LEAP: Library for Evolutionary Algorithms in Python Documentation

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Mark Coletti, Eric O. Scott, and Jeffrey K. Bassett

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QUICKSTART GUIDE

LEAP: Evolutionary Algorithms in Python

Written by Dr. Jeffrey K. Bassett, Dr. Mark Coletti, and Eric Scott

LEAP is a general purpose Evolutionary Computation package that combines readable and easy-to-use syntax for search and optimization algorithms with powerful distribution and visualization features.

LEAP's signature is its operator pipeline, which uses a simple list of functional operators to concisely express a meta-heuristic algorithm's configuration as high-level code. Adding metrics, visualization, or special features (like distribution, coevolution, or island migrations) is often as simple as adding operators into the pipeline.

1.1 Using LEAP

Get the stable version of LEAP from the Python package index with

```
pip install leap_ec
```

1.1.1 Simple Example

The easiest way to use an evolutionary algorithm in LEAP is to use the *leap_ec.simple* package, which contains simple interfaces for pre-built algorithms:

```
from leap_ec.simple import ea_solve

def f(x):
    """A real-valued function to be optimized."""
    return sum(x)**2

ea_solve(f, bounds=[(-5.12, 5.12) for _ in range(5)], maximize=True)
```

1.1.2 Genetic Algorithm Example

The next-easiest way to use LEAP is to configure a custom algorithm via one of the metaheuristic functions in the *leap_ec.algorithms* package. These interfaces off you a flexible way to customize the various operators, representations, and other components that go into a modern evolutionary algorithm.

Here's an example that applies a genetic algorithm variant to solve the *MaxOnes* optimization problem. It uses bitflip mutation, uniform crossover, and binary tournament_selection selection:

```
from leap_ec.algorithm import generational_ea
from leap_ec.decoder import IdentityDecoder
from leap_ec.representation import Representation
from leap_ec.binary_rep.problems import MaxOnes
from leap_ec.binary_rep.initializers import create_binary_sequence
from leap_ec.binary_rep.ops import mutate_bitflip
pop_size = 5
ea = generational_ea(generations=100, pop_size=pop_size,
                     problem=MaxOnes(),             # Solve a MaxOnes Boolean␣
↪optimization problem

                     representation=Representation(
                         decoder=IdentityDecoder(),             # Genotype and phenotype␣
↪are the same for this task
                         initialize=create_binary_sequence(length=10)  # Initial genomes␣
↪are random binary sequences
                     ),

                     # The operator pipeline
                     pipeline=[ops.tournament_selection,                    # Select␣
↪parents via tournament_selection selection
                               ops.clone,                           # Copy them (just to be␣
↪safe)
                                  mutate_bitflip,                   # Basic mutation:␣
↪defaults to a 1/L mutation rate
                               ops.uniform_crossover(p_swap=0.4),   # Crossover with a 40%␣
↪chance of swapping each gene
                               ops.evaluate,                        # Evaluate fitness
                               ops.pool(size=pop_size)              # Collect offspring into␣
↪a new population
                     ])

print('Generation, Best_Individual')
for i, best in ea:
    print(f"{i}, {best}")
```

1.1.3 More Examples

A number of LEAP demo applications are found in the the example directory of the github repository:

```
git clone https://github.com/AureumChaos/LEAP.git
python LEAP/example/island_models.py
```

Fig. 1.1: Demo of LEAP running a 3-population island model on a real-valued optimization problem.

1.2 Documentation

The stable version of LEAP's full documentation is over at ReadTheDocs

If you want to build a fresh set of docs for yourself, you can do so after running *make setup*:

```
make doc
```

This will create HTML documentation in the *docs/build/html/* directory. It might take a while the first time, since building the docs involves generating some plots and executing some example algorithms.

1.3 Installing from Source

To install a source distribution of LEAP, clone the repo:

```
git clone https://github.com/AureumChaos/LEAP.git
```

And use the Makefile to install the package:

```
make setup
```

1.3.1 Run the Test Suite

LEAP ships with a two-part *pytest* harness, divided into fast and slow tests. You can run them with

```
make test-fast
```

and

```
make test-slow
```

respectively.

```
(venv) Erics-MBP:LEAP eric$ make test-fast
py.test -m "not system"
============================================= test session starts ==============================================
platform darwin -- Python 3.7.6, pytest-5.3.2, py-1.8.1, pluggy-0.13.1
rootdir: /Users/eric/code/LEAP, inifile: pytest.ini
plugins: cov-2.8.1
collected 66 items / 1 deselected / 65 selected

leap/algorithm.py .                                                                                    [  1%]
leap/binary_problems.py .                                                                              [  3%]
leap/brains.py ...                                                                                     [  7%]
leap/core.py ...........                                                                               [ 24%]
leap/ops.py ..........                                                                                 [ 40%]
leap/probe.py ..                                                                                       [ 43%]
leap/real_problems.py ............                                                                     [ 63%]
leap/util.py ...                                                                                       [ 67%]
leap/contrib/transfer/sequential.py .                                                                  [ 69%]
tests/test_clone.py .                                                                                  [ 70%]
tests/test_crossover.py .....                                                                          [ 78%]
```

Fig. 1.2: Example of healthy PyTest output.

1.4 Acknowledgements

This effort used resources of the Oak Ridge Leadership Computing Facility for developing LEAP's distributed evaluation capability, and which is a DOE Office of Science User Facility supported under Contract DE-AC05-00OR22725.

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1.5 Citing LEAP

BiBTeX:

```
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        Address = {New York, NY, USA},
        Author = {Coletti, Mark A. and Scott, Eric O. and Bassett, Jeffrey K.},
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```

CHAPTER

TWO

LEAP CONCEPTS

This section summarizes the main classes and the operator pipeline that use them.

2.1 Core Classes

Fig. 2.1: **The core classes** *Individual*, *Problem*, and *Decoder* are the three classes upon which the rest of the toolkit rests.

Three classes work in tandem to represent and evaluate solutions: *Individual*, *Problem*, and *Decoder*. The relationship between these classes is depicted in Fig. 2.1, and shows that the *Individual* is the design's keystone, and encapsulates posed solutions to a *Problem*. *Problem* implements the semantics for a given problem to be solved, and which *Individual* uses to compute its fitness. *Problem* also implements how any two given *Individuals* are "better than" or "equivalent" to one another. The *Decoder* translates an *Individuals* genome into a phenome, or values meaningful to the associated *Problem* for fitness evaluation; for example, a *Decoder* may translate a bit sequence into a vector of real-values that are then passed to the *Problem* as parameters during evaluation.

2.2 Operator Pipeline

If the above classes are the "nouns" of LEAP, the pipeline operators are the "verbs" that work on those "nouns." The overarching concept of the pipeline is similar to *nix style text processing command lines, where a sequence of operators pipe output of one text processing utility into the next one with the last one returning the final results. For example:

```
> cut -d, -f 4,5,8 results.csv | head -4 | column -t -s,
birth_id  scenario  fitness
2         2         -23.2
1         14        6.0
0         36        31.0
```

This shows the output of *cut* is passed to *head* and the output of that is passed to the formatter *column*, which then sends its output to stdout.

Here is an example of a LEAP pipeline:

```
gen = 0
while gen < max_generation:
    offspring = toolz.pipe(parents,
                           ops.tournament_selection,
                           ops.clone,
```

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```
                                mutate_bitflip,
                            ops.evaluate,
                            ops.pool(size=len(parents)))

    parents = offspring
    gen += 1
```

The above code snippet is an example of a very basic genetic algorithm implementation that uses a *toolz.pipe()* function to link together a series of operators to do the following:

1. binary tournament_selection selection on a set of parents
2. clone those that were selected
3. perform mutation bitflip on the clones
4. evaluate the offspring
5. accumulate as many offspring as there are parents

Essentially the *ops.* functions are python co-routines that are driven by the last function, *ops.pool()* , that makes requests of the upstream operators to fill a pool of offspring. Once the pool is filled, it is returned as the next set of offspring, which are then assigned to become the parents for the next generation. (*mutate_bitflip* is in *ops* but the one for binary representations; i.e., *binary_rep/ops.py*. And, since *ops* is already used, we just directly import *mutate_bitflip*, which is why it does not have the *ops* qualifier.)

Fig. 2.2: **LEAP operator pipeline.** This figure depicts a typical LEAP operator pipeline. First is a parent population from which the next operator selects individuals, which are then cloned by the next operator to be followed by operators for mutating and evaluating the individual. (For brevity, a crossover operator was not included, but could also have been freely inserted into this pipeline.) The pool operator is a sink for offspring, and drives the demand for the upstream operators to repeatedly select, clone, mutate, and evaluate individuals repeatedly until the pool has the desired number of offspring. Lastly, another selection operator returns the final set of individuals based on the offspring pool and optionally the parents.

Fig. 2.2 depicts a general pattern of LEAP pipeline operators. Typically, the first pipeline element is a source for individuals followed by some form of selection operator and then a clone operator to create an offspring that is initially just a copy of the selected parent. Following that there are one or more pertubation operators, and though there is only a mutation operator shown in the figure, there can be other configurations that also include crossover, among other pertubation operators. Next, there is an operator to evaluate offspring as they come through pipeline where they are collected by a pooling operator. And, lastly, there can be a survival selection operator to determine survivors for the next generation, such as truncation selection. (The above code snippet does not have survival selection because it replaces the parents with the offspring for every generation.)

2.3 Detailed Explanations

More detailed explanations of the concepts shared here are given in the following sections.

2.3.1 Individuals

This section covers the class *Individual* in more detail.

Class Summary

Fig. 2.3: **The `Individual` class** This class diagram shows the detail for *Individual*. In additional to the association with *Decoder* and *ProbLem*, each *Individual* has a *genome* and *fitness*. There are also several member functions for cloning, decoding, and evaluating individuals. Not shown are such member functions as *__repr__()* and *__str__()*.

An *Individual* poses a unique instance of a solution to the associated *Problem*. Each *Individual* has a *genome*, which contains state representing that posed solution. The *genome* can be a sequence or a matrix or a tree or some other data structure, but in practice a *genome* is usually a binary or a real-value sequence represented as a numpy array. Every *Individual* is connected to an associated *Problem* and relies on the *Problem* to evaluate its fitness and to compare itself with another *Individual* to determine the better of the two.

The *clone()* method will create a duplicate of a given *Individual*; the new *Individual* gets a deep copy of the *genome* and refers to the same *Problem* and *Decoder*; also, the clone gets its own UUID and has its *self.parents* set updated to include the individual from which it was cloned (i.e., its parent). *evaluate()* calls *evaluate_imp()* that, in turn, calls *decode()* to translate the *genome* into phenomes, or values meaningful to the *Problem*, and then passes those values to the *Problem* where it returns a fitness. This fitness is then assigned to the *Individual*.

The reason for the indirection using *evaluate_imp()* is that *evaluate_imp()* allows sub-classes to pass ancillary information to *Problem* during evaluation. For example, an *Individual* may have a UUID that the *Problem* needs in order to create a file or sub-directory using that UUID. *evaluate_imp()* can be over-ridden in a sub-class to pass along the UUID in addition to the decoded *genome*.

The *@total_ordering* class wrapper is used to expand the member functions *__lt__()* and *__eq__()* that are, in turn, heavily used in sorting, selection, and comparison operators.

RobustIndividual

RobustIndividual is a sub-class of *Individual* that over-rides *evaluate()* to handle exceptions thrown during evaluation. If no exceptions are thrown, then *self.is_viable* is set to *True*. If an exception happens, then the following occurs:

- *self.is_viable* is set to *False*
- *self.fitness* is set to *math.nan*
- *self.exception* is assigned the *Exception* object

In turn, this class has another sub-class *leap_ec.distributed.individual.DistributedIndividual*.

Class API

class leap_ec.individual.**Individual**(*genome*, *decoder=IdentityDecoder()*, *problem=None*)

Represents a single solution to a *Problem*.

We represent an *Individual* by a *genome* and a *fitness*. *Individual* also maintains a reference to the *Problem* it will be evaluated on, and an *decoder*, which defines how genomes are converted into phenomes for fitness evaluation.

__init__(*genome*, *decoder=IdentityDecoder()*, *problem=None*)

Initialize an *Individual* with a given genome. A UUID is generated and assigned to *self.uuid*. The *parents* set is initialized to be empty.

We also require *Individual`s to maintain a reference to the `Problem*:

```
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.decoder import IdentityDecoder
>>> import numpy as np
>>> genome = np.array([0, 0, 1, 0, 1])
>>> ind = Individual(genome, decoder=IdentityDecoder(),
...                  problem=MaxOnes())
>>> ind.genome
array([0, 0, 1, 0, 1])
```

Fitness defaults to *None*:

```
>>> ind.fitness is None
True
```

Parameters

- **genome** – is the genome representing the solution. This can be any arbitrary type that your mutation operators, probes, etc., know how to read and manipulate—a list, class, numpy array, etc.
- **decoder** – is a function or *callable* that converts a genome into a phenome.
- **problem** – is the *Problem* associated with this individual.

clone()

Create a 'clone' of this *Individual*, copying the genome, but not fitness.

The fitness of the clone is set to *None*. A new UUID is generated and assigned to *sefl.uuid*. The *parents* set is updated to include the UUID of the parent. A shallow copy of the parent is made, too, so that ancillary state is also copied.

A deep copy of the genome will be created, so if your *Individual* has a custom genome type, it's important that it implements the *__deepcopy__()* method.

```
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.decoder import IdentityDecoder
>>> import numpy as np
>>> genome = np.array([0, 1, 1, 0])
>>> ind = Individual(genome, IdentityDecoder(), MaxOnes())
>>> ind_copy = ind.clone()
>>> ind_copy.genome == ind.genome
```

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```
array([ True,  True,  True,  True])
>>> ind_copy.problem == ind.problem
True
>>> ind_copy.decoder == ind.decoder
True
```

classmethod create_population(*n*, *initialize*, *decoder*, *problem*)

A convenience method for initializing a population of the appropriate subtype.

Parameters

- **n** – The size of the population to generate
- **initialize** – A function f(m) that initializes a genome
- **decoder** – The decoder to attach individuals to
- **problem** – The problem to attach individuals to

Returns

A list of n individuals of this class's (or subclass's) type

decode(**args*, ***kwargs*)

Determine the indivdual's phenome.

This is done by passing the genome *self.decoder*.

The result is both returned and saved to *self.phenome*.

Returns

the decoded value for this individual

evaluate()

determine this individual's fitness

This is done by outsourcing the fitness evaluation to the associated *Problem* object since it "knows" what is good or bad for a given phenome.

See also

ScalarProblem.worse_than

Returns

the calculated fitness

evaluate_imp()

This is the evaluate 'implementation' called by self.evaluate(). It's intended to be optionally over-ridden by sub-classes to give an opportunity to pass in ancillary data to the evaluate process either by tailoring the problem interface or that of the given decoder.

classmethod evaluate_population(*population*)

Convenience function for bulk serial evaluation of a given population

Parameters

population – to be evaluated

Returns

evaluated population

property phenome

If the phenome has not yet been decoded, do so.

class leap_ec.individual.**RobustIndividual**(*genome*, *decoder=IdentityDecoder()*, *problem=None*)

This adds exception handling for evaluations

After evaluation *self.is_viable* is set to True if all went well. However, if an exception is thrown during evaluation, the following happens:

- self.is_viable is set to False
- self.fitness is set to math.nan
- self.exception is assigned the exception

__init__(*genome*, *decoder=IdentityDecoder()*, *problem=None*)

Initialize an *Individual* with a given genome. A UUID is generated and assigned to *self.uuid*. The *parents* set is initialized to be empty.

We also require *Individual`s to maintain a reference to the `Problem*:

```
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.decoder import IdentityDecoder
>>> import numpy as np
>>> genome = np.array([0, 0, 1, 0, 1])
>>> ind = Individual(genome, decoder=IdentityDecoder(),
...                  problem=MaxOnes())
>>> ind.genome
array([0, 0, 1, 0, 1])
```

Fitness defaults to *None*:

```
>>> ind.fitness is None
True
```

Parameters

- **genome** – is the genome representing the solution. This can be any arbitrary type that your mutation operators, probes, etc., know how to read and manipulate—a list, class, numpy array, etc.
- **decoder** – is a function or *callable* that converts a genome into a phenome.
- **problem** – is the *Problem* associated with this individual.

evaluate()

determine this individual's fitness

Note that if an exception is thrown during evaluation, the fitness is set to NaN and *self.is_viable* to False; also, the returned exception is assigned to *self.exception* for possible later inspection. If the individual was successfully evaluated, *self.is_viable* is set to true. NaN fitness values will figure into comparing individuals in that NaN will always be considered worse than non-NaN fitness values.

Returns

the calculated fitness

class leap_ec.individual.**WholeEvaluatedIndividual**(*genome*, *decoder=IdentityDecoder()*, *problem=None*)

An Individual that, when evaluated, passes its whole self to the evaluation function, rather than just its phenome.

In most applications, fitness evaluation requires only phenome information, so that is all that we pass from the Individual to the Problem. This is important, because during distributed evaluation, we want to pass as little information as possible across nodes.

WholeEvaluatedIndividual is used for special cases where fitness evaluation needs access to more information about an individual than its phenome. This is strange in most cases and should be avoided, but can make certain algorithms more elegant (ex. it's helpful when interpreting cooperative coevolution as an island model).

This can dramatically slow down distributed evaluation (i.e. with dask) in some applications because the entire individual will be sent over a TCP/IP connection instead of just the *phenome*, so use with caution.

__init__(*genome*, *decoder=IdentityDecoder()*, *problem=None*)

Initialize an *Individual* with a given genome. A UUID is generated and assigned to *self.uuid*. The *parents* set is initialized to be empty.

We also require *Individual`s to maintain a reference to the `Problem*:

```
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.decoder import IdentityDecoder
>>> import numpy as np
>>> genome = np.array([0, 0, 1, 0, 1])
>>> ind = Individual(genome, decoder=IdentityDecoder(),
...                  problem=MaxOnes())
>>> ind.genome
array([0, 0, 1, 0, 1])
```

Fitness defaults to *None*:

```
>>> ind.fitness is None
True
```

Parameters

- **genome** – is the genome representing the solution. This can be any arbitrary type that your mutation operators, probes, etc., know how to read and manipulate—a list, class, numpy array, etc.
- **decoder** – is a function or *callable* that converts a genome into a phenome.
- **problem** – is the *Problem* associated with this individual.

evaluate_imp()

This is the evaluate 'implementation' called by self.evaluate(). It's intended to be optionally over-ridden by sub-classes to give an opportunity to pass in ancillary data to the evaluate process either by tailoring the problem interface or that of the given decoder.

2.3.2 Decoders

This section covers the *Decoder* class in more detail.

Class Summary

Fig. 2.4: **The Decoder abstract-base class** This class diagram shows the detail for *Decoder*, which is an abstract base class (ABC). It has just a single abstract function, *decode()*, that is intended to be defined by subclasses.

The abstract-base class, *Decoder* , has one function intended to be overridden by sub-classes, *decode()*, that returns a phenome meaningful to a given *Problem*, which is usually a sequence of values. There are a number of supplied *Decoder* classes mostly for converting binary strings into integers or real values.

Note that there is also support for Gray encoding. See *BinarytoIntGrayDecoder* and *BinaryToRealGreyDecoder*.

Class API

Decoder

class leap_ec.decoder.**Decoder**

Decoders in LEAP implement how solutions to a problem are represented.

Specifically, a `Decoder` converts an `Individual`'s *genotype* (which is a format that can easily be manipulated by mutation and recombination operators) into a *phenotype* (which is a format that can be fed directly into a `Problem` object to obtain a fitness value).

Genotypes and phenotypes can be of arbitrary type, from a simple list of numbers to a complex data structure. Choosing a good genotypic representation and genotype-to-phenotype mapping for a given problem domain is a critical part of evolutionary algorithm design: the `Decoder` object that an algorithm uses can have a big impact on the effectiveness of your metaheuristics.

In LEAP, a `Decoder` is typically used by `Individual` as an intermediate step in calculating its own fitness.

For example, say that we want to use a binary-represented `Individual` to solve a real-valued optimization problem, such as `SchwefelProblem`. Here, the genotype is a vector of binary values, whereas the phenotype is its corresponding float vector.

We can use a `BinaryToIntDecoder` to express this mapping. And when we initialize an individual, we give it all three pieces of this information:

```
>>> from leap_ec.binary_rep.decoders import BinaryToRealDecoder
>>> from leap_ec.individual import Individual
>>> from leap_ec.real_rep.problems import SchwefelProblem
>>> import numpy as np
>>> genome = np.array([0, 1, 1, 0, 1, 0, 1, 1])
>>> decoder = BinaryToRealDecoder((4, -5.12, 5.12), (4, -5.12, 5.12))  # Every 4␣
↪bits map to a float on (-5.12, 5.12)
>>> ind = Individual(genome, decoder=decoder, problem=SchwefelProblem())
```

Now we can decode the individual to examine its phenotype:

```
>>> ind.decode()
array([-1.024     ,  2.38933333])
```

This call is just a wrapper for the `Decoder`, which has the same output:

```
>>> decoder.decode(genome)
array([-1.024     ,  2.38933333])
```

But now `Individual` also has everything it needs to evaluate its own fitness:

```
>>> ind.evaluate()
836.4453949...
```

Calling *evaluate()* also has the side effect of setting the fitness attribute:

```
>>> ind.fitness
836.4453949...
```

__init__()

abstract decode(*genome*, **args*, ***kwargs*)

Parameters
genome – a genome you wish to convert

Returns
the phenotype associated with that genome

IdentityDecoder

class leap_ec.decoder.**IdentityDecoder**

A decoder that maps a genome to itself. This acts as a 'direct' or 'phenotypic' encoding: Use this when your genotype and phenotype are the same thing.

__init__()

decode(*genome*, **args*, ***kwargs*)

Returns
the input *genome*.

For example:

```
>>> import numpy as np
>>> d = IdentityDecoder()
>>> d.decode(np.array([0.5, 0.6, 0.7]))
array([0.5, 0.6, 0.7])
```

BinaryToIntDecoder

class leap_ec.binary_rep.decoders.**BinaryToIntDecoder**(**descriptors*)

A decoder that converts a Boolean-vector genome into an integer-vector phenome.

__init__(**descriptors*)

Constructs a decoder that will convert a binary representation into a corresponding int-value vector.

Parameters
descriptors – is a test_sequence of integer that determine how the binary test_sequence is to be broken up into chunks for interpretation

Returns
a function for real-value phenome decoding of a test_sequence of binary digits

The *segments* parameter indicates the number of (genome) bits per (phenome) dimension. For example, if we construct the decoder

```
>>> d = BinaryToIntDecoder(4, 3)
```

then it will look for a genome of length 7, with the first 4 bits mapped to the first phenotypic value, and the last 3 bits making up the second:

```
>>> import numpy as np
>>> d.decode(np.array([0,0,0,0,1,1,1]))
array([0, 7])
```

decode(*genome*, **args*, ***kwargs*)

Converts a Boolean genome to an integer-vector phenome by interpreting each segment of the genome as low-endian binary number.

Parameters
genome – a list of 0s and 1s representing a Boolean genome

Returns
a corresponding list of ints representing the integer-vector phenome

For example, a Boolean representation of [1, 12, 5] can be decoded like this:

```
>>> import numpy as np
>>> d = BinaryToIntDecoder(4, 4, 4)
>>> b = np.array([0,0,0,1, 1, 1, 0, 0, 0, 1, 1, 0])
>>> d.decode(b)
array([ 1, 12,  6])
```

BinaryToRealDecoderCommon

class leap_ec.binary_rep.decoders.**BinaryToRealDecoderCommon**(**segments*)

Common implementation for binary to real decoders.

The base classes BinaryToRealDecoder and BinaryToRealGreyDecoder differ by just the underlying binary to integer decoder. Most all the rest of the binary integer to real-value decoding is the same, hence this class.

__init__(**segments*)

Parameters
segments – is a test_sequence of tuples of the form (number of bits, minimum, maximum) values

Returns
a function for real-value phenome decoding of a test_sequence of binary digits

decode(*genome*, **args*, ***kwargs*)

Convert a list of binary values into a real-valued vector.

BinaryToRealDecoder

class leap_ec.binary_rep.decoders.**BinaryToRealDecoder**(**segments*)

__init__(**segments*)

This returns a function that will convert a binary representation into a corresponding real-value vector. The segments are a collection of tuples that indicate how many bits per segment, and the corresponding real-value bounds for that segment.

Parameters

segments – is a test_sequence of tuples of the form (number of bits, minimum, maximum) values

Returns

a function for real-value phenome decoding of a test_sequence of binary digits

For example, if we construct the decoder then it will look for a genome of length 8, with the first 4 bits mapped to the first phenotypic value, and the last 4 bits making up the second. The traits have a minimum value of -5.12 (corresponding to 0000) and a maximum of 5.12 (corresponding to 1111):

```
>>> import numpy as np
>>> d = BinaryToRealDecoder((4, -5.12, 5.12),(4, -5.12, 5.12))
>>> d.decode(np.array([0, 0, 0, 0, 1, 1, 1, 1]))
array([-5.12,  5.12])
```

BinaryToIntGreyDecoder

class leap_ec.binary_rep.decoders.**BinaryToIntGreyDecoder**(**descriptors*)

This performs Gray encoding when converting from binary strings.

See also: https://en.wikipedia.org/wiki/Gray_code#Converting_to_and_from_Gray_code

For example, a grey encoded Boolean representation of [1, 8, 4] can be decoded like this:

```
>>> import numpy as np
>>> d = BinaryToIntGreyDecoder(4, 4, 4)
>>> b = np.array([0,0,0,1, 1, 1, 0, 0, 0, 1, 1, 0])
>>> d.decode(b)
array([1, 8, 4])
```

__init__(**descriptors*)

Constructs a decoder that will convert a binary representation into a corresponding int-value vector.

Parameters

descriptors – is a test_sequence of integer that determine how the binary test_sequence is to be broken up into chunks for interpretation

Returns

a function for real-value phenome decoding of a test_sequence of binary digits

The *segments* parameter indicates the number of (genome) bits per (phenome) dimension. For example, if we construct the decoder

```
>>> d = BinaryToIntDecoder(4, 3)
```

then it will look for a genome of length 7, with the first 4 bits mapped to the first phenotypic value, and the last 3 bits making up the second:

```
>>> import numpy as np
>>> d.decode(np.array([0,0,0,0,1,1,1]))
array([0, 7])
```

decode(*genome*, **args*, ***kwargs*)

Converts a Boolean genome to an integer-vector phenome by interpreting each segment of the genome as low-endian binary number.

Parameters

genome – a list of 0s and 1s representing a Boolean genome

Returns

a corresponding list of ints representing the integer-vector phenome

For example, a Boolean representation of [1, 12, 5] can be decoded like this:

```
>>> import numpy as np
>>> d = BinaryToIntDecoder(4, 4, 4)
>>> b = np.array([0,0,0,1, 1, 1, 0, 0, 0, 1, 1, 0])
>>> d.decode(b)
array([ 1, 12,  6])
```

BinaryToRealGreyDecoder

class leap_ec.binary_rep.decoders.**BinaryToRealGreyDecoder**(**segments*)

__init__(**segments*)

This returns a function that will convert a binary representation into a corresponding real-value vector. The segments are a collection of tuples that indicate how many bits per segment, and the corresponding real-value bounds for that segment.

Parameters

segments – is a test_sequence of tuples of the form (number of bits, minimum, maximum) values :return: a function for real-value phenome decoding of a test_sequence of binary digits

For example, if we construct the decoder then it will look for a genome of length 8, with the first 4 bits mapped to the first phenotypic value, and the last 4 bits making up the second. The traits have a minimum value of -5.12 (corresponding to 0000) and a maximum of 5.12 (corresponding to 1111):

```
>>> import numpy as np
>>> d = BinaryToRealGreyDecoder((4, -5.12, 5.12),(4, -5.12, 5.12))
>>> d.decode(np.array([0, 0, 0, 0, 1, 1, 1, 1]))
array([-5.12      ,  1.70666667])
```

2.3.3 Representations

When implementing an EA, one of the first design decisions that a practitioner must make is how to represent their problem in an individual. In this section we share how to structure individuals to represent a posed solution instance for a given problem.

Generally, each representation has a specific function, or set of functions, to create genomes for values of that representation type. There is sometimes also a decoders tailored to translate genomes into desired values. And, lastly, there will be a set of pipeline operators specific to that representation.

In summary, representations can have the following:

initializers
: These are for creating random genomes of that representation.

decoders
: These are for translating genomes to usable values; note not all representations need decoders in that you can directly use the genome values, and which is typical for real-valued and integer representations. (Which are a type of _phenotypic_ representation.)

pipeline operators
: Most all representations will have pipeline operators that are specific to that type

Binary representations

A common representation for individuals is as a string of binary digits.

Decoders for binary representations.

class leap_ec.binary_rep.decoders.**BinaryToIntDecoder**(**descriptors*)

Bases: *Decoder*

A decoder that converts a Boolean-vector genome into an integer-vector phenome.

decode(*genome*, **args*, ***kwargs*)

Converts a Boolean genome to an integer-vector phenome by interpreting each segment of the genome as low-endian binary number.

Parameters
: **genome** – a list of 0s and 1s representing a Boolean genome

Returns
: a corresponding list of ints representing the integer-vector phenome

For example, a Boolean representation of [1, 12, 5] can be decoded like this:

```
>>> import numpy as np
>>> d = BinaryToIntDecoder(4, 4, 4)
>>> b = np.array([0,0,0,1, 1, 1, 0, 0, 0, 1, 1, 0])
>>> d.decode(b)
array([ 1, 12,  6])
```

class leap_ec.binary_rep.decoders.**BinaryToIntGreyDecoder**(**descriptors*)

Bases: *BinaryToIntDecoder*

This performs Gray encoding when converting from binary strings.

See also: https://en.wikipedia.org/wiki/Gray_code#Converting_to_and_from_Gray_code

For example, a grey encoded Boolean representation of [1, 8, 4] can be decoded like this:

```
>>> import numpy as np
>>> d = BinaryToIntGreyDecoder(4, 4, 4)
>>> b = np.array([0,0,0,1, 1, 1, 0, 0, 0, 1, 1, 0])
>>> d.decode(b)
array([1, 8, 4])
```

decode(*genome*, **args*, ***kwargs*)

Converts a Boolean genome to an integer-vector phenome by interpreting each segment of the genome as low-endian binary number.

Parameters
genome – a list of 0s and 1s representing a Boolean genome

Returns
a corresponding list of ints representing the integer-vector phenome

For example, a Boolean representation of [1, 12, 5] can be decoded like this:

```
>>> import numpy as np
>>> d = BinaryToIntDecoder(4, 4, 4)
>>> b = np.array([0,0,0,1, 1, 1, 0, 0, 0, 1, 1, 0])
>>> d.decode(b)
array([ 1, 12,  6])
```

class leap_ec.binary_rep.decoders.**BinaryToRealDecoder**(**segments*)

Bases: *BinaryToRealDecoderCommon*

class leap_ec.binary_rep.decoders.**BinaryToRealDecoderCommon**(**segments*)

Bases: *Decoder*

Common implementation for binary to real decoders.

The base classes BinaryToRealDecoder and BinaryToRealGreyDecoder differ by just the underlying binary to integer decoder. Most all the rest of the binary integer to real-value decoding is the same, hence this class.

decode(*genome*, **args*, ***kwargs*)

Convert a list of binary values into a real-valued vector.

class leap_ec.binary_rep.decoders.**BinaryToRealGreyDecoder**(**segments*)

Bases: *BinaryToRealDecoderCommon*

Used to initialize binary sequences

leap_ec.binary_rep.initializers.**create_binary_sequence**(*length*)

A closure for initializing a binary sequences for binary genomes.

Parameters
length – how many genes?

Returns
a function that, when called, generates a binary vector of given length

E.g., can be used for *Individual.create_population*

```
>>> from leap_ec.decoder import IdentityDecoder
>>> from . problems import MaxOnes
>>> population = Individual.create_population(10, create_binary_sequence(length=10),
...                                           decoder=IdentityDecoder(),
...                                           problem=MaxOnes())
```

Binary representation specific pipeline operators.

leap_ec.binary_rep.ops.**genome_mutate_bitflip**(*genome: ndarray = '__no__default__'*, *expected_num_mutations: float = None*, *probability: float = None*) → ndarray

Perform bitflip mutation on a particular genome.

This function can be used by more complex operators to mutate a full population (as in *mutate_bitflip*), to work with genome segments (as in *leap_ec.segmented.ops.apply_mutation*), etc. This way we don't have to copy-and-paste the same code for related operators.

Parameters

- **genome** – of binary digits that we will be mutating
- **expected_num_mutations** – on average how many mutations are we expecting?

Returns
mutated genome

leap_ec.binary_rep.ops.**mutate_bitflip**(*next_individual: Iterator = '__no__default__'*, *expected_num_mutations: float = None*, *probability: float = None*) → Iterator

Perform bit-flip mutation on each individual in an iterator (population).

This assumes that the genomes have a binary representation.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.ops import mutate_bitflip
>>> import numpy as np
```

```
>>> original = Individual(np.array([1, 1]))
>>> op = mutate_bitflip(expected_num_mutations=1)
>>> pop = iter([original])
>>> mutated = next(op(pop))
```

Parameters

- **next_individual** – to be mutated
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)
- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)

Returns
mutated individual

leap_ec.binary_rep.ops.**random**() → x in the interval [0, 1).

Real-valued representations

Another common representation is a vector of real-values.

Initializers for real values.

`leap_ec.real_rep.initializers.`**`create_real_vector`**`(`*bounds*`)`

A closure for initializing lists of real numbers for real-valued genomes, sampled from a uniform distribution.

Having a closure allows us to just call the returned function N times in *Individual.create_population()*.

TODO Allow either a single tuple or a test_sequence of tuples for bounds. —Siggy

Parameters

bounds – a list of (min, max) values bounding the uniform sampline of each element

Returns

A function that, when called, generates a random genome.

E.g., can be used for *Individual.create_population()*

```
>>> from leap_ec.decoder import IdentityDecoder
>>> from . problems import SpheroidProblem
>>> bounds = [(0, 1), (0, 1), (-1, 100)]
>>> population = Individual.create_population(10, create_real_vector(bounds),
...                                           decoder=IdentityDecoder(),
...                                           problem=SpheroidProblem())
```

Pipeline operators for real-valued representations

`leap_ec.real_rep.ops.`**`apply_hard_bounds`**`(`*genome*, *hard_bounds*`)`

A helper that ensures that every gene is contained within the given bounds.

Parameters

- **genome** – list of values to apply bounds to.
- **hard_bounds** – if a *(low, high)* tuple, the same bounds will be used for every gene. If a list of tuples is given, then the ith bounds will be applied to the ith gene.

Both sides of the range are inclusive:

```
>>> genome = np.array([0, 10, 20, 30, 40, 50])
>>> apply_hard_bounds(genome, hard_bounds=(20, 40))
array([20, 20, 20, 30, 40, 40])
```

Different bounds can be used for each locus by passing in a list of tuples:

```
>>> bounds= [ (0, 1), (0, 1), (50, 100), (50, 100), (0, 100), (0, 10) ]
>>> apply_hard_bounds(genome, hard_bounds=bounds)
array([ 0,  1, 50, 50, 40, 10])
```

`leap_ec.real_rep.ops.`**`genome_mutate_gaussian`**`(`*genome='__no__default__', std: float = '__no__default__', expected_num_mutations='__no__default__', bounds: Tuple[float, float] = (-inf, inf), transform_slope: float = 1.0, transform_intercept: float = 0.0*`)`

Perform Gaussian mutation directly on real-valued genes (rather than on an Individual).

This used to be inside *mutate_gaussian*, but was moved outside it so that *leap_ec.segmented.ops.apply_mutation* could directly use this function, thus saving us from doing a copy-n-paste of the same code to the segmented sub-package.

Parameters

- **genome** – of real-valued numbers that will potentially be mutated
- **std** – the mutation width—either a single float that will be used for all genes, or a list of floats specifying the mutation width for each gene individually.
- **expected_num_mutations** – on average how many mutations are expected

Returns

mutated genome

leap_ec.real_rep.ops.**mutate_gaussian**(*next_individual: Iterator = '__no__default__'*, *std='__no__default__'*, *expected_num_mutations: Union[int, str] = None*, *bounds=(-inf, inf)*, *transform_slope: float = 1.0*, *transform_intercept: float = 0.0*) → Iterator

Mutate and return an Individual with a real-valued representation.

This operators on an iterator of Individuals:

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.real_rep.ops import mutate_gaussian
>>> import numpy as np
>>> pop = iter([Individual(np.array([1.0, 0.0]))])
```

Mutation can either use the same parameters for all genes:

```
>>> op = mutate_gaussian(std=1.0, expected_num_mutations='isotropic', bounds=(-5,␣
↪5))
>>> mutated = next(op(pop))
```

Or we can specify the *std* and *bounds* independently for each gene:

```
>>> pop = iter([Individual(np.array([1.0, 0.0]))])
>>> op = mutate_gaussian(std=[0.5, 1.0],
...                      expected_num_mutations='isotropic',
...                      bounds=[(-1, 1), (-10, 10)]
... )
>>> mutated = next(op(pop))
```

Parameters

- **next_individual** – to be mutated
- **std** – standard deviation to be equally applied to all individuals; this can be a scalar value or a "shadow vector" of standard deviations
- **expected_num_mutations** – if an int, the *expected* number of mutations per individual, on average. If 'isotropic', all genes will be mutated.
- **bounds** – to clip for mutations; defaults to (- ∞, ∞)

Returns

a generator of mutated individuals.

Integer representations

A vector of all integer values is also a common representation.

Initializers for integer-valued genomes.

leap_ec.int_rep.initializers.**create_int_vector**(*bounds*)

A closure for initializing lists of integers for int-vector genomes, sampled from a uniform distribution.

Having a closure allows us to just call the returned function N times in *Individual.create_population()*.

TODO Allow either a single tuple or a sequence of tuples for bounds. —Siggy

Parameters

bounds – a list of (min, max) values bounding the uniform sampline of each element

Returns

A function that, when called, generates a random genome.

```
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.real_rep.problems import SpheroidProblem
>>> bounds = [(0, 1), (-5, 5), (-1, 100)]
>>> population = Individual.create_population(10, create_int_vector(bounds),
...                                           decoder=IdentityDecoder(),
...                                           problem=SpheroidProblem())
```

Evolutionary operators for maniuplating integer-vector genomes.

leap_ec.int_rep.ops.**genome_mutate_binomial**(*std='__no__default__', bounds: list = '__no__default__', expected_num_mutations: float = None, probability: float = None, n: int = 10000*)

Perform additive binomial mutation of a particular genome.

```
>>> import numpy as np
>>> genome = np.array([42, 12])
>>> bounds = [(0,50), (-10,20)]
>>> genome_op = genome_mutate_binomial(std=0.5, bounds=bounds,
...                                    expected_num_mutations=1)
>>> new_genome = genome_op(genome)
```

leap_ec.int_rep.ops.**individual_mutate_randint**(*genome='__no__default__', bounds: list = '__no__default__', expected_num_mutations=None, probability=None*)

Perform random-integer mutation on a particular genome.

```
>>> import numpy as np
>>> genome = np.array([42, 12])
>>> bounds = [(0,50), (-10,20)]
>>> new_genome = individual_mutate_randint(genome, bounds, expected_num_mutations=1)
```

Parameters

- **genome** – test_sequence of integers to be mutated
- **bounds** – test_sequence of bounds tuples; e.g., [(1,2),(3,4)]
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)

- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)

leap_ec.int_rep.ops.**mutate_binomial**(*next_individual: Iterator = '__no__default__', std: float = '__no__default__', bounds: list = '__no__default__', expected_num_mutations: float = None, probability: float = None, n: int = 10000*) → Iterator

Mutate genes by adding an integer offset sampled from a binomial distribution centered on the current gene value.

This is very similar to applying additive Gaussian mutation and then rounding to the nearest integer, but does so in a way that is more natural for integer-valued genes.

Parameters

- **std** (*float*) – standard deviation of the binomial distribution
- **bounds** – list of pairs of hard bounds to clip each gene by (to prevent mutation from carrying a gene value outside an allowed range)
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)
- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)
- **n** (*int*) – the number of "coin flips" to use in the binomial process (defaults to 10000)

Usage example:

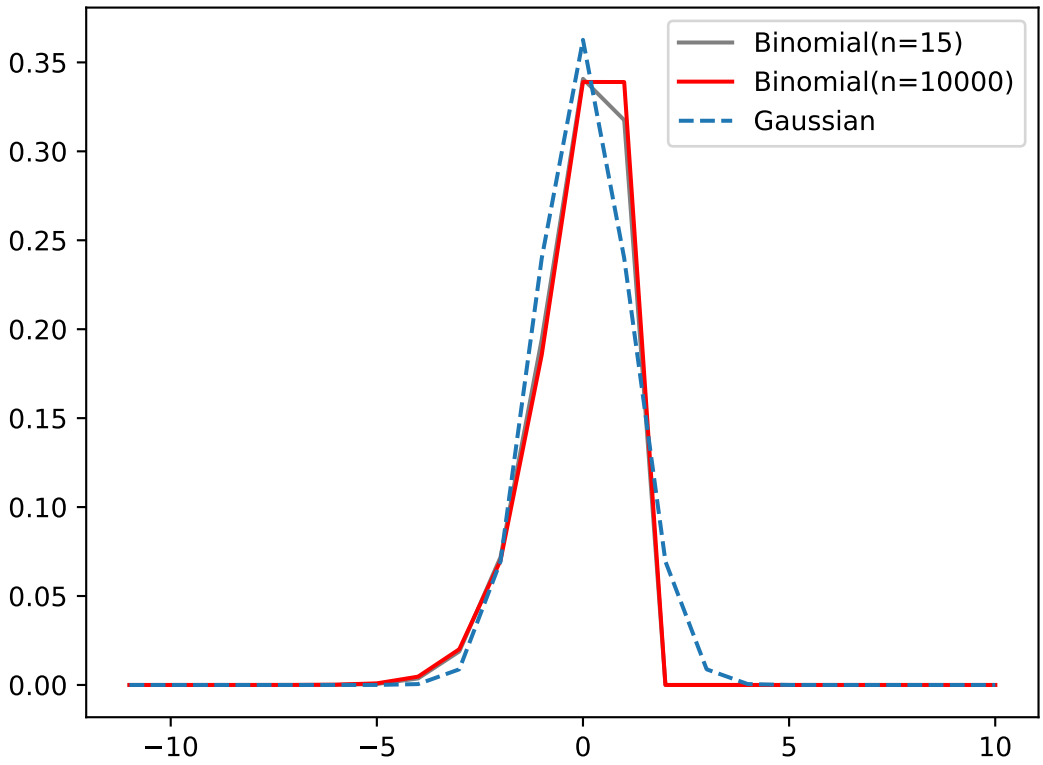
```
>>> from leap_ec.individual import Individual
>>> from leap_ec.int_rep.ops import mutate_binomial
>>> import numpy as np
>>> population = iter([Individual(np.array([1, 1]))])
>>> operator = mutate_binomial(std=2.5,
...                            bounds=[(0, 10), (0, 10)],
...                            expected_num_mutations=1)
>>> mutated = next(operator(population))
```

The *std* parameter can also be given as a list with a value to use for each gene locus:

```
>>> population = iter([Individual(np.array([1, 1]))])
>>> operator = mutate_binomial(std=[2.5, 3.0],
...                            bounds=[(0, 10), (0, 10)],
...                            expected_num_mutations=1)
>>> mutated = next(operator(population))
```

Note: The binomial distribution is defined by two parameters, n and p. Here we simplify the interface by asking instead for an *std* parameter, and fixing a high value of n by default. The value of p needed to obtain the given *std* is computed for you internally.

As the plots below illustrate, the binomial distribution is approximated by a Gaussian. For high n and large standard deviations, the two are effectively equivalent. But when the standard deviation (and thus binomial p parameter) is relatively small, the approximation becomes less accurate, and the binomial differs somewhat from a Gaussian.



---

leap_ec.int_rep.ops.**mutate_randint**(*next_individual: Iterator = '__no__default__', bounds='__no__default__', expected_num_mutations=None, probability=None*) → Iterator

Perform randint mutation on each individual in an iterator (population).

This operator replaces randomly selected genes with an integer samples from a uniform distribution.

Parameters

- **bounds** – test_sequence of bounds tuples; e.g., [(1,2),(3,4)]
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)
- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.int_rep.ops import mutate_randint
>>> import numpy as np
```

```
>>> population = iter([Individual(np.array([1, 1]))])
>>> operator = mutate_randint(expected_num_mutations=1, bounds=[(0, 10), (0, 10)])
>>> mutated = next(operator(population))
```

Segmented representations

Segmented representations are a wrapper around another, arbitrary representation, such as a binary, real-valued, or integer representation. Segmented representations allow for sequences of value "chunks". For example, a Pitt Approach could be implemented using this representation where each segment represents a single rule. Another example would be each segment represents associated hyper-parameters for a convolutional neural network layer.

Used to decode segments

class leap_ec.segmented_rep.decoders.**SegmentedDecoder**(*segment_decoder*)

Bases: *Decoder*

For decoding LEAP segmented representations

```
>>> from leap_ec.binary_rep.decoders import BinaryToIntDecoder
```

This example presumes that each segment has five bits, the first to map to an integer and the remaining three to a different integer.

```
>>> import numpy as np
>>> decoder = SegmentedDecoder(BinaryToIntDecoder(2,3))
>>> genome = np.array([[1, 0, 1, 0, 1],
...                    [0, 0, 1, 1, 1],
...                    [1, 0, 0, 0, 1]])
>>> vals = decoder.decode(genome)
>>> assert np.all(vals == np.array([[2, 5], [0, 7], [2, 1]]))
```

decode(*genome*, **args*, ***kwargs*)

For decoding *genome* which is a list of lists, or a segmented representation.

Parameters

- **genome** (*will be a list of segments (or lists)*) – for a given individual
- **args** (*list*) – optional args
- **kwargs** (*dict*) – optional keyword args

Returns
a list of list of values decoded from *genome*

Return type
list

Used to initialize segments

leap_ec.segmented_rep.initializers.**create_segmented_sequence**(*length*, *seq_initializer*)

Create a segmented test_sequence

A segment is a list of lists. *seq_initializer* is used to create *length* individual segments, which allows for the using any of the pre-supplied initializers for a regular genomic test_sequence, or for making your own.

length denotes how many segments to generate. If it's an integer, then we will create *length* segments. However, if it's a function that draws from a random distribution that returns an int, we will, instead, use that to calculate the number of segments to generate.

```
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> segmented_initializer = create_segmented_sequence(3, create_binary_sequence(3))
>>> segments = segmented_initializer()
>>> assert len(segments) == 3
```

Parameters

- **length** (*int or Callable*) – How many segments?
- **seq_initializer** (*Callable*) – initializer for creating individual sequences

Returns
function that returns a list of segmented

Return type
Callable

Segmented representation specific pipeline operators.

leap_ec.segmented_rep.ops.**add_segment**(*next_individual: Iterator = '__no__default__', seq_initializer: Callable = '__no__default__', probability: float = '__no__default__', append: bool = False*) → Iterator

Possibly add a segment to the given individual

New segments can be always appended, or randomly inserted within the individual's genome.

TODO add a parameter for accepting a function that will yield a distribution for the number of segments to be randomly inserted.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> import numpy as np
>>> original = Individual([np.array([0, 0]), np.array([1, 1])])
>>> mutated = next(add_segment(iter([original]),
...                seq_initializer=create_binary_sequence(2),
...                probability=1.0))
```

Parameters

- **next_individual** – to possibly add a segment
- **seq_initializer** – callable for initializing any new segments
- **probability** – likelihood of adding a segment
- **append** – if True, always append any new segments

Returns
yielded individual with a possible new segment

leap_ec.segmented_rep.ops.**apply_mutation**(*next_individual: Iterator = '__no__default__', mutator: Callable[[list, float], list] = '__no__default__'*) → Iterator

This expects next_individual to have a segmented representation; i.e., a test_sequence of sequences. *mutator* will be applied separately to each sub-test_sequence.

```
>>> from leap_ec.binary_rep.ops import genome_mutate_bitflip
>>> mutation_op = apply_mutation(
...     mutator=genome_mutate_bitflip(
```

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```
...                 expected_num_mutations=0.5
...  ))
>>> import numpy as np
```

```
>>> from leap_ec.individual import Individual
>>> original = Individual(np.array([[0, 0], [1, 1]]))
>>> mutated = next(mutation_op(iter([original])))
```

Parameters

- **next_individual** – to possibly mutate
- **mutator** – function to be applied to each segment in the individual's genome; first argument is a segment, the second the expected probability of mutating each segment element.

Returns

yielded mutated individual

leap_ec.segmented_rep.ops.**copy_segment**(*next_individual: Iterator = '__no__default__', probability: float = '__no__default__', append: bool = False*) → Iterator

with a given probability, randomly select and copy a segment

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> original = Individual([np.array([0, 0])])
>>> mutated = next(copy_segment(iter([original]), probability=1.0))
>>> assert np.all(mutated.genome[0] == [0, 0])             and np.all(mutated.
↪genome[1] == [0, 0])
```

param next_individual
to have a segment possibly removed

param probability
likelihood of doing this

param append
if True, always append any new segments

returns
the next individual

leap_ec.segmented_rep.ops.**remove_segment**(*next_individual: Iterator = '__no__default__', probability: float = '__no__default__'*) → Iterator

for some chance, remove a segment

Nothing happens if the individual has a single segment; i.e., there is no chance for an empty individual to be returned.

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> original = Individual([np.array([0, 0]), np.array([1, 1])])
>>> mutated = next(remove_segment(iter([original]), probability=1.0))
>>> assert np.all(mutated.genome[0] == [0, 0])              or np.all(mutated.
↪genome[0] == [1, 1])
```

param next_individual
to have a segment possibly removed

param probability
likelihood of removing a segment

returns
the next individual

`leap_ec.segmented_rep.ops.`**`segmented_mutate`**(*next_individual: Iterator = '__no__default__'*, *mutator_functions: list = '__no__default__'*)

A mutation operator that applies a different mutation operator to each segment of a segmented genome.

Mixed representations

There is currently no explicit support for mixed representations, but there are plans to implement such at some point. There are a few strategies for implementing mixed values:

- use a binary representation with an associated *Decoder* that decodes values into desired target value formats, such as sequences that are a blend of integers, floating point, and categorical variables
- use a floating point representation that has an associated decoder for mapping certain floating point values to integer or categorical values; an associated mutation function may be necessary to implement pertubations that make sense for individual genes
- likewise use an integer representation with tailored associated decoders and mutators to decode and change values in a bespoke way

Representation convenience class

Since the notion of a representation includes how individuals are created, how they're decoded, and are bound to a particular class for an individual, the class *leap_ec.representation.Representation* was created to bundle those together. By default, the class for individual is *leap_ec.individual.Individual*, but can of course be any of its subclasses.

The *leap_ec.representation.Representation* is used in *leap_ec.algorithm.generational_ea*. In the future this may become a formal python dataclass and be more integrated into LEAP in other functions.

A *Representation* is a simple data structure that wraps the components needed to define, initialize, and decode individuals.

This just serves as some syntactic sugar when we are specifying algorithms—so that representation-related components are grouped together and clearly labeled *Representation*.

class `leap_ec.representation.`**`Representation`**(*initialize*, *decoder=IdentityDecoder()*, *individual_cls=<class 'leap_ec.individual.Individual'>*)

Bases: `object`

Syntactic sugar for some of the monolithic functions that conveniently combines a decoder, initializer, and an Individual class since those always work in tandem, but can still be loosely coupled.

`create_individual`(*problem*)

Make a single individual.

`create_population`(*pop_size*, *problem*)

make a new population

Parameters

- **pop_size** – how many individuals should be in the population
- **problem** – to be solved

Returns
a population of *individual_cls* individuals

2.3.4 Problems

This section covers *Problem* classes in more detail.

Class Summary

Fig. 2.5: **The `Problem` abstract-base class** This class diagram shows the detail for *Problem*, which is an abstract base class (ABC). It has three abstract methods that must be over-ridden by subclasses. *evaluate()* takes a phenome from an individual and compute a fitness from that. *worse_than()* and *equivalent()* compare fitnesses from two different individuals and, as the name suggests, respectively returns the worst of the two or the equivalent within the *Problem* context.

As shown in Fig. 2.5, the *Problem* abstract-base class has three abstract methods. *evaluate()* takes a phenome that was *decode()d* from an *Individual*'s genome, and returns a value denoting the quality, or fitness, of that individual. *Problems* are also used to compare the fitnesses between *Individuals*. *worse_than()* returns true if the first individual is less fit than the second. Similarly, *equivalent()* is used to determine if two given fitnesses are effectively the same.

Class API

Defines the abstract-base classes Problem, ScalarProblem, and FunctionProblem.

class leap_ec.problem.**AlternatingProblem**(*problems*, *modulo*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 20}}*)

equivalent(*first_fitness*, *second_fitness*)

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

get_current_problem()

worse_than(*first_fitness*, *second_fitness*)

class leap_ec.problem.**AverageFitnessProblem**(*wrapped_problem*, *n: int*)

Problem wrapper that copies each genome n times, evaluates them, and averages the results back together to produce a mean-fitness estimate.

This is a common strategy for approaching noisy fitness functions, to make it easier for an optimization algorithm to follow a gradient.

```
>>> from leap_ec.real_rep.problems import NoisyQuarticProblem
>>> p = AverageFitnessProblem(
...                 wrapped_problem = NoisyQuarticProblem(),
...                 n = 20)
>>> x = [ 1, 1, 1, 1 ]
>>> y = p.evaluate(x)
>>> print(f"Fitness: {y}")  # The mean of this will be approximately 10
Fitness: ...
```

equivalent(*first_fitness*, *second_fitness*)

evaluate(*phenome*)

Evaluates the wrapped function n times sequentially and returns the mean.

evaluate_multiple(*phenomes: list*)

Evaluate a collections of phenomes by creating n jobs for each phenome, sending all the jobs to the wrapped evaluate_multiple() function, and then averaging the n results for each phenome into a list of results.

worse_than(*first_fitness*, *second_fitness*)

class leap_ec.problem.**ConstantProblem**(*maximize=False*, *c=1.0*)

A flat landscape, where all phenotypes have the same fitness.

This is sometimes useful for sanity checks or as a control in certain kinds of research.

$$f(\vec{x}) = c$$

Parameters

c (*float*) – the fitness value to return for any input.

```
from leap_ec.problem import ConstantProblem
from leap_ec.real_rep.problems import plot_2d_problem
bounds = ConstantProblem.bounds
plot_2d_problem(ConstantProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (-1.0, 1.0)

evaluate(*phenome*, **args*, ***kwargs*)

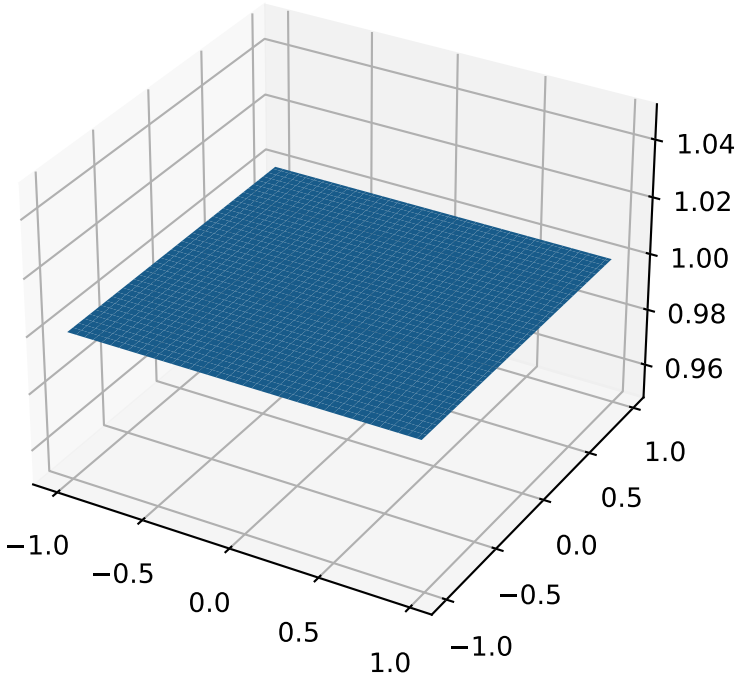
Return a contant value for any input phenome:

```
>>> phenome = [0.5, 0.8, 1.5]
>>> ConstantProblem().evaluate(phenome)
1.0
```

```
>>> ConstantProblem(c=500.0).evaluate('foo bar')
500.0
```

Parameters

phenome – phenome to be evaluated


1.04
1.02
1.00
0.98
0.96
1.0
0.5
0.0
−0.5
−1.0
−1.0
−0.5
0.0
0.5
1.0

Returns
1.0, or the constant defined in the constructor

class leap_ec.problem.**CooperativeProblem**(*wrapped_problem*, *num_trials: int*, *collaborator_selector*, *combined_decoder: ~leap_ec.decoder.Decoder = IdentityDecoder()*, *log_stream=None*, *combine_genomes=<function CooperativeProblem.<lambda>>*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 20}}*)

A Problem that implements cooperative coevolution. This provides a fitness function that takes *partial solutions* as input (i.e. from one of the subpopulations of the cooperative algorithm), and evaluates their fitness by combining them with other individuals in the population.

You can think of a CooperativeProblem as defining a fitness function for a subpopulation in a multi-population model, where the fitness function that is computed is itself a function of the state of the other subpopulations:

..math

mbox{fitness} = f_{p_i}(vec{mathbf{x}}, mathcal{P} \ p_i)

This class works by wrapping another fitness function, which is defined over complete solutions, and by taking a selection operator (which is used to select "collaborators" from other subpopulations to form complete solutions):

```
>>> from leap_ec import ops
>>> from leap_ec.real_rep.problems import SpheroidProblem
>>> complete_problem = SpheroidProblem()
>>> problem = CooperativeProblem(
...             wrapped_problem = SpheroidProblem(),
...             num_trials = 3,
...             collaborator_selector = ops.random_selection)
```

equivalent(*first_fitness*, *second_fitness*)

evaluate(*phenome*, **args*, ***kwargs*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

evaluate_multiple(*phenomes*, *individuals*)

Evaluate multiple phenomes all at once, returning a list of fitness values.

By default this just calls *self.evaluate()* multiple times. Override this if you need to, say, send a group of individuals off to parallel

worse_than(*first_fitness*, *second_fitness*)

class leap_ec.problem.**ExternalProcessProblem**(*command: str*, *maximize: bool*, *args: Optional[list] = None*)

Evaluate individuals by launching an external program, writing phenomes to its stdin as CSV rows, and reading back fitness values from its stdout.

Assumes that individuals are represented with list phenomes with elements that can be cast to strings.

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

evaluate_multiple(*phenomes*, **args*, ***kwargs*)

Evaluate multiple phenomes all at once, returning a list of fitness values.

By default this just calls *self.evaluate()* multiple times. Override this if you need to, say, send a group of individuals off to parallel

class leap_ec.problem.**FitnessOffsetProblem**(*problem*, *fitness_offset*, *maximize=None*)

Takes an existing function and adds a constant value to it output.

$$f'(\mathbf{x}) = f(\mathbf{x}) + c$$

Parameters

- **problem** – the original problem to wrape
- **fitness_offset** (*float*) – the scalar constant to add

evaluate(*phenome*)

Evaluates the phenome's fitness in the wrapped function, then adds the constant.

For example, here the original fitness function returns 5.0, but we subtract 3.5 from it so that it yields 1.5.

```
>>> original = ConstantProblem(c=5.0)
>>> problem = FitnessOffsetProblem(original, fitness_offset=-3.5)
>>> problem.evaluate([0, 1, 2])
1.5
```

class leap_ec.problem.**FunctionProblem**(*fitness_function*, *maximize*)

A convenience wrapper that takes a vanilla function that returns scalar fitness values and makes it usable as an objective function.

evaluate(*phenome*, **args*, ***kwargs*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

class leap_ec.problem.**Problem**

Abstract Base Class used to define problem definitions.

A *Problem* is in charge of two major parts of an EA's behavior:

1. Fitness evaluation (the *evaluate()* method)
2. Fitness comparision (the *worse_than()* and *equivalent()* methods)

abstract equivalent(*first_fitness*, *second_fitness*)

abstract evaluate(*phenome*, **args*, ***kwargs*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

evaluate_multiple(*phenomes*)

Evaluate multiple phenomes all at once, returning a list of fitness values.

By default this just calls *self.evaluate()* multiple times. Override this if you need to, say, send a group of individuals off to parallel

abstract worse_than(*first_fitness*, *second_fitness*)

class leap_ec.problem.**ScalarProblem**(*maximize*)

A problem that compares individuals based on their scalar fitness values.

Inherit from this class and implement the *evaluate()* method to implement an objective function that returns a single real-valued fitness value.

equivalent(*first_fitness*, *second_fitness*)

Used in Individual.__eq__().

By default returns first.fitness== second.fitness. Please over-ride if this does not hold for your problem.

Returns
true if the first individual is equal to the second

worse_than(*first_fitness*, *second_fitness*)

Used in Individual.__lt__().

By default returns first_fitness < second_fitness if a maximization problem, else first_fitness > second_fitness if a minimization problem. Please over-ride if this does not hold for your problem.

Returns
true if the first individual is less fit than the second

leap_ec.problem.**concat_combine**(*collaborators*)

Combine a list of individuals by concatenating their genomes.

This is a convenience function intended for use with CooperativeProblem.

Binary Problems API

A set of standard EA problems that rely on a binary-representation

class leap_ec.binary_rep.problems.**DeceptiveTrap**(*maximize=True*)

A simple bi-modal function whose global optimum is the Boolean vector of all 1's, but in which fitness *decreases* as the number of 1's in the vector *increases*—giving it a local optimum of [0, . . . , 0] with a very wide basin of attraction.

evaluate(*phenome*)

```
>>> import numpy as np
>>> p = DeceptiveTrap()
```

The trap function has a global maximum when the number of one's is maximized:

```
>>> p.evaluate(np.array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1]))
10
```

It's minimized when we have just one zero: >>> p.evaluate(np.array([1, 1, 1, 1, 0, 1, 1, 1, 1, 1])) 0

And has a local optimum when we have no ones at all: >>> p.evaluate(np.array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0])) 9

class leap_ec.binary_rep.problems.**ImageProblem**(*path*, *maximize=True*, *size=(100, 100)*)

A variation on *max_ones* that uses an external image file to define a binary target pattern.

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

class leap_ec.binary_rep.problems.**LeadingOnes**(*target_string=None*, *maximize=True*)

Implementation of the classic leading-ones problem, where the individuals are represented by a bit vector.

By default, the number of consecutve 1's starting from the beginning of the phenome are maximized:

```
>>> p = LeadingOnes()
```

But an optional target string can also be specified, in which case the number of matches to the target are maximized:

```
>>> import numpy as np
>>> p = LeadingOnes(target_string=np.array([1, 1, 0, 1, 1, 0, 0, 0 ,0]))
```

evaluate(*phenome*)

By default this counts the number of consecutive 1's at the start of the string:

```
>>> import numpy as np
>>> p = LeadingOnes()
>>> p.evaluate(np.array([1, 1, 1, 1, 0, 1, 0, 1, 1]))
4
```

Or, if a target string was given, we count matches:

```
>>> p = LeadingOnes(target_string=np.array([1, 1, 0, 1, 1, 0, 0, 0 ,0]))
>>> p.evaluate(np.array([1, 1, 1, 1, 0, 1, 0, 1, 1]))
2
```

class leap_ec.binary_rep.problems.**MaxOnes**(*target_string=None*, *maximize=True*)

Implementation of the classic max-ones problem, where the individuals are represented by a bit vector.

By default, the number of 1's in the phenome are maximized.

```
>>> p = MaxOnes()
```

But an optional target string can also be specified, in which case the number of matches to the target are maximized:

```
>>> import numpy as np
>>> p = MaxOnes(target_string=np.array([1, 1, 1, 1, 1, 0, 0, 0 ,0]))
```

evaluate(*phenome*)

By default this counts the number of 1's:

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> p = MaxOnes()
>>> p.evaluate(np.array([0, 0, 1, 1, 0, 1, 0, 1, 1]))
5
```

Or, if a target string was given, we count matches:

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> p = MaxOnes(target_string=np.array([1, 1, 1, 1, 1, 0, 0, 0 ,0]))
>>> p.evaluate(np.array([0, 0, 1, 1, 0, 1, 0, 1, 1]))
3
```

class leap_ec.binary_rep.problems.**TwoMax**(*maximize=True*)

A simple bi-modal function that returns the number of 1's if there are more 1's than 0's, else the number of 0's.

Also known as the "Twin-Peaks" problem.

evaluate(*phenome*)

```
>>> import numpy as np
>>> p = TwoMax()
```

The TwoMax problems returns the number over 1's if they are in the majority:

```
>>> p.evaluate(np.array([1, 1, 1, 1, 1, 1, 1, 0, 0, 0]))
7
```

Else the number of zeros: >>> p.evaluate(np.array([0, 0, 0, 1, 0, 0, 0, 1, 1, 1])) 6

Real-value Problems API

This module contains a variety of classic real-valued optimization problems that frequently occur in research benchmarks.

It also contains helpers for translating, rotating, and visualizing them.

class leap_ec.real_rep.problems.**AckleyProblem**(*a=20*, *b=0.2*, *c=6.283185307179586*, *maximize=False*)

$$f(\mathbf{x}) = -a \exp\left(-b\sqrt{\frac{1}{d}\sum_{i=1}^{d} x_i^2}\right) - \exp\left(\frac{1}{d}\sum_{i=1}^{d}\cos(cx_i)\right) + a + \exp(1)$$

Parameters

- **a** (*float*) – depth parameter for the bowl-shaped macrostructure
- **b** (*float*) – exponential scale parameter for the bowl
- **c** (*float*) – wavenumber (frequency) of the cosine pattern of local optima
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import AckleyProblem, plot_2d_problem
import math
problem = AckleyProblem(a=20, b=0.2, c=2*math.pi)
bounds = AckleyProblem.bounds  # Contains traditional bounds
plot_2d_problem(problem, xlim=bounds, ylim=bounds, granularity=0.25)
```

bounds = [-32.768, 32.768]

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness.

class leap_ec.real_rep.problems.**CosineFamilyProblem**(*alpha*, *global_optima_counts*, *local_optima_counts*, *maximize=False*)

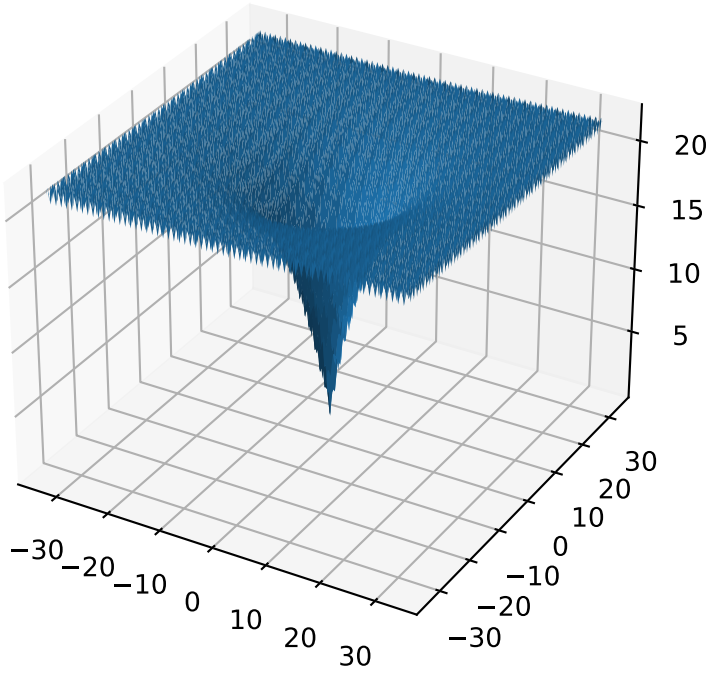
A configurable multi-modal function based on combinations of cosines, taken from the problem generators proposed by Rönkkönen *et al.* [RonkkonenLKL08].

$$f_{\cos}(\mathbf{x}) = \frac{\sum_{i=1}^{n} -\cos((G_i - 1)2\pi x_i) - \alpha \cdot \cos((G_i - 1)2\pi L_i x_i)}{2n}$$

where G_i and L_i are parameters that indicate the number of global and local optima, respectively, in the ith dimension.

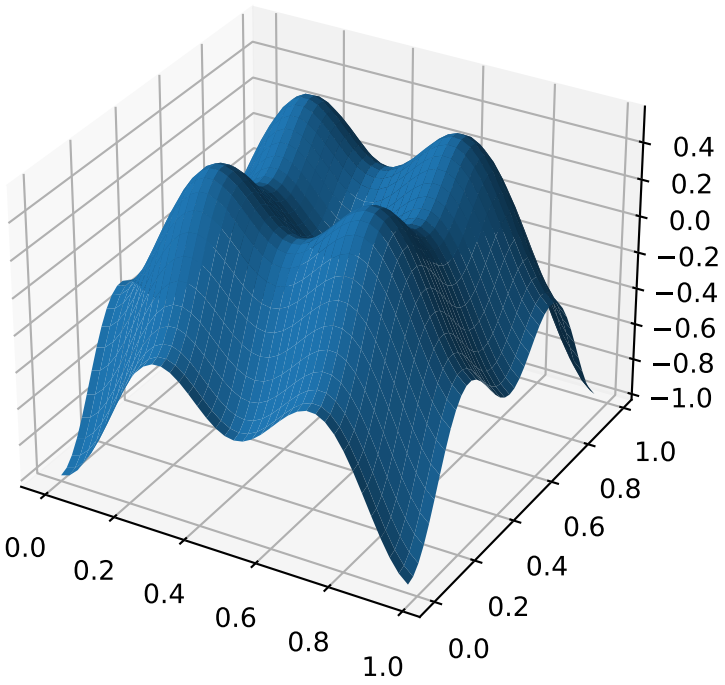
Parameters

- **alpha** (*float*) – parameter that controls the depth of the local optima.
- **global_optima_counts** (*[int]*) – list of integers indicating the number of global optima for each dimension.


