# pygad Module

This section of the PyGAD's library documentation discusses the **pygad** module.

Using the `pygad` module, instances of the genetic algorithm can be created, run, saved, and loaded.

# pygad.GA Class

The first module available in PyGAD is named `pygad` and contains a class named `GA` for building the genetic algorithm. The constructor, methods, function, and attributes within the class are discussed in this section.

## `__init__()`

For creating an instance of the `pygad.GA` class, the constructor accepts several parameters that allow the user to customize the genetic algorithm to different types of applications.

The `pygad.GA` class constructor supports the following parameters:

- `num_generations`: Number of generations.
- `num_parents_mating`: Number of solutions to be selected as parents.
- `fitness_func`: Accepts a function that must accept 2 parameters (a single solution and its index in the population) and return the fitness value of the solution. Available starting from PyGAD 1.0.17 until 1.0.20 with a single parameter representing the solution. Changed in PyGAD 2.0.0 and higher to include a second parameter representing the solution index. Check the **Preparing the ``fitness_func`` Parameter** section for information about creating such a function.
- `initial_population`: A user-defined initial population. It is useful when the user wants to start the generations with a custom initial population. It defaults to `None` which means no initial population is specified by the user. In this case, PyGAD creates an initial population using the `sol_per_pop` and `num_genes` parameters. An exception is raised if the `initial_population` is `None` while any of the 2 parameters (`sol_per_pop` or `num_genes`) is also `None`. Introduced in PyGAD 2.0.0 and higher.
- `sol_per_pop`: Number of solutions (i.e. chromosomes) within the population. This parameter has no action if `initial_population` parameter exists.
- `num_genes`: Number of genes in the solution/chromosome. This parameter is not needed if the user feeds the initial population to the `initial_population` parameter.
- `gene_type=float`: Controls the gene type. It can be assigned to a single data type that is applied to all genes or can specify the data type of each individual gene. It defaults to `float` which means all genes are of `float` data type. Starting from PyGAD 2.9.0, the `gene_type` parameter can be assigned to a numeric value of any of these types: `int`, `float`, and `numpy.int/uint/float(8-64)`. Starting from PyGAD 2.14.0, it can be assigned to a `list`, `tuple`, or a `numpy.ndarray` which hold a data type for each gene (e.g. `gene_type=[int, float, numpy.int8]`). This helps to control the data type of each individual gene. In PyGAD 2.15.0, a precision for the `float` data types can be specified (e.g. `gene_type=[float, 2]`.
- `init_range_low=-4`: The lower value of the random range from which the gene values in the initial population are selected. `init_range_low` defaults to `-4`. Available in PyGAD 1.0.20 and higher. This parameter has no action if the `initial_population` parameter exists.
- `init_range_high=4`: The upper value of the random range from which the gene values in the initial population are selected. `init_range_high` defaults to `+4`. Available in PyGAD 1.0.20 and higher. This parameter has no action if the `initial_population` parameter exists.
- `parent_selection_type="sss"`: The parent selection type. Supported types are `sss` (for steady-state selection), `rws` (for roulette wheel selection), `sus` (for stochastic universal selection), `rank` (for rank selection), `random` (for random selection), and `tournament` (for tournament selection). A custom parent selection function can be passed starting from PyGAD 2.16.0. Check the User-Defined Crossover, Mutation, and Parent Selection Operators section for more details about building a user-defined parent selection function.

