
PyGA Documentation

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Contents: This is the core module for pyga.

Here are the basic vanilla components; genes and a GA. Other variations are sub-classes of these.

class `pyga.Gene` (*values=(None,)*)

” This is the base class for Gene objects. These do not represent a specific gene on one chromosome, rather it represents all possible genes that exist at that position - the different alleles (values).

class `pyga.GeneticAlg` (*populationsize, generations, genomepattern, fitness_function, survival=0.10000000000000001, rng=None, avgmutations=1.0, mutation-rate=None*)

Base class for the Genetic Algorithm itself.

evol_population ()

Evolves a new generation of the population based on the fitness values calculated by `score_population`.

Replaces `self.population` with the new generation.

genome_make ()

Creates a new genome based on `self.chromosomepatterns`. Uses the selfs random number generator, which may have been seeded.

Genome return is a tuple of tuples of alleles.

genome_mutate (*genome*)

Returns a mutated copy of a genome. Genome must match `self.chromosomepatterns`, which it will do if created via `self.genomemake` or `self.genomemutate`. Mutation rate is based on `self.mutationrate`.

This does not do cross-over. This does not do duplication/deletion, and can't unless changes are made to `self.chromosomepatterns` too.

score_population ()

Calculates the fitness of each individual in the population. Then sorts the population in descending fitness order. Ties are broken randomly.

Rather than returning the scores, it sets the `self.scores` variable This it to discourage repeated fitness calculations because it can be a computationally expensive process.

The genomes of the current generation are stored with the scores. This is to make it easy to see which genome got which score, rather than assuming `self.population` and `self.scores` have the same ordering.

write_scores (*filename*)

Dumps current generation to disk. Fomat is tab-separated between score and genome.

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