20
15
10
5
−30
−20
−10
0
10
20
30
30
20
10
0
−10
−20
−30

- **local_optima_counts** (*[int]*) – list of integers indicated the number of local optima for each dimension.
- **maximize** – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import CosineFamilyProblem, plot_2d_problem
problem = CosineFamilyProblem(alpha=1.0, global_optima_counts=[2, 2], local_optima_
↪counts=[2, 2])
bounds = CosineFamilyProblem.bounds  # Contains traditional bounds
plot_2d_problem(problem, xlim=bounds, ylim=bounds, granularity=0.025)
```



The number of optima can be varied independently by each dimension:

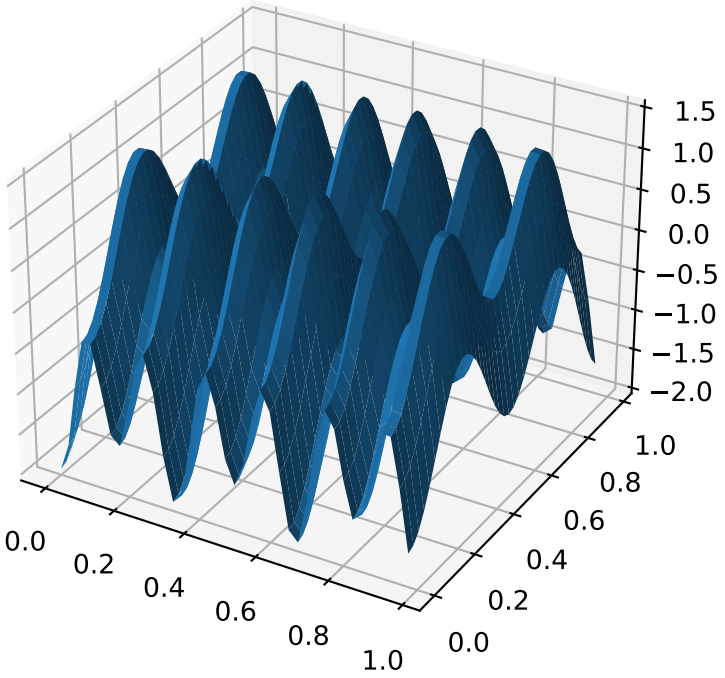
```
from leap_ec.real_rep.problems import CosineFamilyProblem, plot_2d_problem
problem = CosineFamilyProblem(alpha=3.0, global_optima_counts=[4, 2], local_optima_
↪counts=[2, 2])
bounds = CosineFamilyProblem.bounds  # Contains traditional bounds
plot_2d_problem(problem, xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (0, 1)

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters


1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0

phenome – phenome with a real-valued phenome vector to be evaluated

Returns
its fitness.

class leap_ec.real_rep.problems.**GaussianProblem**(*width=1*, *height=1*, *maximize=True*)

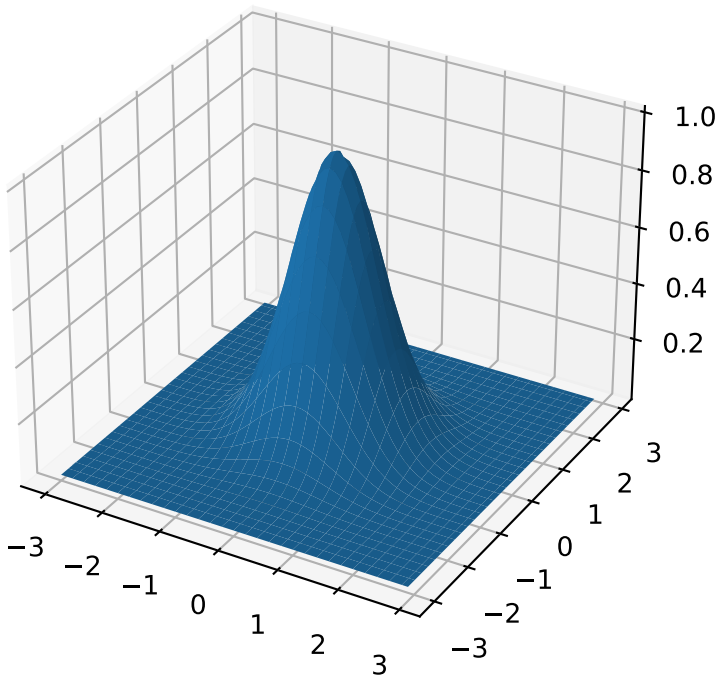
A multidimensional, isotropic Gaussian function, defined by

$$A \exp\left(-\sum_{i}^{n}\left(\frac{x_i}{w}\right)^2\right)$$

Parameters

- **width** (*float*) – the width parameter w
- **height** (*float*) – the height parameter A

```
from leap_ec.real_rep.problems import GaussianProblem, plot_2d_problem
bounds = GaussianProblem.bounds  # Some typical bounds
problem = GaussianProblem(width=1, height=1)
plot_2d_problem(problem, xlim=bounds, ylim=bounds, granularity=0.1)
```



bounds = (-3, 3)

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

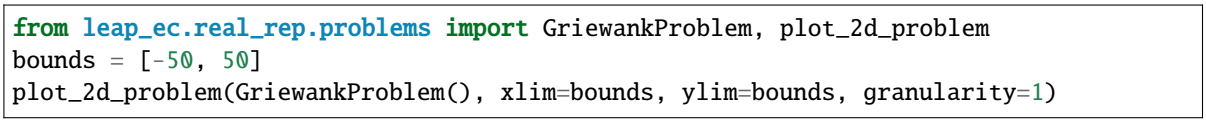
class leap_ec.real_rep.problems.**GriewankProblem**(*maximize=False*)

The classic Griewank problem. Like the `RastriginProblem` function, the Griewank has a quadratic global structure with many local optima that are distrib in a regular pattern.

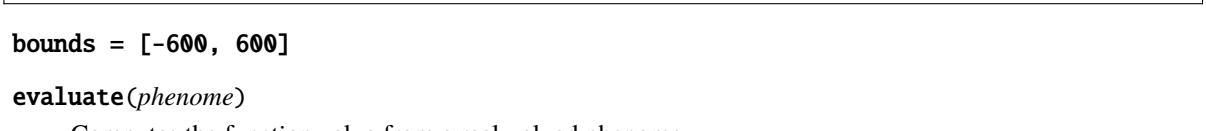
$$f(\mathbf{x}) = \sum_{i=1}^{d} \frac{x_i^2}{4000} - \prod_{i=1}^{d} \cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$$

Parameters
maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import GriewankProblem, plot_2d_problem
bounds = GriewankProblem.bounds  # Contains traditional bounds
plot_2d_problem(GriewankProblem(), xlim=bounds, ylim=bounds, granularity=10)
```



```
from leap_ec.real_rep.problems import GriewankProblem, plot_2d_problem
bounds = [-50, 50]
plot_2d_problem(GriewankProblem(), xlim=bounds, ylim=bounds, granularity=1)
```



bounds = [-600, 600]

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness.

class leap_ec.real_rep.problems.**LangermannProblem**(*m=5, c=(1, 2, 5, 2, 3), a=((3, 5), (5, 2), (2, 1), (1, 4), (7, 9)), maximize=False*)

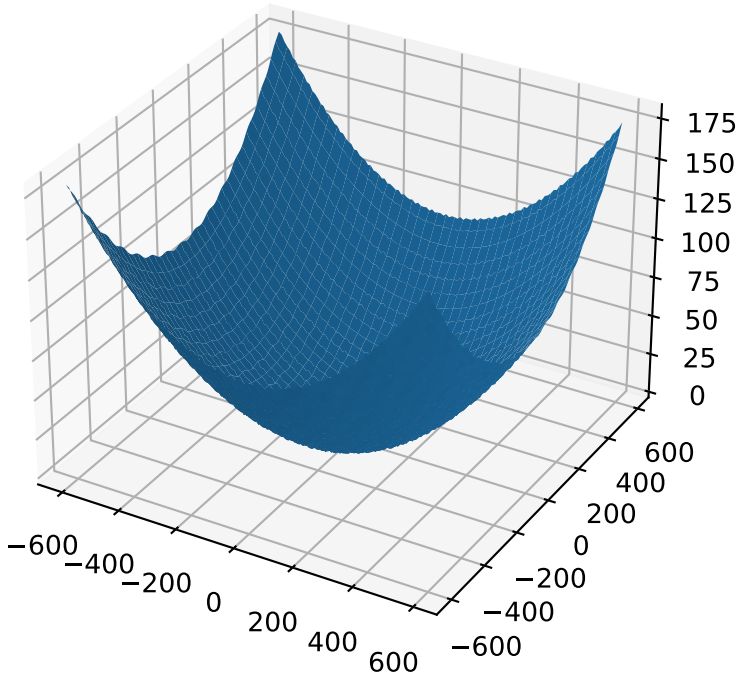
A popular multi-modal test function built by summing together m terms.

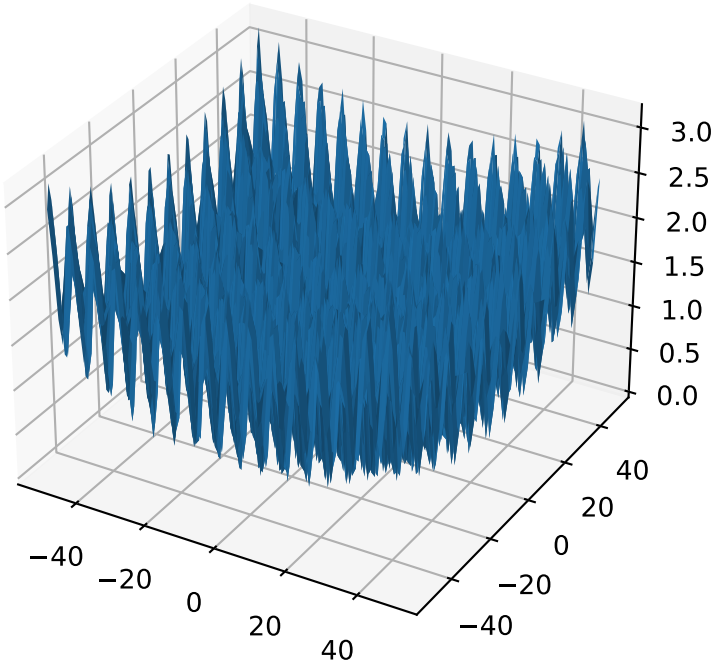
$$f(\mathbf{x}) = -\sum_{i=1}^{m} c_i \exp\left(-\frac{1}{\pi}\sum_{j=1}^{d}(x_j - A_{ij})^2\right) \cos\left(\pi \sum_{j=1}^{d}(x_j - A_{ij})^2\right)$$

Langermann's function is parameterized by a vector c_i of length m and a matrix A_{ij} of dimension $m \times d$. This class uses the traditional parameterization as the default, with $m = 5$ and

$$c = (1, 2, 5, 2, 3)$$

$$A = \begin{bmatrix} 3 & 5 \\ 5 & 2 \\ 2 & 1 \\ 1 & 4 \\ 7 & 9 \end{bmatrix}.$$

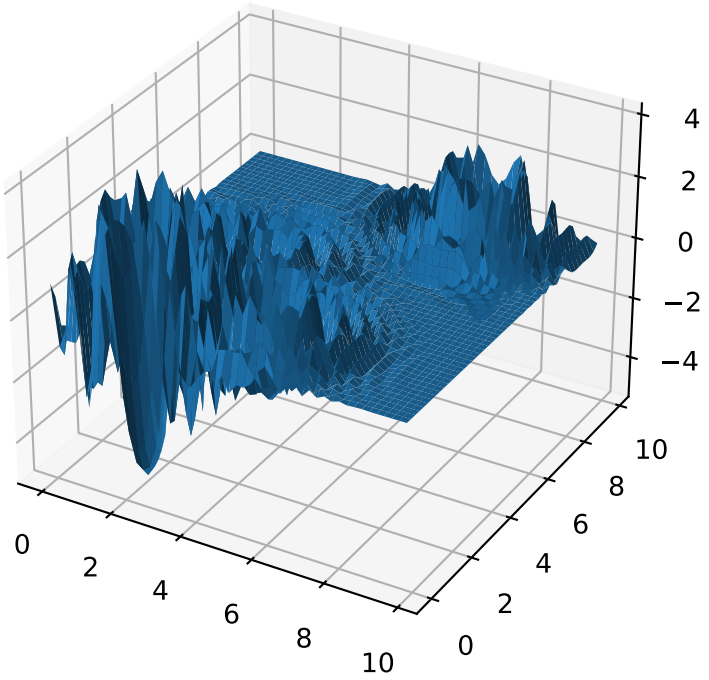

175
150
125
100
75
50
25
0
600
400
200
0
−200
−400
−600
−600
−400
−200
0
200
400
600


3.0
2.5
2.0
1.5
1.0
0.5
0.0
−40
−20
0
20
40
40
20
0
−20
−40

Parameters

- **m** (*int*) – total number of terms in the function's sum
- **c** (*[float]*) – amplitude coefficients for each term
- **a** (*[[float]]*) – offsets points for each term
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import LangermannProblem, plot_2d_problem
bounds = LangermannProblem.bounds  # Contains traditional bounds
plot_2d_problem(LangermannProblem(), xlim=bounds, ylim=bounds, granularity=0.2)
```



bounds = [0, 10]

default_a = ((3, 5), (5, 2), (2, 1), (1, 4), (7, 9))

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters

phenome – real-valued vector to be evaluated

Returns

its fitness.

class leap_ec.real_rep.problems.**LunacekProblem**(*N*, *d=1.0*, *mu_1=2.5*, *mu_2=None*, *s=None*, *maximize=False*)

Lunacek's function is also know as the "double Rastrigin" or "bi-Rastrigin" problem, because it overlays a `RastriginProblem`-style cosine function across a *pair* of spheroid functions.

This function was designed to model the double-funnel macrostructure that occurs in some difficult cases of the Lennard-Jones function (a famous function from molecular dynamics).

$$f(\mathbf{x}) = \min\left(\left\{\sum_{i=1}^{N}(x_i - \mu_1)^2\right\}, \left\{d \cdot N + s \cdot \sum_{i=1}^{N}(x_i - \mu_2)^2\right\}\right) + 10\sum_{i=1}^{N}(1 - \cos(2\pi(x_i - \mu_i))),$$

where N is the dimensionality of the solution vector, and the second sphere center parameter μ_2 is typically given by

$$\mu_2 = -\sqrt{\frac{\mu_1^2 - d}{s}}$$

and s is by default a function on N:

$$s = 1 - \frac{1}{2\sqrt{N + 20} - 8.2}$$

These respective defaults are used for μ_2 and s whenever *mu_2* and *s* are set to *None*.

Because of these complicated defaults, this class requires that you explicitly set the dimensionality of N of the expected input solutions. A warning will be thrown if an input solution is encountered that doesn't match the expected dimensionality.

Parameters

- **N** (*int*) – dimensionality of the anticipated input solutions
- **d** (*float*) – base fitness value of the second spheroid
- **mu_1** (*float*) – offset of the first spheroid
- **mu_2** (*float*) – offset of the second spheroid (if *None*, this will be calculated automatically)
- **s** (*float*) – scale parameter for the second spheroid (if *None*, this will be calculated automatically)
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import LunacekProblem, plot_2d_problem
bounds = LunacekProblem.bounds  # Contains traditional bounds
plot_2d_problem(LunacekProblem(N=2), xlim=bounds, ylim=bounds, granularity=0.1)
```

bounds = (-5, 5)

evaluate(*phenome*)

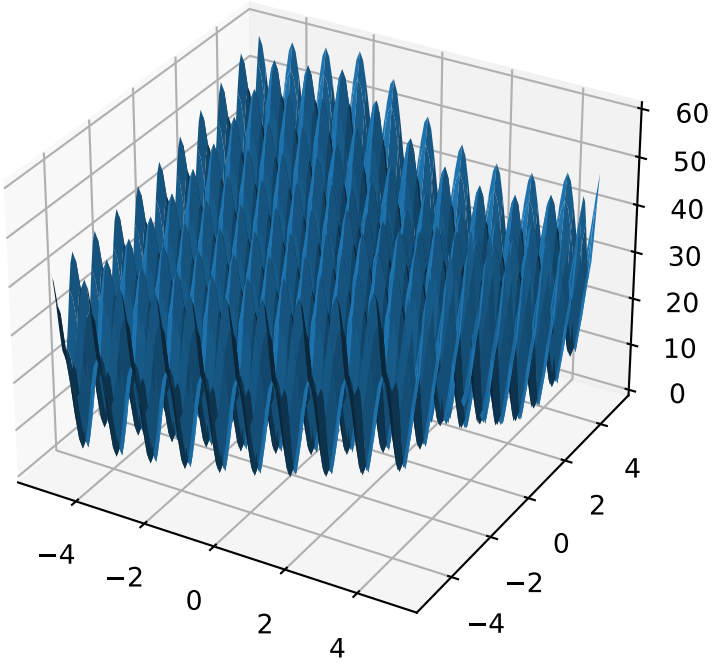
Computes the function value from a real-valued phenome.

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness.

class leap_ec.real_rep.problems.**MatrixTransformedProblem**(*problem*, *matrix*, *maximize=None*)

Apply a linear transformation to a fitness function.


60
50
40
30
20
10
0
−4
−2
0
2
4
−4
−2
0
2
4

Parameters
matrix – an nxn matrix, where n is the genome length.

Returns
a function that first applies -matrix to the input, then applies fun to the transformed input.

For example, here we manually construct a 2x2 rotation matrix and apply it to the `leap.RosenbrockProblem` function:

```
from matplotlib import pyplot as plt
from leap_ec.real_rep.problems import RosenbrockProblem, MatrixTransformedProblem,␣
↪plot_2d_problem

original_problem = RosenbrockProblem()
theta = np.pi/2
matrix = [[np.cos(theta), -np.sin(theta)],                  [np.sin(theta), np.
↪cos(theta)]]

transformed_problem = MatrixTransformedProblem(original_problem, matrix)

fig = plt.figure(figsize=(12, 8))

plt.subplot(221, projection='3d')
bounds = RosenbrockProblem.bounds  # Contains traditional bounds
plot_2d_problem(original_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(222, projection='3d')
plot_2d_problem(transformed_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(223)
plot_2d_problem(original_problem, kind='contour', xlim=bounds, ylim=bounds, ax=plt.
↪gca(), granularity=0.025)

plt.subplot(224)
plot_2d_problem(transformed_problem, kind='contour', xlim=bounds, ylim=bounds,␣
↪ax=plt.gca(), granularity=0.025)
```

evaluate(*phenome*)

Evaluated the fitness of a point on the transformed fitness landscape.

For example, consider a sphere function whose global optimum is situated at (0, 1):

```
>>> import numpy as np
>>> s = TranslatedProblem(SpheroidProblem(), offset=[0, 1])
>>> round(s.evaluate(np.array([0, 1])), 5)
0
```

Now let's take a rotation matrix that transforms the space by pi/2 radians:

```
>>> import numpy as np
>>> theta = np.pi/2
>>> matrix = [[np.cos(theta), -np.sin(theta)],                  [np.
↪sin(theta), np.cos(theta)]]
```

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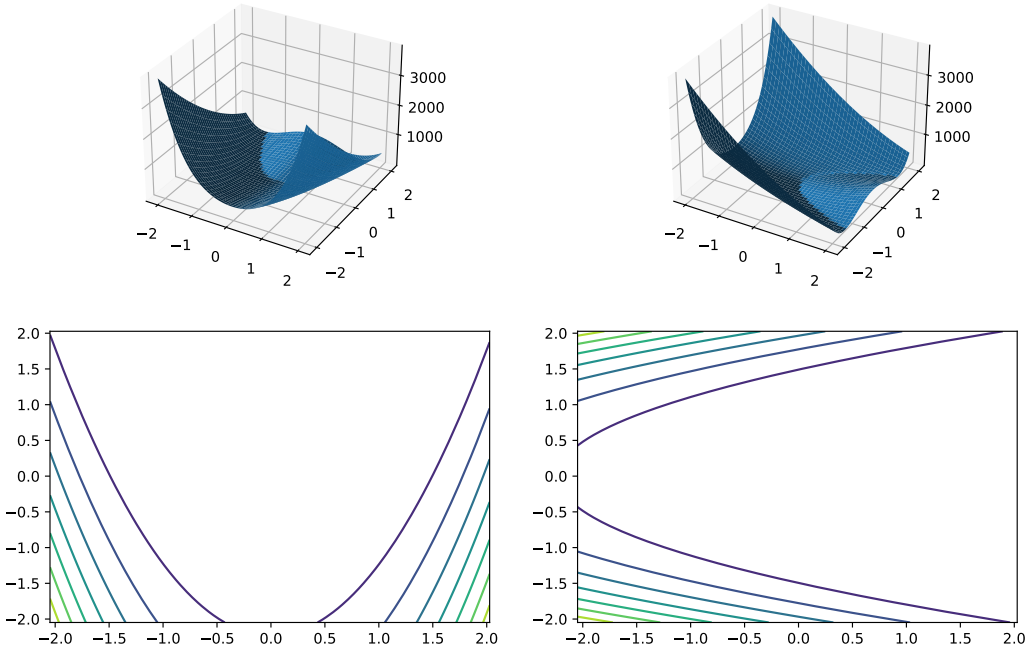

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```
>>> r = MatrixTransformedProblem(s, matrix)
```

The rotation has moved the new global optimum to (1, 0)

```
>>> round(r.evaluate(np.array([1, 0])), 5)
0.0
```

The point (0, 1) lies at a distance of sqrt(2) from the new optimum, and has a fitness of 2:

```
>>> round(r.evaluate(np.array([0, 1])), 5)
2.0
```

classmethod random_orthonormal(*problem*, *dimensions*, *maximize=None*)

Create a `MatrixTransformedProblem` that performs a random rotation and/or inversion of the function.

We accomplish this by generating a random orthonormal basis for R^n and plugging the resulting matrix into `MatrixTransformedProblem`.

The classic algorithm we use here is based on the Gramm-Schmidt process: we first generate a set of random vectors, and then convert them into an orthonormal basis. This approach is described in Hansen and Ostermeier's original CMA-ES paper:

"Completely derandomized self-adaptation in evolution strategies." *Evolutionary Computation* 9.2 (2001): 159-195.

Parameters

- **problem** – the original `ScalarProblem` to apply the transform to.

- **dimensions** (*int*) – the number of elements each vector should have.
- **maximize** (*bool*) – whether to maximize or minimize the resulting fitness function. Defaults to whatever setting the underlying problem uses.

```
from matplotlib import pyplot as plt
from leap_ec.real_rep.problems import CosineFamilyProblem,␣
↪MatrixTransformedProblem, plot_2d_problem

original_problem = CosineFamilyProblem(alpha=1.0, global_optima_counts=[2, 3],␣
↪local_optima_counts=[2, 3])

transformed_problem = MatrixTransformedProblem.random_orthonormal(original_
↪problem, 2)

fig = plt.figure(figsize=(12, 8))

plt.subplot(221, projection='3d')
bounds = original_problem.bounds
plot_2d_problem(original_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(222, projection='3d')
plot_2d_problem(transformed_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(223)
plot_2d_problem(original_problem, kind='contour', xlim=bounds, ylim=bounds,␣
↪ax=plt.gca(), granularity=0.025)

plt.subplot(224)
plot_2d_problem(transformed_problem, kind='contour', xlim=bounds, ylim=bounds,␣
↪ax=plt.gca(), granularity=0.025)
```

class leap_ec.real_rep.problems.**NoisyQuarticProblem**(*maximize=False*)

The classic 'quadratic quartic' function with Gaussian noise:

$$f(\mathbf{x}) = \sum_{i=1}^{n} ix_i^4 + \text{gauss}(0, 1)$$

Parameters

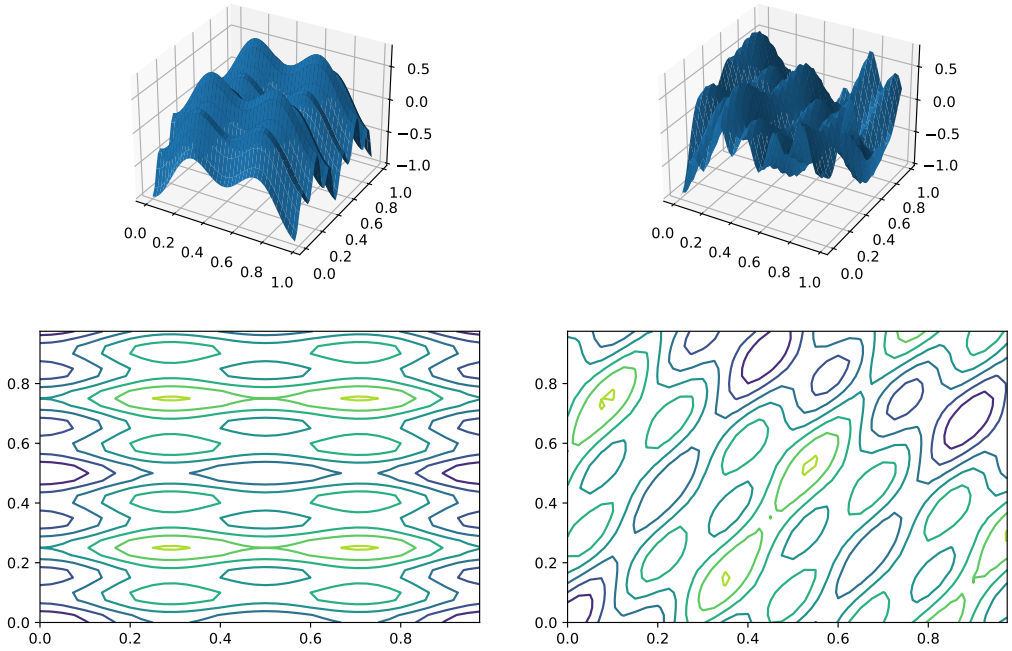
maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import NoisyQuarticProblem, plot_2d_problem
bounds = NoisyQuarticProblem.bounds  # Contains traditional bounds
plot_2d_problem(NoisyQuarticProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (-1.28, 1.28)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome (the output varies, since the function has noise):



```
>>> phenome = [3.5, -3.8, 5.0]
>>> r = NoisyQuarticProblem().evaluate(phenome)
>>> print(f'Result: {r}')
Result: ...
```

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness

worse_than(*first_fitness*, *second_fitness*)

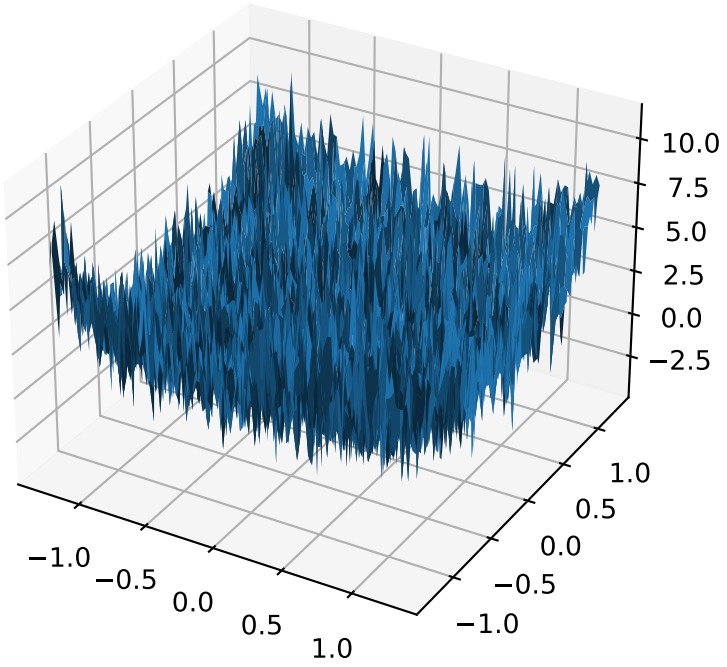
We minimize by default:

```
>>> s = NoisyQuarticProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = NoisyQuarticProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```

class leap_ec.real_rep.problems.**ParabaloidProblem**(*diagonal_matrix: ndarray*, *rotation_matrix: ndarray*, *maximize=False*)

A generalization of the *SpheroidProblem* into parabaloids (including elliptic and hyperbolic parabaloids).


10.0
7.5
5.0
2.5
0.0
−2.5
−1.0
−0.5
0.0
0.5
1.0
1.0
0.5
0.0
−0.5
−1.0

We construct the parabaloid by combining a diagonal matrix (which defines an axis-aligned parabaloid) with an orthornormal rotation. Together, these make up the eigenvalues and eigenbasis, respectively, of an arbitrary parabaloid:

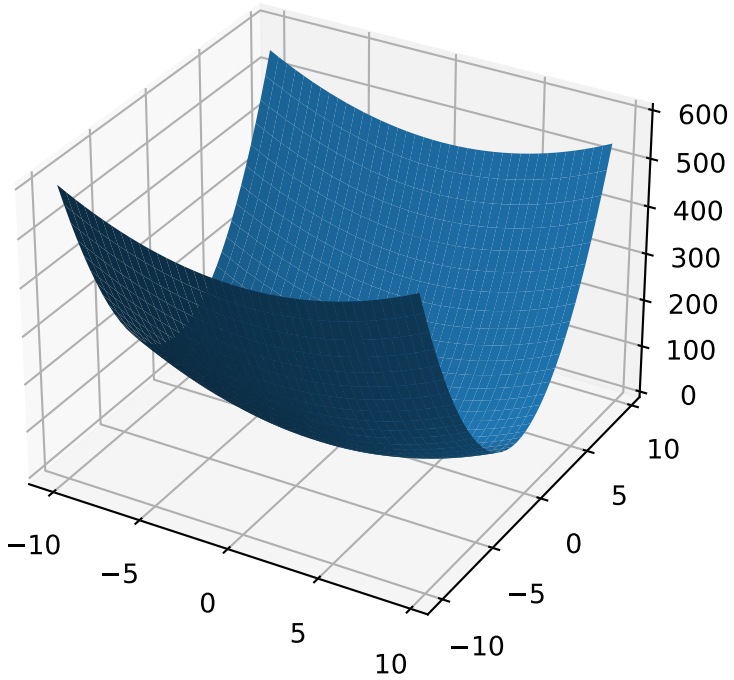
$$\mathbf{A} = \mathbf{R}^\top \mathbf{D} \mathbf{R}$$

We then compute fitness by interpretting A as a quadratic form:

$$f(x) = x^\top \mathbf{A} x$$

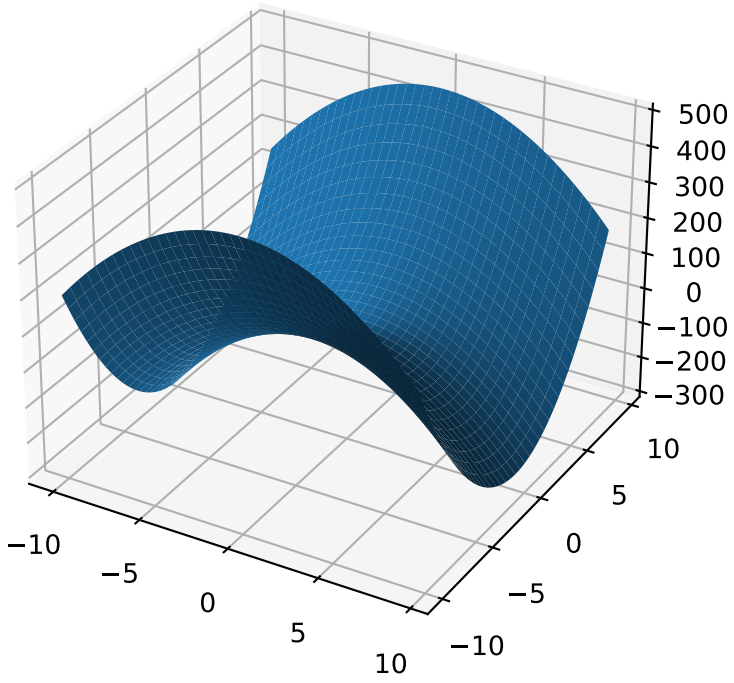
When the eigenvalues are all positive, then the result is an elliptic parabaloid

```
from leap_ec.real_rep .problems import ParabaloidProblem, plot_2d_problem
from matplotlib import pyplot as plt
import numpy as np

p = ParabaloidProblem(diagonal_matrix=np.diag([1, 5]), rotation_matrix=np.
↪identity(2))
plot_2d_problem(p, xlim=(-10, 10), ylim=(-10, 10), granularity=0.5)
plt.show()
```



If one or more eigenvalues are negative, then a hyperbolic parabloid results, which has a saddle shape:

```
from leap_ec.real_rep .problems import ParabaloidProblem, plot_2d_problem
from matplotlib import pyplot as plt
import numpy as np

p = ParabaloidProblem(diagonal_matrix=np.diag([-3, 5]), rotation_matrix=np.
↪identity(2))
plot_2d_problem(p, xlim=(-10, 10), ylim=(-10, 10), granularity=0.5)
plt.show()
```



evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

class leap_ec.real_rep.problems.**QuadraticFamilyProblem**(*diagonal_matrices: list*, *rotation_matrices: list*, *offset_vectors: list*, *fitness_offsets: list*, *maximize=False*)

A configurable multi-modal function based on combinations of spheroids or parabaloids. Taken from the problem generators proposed by Rönkkönen *et al.* [RonkkonenLKL08].

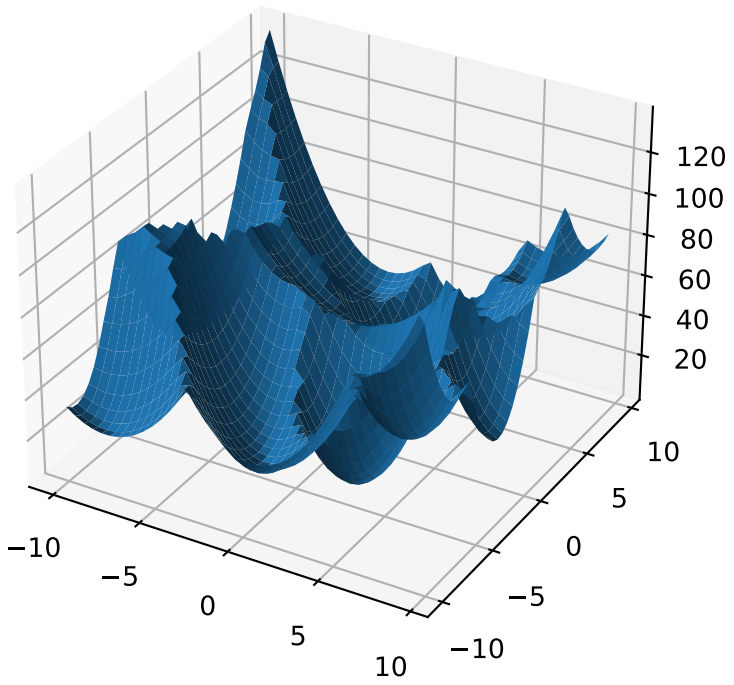
The function is given by

$$f(\mathbf{x}) = \min_{i=1,2,\ldots,q} \left((\mathbf{x} - \mathbf{p}_i)^\top \mathbf{B}_i^{-1} (\mathbf{x} - \mathbf{p}_i) + v_i \right)$$

where the $\mathbf{p}_i$ gives the center of each quadratic (i.e. the location of each local minimum), the v_i give their fitness values, and the $\mathbf{B}_i^{-1}$ are symmetric matrices.

The easiest way to create one of these problems is to use the random generator:

```
from leap_ec.real_rep.problems import QuadraticFamilyProblem, plot_2d_problem
from matplotlib import pyplot as plt

problem = QuadraticFamilyProblem.generate(dimensions=2, num_basins=30)
plot_2d_problem(problem, xlim=(-10, 10), ylim=(-10, 10), granularity=0.5)
plt.show()
```



You can also specify the problem structure directly by providing two matrices for each parabaloid along with an offset vector (for translation) and a scalar offset (to define the minimum fitness value for the basin):

```
from leap_ec.real_rep.problems import QuadraticFamilyProblem, plot_2d_problem,␣
↪random_orthonormal_matrix
```

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```
from matplotlib import pyplot as plt
import numpy as np

# Define the parameters for each parabaloid

diag1 = np.diag([2, 4])     # Diagonal matrix defining the widths (eigenvalues) of␣
↪the basin for each dimension
rot1 = np.identity(2)       # Rotation matrix, in this case the identity (no␣
↪rotation)
offset1 = np.array([-1, -1])  # Offset used to translate the basin location
fitness1 = 0                # Fitness value of the local optimum

diag2 = np.diag([5, 1])
rot2 = random_orthonormal_matrix(dimensions=2)  # Apply a random rotation to the␣
↪second basin
offset2 = np.array([3, 4])
fitness2 = 100.0

# Build the problem
problem = QuadraticFamilyProblem(
    diagonal_matrices = [ diag1, diag2 ],
    rotation_matrices = [ rot1, rot2 ],
    offset_vectors = [ offset1, offset2 ],
    fitness_offsets = [ fitness1, fitness2 ]
)

# Visualize
plot_2d_problem(problem, xlim=(-10, 10), ylim=(-10, 10), granularity=0.5)
plt.show()
```

property dimensions

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

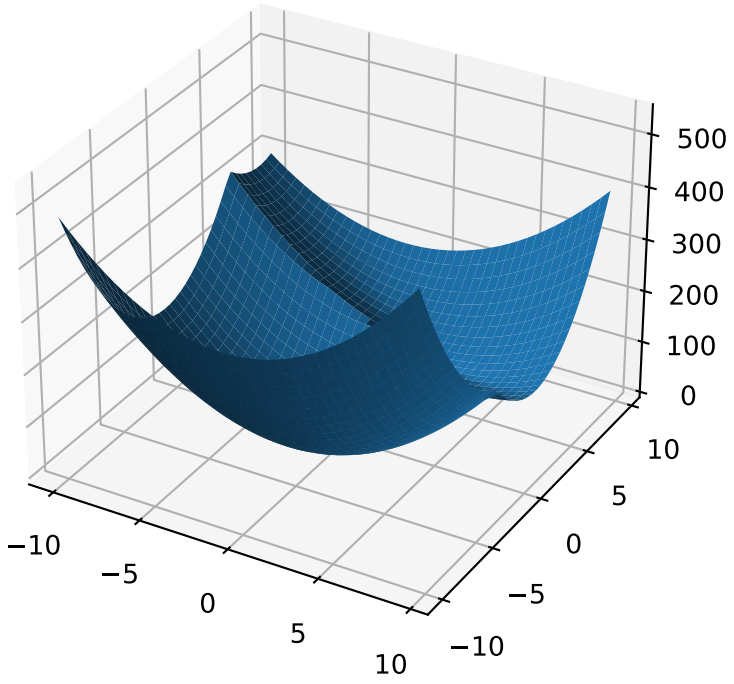
Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

classmethod generate(*dimensions: int*, *num_basins: int*, *num_global_optima: int = 1*, *width_bounds: tuple = (1, 5)*, *offset_bounds: tuple = (-10, 10)*, *fitness_offset_bounds: tuple = (10, 100)*)

Convenient method to generate a QuadraticFamilyProblem by randomly sampling the matrices that define it.

```
>>> problem = QuadraticFamilyProblem.generate(10, 20, num_global_optima = 2)
>>> x = problem.evaluate(np.array([0.0, 0.5, 0.0, 0.6, 0.0, 0.7, 0.6, 0.8, 4.3,␣
↪0.2]))
```


500
400
300
200
100
0
10
5
0
−5
−10
−10
−5
0
5
10

property num_basins

class leap_ec.real_rep.problems.**RastriginProblem**(*a=1.0*, *maximize=False*)

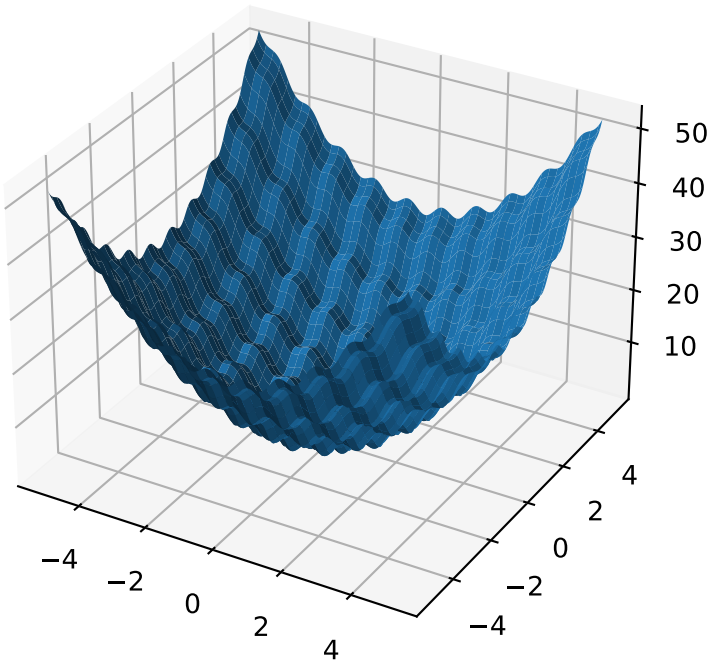
The classic Rastrigin problem. The Rastrigin provides a real-valued fitness landscape with a quadratic global structure (like the SpheroidProblem), plus a sinusoidal local structure with many local optima.

$$f(\vec{x}) = An + \sum_{i=1}^{n} x_i^2 - A\cos(2\pi x_i)$$

Parameters

maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import RastriginProblem, plot_2d_problem
bounds = RastriginProblem.bounds  # Contains traditional bounds
plot_2d_problem(RastriginProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```



bounds = (-5.12, 5.12)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome:

```
>>> phenome = [1.0/12, 0]
>>> RastriginProblem().evaluate(phenome)
0.1409190406...
```

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness

worse_than(*first_fitness*, *second_fitness*)

We minimize by default:

```
>>> s = RastriginProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = RastriginProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```

class leap_ec.real_rep.problems.**RosenbrockProblem**(*maximize=False*)

The classic RosenbrockProblem problem, a.k.a. the "banana" or "valley" function.

$$f(\mathbf{x}) = \sum_{i=1}^{d-1} \left[100(x_{i+1} - x_i^2)^2 + (x_i - 1)^2\right]$$

Parameters
maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import RosenbrockProblem, plot_2d_problem
bounds = RosenbrockProblem.bounds  # Contains traditional bounds
plot_2d_problem(RosenbrockProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (-2.048, 2.048)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome:

```
>>> phenome = [0.5, -0.2, 0.1]
>>> RosenbrockProblem().evaluate(phenome)
22.3
```

Parameters
phenome – real-valued vector to be evaluated

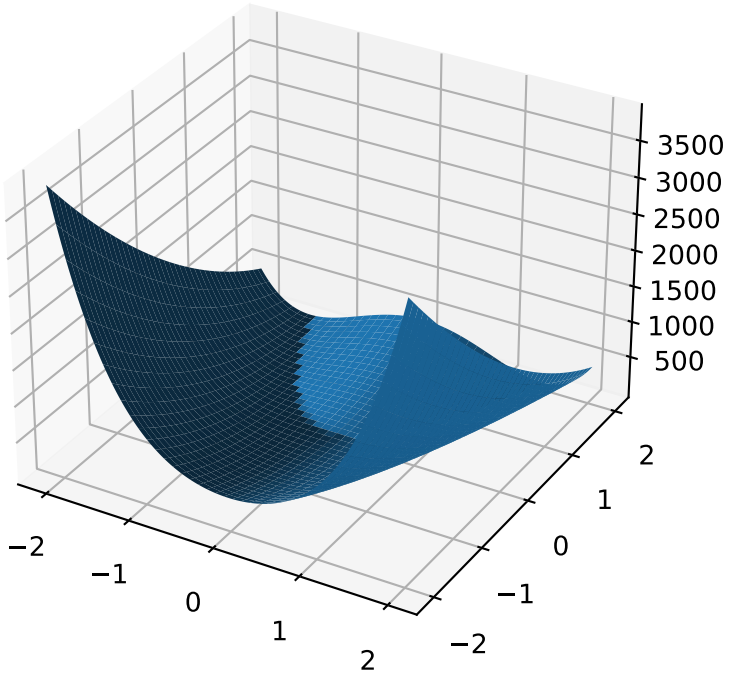
Returns
its fitness

worse_than(*first_fitness*, *second_fitness*)

We minimize by default:

```
>>> s = RosenbrockProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = RosenbrockProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```


3500
3000
2500
2000
1500
1000
500
−2
−1
0
1
2
−2
−1
0
1
2

class leap_ec.real_rep.problems.**ScaledProblem**(*problem*, *new_bounds*, *maximize=None*)

Scale the search space of a fitness function up or down.

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

class leap_ec.real_rep.problems.**SchwefelProblem**(*alpha=418.982887*, *maximize=False*)

Schwefel's function is another traditional multimodal test function whose local optima are distributed in a slightly irregular way, and whose global optimum is out at the edge of the search space (with no gently sloping macrostructure to guide the algorithm toward it).

Compare this to the `RastriginProblem` function, whose global optimum lies at the center of a quadratic bowl with a regular grid of local optima.

$$f(\mathbf{x}) = \sum_{i=1}^{d} \left(-x_i \cdot \sin\left(\sqrt{|x_i|} \right) \right) + \alpha \cdot d$$

Parameters

- **alpha** (*float*) – fitness offset (the default value ensures that the global optimum has zero fitness)
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import SchwefelProblem, plot_2d_problem
bounds = SchwefelProblem.bounds  # Contains traditional bounds
plot_2d_problem(SchwefelProblem(), xlim=bounds, ylim=bounds, granularity=10)
```

bounds = (-512, 512)

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

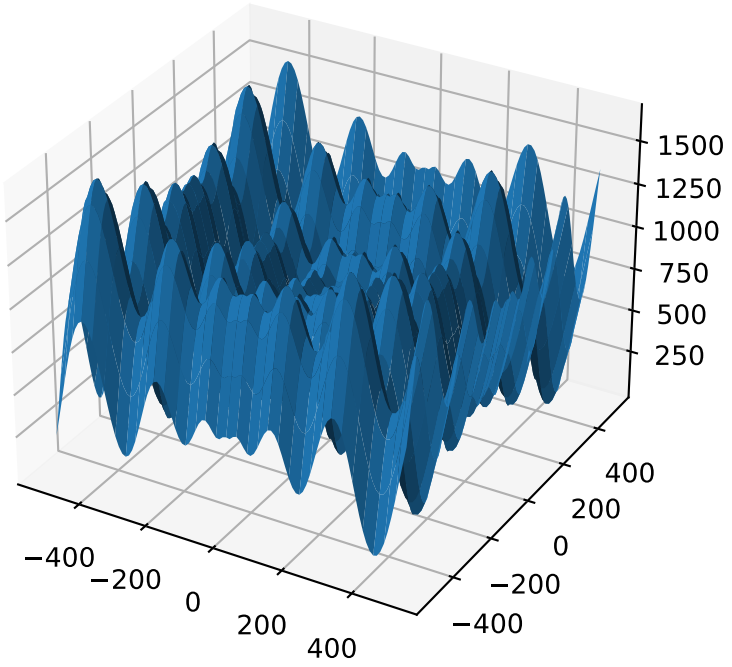
Parameters
phenome – phenome with a real-valued phenome to be evaluated

Returns
its fitness.

class leap_ec.real_rep.problems.**ShekelProblem**(*k=500*, *c=array([1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25])*, *maximize=False*)

The classic 'Shekel's foxholes' function.

$$f(\mathbf{x}) = \frac{1}{\frac{1}{K} + \sum_{j=1}^{25} \frac{1}{f_j(\mathbf{x})}}$$


1500
1250
1000
750
500
250
−400
−200
0
200
400
400
200
0
−200
−400

where

$$f_j(\mathbf{x}) = c_j + \sum_{i=1}^{2}(x_i - a_{ij})^6$$

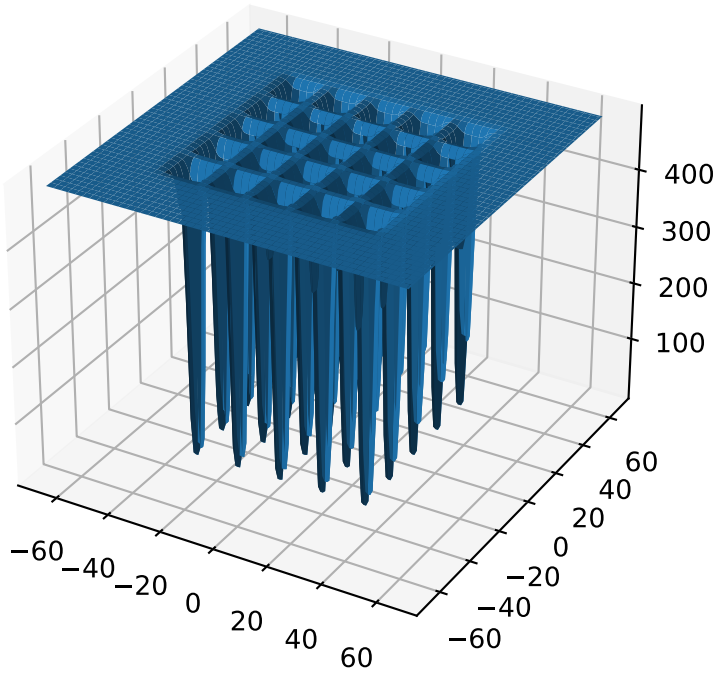
and the points $\{(a_{1j}, a_{2j})\}_{j=1}^{25}$ define the functions various optima, and are given by the following hardcoded matrix:

$$[a_{ij}] = \begin{bmatrix} -32 & -16 & 0 & 16 & 32 & -32 & -16 & \cdots & 0 & 16 & 32 \\ -32 & -32 & -32 & -32 & -32 & -16 & -16 & \cdots & 32 & 32 & 32 \end{bmatrix}.$$

Parameters

- **k** (*int*) – the value of K in the fitness function.
- **c** (*[int]*) – list of values for the function's c_j parameters. Each *c[j]* approximately corresponds to the depth of the jth foxhole.
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.
- **maximize** – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import ShekelProblem, plot_2d_problem
bounds = ShekelProblem.bounds  # Contains traditional bounds
plot_2d_problem(ShekelProblem(), xlim=bounds, ylim=bounds, granularity=0.9)
```



bounds = (-65.536, 65.536)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome (the output varies, since the function has noise).

Parameters
phenome – real-valued to be evaluated

Returns
its fitness

points = array([[-32, -16, 0, 16, 32, -32, -16, 0, 16, 32, -32, -16, 0, 16, 32, -32, -16, 0, 16, 32, -32, -16, 0, 16, 32], [-32, -32, -32, -32, -32, -16, -16, -16, -16, -16, 0, 0, 0, 0, 0, 16, 16, 16, 16, 16, 32, 32, 32, 32, 32]])

worse_than(*first_fitness*, *second_fitness*)

We minimize by default:

```
>>> s = ShekelProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = ShekelProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```

class leap_ec.real_rep.problems.**SpheroidProblem**(*maximize=False*)

Classic paraboloid function, known as the "sphere" or "spheroid" problem, because its equal-fitness contours form (hyper)spheres in n > 2.

$$f(\vec{x}) = \sum_{i}^{n} x_i^2$$

Parameters
maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import SpheroidProblem, plot_2d_problem
bounds = SpheroidProblem.bounds  # Contains traditional bounds
plot_2d_problem(SpheroidProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (-5.12, 5.12)

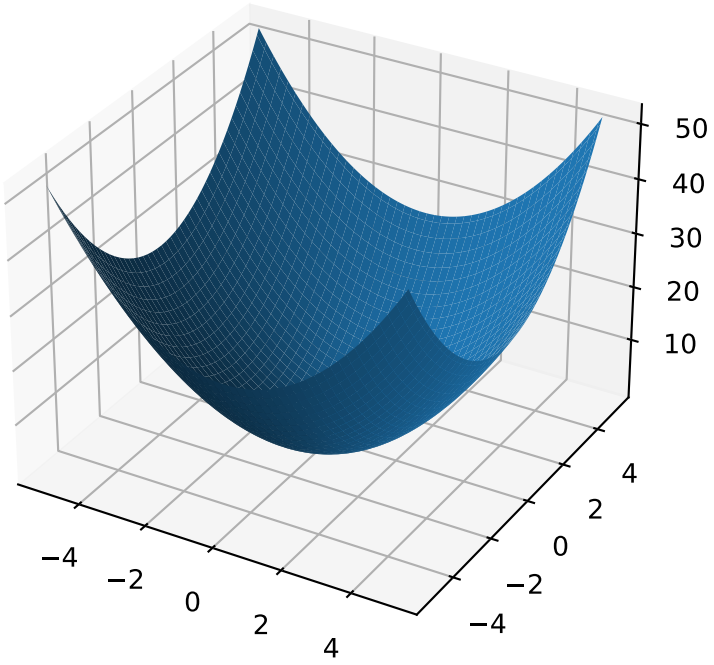
evaluate(*phenome*)

Computes the function value from a real-valued list phenome:

```
>>> phenome = [0.5, 0.8, 1.5]
>>> SpheroidProblem().evaluate(phenome)
3.14
```

Parameters
phenome – real-valued vector to be evaluated

Returns
it's fitness, *sum(phenome**2)*


50
40
30
20
10
−4
−2
0
2
4
4
2
0
−2
−4

worse_than(*first_fitness*, *second_fitness*)

We minimize by default:

```
>>> s = SpheroidProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = SpheroidProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```

class leap_ec.real_rep.problems.**StepProblem**(*maximize=True*)

The classic 'step' function—a function with a linear global structure, but with stair-like plateaus at the local level.

$$f(\mathbf{x}) = \sum_{i=1}^{n} \lfloor x_i \rfloor$$

where $\lfloor x \rfloor$ denotes the floor function.

Parameters

maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import StepProblem, plot_2d_problem
bounds = StepProblem.bounds  # Contains traditional bounds
plot_2d_problem(StepProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (-5.12, 5.12)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome:

```
>>> import numpy as np
>>> phenome = np.array([3.5, -3.8, 5.0])
>>> StepProblem().evaluate(phenome)
4.0
```

Parameters

phenome – real-valued vector to be evaluated

Returns

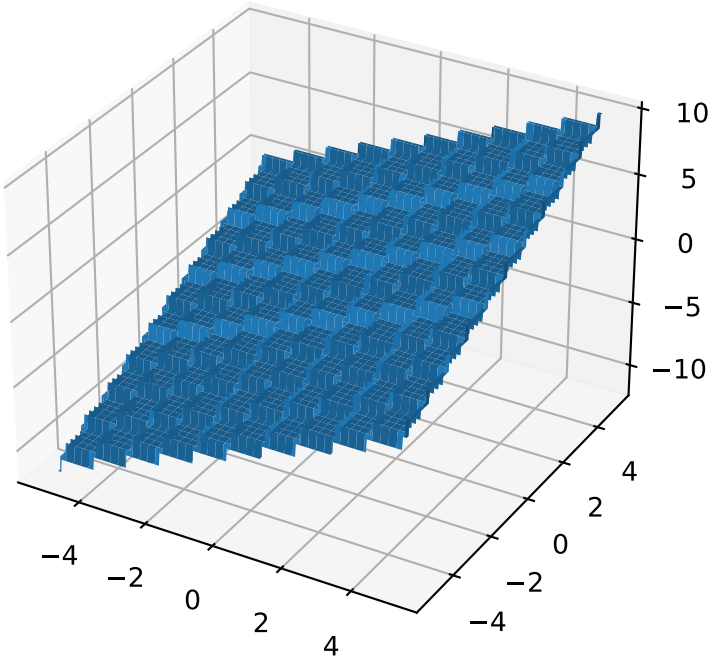
its fitness

worse_than(*first_fitness*, *second_fitness*)

We maximize by default:

```
>>> s = StepProblem()
>>> s.worse_than(100, 10)
False
```

```
>>> s = StepProblem(maximize=False)
>>> s.worse_than(100, 10)
True
```


10
5
0
−5
−10
−4
−2
0
2
4
4
2
0
−2
−4

class leap_ec.real_rep.problems.**TranslatedProblem**(*problem*, *offset*, *maximize=None*)

Takes an existing fitness function and translates it by applying a fixed offset vector.

For example,

```
from matplotlib import pyplot as plt
from leap_ec.real_rep.problems import SpheroidProblem, TranslatedProblem, plot_2d_
↪problem

original_problem = SpheroidProblem()
offset = [-1.0, -2.5]
translated_problem = TranslatedProblem(original_problem, offset)

fig = plt.figure(figsize=(12, 8))

plt.subplot(221, projection='3d')
bounds = SpheroidProblem.bounds  # Contains traditional bounds
plot_2d_problem(original_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(222, projection='3d')
plot_2d_problem(translated_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(223)
plot_2d_problem(original_problem, kind='contour', xlim=bounds, ylim=bounds, ax=plt.
↪gca(), granularity=0.025)

plt.subplot(224)
plot_2d_problem(translated_problem, kind='contour', xlim=bounds, ylim=bounds,␣
↪ax=plt.gca(), granularity=0.025)
```

evaluate(*phenome*)

Evaluate the fitness of a point after translating the fitness function.

Translation can be used in higher than two dimensions:

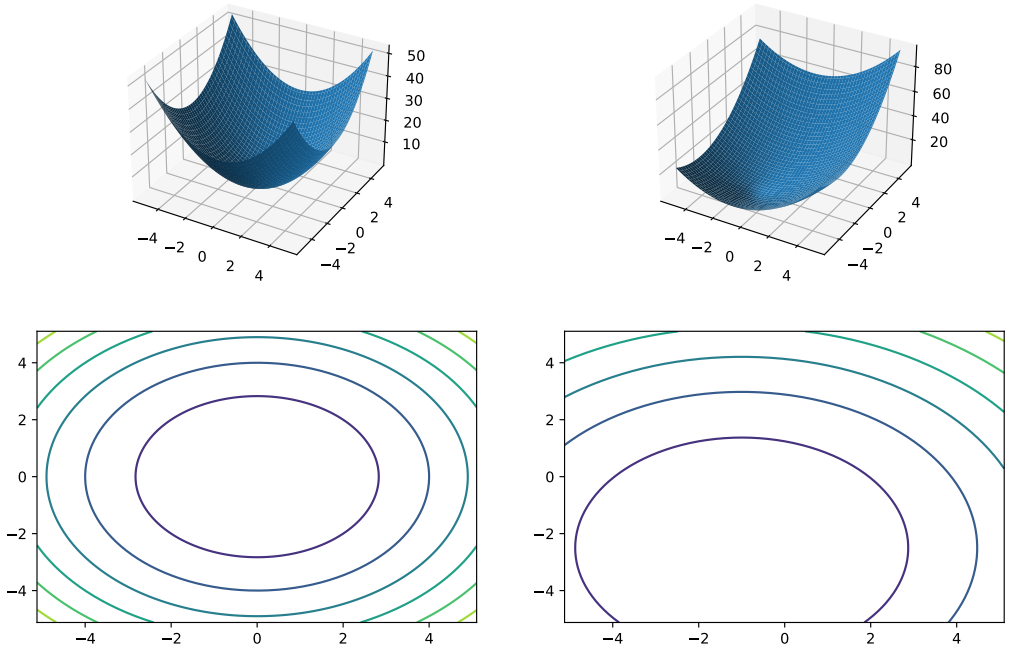
```
>>> import numpy as np
>>> offset = [-1.0, -1.0, 1.0, 1.0, -5.0]
>>> t_sphere = TranslatedProblem(SpheroidProblem(), offset)
>>> genome = np.array([0.5, 2.0, 3.0, 8.5, -0.6])
>>> t_sphere.evaluate(genome)
90.86
```

classmethod random(*problem*, *offset_bounds*, *dimensions*, *maximize=None*)

Apply a random real-valued translation to a fitness function, sampled uniformly between min_offset and max_offset in every dimension.

```
>>> from leap_ec.real_rep.problems import TranslatedProblem, RastriginProblem,␣
↪plot_2d_problem
```

```
>>> original_problem = RastriginProblem()
>>> bounds = RastriginProblem.bounds  # Contains traditional bounds
>>> translated_problem = TranslatedProblem.random(original_problem, bounds, 2)
```



```
>>> plot_2d_problem(translated_problem, kind='contour', xlim=bounds,␣
↪ylim=bounds)
<matplotlib.contour...>
```

```
from leap_ec.real_rep.problems import TranslatedProblem, RastriginProblem, plot_
↪2d_problem

original_problem = RastriginProblem()
bounds = RastriginProblem.bounds  # Contains traditional bounds
translated_problem = TranslatedProblem.random(original_problem, bounds, 2)

plot_2d_problem(translated_problem, kind='contour', xlim=bounds, ylim=bounds)
```

class leap_ec.real_rep.problems.**WeierstrassProblem**(*kmax=20*, *a=0.5*, *b=3*, *maximize=False*)

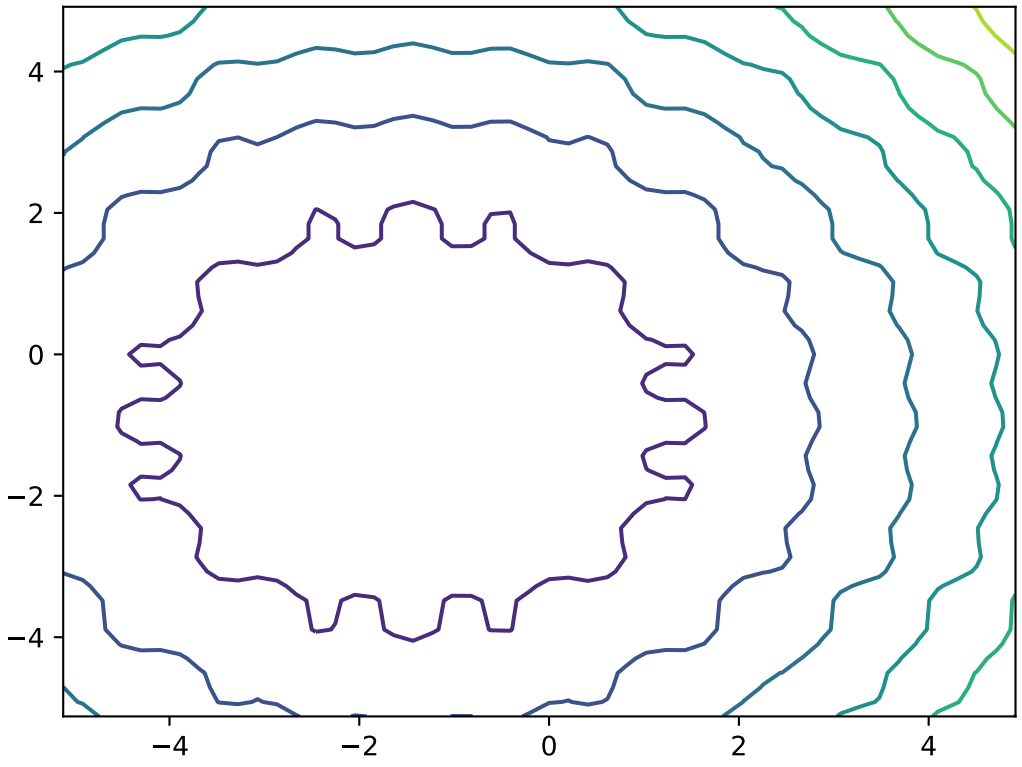
The Weierstrass function is famous for being the first discovered example of a function that is continuous, but not differentiable. Built by adding the terms of a Fourier series, it has a jagged, self-similar structure:

$$f(\mathbf{x}) = \sum_{i=1}^{d} \left[\sum_{k=0}^{kmax} a^k \cos\left(2\pi b^k (x_i + 0.5)\right) - n \sum_{k=0}^{kmax} a^k \cos(\pi b^k) \right]$$

When used in optimization benchmarks, it's typical to carry out the Fourier sum to *kmax=20* terms.

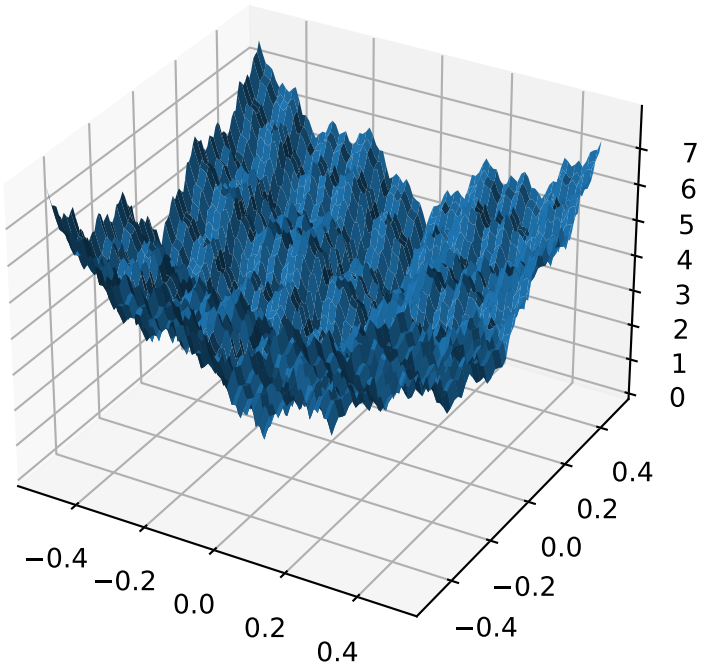
Parameters

- **kmax** (*int*) – number of terms to carry the Fourier sum out to
- **a** (*float*) – amplitude parameter of the cosine terms


4
2
0
−2
−4
−4
−2
0
2
4

- **b** (*float*) – wavenumber (frequency) parameter of the cosine terms
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import WeierstrassProblem, plot_2d_problem
bounds = WeierstrassProblem.bounds  # Contains traditional bounds
plot_2d_problem(WeierstrassProblem(), xlim=bounds, ylim=bounds, granularity=0.01)
```



bounds = [-0.5, 0.5]

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness.

leap_ec.real_rep.problems.**plot_2d_contour**(*fun*, *xlim*, *ylim*, *granularity*, *ax=None*, *title=None*, *pad=None*)

Convenience method for plotting contours for a function that accepts 2-D real-valued inputs and produces a 1-D scalar output.

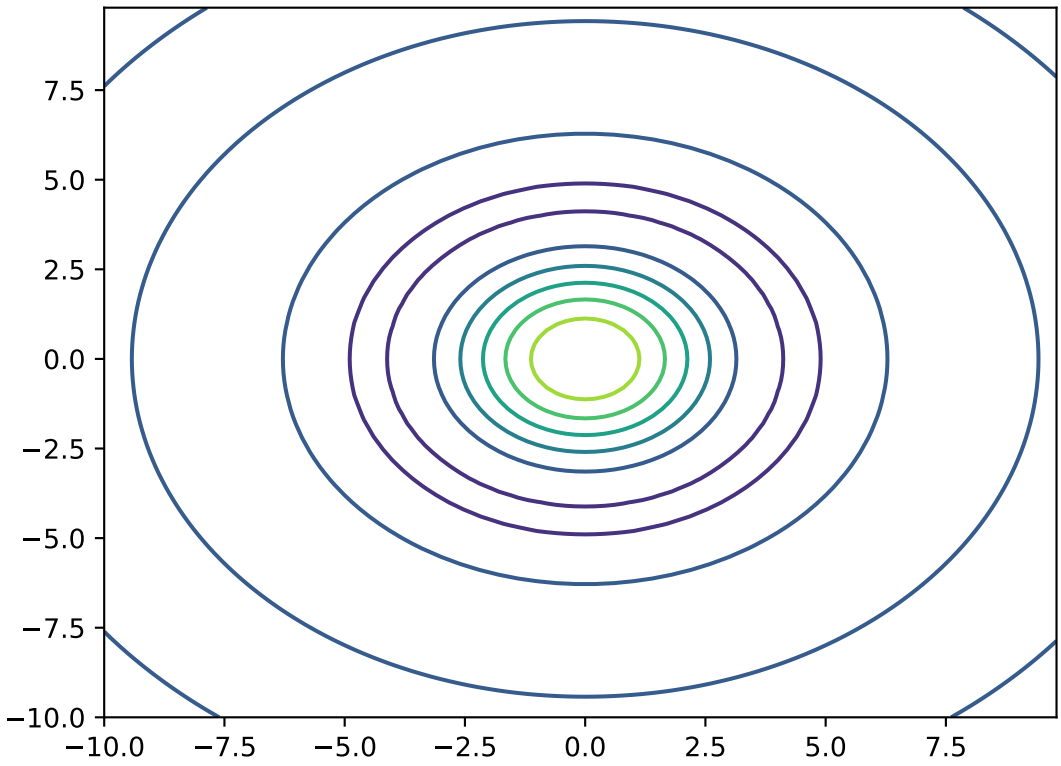
Parameters

- **fun** (*function*) – The function to plot.

- **xlim** (*(float, float)*) – Bounds of the horizontal axes.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **granularity** (*float*) – Spacing of the grid to sample points along.
- **pad** – An array of extra gene values, used to fill in the hidden dimensions with contants while drawing fitness contours.

The difference between this and *plot_2d_problem()* is that this takes a raw function (instead of a `Problem` object).

```
import numpy as np
from scipy import linalg

from leap_ec.real_rep.problems import plot_2d_contour

def sinc_hd(phenome):
    r = linalg.norm(phenome)
    return np.sin(r)/r

plot_2d_contour(sinc_hd, xlim=(-10, 10), ylim=(-10, 10), granularity=0.2)
```



leap_ec.real_rep.problems.**plot_2d_function**(*fun*, *xlim*, *ylim*, *granularity=0.1*, *ax=None*, *title=None*, *pad=None*, ***kwargs*)

Convenience method for plotting a function that accepts 2-D real-valued imputs and produces a 1-D scalar output.

Parameters

- **fun** (*function*) – The function to plot.
- **xlim** (*(float, float)*) – Bounds of the horizontal axes.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **granularity** (*float*) – Spacing of the grid to sample points along.
- **pad** – An array of extra gene values, used to fill in the hidden dimensions with contants while drawing fitness contours.
- **kwargs** – additional keyword arguments to pass along to plot_surface() or contour()

The difference between this and *plot_2d_problem()* is that this takes a raw function (instead of a `Problem` object).

```
import numpy as np
from scipy import linalg

from leap_ec.real_rep.problems import plot_2d_function

def sinc_hd(phenome):
    r = linalg.norm(phenome)
    return np.sin(r)/r

plot_2d_function(sinc_hd, xlim=(-10, 10), ylim=(-10, 10), granularity=0.2)
```

leap_ec.real_rep.problems.**plot_2d_problem**(*problem*, *xlim=None*, *ylim=None*, *kind='surface'*, *ax=None*, *granularity=None*, *title=None*, *pad=None*, ***kwargs*)

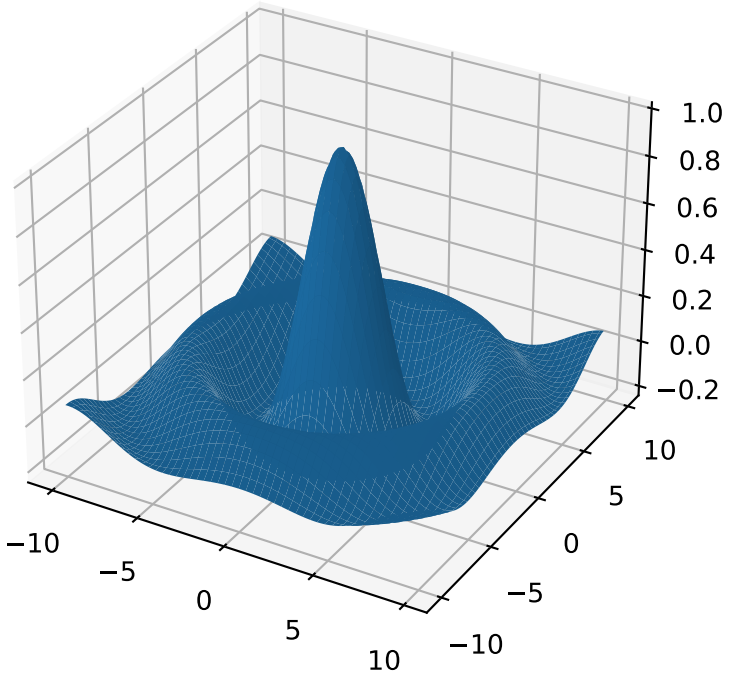
Convenience function for plotting a `Problem` that accepts 2-D real-valued phenomes and produces a 1-D scalar fitness output.

Parameters

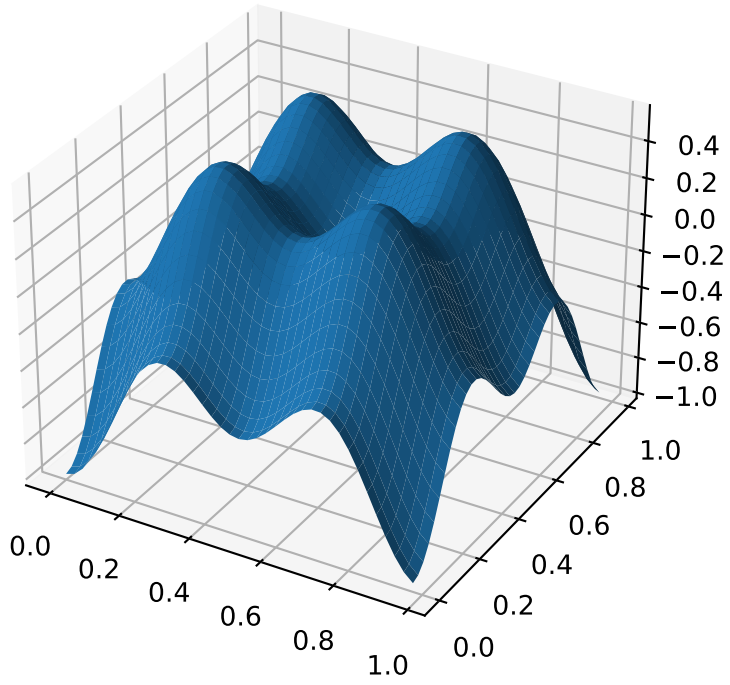
- **fun** (*Problem*) – The `Problem` to plot.
- **xlim** (*(float, float)*) – Bounds of the horizontal axes. If None, uses *problem.bounds*.
- **ylim** (*(float, float)*) – Bounds of the vertical axis. If None, uses *problem.bounds*.
- **kind** (*str*) – The kind of plot to create: 'surface' or 'contour'
- **pad** – An array of extra gene values, used to fill in the hidden dimensions with contants while drawing fitness contours.
- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **granularity** (*float*) – Spacing of the grid to sample points along. If none is given, then the granularity will default to 1/50th of the range of the function's *bounds* attribute.
- **kwargs** – additional keyword arguments to pass along to plot_surface()

The difference between this and *plot_2d_function()* is that this takes a `Problem` object (instead of a raw function).

If no axes are specified, a new figure is created for the plot:


1.0
0.8
0.6
0.4
0.2
0.0
−0.2
−10
−5
0
5
10
10
5
0
−5
−10

```
from leap_ec.real_rep.problems import CosineFamilyProblem, plot_2d_problem
problem = CosineFamilyProblem(alpha=1.0, global_optima_counts=[2, 2], local_optima_
↪counts=[2, 2])
plot_2d_problem(problem, xlim=(0, 1), ylim=(0, 1), granularity=0.025);
```

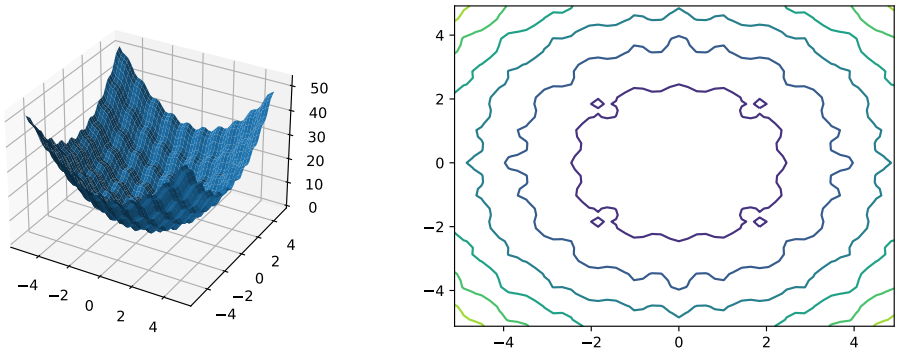


You can also specify axes explicitly (ex. by using *ax=plt.gca()*. When plotting surfaces, you must configure your axes to use *projection='3d'*. Contour plots don't need 3D axes:

```
from matplotlib import pyplot as plt
from leap_ec.real_rep.problems import RastriginProblem, plot_2d_problem

fig = plt.figure(figsize=(12, 4))
bounds=RastriginProblem.bounds  # Contains default bounds

plt.subplot(121, projection='3d')
plot_2d_problem(RastriginProblem(), ax=plt.gca(), xlim=bounds, ylim=bounds)

plt.subplot(122)
plot_2d_problem(RastriginProblem(), ax=plt.gca(), kind='contour', xlim=bounds,␣
↪ylim=bounds)
```

leap_ec.real_rep.problems.**random**(*size=None*)

Return random floats in the half-open interval [0.0, 1.0). Alias for *random_sample* to ease forward-porting to



the new random API.

`leap_ec.real_rep.problems.`**`random_orthonormal_matrix`**(*dimensions: int*)

Generate a random orthornomal matrix using the Gramm-Schmidt process.

Orthonormal matrices represent rotations (and flips) of a space.

The defining property of an orthonormal matrix is that its transpose is its inverse:

```
>>> Q = random_orthonormal_matrix(10)
>>> np.allclose( Q.dot(Q.T), np.identity(10) )
True
```

2.3.5 Pipeline Operators

Fig. 2.6: **LEAP operator pipeline.** This figure depicts a typical LEAP operator pipeline. First is a parent population from which the next operator selects individuals, which are then cloned by the next operator to be followed by operators for mutating and evaluating the individual. (For brevity, a crossover operator was not included, but could also have been freely inserted into this pipeline.) The pool operator is a sink for offspring, and drives the demand for the upstream operators to repeatedly select, clone, mutate, and evaluate individuals repeatedly until the pool has the desired number of offspring. Lastly, another selection operator returns the final set of individuals based on the offspring pool and optionally the parents.

Overview

`leap_ec.individual.Individual`, `leap_ec.problem.Problem`, and `leap_ec.decoder.Decoder` are passive classes that need an external framework to make them function. In *LEAP Concepts* the notion of a pipeline of evolutionary algorithm (EA) operators that use these classes was introduced. That is, *Individual*, *Decoder*, and *Problem* are the "nouns" and the pipeline operators a the verbs that operate on those nouns. The operator pipeline objective is to create a new set of evaluated individuals from an existing set of prospective parents that can be in a new set of prospective parents.

Fig. 2.6 is shown again here to depict a typical set of LEAP pipeline operators. The pipeline generally starts with a "source", or a parent population, from which the next operator typically selects for creating offspring. This is followed by a clone operator that ensure the subsequent pertubation operators do not modify the selected parents. (And so it is critically important that users *always* have a clone operator as a part of the offspring creation pipeline before any mutation, crossover, or other genome altering operators.) The pertubation operators can be mutation or also include a crossover operator. At this point in the pipeline we have a completed offspring with no fitness, so the next operator evaluates the offspring to assign that fitness. Then the evaluated offspring is collected into a pool of offspring that acts as a "sink" for new individuals, and is the principal driving for the pipeline; i.e., it is the need to fill the sink that "pulls" individuals down the pipeline. Once the offspring pool reaches a desired size it returns all the offspring to another selection operator to cull the offspring, and optionally the parents, to return the next set of prospective parents.

Or, more explicitly:

1. Start with a collection of *Individuals* that are prospective parents as the pipeline "source"
2. A selection operator for selecting one or more parents to begin the creation of a new offspring
3. A clone operator that makes a copy of the selected parents to ensure the following operators don't overwrite those parents
4. A set of mutation, crossover, or other operators that perturb the cloned individual's genome, thus (hopefully) giving the new offspring unique values
5. An operator to evaluate the new offspring
6. A pool that serves as a "sink" for evaluated offspring; this pool is sent to the next operator, or is returned from the function, once the pool reaches a specified size
7. Another selection operator to cull the offspring (and optionally parents) to return a population of new prospective parents

This is, the general sequence for most LEAP pipelines, but there will be the occasional variation on this theme. For example, many of the provided "canned" algorithms take just *snippets* of an offspring creation pipeline. E.g., `leap_ec.distributed.asynchronous.steady_state()` has an *offspring_pipeline* parameter that doesn't have parents explicitly as part of the pipeline; instead, for *steady_state()* it's *implied* that the parents will be provided during the run internally.

Implementation Details

The LEAP pipeline is implemented using the `toolz.functoolz.pipe()` function, which has arguments comprised of a collection of data followed by an arbitrary number of functions. When invoked the data is passed as an argument to the first function, and the output of that function is fed as an argument to the next function — this repeats for the rest of the functions. The output of the last function is returned as the overall pipeline output. (See: https://toolz.readthedocs.io/en/latest/api.html#toolz.functoolz.pipe)

Loose-coupling via generator functions

The first "data" argument is a collection of *Individuals* representing prospective parents, which can be a sequence, such as a list or tuple. The design philosophy for the operator functions that follow was to ensure they were as loosely coupled as possible. This was achieved by implementing some operators as generator functions that accept iterators as arguments. That way, new operators can be spliced into the pipeline and they'd automatically "hook up" to their neighbors.

For example, consider the following snippet:

```
gen = 0
while gen < max_generation:
    offspring = toolz.pipe(parents,
                           ops.tournament_selection,
                           ops.clone,
                               mutate_bitflip,
                           ops.evaluate,
                           ops.pool(size=len(parents)))

    parents = offspring
    gen += 1
```

The above code snippet is an example of a very basic genetic algorithm implementation that uses a *toolz.pipe()* function to link together a series of operators to do the following:

1. binary tournament_selection selection on a set of parents
2. clone those that were selected
3. perform mutation bit-bitflip on the clones
4. evaluate the offspring
5. accumulate as many offspring as there are parents

Since we only have mutation in the pipeline, only one parent at a time is selected to be cloned to create an offspring. However, let's make one change to that pipeline by adding crossover:

```
gen = 0
while gen < max_generation:
    offspring = toolz.pipe(parents,
                           ops.tournament_selection,
                           ops.clone,
                               mutate_bitflip,
                           ops.uniform_crossover, # NEW OPERATOR
                           ops.evaluate,
                           ops.pool(size=len(parents)))

    parents = offspring
    gen += 1
```

This does the following:

1. binary tournament_selection selection on a set of parents
2. clone those that were selected
3. perform mutation bitflip on the clones
4. perform uniform crossover between the two offspring

5. evaluate the offspring
6. accumulate as many offspring as there are parents

Adding crossover means that now **two** parents are selected instead of one. However, note that the tournament_selection selection operator wasn't changed. It automatically selects two parents instead of one, as necessary.

Let's take a closer look at *uniform_crossover()* (this is a simplified version; the actual code has more type checking and docstrings).

```
def uniform_crossover(next_individual: Iterator,
                      p_swap: float = 0.5) -> Iterator:
    def _uniform_crossover(ind1, ind2, p_swap):
        for i in range(len(ind1.genome)):
            if random.random() < p_swap:
                ind1.genome[i], ind2.genome[i] = ind2.genome[i], ind1.genome[i]

        return ind1, ind2

    while True:
        parent1 = next(next_individual)
        parent2 = next(next_individual)

        child1, child2 = _uniform_crossover(parent1, parent2, p_swap)

        yield child1
        yield child2
```

Note that the argument *next_individual* is an *Iterator* that "hooks up" to a previously *yielded Individual* from the previous pipeline operator. The *uniform_crossover* operator doesn't care how the previous *Individual* is made, it just has a contract that when *next()* is invoked that it will get another *Individual*. And, since this is a generator function, it *yields* the crossed-over *Individuals*. It also has *two yield* statements that ensures both crossed-over *Individuals* are returned, thus eliminating a potential source of genetic drift by arbitrarily only yielding one and discarding the other.

Operators for collections of *Individuals*

There is another class of operators that work on collections of *Individuals* such as selection and pooling operators. Generally:

***selection* pipeline operators**
: accept a collection of *Individuals* and yield a selected *Individual* (and thus are generator functions)

***pooling* operators**
: accept an *Iterator* from which to get the *next() Individual*, and returns a collection of *Individuals*

Below shows an example of a selection operator, which is a simplified version of the *tournament_selection()* operator:

```
def tournament_selection(population: List, k: int = 2) -> Iterator:
    while True:
        choices = random.choices(population, k=k)
        best = max(choices)

        yield best
```

(Again, the actual *leap_ec.ops.tournament_selection()* has checks and docstrings.)

This depicts how a typical selection pipeline operator works. It accepts a population parameter (plus some optional parameters), and yields the selected individual.

Below is example of a pooling operator:

```
def pool(next_individual: Iterator, size: int) -> List:
    return [next(next_individual) for _ in range(size)]
```

This accepts an *Iterator* from which it gets the next individual, and it uses that iterator to accumulate a specified number of *Individuals* via a list comprehension. Once the desired number of *Individuals* is accumulated, the list of those *Individuals* is returned.

Currying Function Decorators

Some pipeline operators have user-specified parameters. E.g., *leap_ec.ops.pool()* has the mandatory *size* parameter. However, given that *toolz.pipe()* takes functions as parameters, how do we ensure that we pass in functions that have set parameters?

Normally we would use the Standard Python Library's *functools.partial* to set the function parameters and then pass in the function returned from that call. However, *toolz* has a convenient function wrapper that does the same thing, *toolz.functools.curry*. (See: https://toolz.readthedocs.io/en/latest/api.html#toolz.functoolz.curry) Pipeline operators that take on user-settable parameters are all wrapped with *curry* to allow functions with parameters set to be passed into *toolz.pipe()*.

Operator Class

Most of the pipeline operators are implemented as functions. However, from time to time an operator will need to persist state between invocations. For generator functions, that comes with using *yield* in that the next time that function is invoked the next individual is returned. However, there are some operators that use closures, such as *:py:func:leap_ec.ops.migrate*.

In any case, sometimes if one wants persistent state in a pipeline operator a closure or using `yield` isn't enough. In which case, having a *class* that can have objects that persist state might be useful.

To that end, *leap_ec.ops.Operator* is an abstract base-class (ABC) that provides a template of sorts for those kinds of classes. That is, you would write an *Operator* sub-class that provides a *__call__()* member function that would allow objects of that class to be inserted into a LEAP pipeline just like any other operator. Presumably during execution the internal object state would be continually be updated with book-keeping information as *Individuals* flow through it in the pipeline.

leap_ec.ops.CooperativeEvaluate is an example of using this class.

Table of Pipeline Operators

Representation Specificity		Input -> Output	Operator
Representation Agnostic		Iterator → Iterator	clone()
			evaluate()
			uniform_crossover()
			n_ary_crossover()
			CooperativeEvaluate
		Iterator → population	pool()
		population → population	truncation_selection()
			const_evaluate()
			insertion_selection()
			migrate()
		population → Iterator	tournament_selection()
			naive_cyclic_selection()
			cyclic_selection()
			random_selection()
Representation Dependent Dependent	binary_rep	Iterator → Iterator	mutate_bitflip()
	real_rep	Iterator → Iterator	mutate_gaussian()
	int_rep	Iterator → Iterator	mutate_randint()
	segmented_rep	Iterator → Iterator	apply_mutation()
			add_segment()
			remove_segment()
			copy_segment()

Admittedly it can be confusing when considering the full suite of LEAP pipeline operators, especially in remembering what kind of operators "connect" to what. With that in mind, the above table breaks down pipeline operators into different categories. First, there are two broad categories of pipeline operators — operators that don't care about the internal representation of *Individuals*, or "Representation Agnostic" operators; and those operators that do depend on the internal representation, or "Representation Dependent" operators. Most of the operators are "Representation Agnostic" in that it doesn't matter if a given *Individual* has a genome of bits, real-values, or some other representation. Only two operators are dependent on representation, and those will be discussed later.

The next category is broken down by what kind of input and output a given operator takes. That is, generally, an operator takes a population (collection of *Individuals*) or an *Iterator* from which a next *Individual* can be found. Likewise, a given operator can return a population or yield an *Iterator* to a next *Individual*. So, operators that return an *Iterator* can be connected to operators that expect an *Iterator* for input. Similarly, an operator that expects a population can be connected directly to a collection of *Individuals* (e.g., be the second argument to `toolz.pipe()`) or to an operator that returns a collection of *Individuals*.

If you are familiar with evolutionary algorithms, most of these connections are just common sense. For example, selection operators would select from a population.

With regards to "Representation Dependent" operators there currently are only two: `leap_ec.binary_rep.mutate_bitflip()` and `leap_ec.real_rep.mutate_gaussian()`. The former relies on a genome of all bits, and the latter of real-values. In the future, LEAP will support other representations that will similarly have their own operators.

Warning: Are all operators really representation agnostic? In reality, most of the operators assume that *Individual.genome* is a *numpy* array, which may not always be the case. For example, the user may come up with a representation that employs, say, a sparse matrix. In that case, the crossover operators will fail.

In the future we intend on adding support for other popular representations that will show up as LEAP sub-packages. (I.e., just as *binary_rep* and *real_rep* provide support for binary and real-value representations.)

So, in a sense, for where it matters, LEAP currently assumes some sort of sequence for genomes though, again, plans are afoot to add more representation types. In the interim, you will have to add your own operators to support new non-sequence genomic representations.

Type-checking Decorator Functions

However, to help minimize the chances that pipeline operators would be mis-used the operators have function decorates that due parameter type-checking to ensure the correct parameters are being passed in. These are:

iteriter_op
: This checks for signatures of type *Iterator* -> *Iterator*

listlist_op
: Checks for population -> population type operators

listiter_op
: Checks for population -> population type operators

iterlist_op
: Checks for population -> *Iterator* type operators

These can be found in *leap_ec.ops*.

API Documentation

Base operator classes and representation agnostic functions

Fundamental evolutionary operators.

This module provides many of the most important functions that we string together to create EAs out of operator pipelines. You'll find many traditional selection and reproduction strategies here, as well as components for classic algorithms like island models and cooperative coevolution.

Representation-specific operators tend to reside within their own subpackages, rather than here. See for example *leap_ec.real_rep.ops* and *leap_ec.binary_rep.ops*.

class leap_ec.ops.**CooperativeEvaluate**(*num_trials: int*, *collaborator_selector*, *log_stream=None*, *combine=<function concat_combine>*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

Bases: *Operator*

A simple, non-parallel implementation of cooperative coevolutionary fitness evaluation.

Parameters

- **num_trials** (*int*) – the number of combined solutions & fitness estimates to collect when computing a partial solution's fitness.
- **collaborator_selector** – a selection operator that we use to choose individuals from the *other* subpopulations to create a combined solution.
- **context** – the algorithm's state context. Used to access subpopulation information.
- **log_stream** – optional file object to collect statistics about combined individuals to.

- **combine** – the function used to combine partial solutions into combined solutions.

class leap_ec.ops.**Crossover**(*persist_children*, *p_xover*)

Bases: *Operator*

abstract recombine(*parent_a*, *parent_b*)

Perform recombination between two parents to produce two new individuals.

class leap_ec.ops.**NAryCrossover**(*num_points=2*, *p_xover=1.0*, *persist_children=False*)

Bases: *Crossover*

Do crossover between individuals between N crossover points.

1 < n < genome length - 1

We also assume that the passed in individuals are *clones* of parents.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import NAryCrossover
>>> import numpy as np
```

```
>>> genome1 = np.array([0, 0])
>>> genome2 = np.array([1, 1])
>>> first = Individual(genome1)
>>> second = Individual(genome2)
>>> pop = [first, second]
>>> select = naive_cyclic_selection(pop)
```

```
>>> op = NAryCrossover()
>>> result = op(select)
```

```
>>> new_first = next(result)
>>> new_second = next(result)
```

If *persist_children* is True and there is a child that was made by crossover but isn't used in the first call, it will be yielded in a future call.

```
>>> op = NAryCrossover(p_xover=0.0, persist_children=True)
>>>
>>> next(op(select)) is first  # Create an iterator loop with op(select) and␣
↪consume 1 individual
True
>>> next(op(select)) is second # Create a different iterator loop with op(select)
True
```

With *persist_children* set to False, the second child will not be yielded if the iterator is consumed an odd number of times. Instead, on the next call the loop is started anew.

```
>>> op = NAryCrossover(p_xover=0.0, persist_children=False)
>>>
>>> next(op(select)) is first  # Create an iterator loop with op(select) and␣
↪consume 1 individual
True
>>> next(op(select)) is second # Create a different iterator loop with op(select)
False
```

Parameters

- **num_points** – how many crossing points do we use? Defaults to 2, since 2-point crossover has been shown to be the least disruptive choice for this value.
- **p** – the probability that crossover is performed.
- **persist_children** (*bool*) – whether unyielded children should persist between calls. This is useful for *leap_ec.distrib.asynchronous.steady_state*, where the pipeline may only produce one individual at a time.

Returns

a pipeline operator that returns two recombined individuals (with probability p), or two unmodified individuals (with probability 1 - p)

recombine(*parent_a*, *parent_b*)

Perform recombination between two parents to produce two new individuals.

class leap_ec.ops.**Operator**

Bases: ABC

Abstract base class that documents the interface for operators in a LEAP pipeline.

LEAP treats operators as functions of two arguments: the population, and a "context" *dict* that may be used in some algorithms to maintain some global state or parameters independent of the population.

TODO The above description is outdated. –Siggy TODO Also this is for a *population* based operator. We also have operators *for individuals*

You can inherit from this class to define operators as classes. Classes support operators that take extra arguments at construction time (such as a mutation rate) and maintain some internal private state, and they allow certain special patterns (such as multi-function operators).

But inheriting from this class is optional. LEAP can treat any *callable* object that takes two parameters as an operator. You may define your custom operators as closures (which also allow for construction-time arguments and internal state), as simple functions (when no additional arguments are necessary), or as curried functions (i.e. with the help of *toolz.curry(...)*.

class leap_ec.ops.**UniformCrossover**(*p_swap: float = 0.2*, *p_xover: float = 1.0*, *persist_children=False*)

Bases: *Crossover*

Parameterized uniform crossover iterates through two parents' genomes and swaps each of their genes with the given probability.

In a classic paper, De Jong and Spears showed that this operator works particularly well when the swap probability *p_swap* is set to about 0.2. LEAP thus uses this value as its default.

> De Jong, Kenneth A., and W. Spears. "On the virtues of parameterized uniform crossover." *Proceedings of the 4th international conference on genetic algorithms.* Morgan Kaufmann Publishers, 1991.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import UniformCrossover, naive_cyclic_selection
>>> import numpy as np
```

```
>>> genome1 = np.array([0, 0])
>>> genome2 = np.array([1, 1])
>>> first = Individual(genome1)
>>> second = Individual(genome2)
>>> pop = [first, second]
```

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```
>>> select = naive_cyclic_selection(pop)
>>> op = UniformCrossover()
>>> result = op(select)
>>> new_first = next(result)
>>> new_second = next(result)
```

The probability can be tuned via the *p_swap* parameter: >>> op = UniformCrossover(p_swap=0.1) >>> result = op(select)

If *persist_children* is True and there is a child that was made by crossover but isn't used in the first call, it will be yielded in a future call.

```
>>> op = UniformCrossover(p_xover=0.0, persist_children=True)
>>>
>>> next(op(select)) is first  # Create an iterator loop with op(select) and␣
↪consume 1 individual
True
>>> next(op(select)) is second # Create a different iterator loop with op(select)
True
```

With *persist_children* set to False, the second child will not be yielded if the iterator is consumed an odd number of times. Instead, on the next call the loop is started anew.

```
>>> op = UniformCrossover(p_xover=0.0, persist_children=False)
>>>
>>> next(op(select)) is first  # Create an iterator loop with op(select) and␣
↪consume 1 individual
True
>>> next(op(select)) is second # Create a different iterator loop with op(select)
False
```

Parameters

- **p_swap** – how likely are we to swap each pair of genes when crossover is performed
- **p_xover** (*float*) – the probability that crossover is performed in the first place
- **persist_children** (*bool*) – whether unyielded children should persist between calls. This is useful for *leap_ec.distrib.asynchronous.steady_state*, where the pipeline may only produce one individual at a time.

Returns

a pipeline operator that returns two recombined individuals (with probability p_xover), or two unmodified individuals (with probability 1 - p_xover)

recombine(*parent_a*, *parent_b*)

Perform recombination between two parents to produce two new individuals.

leap_ec.ops.**clone**(*next_individual: Iterator = '__no__default__'*) → Iterator

clones and returns the next individual in the pipeline

The clone's fitness is set to None, its parents are set to the individual from which it was cloned (i.e., the parent), and it is assigned its own UUID.

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
```

Create a common decoder and problem for individuals.

```
>>> genome = np.array([1, 1])
>>> original = Individual(genome)
```

```
>>> cloned_generator = clone(iter([original]))
```

Parameters
next_individual – iterator for next individual to be cloned

Returns
copy of next_individual

leap_ec.ops.**compute_expected_probability**(*expected_num_mutations: float*, *individual_genome: List*) → float

Computed the probability of mutation based on the desired average expected mutation and genome length.

The equation here is $p = 1/L *$

Parameters
- **expected_num_mutations** – times individual is to be mutated on average
- **individual_genome** – genome for which to compute the probability

Returns
the corresponding probability of mutation

leap_ec.ops.**compute_population_values**(*population: ~typing.List*, *offset=0*, *exponent: int = 1*, *key=<function <lambda>>*) → ndarray

Returns a list of values where the zero-point of the population is shifted and the values are scaled by exponentiation.

Parameters
- **population** – the population to compute values from.
- **offset** – the offset from zero. Specifying *offset='pop-min'* will use the population's minimum value as the new zero-point. Defaults to 0.
- **exponent** (*int*) – the power to which values are raised to. Defaults to 1.
- **key** – a function that computes a metric based on an *Individual*.

Returns
a numpy array of values that have been shifted by *offset* and scaled by *exponent* corresponding to each individual in the population.

leap_ec.ops.**concat_combine**(*collaborators*)

Combine a list of individuals by concatenating their genomes.

You can choose whether this or some other function is used for combining collaborators by passing it into the *CooperativeEvaluate* constructor.

leap_ec.ops.**const_evaluate**(*population: List = '__no__default__'*, *value='__no__default__'*) → List

An evaluator that assigns a constant fitness to every individual.

This ignores the *Problem* associated with each individual for the purpose of assigning a constant fitness.

This is useful for algorithms that need to assign an arbitrary initial fitness value before using their normal evaluation method. Some forms of cooperative coevolution are an example.

leap_ec.ops.**cyclic_selection**(*population: List = '__no__default__'*) → Iterator

Deterministically returns individuals in order, then shuffles the test_sequence, returns the individuals in that new order, and repeats this process.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import cyclic_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0])),
...        Individual(np.array([0, 1]))]
```

```
>>> cyclic_selector = cyclic_selection(pop)
```

Parameters
population – from which to select

Returns
the next selected individual

leap_ec.ops.**elitist_survival**(*offspring: List = '__no__default__'*, *parents: List = '__no__default__'*, *k: int = 1*, *key=None*) → List

This allows k best parents to compete with the offspring.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> import numpy as np
```

First, let's make a "pretend" population of parents using the MaxOnes problem.

```
>>> pretend_parents = [Individual(np.array([0, 0, 0]), problem=MaxOnes()),
...                    Individual(np.array([1, 1, 1]), problem=MaxOnes())]
```

Then a "pretend" population of offspring. (Pretend in that we're pretending that the offspring came from the parents.)

```
>>> pretend_offspring = [Individual(np.array([0, 0, 0]), problem=MaxOnes()),
...                      Individual(np.array([1, 1, 0]), problem=MaxOnes()),
...                      Individual(np.array([1, 0, 1]), problem=MaxOnes()),
...                      Individual(np.array([0, 1, 1]), problem=MaxOnes()),
...                      Individual(np.array([0, 0, 1]), problem=MaxOnes())]
```

We need to evaluate them to get their fitness to sort them for elitist_survival.

```
>>> pretend_parents = Individual.evaluate_population(pretend_parents)
>>> pretend_offspring = Individual.evaluate_population(pretend_offspring)
```

This will take the best parent, which has [1,1,1], and replace the worst offspring, which has [0,0,0] (because this is the MaxOnes problem) >>> survivors = elitist_survival(pretend_offspring, pretend_parents)

```
>>> assert pretend_parents[1] in survivors # yep, best parent is there
>>> assert pretend_offspring[0] not in survivors # worst guy isn't
```

We orginally ordered 5 offspring, so that's what we better have. >>> assert len(survivors) == 5

Please note that the literature has a number of variations of elitism and other forms of overlapping generations. For example, this may be a good starting point:

De Jong, Kenneth A., and Jayshree Sarma. "Generation gaps revisited." In Foundations of genetic algorithms, vol. 2, pp. 19-28. Elsevier, 1993.

Parameters

- **offspring** – list of created offpring, probably from pool()
- **parents** – list of parents, usually the ones that offspring came from
- **k** – how many elites from parents to keep?
- **key** – optional key criteria for selecting; e.g., can be used to impose parsimony pressure

Returns

surviving population, which will be offspring with offspring replaced by any superior parent elites

leap_ec.ops.**evaluate**(*next_individual: Iterator = '__no__default__'*) → Iterator

Evaluate and returns the next individual in the pipeline

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> import numpy as np
```

We need to specify the decoder and problem so that evaluation is possible.

```
>>> genome = np.array([1, 1])
>>> ind = Individual(genome, decoder=IdentityDecoder(), problem=MaxOnes())
```

```
>>> evaluated_ind = next(evaluate(iter([ind])))
```

Parameters

- **next_individual** – iterator pointing to next individual to be evaluated
- **kwargs** – contains optional context state to pass down the pipeline in context dictionaries

Returns

the evaluated individual

leap_ec.ops.**grouped_evaluate**(*population: list = '__no__default__', max_individuals_per_chunk: int = None*) → list

Evaluate the population by sending groups of multiple individuals to a fitness function so they can be evaluated simultaneously.

This is useful, for example, as a way to evaluate individuals in parallel on a GPU.

leap_ec.ops.**insertion_selection**(*offspring: List = '__no__default__', parents: List = '__no__default__', key=None*) → List

do exclusive selection between offspring and parents

This is typically used for Ken De Jong's EV algorithm for survival selection. Each offspring is deterministically selected and a random parent is selected; if the offspring wins, then it replaces the parent.

Note that we make a _copy_ of the parents and have the offspring compete with the parent copies so that users can optionally preserve the original parents. You may wish to do that, for example, if you want to analyze the composition of the original parents and the modified copy.

Parameters

- **offspring** – population to select from
- **parents** – parents that are copied and which the copies are potentially updated with better offspring
- **key** – optional key for determining max() by other criteria such as for parsimony pressure

Returns
the updated parent population

leap_ec.ops.**iteriter_op**(*f*)

This decorator wraps a function with runtime type checking to ensure that it always receives an iterator as its first argument, and that it returns an iterator.

We use this to make debugging operator pipelines easier in EAs: if you accidentally hook up, say an operator that outputs a list to an operator that expects an iterator, we'll throw an exception that pinpoints the issue.

Parameters
function (*f*) – the function to wrap

leap_ec.ops.**iterlist_op**(*f*)

This decorator wraps a function with runtime type checking to ensure that it always receives an iterator as its first argument, and that it returns a list.

We use this to make debugging operator pipelines easier in EAs: if you accidentally hook up, say an operator that outputs a list to an operator that expects an iterator, we'll throw an exception that pinpoints the issue.

Parameters
function (*f*) – the function to wrap

leap_ec.ops.**listiter_op**(*f*)

This decorator wraps a function with runtime type checking to ensure that it always receives a list as its first argument, and that it returns an iterator.

We use this to make debugging operator pipelines easier in EAs: if you accidentally hook up, say an operator that outputs an iterator to an operator that expects a list, we'll throw an exception that pinpoints the issue.

Parameters
function (*f*) – the function to wrap

leap_ec.ops.**listlist_op**(*f*)

This decorator wraps a function with runtime type checking to ensure that it always receives a list as its first argument, and that it returns a list.

We use this to make debugging operator pipelines easier in EAs: if you accidentally hook up, say an operator that outputs an iterator to an operator that expects a list, we'll throw an exception that pinpoints the issue.

Parameters
function (*f*) – the function to wrap

leap_ec.ops.**migrate**(*topology*, *emigrant_selector*, *replacement_selector*, *migration_gap*, *customs_stamp=<function <lambda>>*, *metric=None*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

A migration operator for use in island models.

This operator works with multi-population algorithms, and is thus meant to used with *leap_ec.algorithm.multi_population_ea*.

Specifically, it assumes that

1. the *population* argument passed into the returned function is a particular sub-population that we want to process "emigration" out of and "immigration" into,
2. the *context* state object contains an integer field *context['leap']['generation']* indicating the current generation count of the algorithm, and
3. the *context* also contains a integer field *context['leap']['current_subpopulation']* indicating the index of the subpopulation that is currently being processed in the overall collection of subpopulations (i.e. the one that *population* belongs to).

These assumptions are essentially what *leap_ec.algorithm.multi_population_ea* implements.

```
>>> import networkx as nx
>>> from leap_ec import ops, context
>>> from leap_ec.data import test_population
>>> pop0 = test_population[:]  # Shallow copy
>>> pop1 = test_population[:]
```

```
>>> op = migrate(topology=nx.complete_graph(2),
...              emigrant_selector=ops.tournament_selection,
...              replacement_selector=ops.random_selection,
...              migration_gap=50)
>>> context['leap']['generation'] = 0
>>> context['leap']['current_subpopulation'] = 0
>>> op(pop0)
[Individual<...>(...), Individual<...>(...), Individual<...>(...), Individual<...>(.
↪..)]
```

```
>>> context['leap']['current_subpopulation'] = 1
>>> op(pop1)
[Individual<...>(...), Individual<...>(...), Individual<...>(...), Individual<...>(.
↪..)]
```

This operator is a stateful closure: it maintains an internal list of all the out-going "emigrations" that occurred in the previous time step, so that it can process them as "immigrations" in the current time step.

Parameters

- **topology** – a *networkx* topology defining the connectivity among islands
- **emigrant_selector** – a selection operator for choosing individuals to leave an island
- **replacement_selector** – a selection operator choosing contestants that will be replaced by an incoming immigrant if the immigrant has higher fitness
- **migration_gap** (*int*) – migration will occur regularly after every *migration_gap* evolutionary steps
- **customs_stamp** – an optional function to transfrom an individual upon its arrival to a new island. This can be used, for example, to change the individual's decoder or problem in a heterogeneous island model.
- **metric** – an optional function of the form *f(generation, immigrant_individual, contestant_indidivudal, success)* for recording information about migration events.
- **context** – the context object to check for EA state, such as the current generation number, and the ID of the subpopulation that is currently being processed.

leap_ec.ops.**migration_metric**(*stream*, *header: bool = True*, *notes: Optional[dict] = None*)

Returns a function that can be used to record migration events.

The purpose of a migration metric is to record information about migrations that occur inside a migration operator. Because these events take place inside the operator (rather than across operators), they cannot be recorded by a LEAP pipeline probe.

In general, the interface for a migration metric function takes four parameters:

- *generation*: the current generation
- *immigrant_ind*: the individual that is attempting to migrate
- *contestant_ind*: the individual that has been chosen to be replaced
- *success*: True if the migration is successful, False otherwise

The metric included here records the fitness of both individuals and writes them (along with the *generation* and *success* values) to a CSV. You can write your own metric if you need to record other information (such as, say, genomes).

```
>>> import sys
>>> from leap_ec import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> m = migration_metric(sys.stdout,
...                      header=True,
...                      notes={'run': 0, 'description': 'Test output'}
... )
run,description,generation,migrant_fitness,contestant_fitness,success
```

```
>>> ind1 = Individual(np.array([1, 1, 1]), problem=MaxOnes())
>>> f = ind1.evaluate()
>>> contestant = Individual(np.array([0, 1, 1]), problem=MaxOnes())
>>> f = contestant.evaluate()
>>> m(0, ind1, contestant, True)
0,Test output,0,3,2,True
```

Parameters

- **stream** – file object to write the CSV data to
- **header** (*bool*) – a CSV header will be written if True
- **notes** (*dict*) – a dict specifying additional constant-value columns to include in the CSV output

leap_ec.ops.**naive_cyclic_selection**(*population: List = '__no__default__'*, *indices: List = None*) → Iterator

Deterministically returns individuals, and repeats the same test_sequence when exhausted.

This is "naive" because it doesn't shuffle the population between complete tours to minimize bias.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import naive_cyclic_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0])),
...        Individual(np.array([0, 1]))]
```

```
>>> cyclic_selector = naive_cyclic_selection(pop)
```

Parameters
population – from which to select

Returns
the next selected individual

leap_ec.ops.**pool**(*next_individual: Iterator = '__no__default__', size: int = '__no__default__'*) → List

'Sink' for creating *size* individuals from preceding pipeline source.

Allows for "pooling" individuals to be processed by next pipeline operator. Typically used to collect offspring from preceding set of selection and birth operators, but could also be used to, say, "pool" individuals to be passed to an EDA as a training set.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import naive_cyclic_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0])),
...        Individual(np.array([0, 1]))]
```

```
>>> cyclic_selector = naive_cyclic_selection(pop)
```

```
>>> pool = pool(cyclic_selector, 3)
```

print(pool) [Individual([0, 0], None, None), Individual([0, 1], None, None), Individual([0, 0], None, None)]

Parameters

- **next_individual** – generator for getting the next offspring
- **size** – how many kids we want

Returns
population of *size* offspring

leap_ec.ops.**proportional_selection**(*population: ~typing.List = '__no__default__', offset=0, exponent: int = 1, key=<function <lambda>>*) → Iterator

Returns an individual from a population in direct proportion to their fitness or another given metric.

To deal with negative fitness values use *offset='pop-min'* or set a custom offset. A *ValueError* is thrown if the result of adding *offset* to a fitness value results in a negative number. The value of an individual is calculated as follows

value = (fitness + offset)^exponent

Parameters

- **population** – the population to select from. Should be a list, not an iterator.
- **offset** – the offset from zero. If negative fitness values are possible and the minimum is unknown use *offest='pop-min'* for an adaptive offset. Defaults to 0.
- **exponent** (*int*) – the power to which fitness values are raised to. This can be tuned to increase or decrease selection pressure by creating larger or smaller differences between fitness values in the population. Defaults to 1.
- **key** – a function that computes the metric used to compare individuals. Defaults to fitness.

Returns
a random individual based on the proportion of the given metric in the population.

```
>>> from leap_ec import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.ops import proportional_selection
>>> import numpy as np
```

```
>>> genome1 = np.array([0, 0, 0])
>>> genome2 = np.array([0, 0, 1])
>>> pop = [Individual(genome1, problem=MaxOnes()),
...        Individual(genome2, problem=MaxOnes())]
>>> pop = Individual.evaluate_population(pop)
>>> selected = proportional_selection(pop)
```

leap_ec.ops.**random_bernoulli_vector**(*shape: Union[int, Tuple]*, *p: float = 0.5*) → ndarray

Generates a random vector of Boolean balues from a Bernoulli process—that is, from a sequence of weighted coin flips.

We use this function throughout LEAP because its implementation was found to be much faster than, say, just calling *np.random.choice([0, 1])*.

```
>>> from leap_ec.ops import random_bernoulli_vector
>>> random_bernoulli_vector(5, p=0.4)
array([..., ..., ..., ..., ...])
```

Parameters

- **shape** – shape of the random vector—can be an integer or a tuple.
- **p** – success probability of the bernoulli trials.

Returns
boolean numpy array

leap_ec.ops.**random_selection**(*population: List = '__no__default__'*, *indices=None*) → Iterator

return a uniformly randomly selected individual from the population

Parameters
population – from which to select

Returns
a uniformly selected individual

leap_ec.ops.**sus_selection**(*population: ~typing.List = '__no__default__'*, *n=None*, *shuffle: bool = True*, *offset=0*, *exponent: int = 1*, *key=<function <lambda>>*) → Iterator

Returns an individual from a population in proportion to their fitness or another given metric using the stochastic universal sampling algorithm.

To deal with negative fitness values use *offset='pop-min'* or set a custom offset. A *ValueError* is thrown if the result of adding *offset* to a fitness value results in a negative number. The value of an individual is calculated as follows

value = (fitness + offset)^exponent

Parameters

- **population** – the population to select from. Should be a list, not an iterator.

- **n** – the number of evenly spaced points to use in the algorithm. Default is None which uses *len(population)*.
- **shuffle** (*bool*) – if True, *n* points are resampled after one full pass over them. If False, selection repeats over the same *n* points. Defaults to True.
- **offset** – the offset from zero. If negative fitness values are possible and the minimum is unknown use *offset='pop-min'* for an adaptive offset. Defaults to 0.
- **exponent** (*int*) – the power to which fitness values are raised to. This can be tuned to increase or decrease selection pressure by creating larger or smaller differences between fitness values in the population. Defaults to 1.
- **key** – a function that computes the metric used to compare individuals. Defaults to fitness.

Returns

a random individual based on the proportion of the given metric in the population.

```
>>> from leap_ec import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.ops import sus_selection
>>> import numpy as np
```

```
>>> genome1 = np.array([0, 0, 0])
>>> genome2 = np.array([1, 1, 1])
>>> pop = [Individual(genome1, problem=MaxOnes()),
...        Individual(genome2, problem=MaxOnes())]
>>> pop = Individual.evaluate_population(pop)
>>> selected = sus_selection(pop)
```

leap_ec.ops.**tournament_selection**(*population: list = '__no__default__', k: int = 2, key=None, select_worst: bool = False, indices=None*) → Iterator

Returns an operator that selects the best individual from k individuals randomly selected from the given population.

Like other selection operators, this assumes that if one individual is "greater than" another, then it is "better than" the other. Whether this indicates maximization or minimization isn't handled here: the *Individual* class determines the semantics of its "greater than" operator.

Parameters

- **population** – the population to select from. Should be a list, not an iterator.
- **k** (*int*) – number of contestants in the tournament. k=2 does binary tournament selection, which approximates linear ranking selection in the expectation. Higher values of k yield greedier selection strategies—k=3, for instance, is equal to quadratic ranking selection in the expectation.
- **key** – an optional function that computes keys to sort over. Defaults to None, in which case Individuals are compared directly.
- **select_worst** (*bool*) – if True, select the worst individual from the tournament instead of the best.
- **indices** (*list*) – an optional list that will be populated with the index of the selected individual.

Returns

the best of k individuals drawn from population

```
>>> from leap_ec import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.ops import tournament_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0, 0]), problem=MaxOnes()),
...        Individual(np.array([0, 0, 1]), problem=MaxOnes())]
>>> pop = Individual.evaluate_population(pop)
>>> best = tournament_selection(pop)
```

leap_ec.ops.**truncation_selection**(*offspring: List = '__no__default__'*, *size: int = '__no__default__'*, *parents: List = None*, *key=None*) → List

return the *size* best individuals from the given population

This defaults to (mu, lambda) if *parents* is not given.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.ops import truncation_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0, 0]), problem=MaxOnes()),
...        Individual(np.array([0, 0, 1]), problem=MaxOnes()),
...        Individual(np.array([1, 1, 0]), problem=MaxOnes()),
...        Individual(np.array([1, 1, 1]), problem=MaxOnes())]
```

We need to evaluate them to get their fitness to sort them for truncation.

```
>>> pop = Individual.evaluate_population(pop)
```

```
>>> truncated = truncation_selection(pop, 2)
```

TODO Do we want an optional context to over-ride the 'parents' parameter?

Parameters

- **offspring** – offspring to truncate down to a smaller population
- **size** – is what to resize population to
- **second_population** – is optional parent population to include with population for down-sizing

Returns

truncated population

Pipeline operators for binary representations

Binary representation specific pipeline operators.

leap_ec.binary_rep.ops.**genome_mutate_bitflip**(*genome: ndarray = '__no__default__'*, *expected_num_mutations: float = None*, *probability: float = None*) → ndarray

Perform bitflip mutation on a particular genome.

This function can be used by more complex operators to mutate a full population (as in *mutate_bitflip*), to work with genome segments (as in *leap_ec.segmented.ops.apply_mutation*), etc. This way we don't have to copy-and-paste the same code for related operators.

Parameters

- **genome** – of binary digits that we will be mutating
- **expected_num_mutations** – on average how many mutations are we expecting?

Returns
mutated genome

leap_ec.binary_rep.ops.**mutate_bitflip**(*next_individual: Iterator = '__no__default__'*, *expected_num_mutations: float = None*, *probability: float = None*) → Iterator

Perform bit-flip mutation on each individual in an iterator (population).

This assumes that the genomes have a binary representation.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.ops import mutate_bitflip
>>> import numpy as np
```

```
>>> original = Individual(np.array([1, 1]))
>>> op = mutate_bitflip(expected_num_mutations=1)
>>> pop = iter([original])
>>> mutated = next(op(pop))
```

Parameters

- **next_individual** – to be mutated
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)
- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)

Returns
mutated individual

leap_ec.binary_rep.ops.**random**() → x in the interval [0, 1).

Pipeline operators for real-valued representations

Pipeline operators for real-valued representations

leap_ec.real_rep.ops.**apply_hard_bounds**(*genome*, *hard_bounds*)

A helper that ensures that every gene is contained within the given bounds.

Parameters

- **genome** – list of values to apply bounds to.
- **hard_bounds** – if a *(low, high)* tuple, the same bounds will be used for every gene. If a list of tuples is given, then the ith bounds will be applied to the ith gene.

Both sides of the range are inclusive:

```
>>> genome = np.array([0, 10, 20, 30, 40, 50])
>>> apply_hard_bounds(genome, hard_bounds=(20, 40))
array([20, 20, 20, 30, 40, 40])
```

Different bounds can be used for each locus by passing in a list of tuples:

```
>>> bounds= [ (0, 1), (0, 1), (50, 100), (50, 100), (0, 100), (0, 10) ]
>>> apply_hard_bounds(genome, hard_bounds=bounds)
array([ 0,  1, 50, 50, 40, 10])
```

leap_ec.real_rep.ops.**genome_mutate_gaussian**(*genome='__no__default__'*, *std: float = '__no__default__'*, *expected_num_mutations='__no__default__'*, *bounds: Tuple[float, float] = (-inf, inf)*, *transform_slope: float = 1.0*, *transform_intercept: float = 0.0*)

Perform Gaussian mutation directly on real-valued genes (rather than on an Individual).

This used to be inside *mutate_gaussian*, but was moved outside it so that *leap_ec.segmented.ops.apply_mutation* could directly use this function, thus saving us from doing a copy-n-paste of the same code to the segmented sub-package.

Parameters

- **genome** – of real-valued numbers that will potentially be mutated
- **std** – the mutation width—either a single float that will be used for all genes, or a list of floats specifying the mutation width for each gene individually.
- **expected_num_mutations** – on average how many mutations are expected

Returns

mutated genome

leap_ec.real_rep.ops.**mutate_gaussian**(*next_individual: Iterator = '__no__default__'*, *std='__no__default__'*, *expected_num_mutations: Union[int, str] = None*, *bounds=(-inf, inf)*, *transform_slope: float = 1.0*, *transform_intercept: float = 0.0*) → Iterator

Mutate and return an Individual with a real-valued representation.

This operators on an iterator of Individuals:

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.real_rep.ops import mutate_gaussian
>>> import numpy as np
>>> pop = iter([Individual(np.array([1.0, 0.0]))])
```

Mutation can either use the same parameters for all genes:

```
>>> op = mutate_gaussian(std=1.0, expected_num_mutations='isotropic', bounds=(-5,␣
↪5))
>>> mutated = next(op(pop))
```

Or we can specify the *std* and *bounds* independently for each gene:

```
>>> pop = iter([Individual(np.array([1.0, 0.0]))])
>>> op = mutate_gaussian(std=[0.5, 1.0],
...                      expected_num_mutations='isotropic',
...                      bounds=[(-1, 1), (-10, 10)]
... )
>>> mutated = next(op(pop))
```

Parameters

- **next_individual** – to be mutated
- **std** – standard deviation to be equally applied to all individuals; this can be a scalar value or a "shadow vector" of standard deviations
- **expected_num_mutations** – if an int, the *expected* number of mutations per individual, on average. If 'isotropic', all genes will be mutated.
- **bounds** – to clip for mutations; defaults to (- ∞, ∞)

Returns

a generator of mutated individuals.

Pipeline operators for segmented representations

Segmented representation specific pipeline operators.

`leap_ec.segmented_rep.ops.`**add_segment**(*next_individual: Iterator = '__no__default__', seq_initializer: Callable = '__no__default__', probability: float = '__no__default__', append: bool = False*) → Iterator

Possibly add a segment to the given individual

New segments can be always appended, or randomly inserted within the individual's genome.

TODO add a parameter for accepting a function that will yield a distribution for the number of segments to be randomly inserted.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> import numpy as np
>>> original = Individual([np.array([0, 0]), np.array([1, 1])])
>>> mutated = next(add_segment(iter([original]),
...                seq_initializer=create_binary_sequence(2),
...                probability=1.0))
```

Parameters

- **next_individual** – to possibly add a segment
- **seq_initializer** – callable for initializing any new segments

- **probability** – likelihood of adding a segment
- **append** – if True, always append any new segments

Returns
yielded individual with a possible new segment

leap_ec.segmented_rep.ops.**apply_mutation**(*next_individual: Iterator = '__no__default__', mutator: Callable[[list, float], list] = '__no__default__'*) → Iterator

This expects next_individual to have a segmented representation; i.e., a test_sequence of sequences. *mutator* will be applied separately to each sub-test_sequence.

```
>>> from leap_ec.binary_rep.ops import genome_mutate_bitflip
>>> mutation_op = apply_mutation(
...     mutator=genome_mutate_bitflip(
...                 expected_num_mutations=0.5
...  ))
>>> import numpy as np
```

```
>>> from leap_ec.individual import Individual
>>> original = Individual(np.array([[0, 0], [1, 1]]))
>>> mutated = next(mutation_op(iter([original])))
```

Parameters

- **next_individual** – to possibly mutate
- **mutator** – function to be applied to each segment in the individual's genome; first argument is a segment, the second the expected probability of mutating each segment element.

Returns
yielded mutated individual

leap_ec.segmented_rep.ops.**copy_segment**(*next_individual: Iterator = '__no__default__', probability: float = '__no__default__', append: bool = False*) → Iterator

with a given probability, randomly select and copy a segment

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> original = Individual([np.array([0, 0])])
>>> mutated = next(copy_segment(iter([original]), probability=1.0))
>>> assert np.all(mutated.genome[0] == [0, 0])            and np.all(mutated.
↪genome[1] == [0, 0])
```

param next_individual
to have a segment possibly removed

param probability
likelihood of doing this

param append
if True, always append any new segments

returns
the next individual

leap_ec.segmented_rep.ops.**remove_segment**(*next_individual: Iterator = '__no__default__', probability: float = '__no__default__'*) → Iterator

for some chance, remove a segment

Nothing happens if the individual has a single segment; i.e., there is no chance for an empty individual to be returned.

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> original = Individual([np.array([0, 0]), np.array([1, 1])])
>>> mutated = next(remove_segment(iter([original]), probability=1.0))
>>> assert np.all(mutated.genome[0] == [0, 0])             or np.all(mutated.
↪genome[0] == [1, 1])
```

param next_individual
to have a segment possibly removed

param probability
likelihood of removing a segment

returns
the next individual

leap_ec.segmented_rep.ops.**segmented_mutate**(*next_individual: Iterator = '__no__default__', mutator_functions: list = '__no__default__'*)

A mutation operator that applies a different mutation operator to each segment of a segmented genome.

2.3.6 Context

From time to time pipeline operators need to consult some sort of state such as the current generation. E.g., *ops.migrate* uses the *context* to track subpopulations.

context is found in *leap_ec.context* and is just a dictionary. The default element, *leap*, is reserved for LEAP data.

Summary of current *leap_ec.context* reserved state:

- ***context['leap']* is for storing general LEAP running state, such as current** generation.
- *context['leap']['distributed']* is for storing *leap.distributed* running state
- ***context['leap']['distributed']['non_viable']* accumulates counts of non-viable** individuals during *distributed.eval_pool()* and *distributed.async_eval_pool()* runs.

2.3.7 Probes

Probes are special pipeline operators that can be used to echo state of passing individuals or other data. For example, you might want to print the state of an individual with two probes, one before a mutation operator is applied, and another afterwards to observe the effects of mutation.

These are probes do more than passive reporting of data that passes through the pipeline – they actually do some data processing and report that.

Probes are pipeline operators to instrument state that passes through the pipeline such as populations or individuals.

class leap_ec.probe.**AttributesCSVProbe**(*attributes=()*, *stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *do_dataframe=False*, *best_only=False*, *header=True*, *do_fitness=False*, *do_genome=False*, *notes=None*, *extra_metrics=None*, *job=None*, *numpy_as_list=True*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

An operator that records the specified attributes for all the individuals (or just the best individual) in *population* in CSV-format to the specified stream and/or to a DataFrame.

Parameters

- **attributes** – list of attribute names to record, as found in the individuals' *attributes* field
- **stream** – a file object to write the CSV rows to (defaults to sys.stdout). Can be *None* if you only want a DataFrame
- **do_dataframe** (*bool*) – if True, data will be collected in memory as a Pandas DataFrame, which can be retrieved by calling the *dataframe* property after (or during) the algorithm run. Defaults to False, since this can consume a lot of memory for long-running algorithms.
- **best_only** (*bool*) – if True, attributes will only be recorded for the best-fitness individual; otherwise a row is recorded for every individual in the population
- **header** (*bool*) – if True (the default), a CSV header is printed as the first row with the column names
- **do_fitness** (*bool*) – if True, the individuals' fitness is included as one of the columns
- **do_genomes** (*bool*) – if True, the individuals' genome is included as one of the columns
- **notes** (*str*) – a dict of optional constant-value columns to include in all rows (ex. to identify and experiment or parameters)
- **extra_metrics** – a dict of *'column_name': function* pairs, to compute optional extra columns. The functions take a the population as input as a list of individuals, and their return value is printed in the column.
- **job** (*int*) – a job ID that will be included as a constant-value column in all rows (ex. typically an integer, indicating the ith run out of many)
- **numpy_as_list** (*bool*) – if True, numpy arrays will be first converted to a python list before printing. This is intended for large genomes and multiobjective fitnesses, where large numpy arrays would be split across multiple csv rows by the default formatter.
- **context** – the algorithm context we use to read the current generation from (so we can write it to a column)

Individuals contain some build-in attributes (namely fitness, genome), and also a *dict* of additional custom attributes called, well, *attributes*. This class allows you to log all of the above.

Most often, you will want to record only the best individual in the population at each step, and you'll just want to know its fitness and genome. You can do this with this class's boolean flags. For example, here's how you'd record the best individual's fitness and genome to a dataframe:

```
>>> from leap_ec.global_vars import context
>>> from leap_ec.data import test_population
>>> probe = AttributesCSVProbe(do_dataframe=True, best_only=True,
...                            do_fitness=True, do_genome=True)
>>> context['leap']['generation'] = 100
>>> probe(test_population) == test_population
True
```

You can retrieve the result programatically from the *dataframe* property:

```
>>> probe.dataframe
   step  fitness           genome
0   100        4  [0, 1, 1, 1, 1]
```

By default, the results are also written to *sys.stdout*. You can pass any file object you like into the *stream* parameter.

Another common use of this task is to record custom attributes that are stored on individuals in certain kinds of experiments. Here's how you would record the values of *ind.foo* and *ind.bar* for every individual in the population. We write to a stream object this time to demonstrate how to use the probe without a dataframe:

```
>>> import io
>>> stream = io.StringIO()
>>> probe = AttributesCSVProbe(attributes=['foo', 'bar'], stream=stream)
>>> context['leap']['generation'] = 100
>>> r = probe(test_population)
>>> print(stream.getvalue())
step,foo,bar
100,GREEN,Colorless
100,15,green
100,BLUE,ideas
100,72.81,sleep
```

property dataframe

Property for retrieving a Pandas DataFrame representation of the collected data.

get_row_dict(*ind*)

Compute a full row of data from a given individual.

class leap_ec.probe.**BestSoFarIterProbe**(*stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *header=True*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

This probe takes an iterator as input and will track the
best-so-far (BSF) individual in the all the individuals it sees.

Insert an object of this class into a pipeline to have it track the the best individual it sees so far. It will write the current best individual for each __call__ invocation to a given stream in CSV format.

Like many operators, this operator checks the context object to retrieve the current generation number for output purposes.

```
>>> from leap_ec import context, data
>>> from leap_ec import probe
>>> pop = data.test_population
>>> context['leap']['generation'] = 12
```

The probe will write its output to the provided stream (default is stdout, but we illustrate here with a StringIO stream):

```
>>> import io
>>> stream = io.StringIO()
>>> probe = BestSoFarIterProbe(stream=stream)
>>> bsf_output_iter = probe(iter(pop))
```

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```
>>> x = next(bsf_output_iter)
>>> x = next(bsf_output_iter)
>>> x = next(bsf_output_iter)
>>> print(stream.getvalue())
step,bsf
12,...
12,...
12,...
```

class leap_ec.probe.**BestSoFarProbe**(*stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *header=True*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

This probe takes an list of individuals as input and will track the
best-so-far (BSF) individual across all the population it has seen.

Insert an object of this class into a pipeline to have it track the the best individual it sees so far. It will write the current best individual for each __call__ invocation to a given stream in CSV format.

Like many operators, this operator checks the context object to retrieve the current generation number for output purposes.

```
>>> from leap_ec import context, data
>>> from leap_ec import probe
>>> pop = data.test_population
>>> context['leap']['generation'] = 12
```

The probe will write its output to the provided stream (default is stdout, but we illustrate here with a StringIO stream):

```
>>> import io
>>> stream = io.StringIO()
>>> probe = BestSoFarProbe(stream=stream)
>>> new_pop = probe(pop)
>>> print(stream.getvalue())
step,bsf
12,4
```

This operator does not change the state of the population: >>> new_pop == pop True

class leap_ec.probe.**CartesianPhenotypePlotProbe**(*ax=None*, *xlim=(-5.12, 5.12)*, *ylim=(-5.12, 5.12)*, *contours=None*, *granularity=None*, *title='Cartesian Phenotypes'*, *modulo=1*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*, *pad=()*)

Measure and plot a scatterplot of the populations' location in a 2-D phenotype space.

Parameters

- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **xlim** (*(float, float)*) – Bounds of the horizontal axis.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **contours** (*Problem*) – a problem defining a 2-D fitness function (this will be used to draw fitness contours in the background of the scatterplot).

- **granularity** (*float*) – (Optional) spacing of the grid to sample points along while drawing the fitness contours. If none is given, then the granularity will default to 1/50th of the range of the function's *bounds* attribute.
- **modulo** (*int*) – take and plot a measurement every *modulo* steps (default 1).
- **pad** – A list of extra gene values, used to fill in the hidden dimensions with contants while drawing fitness contours.

Attach this probe to matplotlib `Axes` and then insert it into an EA's operator pipeline to get a live phenotype plot that updates every *modulo* steps.

```
>>> import matplotlib.pyplot as plt
>>> from leap_ec.probe import CartesianPhenotypePlotProbe
>>> from leap_ec.representation import Representation
```

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.algorithm import generational_ea
```

```
>>> from leap_ec import ops
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.real_rep.problems import CosineFamilyProblem
>>> from leap_ec.real_rep.initializers import create_real_vector
>>> from leap_ec.real_rep.ops import mutate_gaussian
```

```
>>> # The fitness landscape
>>> problem = CosineFamilyProblem(alpha=1.0, global_optima_counts=[2, 2], local_
↪optima_counts=[2, 2])
```

```
>>> # If no axis is provided, a new figure will be created for the probe to write to
>>> trajectory_probe = CartesianPhenotypePlotProbe(contours=problem,
...                                                xlim=(0, 1), ylim=(0, 1),
...                                                granularity=0.025)
```

```
>>> # Create an algorithm that contains the probe in the operator pipeline
```

```
>>> pop_size = 100
>>> ea = generational_ea(max_generations=20, pop_size=pop_size,
...                      problem=problem,
...
...                      representation=Representation(
...                         individual_cls=Individual,
...                         initialize=create_real_vector(bounds=[[0.4, 0.6]] * 2),
...                         decoder=IdentityDecoder()
...                      ),
...
...                      pipeline=[
...                         trajectory_probe,  # Insert the probe into the pipeline␣
↪like so
...                         ops.tournament_selection,
...                         ops.clone,
...                         mutate_gaussian(std=0.05, expected_num_mutations=
↪'isotropic', bounds=(0, 1)),
```

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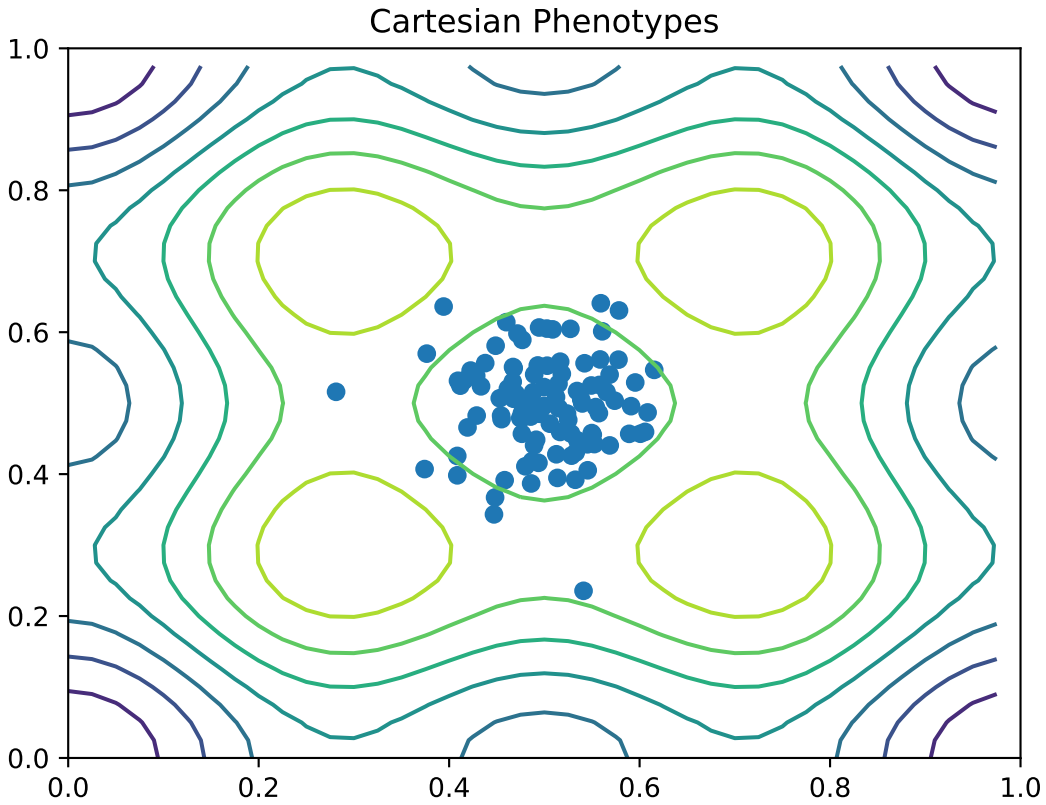
```
...                         ops.evaluate,
...                         ops.pool(size=pop_size)
...                     ])
>>> result = list(ea);
```



class leap_ec.probe.**FitnessPlotProbe**(*ax=None*, *xlim=None*, *ylim=None*, *modulo=1*, *title='Best-of-Generation Fitness'*, *x_axis_value=None*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

Measure and plot a population's fitness trajectory.

Parameters

- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **xlim** (*(float, float)*) – Bounds of the horizontal axis.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **modulo** (*int*) – take and plot a measurement every *modulo* steps (default 1).
- **title** – title to print on the plot
- **x_axis_value** – optional function to define what value gets plotted on the x axis. Defaults to pulling the 'generation' value out of the default *context* object.

- **context** – set a context object to query for the current generation. Defaults to the standard *leap_ec.context* object.

Attach this probe to matplotlib `Axes` and then insert it into an EA's operator pipeline.

```
>>> import matplotlib.pyplot as plt
>>> from leap_ec.probe import FitnessPlotProbe
>>> from leap_ec.representation import Representation
```

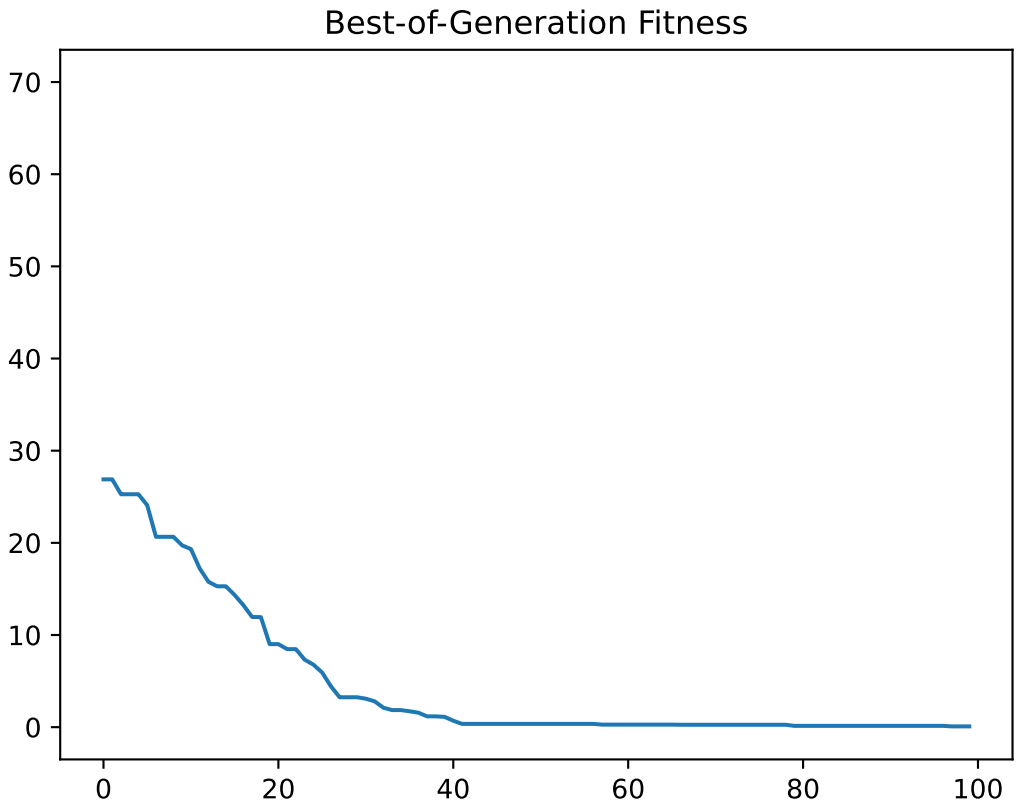
```
>>> f = plt.figure()  # Setup a figure to plot to
>>> plot_probe = FitnessPlotProbe(ylim=(0, 70), ax=plt.gca())
```

```
>>> # Create an algorithm that contains the probe in the operator pipeline
>>> from leap_ec.individual import Individual
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec import ops
>>> from leap_ec.real_rep.problems import SpheroidProblem
>>> from leap_ec.real_rep.ops import mutate_gaussian
>>> from leap_ec.real_rep.initializers import create_real_vector
```

```
>>> from leap_ec.algorithm import generational_ea
```

```
>>> l = 10
>>> pop_size = 10
>>> ea = generational_ea(max_generations=100, pop_size=pop_size,
...                      problem=SpheroidProblem(maximize=False),
...
...                      representation=Representation(
...                         individual_cls=Individual,
...                         decoder=IdentityDecoder(),
...                         initialize=create_real_vector(bounds=[[-5.12, 5.12]] *␣
↪l)
...                      ),
...
...                      pipeline=[
...                         plot_probe,  # Insert the probe into the pipeline like␣
↪so
...                         ops.tournament_selection,
...                         ops.clone,
...                         mutate_gaussian(std=0.2, expected_num_mutations=
↪'isotropic'),
...                         ops.evaluate,
...                         ops.pool(size=pop_size)
...                      ])
>>> result = list(ea);
```

To get a live-updated plot that words like a real-time video of the EA's progress, use this probe in conjunction with the *%matplotlib notebook* magic for Jupyter Notebook (as opposed to *%matplotlib inline*, which only allows static plots).


Best-of-Generation Fitness
70
60
50
40
30
20
10
0
0
20
40
60
80
100

class leap_ec.probe.**FitnessStatsCSVProbe**(*stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *header=True*, *extra_metrics=None*, *comment=None*, *job: ~typing.Optional[str] = None*, *notes: ~typing.Optional[~typing.Dict] = None*, *modulo: int = 1*, *numpy_as_list=True*, *context: ~typing.Dict = {'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

A probe that records basic fitness statistics for a population to a text stream in CSV format.

This is meant to capture the "bread and butter" values you'll typically want to see in any population-based optimization experiment. If you want additional columns with custom values, you can pass in a dict of *notes* with constant values or *extra_metrics* with functions to compute them.

Parameters

- **stream** – the file object to write to (defaults to sys.stdout)
- **header** – whether to print column names in the first line
- **extra_metrics** – a dict of *'column_name': function* pairs, to compute optional extra columns. The functions take a the population as input as a list of individuals, and their return value is printed in the column.
- **job** – optional constant job ID, which will be printed as the first column
- **notes** (*str*) – a dict of optional constant-value columns to include in all rows (ex. to identify and experiment or parameters)
- **numpy_as_list** (*bool*) – if True, numpy arrays will be first converted to a python list before printing. This is intended for multiobjective fitnesses, where large numpy arrays are normally split across csv rows with the default formatter.
- **context** – a LEAP context object, used to retrieve the current generation from the EA state (i.e. from *context['leap']['generation']*)

In this example, we'll set up two three inputs for the probe: an output stream, the generation number, and a population.

We use a *StringIO* stream to print the results here, but in practice you often want to use *sys.stdout* (the default) or a file object:

```
>>> import io
>>> stream = io.StringIO()
```

The probe also relies on LEAP's algorithm *context* to determine the generation number:

```
>>> from leap_ec.global_vars import context
>>> context['leap']['generation'] = 100
```

Here's how we'd compute fitness statistics for a test population. The population is unmodified:

```
>>> from leap_ec.data import test_population
>>> probe = FitnessStatsCSVProbe(stream=stream, job=15, notes={'description': 'just␣
↪a test'})
>>> probe(test_population) == test_population
True
```

and the output has the following columns: >>> print(stream.getvalue()) job, description, step, bsf, mean_fitness, std_fitness, min_fitness, max_fitness 15, just a test, 100, 4, 2.5, 1.11803…, 1, 4 <BLANKLINE>

To add custom columns, use the *extra_metrics* dict. For example, here's a function that computes the median fitness value of a population:

```
>>> import numpy as np
>>> median = lambda p: np.median([ ind.fitness for ind in p ])
```

We can include it in the fitness stats report like so:

```
>>> stream = io.StringIO()
>>> extras_probe = FitnessStatsCSVProbe(stream=stream, job="15", extra_metrics={
↪'median_fitness': median})
>>> extras_probe(test_population) == test_population
True
```

```
>>> print(stream.getvalue())
job, step, bsf, mean_fitness, std_fitness, min_fitness, max_fitness, median_fitness
15, 100, 4, 2.5, 1.11803..., 1, 4, 2.5
```

comment_character = '#'

default_metric_cols = ('bsf', 'mean_fitness', 'std_fitness', 'min_fitness', 'max_fitness')

time_col = 'step'

write_comment(*stream*)

write_header(*stream*)

class leap_ec.probe.**HeatMapPhenotypeProbe**(*ax=None*, *title='HeatMap of Phenotypes'*, *modulo=1*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

class leap_ec.probe.**HistPhenotypePlotProbe**(*ax=None*, *title='Histogram of Phenotypes'*, *modulo=1*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

A visualization probe that uses matplotlib to show a live histogram of the population's phenotypes.

This typically makes the most since for 1-dimensional genotypes.

class leap_ec.probe.**PopulationMetricsPlotProbe**(*ax=None*, *metrics=None*, *xlim=None*, *ylim=None*, *modulo=1*, *title='Population Metrics'*, *x_axis_value=None*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

reset()

class leap_ec.probe.**SumPhenotypePlotProbe**(*ax=None*, *xlim=(-5.12, 5.12)*, *ylim=(-5.12, 5.12)*, *problem=None*, *granularity=1*, *title='Sum Phenotypes'*, *modulo=1*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

Plot the population's location on a fitness landscape that is defined over the sum of a vector phenotype's elements. This is useful for visualizing OneMax functions and similar functions that can be understood in terms of a graph with "the number of ones" along the x axis.

Parameters

- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **xlim** (*(float, float)*) – Bounds of the horizontal axis.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **problem** (*Problem*) – a problem that will be used to draw a fitness curve.
- **granularity** (*float*) – (Optional) spacing of the grid to sample points along while drawing the fitness contours. If none is given, then the granularity will default to 1.0.
- **modulo** (*int*) – take and plot a measurement every *modulo* steps (default 1).

Attach this probe to matplotlib `Axes` and then insert it into an EA's operator pipeline to get a live phenotype plot that updates every *modulo* steps.

```
>>> import matplotlib.pyplot as plt
>>> from leap_ec.probe import SumPhenotypePlotProbe
>>> from leap_ec.representation import Representation
```

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.algorithm import generational_ea
```

```
>>> from leap_ec import ops
>>> from leap_ec.binary_rep.problems import DeceptiveTrap
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> from leap_ec.binary_rep.ops import mutate_bitflip
```

```
>>> # The fitness landscape
>>> problem = DeceptiveTrap()
```

```
>>> # If no axis is provided, a new figure will be created for the probe to write to
>>> dimensions = 20
>>> trajectory_probe = SumPhenotypePlotProbe(problem=problem,
...                                          xlim=(0, dimensions), ylim=(0,␣
↪dimensions))
```

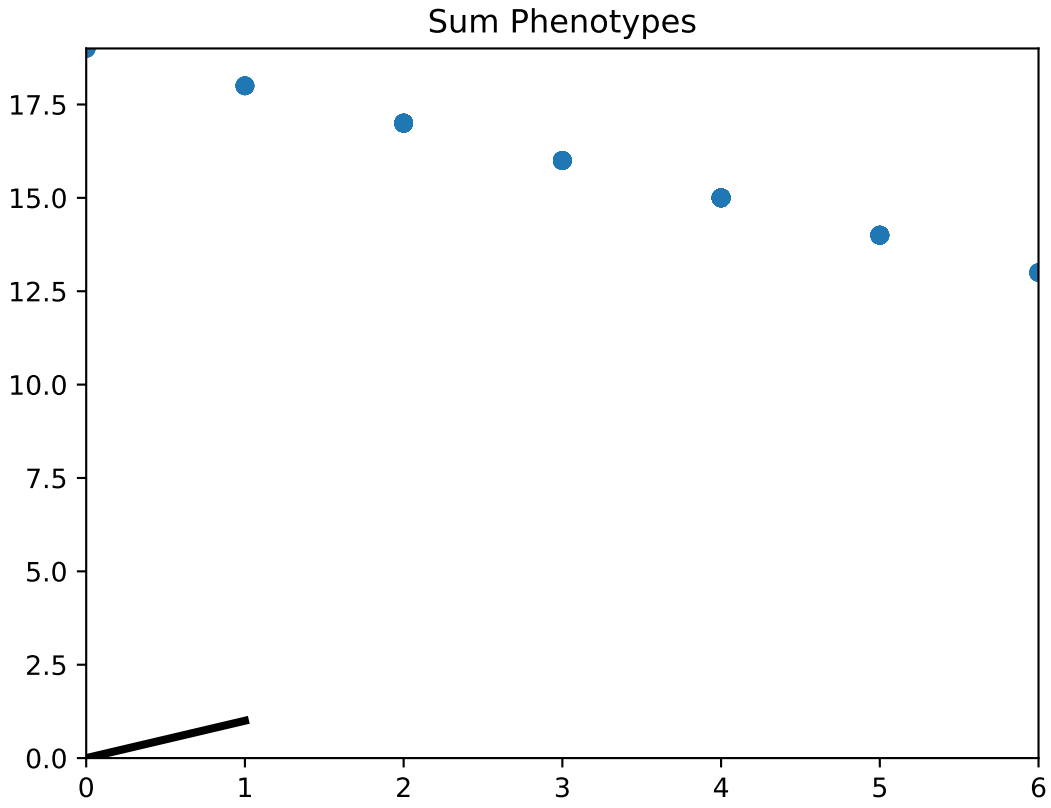
```
>>> # Create an algorithm that contains the probe in the operator pipeline
```

```
>>> pop_size = 100
>>> ea = generational_ea(max_generations=20, pop_size=pop_size,
...                      problem=problem,
...
...                      representation=Representation(
...                         individual_cls=Individual,
...                         initialize=create_binary_sequence(length=dimensions)
...                      ),
...
...                      pipeline=[
...                         trajectory_probe,  # Insert the probe into the pipeline␣
↪like so
...                         ops.tournament_selection,
...                         ops.clone,
...                         mutate_bitflip(expected_num_mutations=1),
...                         ops.evaluate,
```

(continues on next page)

(continued from previous page)

```
...                         ops.pool(size=pop_size)
...                     ])
>>> result = list(ea);
```



leap_ec.probe.**best_of_gen**(*population*)

Syntactic sugar to select the best individual in a population.

Parameters

- **population** – a list of individuals
- **context** – optional *dict* of auxiliary state (ignored)

```
>>> from leap_ec.data import test_population
>>> print(best_of_gen(test_population))
Individual<...> with fitness 4
```

leap_ec.probe.**num_fixated_metric**(*population: list*)

Computes the genetic diversity of the population by counting the number of variables in the genome that have zero variance.

This is a so-called "column-wise" metric, in the sense that it considers each element of the solution vectors independently.

leap_ec.probe.**pairwise_squared_distance_metric**(*population: list*)

Computes the genetic diversity of a population by considering the sum of squared Euclidean distances between individual genomes.

We compute this in $O(n)$ by writing the sum in terms of distance from the population centroid c:

$$\mathcal{D}(\text{population}) = \sum_{i=1}^{n}\sum_{j=1}^{n}\|x_i - x_j\|^2 = 2n\sum_{i=1}^{n}\|x_i - c\|^2$$

leap_ec.probe.**print_individual**(*next_individual: ~typing.Iterator = '__no__default__', prefix='', numpy_as_list=False, stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*) → Iterator

Just echoes the individual from within the pipeline

Uses next_individual.__str__

Parameters

- **next_individual** – iterator for next individual to be printed
- **prefix** – prefix appended to the start of the line
- **numpy_as_list** – If True, numpy arrays are converted to lists before printing
- **stream** – File object passed to print

Returns
the same individual, unchanged

leap_ec.probe.**print_population**(*population*, *generation*, *numpy_as_list=False*)

Convenience function for pretty printing a population that's associated with a given generation

Parameters

- **population** – The population of individuals to be printed
- **generation** – The generation of the population
- **numpy_as_list** – If True, numpy arrays are converted to lists before printing

Returns
None

leap_ec.probe.**print_probe**(*population='__no__default__', probe='__no__default__', stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>, prefix=''*)

pipeline operator for printing the given population

This is really a wrapper around *probe* that, itself, gets passed te entire population.

The optional prefix is used to tag the output. For example, you may want to print 'before' to indicate that the population is before an operator is applied.

Parameters

- **population** – to be printed
- **probe** – secondary probe that gets the poplation as input and for which the output is passed to *stream*
- **stream** – to write output
- **prefix** – optional string prefix to prepend to output

Returns
population

`leap_ec.probe.`**`sum_of_variances_metric`**(*population: list*)

Computes the genetic diversity of a population by considering the sum of the variances of each variable in the genome.

$$\mathcal{D}(\text{population}) = \sum_{i=1}^{L} \mathbb{E}_{j \in P}\left[x_j[i] - \mathbb{E}[x_j[i]]\right]$$

This is a so-called "column-wise" metric, in the sense that it considers each element of the solution vectors independently.

2.3.8 Parsimony Pressure

One common problem with variable length representations is "bloat" whereby genome lengths will gradually increase over time. This may be due to over-fitting or the accumulation of "junk DNA" over time.

LEAP currently provides two approaches to mitigating bloat. First is a very simple "genome tax," or penalty by genome length, popularized by Koza [Koz92]. The second is lexicographical parsimony, or "tie breaking parsimony," where the individual with the shortest genome is returned if their respective fitnesses happen to be equivalent Luke and Panait [LP02].

API

Parsimony pressure functions.

These are intended to be used as *key* parameters for selection operators.

Provided are Koza-style parsimony pressure and lexicographic parsimony key functions.

`leap_ec.parsimony.`**`koza_parsimony`**(*ind='__no__default__'*, *, *penalty='__no__default__'*)

Penalize fitness by genome length times a constant, in the style of Koza [Koz92].

```
>>> import toolz
>>> from leap_ec.individual import Individual
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> import leap_ec.ops as ops
>>> import numpy as np
>>> problem = MaxOnes()
>>> pop = [Individual(np.array([0, 0, 0, 1, 1, 1]), problem=problem),
...        Individual(np.array([0, 0]), problem=problem),
...        Individual(np.array([1, 1]), problem=problem),
...        Individual(np.array([1, 1, 1]), problem=problem)]
>>> pop = Individual.evaluate_population(pop)
>>> best, = ops.truncation_selection(pop, size=1)
>>> print(best.genome, best.fitness)
[0 0 0 1 1 1] 3
```

```
>>> best, = ops.truncation_selection(pop, size=1, key=koza_parsimony(penalty=.5))
>>> print(best.genome, best.fitness)
[1 1 1] 3
```

$$f_p(x) = f(x) - cl(x)$$

Where f(x) is original fitness, c is a penalty constant, and l(x) is the genome length.

Parameters

- **ind** – to be compared
- **penalty** – for denoting penalty strength

Returns
altered comparison criteria

`leap_ec.parsimony.`**`lexical_parsimony`**(*ind*)

If two fitnesses are the same, break the tie with the smallest genome

This implements Lexicographical Parsimony Pressure [LP02], which is essentially where if the fitnesses of two individuals are close, then break the tie with the smallest genome.

```
>>> import toolz
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> import leap_ec.ops as ops
>>> import numpy as np
>>> problem = MaxOnes()
>>> pop = [Individual(np.array([0, 0, 0, 1, 1, 1]), problem=problem),
...        Individual(np.array([0, 0]), problem=problem),
...        Individual(np.array([1, 1]), problem=problem),
...        Individual(np.array([1, 1, 1]), problem=problem)]
>>> pop = Individual.evaluate_population(pop)
>>> best, = ops.truncation_selection(pop, size=1)
>>> print(best.genome, best.fitness)
[0 0 0 1 1 1] 3
```

```
>>> best, = ops.truncation_selection(pop, size=1, key=lexical_parsimony)
>>> print(best.genome, best.fitness)
[1 1 1] 3
```

Parameters
ind – to be compared

Returns
altered comparison criteria

2.3.9 Visualization

Being able to visualize a running evolutionary algorithm is important. Here we describe special pipeline operators that use matplotlib to visualize the state of the population.

Prebuilt Algorithms

LEAP's "prebuilt" algorithms (also sometimes referred to as "monolithic functions") have optional support for visualizations.

`leap_ec.simple.ea_solve` has two optional arguments that control visualization: *viz* and *viz_ylim*. *viz* is a boolean that controls whether or not to display the visualization; if *True* a matplot lib window will appear and update during a run with the . *viz_ylim* is used to supply the initial bounds for the y-axis of the visualization. The plotting is carried out via an instance of `leap_ec.probe.FitnessPlotProbe`, and which is added as a last pipeline operator; this means that it will be plotting the created offspring with each iteration.

The other monolithic function, `leap_ec.algorithm.generational_ea`, offers more fine-tuned control over visualization. Since the user specifies the pipeline, a visualization pipeline operator can be added anywhere in the pipeline. Moreover, since the user is specifying the visualization operator, they're free to tailor how the visualization is done. For example, the user can specify a custom title and the update frequency.

Tailored evolutionary algorithms

Of course many practitioners will want to build their own evolutionary algorithms and forgo the use of the aforementioned monolithic functions. For these users, LEAP offers a number of pipeline operators that can be used to visualize the state of the population merely by inserting an instance of one of these into the pipeline. A full list of such operators is in the next section.

Visualization Pipeline Operators

- `leap_ec.probe.FitnessPlotProbe`
  A pipeline operator that plots the fitness of the population with each iteration.
- `leap_ec.probe.PopulationMetricsPlotProbe`
  A pipeline operator that plots user-specified metrics of the population with each invocation. The user is free to specify which metrics to plot. Please refer to *examples/simple/onemax_style_problems.py* for an example of how to use this operator.
- `leap_ec.probe.CartesianPhenotypePlotProbe`
  A pipeline operator that plots the phenotypes of the population with each iteration. This operator is only useful for problems where the phenotype is a 2D point.
- `leap_ec.probe.HistPhenotypePlotProbe`
  A pipeline operator that shows a dynamic histogram of phenotypes.
- `leap_ec.probe.HeatMapPhenotypeProbe`
  A pipeline operator that shows a heatmap of phenotypes.
- `leap_ec.probe.SumPhenotypePlotProbe`
  This operator plots the sum of the phenotype vector with each iteration. For example, this is good for the MAXONES problem that is literally the sum of all the ones in a binary vector.

Examples

You can find examples on how to use these probes in the following:

- *examples/advanced/custom_stopping_condition.py*
- *examples/advanced/neural_network_cartpole.py*
- *examples/advanced/island_model.py*
- *examples/advanced/cgp_images.py*
- *examples/advanced/cgp.py*
- *examples/advanced/real_rep_with_diversity_metrics.py*
- *examples/advanced/multitask_island_model.py*
- *examples/advanced/external_simulation.py*
- *examples/advanced/pitt_rules_cartpole.py*
- *examples/distributed/simple_sync_distributed.py*
- *examples/simple/int_rep.py*
- *examples/simple/one+one_es.py*
- *examples/simple/onemax_style_problems.py*
- *examples/simple/real_rep_genewise_mutation.py*

CHAPTER

THREE

PREBUILT ALGORITHMS

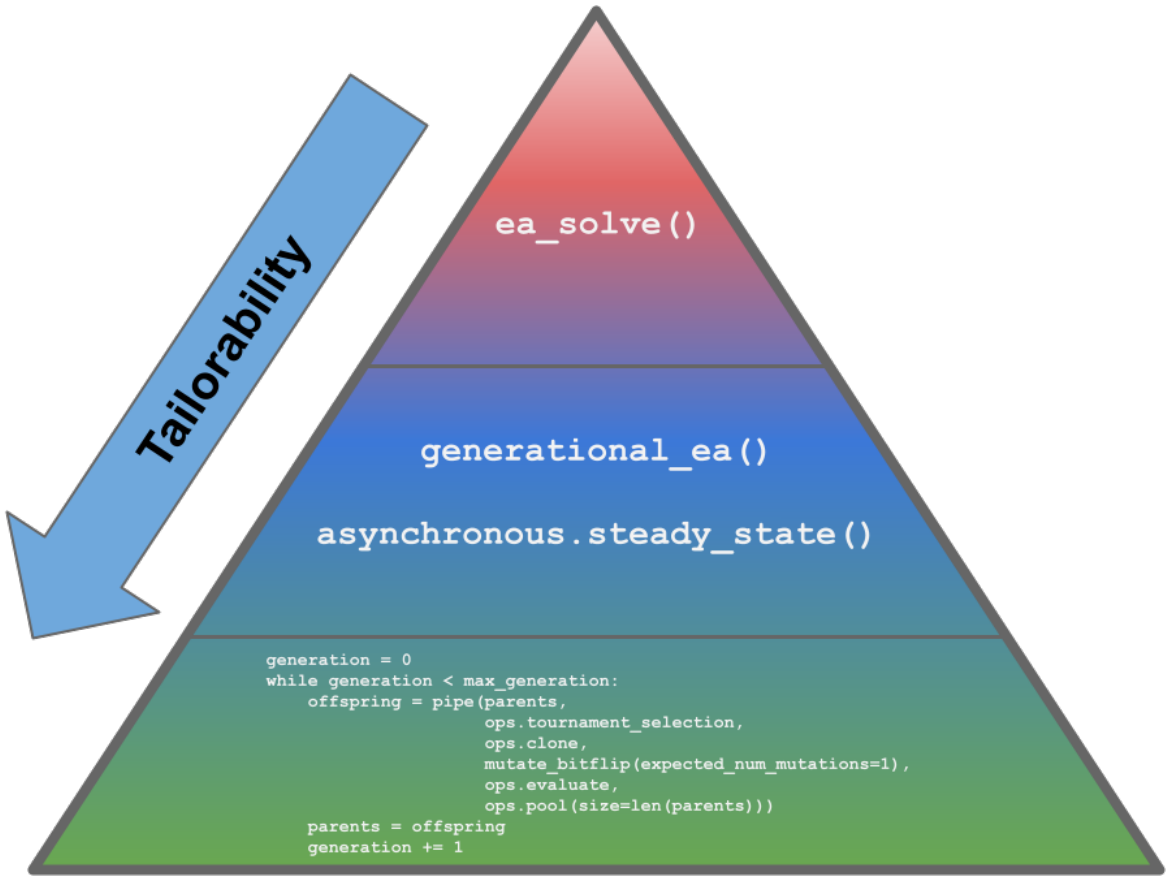


Fig. 3.1: **The three tiers of tailorability for using LEAP.** LEAP has three levels of abstraction with gradually increasing order of customization. The top-level has ea_solve() that is ideal for real-valued optimization problems. The mid-level has two functions that allows for some tailoring of the pipeline and representation, generational_ea() and steady_state(). The bottom-most tier provides maximum flexibility and control over an EA's implementation, and involves the practitioner assembling bespoke EAs using LEAP low-level components, as shown by the code snippet.

Fig. 3.1 depicts the top-level entry-point, *ea_solve()*, and has the least customization, but is ideal for real-valued optimization problems. The mid-level allows for more user customization. *generational_ea()* allows for implementing most traditional evolutionary algorithms, such as genetic algorithms and evolutionary programs. *asynchronous.steady_state()* is used to implement an asynchronous steady-state EA suitable for HPC platforms as they make the best use of HPC resources. The bottom-most level provides the

greatest amount of flexability, and is where users implement their evolutionary algorithms using low-level LEAP components.

ea_solve() and *generational_ea()* is documented below. *asynchronous.steady_state()* is documented in *Asynchronous fitness evaluations*. Information on the bottom-most tier can be found in *Implementing Tailored Evolutionary Algorithms with LEAP*.

3.1 *ea_solve()*

leap_ec.simple.**ea_solve**(*function*, *bounds*, *generations=100*, *pop_size=2*, *mutation_std=1.0*, *maximize=False*, *viz=False*, *viz_ylim=(0, 1)*, *hard_bounds=True*, *dask_client=None*, *stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*)

Provides a simple, top-level interfact that optimizes a real-valued function using a simple generational EA.

Parameters

- **function** – the function to optimize; should take lists of real numbers as input and return a float fitness value
- **bounds** (*[(float, float)]*) – a list of (min, max) bounds to define the search space
- **generations** (*int*) – the number of generations to run for
- **pop_size** (*int*) – the population size
- **mutation_std** (*float*) – the width of the mutation distribution
- **maximize** (*bool*) – whether to maximize the function (else minimize)
- **viz** (*bool*) – whether to display a live best-of-generation plot
- **hard_bounds** (*bool*) – if True, bounds are enforced at all times during evolution; otherwise they are only used to initialize the population.
- **viz_ylim** (*(float, float)*) – initial bounds to use of the plots vertical axis
- **dask_client** – is optional dask Client to enable parallel evaluations
- **stream** – a stream to write best-so-far values to (defaults to stdout)

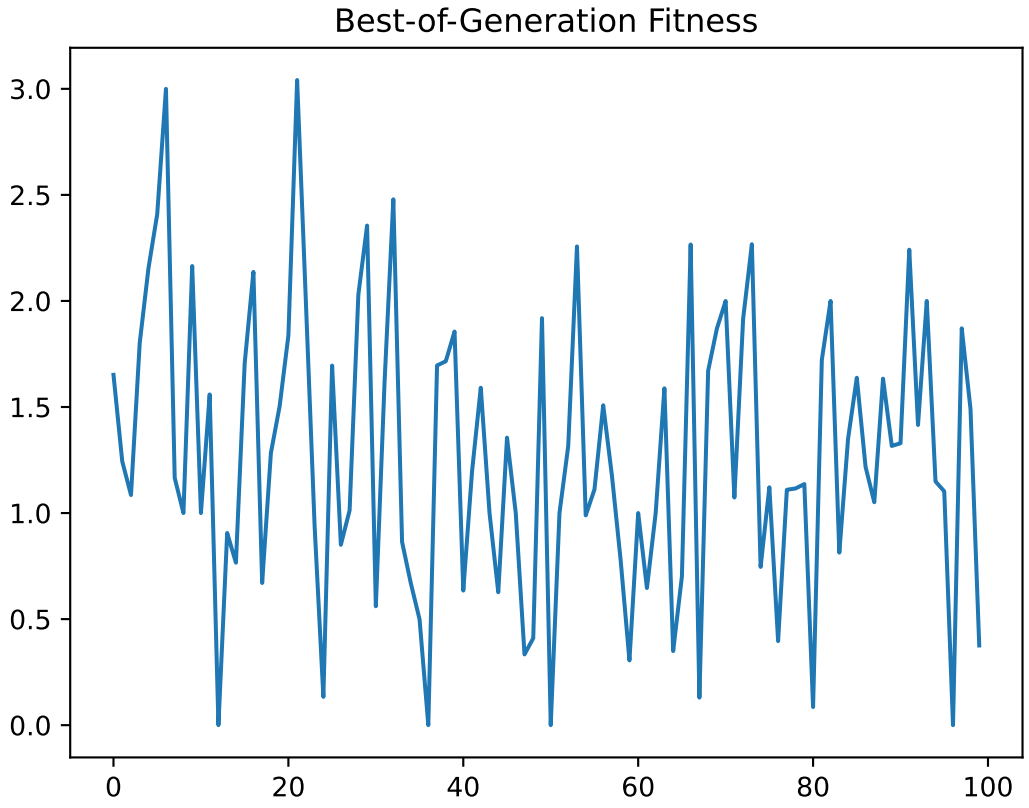
The basic call includes instrumentation that prints the best-so-far fitness value of each generation to stdout:

```
>>> import io
>>> from leap_ec.simple import ea_solve
>>> stream = io.StringIO()
>>> ea_solve(sum, bounds=[(0, 1)]*5, stream=stream)
array([..., ..., ..., ..., ...])
```

The stream captures the best-so-far individual at each iteration of the algorithm: >>> print(stream.getvalue()) # doctest: +ELLIPSIS, +NORMALIZE_WHITESPACE step,bsf 0,… 1,… 2,… … 99,… <BLANKLINE>

When *viz=True*, a live BSF plot will also display:

```
>>> ea_solve(sum, bounds=[(0, 1)]*5, viz=True)
array([..., ..., ..., ..., ...])
```


Best-of-Generation Fitness
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0
20
40
60
80
100

3.1.1 Example

And example using *ea_solve()* can be found in *examples/simple/simple.py*.

3.2 *generational_ea()*

leap_ec.algorithm.**generational_ea**(*max_generations: int*, *pop_size: int*, *problem*, *representation*, *pipeline*, *stop=<function <lambda>>*, *init_evaluate=<bound method Individual.evaluate_population of <class 'leap_ec.individual.Individual'>>*, *k_elites: int = 1*, *start_generation: int = 0*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

This function provides an evolutionary algorithm with a generational population model.

When called this initializes and evaluates a population of size *pop_size* using the *init_evaluate* function and then pipes it through an operator *pipeline* (i.e. a list of operators) to obtain offspring. Wash, rinse, repeat.

The algorithm is provided here at the "metaheuristic" level: in order to apply it to a particular problem, you must parameterize it with implementations of its various components. You must decide the population size, how individuals are represented and initialized, the pipeline of reproductive operators, etc. A metaheuristic template of this kind can be used to implement genetic algorithms, genetic programming, certain evolution strategies, and all manner of other (novel) algorithms by passing in appropriate components as parameters.

Parameters

- **max_generations** (*int*) – The max number of generations to run the algorithm for. Can pass in float('Inf') to run forever or until the *stop* condition is reached.
- **pop_size** (*int*) – Size of the initial population
- **stop** (*int*) – A function that accepts a population and returns True iff it's time to stop evolving.
- **problem** (Problem) – the Problem that should be used to evaluate individuals' fitness
- **representation** – How the problem is represented in individuals
- **pipeline** (*list*) – a list of operators that are applied (in order) to create the offspring population at each generation
- **init_evaluate** – a function used to evaluate the initial population, before the main pipeline is run. The default of *Individual.evaluate_population* is suitable for many cases, but you may wish to pass a different operator in for distributed evaluation or other purposes.
- **k_elites** – keep k elites
- **start_generation** – index of the first generation to count from (defaults to 0). You might want to change this, for example, in experiments that involve stopping and restarting an algorithm.

Returns

the final population

The intent behind this kind of EA interface is to allow the complete configuration of a basic evolutionary algorithm to be defined in a clean and readable way. If you define most of the components in-line when passing them to the named arguments, then the complete configuration of an algorithmic experiment forms one concise code block. Here's what a basic (mu, lambda)-style EA looks like (that is, an EA that throws away the parents at each generation in favor of their offspring):

```
>>> from leap_ec import Individual, Representation
>>> from leap_ec.algorithm import generational_ea, stop_at_generation
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> from leap_ec.binary_rep.ops import mutate_bitflip
>>> import leap_ec.ops as ops
>>> pop_size = 5
>>> final_pop = generational_ea(max_generations=100, pop_size=pop_size,
...
...                         problem=MaxOnes(),      # Solve a MaxOnes Boolean␣
↪optimization problem
...
...                         representation=Representation(
...                             initialize=create_binary_sequence(length=10)  #␣
↪Initial genomes are random binary sequences
...                         ),
...
...                         # The operator pipeline
...                         pipeline=[
...                             ops.tournament_selection,                     # Select␣
↪parents via tournament selection
...                             ops.clone,                              # Copy them (just␣
↪to be safe)
...                             mutate_bitflip(expected_num_mutations=1),     # Basic␣
↪mutation with a 1/L mutation rate
...                             ops.UniformCrossover(p_swap=0.4),  # Crossover with a␣
↪40% chance of swapping each gene
...                             ops.evaluate,                           # Evaluate fitness
...                             ops.pool(size=pop_size)                 # Collect␣
↪offspring into a new population
...                         ])
```

The algorithm runs immediately and returns the final population:

```
>>> print(*final_pop, sep='\n')
Individual<...> ...
Individual<...> ...
Individual<...> ...
...
Individual<...> ...
```

You can get the best individual by using *max* (since comparison on individuals is based on the *Problem* associated with them, this will return the best individaul even on minimization problems):

```
>>> max(final_pop)
Individual<...>...
```

3.2.1 Example

And example using *generational_ea()* can be found in *examples/simple/int_rep.py*.

CHAPTER

FOUR

IMPLEMENTING TAILORED EVOLUTIONARY ALGORITHMS WITH LEAP

The *Prebuilt Algorithms* , *ea_solve()*, *generational_ea()*, and *asynchronous.steady_state()* may not be sufficient to address your problem. This could be that you want to access the state of objects outside the pipeline during a run, or that you want to add complex bookkeeping not easily supported by a prebuilt, among many other possible reasons.

This leaves assembling a bespoke evolutionary algorithm (EA) using low-level LEAP components. Generally, to do that you will need to do the following:

- Come up with a suitable representation for your problem
  - What is the genome going to look like? Is it an indirect representation like a binary representation that must be decoded? Or a phenotypic, or direct representation, such as a real-valued vector? Or something else?
  - How are genomes going to be decoded into a phenotypic representation suitable for the associated Problem class?
  - Is the default *Individual* class suitable? Or will one of its subclasses be more appropriate? Will you have to write your own to keep additional state?
- Define a *Problem* sub-class
- Implement a loop wrapped around a pipeline of appropriate pipeline operators
- Determine what output to generate
- Optionally visualizing a run

These will be described in more detail in the following sub-sections.

4.1 Deciding on a suitable representation

The first design decision you will have to make is how to best represent your problem. There are two broad categories of representations, *genotypic* and *phenotypic*. A *genotypic* representation is a form of indirect representation whereby problem values use data that must be decoded into values that make sense to the associated *Problem* class you will also define. One popular example is using a binary encoding that must be decoded into values, usually integers or real-value sequences, that can then be used by a *Problem* instance to evaluate an individual. (However, there are some problems that directly use the binary sequences without having to interpret the values, such as the *MaxOnes* problem.) A *phenotypic* representation is able to directly represent problem relevant values in some way, usually as a vector of real-values that correspond to problem parameters.

4.1.1 Decoders for binary representations

If you use a binary representation, then you will almost certainly need to define an associated decoder to convert binary sequences within *Individual* genomes into values that the associated *Problem* can use. A variety of premade binary decoders can be found in `leap_ec.binary_rep.decoders`, and these can be used to convert binary sequences to integers or real values. Gray code versions of binary decoders are also included.

Note: Gray encoding Gray encoding is an alternative integer representation that use binary sequences. Gray encoding resolves the issue where bit flip mutation of higher order bits would greatly change the values, whereas a Grey encoded binary integer will only change the value a small amount regardless of which bit was flipped in the binary sequence. (See also: Grey code)

4.1.2 Impact on representation on choice of pipeline operators

There will be two areas where you representation choice is going to have an impact on the code you write. First is in how you initialize individuals with random genomes. The second will be mutation and possibly crossover pipeline operators tailored to that representation. The mutation and crossover pipeline operators are generally going to be specific to the underlying representation. For example, bit flip mutation is relevant to binary representations, and a Gaussian mutation is appropriate for real-value representations. There are sub-packages for integer, real, and binary representations that have an *ops.py* that will contain pertubation (mutation) operators appropriate for the associated representation.

4.1.3 LEAP supports three numeric representations

There are three numeric representations supported by LEAP, that for binary, integer, and real values. You can find initializers that create random values for those value types in their respective sub-packages. You can find them in `leap_ec.binary_rep.initializers`, `leap_ec.int_rep.initializers`, and `leap_ec.real_rep.initializers`, respectively.

4.1.4 Support for exotic representations

LEAP is flexible enough to support other, more exotic representations, such as graphs and matrices. However, you will have to write your own initializers and mutation (and possibly crossover) operators to support such novel genome types.

4.2 Defining a *Problem* subclass

The *Problems* are where you implement how to evaluate an individual to solve your problem. You will need to create a *Problem* sub-class and implement its *evaluate()* member function accordingly.

Problem is an abstract base class (ABC), so you *must* subclass from it. Moreover, there are a number of *Problem* subclasses, so you will need to pick one that is the best fit for your situation. More than likely you will subclass from *ScalarProblem* since it supports real-valued fitnesses and it handles fitnesses that are NaNs, which can happen if you use *RobustIndividual* or *DistributedIndividual* and an exception is thrown during evaluation. (I.e., it was impossible to assign a fitness because the evaluation failed, so we signal that by assigning NaN as the fitness.)

If you use *ScalarProblem* or one of its subclasses, you will also have to specify whether it is a maximization problem via the boolean parameter passed into the class constructor.

There are a number of example *Problem* implementations that can be found in *real_rep.problems* many of which are popular benchmarks.

4.3 Possibly defining or choosing a special *Individual* subclass

Individuals encapsulate a posed solution to a problem and an associated fitness after evaluation. For most situations the default *Individual* class should be fine. However, you can also use *RobustIndividual* if you want individuals to handle exceptions that may be thrown during evaluation. If you are using the synchronous or asynchronous distributed evaluation support, then you may consider using *DistributedIndividual*, which itself is a subclass of *RobustIndividual*, but also assigns a UUID to each individual, a unique birth ID integer, and start and stop evaluation times in UNIX epoch time.

Of course, if none of those *Individual* classes meet your needs, you can freely create your own *Individual* subclass. For example, you may want a subclass that performs additional bookkeeping, such as perhaps maintaining links to its parents and any clones (offspring).

4.4 Putting all that together

Now that you have chosen a representation, an associated *Decoder*, a *Problem*, and an *Individual* class, you are now ready to assemble those components into a functional evolutionary algorithm. Generally, your code will follow this pattern:

```
parents ← create_initial_random_population()

While not done:

    offspring ← toolz.pipe(parents, *pipeline_ops)
    parents ← offspring
```

That is, first a population of parents are randomly created, and then we fall into a loop where we create offspring from those parents by generation until we are done with some sort of arbitrary stopping criteria. Within the loop the old parents are replaced with the offspring. There is, of course, a lot more nuance to that with actual evolutionary algorithms, but that captures the essence of EAs.

The part where the offspring are created merits more discussion. We rely on *toolz.pipe()* to take a source of individuals, the current parents, from which to generate a set of offspring. Individuals are selected by demand from the given sequent of pipeline operators, where each of these operators will manipulate the individuals that pass through them in some way. This concept is described in more detail in *Operator Pipeline*.

4.4.1 Evolutionary algorithm examples

There are a number of examples to steer by found in *examples/simple*. In particular:

- *simple_ep.py* – simple example of an Evolutionary Program
- *simple_es.py* – simple example of an Evolutionary Strategy
- *simple_ga.py* – simple example of a Genetic Algorithm
- *simple_ev.py* – simple example of an Evolutionary Algorithm as defined in Ken De Jong's *Evolutionary Computation: A Unified Approach*.

CHAPTER

FIVE

DISTRIBUTED LEAP

LEAP supports synchronous and asynchronous distributed concurrent fitness evaluations that can significantly speed-up runs. LEAP uses dask (*https://dask.org/*), which is a popular distributed processing python package, to implement parallel fitness evaluations, and which allows easy scaling from laptops to supercomputers.

5.1 Synchronous fitness evaluations

Synchronous fitness evaluations are essentially a map/reduce approach where individuals are fanned out to computing resources to be concurrently evaluated, and then the calling process waits until all the evaluations are done. This is particularly suited for by-generation approaches where offspring are evaluated in a batch, and progress in the EA only proceeds when all individuals have been evaluated.

5.1.1 Components

leap_ec.distrib.synchronous provides two components to implement synchronous individual parallel evaluations.

leap_ec.distrib.synchronous.eval_population
: which evaluates an entire population in parallel, and returns the evaluated population

leap_ec.distrib.synchronous.eval_pool
: is a pipeline operator that will collect offspring and then evaluate them all at once in parallel; the evaluated offspring are returned

5.1.2 Example

The following shows a simple example of how to use the synchronous parallel fitness evaluation in LEAP.

```
#!/usr/bin/env python
""" Simple example of using leap_ec.distrib.synchronous

"""
import os

from distributed import Client
import toolz

from leap_ec import context, test_env_var
from leap_ec import ops
from leap_ec.decoder import IdentityDecoder
```

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```
from leap_ec.binary_rep.initializers import create_binary_sequence
from leap_ec.binary_rep.ops import mutate_bitflip
from leap_ec.binary_rep.problems import MaxOnes
from leap_ec.distrib import DistributedIndividual
from leap_ec.distrib import synchronous
from leap_ec.probe import AttributesCSVProbe


##############################
# Entry point
##############################
if __name__ == '__main__':

    # We've added some additional state to the probe for DistributedIndividual,
    # so we want to capture that.
    probe = AttributesCSVProbe(attributes=['hostname',
                                           'pid',
                                           'uuid',
                                           'birth_id',
                                           'start_eval_time',
                                           'stop_eval_time'],
                               do_fitness=True,
                               do_genome=True,
                               stream=open('simple_sync_distributed.csv', 'w'))

    # Just to demonstrate multiple outputs, we'll have a separate probe that
    # will take snapshots of the offspring before culling.  That way we can
    # compare the before and after to see what specific individuals were culled.
    offspring_probe = AttributesCSVProbe(attributes=['hostname',
                                           'pid',
                                           'uuid',
                                           'birth_id',
                                           'start_eval_time',
                                           'stop_eval_time'],
                               do_fitness=True,
                               stream=open('simple_sync_distributed_offspring.csv', 'w'))

    with Client() as client:
        # create an initial population of 5 parents of 4 bits each for the
        # MAX ONES problem
        parents = DistributedIndividual.create_population(5, # make five individuals
                                                          initialize=create_binary_
↪sequence(
                                                              4), # with four bits
                                                          decoder=IdentityDecoder(),
                                                          problem=MaxOnes())

        # Scatter the initial parents to dask workers for evaluation
        parents = synchronous.eval_population(parents, client=client)

        # probes rely on this information for printing CSV 'step' column
        context['leap']['generation'] = 0
```

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```
    probe(parents) # generation 0 is initial population
    offspring_probe(parents) # generation 0 is initial population

    # When running the test harness, just run for two generations
    # (we use this to quickly ensure our examples don't get bitrot)
    if os.environ.get(test_env_var, False) == 'True':
        generations = 2
    else:
        generations = 5

    for current_generation in range(generations):
        context['leap']['generation'] += 1

        offspring = toolz.pipe(parents,
                               ops.tournament_selection,
                               ops.clone,
                               mutate_bitflip(expected_num_mutations=1),
                               ops.UniformCrossover(),
                               # Scatter offspring to be evaluated
                               synchronous.eval_pool(client=client,
                                                     size=len(parents)),
                               offspring_probe, # snapshot before culling
                               ops.elitist_survival(parents=parents),
                               # snapshot of population after culling
                               # in separate CSV file
                               probe)

        print('generation:', current_generation)
        [print(x.genome, x.fitness) for x in offspring]

        parents = offspring

print('Final population:')
[print(x.genome, x.fitness) for x in parents]
```

This example of a basic genetic algorithm that solves the MAX ONES problem does not use a provided monolithic entry point, such as found with *ea_solve()* or *generational_ea()* but, instead, directly uses LEAP's pipeline architecture. Here, we create a simple *dask Client* that uses the default local cores to do the parallel evaluations. The first step is to create the initial random population, and then distribute those to dask workers for evaluation via *synchronous.eval_population()*, and which returns a set of fully evaluated parents. The *for* loop supports the number of generations we want, and provides a sequence of pipeline operators to create offspring from selected parents. For concurrently evaluating newly created offspring, we use *synchronous.eval_pool*, which is just a variant of the *leap_ec.ops.pool* operator that relies on *dask* to evaluate individuals in parallel.

Note: If you wanted to use resources on a cluster or supercomputer, you would start up *dask-scheduler* and *dask-worker`s first, and then point the `Client* at the scheduler file used by the scheduler and workers. Distributed LEAP is agnostic on what kind of dask client is passed as a *client* parameter – it will generically perform the same whether running on local cores or on a supercomputer.

5.1.3 Separate Examples

There is a jupyter notebook that walks through a synchronous implementation in *examples/distributed/simple_sync_distributed.ipynb*. The above example can also be found at *examples/distributed/simple_sync_distributed.py*.

5.2 Asynchronous fitness evaluations

Asynchronous fitness evaluations are a little more involved in that the EA immediately integrates newly evaluated individuals into the population – it doesn't wait until all the individuals have finished evaluating before proceeding. More specifically, LEAP implements an asynchronous steady-state evolutionary algorithm (ASEA).

Algorithm 1 ASAE design. This shows details on how we asynchronously update a population of individuals of posed solutions.

$P_0 \leftarrow$ init_pop() ▷ Initial population
$b \leftarrow$ size(P_o) ▷ Initial number of births
$P_p \leftarrow \emptyset$ ▷ Initialize an empty pool
async_eval(P_0) ▷ Fan out population to workers
while $I_e \leftarrow$ evaluated() **do** ▷ Next evaluated individual
    if is_full(P_p) **then**
        if $I_e >$ min(P_p) **then** ▷ Replace only if better
            remove(P_p, min(P_p)) ▷ than weakest in pool
            insert(P_p, I_e)
        end if
    else ▷ Pool not full yet, so just insert
        insert(P_p, I_e)
    end if
    if $b <$ birth_budget **then**
        $I_p \leftarrow$ select(P_p) ▷ Select parent
        $I_o \leftarrow$ reproduce(I_p) ▷ Create offspring
        async_submit(I_o) ▷ Send to worker for evaluation
        $b \leftarrow b + 1$ ▷ Increment births
    end if
end while
return P_p ▷ Return best individuals

Fig. 5.1: Algorithm 1: Asynchronous steady-state evolutionary algorithm concurrently updates a population as individuals are evaluated [CSB20].

Algorithm 1 shows the details of how an ASEA works. Newly evaluated individuals are inserted into the population, which then leaves a computing resource available. Offspring are created from one or more selected parents, and are then assigned to that computing resource, thus assuring minimal idle time between evaluations. This is particularly important within HPC contexts as it is often the case that such resources are costly, and therefore there is an implicit need to minimize wasting such resources. By contrast, a synchronous distributed approach risks wasting computing resources because computing resources that finish evaluating individuals before the last individual is evaluated will idle until the next generation.

5.2.1 Example

```
from pprint import pformat

from dask.distributed import Client, LocalCluster

from leap_ec import Representation
from leap_ec import ops
from leap_ec.binary_rep.problems import MaxOnes
from leap_ec.binary_rep.initializers import create_binary_sequence
from leap_ec.binary_rep.ops import mutate_bitflip
from leap_ec.distrib import DistributedIndividual
from leap_ec.distrib import asynchronous
from leap_ec.distrib.probe import log_worker_location, log_pop

MAX_BIRTHS = 500
INIT_POP_SIZE = 20
POP_SIZE = 20
GENOME_LENGTH = 5

with Client(scheduler_file='scheduler.json') as client:
    final_pop = asynchronous.steady_state(client, # dask client
                                  births=MAX_BIRTHS,
                                  init_pop_size=INIT_POP_SIZE,
                                  pop_size=POP_SIZE,

                                  representation=Representation(
                                      initialize=create_binary_sequence(
                                          GENOME_LENGTH),
                                      individual_cls=DistributedIndividual),

                                  problem=MaxOnes(),

                                  offspring_pipeline=[
                                      ops.random_selection,
                                      ops.clone,
                                          mutate_bitflip,
                                      ops.pool(size=1)],

                                  evaluated_probe=track_workers_func,
                                  pop_probe=track_pop_func)

print(f'Final pop: \n{pformat(final_pop)}')
```

The above example is quite different from the synchronous code given earlier. Unlike, with the synchronous code, the asynchronous code does provide a monolithic function entry point, *asynchronous.steady_state()*. The first thing to note is that by nature this EA has a birth budget, not a generation budget, and which is set to 500 in *MAX_BIRTHS*, and passed in via the *births* parameter. We also need to know the size of the initial population, which is given in *init_pop_size*. And, of course, we need the size of the population that is perpetually updated during the lifetime of the run, and which is passed in via the *pop_size* parameter.

The *representation* parameter we have seen before in the other monolithic functions, such as *generational_ea*, which encapsulates the mechanisms for making an individual and how the individual's state is stored. In this case, because it's the MAX ONES problem, we use the *IdentityDecoder* because we want to use the raw bits as is, and we specify a factory

function for creating binary sequences GENOME_LENGTH in size; and, lastly, we override the default class with a new class, *DistributedIndividual*, that contains some additional bookkeeping useful for an ASEA, and is described later.

The *offspring_pipeline* differs from the usual LEAP pipelines. That is, a LEAP pipeline is usally a set of operators that define a workflow for creating offspring from a set of prospective parents. In this case, the pipeline is for creating a *single* offspring from an *implied* population of prospective parents to be evaluated on a recently available dask worker; essentially, as a dask worker finishes evaluating an individual, this pipeline will be used to create a single offspring to be assigned to that worker for evaluation. This gives the user maximum flexibility in how that offspring is created by choosing a selection operator followed by perturbation operators deemed suitable for the given problem. (Not forgetting the critical *clone* operator, the absence of which will cause selected parents to be modified by any applied mutation or crossover operators.)

There are two optional callback function reporting parameters, *evaluated_probe* and *pop_probe*. *evaluated_probe* takes a single *Individual* class, or subclass, as an argument, and can be used to write out that individual's state in a desired format. *distrib.probe.log_worker_location* can be passed in as this argument to write each individual's state as a CSV row to a file; by default it will write to *sys.stdout*. The *pop_probe* parameter is similar, but allows for taking snapshots of the hidden population at preset intervals, also in CSV format.

Also noteworthy is that the *Client* has a *scheduler_file* specified, which indicates that a dask scheduler and one or more dask workers have already been started beforehand outside of LEAP and are awaiting tasking to evaluate individuals.

There are three other optional parameters to *steady_state*, which are summarized as follows:

inserter
: takes a callback function of the signature *(individual, population, max_size)* where *individual* is the newly evaluated individual that is a candidate for inserting into the *population*, and which is the internal population that *steady_state* updates. The value for *max_size* is passed in by *steady_state* that is the user stipulated population size, and is used to determine if the individual should just be inserted into the population when at the start of the run it has yet to reach capacity. That is, when a user invokes *steady_state*, they specify a population size via *pop_size*, and we would just normally insert individuals until the population reaches *pop_size* in capacity, then the function will use criteria to determine whether the individual is worthy of being inserted. (And, if so, at the removal of an individual that was already in the population. Or, colloquially, someone is voted off the island.)

  There are two provided inserters, *steady_state.tournament_insert_into_pop* and *greedy_insert_into_pop*. The first will randomly select an individual from the internal population, and will replace it if its fitness is worse than the new individual. The second will compare the new individual with the current worst in the population, and will replace that individual if it is better. The default for *inserter* is to use the *greedy_insert_into_pop*.

  Of course you can write your own if either of these two inserters do not meet your needs.

count_nonviable
: is a boolean that, if True, means that individuals that are non- viable are counted towards the birth budget; by default, this is *False*. A non-viable individual is one where an exception was thrown during evaluation. (E.g., an individual poses a deep-learner configuration that does not make sense, such as incompatible adjacent convolutional layers, and pytorch or tensorflow throws an exception.)

context
: contains global state where the running number of births and non-viable individuals is kept. This defaults to *context*.

5.2.2 DistributedIndividual

DistributedIndividual is a subclass of *RobustIndividual* that contains some additional state that may be useful for distributed fitness evaluations.

uuid
: is UUID assigned to that individual upon creation

birth_id
: is a unique, monotonically increasing integer assigned to each indidividual on creation, and denotes its birth order

start_eval_time
: is when evaluation began for this individul, and is in *time_t* format

stop_eval_time
: when evaluation completed in *time_t* format

This additional state is set in *distrib.evaluate.evaluate()* and *is_viable* and *exception* are set as with the base class, *core.Individual*.

Note: The *uuid* is useful if one wanted to save, say, a model or some other state in a file; using the *uuid* in the file name will make it easier to associate the file with a given individual later during a run's post mortem analysis.

Note: The *start_eval_time* and *end_eval_time* can be useful for checking whether individuals that take less time to evaluate come to dominate the population, which can be important in ASEA parameter tuning. E.g., initially the population will come to be dominated by individuals that evaluated quickly even if they represent inferior solutions; however, eventually, better solutions that take longer to evaluate will come to dominate the population; so, if one observes that shorter solutions still dominate the population, then increasing the *max_births* should be considered, if feasible, to allow time for solutions that need longer to evaluate time to make a representative presence in the population.

5.2.3 Separate Examples

There is also a jupyter notebook walkthrough for the asynchronous implementation, *examples/distributed/simple_async_distributed.ipynb*. Moreover, there is standalone code in *examples/distributed/simple_async_distributed.py*.

CHAPTER

SIX

MULTIOBJECTIVE OPTIMIZATION

LEAP supports multi-objective optimization via an implementation of [NSGA-II]. There are two ways of using this functionality – using a single function, *leap_ec.mulitobjective.nsga2.generalized_nsga_2* , or by assembling a bespoke NSGA-II using pipeline operators. We will cover both approaches here.

6.1 Using *generalized_nsga_2*

leap_ec.mulitobjective.nsga2.generalized_nsga_2 is similar to other LEAP metaheuristic functions, such as *generational_ea*. It has arguments for specifying the maximum number of generations, population size, stopping criteria, problem representation, and others.

Note that by default a faster rank sorting algorithm is used [Burlacu], but if it is important to use the original NSGA-II rank sorting algorithm, then that can be provided by specifying *leap_ec.mulitobjective.ops.fast_nondominated_sort* for the *rank_func* argument.

6.1.1 Example

```
from leap_ec.representation import Representation
from leap_ec.ops import random_selection, clone, evaluate, pool
from leap_ec.real_rep.initializers import create_real_vector
from leap_ec.real_rep.ops import mutate_gaussian
from leap_ec.multiobjective.nsga2 import generalized_nsga_2
from leap_ec.multiobjective.problems import SCHProblem
pop_size = 10
max_generations = 5
final_pop = generalized_nsga_2(
    max_generations=max_generations, pop_size=pop_size,

    problem=SCHProblem(),

    representation=Representation(
        initialize=create_real_vector(bounds=[(-10, 10)])
    ),

    pipeline=[
        random_selection,
        clone,
        mutate_gaussian(std=0.5, expected_num_mutations=1),
        evaluate,
```

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```
        pool(size=pop_size),
    ]
)
```

The above code snippet shows how to set up NSGA-II for one of the benchmark multiobjective problems, *SCHProblem*. We specify the maximum number of generations, the population size, representation, and give a reproduction pipeline. The representation is a simple single valued gene, that we see on line 15 is initialized in the range of [-10,10].

The reproduction pipeline given on lines 18-24 is used to create the offspring for each generation. It is spliced into another pipeline so that the offspring created via this pipeline are then passed to the rank sorting and crowding distance functions. Then truncation selection based on rank and crowding distance is used to return the final set of offspring that then become the parents for the next generation.

6.2 Creating a tailored NSGA-II

However, it may be desirable to have fine-grained control over the NSGA-II implementation, maybe to more conveniently perform some necessary ancillary calculations during a run. In that case, the lower-level NSGA-II operators can be directly used in a full LEAP pipeline, as shown below.

6.2.1 Example

```
# represenations have a convenience function for creating
# initial random population
parents = representation.create_population(int(config.ea.pop_size),
                                           problem=problem)

generation_counter = util.inc_generation(context=context)

# Scatter the initial parents to dask workers for evaluation
parents = synchronous.eval_population(parents, client=client)

context['std'] = np.array([0.001,  # start_lr
                           0.0001, # stop_lr
                           0.0625, # rcut
                           0.0625, # rcut smth
                           0.0625, # training batch
                           0.0625, # valid. batch
                           0.0625, # scale by worker
                           0.0625, # des activ func
                           0.0625, # fitting activ func
                           ])

try:
    while generation_counter.generation() < max_generations:
        generation_counter()  # Increment to the next generation

        offspring = pipe(parents,
                         ops.random_selection,
                         ops.clone,
                         mutate_gaussian(
```

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```
30                              std=context['std'],
31                              expected_num_mutations='isotropic', # zap all genes
32                              hard_bounds=DeepMDRepresentation.bounds),
33                          eval_pool(client=client, size=len(parents)),
34                          rank_ordinal_sort(parents=parents),
35                          crowding_distance_calc,
36                          ops.truncation_selection(size=len(parents),
37                                                   key=lambda x: (-x.rank,
38                                                                  x.distance)),
39                          )
40
41          parents = offspring  # Make offspring new parents for next generation
42
43          context['std'] *= .85
```

The above code demonstrates how to use the NSGA operators, *rank_ordinal_sort* and *crowding_distance_calc*, in a LEAP reproductive operator pipeline to do the rank sorting and crowding distance calculation on newly formed offspring. The truncation selection operator uses the rank and distances that are added as attributes to individuals as they pass through the pipeline by those operators.

Also shown is how to use Dask to perform parallel fitness evaluations. On line 9 the initial random population is scattered to preassigned Dask workers for evaluation. Line 33 performs a similar operation with newly created offspring.

And, finally, this shows how to add some ancillary computation, in this case updating a vector of standard deviations to be used with the Gaussian mutation operator. The vector is assigned to the LEAP global dictionary, *context*, on line 11, and is updated every generation on line 43. The mutation operator, itself, is on line 29. Although a special pipeline operator could have been made to do this same update to enable use of *generalized_nsga_2* , it was cleaner to separate out this update outside the pipeline.

6.3 Representing multiple fitnesses

Normally a fitness is a real-valued scalar, but in the case of multiple objectives, LEAP uses a numpy array of floats for fitnesses, with each element of the array corresponding to one objective. Be mindful to *not* use a python tuple or list to hold fitnesses.

Another caveat if using *DistributedIndividual* is that class will assign NaNs as fitnesses if something should go wrong while evaluating an individual's fitness. E.g., if optimizing a neural network architecture and exception is thrown during model training due to a hardware failure. This poses a problem for rank sorting since sorting floating point values with NaNs leads to undefined behavior. In which case it's advisable to create a`DistributedIndividual` subclass that overrides this behavior and assigns, say, MAXINT or -MAXINT (as appropriate for maximizing or minimizing objectives) for fitnesses where there was a problem in performing the fitness evaluation.

6.4 Asynchronous steady-state multiobjective optimization

LEAP also supports a distributed asynchronous-steady state version of NSGA-II. This is useful for HPC clusters where it is desirable to have a large number of workers evaluating individuals in parallel. Moreover, this allows for minimizing worker idle time in that new offspring are allocated to workers that finished evaluating their previous individuals. This is in contrast to the traditional synchronous version of NSGA-II where all workers must finish evaluating their individuals before the next generation can be created; within an HPC context this would mean that some workers would be idle while waiting for others to finish, thus wasting computational resources. As with the other distributed support in LEAP, this functionality is implemented using Dask, and so a Dask client must be provided.

The asynchronous steady-state version of NSGA-II is implemented in `leap_ec.multiobjective.asynchronous.steady_state_nsga_2()`. An example of use is in the *examples/distributed/multiobjective_async_distributed.ipynb* notebook.

6.5 References

CHAPTER

SEVEN

LEAP COOKBOOK

This is a collection of "recipes" in the spirit of the O'Reilly "Cookbook" series. That is, it's a collection of common howtos and examples for using LEAP.

7.1 Enforcing problem bounds constraints

There are two overall types of bounds enforcement within EAs, soft bounds and hard bounds:

soft bounds
: where the boundaries are enforced only at initialization, but mutation allows for exploring beyond those initial boundaries

hard bounds
: boundaries are strictly enforced at initialization as well as during mutation and crossover. In the latter case this can be done by clamping new values to a given range, or flagging an individual that violates such constraints as non-viable by throwing an exception during fitness evaluation. (That is, during evaluation, exceptions are caught, which causes the individual's fitness to be set to NaN and its *is_viable* internal flag set to false; then selection should hopefully weed out this individual from the population.)

7.1.1 Bounds for initialization

When initializing a population with genomes of numeric values, such as integers or real-valued numbers, the bounds for each gene needs to be specified so that we know in what range to initialize the genes.

For real-valued genomes, `leap_ec.real_rep.create_real_vector()` takes a list of tuples where each tuple is a pair of lower and upper bounds for each gene. For example, the following initializes a genome with three genes, where each gene is in the range [0, 1], [0, 1], and [-1, 100], respectively:

```
from leap_ec.real_rep import create_real_vector
bounds = [(0, 1), (0, 1), (-1, 100)]
genome = create_real_vector(bounds)
```

For integer-valued genomes, `leap_ec.int_rep.create_int_vector()` works identically. That is, *create_int_vector* accepts a collection of tuples of pairs of lower and upper bounds for each gene.

7.1.2 Enforcing bounds during mutation

That's great for _initializing_ a population, but what about when we mutate? If no precautions are taken, then mutation is free to create genes that are well outside the initialization bounds. Fortunately for any numeric mutation operator, we can specify a bounds constraint that will be enforced during mutation. The functions *leap_ec.int_rep.ops.mutate_randint()*, `leap_ec.int_rep.ops.binomial()`, *leap_ec.real_rep.ops.mutate_gaussian()* accept a *bounds* parameter that, as with the initializers, is a list of tuples of lower and upper bounds for each gene. Mutations that stray outside of these bounds are clamped to the nearest boundary. *numpy.clip* is used to efficiently clip the values to the bounds.

CHAPTER

EIGHT

COMMON PROBLEMS

Here we address common problems that may arise when using LEAP.

8.1 *min()* returns the worst individual for minimization problems

min() and *max()* works the opposite you may expect for minimization problems because the < operator has been overriden to consider fitness scalars that are numerically less than than another to be "better". So *min()* takes into consideration the problem semantics not the raw number values.

E.g., for a given minimization problem:

```
min(parents).fitness
Out[2]: 66.49057507514954
max(parents).fitness
Out[3]: 59.87865996360779
```

The above shows that the value *59.87865996360779* is "better" than *66.49057507514954* even though _numerically_ it is less than the other value.

It was important for LEAP to override the < operator for `Individual`s because it uses native sort operations to find the "best" and "worst", and so minimization vs. maximization semantics needed to be taken into account.

8.2 Missing pipeline operator arguments

If you see an error like this:

` TypeError: mutate_binomial() missing 1 required positional argument: 'next_individual' `

The corresponding code may look like this:

```
int_ops.mutate_binomial(std=[context['leap']['std0'],
                             context['leap']['std1']],
                        hard_bounds=[(1, 127), (0, 255)],
                        probability=context['leap']['mutation']),
```

In this case, the API for *leap_ec.int_rep.ops.mutate_binomial()* had changed such that the argument *hard_bounds* had been shortened to *bounds*. Renaming that argument to *bounds* fixed this instance of the problem.

In general, if you see an error like this, you should check the API documentation and ensure that all mandatory function arguments are getting passed into the pipeline operator.

CHAPTER

NINE

ROADMAP

Please see the CHANGELOG.md for a history of feature implementations.

Future features, in no particular order of priority:

- **Documentation**
  - add write-up on probes
  - more recipes for common use cases in “cookbook”
  - technical report
- Checkpoint / restart support
- Asynchronous multiobjective optimization
- Hall of fame
- **Rule systems**
  - Mich Approach
  - Pitt Approach
- Koza-style Genetic Programming (GP)
- **Estimation of Distribution Algorithms (EDA)**
  - Covariance Matrix Adaptation Evolution Strategy (CMA-ES)
  - Population-based Incremental Learning (PBIL)
  - Bayesian Optimization Algorithm (BOA)

CHAPTER

TEN

LEAP_EC PACKAGE

10.1 Subpackages

10.1.1 leap_ec.binary_rep package

Submodules

leap_ec.binary_rep.decoders module

Decoders for binary representations.

class leap_ec.binary_rep.decoders.**BinaryToIntDecoder**(**descriptors*)

Bases: *Decoder*

A decoder that converts a Boolean-vector genome into an integer-vector phenome.

decode(*genome*, **args*, ***kwargs*)

Converts a Boolean genome to an integer-vector phenome by interpreting each segment of the genome as low-endian binary number.

Parameters
genome – a list of 0s and 1s representing a Boolean genome

Returns
a corresponding list of ints representing the integer-vector phenome

For example, a Boolean representation of [1, 12, 5] can be decoded like this:

```
>>> import numpy as np
>>> d = BinaryToIntDecoder(4, 4, 4)
>>> b = np.array([0,0,0,1, 1, 1, 0, 0, 0, 1, 1, 0])
>>> d.decode(b)
array([ 1, 12,  6])
```

class leap_ec.binary_rep.decoders.**BinaryToIntGreyDecoder**(**descriptors*)

Bases: *BinaryToIntDecoder*

This performs Gray encoding when converting from binary strings.

See also: https://en.wikipedia.org/wiki/Gray_code#Converting_to_and_from_Gray_code

For example, a grey encoded Boolean representation of [1, 8, 4] can be decoded like this:

```
>>> import numpy as np
>>> d = BinaryToIntGreyDecoder(4, 4, 4)
>>> b = np.array([0,0,0,1, 1, 1, 0, 0, 0, 1, 1, 0])
>>> d.decode(b)
array([1, 8, 4])
```

decode(*genome*, **args*, ***kwargs*)

Converts a Boolean genome to an integer-vector phenome by interpreting each segment of the genome as low-endian binary number.

Parameters
genome – a list of 0s and 1s representing a Boolean genome

Returns
a corresponding list of ints representing the integer-vector phenome

For example, a Boolean representation of [1, 12, 5] can be decoded like this:

```
>>> import numpy as np
>>> d = BinaryToIntDecoder(4, 4, 4)
>>> b = np.array([0,0,0,1, 1, 1, 0, 0, 0, 1, 1, 0])
>>> d.decode(b)
array([ 1, 12,  6])
```

class leap_ec.binary_rep.decoders.**BinaryToRealDecoder**(**segments*)

Bases: *BinaryToRealDecoderCommon*

class leap_ec.binary_rep.decoders.**BinaryToRealDecoderCommon**(**segments*)

Bases: *Decoder*

Common implementation for binary to real decoders.

The base classes BinaryToRealDecoder and BinaryToRealGreyDecoder differ by just the underlying binary to integer decoder. Most all the rest of the binary integer to real-value decoding is the same, hence this class.

decode(*genome*, **args*, ***kwargs*)

Convert a list of binary values into a real-valued vector.

class leap_ec.binary_rep.decoders.**BinaryToRealGreyDecoder**(**segments*)

Bases: *BinaryToRealDecoderCommon*

leap_ec.binary_rep.initializers module

Used to initialize binary sequences

leap_ec.binary_rep.initializers.**create_binary_sequence**(*length*)

A closure for initializing a binary sequences for binary genomes.

Parameters
length – how many genes?

Returns
a function that, when called, generates a binary vector of given length

E.g., can be used for *Individual.create_population*

```
>>> from leap_ec.decoder import IdentityDecoder
>>> from . problems import MaxOnes
>>> population = Individual.create_population(10, create_binary_sequence(length=10),
...                                           decoder=IdentityDecoder(),
...                                           problem=MaxOnes())
```

leap_ec.binary_rep.ops module

Binary representation specific pipeline operators.

leap_ec.binary_rep.ops.**genome_mutate_bitflip**(*genome: ndarray = '__no__default__'*, *expected_num_mutations: float = None*, *probability: float = None*) → ndarray

Perform bitflip mutation on a particular genome.

This function can be used by more complex operators to mutate a full population (as in *mutate_bitflip*), to work with genome segments (as in *leap_ec.segmented.ops.apply_mutation*), etc. This way we don't have to copy-and-paste the same code for related operators.

Parameters

- **genome** – of binary digits that we will be mutating
- **expected_num_mutations** – on average how many mutations are we expecting?

Returns

mutated genome

leap_ec.binary_rep.ops.**mutate_bitflip**(*next_individual: Iterator = '__no__default__'*, *expected_num_mutations: float = None*, *probability: float = None*) → Iterator

Perform bit-flip mutation on each individual in an iterator (population).

This assumes that the genomes have a binary representation.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.ops import mutate_bitflip
>>> import numpy as np
```

```
>>> original = Individual(np.array([1, 1]))
>>> op = mutate_bitflip(expected_num_mutations=1)
>>> pop = iter([original])
>>> mutated = next(op(pop))
```

Parameters

- **next_individual** – to be mutated
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)
- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)

Returns

mutated individual

leap_ec.binary_rep.ops.**random**() → x in the interval [0, 1).

leap_ec.binary_rep.problems module

A set of standard EA problems that rely on a binary-representation

class leap_ec.binary_rep.problems.**DeceptiveTrap**(*maximize=True*)

Bases: *ScalarProblem*

A simple bi-modal function whose global optimum is the Boolean vector of all 1's, but in which fitness *decreases* as the number of 1's in the vector *increases*—giving it a local optimum of [0, . . . , 0] with a very wide basin of attraction.

evaluate(*phenome*)

```
>>> import numpy as np
>>> p = DeceptiveTrap()
```

The trap function has a global maximum when the number of one's is maximized:

```
>>> p.evaluate(np.array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1]))
10
```

It's minimized when we have just one zero: >>> p.evaluate(np.array([1, 1, 1, 1, 0, 1, 1, 1, 1, 1])) 0

And has a local optimum when we have no ones at all: >>> p.evaluate(np.array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0])) 9

class leap_ec.binary_rep.problems.**ImageProblem**(*path*, *maximize=True*, *size=(100, 100)*)

Bases: *ScalarProblem*

A variation on *max_ones* that uses an external image file to define a binary target pattern.

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

class leap_ec.binary_rep.problems.**LeadingOnes**(*target_string=None*, *maximize=True*)

Bases: *ScalarProblem*

Implementation of the classic leading-ones problem, where the individuals are represented by a bit vector.

By default, the number of consecutve 1's starting from the beginning of the phenome are maximized:

```
>>> p = LeadingOnes()
```

But an optional target string can also be specified, in which case the number of matches to the target are maximized:

```
>>> import numpy as np
>>> p = LeadingOnes(target_string=np.array([1, 1, 0, 1, 1, 0, 0, 0 ,0]))
```

evaluate(*phenome*)

By default this counts the number of consecutive 1's at the start of the string:

```
>>> import numpy as np
>>> p = LeadingOnes()
>>> p.evaluate(np.array([1, 1, 1, 1, 0, 1, 0, 1, 1]))
4
```

Or, if a target string was given, we count matches:

```
>>> p = LeadingOnes(target_string=np.array([1, 1, 0, 1, 1, 0, 0, 0 ,0]))
>>> p.evaluate(np.array([1, 1, 1, 1, 0, 1, 0, 1, 1]))
2
```

class leap_ec.binary_rep.problems.**MaxOnes**(*target_string=None*, *maximize=True*)

Bases: *ScalarProblem*

Implementation of the classic max-ones problem, where the individuals are represented by a bit vector.

By default, the number of 1's in the phenome are maximized.

```
>>> p = MaxOnes()
```

But an optional target string can also be specified, in which case the number of matches to the target are maximized:

```
>>> import numpy as np
>>> p = MaxOnes(target_string=np.array([1, 1, 1, 1, 1, 0, 0, 0 ,0]))
```

evaluate(*phenome*)

By default this counts the number of 1's:

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> p = MaxOnes()
>>> p.evaluate(np.array([0, 0, 1, 1, 0, 1, 0, 1, 1]))
5
```

Or, if a target string was given, we count matches:

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> p = MaxOnes(target_string=np.array([1, 1, 1, 1, 1, 0, 0, 0 ,0]))
>>> p.evaluate(np.array([0, 0, 1, 1, 0, 1, 0, 1, 1]))
3
```

class leap_ec.binary_rep.problems.**TwoMax**(*maximize=True*)

Bases: *ScalarProblem*

A simple bi-modal function that returns the number of 1's if there are more 1's than 0's, else the number of 0's.

Also known as the "Twin-Peaks" problem.

evaluate(*phenome*)

```
>>> import numpy as np
>>> p = TwoMax()
```

The TwoMax problems returns the number over 1's if they are in the majority:

```
>>> p.evaluate(np.array([1, 1, 1, 1, 1, 1, 1, 0, 0, 0]))
7
```

Else the number of zeros: >>> p.evaluate(np.array([0, 0, 0, 1, 0, 0, 0, 1, 1, 1])) 6

Module contents

10.1.2 leap_ec.contrib package

Subpackages

leap_ec.contrib.transfer package

Submodules

leap_ec.contrib.transfer.sequential module

Experimental algorithms for sequential evolutionary transfer.

This module provides general mechanisms that allow an algorithm to learn from experience on past problems, and to reuse that experience on future problems.

class leap_ec.contrib.transfer.sequential.**PopulationSeedingRepertoire**(*initialize*, *algorithm*, *repfile=None*)

Bases: object

A repertoire method that works by seeding the population with individuals that were successful on past problems.

This works by injecting an *initialize* function into the wrapped algorithm's parameterization. During training, we inject a standard initializer (i.e. that create a random population), but when applying the repertoire, we use a special initializer that draws individuals from the repertoire's memory.

Parameters

- **initialize** – a standard initializer to create random populations during training.
- **algorithm** – the wrapped algorithm, which should take an initialize argument.
- **repfile** – an optional path to save the repertoire's memory to.

apply(*problem*, ***kwargs*)

Solve a new problem by injecting the all the individuals from the repertoire into the new initial population.

build_repertoire(*problems*, *problem_kwargs*)

Train the repertoire on a set of problems.

The best solution found on each problem will be saved into the repertoire.

export(*path*)

Write the repertoire of saved individuals out to a CSV file.

class leap_ec.contrib.transfer.sequential.**Repertoire**

Bases: ABC

Abstract definition of a 'repertoire' algorithm for evolutionary transfer.

A repertoire is a wrapper for an algorithm that can be trained on a set of problems, from which is learns and encodes some form of memory, which can be applied to new problems.

abstract apply(*problem*, *algorithm*)

Apply the repertoire to a new problem.

Parameters

- **problem** – the Problem to solve.
- **algorithm** – the algorithm to apply.

abstract build_repertoire(*problems*, *initialize*, *algorithm*)

Train the repertoire on a set of problems.

Parameters

- **problems** – a list of Problems to train on.
- **initialize** – a function that generates a population.
- **algorithm** – an algorithm function, which may be parameterized with an initialize function.

leap_ec.contrib.transfer.sequential.**initialize_seeded**(*initialize*, *seed_pop*)

A population initializer that injects a fixed list of seed individuals into the population, and fills the remaining space with newly generated individuals.

```
>>> import numpy as np
>>> from leap_ec.real_rep.initializers import create_real_vector
>>> random_init = create_real_vector(bounds=[[0, 0]] * 2)
>>> init = initialize_seeded(random_init, [np.array([5.0, 5.0]), np.array([4.5, -
↪6])])
>>> [init() for _ in range(5)]
[array([5., 5.]), array([ 4.5, -6. ]), array([0., 0.]), array([0., 0.]), array([0.,␣
↪0.])]
```

Module contents

Submodules

leap_ec.contrib.analysis module

Module contents

10.1.3 leap_ec.distrib package

Submodules

leap_ec.distrib.asynchronous module

This provides an asynchronous steady-state fitness evaluation pipeline operator.

A common feature here is a population of evaluated individuals that is asynchronously updated via dask.

leap_ec.distrib.asynchronous.**eval_population**(*population*, *client*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

Concurrently evaluate all the individuals in the given population

Parameters

- **population** – to be evaluated
- **client** – dask client
- **context** – for storing count of non-viable individuals

Returns
dask distrib iterator for futures

leap_ec.distrib.asynchronous.**greedy_insert_into_pop**(*individual*, *pop*, *max_size*)

Insert the given individual into the pop of evaluated individuals.

This is greedy because we always compare the new *individual* with the current weakest in the pop. This is similar to tournament selection.

Just insert individuals if the pop isn't at capacity yet

Parameters

- **individual** – that was just evaluated
- **pop** – of already evaluated individuals

Returns
None

leap_ec.distrib.asynchronous.**replace_if**(*new_individual*, *pop*, *index*)

Convenience function for possibly replacing pop[index] individual with new_individual depending on which has higher fitness.

Parameters

- **new_individual** – is a newly evaluated individual
- **pop** – of already evaluated individuals
- **index** – of individual in pop to be compared against

Returns
None

leap_ec.distrib.asynchronous.**steady_state**(*client*, *max_births*, *init_pop_size*, *pop_size*, *representation*, *problem*, *offspring_pipeline*, *inserter=<function greedy_insert_into_pop>*, *count_nonviable=False*, *evaluated_probe=None*, *pop_probe=None*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

Implements an asynchronous steady-state EA

Parameters

- **client** – Dask client that should already be set-up
- **max_births** – how many births are we allowing?

- **init_pop_size** – size of initial population sent directly to workers at start
- **pop_size** – how large should the population be?
- **representation** – of the individuals
- **problem** – to be solved
- **offspring_pipeline** – for creating new offspring from the pop
- **inserter** – function with signature (new_individual, pop, popsize) used to insert newly evaluated individuals into the population; defaults to greedy_insert_into_pop()
- **count_nonviable** – True if we want to count non-viable individuals towards the birth budget
- **evaluated_probe** – is a function taking an individual that is given the next evaluated individual; can be used to print newly evaluated individuals
- **pop_probe** – is an optional function that writes a snapshot of the population to a CSV formatted stream ever N births

Returns
the population containing the final individuals

leap_ec.distrib.asynchronous.**tournament_insert_into_pop**(*individual*, *pop*, *max_size*)

Insert the given individual into the pop of evaluated individuals.

Randomly select an individual in the pop, and the *individual* will replace the selected individual iff it has a better fitness. This is essentially binary tournament selection.

Just insert individuals if the pop isn't at capacity yet

TODO as with tournament selection, we should have an optional *k* to specify the tournament size. However, we have to be mindful that this is already k=2, so we would have to draw k-1 individuals from the population for comparison.

Parameters

- **individual** – that was just evaluated
- **pop** – of already evaluated individuals
- **max_size** – of the pop

Returns
None

leap_ec.distrib.evaluate module

contains common evaluate() used in sync.eval_pool and async.eval_pool

leap_ec.distrib.evaluate.**evaluate**(*individual='__no__default__'*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

concurrently evaluate the given individual

This is what's invoked on each dask worker to evaluate each individual.

We log the start and end times for evaluation.

An individual is viable if an exception is NOT thrown, else it is NOT a viable individual. If not viable, we increment the context['leap']['distrib'][‘non_viable’] count to track such instances.

This function sets:

individual.start_eval_time has the time() of when evaluation started. individual.stop_eval_time has the time() of when evaluation finished. individual.is_viable is True if viable, else False individual.exception will be assigned any raised exceptions individual.fitness will be NaN if not viable, else the calculated fitness individual.hostname is the name of the host on which this individual was evaluated individual.pid is the process ID associated with evaluating the individual

Parameters
individual – to be evaluated

Returns
evaluated individual

`leap_ec.distrib.evaluate.`**`is_viable`**(*individual*)

evaluate.evaluate() will set an individual's fitness to NaN and the attributes *is_viable* to False, and will assign any exception triggered during the individuals evaluation to *exception*. This just checks the individual's *is_viable*; if it doesn't have one, this assumes it is viable.

Parameters
individual – to be checked if viable

Returns
True if individual is viable

leap_ec.distrib.individual module

Subclass of core.Individual that adds some state relevant for distrib runs.

Adds:

- uuid for each individual
- birth ID, a unique birth number; first individual has ID 0, the last N-1.

class `leap_ec.distrib.individual.`**`DistributedIndividual`**(*genome*, *decoder=None*, *problem=None*)

Bases: *RobustIndividual*

`birth_id = count(202)`

Core individual that has unique UUID and birth ID.

`clone`()

Create a 'clone' of this *Individual*, copying the genome, but not fitness.

The fitness of the clone is set to *None*. A new UUID is generated and assigned to *sefl.uuid*. The *parents* set is updated to include the UUID of the parent. A shallow copy of the parent is made, too, so that ancillary state is also copied.

A deep copy of the genome will be created, so if your *Individual* has a custom genome type, it's important that it implements the *__deepcopy__()* method.

```
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.decoder import IdentityDecoder
>>> import numpy as np
>>> genome = np.array([0, 1, 1, 0])
>>> ind = Individual(genome, IdentityDecoder(), MaxOnes())
>>> ind_copy = ind.clone()
>>> ind_copy.genome == ind.genome
array([ True,  True,  True,  True])
>>> ind_copy.problem == ind.problem
```

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```
True
>>> ind_copy.decoder == ind.decoder
True
```

leap_ec.distrib.logger module

This provides a dask logging plugin that reports the hostname, worker ID, and process ID for each worker. This is useful for checking that all workers have been sanely assigned to targeted resources.

Note that once this plugin is installed that dask will ensure that each worker restarted after a failure gets the plugin re-installed, too.

class leap_ec.distrib.logger.**EvaluatorLogFilter**

Bases: `Filter`

Convenience for adding hostname and worker ID to log messages

Cribbed from https://stackoverflow.com/questions/55584115/python-logging-how-to-track-hostname-in-logs

filter(*record*)

Determine if the specified record is to be logged.

Is the specified record to be logged? Returns 0 for no, nonzero for yes. If deemed appropriate, the record may be modified in-place.

class leap_ec.distrib.logger.**WorkerLoggerPlugin**(*verbose=False*, **args*, ***kwargs*)

Bases: `WorkerPlugin`

This dask worker plugin adds a logger for each worker that reports the hostname, worker ID, and process ID.

Usage:

client.register_worker_plugin(WorkerLoggerPlugin()) after dask client is setup.

Then in code sent to worker:

worker = get_worker() worker.logger.info('This is a log message')

setup(*worker: Worker*)

This is invoked once for each worker on their startup. The scheduler will also ensure that all workers invoke this.

setup_logger(*worker*)

teardown(*worker: Worker*)

Run when the worker to which the plugin is attached to is closed

leap_ec.distrib.probe module

A collection of probe functions tailored for distrib evaluation

leap_ec.distrib.probe.**log_pop**(*update_interval*, *stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *header=True*)

Regularly update a CSV formatted stream with snapshots of the given population.

This is useful for asynchronous.steady_state() to regularly probe the regularly updated population.

Parameters

- **update_interval** – how often should we write a row?
- **stream** – open stream to which to write rows
- **header** – True if we want a header for the CSV file

Returns
a function for saving regular population snapshots

leap_ec.distrib.probe.**log_worker_location**(*stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *header=True*)

When debugging dask distribution configurations, this function can be used to track what machine and process was used to evaluate a given individual. Accumulates this information to the given stream as a CSV.

Suitable for being passed as the *evaluated_probe* argument for leap.distrib.asynchronous.steady_state().

Parameters

- **stream** – to which we want to write the machine details
- **header** – True if we want a header for the CSV file

Returns
a function for recording where individuals are evaluated

leap_ec.distrib.synchronous module

This provides a synchronous fitness evaluation pipeline operator.

leap_ec.distrib.synchronous.**eval_pool**(*next_individual='__no__default__'*, *client='__no__default__'*, *size='__no__default__'*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

concurrently evaluate *size* individuals

This is similar to ops.pool() in that it's a "sink" for accumulating individuals by "pulling" individuals from upstream the pipeline via *next_individual*. However, it's also like ops.evaluate() in that these individuals are concurrently evaluated via a map/reduce approach. We use dask to implement this evaluation mechanism.

If an exception is thrown while evaluating an individual, NaN is assigned as its fitness, individual.is_viable is set to False, and the associated exception is assigned to individual.exception as a post mortem aid; also core.context['leap']['distrib']['non_viables'] count is incremented if you want to track the number of non-viable individuals (i.e., those that have an exception thrown during evaluation); just remember to reset that between runs if that variable has been updated.

Parameters

- **next_individual** – iterator/generator for individual provider
- **client** – dask client through which we submit individuals to be evaluated
- **size** – how many individuals to evaluate simultaneously.
- **context** – for storing count of non-viable individuals

Returns
the pool of evaluated individuals

leap_ec.distrib.synchronous.**eval_population**(*population='__no__default__'*, *client='__no__default__'*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

Concurrently evaluate all the individuals in the given population

Parameters

- **population** – to be evaluated
- **client** – dask client
- **context** – for storing count of non-viable individuals

Returns
evaluated population

Module contents

10.1.4 leap_ec.executable_rep package

Submodules

leap_ec.executable_rep.cgp module

Cartesian genetic programming (CGP) representation.

The CGPDecoder does most of the work here: it converts a linear genome into a graph structure, and wraps the latter in a CGPExecutable (which knows how to execute the graph).

class leap_ec.executable_rep.cgp.**CGPDecoder**(*primitives*, *num_inputs*, *num_outputs*, *num_layers*, *nodes_per_layer*, *max_arity*, *prune: bool = True*, *levels_back=None*)

Bases: *Decoder*

Implements the genotype-phenotype decoding for Cartesian genetic programming (CGP).

A CGP genome is linear, but made up of one sub-sequence for each circuit element. In our version here, the first gene in each sub-sequence indicates the primitive (i.e., function) that node computes, and the subsequence genes indicate the inputs to that primitive.

That is, each node is specified by three genes *[p_id, i_1, i_2]*, where *p_id* is the index of the node's primitive, and *i_1, i_2* are the indices of the nodes that feed into it.

The sequence *[0, 2, 3]* indicates an element that computes the 0th primitive (as an index of the *primitives* list) and takes its inputs from nodes 2 and 3, respectively.

bounds()

Return the (min, max) allowed value they every gene may assume, taking into account the levels structure.

These values should be used by initialization and mutation operators to ensure that CGP's constraints are met.

```
>>> primitives = [ sum, lambda x: x[0] - x[1], lambda x: x[0] * x[1] ]
>>> decoder = CGPDecoder(primitives, num_inputs=2, num_outputs=2, num_layers=2,␣
↪nodes_per_layer=2, max_arity=2, levels_back=1)
>>> decoder.bounds()
[(0, 2), (0, 1), (0, 1), (0, 2), (0, 1), (0, 1), (0, 2), (2, 3), (2, 3), (0, 2),
↪ (2, 3), (2, 3), (0, 5), (0, 5)]
```

check_constraints(*next_individual: Iterator*)

An operator that checks whether individual's genomes satisfy the CGP constraints.

For example, say we have the following population:

```
>>> from leap_ec import Individual
>>> genome0 = np.array([ 0, 0, 1, 1, 0, 1, 2, 2, 3, 0, 2, 3, 4, 5 ])
>>> genome1 = np.array([ 0, 0, 1, 1, 0, 1, 2, 2, 3, 0, 2, 1, 4, 5 ])
>>> genome2 = np.array([ 0, 0, 1, 4, 0, 1, 2, 2, 3, 0, 2, 3, 4, 5 ])
>>> genome3 = np.array([ 0, 0, 1, 1, 0, 1, 2, 2, 3, 0, 2, 3, 4, 5, 3, 4, 5 ])
>>> genome4 = np.array([ 0.0, 0.0, 1.0, 1.0, 0, 1.0, 2.0, 2.0, 3.0, 0.0, 2.0, 3.
↪0, 4.0, 5.0 ])
>>> population = iter([ Individual(genome0),
...                     Individual(genome1),
...                     Individual(genome2),
...                     Individual(genome3),
...                     Individual(genome4) ])
```

Then given this decoder:

```
>>> primitives = [ sum, lambda x: x[0] - x[1], lambda x: x[0] * x[1] ]
>>> decoder = CGPDecoder(primitives, num_inputs=2, num_outputs=2, num_layers=2,␣
↪nodes_per_layer=2, max_arity=2, levels_back=1)
```

The first individual (genome0) satisfies the constraints:

```
>>> op = decoder.check_constraints
>>> next(op(population))
Individual<...>(...)
```

The next fails (genome1), however, because it violates the levels_back constraint:

```
>>> next(op(population))
Traceback (most recent call last):
...
ValueError: CGP constraints violated by individual: expected gene at locus 11␣
↪to be between the values of (2, 3) (inclusive), but found a value of 1.
```

Then genome2 fails because it contains a cycle:

```
>>> next(op(population))
Traceback (most recent call last):
...
ValueError: CGP constraints violated by individual: expected gene at locus 3 to␣
↪be between the values of (0, 2) (inclusive), but found a value of 4.
```

The new (genome3) fails because it has the incorrect genome length:

```
>>> next(op(population))
Traceback (most recent call last):
...
ValueError: CGP constraints violated by individual: genome of length 17 found,␣
↪but expected 14 genes.
```

And the last (genome4) fails because the genes are of the wrong type:

```
>>> next(op(population))
Traceback (most recent call last):
...
```

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```
ValueError: CGP constraints violated by individual: genome must contain only␣
↪integers, but the gene at locus 0 has a non-integral value of 0.0.
```

decode(*genome*, **args*, ***kwargs*)

Decode a linear CGP genome into an executable circuit.

```
>>> primitives = [ sum, lambda x: x[0] - x[1], lambda x: x[0] * x[1] ]
>>> decoder = CGPDecoder(primitives, num_inputs=2, num_outputs=2, num_layers=2,␣
↪nodes_per_layer=2, max_arity=2)
>>> genome = [ 0, 0, 1, 1, 0, 1, 2, 2, 3, 0, 2, 3, 4, 5 ]
>>> decoder.decode(genome)
<leap_ec.executable_rep.cgp.CGPExecutable object at ...>
```

get_input_sources(*genome*, *layer*, *node*)

Given a linear CGP genome, return the list of all of the input sources (as integers) which feed into the given node in the given layer.

get_output_sources(*genome*)

Given a linear CGP genome, return the list of nodes that connect to each output.

get_primitive(*genome*, *layer*, *node*)

Given a linear CGP genome, return the primitive object for the given node in the given layer.

initializer()

Convenience method that returns an initialization function for creating integer-vector genomes that obey this CGP representation's constraints.

num_cgp_nodes()

Return the total number of nodes that will be in the resulting CGP graph, including inputs and outputs.

For example, a 2x2 CGP individual with 2 outputs and 2 inputs will have $4 + 2 + 2 = 8$ total graph nodes.

```
>>> decoder = CGPDecoder([sum], num_inputs=2, num_outputs=2, num_layers=2,␣
↪nodes_per_layer=2, max_arity=2, levels_back=1)
>>> decoder.num_cgp_nodes()
8
```

num_genes()

The number of genes we expect to find in each genome. This will equal the number of outputs plus the total number of genes needed to specify the nodes of the graph.

The number of inputs has no effect on the size of the genome.

For example, a 2x2 CGP individual with 2 outputs an a *max_arity* of 2 will have 14 genes: $3*4 = 12$ genes to specify the primitive and inputs (1 + 2) for each internal node, plus 2 genes to specify the circuit outputs.

```
>>> decoder = CGPDecoder([sum], num_inputs=2, num_outputs=2, num_layers=2,␣
↪nodes_per_layer=2, max_arity=2, levels_back=1)
>>> decoder.num_genes()
14
```

static prune_graph(*graph*, *num_inputs: int*, *num_outputs: int*)

Prune parts of the graph that do not feed into any of the output nodes.

class leap_ec.executable_rep.cgp.**CGPExecutable**(*primitives*, *num_inputs*, *num_outputs*, *graph*)

Bases: *Executable*

Represents a decoded CGP circuit, which can be executed on inputs.

class leap_ec.executable_rep.cgp.**CGPWithParametersDecoder**(*primitives*, *num_inputs: int*, *num_outputs: int*, *num_layers: int*, *nodes_per_layer: int*, *max_arity: int*, *num_parameters_per_node: int*, *prune: bool = True*, *levels_back=None*)

Bases: *CGPDecoder*

A CGP decoder that takes a genome with two segments: an integer vector defining the usual CGP genome (functions and connectivity), and an auxiliary vector defining additional constant parameters to be fed into each node's function.

Much like bias weights in a neural network, these parameters allow a slightly different computation to be performed at different nodes that use the same primitive function.

decode(*genome*, **args*, ***kwargs*)

Decode a genome containing both a CGP graph and a list of auxiliary parameters.

```
>>> primitives=[
...                 lambda x, y, z: sum([x, y, z]),
...                 lambda x, y, z: (x - y)*z,
...                 lambda x, y, z: (x*y)*z
...             ]
>>> decoder = CGPWithParametersDecoder(primitives, num_inputs=2, num_outputs=2,␣
↪num_layers=2, nodes_per_layer=2, max_arity=2, num_parameters_per_node=1)
>>> genome = [ [ 0, 0, 1, 1, 0, 1, 2, 2, 3, 0, 2, 3, 4, 5 ], [ 0.5, 15, 2.7, 0.
↪0 ] ]
>>> executable = decoder.decode(genome)
>>> executable
<leap_ec.executable_rep.cgp.CGPExecutable object at ...>
```

Now node #2 (i.e. the first computational node, skipping the two inputs #0 and #1) should have a parameter value of 0.5, and so on:

```
>>> executable.graph.nodes[2]['parameters']
[0.5]
>>> executable.graph.nodes[3]['parameters']
[15]
>>> executable.graph.nodes[4]['parameters']
[2.7]
>>> executable.graph.nodes[5]['parameters']
[0.0]
```

initialize(*parameters_initializer*)

Return an initializer for creating the two-segment genomes that this decoder expects as input.

The first segment will be initialized with our standard CGP initializer. The second will use the provided initializer.

class leap_ec.executable_rep.cgp.**FunctionPrimitive**(*func*, *f_arity: int*)

Bases: *Primitive*

A convenience wrapper that defines a generic primitive function for CGP from a function (ex. a lambda). Basically this lets us define a function that we can also query the arity of.

```
>>> f = FunctionPrimitive(lambda x, y: x ^ y, 2)
>>> f(True, False)
True
>>> f.arity
2
```

property arity

How many args are used inside the __call__ function

class leap_ec.executable_rep.cgp.**NAND**

Bases: *Primitive*

Primitive NAND function for use in genetic programming.

```
>>> f = NAND()
>>> f(True, True)
False
>>> f(True, False)
True
```

property arity

How many args are used inside the __call__ function

class leap_ec.executable_rep.cgp.**NotX**

Bases: *Primitive*

Primitive NOT function for use in genetic programming.

```
>>> f = NotX()
>>> f(True)
False
>>> f(False)
True
```

property arity

How many args are used inside the __call__ function

class leap_ec.executable_rep.cgp.**Primitive**

Bases: ABC

Abstract class that primitive functions inherit from for CGP.

You don't need to use this class to define primitive for CGP. But if you do, it allows CGP to know the arity of each function— which CGPDecoder can use to prune un-needed edges in the resulting graph. This sometimes leads better performance or simpler graphs.

abstract property arity: int

How many args are used inside the __call__ function

leap_ec.executable_rep.cgp.**cgp_art_primitives**()

Returns a standard set of primitives that Ashmore and Miller originally published in an online report on "Evolutionary Art with Cartesian Genetic Programming" (2004).

leap_ec.executable_rep.cgp.**cgp_genome_mutate**(*cgp_decoder*, *expected_num_mutations: Optional[float] = None*, *probability: Optional[float] = None*)

leap_ec.executable_rep.cgp.**cgp_mutate**(*cgp_decoder*, *expected_num_mutations: Optional[float] = None*, *probability: Optional[float] = None*)

A special integer-vector mutation operator that respects the constraints on valid genomes that are implied by the parameters of the given CGPDecoder.

Parameters

- **cgp_decoder** – the Decoder, which informs us about the bounds genes should obey
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)
- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)

leap_ec.executable_rep.cgp.**create_cgp_vector**(*cgp_decoder*)

leap_ec.executable_rep.executable module

This module provides executable object representations. An *Executable* in LEAP represents problem solutions as functions, agent controllers, etc.

A LEAP *Executable* is a kind of phenotype, typically constructed when we use a `Decoder` to convert a genotypic representation of the object into an executable phenotype.

Executable are also just callable functors, so you can use them in your code like any other function.

class leap_ec.executable_rep.executable.**ArgmaxExecutable**(*wrapped_executable*)

Bases: *Executable*

Wraps another *Executable* with logic that returns the index of the highest output.

For example, we can use this to convert the class selection distribution output by a softmax layer to an integer representing the index of the most likely class:

```
>>> executable = lambda x: [ x[0] ^ x[1], x[0] & x[1], x[0] + x[1] ]
>>> wrapped = ArgmaxExecutable(executable)
```

```
>>> executable([1, 1])
[0, 1, 2]
```

```
>>> wrapped([1, 1])
2
```

class leap_ec.executable_rep.executable.**Executable**

Bases: `ABC`

class leap_ec.executable_rep.executable.**KeyboardExecutable**(*input_space*, *output_space*, *keymap=<function KeyboardExecutable.<lambda>>*)

Bases: *Executable*

A non-autonomous *Executable* phenotype that allows users to control an agent via the keyboard.

Parameters

- **input_space** – space of possible inputs (ignored)
- **output_space** – the space of possible actions to sample from, satisfying the *Space* interface used by OpenAI Gym
- **keymap** – *dict* mapping keys to elements of the output space

key_press(*key*, *mod*)

You'll need to assign this function to your environment's key_press handler.

key_release(*key*, *mod*)

You'll need to assign this function to your environment's key_release handler.

class leap_ec.executable_rep.executable.**RandomExecutable**(*input_space*, *output_space*)

Bases: *Executable*

A trivial *Executable* phenotype that samples a random value from its output space.

Parameters

- **input_space** – space of possible inputs (ignored)
- **output_space** – the space of possible actions to sample from, satisfying the *Space* interface used by OpenAI Gym

class leap_ec.executable_rep.executable.**WrapperDecoder**(*wrapped_decoder*, *decorator*)

Bases: *Decoder*

A decoder that takes an executable object output by the wrapped *Decoder*, and then wrapps that *Executable* with an additional decorator function.

For example, if we have a *Decoder* that produces *Executable* objects whose output is governed by a softmax layer (i.e. a distribution), we can use this class to decorate them with an *ArgmaxExecutable* to transform their output into an integer.

decode(*genome*, **args*, ***kwargs*)

Parameters
genome – a genome you wish to convert

Returns
the phenotype associated with that genome

leap_ec.executable_rep.neural_network module

Tools for decoding and executing a neural network from its genetic representation.

class leap_ec.executable_rep.neural_network.**GraphPhenotypeProbe**(*modulo=1*, *ax=None*, *weights: bool = False*, *weight_multiplier: float = 1.0*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

Bases: `object`

Visualize the graph for the best individual in the population.

This requires that the phenotypes of the individuals in the population have a *graph* attribute that provides a *networkx* graph object.

class leap_ec.executable_rep.neural_network.**SimpleNeuralNetworkDecoder**(*shape: ~typing.Tuple[int], activation=<function sigmoid>*)

Bases: `object`

Decode a real-vector genome into a neural network by treating it as a test_sequence of weight matrices.

For example, say we have a linear real-valued made up of 29 values:

```
>>> genome = list(range(0, 29))
```

We can decode this into a neural network with 4 inputs, two hidden layers (of size 3 and 2), and 2 outputs like so:

```
>>> from leap_ec.executable_rep import neural_network
>>> dec = neural_network.SimpleNeuralNetworkDecoder([ 4, 3, 2, 2 ])
>>> nn = dec.decode(genome)
```

Parameters

shape (*(int)*) – the size of each layer of the network, i.e. (inputs, hidden nodes, outputs). The shape tuple must have at least two elements (inputs + bias weight and outputs): each additional value is treated as a hidden layer. Note also that we expect a bias weight to exist for the inputs of each layer, so the number of weights at each layer will be set to 1 greater than the number of inputs you specify for that layer.

decode(*genome*, **args*, ***kwargs*)

Decode a genome into a *SimpleNeuralNetworkExecutable*.

class leap_ec.executable_rep.neural_network.**SimpleNeuralNetworkExecutable**(*weight_matrices*, *activation*)

Bases: *Executable*

A simple fixed-architecture neural network that can be executed on inputs.

Takes a list of weight matrices and an activation function as arguments. The weight matrices each must have 1 row more than the previous layer's outputs, to support a bias node that is implicitly connected to each layer.

For example, here we build a network with 10 inputs, two hidden layers (with 5 and 3 nodes, respectively), and 5 output nodes, and random weights:

```
>>> import numpy as np
>>> from leap_ec.executable_rep import neural_network
>>> n_inputs = 10
>>> n_hidden1, n_hidden2 = 5, 3
>>> n_outputs = 5
>>> weights = [ np.random.uniform((n_inputs + 1, n_hidden1)),
...             np.random.uniform((n_hidden1 + 1, n_hidden2)),
...             np.random.uniform((n_hidden2 + 1, n_outputs)) ]
>>> nn = neural_network.SimpleNeuralNetworkExecutable(weights, neural_network.
↪sigmoid)
```

property graph

Create a graph representation of this neural network (ex., for visualization).

property num_hidden_layers

The number of hidden layers in this network.

property num_inputs

The number of inputs the network receives.

property num_outputs

The number of outputs the network produces.

leap_ec.executable_rep.neural_network.**relu**(*x*)

A rectified linear unit (ReLu) activation function. Accept array-like inputs, and uses NumPy for efficient computation.

leap_ec.executable_rep.neural_network.**sigmoid**(*x*)

A logistic sigmoid activation function. Accepts array-like inputs, and uses NumPy for efficient computation.

leap_ec.executable_rep.neural_network.**softmax**(*x*)

A softmax activation function. Accepts array-like input and normalizes each element relative to the others.

leap_ec.executable_rep.problems module

class leap_ec.executable_rep.problems.**EnvironmentProblem**(*runs: int*, *steps: int*, *environment*, *fitness_type: str*, *gui: bool*, *stop_on_done=True*, *maximize=True*)

Bases: *ScalarProblem*

Defines a fitness function over `Executable` by evaluating them within a given environment.

Parameters

- **runs** (*int*) – The number of independent runs to aggregate data over.
- **steps** (*int*) – The number of steps to run the simulation for within each run.
- **environment** – A simulation environment corresponding to the OpenAI Gym environment interface.
- **behavior_fitness** – A function

evaluate(*phenome*)

Run the environmental simulation using *executable* phenotype as a controller, and use the resulting observations & rewards to compute a fitness value.

property num_inputs

Return the number of dimensions in the environment's input space.

property num_outputs

Return the number of dimensions in the environment's action space.

static space_dimensions(*observation_space*) → int

Helper to get the number of dimensions (variables) in an OpenAI Gym space.

The point of this helper is that it works on simple spaces:

```
>>> from gymnasium import spaces
>>> discrete = spaces.Discrete(8)
>>> EnvironmentProblem.space_dimensions(discrete)
1
```

Box spaces:

```
>>> box = spaces.Box(low=-1.0, high=2.0, shape=(3, 4), dtype=np.float32)
>>> EnvironmentProblem.space_dimensions(box)
12
```

And Tuple spaces:

```
>>> tup = spaces.Tuple([discrete, box])
>>> EnvironmentProblem.space_dimensions(tup)
13
```

class leap_ec.executable_rep.problems.**ImageXYProblem**(*path*, *maximize=False*)

Bases: *ScalarProblem*

A problem that takes a function that generates an image defined over (x, y) coordinates and computed its fitness based on its match to an externally-defined image.

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

static generate_image(*executable*, *width*, *height*)

class leap_ec.executable_rep.problems.**TruthTableProblem**(*boolean_function*, *num_inputs*, *num_outputs*, *name: Optional[str] = None*, *pad_inputs=False*, *maximize=True*)

Bases: *ScalarProblem*

Defines a fitness function over a `Executable` by evaluating it against each row of a given Boolean function's truth table.

Both the executable we receive and the *boolean_function* we compare against should return a list of 1 or more outputs.

evaluate(*phenome*)

Say our object function is $(x_0 \wedge x_1) \vee x_3$:

```
>>> problem = TruthTableProblem(lambda x: [ (x[0] and x[1]) or x[2] ], num_
↪inputs=3, num_outputs=1)
```

The truth table for this Boolean function has eight entries:

F F F=F F F T=T F T F=F F T T=T T F F=F T F T=T T T F=T T T T=T

Now consider a different function, $(x_0 \wedge x_1) \oplus x_3$.

```
>>> executable = lambda x: [ (x[0] and x[1]) ^ x[2] ]
```

This function's truth table differs from the first one by exactly one entry (in the second one, TTT=F). So we expect a fitness value of $7/8 = 0.875$:

```
>>> from leap_ec import Individual
>>> problem.evaluate(executable)
0.875
```

Note that we our lambda functions above return a list that contains a computed value, rather than just the value directly. This is because this framework allows us to work with functions of more than one output:

```
>>> problem = TruthTableProblem(lambda x: [ x[0] and x[1], x[0] or x[1] ], num_
↪inputs=3, num_outputs=2)
>>> problem.evaluate(lambda x: [ x[0] and x[1], x[0] or x[1] ])
1.0
```

leap_ec.executable_rep.rules module

Pitt-approach rule systems are one of the two basic approach to evolving rule-based programs (alongside Michigan-approach systems). In Pitt systems, every individual encodes a complete set of rules for producing an output given a set of inputs.

Evolutionary rule systems (also known as learning classifier systems) are often used to create controller for agents (i.e. for reinforcement learning problems), or to evolve classifiers for pattern recognition (i.e. supervised learning).

This module provides a basic Pitt-approach system that uses the *spaces* API from OpenAI Gym to define input and output spaces for rule conditions and actions, respectively.

class leap_ec.executable_rep.rules.**PittRulesDecoder**(*input_space*, *output_space*, *memory_space=None*, *priority_metric=None*)

Bases: *Decoder*

A Decoder that contructs a Pitt-approach rule system phenotype (*PittRulesExecutable*) out of a real-valued genome.

We use the OpenAI Gym *spaces* API to define the types and dimensionality of the rule system's inputs and outputs.

Parameters

- **input_space** – an OpenAI-gym-style space defining the inputs
- **output_space** – an OpenAI-gym-style space defining the outputs
- **priority_metric** – a PittRulesExecutable.PriorityMetric enum value defining how matching rules are deconflicted within the controller
- **num_memory_registers** – the number of stateful memory registers that each rule considers as additional inputs

If, for example, we want to evolve controllers for a robot that has 3 real-valued sensor inputs and 4 mutually exclusive actions to choose from, we might use a Box and Discrete space, respectively, from *gym.spaces*:

```
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=0, high=1.0, shape=(1, 3), dtype=np.float32)
>>> out_ = spaces.Discrete(4)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

property action_bounds

The bounds of permitted values on action genes within each rule.

For example, the following *decoder*

```
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=0, high=1.5, shape=(1, 3), dtype=np.float32)
>>> out_ = spaces.Discrete(4)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

allows just one output value gene in each rule, with a maximum value of 4.

Bounds are inclusive, so they look like this:

```
>>> decoder.action_bounds
[(0, 3)]
```

bounds(*num_rules*)

Return the (low, high) bounds that it makes sense for each gene to vary within.

```
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=0, high=1.0, shape=(1, 3), dtype=np.float32)
>>> out_ = spaces.Discrete(4)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
>>> decoder.bounds(num_rules=4)
[[(0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0,␣
↪3)], [(0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0),␣
↪(0, 3)], [(0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.
↪0), (0, 3)], [(0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.0, 1.0), (0.
↪0, 1.0), (0, 3)]]
```

property condition_bounds

The bounds of permitted values on condition genes within each rule.

For example, the following *decoder*

```
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=0, high=1.5, shape=(1, 3), dtype=np.float32)
>>> out_ = spaces.Discrete(4)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

produces bounds that restrict the *low* and *high* value of each condition's range between 0 and 1.5:

```
>>> decoder.condition_bounds
[(0.0, 1.5), (0.0, 1.5), (0.0, 1.5), (0.0, 1.5), (0.0, 1.5), (0.0, 1.5)]
```

decode(*genome*, **args*, ***kwargs*)

Decodes a real-valued genome into a PittRulesExecutable.

For example, say we have a Decoder that takes continuous inputs from a 2-D box and selects between two discrete actions:

```
>>> import numpy as np
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=np.array((0, 0)), high=np.array((1.0, 1.0)), dtype=np.
```

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```
↪float32)
>>> out_ = spaces.Discrete(2)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

Now we can take genomes that represent each rule as as segment of the form *[low, high, low, high, action]* and converts them into executable controllers:

```
>>> genome = [ [ 0.0,0.6, 0.0,0.4, 0],
...             [ 0.4,1.0, 0.6,1.0, 1] ]
>>> decoder.decode(genome)
<leap_ec.executable_rep.rules.PittRulesExecutable object at ...>
```

genome_to_rules(*genome*)

Convert a genome into a list of Rules.

Usage example:

```
>>> import numpy as np
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=np.array((0, 0)), high=np.array((1.0, 1.0)), dtype=np.
↪float32)
>>> out_ = spaces.Discrete(2)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

Now we can take genomes that represent each rule as as segment of the form *[low, high, low, high, action]* and converts them into *Rule* objects:

```
>>> genome = [ [ 0.0,0.6, 0.0,0.4, 0],
...             [ 0.4,1.0, 0.6,1.0, 1] ]
>>> decoder.genome_to_rules(genome)
[Rule(conditions=[(0.0, 0.6), (0.0, 0.4)], actions=[0]), Rule(conditions=[(0.4,␣
↪1.0), (0.6, 1.0)], actions=[1])]
```

initializer(*num_rules: int*)

Returns an initializer function that can generate genomes according to the segmented scheme that we use for rule sets—i.e. with the appropriate number of segments, inputs, outputs, and hidden registers.

For instance, if we have the following decoder:

```
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=0, high=1.0, shape=(1, 3), dtype=np.float32)
>>> out_ = spaces.Discrete(4)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

Then we can get an initializer like so that creates genomes compatible with the decoder when called:

```
>>> initialize = decoder.initializer(num_rules=4)
>>> initialize()
[array(...), array(...), array(...), array(...)]
```

Notice that it creates four top-level segments (one for each rule), and that the condition bounds for each input within a rule are wrapped in tuple sub-segments.

mutator(*condition_mutator*, *action_mutator*)

Returns a mutation operator that properly handles the segmented genome representation used for rule sets.

This wraps two different mutation operators you provide, so that mutation can be configured differently for rule conditions and rule actions, respectively.

Parameters

- **condition_mutator** – a mutation operator to use for the condition genes in each rule.
- **action_mutator** – a mutation operator to use for the action genes in each rule.

For example, often we'll apply a rule system to a real-valued observation space and an integer-valued action space.

```
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=0, high=1.0, shape=(1, 3), dtype=np.float32)
>>> out_ = spaces.Discrete(4)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

These two spaces call for different mutation strategies:

```
>>> from leap_ec.real_rep.ops import genome_mutate_gaussian
>>> from leap_ec.int_rep.ops import individual_mutate_randint
>>> mutator = decoder.mutator(
...                     condition_mutator=genome_mutate_gaussian,
...                     action_mutator=individual_mutate_randint
... )
```

property num_genes_per_rule

This property reports the total number of genes that specify each rule.

For example, the following *decoder*

```
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=0, high=1.0, shape=(1, 3), dtype=np.float32)
>>> out_ = spaces.Discrete(4)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

takes rule genomes that have 7 values in each segment: 6 to specify the condition ranges (*(low, high)* for each of 3 inputs), and 1 to specify the output action.

```
>>> decoder.num_genes_per_rule
7
```

property num_inputs

This property reports the number of dimensions in the system's input space.

For example, the following *decoder*

```
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=0, high=1.0, shape=(1, 12), dtype=np.float32)
>>> out_ = spaces.Discrete(4)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

has a 12-dimensional input space:

```
>>> decoder.num_inputs
12
```

property num_memory_registers

property num_outputs

This property reports the number of dimensions in the system's output space.

For example, the following *decoder*

```
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=0, high=1.0, shape=(1, 12), dtype=np.float32)
>>> out_ = spaces.Discrete(4)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

has a 1-dimensional output space:

```
>>> decoder.num_outputs
1
```

class leap_ec.executable_rep.rules.**PittRulesExecutable**(*input_space*, *output_space*, *rules*, *priority_metric*, *init_mem=[]*)

Bases: *Executable*

An *Executable* phenotype that interprets a Pittsburgh-style ruleset and outputs the appropriate action.

Parameters

- **input_space** – an OpenAI-gym-style space defining the inputs
- **output_space** – an OpenAI-gym-style space defining the outputs
- **init_memory** – a list of initial values for the memory registers
- **rules** – a list of *Rule* objects
- **priority_metric** – the rule prioritization strategy used to resolve conflicts

Rulesets are lists of rules. Rules are lists of the form *[c1 c1' c2 c2' … cn cn' a1 … am m1 … mr]*, where *(cx, cx')* are are the min and max bounds that the rule covers, *a1 .. am* are the output actions, and *m1 … mr* are values to write to the memory registers.

For example, this ruleset has two rules. The first rule covers the square bounded by *(0.0, 0.6)' and `(0.0, 0.4)*, returning the output action *0* if the input falls within that range:

```
>>> rules = [ Rule(conditions=[(0.0, 0.6), (0.0, 0.4)], actions=[0]),
...           Rule(conditions=[(0.4, 1.0), (0.6, 1.0)], actions=[1])
...         ]
```

The input and output spaces are defined in the style of OpenAI gym. For example, here's how you would set up a PittRulesExecutable with the above ruleset that takes two continuous input variables on *(0.0, 1.0)*, and outputs discrete values in *{0, 1}*:

```
>>> import numpy as np
>>> from gymnasium import spaces
>>> input_space = spaces.Box(low=np.array((0, 0)), high=np.array((1.0, 1.0)),␣
↪dtype=np.float32)
>>> output_space = spaces.Discrete(2)
```

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```
>>> rules = PittRulesExecutable(input_space, output_space, rules,
...                             priority_metric=PittRulesExecutable.PriorityMetric.
↪RULE_ORDER)
```

class PriorityMetric(*value*)

Bases: Enum

An enumeration.

GENERALITY = 2

PERIMETER = 3

RULE_ORDER = 1

class leap_ec.executable_rep.rules.**PlotPittRuleProbe**(*decoder*, *plot_dimensions: (<class 'int'>, <class 'int'>) = (0, 1)*, *ax=None*, *xlim=(0, 1)*, *ylim=(0, 1)*, *modulo=1*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

Bases: object

A visualization operator that takes the best individual in the population and plots the condition bounds for each rule, i.e. as boxes over the input space.

Parameters

- **num_inputs** (*int*) – the number of inputs in the sensor space
- **num_outputs** (*int*) – the number of output actions
- **plot_dimensions** ((*int, int*)) – which two dimensions of the input space to visualize along the x and y axes; defaults to the first two dimensions, (0, 1)
- **ax** – the matplotlib axis to plot to; if None (the default), new Axes are created
- **xlim** ((*float, float*)) – bounds for the horizontal axis
- **ylim** ((*float, float*)) – bounds for the vertical axis
- **modulo** (*int*) – the interval (in generations) to go between each visualization; i.e. if set to 10, then the visualization will be updated every 10 generations
- **context** – the context objected that the generation count is read from (should be updated by the algorithm at each generation)

This probe requires a *decoder*, which it uses to parse individual genomes into sets of rules that it can visualize:

```
>>> import numpy as np
>>> from gymnasium import spaces
>>> in_ = spaces.Box(low=np.array((0, 0)), high=np.array((1.0, 1.0)), dtype=np.
↪float32)
>>> out_ = spaces.Discrete(2)
>>> decoder = PittRulesDecoder(input_space=in_, output_space=out_)
```

Now we can create the probe itself:

```
>>> probe = PlotPittRuleProbe(decoder)
```

If we feed it a population of a single individual, we'll see all that individual's rules visualized. Like all LEAP probes, it returns the population unmodified. This allows the probe to be inserted into an EA's operator pipeline.

```
>>> from leap_ec.individual import Individual
>>> ruleset = np.array([[0.0, 0.6, 0.0, 0.5, 0],
...                     [0.4, 1.0, 0.3, 1.0, 1],
...                     [0.1, 0.2, 0.1, 0.2, 0],
...                     [0.5, 0.6, 0.8, 1.0, 1]])
>>> pop = [Individual(genome=ruleset)]
>>> probe(pop)
[Individual<...>(...)]
```

class leap_ec.executable_rep.rules.**Rule**(*conditions*, *actions*)

Bases: tuple

property actions

Alias for field number 1

property conditions

Alias for field number 0

Module contents

10.1.5 leap_ec.int_rep package

Submodules

leap_ec.int_rep.initializers module

Initializers for integer-valued genomes.

leap_ec.int_rep.initializers.**create_int_vector**(*bounds*)

A closure for initializing lists of integers for int-vector genomes, sampled from a uniform distribution.

Having a closure allows us to just call the returned function N times in *Individual.create_population()*.

TODO Allow either a single tuple or a sequence of tuples for bounds. —Siggy

Parameters

bounds – a list of (min, max) values bounding the uniform sampline of each element

Returns

A function that, when called, generates a random genome.

```
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.real_rep.problems import SpheroidProblem
>>> bounds = [(0, 1), (-5, 5), (-1, 100)]
>>> population = Individual.create_population(10, create_int_vector(bounds),
...                                           decoder=IdentityDecoder(),
...                                           problem=SpheroidProblem())
```

leap_ec.int_rep.ops module

Evolutionary operators for maniuplating integer-vector genomes.

leap_ec.int_rep.ops.**genome_mutate_binomial**(*std='__no__default__', bounds: list = '__no__default__', expected_num_mutations: float = None, probability: float = None, n: int = 10000*)

Perform additive binomial mutation of a particular genome.

```
>>> import numpy as np
>>> genome = np.array([42, 12])
>>> bounds = [(0,50), (-10,20)]
>>> genome_op = genome_mutate_binomial(std=0.5, bounds=bounds,
...                                    expected_num_mutations=1)
>>> new_genome = genome_op(genome)
```

leap_ec.int_rep.ops.**individual_mutate_randint**(*genome='__no__default__', bounds: list = '__no__default__', expected_num_mutations=None, probability=None*)

Perform random-integer mutation on a particular genome.

```
>>> import numpy as np
>>> genome = np.array([42, 12])
>>> bounds = [(0,50), (-10,20)]
>>> new_genome = individual_mutate_randint(genome, bounds, expected_num_mutations=1)
```

Parameters

- **genome** – test_sequence of integers to be mutated
- **bounds** – test_sequence of bounds tuples; e.g., [(1,2),(3,4)]
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)
- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)

leap_ec.int_rep.ops.**mutate_binomial**(*next_individual: Iterator = '__no__default__', std: float = '__no__default__', bounds: list = '__no__default__', expected_num_mutations: float = None, probability: float = None, n: int = 10000*) → Iterator

Mutate genes by adding an integer offset sampled from a binomial distribution centered on the current gene value.

This is very similar to applying additive Gaussian mutation and then rounding to the nearest integer, but does so in a way that is more natural for integer-valued genes.

Parameters

- **std** (*float*) – standard deviation of the binomial distribution
- **bounds** – list of pairs of hard bounds to clip each gene by (to prevent mutation from carrying a gene value outside an allowed range)
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)

- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)
- **n** (*int*) – the number of "coin flips" to use in the binomial process (defaults to 10000)

Usage example:

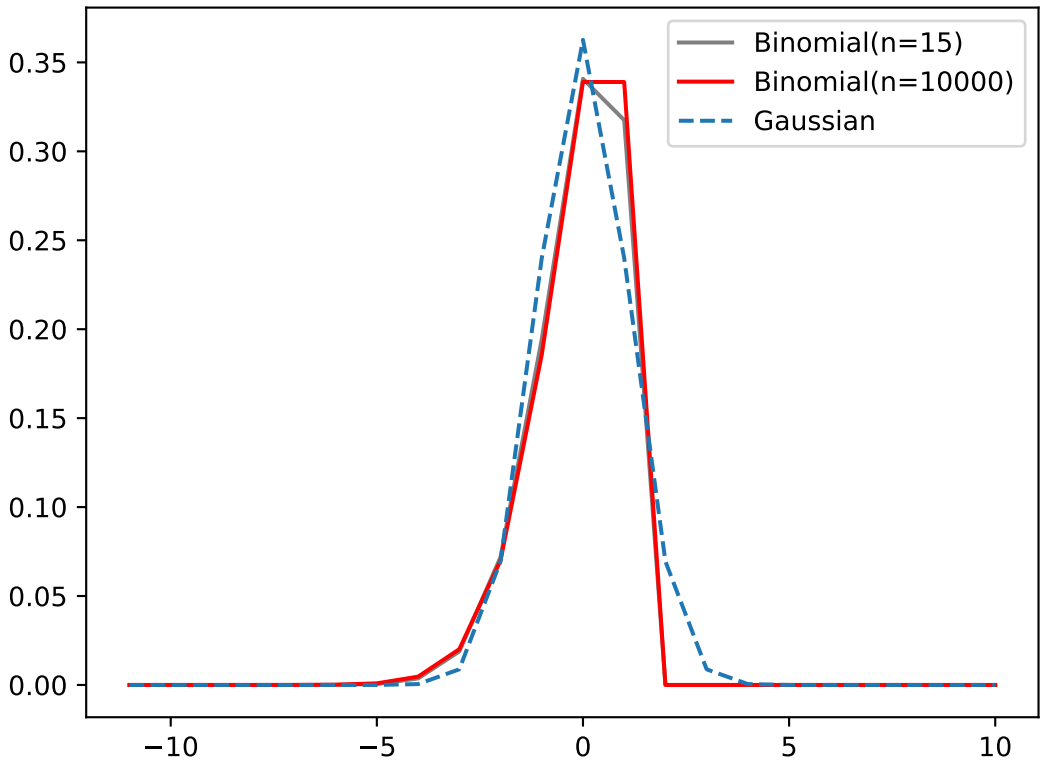
```
>>> from leap_ec.individual import Individual
>>> from leap_ec.int_rep.ops import mutate_binomial
>>> import numpy as np
>>> population = iter([Individual(np.array([1, 1]))])
>>> operator = mutate_binomial(std=2.5,
...                            bounds=[(0, 10), (0, 10)],
...                            expected_num_mutations=1)
>>> mutated = next(operator(population))
```

The *std* parameter can also be given as a list with a value to use for each gene locus:

```
>>> population = iter([Individual(np.array([1, 1]))])
>>> operator = mutate_binomial(std=[2.5, 3.0],
...                            bounds=[(0, 10), (0, 10)],
...                            expected_num_mutations=1)
>>> mutated = next(operator(population))
```

Note: The binomial distribution is defined by two parameters, n and p. Here we simplify the interface by asking instead for an *std* parameter, and fixing a high value of n by default. The value of p needed to obtain the given *std* is computed for you internally.

As the plots below illustrate, the binomial distribution is approximated by a Gaussian. For high n and large standard deviations, the two are effectively equivalent. But when the standard deviation (and thus binomial p parameter) is relatively small, the approximation becomes less accurate, and the binomial differs somewhat from a Gaussian.



---

leap_ec.int_rep.ops.**mutate_randint**(*next_individual: Iterator = '__no__default__', bounds='__no__default__', expected_num_mutations=None, probability=None*) → Iterator

Perform randint mutation on each individual in an iterator (population).

This operator replaces randomly selected genes with an integer samples from a uniform distribution.

Parameters

- **bounds** – test_sequence of bounds tuples; e.g., [(1,2),(3,4)]
- **expected_num_mutations** – on average how many mutations done (specificy either this or probability, but not both)
- **probability** – the probability of mutating any given gene (specificy either this or expected_num_mutations, but not both)

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.int_rep.ops import mutate_randint
>>> import numpy as np
```

```
>>> population = iter([Individual(np.array([1, 1]))])
>>> operator = mutate_randint(expected_num_mutations=1, bounds=[(0, 10), (0, 10)])
>>> mutated = next(operator(population))
```

Module contents

10.1.6 leap_ec.landscape_features package

Submodules

leap_ec.landscape_features.exploratory module

This module implements features that are common in exploratory landscape analysis (ELA).

The gist of exploratory landscape analysis is that it provides a set of

1. statistical features for measuring properties of continuous fitness landscapes, with
2. an emphasis on using a small number of fitness samples to compute the features.

The big idea is that these are features you can use to measure and understand a problem before solving it.

There are dozens of traditional ELA features. Most are described in the following two seminal papers:

- Mersmann, Olaf, et al. "Exploratory landscape analysis." *Proceedings of the 13th annual conference on Genetic and evolutionary computation.* 2011.
- Kerschke, Pascal, et al. "Cell mapping techniques for exploratory landscape analysis." *EVOLVE-A Bridge between Probability, Set Oriented Numerics, and Evolutionary Computation V.* Springer, Cham, 2014. 115-131.

class leap_ec.landscape_features.exploratory.**ELAConvexity**(*problem*, *representation*, *design_individuals: list*, *num_convexity_tests: int = 1000*)

Bases: `object`

This class provides features that empirically estimate the degree to which a landscape is convex or linear.

Parameters

- **problem** – the fitness landscape to analyze (must accept real-vector phenomes).
- **representation** – a `Representation` that can be used to sample and decode new individuals (must decode individuals into a real-vector phenome).
- **design_individuals** – an initial sample individuals that is used as the basis for analysis (their fitnesses must already have been evaluated).
- **num_convexity_tests** (*int*) – the number of pairwises tests (and additional fitness samples) to use in estimating convexity features.

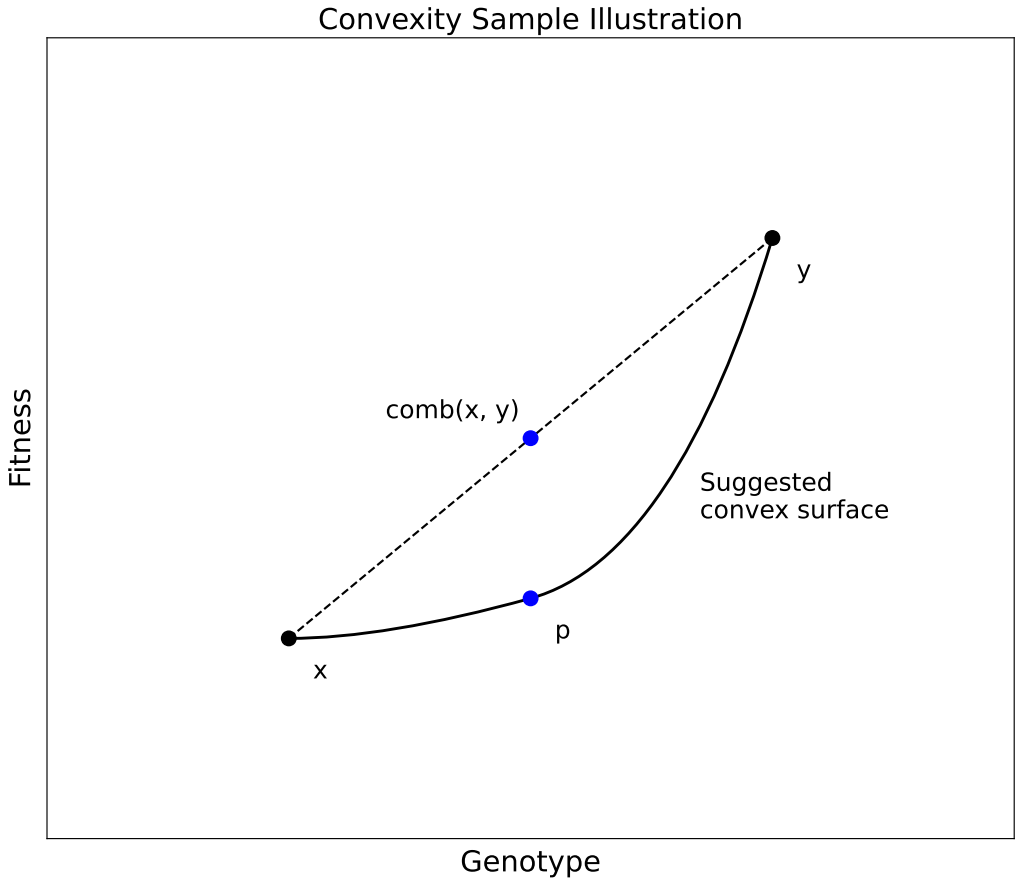
The algorithm used here is best explained by the following graphic:

We take a number of random pairs x, y of individuals from the initial design (sample), and compute a third point p from them via a convex combination of the original two points (i.e. a random point lying along the line between the original points). Then we compare the fitness $f(p)$ of the new point to the fitness that the point *would* have if the landscape were perfectly linear between the original points. That is, we compute the *difference* between the complex combination of the parents' *fitness values* $f(x)$ and $f(y)$ and the fitness value of their *genomes'* complex combination, $f(p)$.

$$\delta = f(p) - \text{comb}(f(x), f(y))$$

When $\delta \approx 0$, it suggests local linearity of the fitness landscape, whereas when $\delta < 0$, convexity is suggested.

To compute these features, we'll need a problem and a representation:


Convexity Sample Illustration
Fitness
Genotype
y
comb(x, y)
Suggested
convex surface
p
x

```
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.individual import Individual
>>> from leap_ec.representation import Representation
>>> from leap_ec.real_rep import initializers, problems
```

```
>>> DIMENSIONS = 10
>>> N_SAMPLES = 50*DIMENSIONS
>>> problem = problems.SpheroidProblem()
```

```
>>> representation = Representation(
...     initialize=initializers.create_real_vector(bounds=[(-5.12, 5.
↪12)]*DIMENSIONS)
... )
```

We'll also need an initial sample of individuals must be provided, with its fitnesses already evaluated:

```
>>> initial_sample = representation.create_population(N_SAMPLES, problem)
>>> initial_sample = Individual.evaluate_population(initial_sample);
```

The feature computation uses this as its initial "experiment design," and then takes additional fitness samples as needed when we call the constructor:

```
>>> convex = ELAConvexity(problem, representation, design_individuals=initial_
↪sample)
```

The resulting object can be used to compute the various feature calculations:

```
>>> x = convex.convex_p()
```

```
>>> x = convex.linear_p()
```

```
>>> x = convex.linear_deviation()
```

property combinations

Contains the list of *(f, p)* pairs, where f is the convex combination of the fitness pair that was used in the ith test, and p is the individual formed from the convex combination of their genomes.

convex_p(*threshold: float = -1e-10*)

Estimate the probability that the landscape is convex by calculating the frequency with which

$$\delta < \tau$$

where τ is a small negative threshold (typically -10^{-10}).

Parameters

threshold (*float*) – the value of τ.

property deltas

Contains the list of $\delta = f(p) - \text{comb}(f(x), f(y))$ values that were computed for the convexity tests.

linear_deviation()

Estimate the deviation of the landscape from linearity by averaging the δ values.

linear_deviation_abs()

Estimate the deviation of the landscape of linearity by averagin the absolute value $|\delta|$ of the computed deltas.

Sometimes this is simply the negative of linear_deviation() (ex. when the function is completely convex), but other times the two values differ considerably.

linear_p(*threshold: float = -1e-10*)

Estimate the probability that the landscape is linear by calculating the frequency with which

$$|\delta| < \tau$$

where τ is a small negative threshold (typically -10^{-10}).

Parameters
threshold (*float*) – the value of τ.

property pairs

Contains all of the pairs of original individuals that were used in the convexity tests.

results_table(*function_name=None*)

Return a Pandas dataframe as a convenience, with one row for each computed feature.

Module contents

This package contains algorithms for computing statistical properties of landscapes.

Much of the research on landscape features is focused on understanding why some problems are easy or hard to solve for certain algorithms, or on how we might use statistical features to train machine learning models to assist in algorithm selection.

For a good survey of the field, look to the following paper:

- Malan, Katherine Mary. "A Survey of Advances in Landscape Analysis for Optimisation." *Algorithms* 14.2 (2021): 40.

10.1.7 leap_ec.multiobjective package

Submodules

leap_ec.multiobjective.asynchronous module

class leap_ec.multiobjective.asynchronous.**ENLUInserter**

Bases: object

leap_ec.multiobjective.asynchronous.**enlu_inds_rank**(*start_point*, *layer_pops*)

Performs the incremental non-dominated sorting ranking process.

Based on the ENLU insertion algorithm with the modification of a binary search for the start point. Locates the highest layer where the individual is nondominated and inserts it, propagating layer composition changes down the rankings.

- K. Li, K. Deb, Q. Zhang and Q. Zhang, "Efficient Nondomination Level Update Method for Steady-State Evolutionary Multiobjective Optimization," in IEEE Transactions on Cybernetics, vol. 47, no. 9, pp. 2838-2849, Sept. 2017, doi: 10.1109/TCYB.2016.2621008.

Parameters

- **points** (*moving*) – the set of points descending in rank from the previous layer. In the first recursion this is the inserted individual.
- **layer_pops** – the population separated into non-dominating layers.
- **rank_func** – the ranking function used to separate out the dominated group at each recursion.
- **depth** – the current layer depth the moving points set is dominating.

leap_ec.multiobjective.asynchronous.**steady_state_nsga_2**(*client*, *max_births: int*, *init_pop_size: int*, *pop_size: int*, *problem:* MultiObjectiveProblem, *representation*, *offspring_pipeline*, *count_nonviable=False*, *evaluated_probe=None*, *pop_probe=None*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

A steady state version of the NSGA-II multi-objective evolutionary algorithm.

Functionally, a wrapper around steady_state that chooses the inserter for you.

- K. Li, K. Deb, Q. Zhang and Q. Zhang, "Efficient Nondomination Level Update Method for Steady-State Evolutionary Multiobjective Optimization," in IEEE Transactions on Cybernetics, vol. 47, no. 9, pp. 2838-2849, Sept. 2017, doi: 10.1109/TCYB.2016.2621008.

Parameters

- **client** – Dask client that should already be set-up
- **max_births** – how many births are we allowing?
- **init_pop_size** – size of initial population sent directly to workers at start
- **pop_size** – how large should the population be?
- **representation** – of the individuals
- **problem** – to be solved
- **offspring_pipeline** – for creating new offspring from the pop
- **count_nonviable** – True if we want to count non-viable individuals towards the birth budget
- **evaluated_probe** – is a function taking an individual that is given the next evaluated individual; can be used to print newly evaluated individuals
- **pop_probe** – is an optional function that writes a snapshot of the population to a CSV formatted stream ever N births

Returns

the population containing the final individuals

leap_ec.multiobjective.nsga2 module

Implementation of Non-dominated sorted genetic algorithm II (NSGA-II).

- Deb, Kalyanmoy, Amrit Pratap, Sameer Agarwal, and T. A. M. T. Meyarivan. "A Fast and Elitist Multiobjective Genetic Algorithm: NSGA-II." IEEE transactions on evolutionary computation 6, no. 2 (2002): 182-197.

leap_ec.multiobjective.nsga2.**generalized_nsga_2**(*max_generations: int*, *pop_size: int*, *problem: ~leap_ec.multiobjective.problems.MultiObjectiveProblem*, *representation*, *pipeline*, *rank_func=<function rank_ordinal_sort>*, *stop=<function <lambda>>*, *init_evaluate=<bound method Individual.evaluate_population of <class 'leap_ec.individual.Individual'>>*, *start_generation: int = 0*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

NSGA-II multi-objective evolutionary algorithm.

- **Deb, Kalyanmoy, Amrit Pratap, Sameer Agarwal, and T. A. M. T. Meyarivan.** "A Fast and Elitist Multiobjective Genetic Algorithm: NSGA-II." IEEE transactions on evolutionary computation 6, no. 2 (2002): 182-197.
- **Bogdan Burlacu. 2022. Rank-based Non-dominated Sorting. arXiv.** DOI:https://doi.org/10.48550/ARXIV.2203.13654

This classic algorithm relies on the idea of "non-dominated sorting" and de-crowding to evolve a diverse Pareto front. The "generalized" NSGA-II we implement here differs slightly from the canonical algorithm, in that we default to a faster sorting algorithm devised by Burlacu (2022).

If you wish the algorithm to use the original NSGA-II behavior instead (which runs much slower), you can select the original operator by passing in *rank_func=fast_nondominated_sort*.

```
>>> from leap_ec.representation import Representation
>>> from leap_ec.ops import random_selection, clone, evaluate, pool
>>> from leap_ec.real_rep.initializers import create_real_vector
>>> from leap_ec.real_rep.ops import mutate_gaussian
>>> from leap_ec.multiobjective.nsga2 import generalized_nsga_2
>>> from leap_ec.multiobjective.problems import SCHProblem
>>> pop_size = 10
>>> max_generations = 5
>>> final_pop = generalized_nsga_2(
...     max_generations=max_generations, pop_size=pop_size,
...
...     problem=SCHProblem(),
...
...     representation=Representation(
...         initialize=create_real_vector(bounds=[(-10, 10)])
...     ),
...
...     pipeline=[
...         random_selection,
...         clone,
...         mutate_gaussian(std=0.5, expected_num_mutations=1),
...         evaluate,
...         pool(size=pop_size),
```

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```
...     ]
... )
```

[Individual(...), Individual(...), Individual(...), ... Individual(...)]

Note

You will need a selection as first operator in *pipeline*. This will use Deb's multiobjective criteria for comparing individuals as dictated in *MultiobjectiveProblem*.

Parameters

- **max_generations** (*int*) – The max number of generations to run the algorithm for. Can pass in float('Inf') to run forever or until the *stop* condition is reached.
- **pop_size** (*int*) – Size of the initial population
- **rank_func** – the function used to calculate non-domination rankings for the individuals of the population.
- **stop** (*int*) – A function that accepts a population and returns True iff it's time to stop evolving.
- **problem** (Problem) – the Problem that should be used to evaluate individuals' fitness
- **representation** – How the problem is represented in individuals
- **pipeline** (*list*) – a list of operators that are applied (in order) to create the offspring population at each generation
- **init_evaluate** – a function used to evaluate the initial population, before the main pipeline is run. The default of *Individual.evaluate_population* is suitable for many cases, but you may wish to pass a different operator in for distributed evaluation or other purposes.
- **start_generation** – index of the first generation to count from (defaults to 0). You might want to change this, for example, in experiments that involve stopping and restarting an algorithm.

Returns

a list of the final population

leap_ec.multiobjective.ops module

LEAP pipeline operators for multiobjective optimization.

For now this just implements NSGA-II, but other multiobjective approaches will eventually be included.

leap_ec.multiobjective.ops.**crowding_distance_calc**(*population: list = '__no__default__'*) → list

This implements the NSGA-II crowding-distance-assignment()

Note that this assumes that all the individuals have had their ranks computed since we do crowding distance calculations within ranks.

- Deb, Kalyanmoy, Amrit Pratap, Sameer Agarwal, and T. A. M. T. Meyarivan. "A Fast and Elitist Multiobjective Genetic Algorithm: NSGA-II." IEEE transactions on evolutionary computation 6, no. 2 (2002): 182-197.

Parameters

population – population to calculate crowding distances

Returns
individuals with crowding distance calculated

leap_ec.multiobjective.ops.**fast_nondominated_sort**(*population: list = '__no__default__'*, *parents: list = None*) → list

This implements the NSGA-II fast-non-dominated-sort()

This is really *binning* the population by ranks. In any case, the returned population will have an attribute, *rank*, that will denote the corresponding rank in which it is a member.

- Deb, Kalyanmoy, Amrit Pratap, Sameer Agarwal, and T. A. M. T. Meyarivan. "A Fast and Elitist Multiobjective Genetic Algorithm: NSGA-II." IEEE transactions on evolutionary computation 6, no. 2 (2002): 182-197.

Parameters

- **population** – population to be ranked
- **parents** – optional parents population to be included with the ranking process

Returns
individuals binned by ranks

leap_ec.multiobjective.ops.**per_rank_crowding_calc**(*ranked_population: list*, *is_maximizing*) → list

Calculate crowding distance within rank :param ranked_population: A population of entirely one rank :returns: population with crowding distance calculate for one rank

leap_ec.multiobjective.ops.**rank_ordinal_sort**(*population: list = '__no__default__'*, *parents: list = None*) → list

This implements Rank Ordinal Sort from Rank-based Non-dominated Sorting

Produces identical *rank* values to *fast_nondominated_sort* from the original NSGA-II implementation, however performs much faster.

- Bogdan Burlacu. 2022. Rank-based Non-dominated Sorting. arXiv. DOI:https://doi.org/10.48550/ARXIV.2203.13654

Parameters

- **population** – population to be ranked
- **parents** – optional parents population to be included with the ranking process

Returns
individuals binned by ranks

leap_ec.multiobjective.ops.**sort_by_dominance**(*population: list = '__no__default__'*) → list

Sort population by rank and distance

This presumes that fast_nondominated_sort() *and* crowding_distance_calc have been used on *all* individuals in *population*.

Parameters
population – to be sorted

Returns
sorted population

leap_ec.multiobjective.probe module

Visualization pipeline operators tailored for multiple objectives

class leap_ec.multiobjective.probe.**ParetoPlotProbe2D**(*ax=None*, *metrics=None*, *xlim=(0, 1)*, *ylim=(0, 1)*, *title='Pareto Front'*, *step=1*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*)

Bases: *PopulationMetricsPlotProbe*

Plot a 2D Pareto front of a population that has been assigned multi-objective fitness values.

If the fitness space has more than two dimensions, only the first two are plotted.

reset()

leap_ec.multiobjective.problems module

LEAP Problem classes for multiobjective optimization.

class leap_ec.multiobjective.problems.**MultiObjectiveProblem**(*maximize: Sequence[bool]*)

Bases: *Problem*

A problem that compares individuals based on Pareto dominance.

Inherit from this class and implement the *evaluate()* method to implement an objective function that returns a list of real-value fitness values.

In Pareto-dominance, an individual A is only considered "better than" an individual B if A is unambiguously better than B: i.e. it is at least as good as B on all objectives, and it is strictly better than B on at least one objective.

equivalent(*first_fitnesses*, *second_fitnesses*)

Return true if first_fitness and second_fitness are mutually Pareto non-dominating.

$$a \not\succ b \text{ and } b \not\succ a$$

Parameters

- **first_fitnesses** – a np array of real-valued fitnesses for an individual, where each element corresponds to a single objective
- **second_fitnesses** – same as *first_fitnesses*, but for a different individual

worse_than(*first_fitnesses*, *second_fitnesses*)

Return true if first_fitnesses is Pareto-dominated by second_fitnesses.

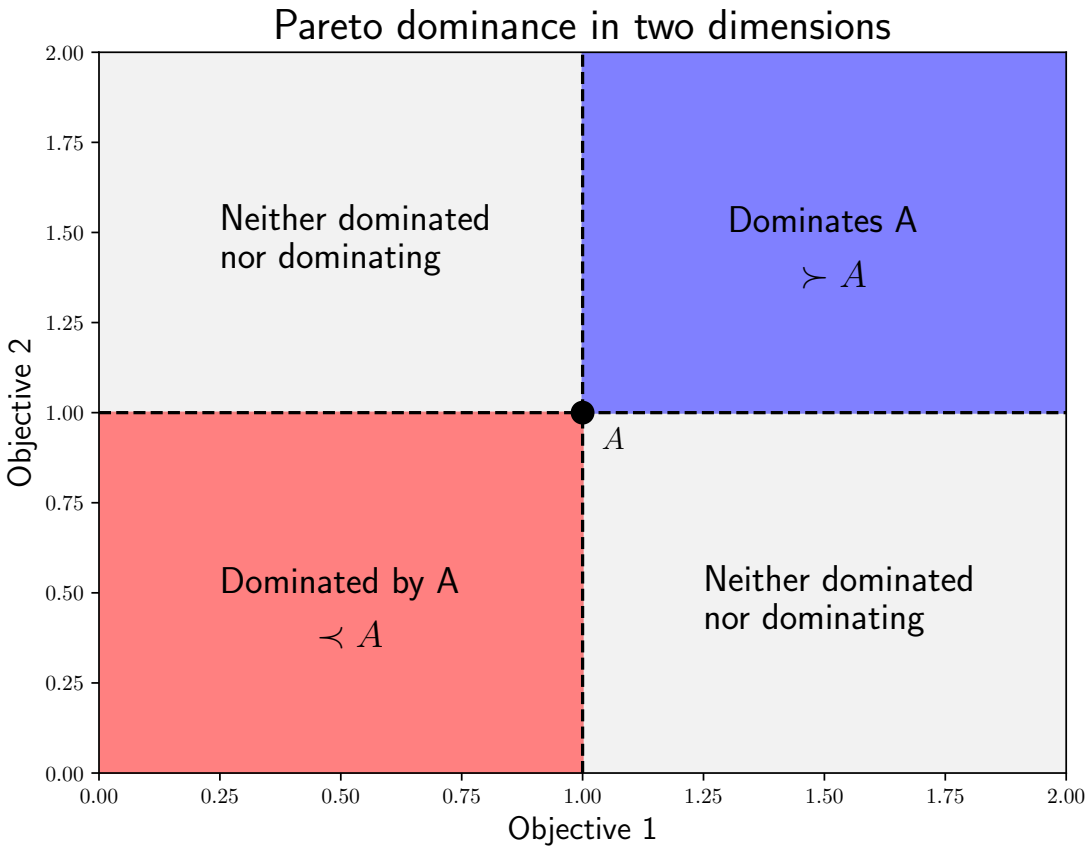
In the case of maximization over all objectives, a solution b dominates a, written $b \succ a$, if and only if

$$\begin{aligned} f_i(b) &\geq f_i(a) \quad \forall i, \text{ and} \\ f_i(b) &> f_j(a) \quad \text{for some } j. \end{aligned}$$

Here we may maximize over some objectives, and minimize over others, depending on the values in the *self.maximize* list.

Parameters

- **first_fitnesses** – a np array of real-valued fitnesses for an individual, where each element corresponds to a single objective
- **second_fitnesses** – same as *first_fitnesses*, but for a different individual


Pareto dominance in two dimensions
Neither dominated
nor dominating
Dominates A
$\succ A$
A
Dominated by A
$\prec A$
Neither dominated
nor dominating
Objective 1
Objective 2
0.00
0.25
0.50
0.75
1.00
1.25
1.50
1.75
2.00

class leap_ec.multiobjective.problems.**SCHProblem**

Bases: *MultiObjectiveProblem*

SCH problem from Deb et al's benchmarks

This expects a numpy scalar (zero dimensional) for a phenome.

$$f_1(x) = x^2 \tag{10.1}$$
$$f_2(x) = (x - 2)^2 \tag{10.2}$$
$$-10^3 \leq x \leq 10^3 \tag{10.3}$$

- Deb, Kalyanmoy, Amrit Pratap, Sameer Agarwal, and T. A. M. T. Meyarivan. "A Fast and Elitist Multiobjective Genetic Algorithm: NSGA-II." IEEE transactions on evolutionary computation 6, no. 2 (2002): 182-197.

evaluate(*phenome*)

Parameters
phenome – argument for objective functions

Returns
two fitnesses, one for $f_1(x)$ and $f_2(x)$

class leap_ec.multiobjective.problems.**ZDT1Problem**(*n=30*, *check_phenome=True*)

Bases: *ZDTBenchmarkProblem*

The first problem from the classic Zitzler, Deb, and Thiele (ZDT) benchmark suite. It's meant to provide a simple multi-objective problem with a *convex* Pareto-optimal front.

$$f_1(x_1) = x_1 \tag{10.4}$$
$$g(x_2, \ldots, x_n) = 1 + 9 \cdot \sum_{i=2}^{n} x_i/(n-1) \tag{10.5}$$
$$h(f_1, g) = 1 - \sqrt{f_1/g} \tag{10.6}$$
$$f_2(x) = g(x_2, \ldots, x_n) h(f_1(x_1), g(x_2, \ldots, x_n)) \tag{10.7}$$
(10.8)
(10.9)
$$x_i \in [0, 1] \tag{10.10}$$

Traditionally the problem is used with $|x| = 30$ dimensions in the solution space.

- Zitzler, Eckart, Kalyanmoy Deb, and Lothar Thiele. "Comparison of multiobjective evolutionary algorithms: Empirical results." *Evolutionary computation* 8.2 (2000): 173-195.

property bounds

Returns
the bounds of the phenome

evaluate(*phenome*)

Parameters
phenome – contains x

Returns
two fitnesses, one for $f_1(x)$ and $f_2(x)$

class leap_ec.multiobjective.problems.**ZDT2Problem**(*n=30*, *check_phenome=True*)

Bases: *ZDTBenchmarkProblem*

The second problem from the classic Zitzler, Deb, and Thiele (ZDT) benchmark suite. This is similar to `leap_ec.problem.ZDT1Problem`, except that it has a *non-convex* Pareto front.

$$f_1(x_1) = x_1 \tag{10.11}$$

$$g(x_2, \ldots, x_n) = 1 + 9 \cdot \sum_{i=2}^{n} x_i / (n-1) \tag{10.12}$$

$$h(f_1, g) = 1 - (f_1/g)^2 \tag{10.13}$$

$$f_2(x) = g(x_2, \ldots, x_n) h(f_1(x_1), g(x_2, \ldots, x_n)) \tag{10.14}$$

(10.15)

(10.16)

$$x_i \in [0, 1] \tag{10.17}$$

Traditionally the problem is used with $|x| = 30$ dimensions in the solution space.

- Zitzler, Eckart, Kalyanmoy Deb, and Lothar Thiele. "Comparison of multiobjective evolutionary algorithms: Empirical results." *Evolutionary computation* 8.2 (2000): 173-195.

property bounds

Returns
the bounds of the phenome

evaluate(*phenome*)

Parameters
phenome – contains x

Returns
two fitnesses, one for $f_1(x)$ and $f_2(x)$

class leap_ec.multiobjective.problems.**ZDT3Problem**(*n=10*, *check_phenome=True*)

Bases: *ZDTBenchmarkProblem*

The third problem from the classic Zitzler, Deb, and Thiele (ZDT) benchmark suite. This function differs from `leap_ec.problem.ZDT1Problem` and `leap_ec.problem.ZDT1Problem` in that the pareto-optimal front has discontinuity.

$$f_1(x_1) = x_1 \tag{10.18}$$

$$g(x_2, \ldots, x_n) = 1 + 9 \cdot \sum_{i=2}^{n} x_i / (n-1) \tag{10.19}$$

$$h(f_1, g) = 1 - \sqrt{f_1/g} - (f_1/g) \sin(10 \pi f_1) \tag{10.20}$$

$$f_2(x) = g(x_2, \ldots, x_n) h(f_1(x_1), g(x_2, \ldots, x_n)) \tag{10.21}$$

(10.22)

(10.23)

$$x_i \in [0, 1] \tag{10.24}$$

Traditionally the problem is used with $|x| = 10$ dimensions in the solution space.

- Zitzler, Eckart, Kalyanmoy Deb, and Lothar Thiele. "Comparison of multiobjective evolutionary algorithms: Empirical results." *Evolutionary computation* 8.2 (2000): 173-195.

property bounds

Returns
the bounds of the phenome

evaluate(*phenome*)

Parameters
phenome – contains x

Returns
two fitnesses, one for $f_1(x)$ and $f_2(x)$

class leap_ec.multiobjective.problems.**ZDT4Problem**(*n=30*, *check_phenome=True*)

Bases: *ZDTBenchmarkProblem*

The fourth problem from the classic Zitzler, Deb, and Thiele (ZDT) benchmark suite. ZDT4 contains 21^9 local pareto-optimal front for the default parameters, allowing it to test for the EA's ability to handle multimodality.

$$f_1(x_1) = x_1 \tag{10.25}$$

$$g(x_2, \ldots, x_n) = 1 + 10(n-1) + \sum_{i=2}^{n} (x_i^2 - 10\cos(4\pi x_i)) \tag{10.26}$$

$$h(f_1, g) = 1 - \sqrt{f_1/g} \tag{10.27}$$

$$f_2(x) = g(x_2, \ldots, x_n) h(f_1(x_1), g(x_2, \ldots, x_n)) \tag{10.28}$$

(10.29)

(10.30)

$$x_1 \in [0, 1] \quad x_2, \ldots, x_n \in [-5, 5] \tag{10.31}$$

Traditionally the problem is used with $|x| = 30$ dimensions in the solution space.

- Zitzler, Eckart, Kalyanmoy Deb, and Lothar Thiele. "Comparison of multiobjective evolutionary algorithms: Empirical results." *Evolutionary computation* 8.2 (2000): 173-195.

property bounds

Returns
the bounds of the phenome

evaluate(*phenome*)

Parameters
phenome – contains x

Returns
two fitnesses, one for $f_1(x)$ and $f_2(x)$

class leap_ec.multiobjective.problems.**ZDT5Problem**(*n=11*, *check_phenome=True*)

Bases: *ZDTBenchmarkProblem*

The fifth problem from the classic Zitzler, Deb, and Thiele (ZDT) benchmark suite. In contrast to the other ZDT problems, ZDT5 takes a binary string as input.

Unlike the other ZDT problems, *ZDT5Problem* additionally provides a *phenome_length* property, denoting the length of the flattened binary sequence *x*. This property is intended to ease the creation of binary sequence

phenomes for input into the problem.

$$u(x_i) = \text{unitation}(x_i) \tag{10.32}$$

$$v(u(x_i)) = \begin{cases} 2 + u(x_i) & if u(x_i) < 5 \\ 1 & if u(x_i) = 5 \end{cases} \tag{10.33}$$

(10.34)

(10.35)

$$f_1(x_1) = 1 + (10.36)$$

$$g(x_2, \ldots, x_n) = \sum_{i=2}^{n} v(u(x_i)) \tag{10.37}$$

$$h(f_1, g) = 1 - (10.38)$$

$$f_2(x) = g(x_2, \ldots, x_n) h(f_1(x_1), g(x_2, \ldots, x_n)) \tag{10.39}$$

(10.40)

(10.41)

$$x_1 \in \{0, 1\}^{30} \quad x_2, \ldots, x_n \in \{0, 1\}^5 \tag{10.42}$$

Traditionally the problem is used with $|x| = 11$ dimensions in the solution space. This translates to a flattened binary sequence of $|phenome_x| = 80$.

- Zitzler, Eckart, Kalyanmoy Deb, and Lothar Thiele. "Comparison of multiobjective evolutionary algorithms: Empirical results." *Evolutionary computation* 8.2 (2000): 173-195.

property bounds

Returns
the bounds of the phenome

evaluate(*phenome*)

Parameters
phenome – the flattened binary sequence x

Returns
two fitnesses, one for $f_1(x)$ and $f_2(x)$

property phenome_length

Returns
the length of the flattened binary sequence x

class leap_ec.multiobjective.problems.**ZDT6Problem**(*n=10*, *check_phenome=True*)

Bases: *ZDTBenchmarkProblem*

The sixth problem from the classic Zitzler, Deb, and Thiele (ZDT) benchmark suite. This function exhibits a nonuniformly distributed pareto front, as well as a lower density of solutions nearer to the pareto front.

$$f_1(x_1) = 1 - \exp(-4x_1) \sin^6(6\pi x_1) \tag{10.43}$$

$$g(x_2, \ldots, x_n) = 1 + 9 \cdot ((\sum_{i=2}^{n} x_i)/(n-1))^{0.25} \tag{10.44}$$

$$h(f_1, g) = 1 - ((f_1)/g)^2 \tag{10.45}$$

$$f_2(x) = g(x_2, \ldots, x_n) h(f_1(x_1), g(x_2, \ldots, x_n)) \tag{10.46}$$

(10.47)

(10.48)

$$x_i \in [0, 1] \tag{10.49}$$

Traditionally the problem is used with $|x| = 10$ dimensions in the solution space.

- Zitzler, Eckart, Kalyanmoy Deb, and Lothar Thiele. "Comparison of multiobjective evolutionary algorithms: Empirical results." *Evolutionary computation* 8.2 (2000): 173-195.

property bounds

Returns
the bounds of the phenome

evaluate(*phenome*)

Parameters
phenome – contains x

Returns
two fitnesses, one for $f_1(x)$ and $f_2(x)$

class leap_ec.multiobjective.problems.**ZDTBenchmarkProblem**(*n*, *check_phenome=True*)

Bases: *MultiObjectiveProblem*

The base class for problems from the classic Zitzler, Deb, and Thiele (ZDT) benchmark suite.

Each problem is of the form:

$$\begin{aligned} \text{Minimize} \quad \mathcal{T}(x) &= (f_1(x_1), f_2(x)) && (10.50)\\ \text{subject to} \quad f_2(x) &= g(x_2, \ldots, x_n)h(f_1(x_1), g(x_2, \ldots, x_n)) && (10.51)\\ \text{where} \quad x &= (x_1, \ldots, x_n) && (10.52)\\ && && (10.53) \end{aligned}$$

For reliability when testing, each problem has been provided with a *check_phenome* parameter to ensure that phenomes match the expected form and bounds of the problem.

- Zitzler, Eckart, Kalyanmoy Deb, and Lothar Thiele. "Comparison of multiobjective evolutionary algorithms: Empirical results." *Evolutionary computation* 8.2 (2000): 173-195.

abstract property bounds

Returns
the bounds of the phenome

Module contents

10.1.8 leap_ec.real_rep package

Submodules

leap_ec.real_rep.initializers module

Initializers for real values.

leap_ec.real_rep.initializers.**create_real_vector**(*bounds*)

A closure for initializing lists of real numbers for real-valued genomes, sampled from a uniform distribution.

Having a closure allows us to just call the returned function N times in *Individual.create_population()*.

TODO Allow either a single tuple or a test_sequence of tuples for bounds. —Siggy

Parameters
bounds – a list of (min, max) values bounding the uniform sampline of each element

Returns
A function that, when called, generates a random genome.

E.g., can be used for *Individual.create_population()*

```
>>> from leap_ec.decoder import IdentityDecoder
>>> from . problems import SpheroidProblem
>>> bounds = [(0, 1), (0, 1), (-1, 100)]
>>> population = Individual.create_population(10, create_real_vector(bounds),
...                                           decoder=IdentityDecoder(),
...                                           problem=SpheroidProblem())
```

leap_ec.real_rep.ops module

Pipeline operators for real-valued representations

leap_ec.real_rep.ops.**apply_hard_bounds**(*genome*, *hard_bounds*)

A helper that ensures that every gene is contained within the given bounds.

Parameters

- **genome** – list of values to apply bounds to.
- **hard_bounds** – if a *(low, high)* tuple, the same bounds will be used for every gene. If a list of tuples is given, then the ith bounds will be applied to the ith gene.

Both sides of the range are inclusive:

```
>>> genome = np.array([0, 10, 20, 30, 40, 50])
>>> apply_hard_bounds(genome, hard_bounds=(20, 40))
array([20, 20, 20, 30, 40, 40])
```

Different bounds can be used for each locus by passing in a list of tuples:

```
>>> bounds= [ (0, 1), (0, 1), (50, 100), (50, 100), (0, 100), (0, 10) ]
>>> apply_hard_bounds(genome, hard_bounds=bounds)
array([ 0,  1, 50, 50, 40, 10])
```

leap_ec.real_rep.ops.**genome_mutate_gaussian**(*genome='__no__default__'*, *std: float = '__no__default__'*, *expected_num_mutations='__no__default__'*, *bounds: Tuple[float, float] = (-inf, inf)*, *transform_slope: float = 1.0*, *transform_intercept: float = 0.0*)

Perform Gaussian mutation directly on real-valued genes (rather than on an Individual).

This used to be inside *mutate_gaussian*, but was moved outside it so that *leap_ec.segmented.ops.apply_mutation* could directly use this function, thus saving us from doing a copy-n-paste of the same code to the segmented sub-package.

Parameters

- **genome** – of real-valued numbers that will potentially be mutated
- **std** – the mutation width—either a single float that will be used for all genes, or a list of floats specifying the mutation width for each gene individually.
- **expected_num_mutations** – on average how many mutations are expected

Returns
mutated genome

leap_ec.real_rep.ops.**mutate_gaussian**(*next_individual: Iterator = '__no__default__', std='__no__default__', expected_num_mutations: Union[int, str] = None, bounds=(-inf, inf), transform_slope: float = 1.0, transform_intercept: float = 0.0*) → Iterator

Mutate and return an Individual with a real-valued representation.

This operators on an iterator of Individuals:

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.real_rep.ops import mutate_gaussian
>>> import numpy as np
>>> pop = iter([Individual(np.array([1.0, 0.0]))])
```

Mutation can either use the same parameters for all genes:

```
>>> op = mutate_gaussian(std=1.0, expected_num_mutations='isotropic', bounds=(-5,␣
↪5))
>>> mutated = next(op(pop))
```

Or we can specify the *std* and *bounds* independently for each gene:

```
>>> pop = iter([Individual(np.array([1.0, 0.0]))])
>>> op = mutate_gaussian(std=[0.5, 1.0],
...                      expected_num_mutations='isotropic',
...                      bounds=[(-1, 1), (-10, 10)]
... )
>>> mutated = next(op(pop))
```

Parameters

- **next_individual** – to be mutated
- **std** – standard deviation to be equally applied to all individuals; this can be a scalar value or a "shadow vector" of standard deviations
- **expected_num_mutations** – if an int, the *expected* number of mutations per individual, on average. If 'isotropic', all genes will be mutated.
- **bounds** – to clip for mutations; defaults to (- ∞, ∞)

Returns

a generator of mutated individuals.

leap_ec.real_rep.problems module

This module contains a variety of classic real-valued optimization problems that frequently occur in research benchmarks.

It also contains helpers for translating, rotating, and visualizing them.

class leap_ec.real_rep.problems.**AckleyProblem**(*a=20, b=0.2, c=6.283185307179586, maximize=False*)

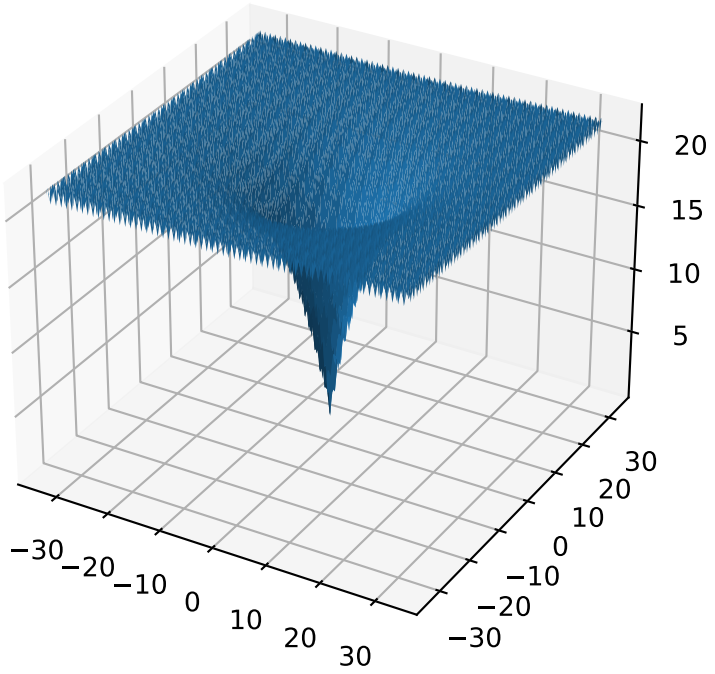
Bases: *ScalarProblem*

$$f(\mathbf{x}) = -a \exp\left(-b\sqrt{\frac{1}{d}\sum_{i=1}^{d} x_i^2}\right) - \exp\left(\frac{1}{d}\sum_{i=1}^{d}\cos(cx_i)\right) + a + \exp(1)$$

Parameters

- **a** (*float*) – depth parameter for the bowl-shaped macrostructure
- **b** (*float*) – exponential scale parameter for the bowl
- **c** (*float*) – wavenumber (frequency) of the cosine pattern of local optima
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import AckleyProblem, plot_2d_problem
import math
problem = AckleyProblem(a=20, b=0.2, c=2*math.pi)
bounds = AckleyProblem.bounds  # Contains traditional bounds
plot_2d_problem(problem, xlim=bounds, ylim=bounds, granularity=0.25)
```



bounds = [-32.768, 32.768]

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness.

class leap_ec.real_rep.problems.**CosineFamilyProblem**(*alpha*, *global_optima_counts*, *local_optima_counts*, *maximize=False*)

Bases: *ScalarProblem*

A configurable multi-modal function based on combinations of cosines, taken from the problem generators proposed by Rönkkönen *et al.* [RonkkonenLKL08].

$$f_{\cos}(\mathbf{x}) = \frac{\sum_{i=1}^{n} -\cos((G_i - 1)2\pi x_i) - \alpha \cdot \cos((G_i - 1)2\pi L_i x_i)}{2n}$$

where G_i and L_i are parameters that indicate the number of global and local optima, respectively, in the ith dimension.

Parameters

- **alpha** (*float*) – parameter that controls the depth of the local optima.
- **global_optima_counts** (*[int]*) – list of integers indicating the number of global optima for each dimension.
- **local_optima_counts** (*[int]*) – list of integers indicated the number of local optima for each dimension.
- **maximize** – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import CosineFamilyProblem, plot_2d_problem
problem = CosineFamilyProblem(alpha=1.0, global_optima_counts=[2, 2], local_optima_
↪counts=[2, 2])
bounds = CosineFamilyProblem.bounds  # Contains traditional bounds
plot_2d_problem(problem, xlim=bounds, ylim=bounds, granularity=0.025)
```

The number of optima can be varied independently by each dimension:

```
from leap_ec.real_rep.problems import CosineFamilyProblem, plot_2d_problem
problem = CosineFamilyProblem(alpha=3.0, global_optima_counts=[4, 2], local_optima_
↪counts=[2, 2])
bounds = CosineFamilyProblem.bounds  # Contains traditional bounds
plot_2d_problem(problem, xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (0, 1)

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters
phenome – phenome with a real-valued phenome vector to be evaluated

Returns
its fitness.

class leap_ec.real_rep.problems.**GaussianProblem**(*width=1*, *height=1*, *maximize=True*)

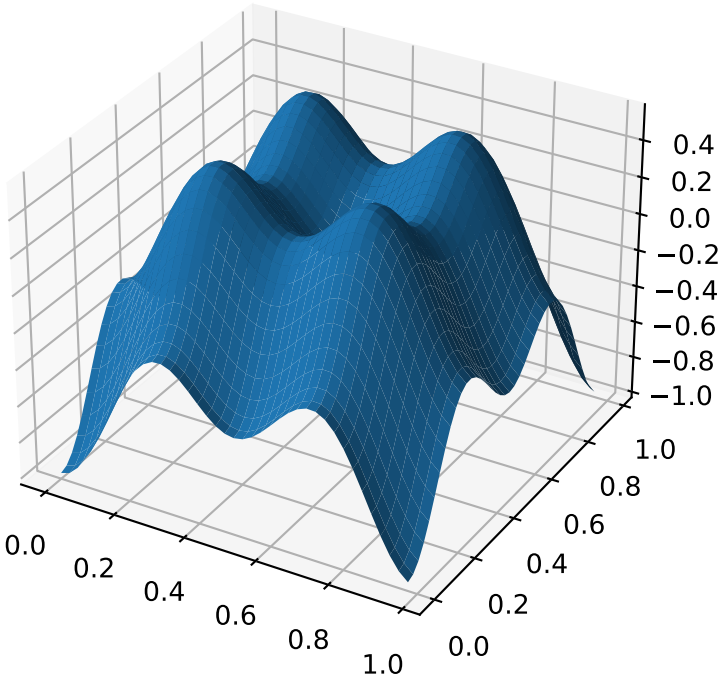
Bases: *ScalarProblem*

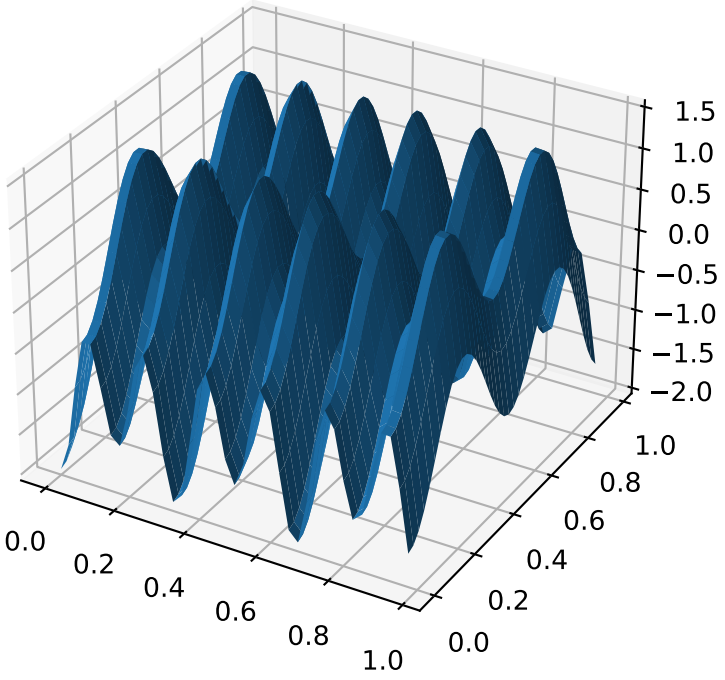
A multidimensional, isotropic Gaussian function, defined by

$$A \exp\left(-\sum_{i}^{n}\left(\frac{x_i}{w}\right)^2\right)$$

Parameters

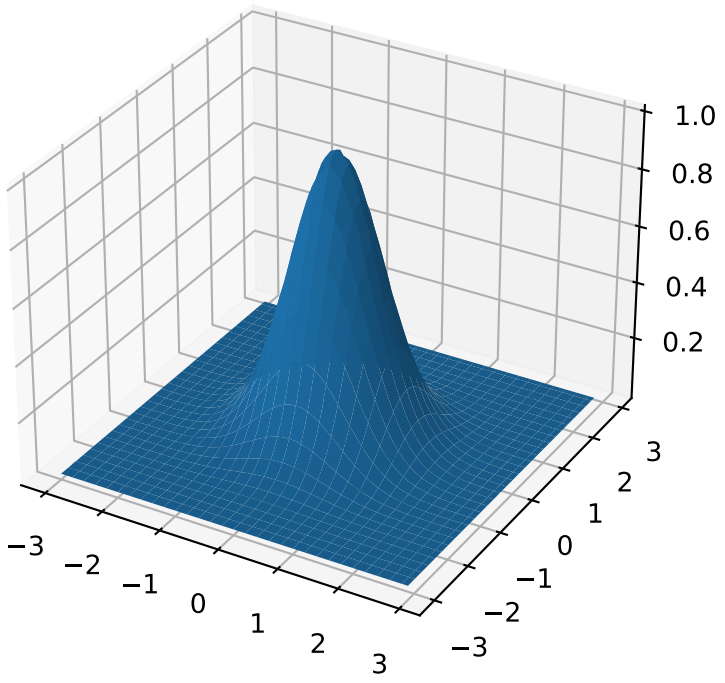
- **width** (*float*) – the width parameter w


0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0


1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
0.0
0.2
0.4
0.6
0.8
1.0
0.0
0.2
0.4
0.6
0.8
1.0

- **height** (*float*) – the height parameter A

```
from leap_ec.real_rep.problems import GaussianProblem, plot_2d_problem
bounds = GaussianProblem.bounds  # Some typical bounds
problem = GaussianProblem(width=1, height=1)
plot_2d_problem(problem, xlim=bounds, ylim=bounds, granularity=0.1)
```



bounds = (-3, 3)

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

class leap_ec.real_rep.problems.**GriewankProblem**(*maximize=False*)

Bases: *ScalarProblem*

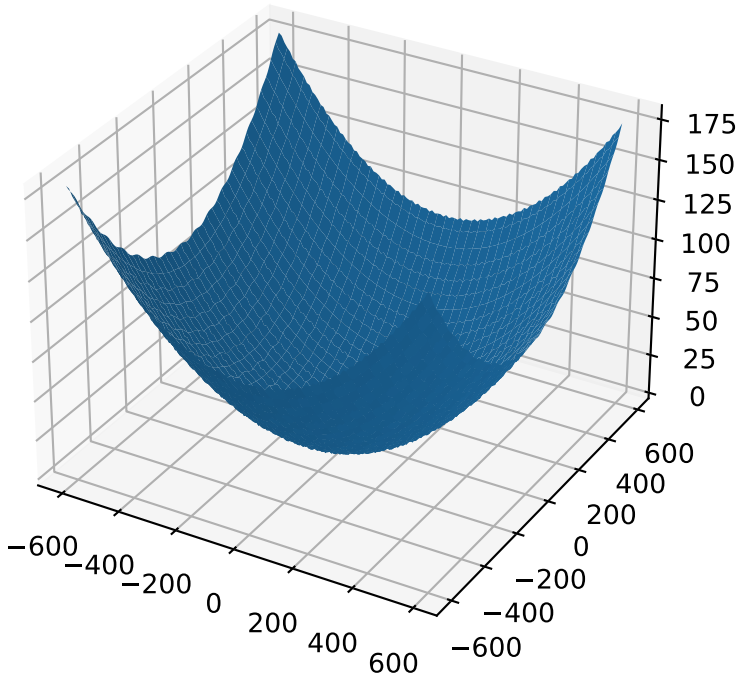
The classic Griewank problem. Like the `RastriginProblem` function, the Griewank has a quadratic global structure with many local optima that are distrib in a regular pattern.

$$f(\mathbf{x}) = \sum_{i=1}^{d} \frac{x_i^2}{4000} - \prod_{i=1}^{d} \cos\left(\frac{x_i}{\sqrt{i}}\right) + 1$$

Parameters

maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import GriewankProblem, plot_2d_problem
bounds = GriewankProblem.bounds  # Contains traditional bounds
plot_2d_problem(GriewankProblem(), xlim=bounds, ylim=bounds, granularity=10)
```




```
from leap_ec.real_rep.problems import GriewankProblem, plot_2d_problem
bounds = [-50, 50]
plot_2d_problem(GriewankProblem(), xlim=bounds, ylim=bounds, granularity=1)
```

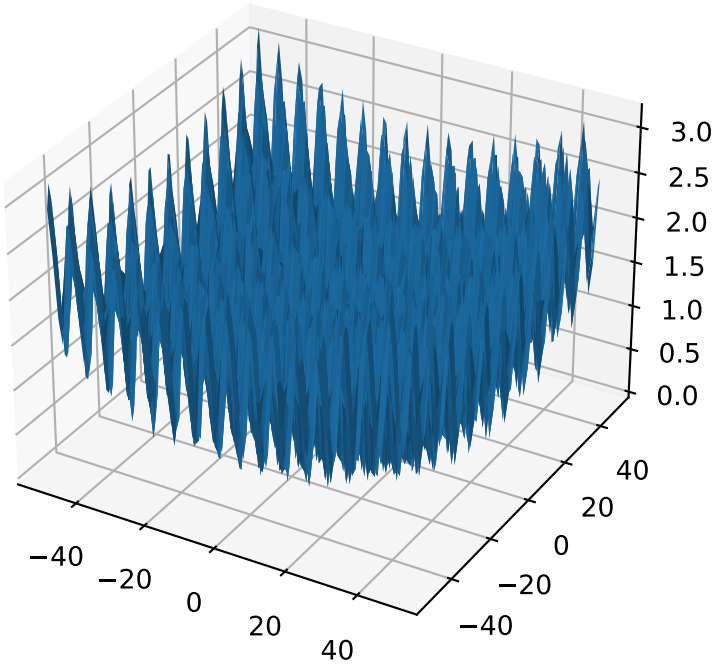
bounds = [-600, 600]

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters

phenome – real-valued vector to be evaluated


3.0
2.5
2.0
1.5
1.0
0.5
0.0
−40
−20
0
20
40
40
20
0
−20
−40

Returns
its fitness.

class leap_ec.real_rep.problems.**LangermannProblem**(*m=5*, *c=(1, 2, 5, 2, 3)*, *a=((3, 5), (5, 2), (2, 1), (1, 4), (7, 9))*, *maximize=False*)

Bases: *ScalarProblem*

A popular multi-modal test function built by summing together m terms.

$$f(\mathbf{x}) = -\sum_{i=1}^{m} c_i \exp\left(-\frac{1}{\pi}\sum_{j=1}^{d}(x_j - A_{ij})^2\right)\cos\left(\pi\sum_{j=1}^{d}(x_j - A_{ij})^2\right)$$

Langermann's function is parameterized by a vector c_i of length m and a matrix A_{ij} of dimension $m \times d$. This class uses the traditional parameterization as the default, with $m = 5$ and

$$c = (1, 2, 5, 2, 3)$$
$$A = \begin{bmatrix} 3 & 5 \\ 5 & 2 \\ 2 & 1 \\ 1 & 4 \\ 7 & 9 \end{bmatrix}.$$

Parameters

- **m** (*int*) – total number of terms in the function's sum
- **c** (*[float]*) – amplitude coefficients for each term
- **a** (*[[float]]*) – offsets points for each term
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import LangermannProblem, plot_2d_problem
bounds = LangermannProblem.bounds  # Contains traditional bounds
plot_2d_problem(LangermannProblem(), xlim=bounds, ylim=bounds, granularity=0.2)
```

bounds = [0, 10]

default_a = ((3, 5), (5, 2), (2, 1), (1, 4), (7, 9))

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness.

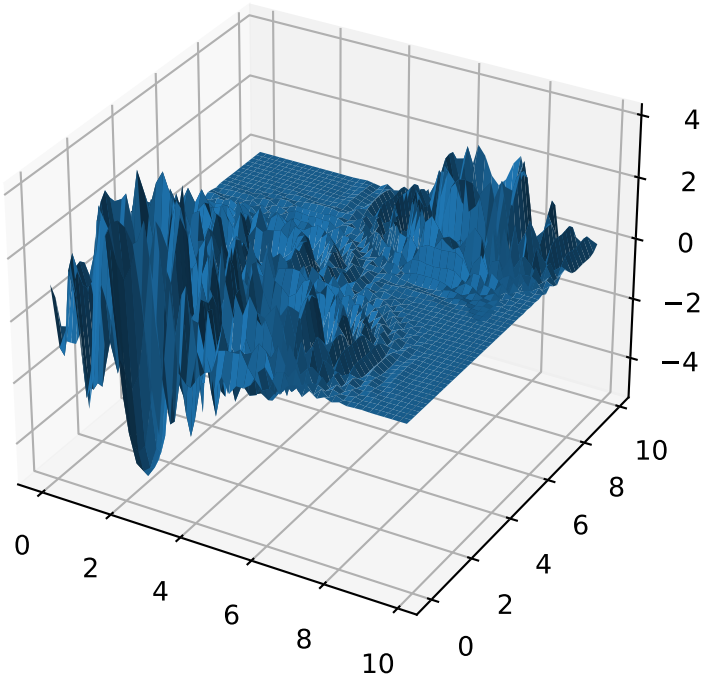
class leap_ec.real_rep.problems.**LunacekProblem**(*N*, *d=1.0*, *mu_1=2.5*, *mu_2=None*, *s=None*, *maximize=False*)

Bases: *ScalarProblem*

Lunacek's function is also know as the "double Rastrigin" or "bi-Rastrigin" problem, because it overlays a `RastriginProblem`-style cosine function across a *pair* of spheroid functions.

This function was designed to model the double-funnel macrostructure that occurs in some difficult cases of the Lennard-Jones function (a famous function from molecular dynamics).

$$f(\mathbf{x}) = \min\left(\left\{\sum_{i=1}^{N}(x_i - \mu_1)^2\right\}, \left\{d \cdot N + s \cdot \sum_{i=1}^{N}(x_i - \mu_2)^2\right\}\right) + 10\sum_{i=1}^{N}(1 - \cos(2\pi(x_i - \mu_i))),$$


4
2
0
−2
−4
0
2
4
6
8
10
0
2
4
6
8
10

where N is the dimensionality of the solution vector, and the second sphere center parameter μ_2 is typically given by

$$\mu_2 = -\sqrt{\frac{\mu_1^2 - d}{s}}$$

and s is by default a function on N:

$$s = 1 - \frac{1}{2\sqrt{N + 20} - 8.2}$$

These respective defaults are used for μ_2 and s whenever *mu_2* and *s* are set to *None*.

Because of these complicated defaults, this class requires that you explicitly set the dimensionality of N of the expected input solutions. A warning will be thrown if an input solution is encountered that doesn't match the expected dimensionality.

Parameters

- **N** (*int*) – dimensionality of the anticipated input solutions
- **d** (*float*) – base fitness value of the second spheroid
- **mu_1** (*float*) – offset of the first spheroid
- **mu_2** (*float*) – offset of the second spheroid (if *None*, this will be calculated automatically)
- **s** (*float*) – scale parameter for the second spheroid (if *None*, this will be calculated automatically)
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import LunacekProblem, plot_2d_problem
bounds = LunacekProblem.bounds  # Contains traditional bounds
plot_2d_problem(LunacekProblem(N=2), xlim=bounds, ylim=bounds, granularity=0.1)
```

bounds = (-5, 5)

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness.

class leap_ec.real_rep.problems.**MatrixTransformedProblem**(*problem*, *matrix*, *maximize=None*)

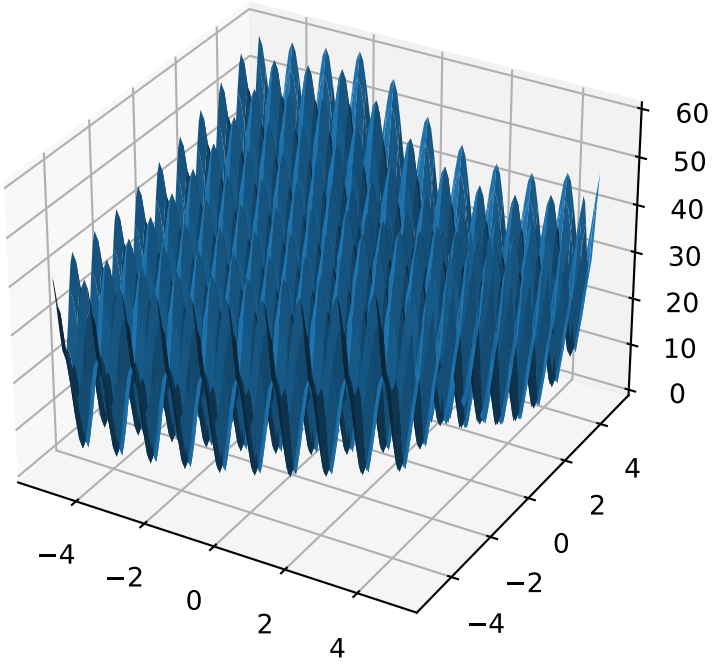
Bases: *ScalarProblem*

Apply a linear transformation to a fitness function.

Parameters
matrix – an nxn matrix, where n is the genome length.

Returns
a function that first applies -matrix to the input, then applies fun to the transformed input.

For example, here we manually construct a 2x2 rotation matrix and apply it to the `leap.RosenbrockProblem` function:


60
50
40
30
20
10
0
−4
−2
0
2
4
−4
−2
0
2
4

```
from matplotlib import pyplot as plt
from leap_ec.real_rep.problems import RosenbrockProblem, MatrixTransformedProblem,␣
↪plot_2d_problem

original_problem = RosenbrockProblem()
theta = np.pi/2
matrix = [[np.cos(theta), -np.sin(theta)],                [np.sin(theta), np.
↪cos(theta)]]

transformed_problem = MatrixTransformedProblem(original_problem, matrix)

fig = plt.figure(figsize=(12, 8))

plt.subplot(221, projection='3d')
bounds = RosenbrockProblem.bounds  # Contains traditional bounds
plot_2d_problem(original_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(222, projection='3d')
plot_2d_problem(transformed_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(223)
plot_2d_problem(original_problem, kind='contour', xlim=bounds, ylim=bounds, ax=plt.
↪gca(), granularity=0.025)

plt.subplot(224)
plot_2d_problem(transformed_problem, kind='contour', xlim=bounds, ylim=bounds,␣
↪ax=plt.gca(), granularity=0.025)
```

evaluate(*phenome*)

Evaluated the fitness of a point on the transformed fitness landscape.

For example, consider a sphere function whose global optimum is situated at (0, 1):

```
>>> import numpy as np
>>> s = TranslatedProblem(SpheroidProblem(), offset=[0, 1])
>>> round(s.evaluate(np.array([0, 1])), 5)
0
```

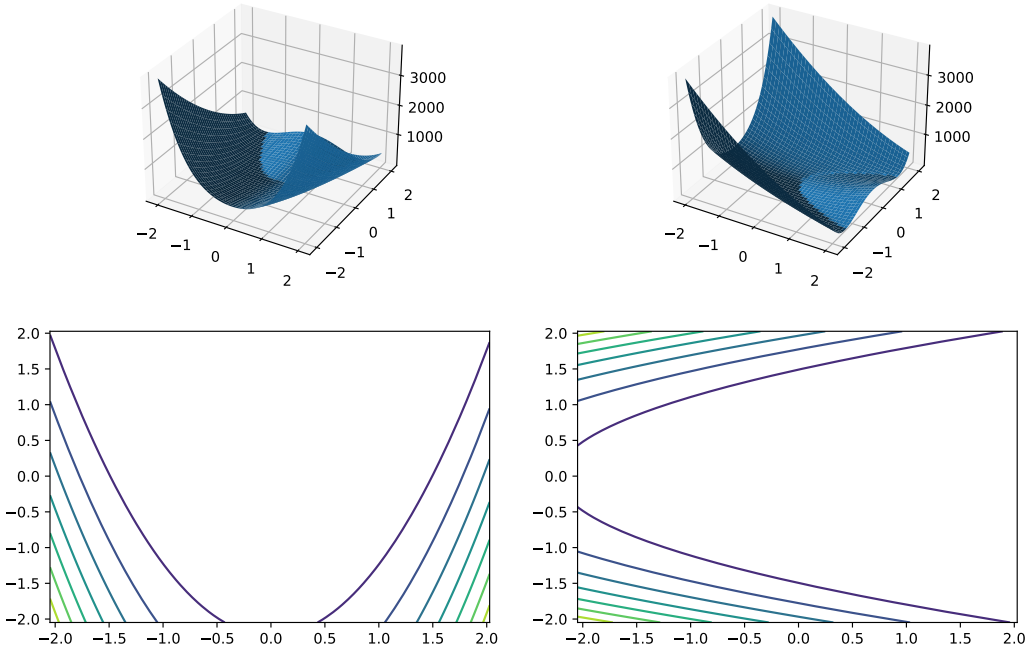
Now let's take a rotation matrix that transforms the space by pi/2 radians:

```
>>> import numpy as np
>>> theta = np.pi/2
>>> matrix = [[np.cos(theta), -np.sin(theta)],                    [np.
↪sin(theta), np.cos(theta)]]
>>> r = MatrixTransformedProblem(s, matrix)
```

The rotation has moved the new global optimum to (1, 0)

```
>>> round(r.evaluate(np.array([1, 0])), 5)
0.0
```

The point (0, 1) lies at a distance of sqrt(2) from the new optimum, and has a fitness of 2:




```
>>> round(r.evaluate(np.array([0, 1])), 5)
2.0
```

classmethod random_orthonormal(*problem*, *dimensions*, *maximize=None*)

Create a `MatrixTransformedProblem` that performs a random rotation and/or inversion of the function.

We accomplish this by generating a random orthonormal basis for R^n and plugging the resulting matrix into `MatrixTransformedProblem`.

The classic algorithm we use here is based on the Gramm-Schmidt process: we first generate a set of random vectors, and then convert them into an orthonormal basis. This approach is described in Hansen and Ostermeier's original CMA-ES paper:

"Completely derandomized self-adaptation in evolution strategies." *Evolutionary Computation* 9.2 (2001): 159-195.

Parameters

- **problem** – the original `ScalarProblem` to apply the transform to.
- **dimensions** (*int*) – the number of elements each vector should have.
- **maximize** (*bool*) – whether to maximize or minimize the resulting fitness function. Defaults to whatever setting the underlying problem uses.

```
from matplotlib import pyplot as plt
from leap_ec.real_rep.problems import CosineFamilyProblem,␣
↪MatrixTransformedProblem, plot_2d_problem
```

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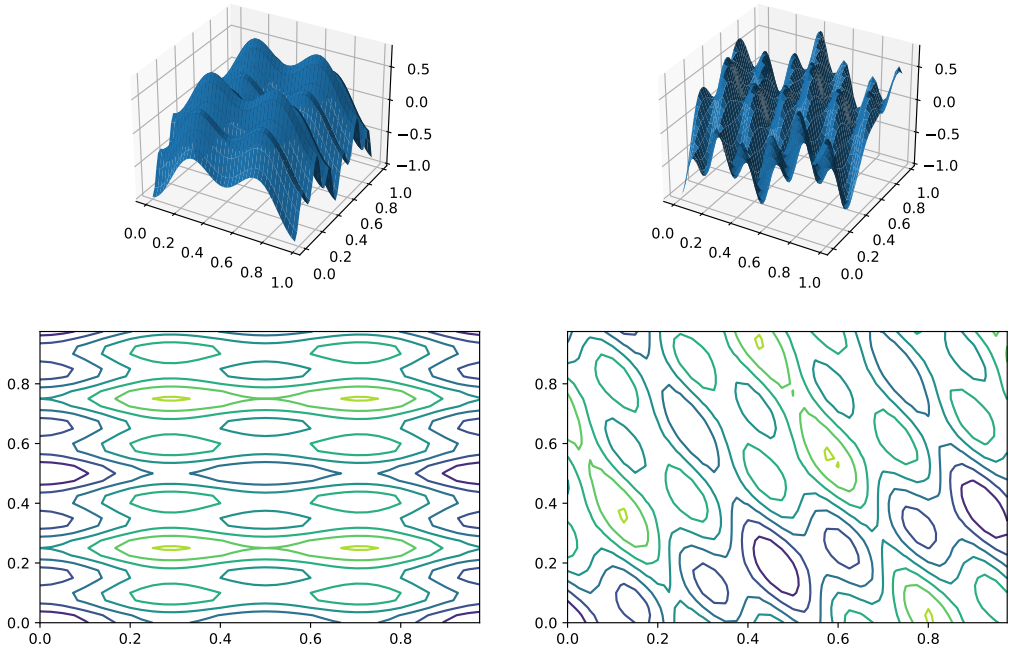
```
original_problem = CosineFamilyProblem(alpha=1.0, global_optima_counts=[2, 3],␣
↪local_optima_counts=[2, 3])

transformed_problem = MatrixTransformedProblem.random_orthonormal(original_
↪problem, 2)

fig = plt.figure(figsize=(12, 8))

plt.subplot(221, projection='3d')
bounds = original_problem.bounds
plot_2d_problem(original_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(222, projection='3d')
plot_2d_problem(transformed_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(223)
plot_2d_problem(original_problem, kind='contour', xlim=bounds, ylim=bounds,␣
↪ax=plt.gca(), granularity=0.025)

plt.subplot(224)
plot_2d_problem(transformed_problem, kind='contour', xlim=bounds, ylim=bounds,␣
↪ax=plt.gca(), granularity=0.025)
```



class leap_ec.real_rep.problems.**NoisyQuarticProblem**(*maximize=False*)

Bases: *ScalarProblem*

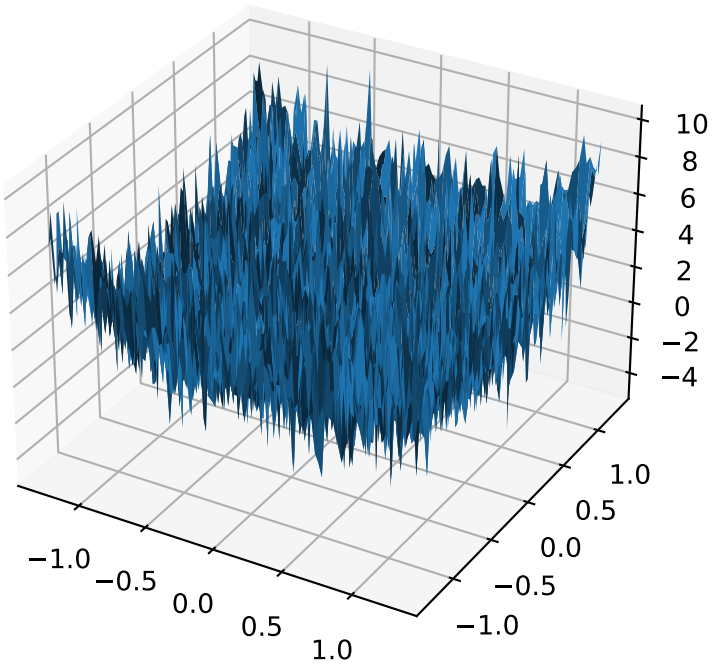
The classic 'quadratic quartic' function with Gaussian noise:

$$f(\mathbf{x}) = \sum_{i=1}^{n} ix_i^4 + \text{gauss}(0, 1)$$

Parameters

maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import NoisyQuarticProblem, plot_2d_problem
bounds = NoisyQuarticProblem.bounds  # Contains traditional bounds
plot_2d_problem(NoisyQuarticProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```



bounds = (-1.28, 1.28)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome (the output varies, since the function has noise):

```
>>> phenome = [3.5, -3.8, 5.0]
>>> r = NoisyQuarticProblem().evaluate(phenome)
>>> print(f'Result: {r}')
Result: ...
```

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness

worse_than(*first_fitness*, *second_fitness*)

We minimize by default:

```
>>> s = NoisyQuarticProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = NoisyQuarticProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```

class leap_ec.real_rep.problems.**ParabaloidProblem**(*diagonal_matrix: ndarray*, *rotation_matrix: ndarray*, *maximize=False*)

Bases: *ScalarProblem*

A generalization of the *SpheroidProblem* into parabaloids (including elliptic and hyperbolic parabaloids).

We construct the parabaloid by combining a diagonal matrix (which defines an axis-aligned parabaloid) with an orthornormal rotation. Together, these make up the eigenvalues and eigenbasis, respectively, of an arbitrary parabaloid:

$$\mathbf{A} = \mathbf{R}^\top \mathbf{D} \mathbf{R}$$

We then compute fitness by interpretting A as a quadratic form:

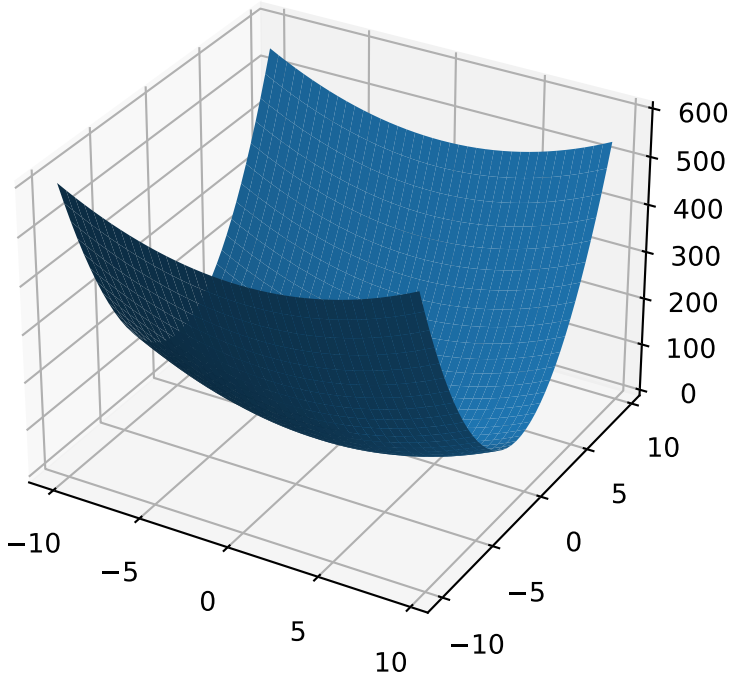
$$f(x) = x^\top \mathbf{A} x$$

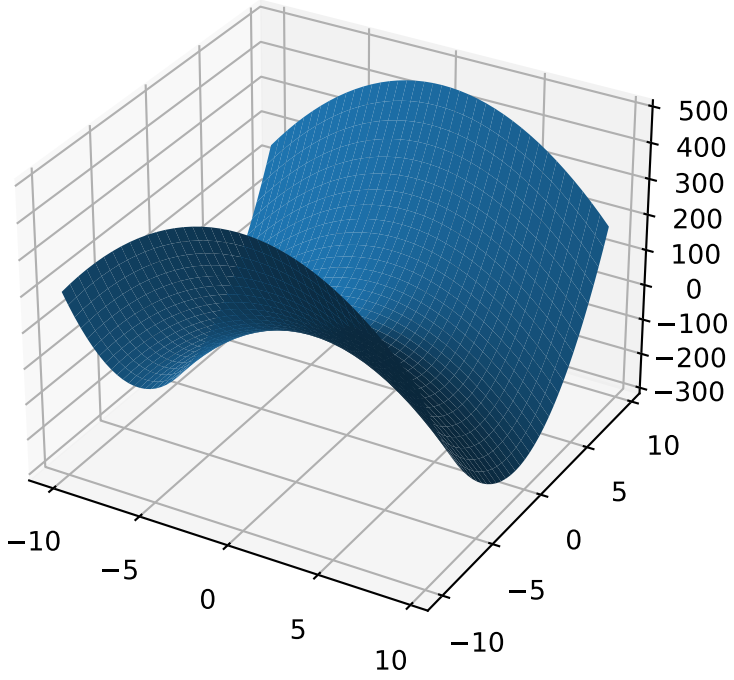
When the eigenvalues are all positive, then the result is an elliptic parabaloid

```
from leap_ec.real_rep .problems import ParabaloidProblem, plot_2d_problem
from matplotlib import pyplot as plt
import numpy as np

p = ParabaloidProblem(diagonal_matrix=np.diag([1, 5]), rotation_matrix=np.
↪identity(2))
plot_2d_problem(p, xlim=(-10, 10), ylim=(-10, 10), granularity=0.5)
plt.show()
```

If one or more eigenvalues are negative, then a hyperbolic parabloid results, which has a saddle shape:

```
from leap_ec.real_rep .problems import ParabaloidProblem, plot_2d_problem
from matplotlib import pyplot as plt
import numpy as np

p = ParabaloidProblem(diagonal_matrix=np.diag([-3, 5]), rotation_matrix=np.
↪identity(2))
plot_2d_problem(p, xlim=(-10, 10), ylim=(-10, 10), granularity=0.5)
plt.show()
```


600
500
400
300
200
100
0
10
5
0
−5
−10
−10
−5
0
5
10


500
400
300
200
100
0
−100
−200
−300
−10
−5
0
5
10
10
5
0
−5
−10

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

class leap_ec.real_rep.problems.**QuadraticFamilyProblem**(*diagonal_matrices: list*, *rotation_matrices: list*, *offset_vectors: list*, *fitness_offsets: list*, *maximize=False*)

Bases: *ScalarProblem*

A configurable multi-modal function based on combinations of spheroids or parabaloids. Taken from the problem generators proposed by Rönkkönen *et al.* [RonkkonenLKL08].

The function is given by

$$f(\mathbf{x}) = \min_{i=1,2,\ldots,q} \left((\mathbf{x} - \mathbf{p}_i)^\top \mathbf{B}_i^{-1} (\mathbf{x} - \mathbf{p}_i) + v_i \right)$$

where the $\mathbf{p}_i$ gives the center of each quadratic (i.e. the location of each local minimum), the v_i give their fitness values, and the $\mathbf{B}_i^{-1}$ are symmetric matrices.

The easiest way to create one of these problems is to use the random generator:

```
from leap_ec.real_rep.problems import QuadraticFamilyProblem, plot_2d_problem
from matplotlib import pyplot as plt

problem = QuadraticFamilyProblem.generate(dimensions=2, num_basins=30)
plot_2d_problem(problem, xlim=(-10, 10), ylim=(-10, 10), granularity=0.5)
plt.show()
```

You can also specify the problem structure directly by providing two matrices for each parabaloid along with an offset vector (for translation) and a scalar offset (to define the minimum fitness value for the basin):

```
from leap_ec.real_rep.problems import QuadraticFamilyProblem, plot_2d_problem,␣
↪random_orthonormal_matrix
from matplotlib import pyplot as plt
import numpy as np

# Define the parameters for each parabaloid

diag1 = np.diag([2, 4])     # Diagonal matrix defining the widths (eigenvalues) of␣
↪the basin for each dimension
rot1 = np.identity(2)       # Rotation matrix, in this case the identity (no␣
↪rotation)
offset1 = np.array([-1, -1])  # Offset used to translate the basin location
fitness1 = 0                # Fitness value of the local optimum

diag2 = np.diag([5, 1])
rot2 = random_orthonormal_matrix(dimensions=2)  # Apply a random rotation to the␣
```

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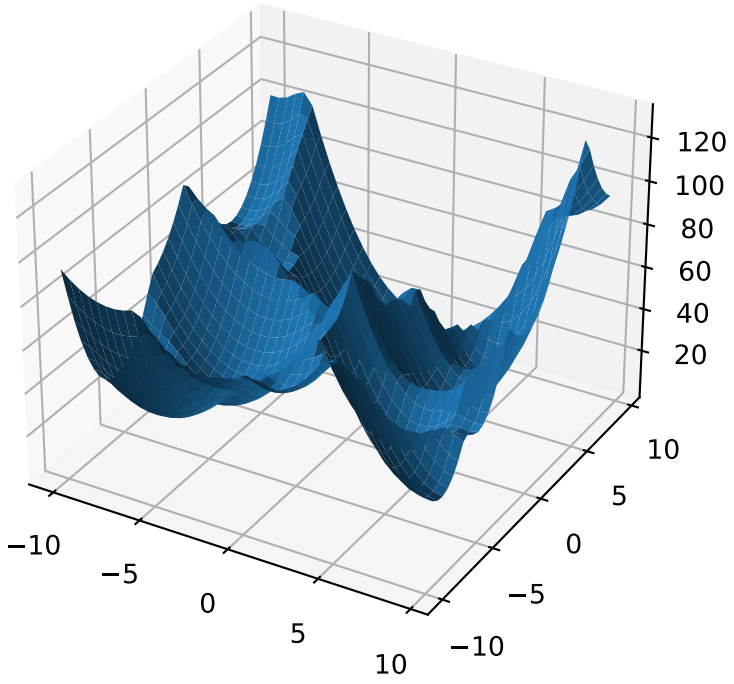
120
100
80
60
40
20
−10
−5
0
5
10
−10
−5
0
5
10

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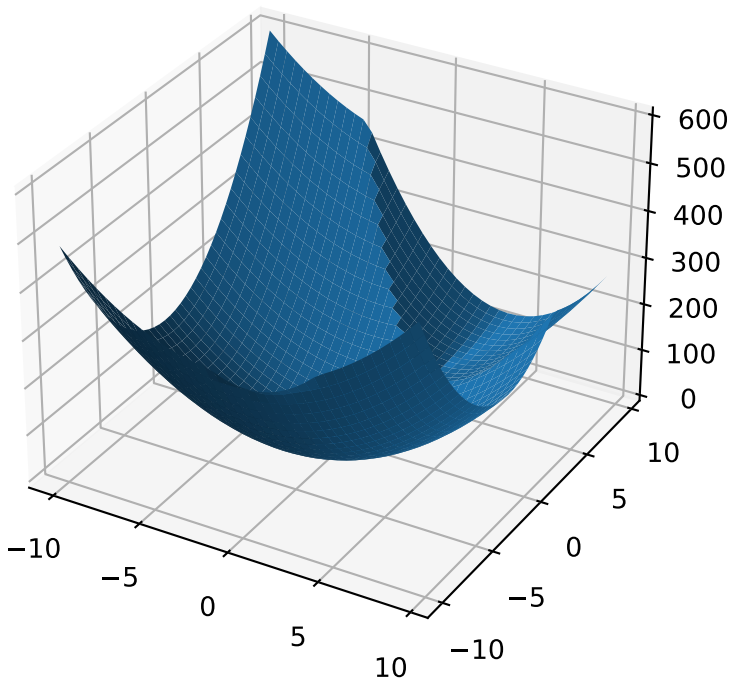
```
↪second basin
offset2 = np.array([3, 4])
fitness2 = 100.0

# Build the problem
problem = QuadraticFamilyProblem(
    diagonal_matrices = [ diag1, diag2 ],
    rotation_matrices = [ rot1, rot2 ],
    offset_vectors = [ offset1, offset2 ],
    fitness_offsets = [ fitness1, fitness2 ]
)

# Visualize
plot_2d_problem(problem, xlim=(-10, 10), ylim=(-10, 10), granularity=0.5)
plt.show()
```



property dimensions

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

classmethod generate(*dimensions: int*, *num_basins: int*, *num_global_optima: int = 1*, *width_bounds: tuple = (1, 5)*, *offset_bounds: tuple = (-10, 10)*, *fitness_offset_bounds: tuple = (10, 100)*)

Convenient method to generate a QuadraticFamilyProblem by randomly sampling the matrices that define it.

```
>>> problem = QuadraticFamilyProblem.generate(10, 20, num_global_optima = 2)
>>> x = problem.evaluate(np.array([0.0, 0.5, 0.0, 0.6, 0.0, 0.7, 0.6, 0.8, 4.3,␣
↪0.2]))
```

property num_basins

class leap_ec.real_rep.problems.**RastriginProblem**(*a=1.0*, *maximize=False*)

Bases: *ScalarProblem*

The classic Rastrigin problem. The Rastrigin provides a real-valued fitness landscape with a quadratic global structure (like the SpheroidProblem), plus a sinusoidal local structure with many local optima.

$$f(\vec{x}) = An + \sum_{i=1}^{n} x_i^2 - A\cos(2\pi x_i)$$

Parameters
maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import RastriginProblem, plot_2d_problem
bounds = RastriginProblem.bounds  # Contains traditional bounds
plot_2d_problem(RastriginProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (-5.12, 5.12)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome:

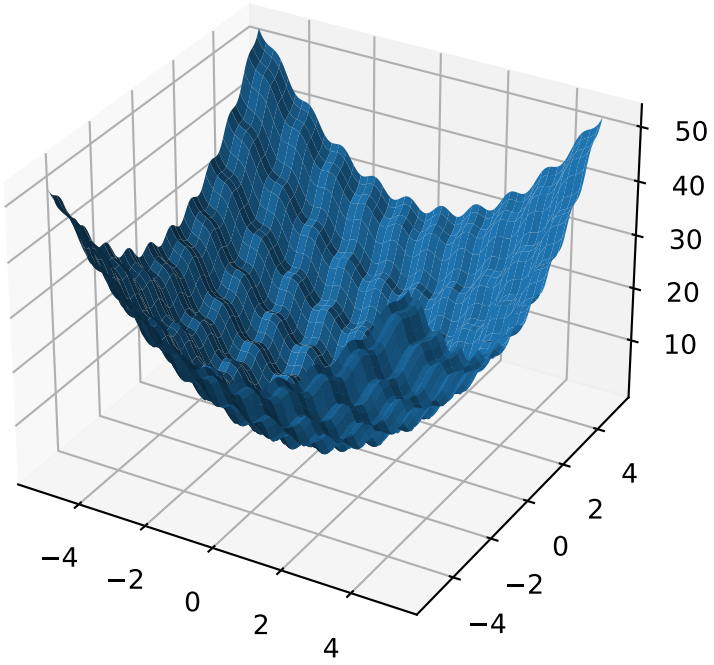
```
>>> phenome = [1.0/12, 0]
>>> RastriginProblem().evaluate(phenome)
0.1409190406...
```

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness

worse_than(*first_fitness*, *second_fitness*)

We minimize by default:


50
40
30
20
10
−4
−2
0
2
4
4
2
0
−2
−4

```
>>> s = RastriginProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = RastriginProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```

class leap_ec.real_rep.problems.**RosenbrockProblem**(*maximize=False*)

Bases: *ScalarProblem*

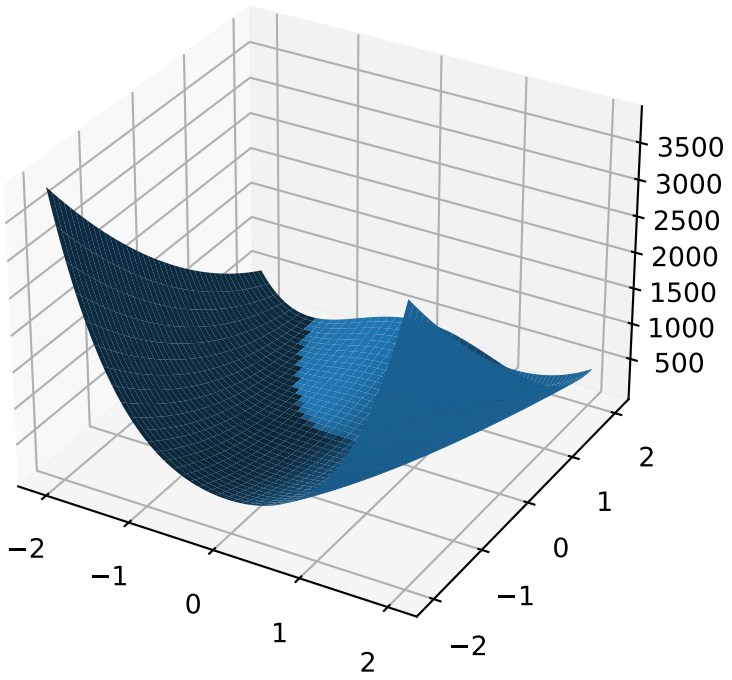
The classic RosenbrockProblem problem, a.k.a. the "banana" or "valley" function.

$$f(\mathbf{x}) = \sum_{i=1}^{d-1} \left[100(x_{i+1} - x_i^2)^2 + (x_i - 1)^2\right]$$

Parameters

maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import RosenbrockProblem, plot_2d_problem
bounds = RosenbrockProblem.bounds  # Contains traditional bounds
plot_2d_problem(RosenbrockProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```



bounds = (-2.048, 2.048)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome:

```
>>> phenome = [0.5, -0.2, 0.1]
>>> RosenbrockProblem().evaluate(phenome)
22.3
```

Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness

worse_than(*first_fitness*, *second_fitness*)

We minimize by default:

```
>>> s = RosenbrockProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = RosenbrockProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```

class leap_ec.real_rep.problems.**ScaledProblem**(*problem*, *new_bounds*, *maximize=None*)

Bases: *ScalarProblem*

Scale the search space of a fitness function up or down.

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

class leap_ec.real_rep.problems.**SchwefelProblem**(*alpha=418.982887*, *maximize=False*)

Bases: *ScalarProblem*

Schwefel's function is another traditional multimodal test function whose local optima are distributed in a slightly irregular way, and whose global optimum is out at the edge of the search space (with no gently sloping macrostructure to guide the algorithm toward it).

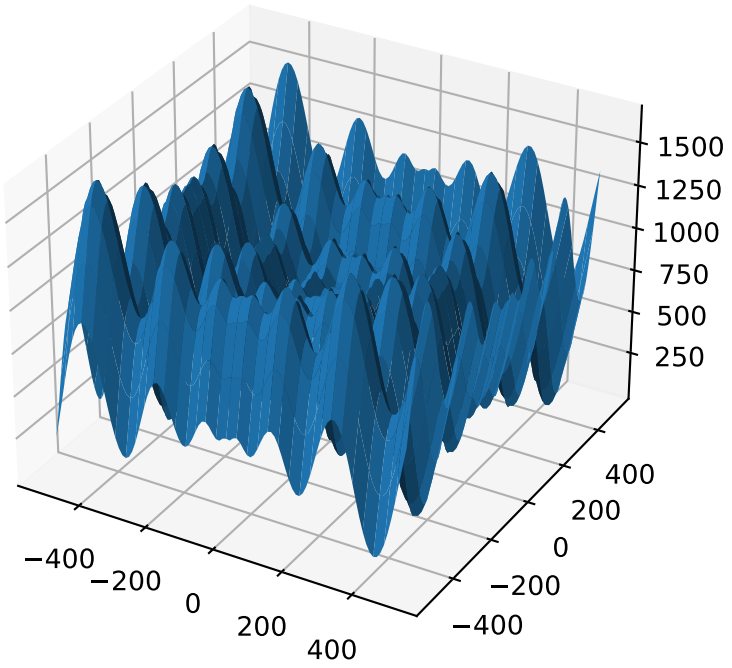
Compare this to the `RastriginProblem` function, whose global optimum lies at the center of a quadratic bowl with a regular grid of local optima.

$$f(\mathbf{x}) = \sum_{i=1}^{d} \left(-x_i \cdot \sin\left(\sqrt{|x_i|} \right) \right) + \alpha \cdot d$$

Parameters

- **alpha** (*float*) – fitness offset (the default value ensures that the global optimum has zero fitness)
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import SchwefelProblem, plot_2d_problem
bounds = SchwefelProblem.bounds  # Contains traditional bounds
plot_2d_problem(SchwefelProblem(), xlim=bounds, ylim=bounds, granularity=10)
```



bounds = (-512, 512)

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters
phenome – phenome with a real-valued phenome to be evaluated

Returns
its fitness.

class leap_ec.real_rep.problems.**ShekelProblem**(*k=500*, *c=array([1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25])*, *maximize=False*)

Bases: *ScalarProblem*

The classic 'Shekel's foxholes' function.

$$f(\mathbf{x}) = \frac{1}{\frac{1}{K} + \sum_{j=1}^{25} \frac{1}{f_j(\mathbf{x})}}$$

where

$$f_j(\mathbf{x}) = c_j + \sum_{i=1}^{2} (x_i - a_{ij})^6$$

and the points $\{(a_{1j}, a_{2j})\}_{j=1}^{25}$ define the functions various optima, and are given by the following hardcoded matrix:

$$[a_{ij}] = \begin{bmatrix} -32 & -16 & 0 & 16 & 32 & -32 & -16 & \cdots & 0 & 16 & 32 \\ -32 & -32 & -32 & -32 & -32 & -16 & -16 & \cdots & 32 & 32 & 32 \end{bmatrix}.$$

Parameters

- **k** (*int*) – the value of K in the fitness function.
- **c** (*[int]*) – list of values for the function's c_j parameters. Each *c[j]* approximately corresponds to the depth of the jth foxhole.
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.
- **maximize** – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import ShekelProblem, plot_2d_problem
bounds = ShekelProblem.bounds  # Contains traditional bounds
plot_2d_problem(ShekelProblem(), xlim=bounds, ylim=bounds, granularity=0.9)
```

bounds = (-65.536, 65.536)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome (the output varies, since the function has noise).

Parameters
phenome – real-valued to be evaluated

Returns
its fitness

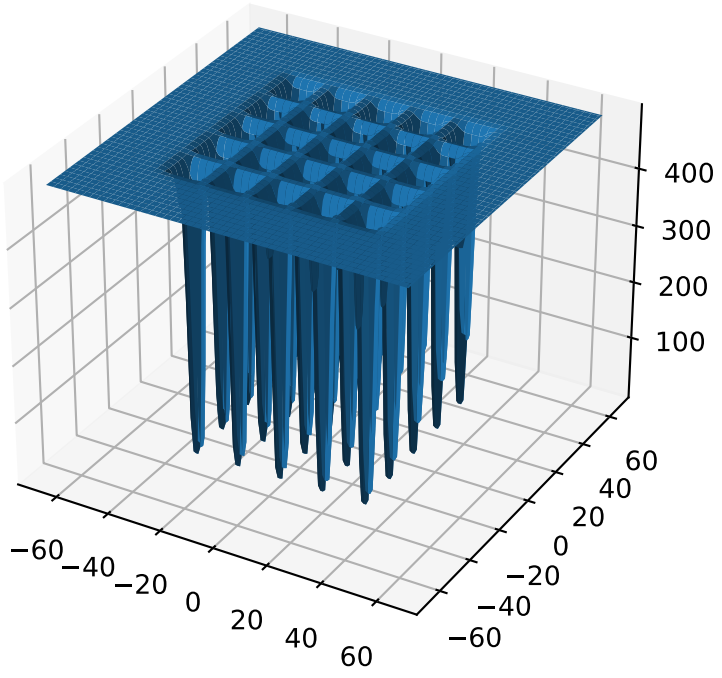
points = array([[-32, -16, 0, 16, 32, -32, -16, 0, 16, 32, -32, -16, 0, 16, 32, -32, -16, 0, 16, 32, -32, -16, 0, 16, 32], [-32, -32, -32, -32, -32, -16, -16, -16, -16, -16, 0, 0, 0, 0, 0, 16, 16, 16, 16, 16, 32, 32, 32, 32, 32]])

worse_than(*first_fitness*, *second_fitness*)

We minimize by default:

```
>>> s = ShekelProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = ShekelProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```


400
300
200
100
−60
−40
−20
0
20
40
60
60
40
20
0
−20
−40
−60

class leap_ec.real_rep.problems.**SpheroidProblem**(*maximize=False*)

Bases: *ScalarProblem*

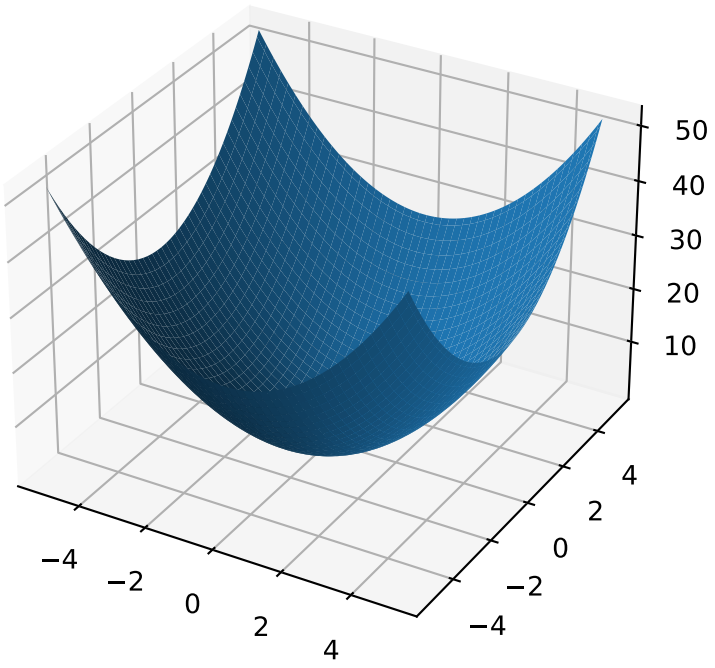
Classic paraboloid function, known as the "sphere" or "spheroid" problem, because its equal-fitness contours form (hyper)spheres in n > 2.

$$f(\vec{x}) = \sum_{i}^{n} x_i^2$$

Parameters

maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import SpheroidProblem, plot_2d_problem
bounds = SpheroidProblem.bounds  # Contains traditional bounds
plot_2d_problem(SpheroidProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```



bounds = (-5.12, 5.12)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome:

```
>>> phenome = [0.5, 0.8, 1.5]
>>> SpheroidProblem().evaluate(phenome)
3.14
```

Parameters
phenome – real-valued vector to be evaluated

Returns
it's fitness, *sum(phenome**2)*

worse_than(*first_fitness*, *second_fitness*)

We minimize by default:

```
>>> s = SpheroidProblem()
>>> s.worse_than(100, 10)
True
```

```
>>> s = SpheroidProblem(maximize=True)
>>> s.worse_than(100, 10)
False
```

class leap_ec.real_rep.problems.**StepProblem**(*maximize=True*)

Bases: *ScalarProblem*

The classic 'step' function—a function with a linear global structure, but with stair-like plateaus at the local level.

$$f(\mathbf{x}) = \sum_{i=1}^{n} \lfloor x_i \rfloor$$

where $\lfloor x \rfloor$ denotes the floor function.

Parameters
maximize (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import StepProblem, plot_2d_problem
bounds = StepProblem.bounds  # Contains traditional bounds
plot_2d_problem(StepProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (-5.12, 5.12)

evaluate(*phenome*)

Computes the function value from a real-valued list phenome:

```
>>> import numpy as np
>>> phenome = np.array([3.5, -3.8, 5.0])
>>> StepProblem().evaluate(phenome)
4.0
```

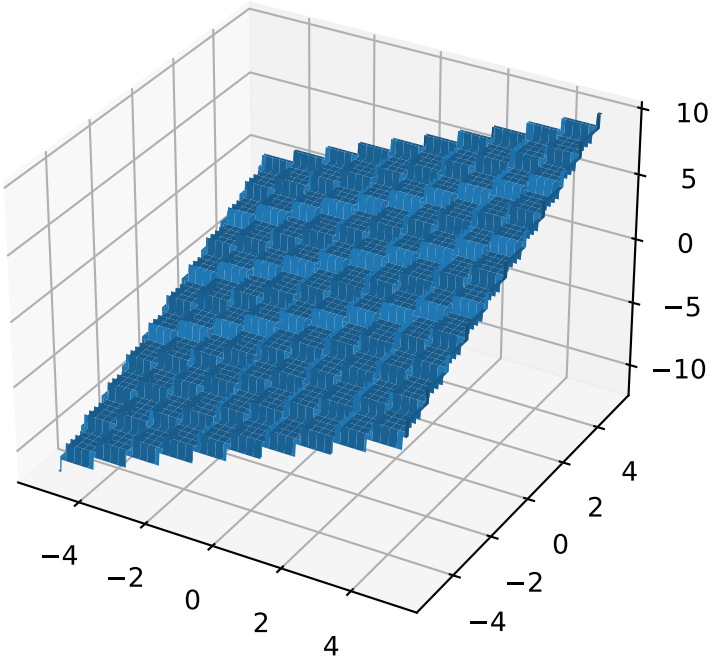
Parameters
phenome – real-valued vector to be evaluated

Returns
its fitness

worse_than(*first_fitness*, *second_fitness*)

We maximize by default:

```
>>> s = StepProblem()
>>> s.worse_than(100, 10)
False
```


10
5
0
−5
−10
−4
−2
0
2
4
−4
−2
0
2
4

```
>>> s = StepProblem(maximize=False)
>>> s.worse_than(100, 10)
True
```

class leap_ec.real_rep.problems.**TranslatedProblem**(*problem*, *offset*, *maximize=None*)

Bases: *ScalarProblem*

Takes an existing fitness function and translates it by applying a fixed offset vector.

For example,

```
from matplotlib import pyplot as plt
from leap_ec.real_rep.problems import SpheroidProblem, TranslatedProblem, plot_2d_
↪problem

original_problem = SpheroidProblem()
offset = [-1.0, -2.5]
translated_problem = TranslatedProblem(original_problem, offset)

fig = plt.figure(figsize=(12, 8))

plt.subplot(221, projection='3d')
bounds = SpheroidProblem.bounds  # Contains traditional bounds
plot_2d_problem(original_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(222, projection='3d')
plot_2d_problem(translated_problem, xlim=bounds, ylim=bounds, ax=plt.gca(),␣
↪granularity=0.025)

plt.subplot(223)
plot_2d_problem(original_problem, kind='contour', xlim=bounds, ylim=bounds, ax=plt.
↪gca(), granularity=0.025)

plt.subplot(224)
plot_2d_problem(translated_problem, kind='contour', xlim=bounds, ylim=bounds,␣
↪ax=plt.gca(), granularity=0.025)
```

evaluate(*phenome*)

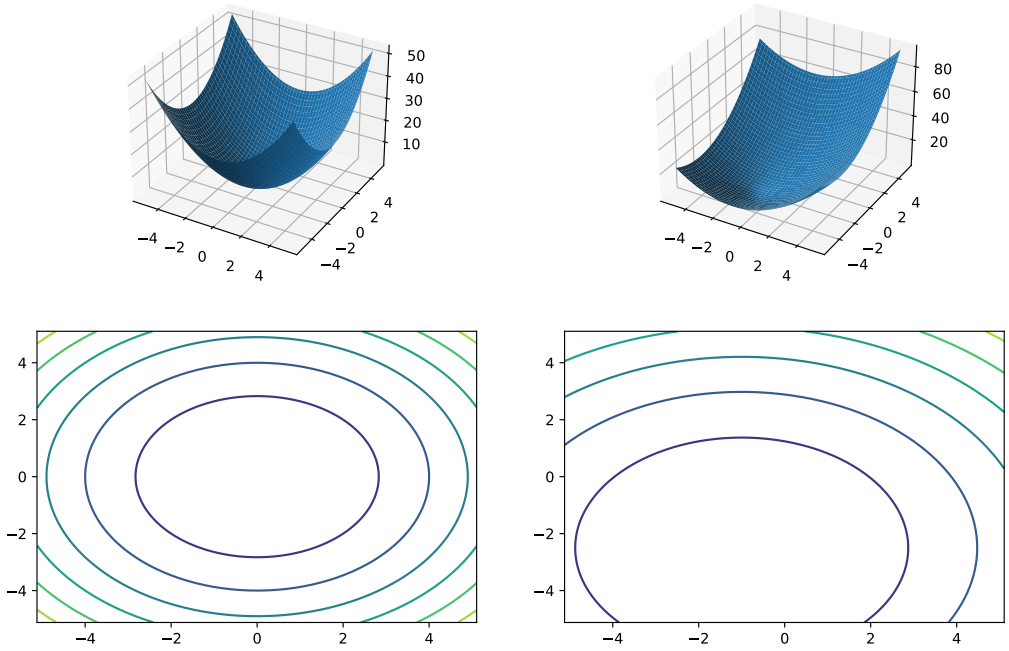
Evaluate the fitness of a point after translating the fitness function.

Translation can be used in higher than two dimensions:

```
>>> import numpy as np
>>> offset = [-1.0, -1.0, 1.0, 1.0, -5.0]
>>> t_sphere = TranslatedProblem(SpheroidProblem(), offset)
>>> genome = np.array([0.5, 2.0, 3.0, 8.5, -0.6])
>>> t_sphere.evaluate(genome)
90.86
```

classmethod random(*problem*, *offset_bounds*, *dimensions*, *maximize=None*)

Apply a random real-valued translation to a fitness function, sampled uniformly between min_offset and max_offset in every dimension.



```
>>> from leap_ec.real_rep.problems import TranslatedProblem, RastriginProblem,␣
↪plot_2d_problem
```

```
>>> original_problem = RastriginProblem()
>>> bounds = RastriginProblem.bounds  # Contains traditional bounds
>>> translated_problem = TranslatedProblem.random(original_problem, bounds, 2)
```

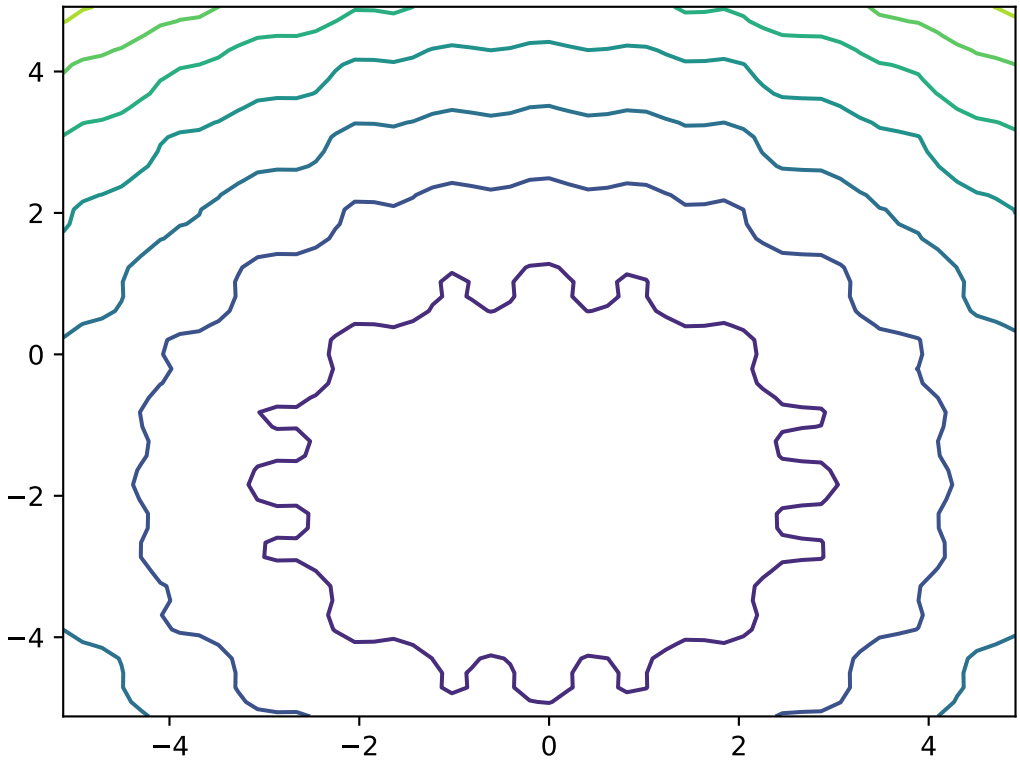
```
>>> plot_2d_problem(translated_problem, kind='contour', xlim=bounds,␣
↪ylim=bounds)
<matplotlib.contour...>
```

```
from leap_ec.real_rep.problems import TranslatedProblem, RastriginProblem, plot_
↪2d_problem

original_problem = RastriginProblem()
bounds = RastriginProblem.bounds  # Contains traditional bounds
translated_problem = TranslatedProblem.random(original_problem, bounds, 2)

plot_2d_problem(translated_problem, kind='contour', xlim=bounds, ylim=bounds)
```

class leap_ec.real_rep.problems.**WeierstrassProblem**(*kmax=20*, *a=0.5*, *b=3*, *maximize=False*)

Bases: *ScalarProblem*

The Weierstrass function is famous for being the first discovered example of a function that is continuous, but


4
2
0
−2
−4
−4
−2
0
2
4

not differentiable. Built by adding the terms of a Fourier series, it has a jagged, self-similar structure:

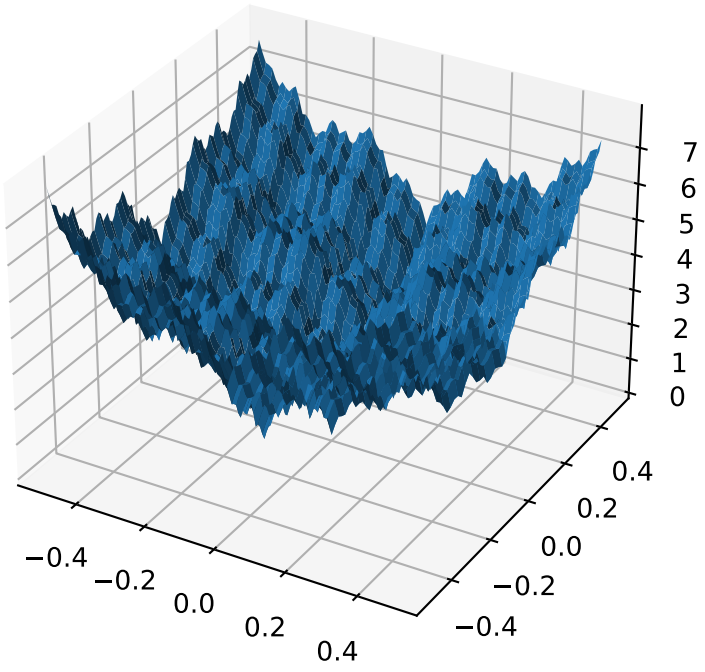
$$f(\mathbf{x}) = \sum_{i=1}^{d} \left[\sum_{k=0}^{kmax} a^k \cos\left(2\pi b^k (x_i + 0.5)\right) - n \sum_{k=0}^{kmax} a^k \cos(\pi b^k) \right]$$

When used in optimization benchmarks, it's typical to carry out the Fourier sum to *kmax=20* terms.

Parameters

- **kmax** (*int*) – number of terms to carry the Fourier sum out to
- **a** (*float*) – amplitude parameter of the cosine terms
- **b** (*float*) – wavenumber (frequency) parameter of the cosine terms
- **maximize** (*bool*) – the function is maximized if *True*, else minimized.

```
from leap_ec.real_rep.problems import WeierstrassProblem, plot_2d_problem
bounds = WeierstrassProblem.bounds  # Contains traditional bounds
plot_2d_problem(WeierstrassProblem(), xlim=bounds, ylim=bounds, granularity=0.01)
```



bounds = [-0.5, 0.5]

evaluate(*phenome*)

Computes the function value from a real-valued phenome.

Parameters

phenome – real-valued vector to be evaluated

Returns
its fitness.

leap_ec.real_rep.problems.**plot_2d_contour**(*fun*, *xlim*, *ylim*, *granularity*, *ax=None*, *title=None*, *pad=None*)

Convenience method for plotting contours for a function that accepts 2-D real-valued inputs and produces a 1-D scalar output.

Parameters

- **fun** (*function*) – The function to plot.
- **xlim** (*(float, float)*) – Bounds of the horizontal axes.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **granularity** (*float*) – Spacing of the grid to sample points along.
- **pad** – An array of extra gene values, used to fill in the hidden dimensions with contants while drawing fitness contours.

The difference between this and *plot_2d_problem()* is that this takes a raw function (instead of a Problem object).

```
import numpy as np
from scipy import linalg

from leap_ec.real_rep.problems import plot_2d_contour

def sinc_hd(phenome):
    r = linalg.norm(phenome)
    return np.sin(r)/r

plot_2d_contour(sinc_hd, xlim=(-10, 10), ylim=(-10, 10), granularity=0.2)
```

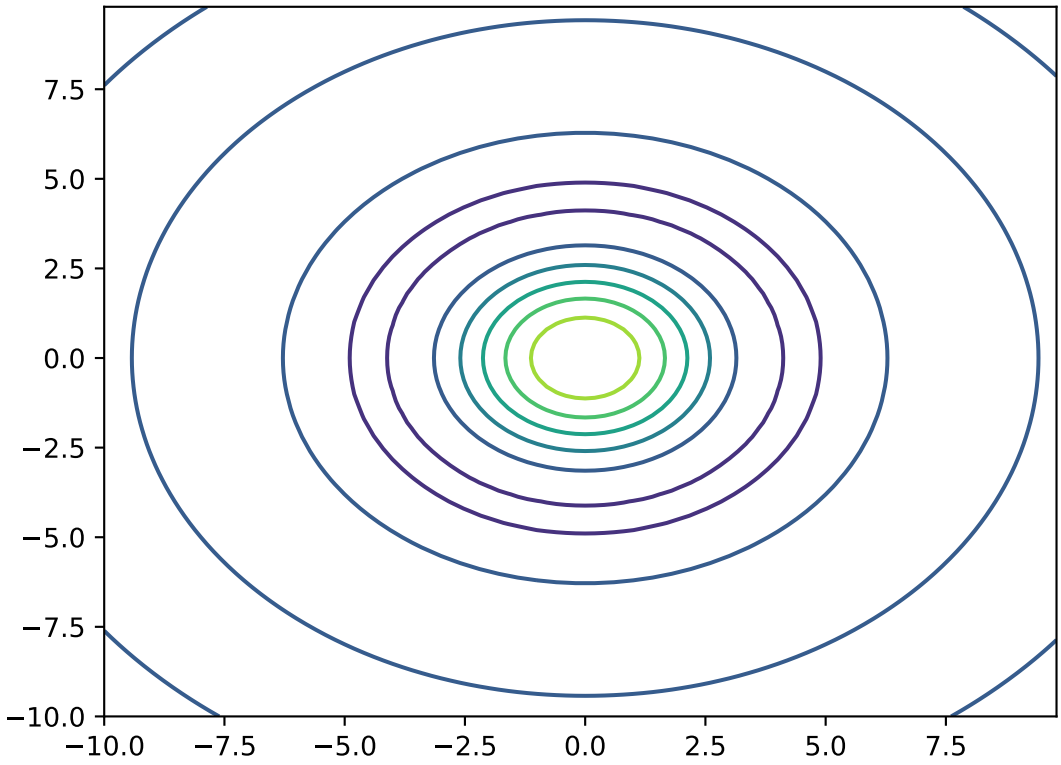
leap_ec.real_rep.problems.**plot_2d_function**(*fun*, *xlim*, *ylim*, *granularity=0.1*, *ax=None*, *title=None*, *pad=None*, ***kwargs*)

Convenience method for plotting a function that accepts 2-D real-valued imputs and produces a 1-D scalar output.

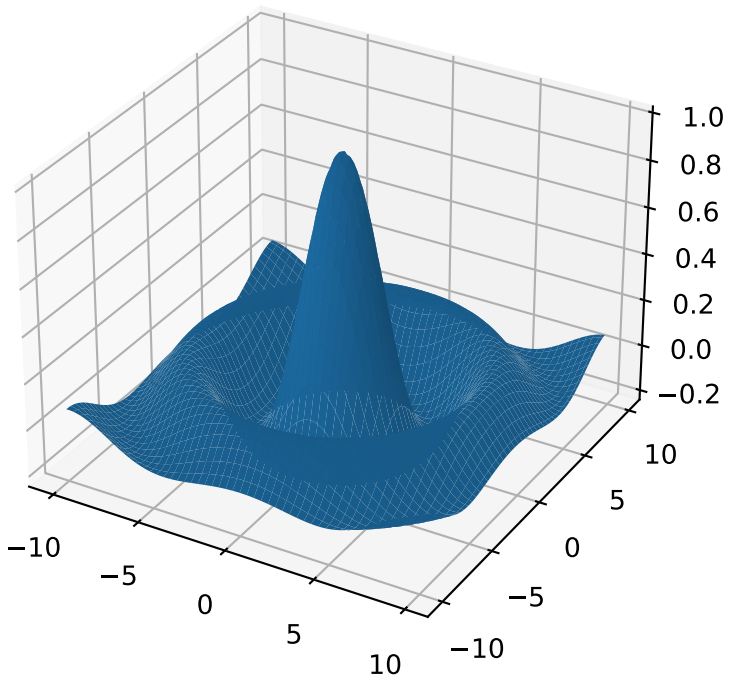
Parameters

- **fun** (*function*) – The function to plot.
- **xlim** (*(float, float)*) – Bounds of the horizontal axes.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **granularity** (*float*) – Spacing of the grid to sample points along.
- **pad** – An array of extra gene values, used to fill in the hidden dimensions with contants while drawing fitness contours.
- **kwargs** – additional keyword arguments to pass along to plot_surface() or contour()

The difference between this and *plot_2d_problem()* is that this takes a raw function (instead of a Problem object).


7.5
5.0
2.5
0.0
−2.5
−5.0
−7.5
−10.0
−10.0
−7.5
−5.0
−2.5
0.0
2.5
5.0
7.5

```
import numpy as np
from scipy import linalg

from leap_ec.real_rep.problems import plot_2d_function

def sinc_hd(phenome):
    r = linalg.norm(phenome)
    return np.sin(r)/r

plot_2d_function(sinc_hd, xlim=(-10, 10), ylim=(-10, 10), granularity=0.2)
```



leap_ec.real_rep.problems.**plot_2d_problem**(*problem*, *xlim=None*, *ylim=None*, *kind='surface'*, *ax=None*, *granularity=None*, *title=None*, *pad=None*, ***kwargs*)

Convenience function for plotting a `Problem` that accepts 2-D real-valued phenomes and produces a 1-D scalar fitness output.

Parameters

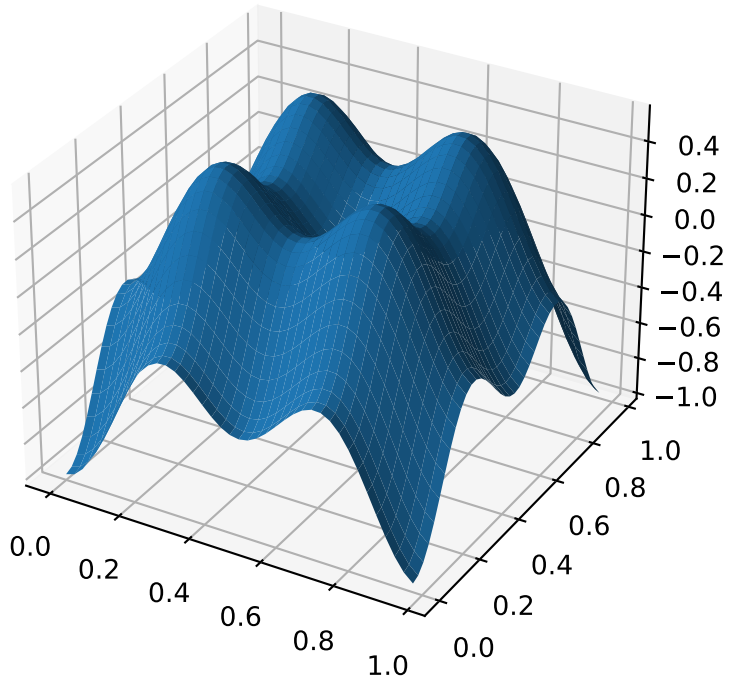
- **fun** (*Problem*) – The `Problem` to plot.
- **xlim** (*(float, float)*) – Bounds of the horizontal axes. If None, uses *problem.bounds*.
- **ylim** (*(float, float)*) – Bounds of the vertical axis. If None, uses *problem.bounds*.
- **kind** (*str*) – The kind of plot to create: 'surface' or 'contour'

- **pad** – An array of extra gene values, used to fill in the hidden dimensions with contants while drawing fitness contours.
- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **granularity** (*float*) – Spacing of the grid to sample points along. If none is given, then the granularity will default to 1/50th of the range of the function's *bounds* attribute.
- **kwargs** – additional keyword arguments to pass along to plot_surface()

The difference between this and *plot_2d_function()* is that this takes a `Problem` object (instead of a raw function).

If no axes are specified, a new figure is created for the plot:

```
from leap_ec.real_rep.problems import CosineFamilyProblem, plot_2d_problem
problem = CosineFamilyProblem(alpha=1.0, global_optima_counts=[2, 2], local_optima_
↪counts=[2, 2])
plot_2d_problem(problem, xlim=(0, 1), ylim=(0, 1), granularity=0.025);
```



You can also specify axes explicitly (ex. by using *ax=plt.gca()*. When plotting surfaces, you must configure your axes to use *projection='3d'*. Contour plots don't need 3D axes:

```
from matplotlib import pyplot as plt
from leap_ec.real_rep.problems import RastriginProblem, plot_2d_problem

```

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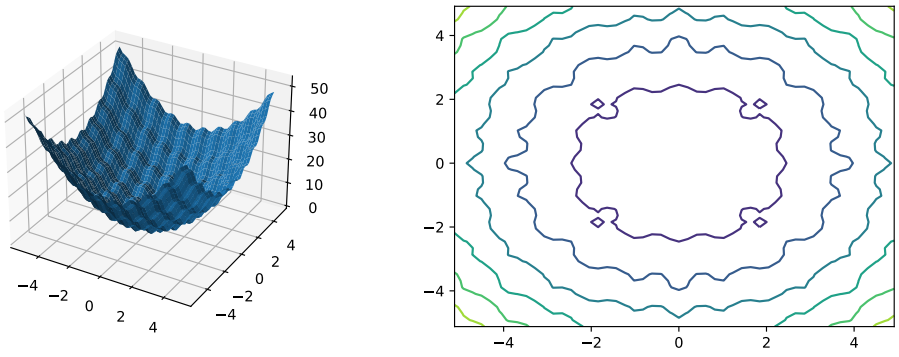
```
fig = plt.figure(figsize=(12, 4))
bounds=RastriginProblem.bounds  # Contains default bounds

plt.subplot(121, projection='3d')
plot_2d_problem(RastriginProblem(), ax=plt.gca(), xlim=bounds, ylim=bounds)

plt.subplot(122)
plot_2d_problem(RastriginProblem(), ax=plt.gca(), kind='contour', xlim=bounds,␣
↪ylim=bounds)
```



leap_ec.real_rep.problems.**random**(*size=None*)

Return random floats in the half-open interval [0.0, 1.0). Alias for *random_sample* to ease forward-porting to the new random API.

leap_ec.real_rep.problems.**random_orthonormal_matrix**(*dimensions: int*)

Generate a random orthornomal matrix using the Gramm-Schmidt process.

Orthonormal matrices represent rotations (and flips) of a space.

The defining property of an orthonormal matrix is that its transpose is its inverse:

```
>>> Q = random_orthonormal_matrix(10)
>>> np.allclose( Q.dot(Q.T), np.identity(10) )
True
```

Module contents

10.1.9 leap_ec.segmented_rep package

Submodules

leap_ec.segmented_rep.decoders module

Used to decode segments

class leap_ec.segmented_rep.decoders.**SegmentedDecoder**(*segment_decoder*)

Bases: *Decoder*

For decoding LEAP segmented representations

```
>>> from leap_ec.binary_rep.decoders import BinaryToIntDecoder
```

This example presumes that each segment has five bits, the first to map to an integer and the remaining three to a different integer.

```
>>> import numpy as np
>>> decoder = SegmentedDecoder(BinaryToIntDecoder(2,3))
>>> genome = np.array([[1, 0, 1, 0, 1],
...                    [0, 0, 1, 1, 1],
...                    [1, 0, 0, 0, 1]])
>>> vals = decoder.decode(genome)
>>> assert np.all(vals == np.array([[2, 5], [0, 7], [2, 1]]))
```

decode(*genome*, **args*, ***kwargs*)

For decoding *genome* which is a list of lists, or a segmented representation.

Parameters

- **genome** (*will be a list of segments (or lists)*) – for a given individual
- **args** (*list*) – optional args
- **kwargs** (*dict*) – optional keyword args

Returns
a list of list of values decoded from *genome*

Return type
list

leap_ec.segmented_rep.initializers module

Used to initialize segments

leap_ec.segmented_rep.initializers.**create_segmented_sequence**(*length*, *seq_initializer*)

Create a segmented test_sequence

A segment is a list of lists. *seq_initializer* is used to create *length* individual segments, which allows for the using any of the pre-supplied initializers for a regular genomic test_sequence, or for making your own.

length denotes how many segments to generate. If it's an integer, then we will create *length* segments. However, if it's a function that draws from a random distribution that returns an int, we will, instead, use that to calculate the number of segments to generate.

```
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> segmented_initializer = create_segmented_sequence(3, create_binary_sequence(3))
>>> segments = segmented_initializer()
>>> assert len(segments) == 3
```

Parameters

- **length** (*int or Callable*) – How many segments?
- **seq_initializer** (*Callable*) – initializer for creating individual sequences

Returns
function that returns a list of segmented

Return type
Callable

leap_ec.segmented_rep.ops module

Segmented representation specific pipeline operators.

leap_ec.segmented_rep.ops.**add_segment**(*next_individual: Iterator = '__no__default__', seq_initializer: Callable = '__no__default__', probability: float = '__no__default__', append: bool = False*) → Iterator

Possibly add a segment to the given individual

New segments can be always appended, or randomly inserted within the individual's genome.

TODO add a parameter for accepting a function that will yield a distribution for the number of segments to be randomly inserted.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> import numpy as np
>>> original = Individual([np.array([0, 0]), np.array([1, 1])])
>>> mutated = next(add_segment(iter([original]),
...                seq_initializer=create_binary_sequence(2),
...                probability=1.0))
```

Parameters

- **next_individual** – to possibly add a segment
- **seq_initializer** – callable for initializing any new segments
- **probability** – likelihood of adding a segment
- **append** – if True, always append any new segments

Returns
yielded individual with a possible new segment

leap_ec.segmented_rep.ops.**apply_mutation**(*next_individual: Iterator = '__no__default__', mutator: Callable[[list, float], list] = '__no__default__'*) → Iterator

This expects next_individual to have a segmented representation; i.e., a test_sequence of sequences. *mutator* will be applied separately to each sub-test_sequence.

```
>>> from leap_ec.binary_rep.ops import genome_mutate_bitflip
>>> mutation_op = apply_mutation(
...     mutator=genome_mutate_bitflip(
...                 expected_num_mutations=0.5
...  ))
>>> import numpy as np
```

```
>>> from leap_ec.individual import Individual
>>> original = Individual(np.array([[0, 0], [1, 1]]))
>>> mutated = next(mutation_op(iter([original])))
```

Parameters

- **next_individual** – to possibly mutate
- **mutator** – function to be applied to each segment in the individual's genome; first argument is a segment, the second the expected probability of mutating each segment element.

Returns
yielded mutated individual

leap_ec.segmented_rep.ops.**copy_segment**(*next_individual: Iterator = '__no__default__', probability: float = '__no__default__', append: bool = False*) → Iterator

with a given probability, randomly select and copy a segment

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> original = Individual([np.array([0, 0])])
>>> mutated = next(copy_segment(iter([original]), probability=1.0))
>>> assert np.all(mutated.genome[0] == [0, 0])            and np.all(mutated.
↪genome[1] == [0, 0])
```

param next_individual
to have a segment possibly removed

param probability
likelihood of doing this

param append
if True, always append any new segments

returns
the next individual

leap_ec.segmented_rep.ops.**remove_segment**(*next_individual: Iterator = '__no__default__', probability: float = '__no__default__'*) → Iterator

for some chance, remove a segment

Nothing happens if the individual has a single segment; i.e., there is no chance for an empty individual to be returned.

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> original = Individual([np.array([0, 0]), np.array([1, 1])])
>>> mutated = next(remove_segment(iter([original]), probability=1.0))
>>> assert np.all(mutated.genome[0] == [0, 0])             or np.all(mutated.
↪genome[0] == [1, 1])
```

param next_individual
to have a segment possibly removed

param probability
likelihood of removing a segment

returns
the next individual

leap_ec.segmented_rep.ops.**segmented_mutate**(*next_individual: Iterator = '__no__default__', mutator_functions: list = '__no__default__'*)

A mutation operator that applies a different mutation operator to each segment of a segmented genome.

Module contents

10.2 Submodules

10.3 leap_ec.algorithm module

Provides convenient monolithic functions that wrap a lot of common function- ality.

- generational_ea() for a typical generational model
- multi_population_ea() for invoking an EA using sub-populations
- random_search() for a more naive strategy

leap_ec.algorithm.**generational_ea**(*max_generations: int*, *pop_size: int*, *problem*, *representation*, *pipeline*, *stop=<function <lambda>>*, *init_evaluate=<bound method Individual.evaluate_population of <class 'leap_ec.individual.Individual'>>*, *k_elites: int = 1*, *start_generation: int = 0*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

This function provides an evolutionary algorithm with a generational population model.

When called this initializes and evaluates a population of size *pop_size* using the *init_evaluate* function and then pipes it through an operator *pipeline* (i.e. a list of operators) to obtain offspring. Wash, rinse, repeat.

The algorithm is provided here at the "metaheuristic" level: in order to apply it to a particular problem, you must parameterize it with implementations of its various components. You must decide the population size, how individuals are represented and initialized, the pipeline of reproductive operators, etc. A metaheuristic template of this kind can be used to implement genetic algorithms, genetic programming, certain evolution strategies, and all manner of other (novel) algorithms by passing in appropriate components as parameters.

Parameters

- **max_generations** (*int*) – The max number of generations to run the algorithm for. Can pass in float('Inf') to run forever or until the *stop* condition is reached.
- **pop_size** (*int*) – Size of the initial population
- **stop** (*int*) – A function that accepts a population and returns True iff it's time to stop evolving.
- **problem** (Problem) – the Problem that should be used to evaluate individuals' fitness
- **representation** – How the problem is represented in individuals
- **pipeline** (*list*) – a list of operators that are applied (in order) to create the offspring population at each generation
- **init_evaluate** – a function used to evaluate the initial population, before the main pipeline is run. The default of *Individual.evaluate_population* is suitable for many cases, but you may wish to pass a different operator in for distributed evaluation or other purposes.
- **k_elites** – keep k elites
- **start_generation** – index of the first generation to count from (defaults to 0). You might want to change this, for example, in experiments that involve stopping and restarting an algorithm.

Returns
the final population

The intent behind this kind of EA interface is to allow the complete configuration of a basic evolutionary algorithm to be defined in a clean and readable way. If you define most of the components in-line when passing them to the named arguments, then the complete configuration of an algorithmic experiment forms one concise code block. Here's what a basic (mu, lambda)-style EA looks like (that is, an EA that throws away the parents at each generation in favor of their offspring):

```
>>> from leap_ec import Individual, Representation
>>> from leap_ec.algorithm import generational_ea, stop_at_generation
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> from leap_ec.binary_rep.ops import mutate_bitflip
>>> import leap_ec.ops as ops
>>> pop_size = 5
>>> final_pop = generational_ea(max_generations=100, pop_size=pop_size,
...
...                         problem=MaxOnes(),      # Solve a MaxOnes Boolean␣
↪optimization problem
...
...                         representation=Representation(
...                             initialize=create_binary_sequence(length=10)  #␣
↪Initial genomes are random binary sequences
...                         ),
...
...                         # The operator pipeline
...                         pipeline=[
...                             ops.tournament_selection,                    # Select␣
↪parents via tournament selection
...                             ops.clone,                              # Copy them (just␣
↪to be safe)
...                             mutate_bitflip(expected_num_mutations=1),     # Basic␣
↪mutation with a 1/L mutation rate
...                             ops.UniformCrossover(p_swap=0.4),  # Crossover with a␣
↪40% chance of swapping each gene
...                             ops.evaluate,                           # Evaluate fitness
...                             ops.pool(size=pop_size)                 # Collect␣
↪offspring into a new population
...                         ])
```

The algorithm runs immediately and returns the final population:

```
>>> print(*final_pop, sep='\n')
Individual<...> ...
Individual<...> ...
Individual<...> ...
...
Individual<...> ...
```

You can get the best individual by using *max* (since comparison on individuals is based on the *Problem* associated with them, this will return the best individaul even on minimization problems):

```
>>> max(final_pop)
Individual<...>...
```

leap_ec.algorithm.**multi_population_ea**(*max_generations*, *num_populations*, *pop_size*, *problem*, *representation*, *shared_pipeline*, *subpop_pipelines=None*, *stop=<function <lambda>>*, *init_evaluate=<bound method Individual.evaluate_population of <class 'leap_ec.individual.Individual'>>*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

An EA that maintains multiple (interacting) subpopulations, i.e. for implementing island models.

This effectively executes several EAs concurrently that share the same generation counter, and which share the same representation (`Individual`, `Decoder`) and objective function (`Problem`), and which share all or part of the same operator pipeline.

Parameters

- **max_generations** (*int*) – The max number of generations to run the algorithm for. Can pass in float('Inf') to run forever or until the *stop* condition is reached.
- **num_populations** (*int*) – The number of separate populations to maintain.
- **pop_size** (*int*) – Size of each initial subpopulation
- **stop** (*int*) – A function that accepts a list of populations and returns True iff it's time to stop evolving.
- **problem** (Problem) – the Problem that should be used to evaluate individuals' fitness
- **representation** – the *Representation* that governs the creation and decoding of individuals. If a list of *Representation* objects is given, then different representations will be used for different subpopulations; else the same representation will be used for all subpopulations.
- **shared_pipeline** (*list*) – a list of operators that every population will use to create the offspring population at each generation
- **subpop_pipelines** (*list*) – a list of population-specific operator lists, the ith of which will only be applied to the ith population (after the *shared_pipeline*). Ignored if *None*.
- **init_evaluate** – a function used to evaluate the initial population, before the main pipeline is run. The default of *Individual.evaluate_population* is suitable for many cases, but you may wish to pass a different operator in for distributed evaluation or other purposes.

Returns

a list of lists of each of the subpopulations.

To turn a multi-population EA into an island model, use the *leap_ec.ops.migrate()* operator in the shared pipeline. This operator takes a *NetworkX* graph describing the topology of connections between islands as input.

For example, here's how we might define a fully connected 4-island model that solves a *leap_ec.real_rep.problems.SchwefelProblem* using a real-vector representation:

```
>>> import networkx as nx
>>> from leap_ec.algorithm import multi_population_ea
>>> from leap_ec import ops
>>> from leap_ec.real_rep.ops import mutate_gaussian
>>> from leap_ec.real_rep import problems
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.representation import Representation
>>> from leap_ec.real_rep.initializers import create_real_vector
>>>
>>> topology = nx.complete_graph(4)
>>> nx.draw_networkx(topology, with_labels=True)
```

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```
>>> problem = problems.SchwefelProblem(maximize=False)
...
>>> l = 2  # Length of the genome
>>> pop_size = 10
>>> pops = multi_population_ea(max_generations=10,
...                            num_populations=topology.number_of_nodes(),
...                            pop_size=pop_size,
...
...                            problem=problem,
...
...                            representation=Representation(
...                                individual_cls=Individual,
...                                decoder=IdentityDecoder(),
...                                initialize=create_real_vector(bounds=[problem.
↪bounds] * l)
...                                ),
...
...                            shared_pipeline=[
...                                ops.tournament_selection,
...                                ops.clone,
...                                mutate_gaussian(std=30,
...                                                expected_num_mutations='isotropic
↪',
...                                                bounds=problem.bounds),
...                                ops.evaluate,
...                                ops.pool(size=pop_size),
...                                ops.migrate(topology=topology,
...                                            emigrant_selector=ops.tournament_
↪selection,
...                                            replacement_selector=ops.random_
↪selection,
...                                            migration_gap=5)
...                            ])
>>> pops
[[Individual<...>(...), ..., Individual<...>(...)], ..., [Individual<...>(...), ...,
↪ Individual<...>(...)]]
```

We can now run the algorithm by pulling output from its generator, which gives us the best individual in each population at each generation:

While each population is executing, *multi_population_ea* writes the index of the current subpopulation to *context['leap']['subpopulation']*. That way shared operators (such as `leap.ops.migrate()`) have the option of accessing the share context to learn which subpopulation they are currently working with.

TODO find a way to use Dask to parallelize populations, likely by having a Dask worker for each sub-poplulation.

`leap_ec.algorithm.`**`random_search`**(*evaluations*, *problem*, *representation*, *pipeline*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

This function performs random search of a solution space using the given representation and problem.

Random search is often used as a control in evolutionary algorithm experiments: if your pet algorithm can't perform better than random search, then it's a sign that you've barked up the wrong tree!

This implementation also allows you to pass in an operator pipeline, which will be applied to each individual. The pipeline must have the following types of operators:

- **a selection operator, probably cyclic_selection since there will be only**
  one individual from which to choose
- clone operator to ensure we don't overwrite the previous individual
- a pertubation operator, likely a simple mutation pipeline operator
- evaluate operator so we know where the new individual is in the space
- pool(size=1) to act as a pipeline sink to pull the new individuals through

Parameters

- **evaluations** – how many evaluations to perform
- **problem** – the Problem instance to use for evaluating individuals
- **representation** – the Representation describing individuals
- **pipeline** – reproductive operator pipeline
- **context** – optional context for storing state as algorithm progresses

Returns
the series of individuals that describe a random walk

```
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> from leap_ec.binary_rep.ops import mutate_bitflip
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.representation import Representation
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import evaluate, clone, cyclic_selection, pool
>>> result = random_search(evaluations=5,
...                       problem=MaxOnes(),      # Solve a MaxOnes Boolean␣
↪optimization problem
...
...                       representation=Representation(
...                           individual_cls=Individual,     # Use the standard␣
↪Individual as the prototype for the population
...                           decoder=IdentityDecoder(),     # Genotype and phenotype␣
↪are the same for this task
...                           initialize=create_binary_sequence(length=3)  # Initial␣
↪genomes are random binary sequences
...                       ),
...                        pipeline=[cyclic_selection,
...                                  clone,
...                                  mutate_bitflip(expected_num_mutations=3),
...                                  evaluate,
...                                  pool(size=1)])
>>> assert(len(result) == 5)
```

The algorithm outputs a list containing all the generated individuals.

leap_ec.algorithm.**stop_at_generation**(*max_generation: int*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

A stopping criterion function that checks the 'generation' count in the *context* object and returns True iff it is >= *max_generation*.

The resulting function takes a *population* argument, which is ignored.

For example:

```
>>> from leap_ec import context
>>> stop = stop_at_generation(100)
```

If we set the generation field in the context object (this value will typically be updated by the algorithm as it runs) like so:

```
>>> context['leap']['generation'] = 15
```

Then we don't stop yet:

```
>>> stop(population=[])
False
```

We do stop at the 100th generation:

```
>>> context['leap']['generation'] = 100
>>> stop([])
True
```

10.4 leap_ec.data module

A module for synthetic data that we use in test and examples.

10.5 leap_ec.decoder module

Defines the *Decoder* base class.

Decoders are used to translate from genotypic to phenotypic space. E.g., binary strings may have to be decoded into corresponding integers or real values meaningful to a *Problem*.

class leap_ec.decoder.**Decoder**

Bases: ABC

Decoders in LEAP implement how solutions to a problem are represented.

Specifically, a `Decoder` converts an `Individual`'s *genotype* (which is a format that can easily be manipulated by mutation and recombination operators) into a *phenotype* (which is a format that can be fed directly into a `Problem` object to obtain a fitness value).

Genotypes and phenotypes can be of arbitrary type, from a simple list of numbers to a complex data structure. Choosing a good genotypic representation and genotype-to-phenotype mapping for a given problem domain is a critical part of evolutionary algorithm design: the `Decoder` object that an algorithm uses can have a big impact on the effectiveness of your metaheuristics.

In LEAP, a `Decoder` is typically used by `Individual` as an intermediate step in calculating its own fitness.

For example, say that we want to use a binary-represented `Individual` to solve a real-valued optimization problem, such as `SchwefelProblem`. Here, the genotype is a vector of binary values, whereas the phenotype is its corresponding float vector.

We can use a `BinaryToIntDecoder` to express this mapping. And when we initialize an individual, we give it all three pieces of this information:

```
>>> from leap_ec.binary_rep.decoders import BinaryToRealDecoder
>>> from leap_ec.individual import Individual
>>> from leap_ec.real_rep.problems import SchwefelProblem
>>> import numpy as np
>>> genome = np.array([0, 1, 1, 0, 1, 0, 1, 1])
>>> decoder = BinaryToRealDecoder((4, -5.12, 5.12), (4, -5.12, 5.12))  # Every 4␣
↪bits map to a float on (-5.12, 5.12)
>>> ind = Individual(genome, decoder=decoder, problem=SchwefelProblem())
```

Now we can decode the individual to examine its phenotype:

```
>>> ind.decode()
array([-1.024     ,  2.38933333])
```

This call is just a wrapper for the `Decoder`, which has the same output:

```
>>> decoder.decode(genome)
array([-1.024     ,  2.38933333])
```

But now `Individual` also has everything it needs to evaluate its own fitness:

```
>>> ind.evaluate()
836.4453949...
```

Calling *evaluate()* also has the side effect of setting the fitness attribute:

```
>>> ind.fitness
836.4453949...
```

abstract decode(*genome*, **args*, ***kwargs*)

Parameters
genome – a genome you wish to convert

Returns
the phenotype associated with that genome

class leap_ec.decoder.**IdentityDecoder**

Bases: *Decoder*

A decoder that maps a genome to itself. This acts as a 'direct' or 'phenotypic' encoding: Use this when your genotype and phenotype are the same thing.

decode(*genome*, **args*, ***kwargs*)

Returns
the input *genome*.

For example:

```
>>> import numpy as np
>>> d = IdentityDecoder()
>>> d.decode(np.array([0.5, 0.6, 0.7]))
array([0.5, 0.6, 0.7])
```

10.6 leap_ec.distrib module

10.7 leap_ec.global_vars module

This defines a global context that is a dictionary of dictionaries. The intent is for certain operators and functions to add to and modify this context. Third party operators and functions will just add a new top-level dedicated key.

context['leap'] is for storing general LEAP running state, such as current generation.

context['leap']['distrib'] is for storing leap.distrib running state

context['leap']['distrib']['non_viable'] accumulates counts of non-viable individuals during distrib.eval_pool() and distrib.async_eval_pool() runs.

10.8 leap_ec.individual module

Defines *Individual*

class leap_ec.individual.**Individual**(*genome*, *decoder=IdentityDecoder()*, *problem=None*)

Bases: `object`

Represents a single solution to a *Problem*.

We represent an *Individual* by a *genome* and a *fitness*. *Individual* also maintains a reference to the *Problem* it will be evaluated on, and an *decoder*, which defines how genomes are converted into phenomes for fitness evaluation.

clone()

Create a 'clone' of this *Individual*, copying the genome, but not fitness.

The fitness of the clone is set to *None*. A new UUID is generated and assigned to *sefl.uuid*. The *parents* set is updated to include the UUID of the parent. A shallow copy of the parent is made, too, so that ancillary state is also copied.

A deep copy of the genome will be created, so if your *Individual* has a custom genome type, it's important that it implements the *__deepcopy__()* method.

```
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.decoder import IdentityDecoder
>>> import numpy as np
>>> genome = np.array([0, 1, 1, 0])
>>> ind = Individual(genome, IdentityDecoder(), MaxOnes())
>>> ind_copy = ind.clone()
>>> ind_copy.genome == ind.genome
array([ True,  True,  True,  True])
>>> ind_copy.problem == ind.problem
True
>>> ind_copy.decoder == ind.decoder
True
```

classmethod create_population(*n*, *initialize*, *decoder*, *problem*)

A convenience method for initializing a population of the appropriate subtype.

Parameters

- **n** – The size of the population to generate

- **initialize** – A function f(m) that initializes a genome
- **decoder** – The decoder to attach individuals to
- **problem** – The problem to attach individuals to

Returns
A list of n individuals of this class's (or subclass's) type

decode(**args*, ***kwargs*)

Determine the indivdual's phenome.

This is done by passing the genome *self.decoder*.

The result is both returned and saved to *self.phenome*.

Returns
the decoded value for this individual

evaluate()

determine this individual's fitness

This is done by outsourcing the fitness evaluation to the associated *Problem* object since it "knows" what is good or bad for a given phenome.

See also
ScalarProblem.worse_than

Returns
the calculated fitness

evaluate_imp()

This is the evaluate 'implementation' called by self.evaluate(). It's intended to be optionally over-ridden by sub-classes to give an opportunity to pass in ancillary data to the evaluate process either by tailoring the problem interface or that of the given decoder.

classmethod evaluate_population(*population*)

Convenience function for bulk serial evaluation of a given population

Parameters
population – to be evaluated

Returns
evaluated population

property phenome

If the phenome has not yet been decoded, do so.

class leap_ec.individual.**RobustIndividual**(*genome*, *decoder=IdentityDecoder()*, *problem=None*)

Bases: *Individual*

This adds exception handling for evaluations

After evaluation *self.is_viable* is set to True if all went well. However, if an exception is thrown during evaluation, the following happens:

- self.is_viable is set to False
- self.fitness is set to math.nan
- self.exception is assigned the exception

evaluate()

determine this individual's fitness

Note that if an exception is thrown during evaluation, the fitness is set to NaN and *self.is_viable* to False; also, the returned exception is assigned to *self.exception* for possible later inspection. If the individual was successfully evaluated, *self.is_viable* is set to true. NaN fitness values will figure into comparing individuals in that NaN will always be considered worse than non-NaN fitness values.

Returns
the calculated fitness

class leap_ec.individual.**WholeEvaluatedIndividual**(*genome*, *decoder=IdentityDecoder()*, *problem=None*)

Bases: *Individual*

An Individual that, when evaluated, passes its whole self to the evaluation function, rather than just its phenome.

In most applications, fitness evaluation requires only phenome information, so that is all that we pass from the Individual to the Problem. This is important, because during distributed evaluation, we want to pass as little information as possible across nodes.

WholeEvaluatedIndividual is used for special cases where fitness evaluation needs access to more information about an individual than its phenome. This is strange in most cases and should be avoided, but can make certain algorithms more elegant (ex. it's helpful when interpreting cooperative coevolution as an island model).

This can dramatically slow down distributed evaluation (i.e. with dask) in some applications because the entire individual will be sent over a TCP/IP connection instead of just the *phenome*, so use with caution.

evaluate_imp()

This is the evaluate 'implementation' called by self.evaluate(). It's intended to be optionally over-ridden by sub-classes to give an opportunity to pass in ancillary data to the evaluate process either by tailoring the problem interface or that of the given decoder.

10.9 leap_ec.multiobjective module

10.10 leap_ec.ops module

Fundamental evolutionary operators.

This module provides many of the most important functions that we string together to create EAs out of operator pipelines. You'll find many traditional selection and reproduction strategies here, as well as components for classic algorithms like island models and cooperative coevolution.

Representation-specific operators tend to reside within their own subpackages, rather than here. See for example *leap_ec.real_rep.ops* and *leap_ec.binary_rep.ops*.

class leap_ec.ops.**CooperativeEvaluate**(*num_trials: int*, *collaborator_selector*, *log_stream=None*, *combine=<function concat_combine>*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

Bases: *Operator*

A simple, non-parallel implementation of cooperative coevolutionary fitness evaluation.

Parameters

- **num_trials** (*int*) – the number of combined solutions & fitness estimates to collect when computing a partial solution's fitness.

- **collaborator_selector** – a selection operator that we use to choose individuals from the *other* subpopulations to create a combined solution.
- **context** – the algorithm's state context. Used to access subpopulation information.
- **log_stream** – optional file object to collect statistics about combined individuals to.
- **combine** – the function used to combine partial solutions into combined solutions.

class leap_ec.ops.**Crossover**(*persist_children*, *p_xover*)

Bases: *Operator*

abstract recombine(*parent_a*, *parent_b*)

Perform recombination between two parents to produce two new individuals.

class leap_ec.ops.**NAryCrossover**(*num_points=2*, *p_xover=1.0*, *persist_children=False*)

Bases: *Crossover*

Do crossover between individuals between N crossover points.

1 < n < genome length - 1

We also assume that the passed in individuals are *clones* of parents.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import NAryCrossover
>>> import numpy as np
```

```
>>> genome1 = np.array([0, 0])
>>> genome2 = np.array([1, 1])
>>> first = Individual(genome1)
>>> second = Individual(genome2)
>>> pop = [first, second]
>>> select = naive_cyclic_selection(pop)
```

```
>>> op = NAryCrossover()
>>> result = op(select)
```

```
>>> new_first = next(result)
>>> new_second = next(result)
```

If *persist_children* is True and there is a child that was made by crossover but isn't used in the first call, it will be yielded in a future call.

```
>>> op = NAryCrossover(p_xover=0.0, persist_children=True)
>>>
>>> next(op(select)) is first  # Create an iterator loop with op(select) and␣
↪consume 1 individual
True
>>> next(op(select)) is second # Create a different iterator loop with op(select)
True
```

With *persist_children* set to False, the second child will not be yielded if the iterator is consumed an odd number of times. Instead, on the next call the loop is started anew.

```
>>> op = NAryCrossover(p_xover=0.0, persist_children=False)
>>>
>>> next(op(select)) is first  # Create an iterator loop with op(select) and␣
↪consume 1 individual
True
>>> next(op(select)) is second # Create a different iterator loop with op(select)
False
```

Parameters

- **num_points** – how many crossing points do we use? Defaults to 2, since 2-point crossover has been shown to be the least disruptive choice for this value.
- **p** – the probability that crossover is performed.
- **persist_children** (*bool*) – whether unyielded children should persist between calls. This is useful for *leap_ec.distrib.asynchronous.steady_state*, where the pipeline may only produce one individual at a time.

Returns

a pipeline operator that returns two recombined individuals (with probability p), or two unmodified individuals (with probability 1 - p)

recombine(*parent_a*, *parent_b*)

Perform recombination between two parents to produce two new individuals.

class leap_ec.ops.**Operator**

Bases: ABC

Abstract base class that documents the interface for operators in a LEAP pipeline.

LEAP treats operators as functions of two arguments: the population, and a "context" *dict* that may be used in some algorithms to maintain some global state or parameters independent of the population.

TODO The above description is outdated. –Siggy TODO Also this is for a *population* based operator. We also have operators *for individuals*

You can inherit from this class to define operators as classes. Classes support operators that take extra arguments at construction time (such as a mutation rate) and maintain some internal private state, and they allow certain special patterns (such as multi-function operators).

But inheriting from this class is optional. LEAP can treat any *callable* object that takes two parameters as an operator. You may define your custom operators as closures (which also allow for construction-time arguments and internal state), as simple functions (when no additional arguments are necessary), or as curried functions (i.e. with the help of *toolz.curry(...)*.

class leap_ec.ops.**UniformCrossover**(*p_swap: float = 0.2*, *p_xover: float = 1.0*, *persist_children=False*)

Bases: *Crossover*

Parameterized uniform crossover iterates through two parents' genomes and swaps each of their genes with the given probability.

In a classic paper, De Jong and Spears showed that this operator works particularly well when the swap probability *p_swap* is set to about 0.2. LEAP thus uses this value as its default.

> De Jong, Kenneth A., and W. Spears. "On the virtues of parameterized uniform crossover." *Proceedings of the 4th international conference on genetic algorithms.* Morgan Kaufmann Publishers, 1991.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import UniformCrossover, naive_cyclic_selection
>>> import numpy as np
```

```
>>> genome1 = np.array([0, 0])
>>> genome2 = np.array([1, 1])
>>> first = Individual(genome1)
>>> second = Individual(genome2)
>>> pop = [first, second]
>>> select = naive_cyclic_selection(pop)
>>> op = UniformCrossover()
>>> result = op(select)
>>> new_first = next(result)
>>> new_second = next(result)
```

The probability can be tuned via the *p_swap* parameter: >>> op = UniformCrossover(p_swap=0.1) >>> result = op(select)

If *persist_children* is True and there is a child that was made by crossover but isn't used in the first call, it will be yielded in a future call.

```
>>> op = UniformCrossover(p_xover=0.0, persist_children=True)
>>>
>>> next(op(select)) is first  # Create an iterator loop with op(select) and␣
↪consume 1 individual
True
>>> next(op(select)) is second # Create a different iterator loop with op(select)
True
```

With *persist_children* set to False, the second child will not be yielded if the iterator is consumed an odd number of times. Instead, on the next call the loop is started anew.

```
>>> op = UniformCrossover(p_xover=0.0, persist_children=False)
>>>
>>> next(op(select)) is first  # Create an iterator loop with op(select) and␣
↪consume 1 individual
True
>>> next(op(select)) is second # Create a different iterator loop with op(select)
False
```

Parameters

- **p_swap** – how likely are we to swap each pair of genes when crossover is performed
- **p_xover** (*float*) – the probability that crossover is performed in the first place
- **persist_children** (*bool*) – whether unyielded children should persist between calls. This is useful for *leap_ec.distrib.asynchronous.steady_state*, where the pipeline may only produce one individual at a time.

Returns

a pipeline operator that returns two recombined individuals (with probability p_xover), or two unmodified individuals (with probability 1 - p_xover)

recombine(*parent_a*, *parent_b*)

Perform recombination between two parents to produce two new individuals.

leap_ec.ops.**clone**(*next_individual: Iterator = '__no__default__'*) → Iterator

clones and returns the next individual in the pipeline

The clone's fitness is set to None, its parents are set to the individual from which it was cloned (i.e., the parent), and it is assigned its own UUID.

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
```

Create a common decoder and problem for individuals.

```
>>> genome = np.array([1, 1])
>>> original = Individual(genome)
```

```
>>> cloned_generator = clone(iter([original]))
```

Parameters

next_individual – iterator for next individual to be cloned

Returns

copy of next_individual

leap_ec.ops.**compute_expected_probability**(*expected_num_mutations: float*, *individual_genome: List*) → float

Computed the probability of mutation based on the desired average expected mutation and genome length.

The equation here is $p = 1/L *$

Parameters

- **expected_num_mutations** – times individual is to be mutated on average
- **individual_genome** – genome for which to compute the probability

Returns

the corresponding probability of mutation

leap_ec.ops.**compute_population_values**(*population: ~typing.List*, *offset=0*, *exponent: int = 1*, *key=<function <lambda>>*) → ndarray

Returns a list of values where the zero-point of the population is shifted and the values are scaled by exponentiation.

Parameters

- **population** – the population to compute values from.
- **offset** – the offset from zero. Specifying *offset='pop-min'* will use the population's minimum value as the new zero-point. Defaults to 0.
- **exponent** (*int*) – the power to which values are raised to. Defaults to 1.
- **key** – a function that computes a metric based on an *Individual*.

Returns

a numpy array of values that have been shifted by *offset* and scaled by *exponent* corresponding to each individual in the population.

leap_ec.ops.**concat_combine**(*collaborators*)

Combine a list of individuals by concatenating their genomes.

You can choose whether this or some other function is used for combining collaborators by passing it into the *CooperativeEvaluate* constructor.

leap_ec.ops.**const_evaluate**(*population: List = '__no__default__'*, *value='__no__default__'*) → List

An evaluator that assigns a constant fitness to every individual.

This ignores the *Problem* associated with each individual for the purpose of assigning a constant fitness.

This is useful for algorithms that need to assign an arbitrary initial fitness value before using their normal evaluation method. Some forms of cooperative coevolution are an example.

leap_ec.ops.**cyclic_selection**(*population: List = '__no__default__'*) → Iterator

Deterministically returns individuals in order, then shuffles the test_sequence, returns the individuals in that new order, and repeats this process.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import cyclic_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0])),
...        Individual(np.array([0, 1]))]
```

```
>>> cyclic_selector = cyclic_selection(pop)
```

Parameters
population – from which to select

Returns
the next selected individual

leap_ec.ops.**elitist_survival**(*offspring: List = '__no__default__'*, *parents: List = '__no__default__'*, *k: int = 1*, *key=None*) → List

This allows k best parents to compete with the offspring.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> import numpy as np
```

First, let's make a "pretend" population of parents using the MaxOnes problem.

```
>>> pretend_parents = [Individual(np.array([0, 0, 0]), problem=MaxOnes()),
...                    Individual(np.array([1, 1, 1]), problem=MaxOnes())]
```

Then a "pretend" population of offspring. (Pretend in that we're pretending that the offspring came from the parents.)

```
>>> pretend_offspring = [Individual(np.array([0, 0, 0]), problem=MaxOnes()),
...                      Individual(np.array([1, 1, 0]), problem=MaxOnes()),
...                      Individual(np.array([1, 0, 1]), problem=MaxOnes()),
...                      Individual(np.array([0, 1, 1]), problem=MaxOnes()),
...                      Individual(np.array([0, 0, 1]), problem=MaxOnes())]
```

We need to evaluate them to get their fitness to sort them for elitist_survival.

```
>>> pretend_parents = Individual.evaluate_population(pretend_parents)
>>> pretend_offspring = Individual.evaluate_population(pretend_offspring)
```

This will take the best parent, which has [1,1,1], and replace the worst offspring, which has [0,0,0] (because this is the MaxOnes problem) >>> survivors = elitist_survival(pretend_offspring, pretend_parents)

```
>>> assert pretend_parents[1] in survivors # yep, best parent is there
>>> assert pretend_offspring[0] not in survivors # worst guy isn't
```

We orginally ordered 5 offspring, so that's what we better have. >>> assert len(survivors) == 5

Please note that the literature has a number of variations of elitism and other forms of overlapping generations. For example, this may be a good starting point:

De Jong, Kenneth A., and Jayshree Sarma. "Generation gaps revisited." In Foundations of genetic algorithms, vol. 2, pp. 19-28. Elsevier, 1993.

Parameters

- **offspring** – list of created offpring, probably from pool()
- **parents** – list of parents, usually the ones that offspring came from
- **k** – how many elites from parents to keep?
- **key** – optional key criteria for selecting; e.g., can be used to impose parsimony pressure

Returns

surviving population, which will be offspring with offspring replaced by any superior parent elites

leap_ec.ops.**evaluate**(*next_individual: Iterator = '__no__default__'*) → Iterator

Evaluate and returns the next individual in the pipeline

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> import numpy as np
```

We need to specify the decoder and problem so that evaluation is possible.

```
>>> genome = np.array([1, 1])
>>> ind = Individual(genome, decoder=IdentityDecoder(), problem=MaxOnes())
```

```
>>> evaluated_ind = next(evaluate(iter([ind])))
```

Parameters

- **next_individual** – iterator pointing to next individual to be evaluated
- **kwargs** – contains optional context state to pass down the pipeline in context dictionaries

Returns

the evaluated individual

leap_ec.ops.**grouped_evaluate**(*population: list = '__no__default__', max_individuals_per_chunk: int = None*) → list

Evaluate the population by sending groups of multiple individuals to a fitness function so they can be evaluated simultaneously.

This is useful, for example, as a way to evaluate individuals in parallel on a GPU.

leap_ec.ops.**insertion_selection**(*offspring: List = '__no__default__', parents: List = '__no__default__', key=None*) → List

do exclusive selection between offspring and parents

This is typically used for Ken De Jong's EV algorithm for survival selection. Each offspring is deterministically selected and a random parent is selected; if the offspring wins, then it replaces the parent.

Note that we make a _copy_ of the parents and have the offspring compete with the parent copies so that users can optionally preserve the original parents. You may wish to do that, for example, if you want to analyze the composition of the original parents and the modified copy.

Parameters

- **offspring** – population to select from
- **parents** – parents that are copied and which the copies are potentially updated with better offspring
- **key** – optional key for determining max() by other criteria such as for parsimony pressure

Returns
the updated parent population

leap_ec.ops.**iteriter_op**(*f*)

This decorator wraps a function with runtime type checking to ensure that it always receives an iterator as its first argument, and that it returns an iterator.

We use this to make debugging operator pipelines easier in EAs: if you accidentally hook up, say an operator that outputs a list to an operator that expects an iterator, we'll throw an exception that pinpoints the issue.

Parameters
function (*f*) – the function to wrap

leap_ec.ops.**iterlist_op**(*f*)

This decorator wraps a function with runtime type checking to ensure that it always receives an iterator as its first argument, and that it returns a list.

We use this to make debugging operator pipelines easier in EAs: if you accidentally hook up, say an operator that outputs a list to an operator that expects an iterator, we'll throw an exception that pinpoints the issue.

Parameters
function (*f*) – the function to wrap

leap_ec.ops.**listiter_op**(*f*)

This decorator wraps a function with runtime type checking to ensure that it always receives a list as its first argument, and that it returns an iterator.

We use this to make debugging operator pipelines easier in EAs: if you accidentally hook up, say an operator that outputs an iterator to an operator that expects a list, we'll throw an exception that pinpoints the issue.

Parameters
function (*f*) – the function to wrap

leap_ec.ops.**listlist_op**(*f*)

This decorator wraps a function with runtime type checking to ensure that it always receives a list as its first argument, and that it returns a list.

We use this to make debugging operator pipelines easier in EAs: if you accidentally hook up, say an operator that outputs an iterator to an operator that expects a list, we'll throw an exception that pinpoints the issue.

Parameters
function (*f*) – the function to wrap

leap_ec.ops.**migrate**(*topology*, *emigrant_selector*, *replacement_selector*, *migration_gap*, *customs_stamp=<function <lambda>>*, *metric=None*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

A migration operator for use in island models.

This operator works with multi-population algorithms, and is thus meant to used with *leap_ec.algorithm.multi_population_ea*.

Specifically, it assumes that

1. the *population* argument passed into the returned function is a particular sub-population that we want to process "emigration" out of and "immigration" into,
2. the *context* state object contains an integer field *context['leap']['generation']* indicating the current generation count of the algorithm, and
3. the *context* also contains a integer field *context['leap']['current_subpopulation']* indicating the index of the subpopulation that is currently being processed in the overall collection of subpopulations (i.e. the one that *population* belongs to).

These assumptions are essentially what *leap_ec.algorithm.multi_population_ea* implements.

```
>>> import networkx as nx
>>> from leap_ec import ops, context
>>> from leap_ec.data import test_population
>>> pop0 = test_population[:]  # Shallow copy
>>> pop1 = test_population[:]
```

```
>>> op = migrate(topology=nx.complete_graph(2),
...              emigrant_selector=ops.tournament_selection,
...              replacement_selector=ops.random_selection,
...              migration_gap=50)
>>> context['leap']['generation'] = 0
>>> context['leap']['current_subpopulation'] = 0
>>> op(pop0)
[Individual<...>(...), Individual<...>(...), Individual<...>(...), Individual<...>(.
↪..)]
```

```
>>> context['leap']['current_subpopulation'] = 1
>>> op(pop1)
[Individual<...>(...), Individual<...>(...), Individual<...>(...), Individual<...>(.
↪..)]
```

This operator is a stateful closure: it maintains an internal list of all the out-going "emigrations" that occurred in the previous time step, so that it can process them as "immigrations" in the current time step.

Parameters

- **topology** – a *networkx* topology defining the connectivity among islands

- **emigrant_selector** – a selection operator for choosing individuals to leave an island
- **replacement_selector** – a selection operator choosing contestants that will be replaced by an incoming immigrant if the immigrant has higher fitness
- **migration_gap** (*int*) – migration will occur regularly after every *migration_gap* evolutionary steps
- **customs_stamp** – an optional function to transfrom an individual upon its arrival to a new island. This can be used, for example, to change the individual's decoder or problem in a heterogeneous island model.
- **metric** – an optional function of the form *f(generation, immigrant_individual, contestant_indidivudal, success)* for recording information about migration events.
- **context** – the context object to check for EA state, such as the current generation number, and the ID of the subpopulation that is currently being processed.

leap_ec.ops.**migration_metric**(*stream*, *header: bool = True*, *notes: Optional[dict] = None*)

Returns a function that can be used to record migration events.

The purpose of a migration metric is to record information about migrations that occur inside a migration operator. Because these events take place inside the operator (rather than across operators), they cannot be recorded by a LEAP pipeline probe.

In general, the interface for a migration metric function takes four parameters:

- *generation*: the current generation
- *immigrant_ind*: the individual that is attempting to migrate
- *contestant_ind*: the individual that has been chosen to be replaced
- *success*: True if the migration is successful, False otherwise

The metric included here records the fitness of both individuals and writes them (along with the *generation* and *success* values) to a CSV. You can write your own metric if you need to record other information (such as, say, genomes).

```
>>> import sys
>>> from leap_ec import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> m = migration_metric(sys.stdout,
...                      header=True,
...                      notes={'run': 0, 'description': 'Test output'}
... )
run,description,generation,migrant_fitness,contestant_fitness,success
```

```
>>> ind1 = Individual(np.array([1, 1, 1]), problem=MaxOnes())
>>> f = ind1.evaluate()
>>> contestant = Individual(np.array([0, 1, 1]), problem=MaxOnes())
>>> f = contestant.evaluate()
>>> m(0, ind1, contestant, True)
0,Test output,0,3,2,True
```

Parameters

- **stream** – file object to write the CSV data to
- **header** (*bool*) – a CSV header will be written if True

- **notes** (*dict*) – a dict specifying additional constant-value columns to include in the CSV output

leap_ec.ops.**naive_cyclic_selection**(*population: List = '__no__default__', indices: List = None*) → Iterator

Deterministically returns individuals, and repeats the same test_sequence when exhausted.

This is "naive" because it doesn't shuffle the population between complete tours to minimize bias.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import naive_cyclic_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0])),
...        Individual(np.array([0, 1]))]
```

```
>>> cyclic_selector = naive_cyclic_selection(pop)
```

Parameters
population – from which to select

Returns
the next selected individual

leap_ec.ops.**pool**(*next_individual: Iterator = '__no__default__', size: int = '__no__default__'*) → List

'Sink' for creating *size* individuals from preceding pipeline source.

Allows for "pooling" individuals to be processed by next pipeline operator. Typically used to collect offspring from preceding set of selection and birth operators, but could also be used to, say, "pool" individuals to be passed to an EDA as a training set.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.ops import naive_cyclic_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0])),
...        Individual(np.array([0, 1]))]
```

```
>>> cyclic_selector = naive_cyclic_selection(pop)
```

```
>>> pool = pool(cyclic_selector, 3)
```

print(pool) [Individual([0, 0], None, None), Individual([0, 1], None, None), Individual([0, 0], None, None)]

Parameters

- **next_individual** – generator for getting the next offspring
- **size** – how many kids we want

Returns
population of *size* offspring

leap_ec.ops.**proportional_selection**(*population: ~typing.List = '__no__default__', offset=0, exponent: int = 1, key=<function <lambda>>*) → Iterator

Returns an individual from a population in direct proportion to their fitness or another given metric.

To deal with negative fitness values use *offset='pop-min'* or set a custom offset. A *ValueError* is thrown if the result of adding *offset* to a fitness value results in a negative number. The value of an individual is calculated as follows

value = (fitness + offset)^exponent

Parameters

- **population** – the population to select from. Should be a list, not an iterator.
- **offset** – the offset from zero. If negative fitness values are possible and the minimum is unknown use *offest='pop-min'* for an adaptive offset. Defaults to 0.
- **exponent** (*int*) – the power to which fitness values are raised to. This can be tuned to increase or decrease selection pressure by creating larger or smaller differences between fitness values in the population. Defaults to 1.
- **key** – a function that computes the metric used to compare individuals. Defaults to fitness.

Returns

a random individual based on the proportion of the given metric in the population.

```
>>> from leap_ec import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.ops import proportional_selection
>>> import numpy as np
```

```
>>> genome1 = np.array([0, 0, 0])
>>> genome2 = np.array([0, 0, 1])
>>> pop = [Individual(genome1, problem=MaxOnes()),
...        Individual(genome2, problem=MaxOnes())]
>>> pop = Individual.evaluate_population(pop)
>>> selected = proportional_selection(pop)
```

leap_ec.ops.**random_bernoulli_vector**(*shape: Union[int, Tuple]*, *p: float = 0.5*) → ndarray

Generates a random vector of Boolean balues from a Bernoulli process—that is, from a sequence of weighted coin flips.

We use this function throughout LEAP because its implementation was found to be much faster than, say, just calling *np.random.choice([0, 1])*.

```
>>> from leap_ec.ops import random_bernoulli_vector
>>> random_bernoulli_vector(5, p=0.4)
array([..., ..., ..., ..., ...])
```

Parameters

- **shape** – shape of the random vector—can be an integer or a tuple.
- **p** – success probability of the bernoulli trials.

Returns

boolean numpy array

leap_ec.ops.**random_selection**(*population: List = '__no__default__'*, *indices=None*) → Iterator

return a uniformly randomly selected individual from the population

Parameters

population – from which to select

Returns
a uniformly selected individual

leap_ec.ops.**sus_selection**(*population: ~typing.List = '__no__default__', n=None, shuffle: bool = True, offset=0, exponent: int = 1, key=<function <lambda>>*) → Iterator

Returns an individual from a population in proportion to their fitness or another given metric using the stochastic universal sampling algorithm.

To deal with negative fitness values use *offset='pop-min'* or set a custom offset. A *ValueError* is thrown if the result of adding *offset* to a fitness value results in a negative number. The value of an individual is calculated as follows

value = (fitness + offset)^exponent

Parameters

- **population** – the population to select from. Should be a list, not an iterator.
- **n** – the number of evenly spaced points to use in the algorithm. Default is None which uses *len(population)*.
- **shuffle** (*bool*) – if True, *n* points are resampled after one full pass over them. If False, selection repeats over the same *n* points. Defaults to True.
- **offset** – the offset from zero. If negative fitness values are possible and the minimum is unknown use *offset='pop-min'* for an adaptive offset. Defaults to 0.
- **exponent** (*int*) – the power to which fitness values are raised to. This can be tuned to increase or decrease selection pressure by creating larger or smaller differences between fitness values in the population. Defaults to 1.
- **key** – a function that computes the metric used to compare individuals. Defaults to fitness.

Returns
a random individual based on the proportion of the given metric in the population.

```
>>> from leap_ec import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.ops import sus_selection
>>> import numpy as np
```

```
>>> genome1 = np.array([0, 0, 0])
>>> genome2 = np.array([1, 1, 1])
>>> pop = [Individual(genome1, problem=MaxOnes()),
...        Individual(genome2, problem=MaxOnes())]
>>> pop = Individual.evaluate_population(pop)
>>> selected = sus_selection(pop)
```

leap_ec.ops.**tournament_selection**(*population: list = '__no__default__', k: int = 2, key=None, select_worst: bool = False, indices=None*) → Iterator

Returns an operator that selects the best individual from k individuals randomly selected from the given population.

Like other selection operators, this assumes that if one individual is "greater than" another, then it is "better than" the other. Whether this indicates maximization or minimization isn't handled here: the *Individual* class determines the semantics of its "greater than" operator.

Parameters

- **population** – the population to select from. Should be a list, not an iterator.

- **k** (*int*) – number of contestants in the tournament. k=2 does binary tournament selection, which approximates linear ranking selection in the expectation. Higher values of k yield greedier selection strategies—k=3, for instance, is equal to quadratic ranking selection in the expectation.
- **key** – an optional function that computes keys to sort over. Defaults to None, in which case Individuals are compared directly.
- **select_worst** (*bool*) – if True, select the worst individual from the tournament instead of the best.
- **indices** (*list*) – an optional list that will be populated with the index of the selected individual.

Returns

the best of k individuals drawn from population

```
>>> from leap_ec import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.ops import tournament_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0, 0]), problem=MaxOnes()),
...        Individual(np.array([0, 0, 1]), problem=MaxOnes())]
>>> pop = Individual.evaluate_population(pop)
>>> best = tournament_selection(pop)
```

leap_ec.ops.**truncation_selection**(*offspring: List = '__no__default__'*, *size: int = '__no__default__'*, *parents: List = None*, *key=None*) → List

return the *size* best individuals from the given population

This defaults to (mu, lambda) if *parents* is not given.

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> from leap_ec.ops import truncation_selection
>>> import numpy as np
```

```
>>> pop = [Individual(np.array([0, 0, 0]), problem=MaxOnes()),
...        Individual(np.array([0, 0, 1]), problem=MaxOnes()),
...        Individual(np.array([1, 1, 0]), problem=MaxOnes()),
...        Individual(np.array([1, 1, 1]), problem=MaxOnes())]
```

We need to evaluate them to get their fitness to sort them for truncation.

```
>>> pop = Individual.evaluate_population(pop)
```

```
>>> truncated = truncation_selection(pop, 2)
```

TODO Do we want an optional context to over-ride the 'parents' parameter?

Parameters

- **offspring** – offspring to truncate down to a smaller population
- **size** – is what to resize population to

- **second_population** – is optional parent population to include with population for downsizing

Returns
truncated population

10.11 leap_ec.parsimony module

Parsimony pressure functions.

These are intended to be used as *key* parameters for selection operators.

Provided are Koza-style parsimony pressure and lexicographic parsimony key functions.

leap_ec.parsimony.**koza_parsimony**(*ind='__no__default__'*, *, *penalty='__no__default__'*)

Penalize fitness by genome length times a constant, in the style of Koza [Koz92].

```
>>> import toolz
>>> from leap_ec.individual import Individual
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> import leap_ec.ops as ops
>>> import numpy as np
>>> problem = MaxOnes()
>>> pop = [Individual(np.array([0, 0, 0, 1, 1, 1]), problem=problem),
...        Individual(np.array([0, 0]), problem=problem),
...        Individual(np.array([1, 1]), problem=problem),
...        Individual(np.array([1, 1, 1]), problem=problem)]
>>> pop = Individual.evaluate_population(pop)
>>> best, = ops.truncation_selection(pop, size=1)
>>> print(best.genome, best.fitness)
[0 0 0 1 1 1] 3
```

```
>>> best, = ops.truncation_selection(pop, size=1, key=koza_parsimony(penalty=.5))
>>> print(best.genome, best.fitness)
[1 1 1] 3
```

$$f_p(x) = f(x) - cl(x)$$

Where f(x) is original fitness, c is a penalty constant, and l(x) is the genome length.

Parameters

- **ind** – to be compared
- **penalty** – for denoting penalty strength

Returns
altered comparison criteria

leap_ec.parsimony.**lexical_parsimony**(*ind*)

If two fitnesses are the same, break the tie with the smallest genome

This implements Lexicographical Parsimony Pressure [LP02], which is essentially where if the fitnesses of two individuals are close, then break the tie with the smallest genome.

```
>>> import toolz
>>> from leap_ec.individual import Individual
>>> from leap_ec.binary_rep.problems import MaxOnes
>>> import leap_ec.ops as ops
>>> import numpy as np
>>> problem = MaxOnes()
>>> pop = [Individual(np.array([0, 0, 0, 1, 1, 1]), problem=problem),
...        Individual(np.array([0, 0]), problem=problem),
...        Individual(np.array([1, 1]), problem=problem),
...        Individual(np.array([1, 1, 1]), problem=problem)]
>>> pop = Individual.evaluate_population(pop)
>>> best, = ops.truncation_selection(pop, size=1)
>>> print(best.genome, best.fitness)
[0 0 0 1 1 1] 3
```

```
>>> best, = ops.truncation_selection(pop, size=1, key=lexical_parsimony)
>>> print(best.genome, best.fitness)
[1 1 1] 3
```

Parameters
ind – to be compared

Returns
altered comparison criteria

10.12 leap_ec.probe module

Probes are pipeline operators to instrument state that passes through the pipeline such as populations or individuals.

class leap_ec.probe.**AttributesCSVProbe**(*attributes=()*, *stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *do_dataframe=False*, *best_only=False*, *header=True*, *do_fitness=False*, *do_genome=False*, *notes=None*, *extra_metrics=None*, *job=None*, *numpy_as_list=True*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

Bases: *Operator*

An operator that records the specified attributes for all the individuals (or just the best individual) in *population* in CSV-format to the specified stream and/or to a DataFrame.

Parameters

- **attributes** – list of attribute names to record, as found in the individuals' *attributes* field
- **stream** – a file object to write the CSV rows to (defaults to sys.stdout). Can be *None* if you only want a DataFrame
- **do_dataframe** (*bool*) – if True, data will be collected in memory as a Pandas DataFrame, which can be retrieved by calling the *dataframe* property after (or during) the algorithm run. Defaults to False, since this can consume a lot of memory for long-running algorithms.
- **best_only** (*bool*) – if True, attributes will only be recorded for the best-fitness individual; otherwise a row is recorded for every individual in the population

- **header** (*bool*) – if True (the default), a CSV header is printed as the first row with the column names
- **do_fitness** (*bool*) – if True, the individuals' fitness is included as one of the columns
- **do_genomes** (*bool*) – if True, the individuals' genome is included as one of the columns
- **notes** (*str*) – a dict of optional constant-value columns to include in all rows (ex. to identify and experiment or parameters)
- **extra_metrics** – a dict of *'column_name': function* pairs, to compute optional extra columns. The functions take a the population as input as a list of individuals, and their return value is printed in the column.
- **job** (*int*) – a job ID that will be included as a constant-value column in all rows (ex. typically an integer, indicating the ith run out of many)
- **numpy_as_list** (*bool*) – if True, numpy arrays will be first converted to a python list before printing. This is intended for large genomes and multiobjective fitnesses, where large numpy arrays would be split across multiple csv rows by the default formatter.
- **context** – the algorithm context we use to read the current generation from (so we can write it to a column)

Individuals contain some build-in attributes (namely fitness, genome), and also a *dict* of additional custom attributes called, well, *attributes*. This class allows you to log all of the above.

Most often, you will want to record only the best individual in the population at each step, and you'll just want to know its fitness and genome. You can do this with this class's boolean flags. For example, here's how you'd record the best individual's fitness and genome to a dataframe:

```
>>> from leap_ec.global_vars import context
>>> from leap_ec.data import test_population
>>> probe = AttributesCSVProbe(do_dataframe=True, best_only=True,
...                            do_fitness=True, do_genome=True)
>>> context['leap']['generation'] = 100
>>> probe(test_population) == test_population
True
```

You can retrieve the result programatically from the *dataframe* property:

```
>>> probe.dataframe
   step  fitness           genome
0   100        4  [0, 1, 1, 1, 1]
```

By default, the results are also written to *sys.stdout*. You can pass any file object you like into the *stream* parameter.

Another common use of this task is to record custom attributes that are stored on individuals in certain kinds of experiments. Here's how you would record the values of *ind.foo* and *ind.bar* for every individual in the population. We write to a stream object this time to demonstrate how to use the probe without a dataframe:

```
>>> import io
>>> stream = io.StringIO()
>>> probe = AttributesCSVProbe(attributes=['foo', 'bar'], stream=stream)
>>> context['leap']['generation'] = 100
>>> r = probe(test_population)
>>> print(stream.getvalue())
step,foo,bar
```

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```
100,GREEN,Colorless
100,15,green
100,BLUE,ideas
100,72.81,sleep
```

property dataframe

Property for retrieving a Pandas DataFrame representation of the collected data.

get_row_dict(*ind*)

Compute a full row of data from a given individual.

class leap_ec.probe.**BestSoFarIterProbe**(*stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *header=True*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

Bases: *Operator*

This probe takes an iterator as input and will track the
best-so-far (BSF) individual in the all the individuals it sees.

Insert an object of this class into a pipeline to have it track the the best individual it sees so far. It will write the current best individual for each __call__ invocation to a given stream in CSV format.

Like many operators, this operator checks the context object to retrieve the current generation number for output purposes.

```
>>> from leap_ec import context, data
>>> from leap_ec import probe
>>> pop = data.test_population
>>> context['leap']['generation'] = 12
```

The probe will write its output to the provided stream (default is stdout, but we illustrate here with a StringIO stream):

```
>>> import io
>>> stream = io.StringIO()
>>> probe = BestSoFarIterProbe(stream=stream)
>>> bsf_output_iter = probe(iter(pop))
>>> x = next(bsf_output_iter)
>>> x = next(bsf_output_iter)
>>> x = next(bsf_output_iter)
>>> print(stream.getvalue())
step,bsf
12,...
12,...
12,...
```

class leap_ec.probe.**BestSoFarProbe**(*stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *header=True*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

Bases: *Operator*

This probe takes an list of individuals as input and will track the
best-so-far (BSF) individual across all the population it has seen.

Insert an object of this class into a pipeline to have it track the the best individual it sees so far. It will write the current best individual for each __call__ invocation to a given stream in CSV format.

Like many operators, this operator checks the context object to retrieve the current generation number for output purposes.

```
>>> from leap_ec import context, data
>>> from leap_ec import probe
>>> pop = data.test_population
>>> context['leap']['generation'] = 12
```

The probe will write its output to the provided stream (default is stdout, but we illustrate here with a StringIO stream):

```
>>> import io
>>> stream = io.StringIO()
>>> probe = BestSoFarProbe(stream=stream)
>>> new_pop = probe(pop)
>>> print(stream.getvalue())
step,bsf
12,4
```

This operator does not change the state of the population: >>> new_pop == pop True

class leap_ec.probe.**CartesianPhenotypePlotProbe**(*ax=None*, *xlim=(-5.12, 5.12)*, *ylim=(-5.12, 5.12)*, *contours=None*, *granularity=None*, *title='Cartesian Phenotypes'*, *modulo=1*, *context={'leap': {'distrib': {'non_viable': 0}}}*, *pad=()*)

Bases: `object`

Measure and plot a scatterplot of the populations' location in a 2-D phenotype space.

Parameters

- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **xlim** (*(float, float)*) – Bounds of the horizontal axis.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **contours** (*Problem*) – a problem defining a 2-D fitness function (this will be used to draw fitness contours in the background of the scatterplot).
- **granularity** (*float*) – (Optional) spacing of the grid to sample points along while drawing the fitness contours. If none is given, then the granularity will default to 1/50th of the range of the function's *bounds* attribute.
- **modulo** (*int*) – take and plot a measurement every *modulo* steps (default 1).
- **pad** – A list of extra gene values, used to fill in the hidden dimensions with contants while drawing fitness contours.

Attach this probe to matplotlib `Axes` and then insert it into an EA's operator pipeline to get a live phenotype plot that updates every *modulo* steps.

```
>>> import matplotlib.pyplot as plt
>>> from leap_ec.probe import CartesianPhenotypePlotProbe
>>> from leap_ec.representation import Representation
```

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.algorithm import generational_ea
```

```
>>> from leap_ec import ops
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec.real_rep.problems import CosineFamilyProblem
>>> from leap_ec.real_rep.initializers import create_real_vector
>>> from leap_ec.real_rep.ops import mutate_gaussian
```

```
>>> # The fitness landscape
>>> problem = CosineFamilyProblem(alpha=1.0, global_optima_counts=[2, 2], local_
↪optima_counts=[2, 2])
```

```
>>> # If no axis is provided, a new figure will be created for the probe to write to
>>> trajectory_probe = CartesianPhenotypePlotProbe(contours=problem,
...                                                xlim=(0, 1), ylim=(0, 1),
...                                                granularity=0.025)
```

```
>>> # Create an algorithm that contains the probe in the operator pipeline
```

```
>>> pop_size = 100
>>> ea = generational_ea(max_generations=20, pop_size=pop_size,
...                      problem=problem,
...
...                      representation=Representation(
...                         individual_cls=Individual,
...                         initialize=create_real_vector(bounds=[[0.4, 0.6]] * 2),
...                         decoder=IdentityDecoder()
...                      ),
...
...                      pipeline=[
...                         trajectory_probe,  # Insert the probe into the pipeline␣
↪like so
...                         ops.tournament_selection,
...                         ops.clone,
...                         mutate_gaussian(std=0.05, expected_num_mutations=
↪'isotropic', bounds=(0, 1)),
...                         ops.evaluate,
...                         ops.pool(size=pop_size)
...                      ])
>>> result = list(ea);
```

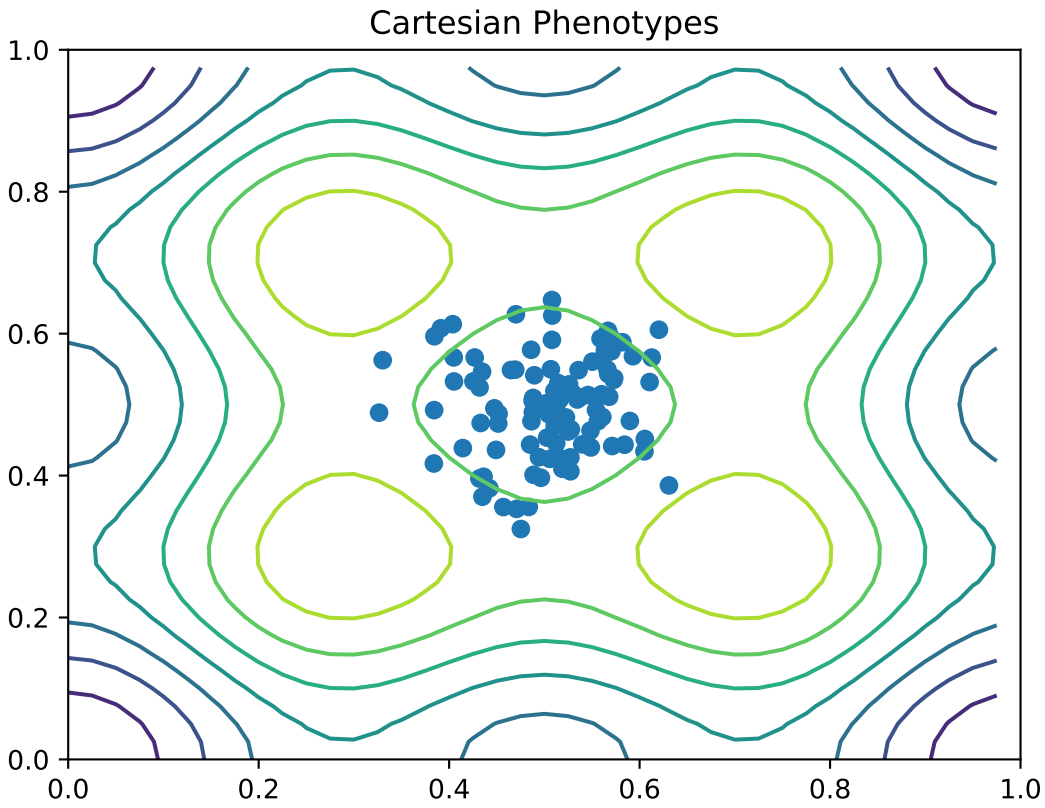
class leap_ec.probe.**FitnessPlotProbe**(*ax=None*, *xlim=None*, *ylim=None*, *modulo=1*, *title='Best-of-Generation Fitness'*, *x_axis_value=None*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

Bases: *PopulationMetricsPlotProbe*

Measure and plot a population's fitness trajectory.

Parameters

- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **xlim** (*(float, float)*) – Bounds of the horizontal axis.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **modulo** (*int*) – take and plot a measurement every *modulo* steps (default 1).


Cartesian Phenotypes
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0

- **title** – title to print on the plot
- **x_axis_value** – optional function to define what value gets plotted on the x axis. Defaults to pulling the 'generation' value out of the default *context* object.
- **context** – set a context object to query for the current generation. Defaults to the standard *leap_ec.context* object.

Attach this probe to matplotlib `Axes` and then insert it into an EA's operator pipeline.

```
>>> import matplotlib.pyplot as plt
>>> from leap_ec.probe import FitnessPlotProbe
>>> from leap_ec.representation import Representation
```

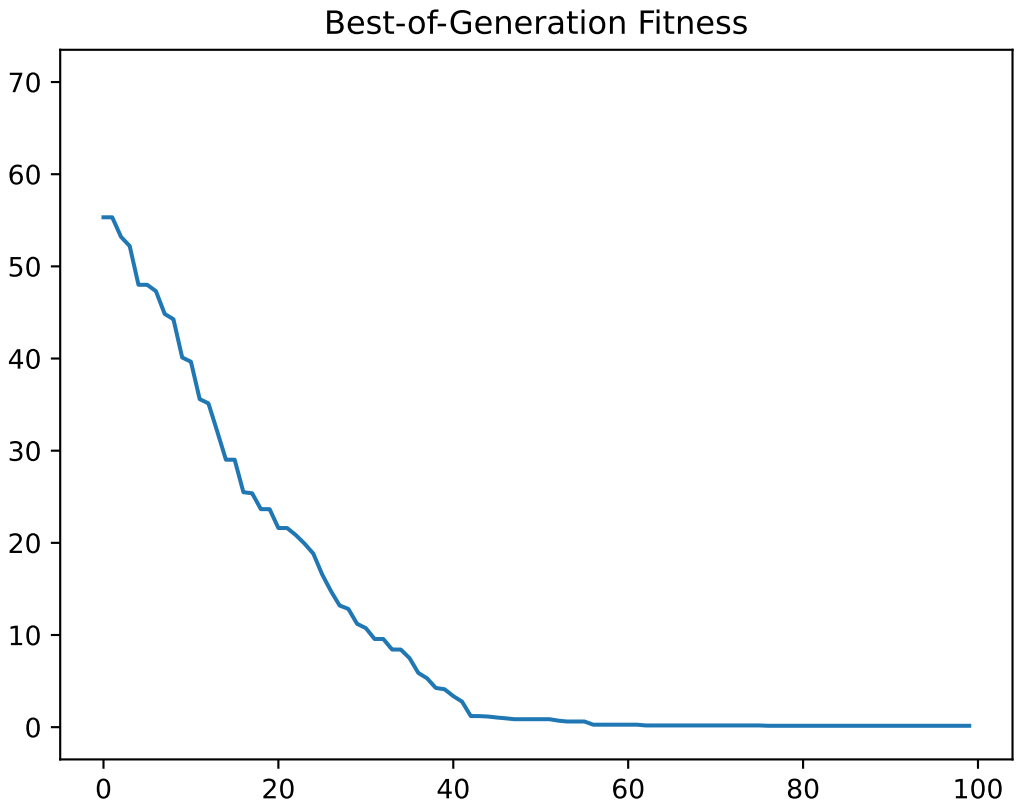
```
>>> f = plt.figure()  # Setup a figure to plot to
>>> plot_probe = FitnessPlotProbe(ylim=(0, 70), ax=plt.gca())
```

```
>>> # Create an algorithm that contains the probe in the operator pipeline
>>> from leap_ec.individual import Individual
>>> from leap_ec.decoder import IdentityDecoder
>>> from leap_ec import ops
>>> from leap_ec.real_rep.problems import SpheroidProblem
>>> from leap_ec.real_rep.ops import mutate_gaussian
>>> from leap_ec.real_rep.initializers import create_real_vector
```

```
>>> from leap_ec.algorithm import generational_ea
```

```
>>> l = 10
>>> pop_size = 10
>>> ea = generational_ea(max_generations=100, pop_size=pop_size,
...                      problem=SpheroidProblem(maximize=False),
...
...                      representation=Representation(
...                         individual_cls=Individual,
...                         decoder=IdentityDecoder(),
...                         initialize=create_real_vector(bounds=[[-5.12, 5.12]] *␣
↪l)
...                      ),
...
...                      pipeline=[
...                         plot_probe,  # Insert the probe into the pipeline like␣
↪so
...                         ops.tournament_selection,
...                         ops.clone,
...                         mutate_gaussian(std=0.2, expected_num_mutations=
↪'isotropic'),
...                         ops.evaluate,
...                         ops.pool(size=pop_size)
...                      ])
>>> result = list(ea);
```

To get a live-updated plot that words like a real-time video of the EA's progress, use this probe in conjunction with the *%matplotlib notebook* magic for Jupyter Notebook (as opposed to *%matplotlib inline*, which only allows static plots).


Best-of-Generation Fitness
70
60
50
40
30
20
10
0
0
20
40
60
80
100

class leap_ec.probe.**FitnessStatsCSVProbe**(*stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*, *header=True*, *extra_metrics=None*, *comment=None*, *job: ~typing.Optional[str] = None*, *notes: ~typing.Optional[~typing.Dict] = None*, *modulo: int = 1*, *numpy_as_list=True*, *context: ~typing.Dict = {'leap': {'distrib': {'non_viable': 0}}}*)

Bases: *Operator*

A probe that records basic fitness statistics for a population to a text stream in CSV format.

This is meant to capture the "bread and butter" values you'll typically want to see in any population-based optimization experiment. If you want additional columns with custom values, you can pass in a dict of *notes* with constant values or *extra_metrics* with functions to compute them.

Parameters

- **stream** – the file object to write to (defaults to sys.stdout)
- **header** – whether to print column names in the first line
- **extra_metrics** – a dict of *'column_name': function* pairs, to compute optional extra columns. The functions take a the population as input as a list of individuals, and their return value is printed in the column.
- **job** – optional constant job ID, which will be printed as the first column
- **notes** (*str*) – a dict of optional constant-value columns to include in all rows (ex. to identify and experiment or parameters)
- **numpy_as_list** (*bool*) – if True, numpy arrays will be first converted to a python list before printing. This is intended for multiobjective fitnesses, where large numpy arrays are normally split across csv rows with the default formatter.
- **context** – a LEAP context object, used to retrieve the current generation from the EA state (i.e. from *context['leap']['generation']*)

In this example, we'll set up two three inputs for the probe: an output stream, the generation number, and a population.

We use a *StringIO* stream to print the results here, but in practice you often want to use *sys.stdout* (the default) or a file object:

```
>>> import io
>>> stream = io.StringIO()
```

The probe also relies on LEAP's algorithm *context* to determine the generation number:

```
>>> from leap_ec.global_vars import context
>>> context['leap']['generation'] = 100
```

Here's how we'd compute fitness statistics for a test population. The population is unmodified:

```
>>> from leap_ec.data import test_population
>>> probe = FitnessStatsCSVProbe(stream=stream, job=15, notes={'description': 'just␣
↪a test'})
>>> probe(test_population) == test_population
True
```

and the output has the following columns: >>> print(stream.getvalue()) job, description, step, bsf, mean_fitness, std_fitness, min_fitness, max_fitness 15, just a test, 100, 4, 2.5, 1.11803…, 1, 4 <BLANKLINE>

To add custom columns, use the *extra_metrics* dict. For example, here's a function that computes the median fitness value of a population:

```
>>> import numpy as np
>>> median = lambda p: np.median([ ind.fitness for ind in p ])
```

We can include it in the fitness stats report like so:

```
>>> stream = io.StringIO()
>>> extras_probe = FitnessStatsCSVProbe(stream=stream, job="15", extra_metrics={
↪'median_fitness': median})
>>> extras_probe(test_population) == test_population
True
```

```
>>> print(stream.getvalue())
job, step, bsf, mean_fitness, std_fitness, min_fitness, max_fitness, median_fitness
15, 100, 4, 2.5, 1.11803..., 1, 4, 2.5
```

comment_character = '#'

default_metric_cols = ('bsf', 'mean_fitness', 'std_fitness', 'min_fitness', 'max_fitness')

time_col = 'step'

write_comment(*stream*)

write_header(*stream*)

class leap_ec.probe.**HeatMapPhenotypeProbe**(*ax=None*, *title='HeatMap of Phenotypes'*, *modulo=1*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

Bases: object

class leap_ec.probe.**HistPhenotypePlotProbe**(*ax=None*, *title='Histogram of Phenotypes'*, *modulo=1*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

Bases: object

A visualization probe that uses matplotlib to show a live histogram of the population's phenotypes.

This typically makes the most since for 1-dimensional genotypes.

class leap_ec.probe.**PopulationMetricsPlotProbe**(*ax=None*, *metrics=None*, *xlim=None*, *ylim=None*, *modulo=1*, *title='Population Metrics'*, *x_axis_value=None*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

Bases: object

reset()

class leap_ec.probe.**SumPhenotypePlotProbe**(*ax=None*, *xlim=(-5.12, 5.12)*, *ylim=(-5.12, 5.12)*, *problem=None*, *granularity=1*, *title='Sum Phenotypes'*, *modulo=1*, *context={'leap': {'distrib': {'non_viable': 0}}}*)

Bases: object

Plot the population's location on a fitness landscape that is defined over the sum of a vector phenotype's elements. This is useful for visualizing OneMax functions and similar functions that can be understood in terms of a graph with "the number of ones" along the x axis.

Parameters

- **ax** (*Axes*) – Matplotlib axes to plot to (if *None*, a new figure will be created).
- **xlim** (*(float, float)*) – Bounds of the horizontal axis.
- **ylim** (*(float, float)*) – Bounds of the vertical axis.
- **problem** (*Problem*) – a problem that will be used to draw a fitness curve.
- **granularity** (*float*) – (Optional) spacing of the grid to sample points along while drawing the fitness contours. If none is given, then the granularity will default to 1.0.
- **modulo** (*int*) – take and plot a measurement every *modulo* steps (default 1).

Attach this probe to matplotlib `Axes` and then insert it into an EA's operator pipeline to get a live phenotype plot that updates every *modulo* steps.

```
>>> import matplotlib.pyplot as plt
>>> from leap_ec.probe import SumPhenotypePlotProbe
>>> from leap_ec.representation import Representation
```

```
>>> from leap_ec.individual import Individual
>>> from leap_ec.algorithm import generational_ea
```

```
>>> from leap_ec import ops
>>> from leap_ec.binary_rep.problems import DeceptiveTrap
>>> from leap_ec.binary_rep.initializers import create_binary_sequence
>>> from leap_ec.binary_rep.ops import mutate_bitflip
```

```
>>> # The fitness landscape
>>> problem = DeceptiveTrap()
```

```
>>> # If no axis is provided, a new figure will be created for the probe to write to
>>> dimensions = 20
>>> trajectory_probe = SumPhenotypePlotProbe(problem=problem,
...                                          xlim=(0, dimensions), ylim=(0,␣
↪dimensions))
```

```
>>> # Create an algorithm that contains the probe in the operator pipeline
```

```
>>> pop_size = 100
>>> ea = generational_ea(max_generations=20, pop_size=pop_size,
...                      problem=problem,
...
...                      representation=Representation(
...                         individual_cls=Individual,
...                         initialize=create_binary_sequence(length=dimensions)
...                      ),
...
...                      pipeline=[
...                         trajectory_probe,  # Insert the probe into the pipeline␣
↪like so
...                         ops.tournament_selection,
...                         ops.clone,
```

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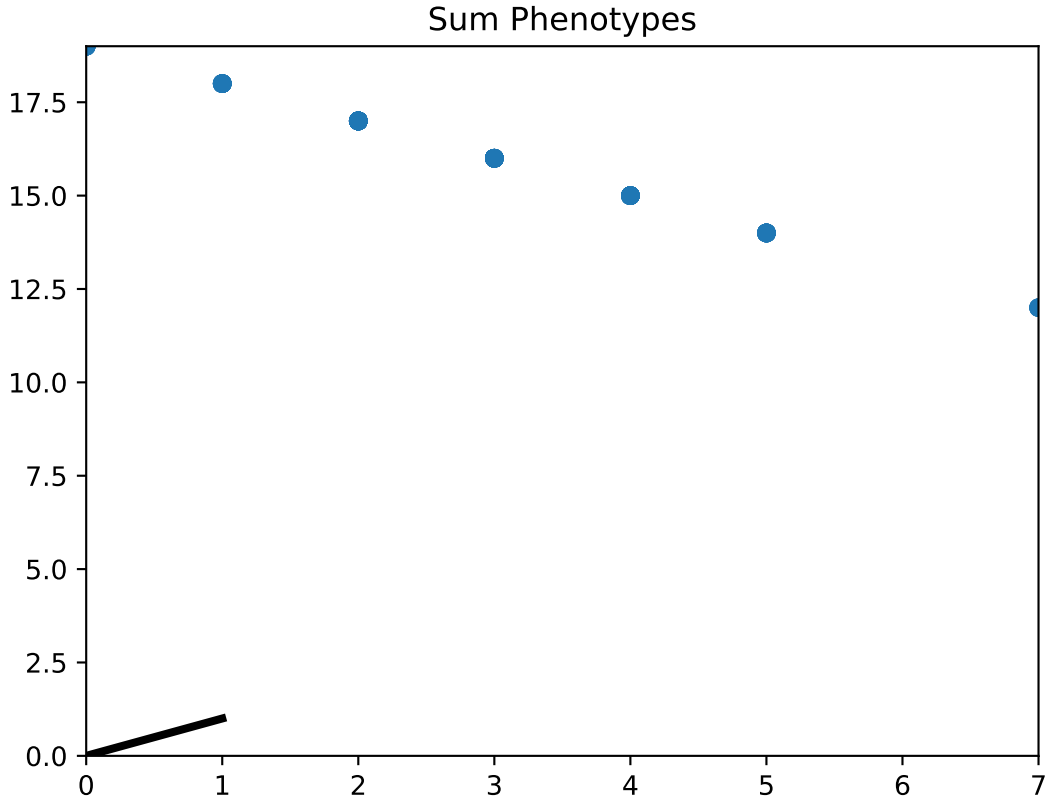
```
...                         mutate_bitflip(expected_num_mutations=1),
...                         ops.evaluate,
...                         ops.pool(size=pop_size)
...                     ])
>>> result = list(ea);
```



leap_ec.probe.**best_of_gen**(*population*)

Syntactic sugar to select the best individual in a population.

Parameters

- **population** – a list of individuals
- **context** – optional *dict* of auxiliary state (ignored)

```
>>> from leap_ec.data import test_population
>>> print(best_of_gen(test_population))
Individual<...> with fitness 4
```

leap_ec.probe.**num_fixated_metric**(*population: list*)

Computes the genetic diversity of the population by counting the number of variables in the genome that have zero variance.

This is a so-called "column-wise" metric, in the sense that it considers each element of the solution vectors

independently.

leap_ec.probe.**pairwise_squared_distance_metric**(*population: list*)

Computes the genetic diversity of a population by considering the sum of squared Euclidean distances between individual genomes.

We compute this in $O(n)$ by writing the sum in terms of distance from the population centroid c:

$$\mathcal{D}(\text{population}) = \sum_{i=1}^{n}\sum_{j=1}^{n} \|x_i - x_j\|^2 = 2n\sum_{i=1}^{n} \|x_i - c\|^2$$

leap_ec.probe.**print_individual**(*next_individual: ~typing.Iterator = '__no__default__', prefix='', numpy_as_list=False, stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*) → Iterator

Just echoes the individual from within the pipeline

Uses next_individual.__str__

Parameters

- **next_individual** – iterator for next individual to be printed
- **prefix** – prefix appended to the start of the line
- **numpy_as_list** – If True, numpy arrays are converted to lists before printing
- **stream** – File object passed to print

Returns
the same individual, unchanged

leap_ec.probe.**print_population**(*population*, *generation*, *numpy_as_list=False*)

Convenience function for pretty printing a population that's associated with a given generation

Parameters

- **population** – The population of individuals to be printed
- **generation** – The generation of the population
- **numpy_as_list** – If True, numpy arrays are converted to lists before printing

Returns
None

leap_ec.probe.**print_probe**(*population='__no__default__', probe='__no__default__', stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>, prefix=''*)

pipeline operator for printing the given population

This is really a wrapper around *probe* that, itself, gets passed te entire population.

The optional prefix is used to tag the output. For example, you may want to print 'before' to indicate that the population is before an operator is applied.

Parameters

- **population** – to be printed
- **probe** – secondary probe that gets the poplation as input and for which the output is passed to *stream*
- **stream** – to write output

- **prefix** – optional string prefix to prepend to output

Returns
population

leap_ec.probe.**sum_of_variances_metric**(*population: list*)

Computes the genetic diversity of a population by considering the sum of the variances of each variable in the genome.

$$\mathcal{D}(\text{population}) = \sum_{i=1}^{L} \mathbb{E}_{j \in P}\left[x_j[i] - \mathbb{E}[x_j[i]]\right]$$

This is a so-called "column-wise" metric, in the sense that it considers each element of the solution vectors independently.

10.13 leap_ec.problem module

Defines the abstract-base classes Problem, ScalarProblem, and FunctionProblem.

class leap_ec.problem.**AlternatingProblem**(*problems*, *modulo*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 20}}*)

Bases: *Problem*

equivalent(*first_fitness*, *second_fitness*)

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

get_current_problem()

worse_than(*first_fitness*, *second_fitness*)

class leap_ec.problem.**AverageFitnessProblem**(*wrapped_problem*, *n: int*)

Bases: *Problem*

Problem wrapper that copies each genome n times, evaluates them, and averages the results back together to produce a mean-fitness estimate.

This is a common strategy for approaching noisy fitness functions, to make it easier for an optimization algorithm to follow a gradient.

```
>>> from leap_ec.real_rep.problems import NoisyQuarticProblem
>>> p = AverageFitnessProblem(
...                 wrapped_problem = NoisyQuarticProblem(),
...                 n = 20)
>>> x = [ 1, 1, 1, 1 ]
```

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```
>>> y = p.evaluate(x)
>>> print(f"Fitness: {y}")  # The mean of this will be approximately 10
Fitness: ...
```

equivalent(*first_fitness*, *second_fitness*)

evaluate(*phenome*)

Evaluates the wrapped function n times sequentially and returns the mean.

evaluate_multiple(*phenomes: list*)

Evaluate a collections of phenomes by creating n jobs for each phenome, sending all the jobs to the wrapped evaluate_multiple() function, and then averaging the n results for each phenome into a list of results.

worse_than(*first_fitness*, *second_fitness*)

class leap_ec.problem.**ConstantProblem**(*maximize=False*, *c=1.0*)

Bases: *ScalarProblem*

A flat landscape, where all phenotypes have the same fitness.

This is sometimes useful for sanity checks or as a control in certain kinds of research.

$$f(\vec{x}) = c$$

Parameters

c (*float*) – the fitness value to return for any input.

```
from leap_ec.problem import ConstantProblem
from leap_ec.real_rep.problems import plot_2d_problem
bounds = ConstantProblem.bounds
plot_2d_problem(ConstantProblem(), xlim=bounds, ylim=bounds, granularity=0.025)
```

bounds = (-1.0, 1.0)

evaluate(*phenome*, **args*, ***kwargs*)

Return a contant value for any input phenome:

```
>>> phenome = [0.5, 0.8, 1.5]
>>> ConstantProblem().evaluate(phenome)
1.0
```

```
>>> ConstantProblem(c=500.0).evaluate('foo bar')
500.0
```

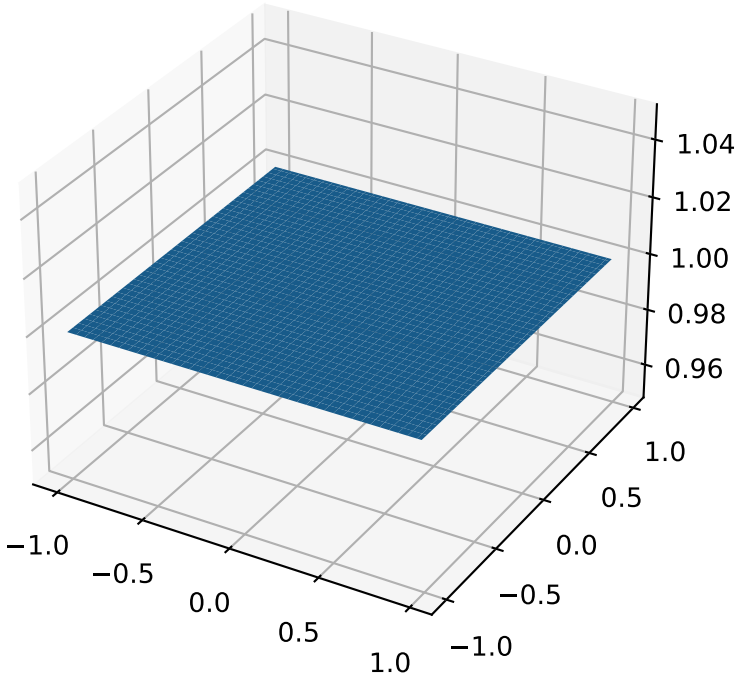
Parameters

phenome – phenome to be evaluated

Returns

1.0, or the constant defined in the constructor

class leap_ec.problem.**CooperativeProblem**(*wrapped_problem*, *num_trials: int*, *collaborator_selector*, *combined_decoder: ~leap_ec.decoder.Decoder = IdentityDecoder()*, *log_stream=None*, *combine_genomes=<function CooperativeProblem.<lambda>>*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 20}}*)


1.04
1.02
1.00
0.98
0.96
1.0
0.5
0.0
−0.5
−1.0
−1.0
−0.5
0.0
0.5
1.0

Bases: *Problem*

A Problem that implements cooperative coevolution. This provides a fitness function that takes *partial solutions* as input (i.e. from one of the subpopulations of the cooperative algorithm), and evaluates their fitness by combining them with other individuals in the population.

You can think of a CooperativeProblem as defining a fitness function for a subpopulation in a multi-population model, where the fitness function that is computed is itself a function of the state of the other subpopulations:

..math

mbox{fitness} = f_{p_i}(vec{mathbf{x}}, mathcal{P} \ p_i)

This class works by wrapping another fitness function, which is defined over complete solutions, and by taking a selection operator (which is used to select "collaborators" from other subpopulations to form complete solutions):

```
>>> from leap_ec import ops
>>> from leap_ec.real_rep.problems import SpheroidProblem
>>> complete_problem = SpheroidProblem()
>>> problem = CooperativeProblem(
...             wrapped_problem = SpheroidProblem(),
...             num_trials = 3,
...             collaborator_selector = ops.random_selection)
```

equivalent(*first_fitness*, *second_fitness*)

evaluate(*phenome*, **args*, ***kwargs*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

evaluate_multiple(*phenomes*, *individuals*)

Evaluate multiple phenomes all at once, returning a list of fitness values.

By default this just calls *self.evaluate()* multiple times. Override this if you need to, say, send a group of individuals off to parallel

worse_than(*first_fitness*, *second_fitness*)

class leap_ec.problem.**ExternalProcessProblem**(*command: str*, *maximize: bool*, *args: Optional[list] = None*)

Bases: *ScalarProblem*

Evaluate individuals by launching an external program, writing phenomes to its stdin as CSV rows, and reading back fitness values from its stdout.

Assumes that individuals are represented with list phenomes with elements that can be cast to strings.

evaluate(*phenome*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

evaluate_multiple(*phenomes*, **args*, ***kwargs*)

Evaluate multiple phenomes all at once, returning a list of fitness values.

By default this just calls *self.evaluate()* multiple times. Override this if you need to, say, send a group of individuals off to parallel

class leap_ec.problem.**FitnessOffsetProblem**(*problem*, *fitness_offset*, *maximize=None*)

Bases: *ScalarProblem*

Takes an existing function and adds a constant value to it output.

$$f'(\mathbf{x}) = f(\mathbf{x}) + c$$

Parameters

- **problem** – the original problem to wrape
- **fitness_offset** (*float*) – the scalar constant to add

evaluate(*phenome*)

Evaluates the phenome's fitness in the wrapped function, then adds the constant.

For example, here the original fitness function returns 5.0, but we subtract 3.5 from it so that it yields 1.5.

```
>>> original = ConstantProblem(c=5.0)
>>> problem = FitnessOffsetProblem(original, fitness_offset=-3.5)
>>> problem.evaluate([0, 1, 2])
1.5
```

class leap_ec.problem.**FunctionProblem**(*fitness_function*, *maximize*)

Bases: *ScalarProblem*

A convenience wrapper that takes a vanilla function that returns scalar fitness values and makes it usable as an objective function.

evaluate(*phenome*, **args*, ***kwargs*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

class leap_ec.problem.**Problem**

Bases: ABC

Abstract Base Class used to define problem definitions.

A *Problem* is in charge of two major parts of an EA's behavior:

1. Fitness evaluation (the *evaluate()* method)
2. Fitness comparision (the *worse_than()* and *equivalent()* methods)

abstract equivalent(*first_fitness*, *second_fitness*)

abstract evaluate(*phenome*, **args*, ***kwargs*)

Evaluate the given phenome.

Practitioners *must* over-ride this member function.

Note that by default the individual comparison operators assume a maximization problem; if this is a minimization problem, then just negate the value when returning the fitness.

Parameters
phenome – the phenome to evaluate (this will *not be modified*)

Returns
the fitness value

evaluate_multiple(*phenomes*)

Evaluate multiple phenomes all at once, returning a list of fitness values.

By default this just calls *self.evaluate()* multiple times. Override this if you need to, say, send a group of individuals off to parallel

abstract worse_than(*first_fitness*, *second_fitness*)

class leap_ec.problem.**ScalarProblem**(*maximize*)

Bases: *Problem*

A problem that compares individuals based on their scalar fitness values.

Inherit from this class and implement the *evaluate()* method to implement an objective function that returns a single real-valued fitness value.

equivalent(*first_fitness*, *second_fitness*)

Used in Individual.__eq__().

By default returns first.fitness== second.fitness. Please over-ride if this does not hold for your problem.

Returns
true if the first individual is equal to the second

worse_than(*first_fitness*, *second_fitness*)

Used in Individual.__lt__().

By default returns first_fitness < second_fitness if a maximization problem, else first_fitness > second_fitness if a minimization problem. Please over-ride if this does not hold for your problem.

Returns
true if the first individual is less fit than the second

leap_ec.problem.**concat_combine**(*collaborators*)

Combine a list of individuals by concatenating their genomes.

This is a convenience function intended for use with CooperativeProblem.

10.14 leap_ec.representation module

A *Representation* is a simple data structure that wraps the components needed to define, initialize, and decode individuals.

This just serves as some syntactic sugar when we are specifying algorithms—so that representation-related components are grouped together and clearly labeled *Representation*.

class leap_ec.representation.**Representation**(*initialize*, *decoder=IdentityDecoder()*, *individual_cls=<class 'leap_ec.individual.Individual'>*)

Bases: object

Syntactic sugar for some of the monolithic functions that conveniently combines a decoder, initializer, and an Individual class since those always work in tandem, but can still be loosely coupled.

create_individual(*problem*)

Make a single individual.

create_population(*pop_size*, *problem*)

make a new population

Parameters

- **pop_size** – how many individuals should be in the population
- **problem** – to be solved

Returns
a population of *individual_cls* individuals

10.15 leap_ec.simple module

Provides a very high-level convenience function for a very general EA, ea_solve().

leap_ec.simple.**ea_solve**(*function*, *bounds*, *generations=100*, *pop_size=2*, *mutation_std=1.0*, *maximize=False*, *viz=False*, *viz_ylim=(0, 1)*, *hard_bounds=True*, *dask_client=None*, *stream=<_io.TextIOWrapper name='<stdout>' mode='w' encoding='UTF-8'>*)

Provides a simple, top-level interfact that optimizes a real-valued function using a simple generational EA.

Parameters

- **function** – the function to optimize; should take lists of real numbers as input and return a float fitness value
- **bounds** (*[(float, float)]*) – a list of (min, max) bounds to define the search space
- **generations** (*int*) – the number of generations to run for
- **pop_size** (*int*) – the population size
- **mutation_std** (*float*) – the width of the mutation distribution
- **maximize** (*bool*) – whether to maximize the function (else minimize)
- **viz** (*bool*) – whether to display a live best-of-generation plot
- **hard_bounds** (*bool*) – if True, bounds are enforced at all times during evolution; otherwise they are only used to initialize the population.
- **viz_ylim** (*(float, float)*) – initial bounds to use of the plots vertical axis

- **dask_client** – is optional dask Client to enable parallel evaluations
- **stream** – a stream to write best-so-far values to (defaults to stdout)

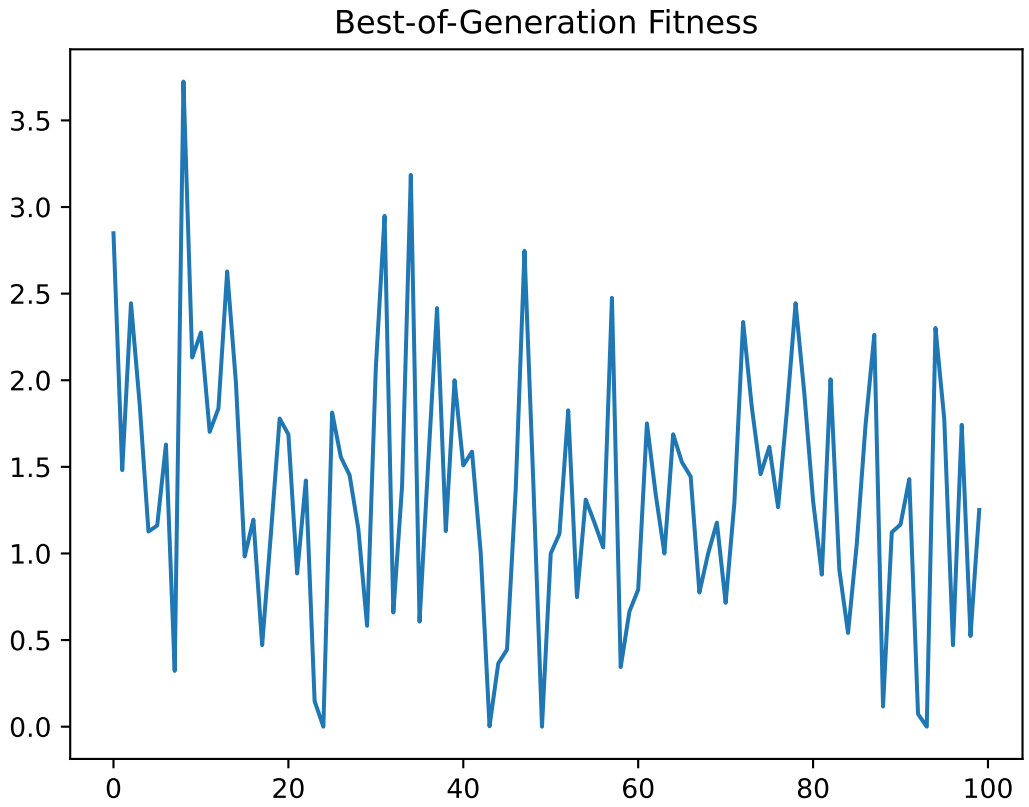
The basic call includes instrumentation that prints the best-so-far fitness value of each generation to stdout:

```
>>> import io
>>> from leap_ec.simple import ea_solve
>>> stream = io.StringIO()
>>> ea_solve(sum, bounds=[(0, 1)]*5, stream=stream)
array([..., ..., ..., ..., ...])
```

The stream captures the best-so-far individual at each iteration of the algorithm: >>> print(stream.getvalue()) # doctest: +ELLIPSIS, +NORMALIZE_WHITESPACE step,bsf 0,… 1,… 2,… … 99,… <BLANKLINE>

When *viz=True*, a live BSF plot will also display:

```
>>> ea_solve(sum, bounds=[(0, 1)]*5, viz=True)
array([..., ..., ..., ..., ...])
```



10.16 leap_ec.statistical_helpers module

Helpers for testing the output of stochastic functions.

leap_ec.statistical_helpers.**collect_distribution**(*function*, *samples: int*)

Count the number of times the given function returns each output value.

leap_ec.statistical_helpers.**equals_gaussian**(*observed_samples*, *reference_mean: float*, *reference_std: float*, *num_reference_observations: int*, *p: float*) → bool

A convenience function for computing a t-test for equality of two independent samples, using samples from one and test statistics from the other.

Assumes equal variance samples.

```
>>> import numpy as np
>>> observed = np.random.normal(15, 1, size=1000)
>>> equals_gaussian(observed, 15, 1, 1000, p=0.05)
True
```

leap_ec.statistical_helpers.**equals_uniform**(*observed_distribution: Dict*, *p: float*) → bool

Use a chi^2 test to determine whether the observed distribution is uniform.

This offers convenience over stochastic_equals(), because the expected distribution doesn't have to be manually specified.

For example, we do not reject the hypothesis that *[5060, 4940]* comes from a uniform distribution:

```
>>> observed = { 0: 5060, 1: 4940 }
>>> equals_uniform(observed, p=0.01)
True
```

The keys are arbitrary, so we can use them to clearly express what we are testing:

```
>>> observed = { 'Left': 101, 'Right': 100, 'Up': 99, 'Down': 100 }
>>> equals_uniform(observed, p=0.01)
True
```

leap_ec.statistical_helpers.**stochastic_chisquare**(*expected_distribution*, *distribution*)

Use a chi^2 distribution to compute a p-value for the probability of rejecting the hypothesis that the given distribution matches the expected distribution.

The null hypothesis here is that the distributions are equal.

This takes two dictionaries of values:

```
>>> expected_distribution = { 1: 10, 2: 10, 3: 10, 4: 10, 5: 10, 6: 10}
>>> distribution = { 1: 5, 2: 8, 3: 9, 4: 8, 5: 10, 6: 20}
>>> stochastic_chisquare(expected_distribution, distribution)
0.01990...
```

The p-value is low, because the samples are quite different, so the "probability of seeing that big a difference or greater if the two distributions are equal" is low.

Very similar samples, by contrast, yield high p values:

```
>>> expected_distribution = { 1: 10, 2: 10, 3: 10, 4: 10, 5: 10, 6: 10}
>>> distribution = { 1: 10, 2: 10, 3: 10, 4: 10, 5: 10, 6: 10}
>>> stochastic_chisquare(expected_distribution, distribution)
1.0
```

leap_ec.statistical_helpers.**stochastic_equals**(*expected_distribution: Dict*, *observed_distribution: Dict*, *p: float*) → bool

Use a chi^2 test to determine whether two discrete distributions are equal. Specifically, this returns false if we *reject the hypothesis* that they are equal at the given p-value.

Lower p-value thresholds make the test more conservative, in the sense that it will assume the distributions are equal unless there is very good evidence to the contrary. We typically want to use low p-value thresholds for unit tests, for example, to avoid false test failures (type-I errors).

For example, we do not reject the hypothesis that *[5060, 4940]* comes from a uniform distribution:

```
>>> expected = { 0: 5000, 1: 5000 }
>>> observed = { 0: 5060, 1: 4940 }
>>> stochastic_equals(expected, observed, p=0.01)
True
```

Here we also do not reject the hypothesis that a 6-sided die is unbiased:

```
>>> expected = { 1: 10, 2: 10, 3: 10, 4: 10, 5: 10, 6: 10}
>>> observed = { 1: 5, 2: 8, 3: 9, 4: 8, 5: 10, 6: 20}
>>> stochastic_equals(expected, observed, p=0.01)
True
```

If we relax the p-value threshold, we can conclude that the die is in fact biased (but with some increased risk of type-I error):

But we would have if we used a 95% significance level instead of 99%: >>> stochastic_equals(expected, observed, p=0.05) False

10.17 leap_ec.util module

Defines miscellaneous utility functions.

TODO we have two almost identical counters that could be consolidated into a single class.

print_list : for pretty printing a list when pprint isn't sufficient.

leap_ec.util.**birth_brander**()

This pipeline operator will add or update a "birth" attribute for passing individuals.

If the individual already has a birth, just let it float by with the original value. If it doesn't, assign the individual the current birth ID, and then increment the global, stored birth count.

We don't increment a birth ID in the ctor because that overall birth count will bloat due to clone operations. Inserting this operator into the pipeline will ensure that each individual that passes through is properly "branded" with a unique birth ID. However, care must be made to ensure that the initial population is similarly branded.

Provides:

- **brand_population() to brand an entire population all at once,**
  which is useful for branding initial populations.

- brand() for explicitly branding a single individual

Parameters
next_thing – preceding individual in the pipeline

Returns
branded individual

leap_ec.util.**get_step**(*context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*, *use_generation=None*, *use_births=None*)

Returns the current step of an algorithm using *context*. Will infer which to use if neither is specified with *use_generation* or *use_births*. If both are set to True, will raise an error.

Parameters

- **context** – the context from which the generations or births is taken from.
- **use_generation** – an override to use generation.
- **use_births** – an override to use births.

leap_ec.util.**inc_births**(*context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*, *start=0*, *callbacks=()*)

This tracks the current number of births

The *context* is used to report the current births, though that can also be obtained by inc_births.births()

This will optionally call all the given callback functions whenever the births are incremented. The registered callback functions should have a signature f(int), where the int is the new birth.

```
>>> from leap_ec.global_vars import context
>>> my_inc_births = inc_births(context)
```

Each time we call the object, the birth count is incremented and returned:

```
>>> my_inc_births()
1
```

```
>>> my_inc_births()
2
```

```
>>> my_inc_births()
3
```

The count can be viewed without changing it like so:

```
>>> my_inc_births.births()
3
```

And decremented like so:

```
>>> my_inc_births.do_decrement()
2
```

Parameters

- **context** – will set ['leap']['births'] to the incremented births

- **start** – if we want to start counter at a higher value; e.g., take into consideration births of an initial population
- **callbacks** – optional list of callback function to call when a birth numberis incremented

Returns
function for incrementing births

leap_ec.util.**inc_generation**(*start_generation: int = 0*, *context={'leap': {'distrib': {'non_viable': 0}, 'generation': 100}}*, *callbacks=()*)

This tracks the current generation

The *context* is used to report the current generation, though that can also be given by inc_generation.generation().

This will optionally call all the given callback functions whenever the generation is incremented. The registered callback functions should have a signature f(int), where the int is the new generation.

```
>>> from leap_ec.global_vars import context
>>> my_inc_generation = inc_generation(context)
```

Parameters

- **context** – will set ['leap']['generation'] to the incremented generation
- **callbacks** – optional list of callback function to call when a generation is incremented

Returns
function for incrementing generations

leap_ec.util.**is_flat**(*obj*)

Returns
True if obj is a flat collection (as opposed to, say, a hierarchical list of lists).

```
>>> is_flat((0, 1))
True
```

```
>>> is_flat(1)
False
```

```
>>> is_flat([(0, 1), (0, 1)])
False
```

leap_ec.util.**is_iterable**(*obj*)

Parameters
obj – that we want to determine is a generator

Returns
True if obj can use next(obj)

leap_ec.util.**is_sequence**(*obj*)

Returns
True if obj is a test_sequence

Cribbed from https://stackoverflow.com/questions/2937114/python-check-if-an-object-is-a-sequence?lq=1

E.g., used to determine if gaussian mutation has a single specified standard deviation, or a vector of standard deviations.

```
>>> is_sequence(0.5)
False
```

```
>>> is_sequence([0.1, 0.2, 0.3])
True
```

leap_ec.util.**print_list**(*l*)

Return a string representation of a list.

This uses __str__() to resolve the elements of the list:

```
>>> from leap_ec.individual import Individual
>>> import numpy as np
>>> l = [Individual(np.array([0, 1, 2])),
...      Individual(np.array([3, 4, 5]))]
>>> print_list(l)
[Individual<...> ..., Individual<...> ...]
```

As opposed to the standard printing mechanism, which calls __repr__() on the elements to produce

```
>>> print(l)
[Individual<...>(...), Individual<...>(...)]
```

Parameters
l –

Returns

leap_ec.util.**wrap_curry**(*f*)

Wraps and curries in conjunction, so the function signature remains.

10.18 Module contents

leap_ec.**leap_logger_name = 'leap_ec'**

The environment variable we use to signal that our test harness is being run.

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BIBLIOGRAPHY

[NSGA-II] Deb, Kalyanmoy, Amrit Pratap, Sameer Agarwal, and T. A. M. T. Meyarivan. "A Fast and Elitist Multiobjective Genetic Algorithm: NSGA-II." IEEE transactions on evolutionary computation 6, no. 2 (2002): 182-197.

[Burlacu] Bogdan Burlacu. 2022. "Rank-based Non-dominated Sorting". arXiv. DOI:https://doi.org/10.48550/ARXIV.2203.13654

[CSB20] Mark A. Coletti, Eric O. Scott, and Jeffrey K. Bassett. Library for evolutionary algorithms in python (leap). In *Proceedings of the 2020 Genetic and Evolutionary Computation Conference Companion*, GECCO '20, 1571–1579. New York, NY, USA, 2020. Association for Computing Machinery. URL: https://doi.org/10.1145/3377929.3398147, doi:10.1145/3377929.3398147.

[Koz92] John R Koza. *Genetic programming: on the programming of computers by means of natural selection*. Volume 1. MIT press, 1992.

[LP02] Sean Luke and Liviu Panait. Lexicographic parsimony pressure. In *Proceedings of the 4th Annual Conference on Genetic and Evolutionary Computation*, 829–836. 2002.

[RonkkonenLKL08] Jani Rönkkönen, Xiaodong Li, Ville Kyrki, and Jouni Lampinen. A generator for multimodal test functions with multiple global optima. In *Simulated Evolution and Learning: 7th International Conference, SEAL 2008, Melbourne, Australia, December 7-10, 2008. Proceedings 7*, 239–248. Springer, 2008.

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