- `keep_parents=-1`: Number of parents to keep in the current population. `-1` (default) means to keep all parents in the next population. `0` means keep no parents in the next population. A value `greater than 0` means keeps the specified number of parents in the next population. Note that the value assigned to `keep_parents` cannot be `< - 1` or greater than the number of solutions within the population `sol_per_pop`.
- `K_tournament=3`: In case that the parent selection type is `tournament`, the `K_tournament` specifies the number of parents participating in the tournament selection. It defaults to `3`.
- `crossover_type="single_point"`: Type of the crossover operation. Supported types are `single_point` (for single-point crossover), `two_points` (for two points crossover), `uniform` (for uniform crossover), and `scattered` (for scattered crossover). Scattered crossover is supported from PyGAD 2.9.0 and higher. It defaults to `single_point`. A custom crossover function can be passed starting from PyGAD 2.16.0. Check the User-Defined Crossover, Mutation, and Parent Selection Operators section for more details about creating a user-defined crossover function. Starting from PyGAD 2.2.2 and higher, if `crossover_type=None`, then the crossover step is bypassed which means no crossover is applied and thus no offspring will be created in the next generations. The next generation will use the solutions in the current population.
- `crossover_probability=None`: The probability of selecting a parent for applying the crossover operation. Its value must be between 0.0 and 1.0 inclusive. For each parent, a random value between 0.0 and 1.0 is generated. If this random value is less than or equal to the value assigned to the `crossover_probability` parameter, then the parent is selected. Added in PyGAD 2.5.0 and higher.
- `mutation_type="random"`: Type of the mutation operation. Supported types are `random` (for random mutation), `swap` (for swap mutation), `inversion` (for inversion mutation), `scramble` (for scramble mutation), and `adaptive` (for adaptive mutation). It defaults to `random`. A custom mutation function can be passed starting from PyGAD 2.16.0. Check the User-Defined Crossover, Mutation, and Parent Selection Operators section for more details about creating a user-defined mutation function. Starting from PyGAD 2.2.2 and higher, if `mutation_type=None`, then the mutation step is bypassed which means no mutation is applied and thus no changes are applied to the offspring created using the crossover operation. The offspring will be used unchanged in the next generation. `Adaptive` mutation is supported starting from PyGAD 2.10.0. For more information about adaptive mutation, go the the Adaptive Mutation section. For example about using adaptive mutation, check the Use Adaptive Mutation in PyGAD section.
- `mutation_probability=None`: The probability of selecting a gene for applying the mutation operation. Its value must be between 0.0 and 1.0 inclusive. For each gene in a solution, a random value between 0.0 and 1.0 is generated. If this random value is less than or equal to the value assigned to the `mutation_probability` parameter, then the gene is selected. If this parameter exists, then there is no need for the 2 parameters `mutation_percent_genes` and `mutation_num_genes`. Added in PyGAD 2.5.0 and higher.
- `mutation_by_replacement=False`: An optional bool parameter. It works only when the selected type of mutation is random (`mutation_type="random"`). In this case, `mutation_by_replacement=True` means replace the gene by the randomly generated value. If False, then it has no effect and random mutation works by adding the random value to the gene. Supported in PyGAD 2.2.2 and higher. Check the changes in PyGAD 2.2.2 under the Release History section for an example.
- `mutation_percent_genes="default"`: Percentage of genes to mutate. It defaults to the string `"default"` which is later translated into the integer `10` which means 10% of the genes will be mutated. It must be `>0` and `<=100`. Out of this percentage, the number of genes to mutate is deduced which is assigned to the `mutation_num_genes` parameter. The `mutation_percent_genes` parameter has no action if `mutation_probability` or `mutation_num_genes` exist. Starting from PyGAD 2.2.2 and higher, this parameter has no action if `mutation_type` is `None`.
- `mutation_num_genes=None`: Number of genes to mutate which defaults to `None` meaning that no number is specified. The `mutation_num_genes` parameter has no action if the parameter `mutation_probability` exists. Starting from PyGAD 2.2.2 and higher, this parameter has no action if `mutation_type` is `None`.
- `random_mutation_min_val=-1.0`: For `random` mutation, the `random_mutation_min_val` parameter specifies the start value of the range from which a random value is selected to be added to the gene. It defaults to `-1`. Starting from PyGAD 2.2.2 and higher, this parameter has no action if `mutation_type` is `None`.

- `random_mutation_max_val=1.0`: For `random` mutation, the `random_mutation_max_val` parameter specifies the end value of the range from which a random value is selected to be added to the gene. It defaults to `+1`. Starting from PyGAD 2.2.2 and higher, this parameter has no action if `mutation_type` is `None`.
- `gene_space=None`: It is used to specify the possible values for each gene in case the user wants to restrict the gene values. It is useful if the gene space is restricted to a certain range or to discrete values. It accepts a `list`, `tuple`, `range`, or `numpy.ndarray`. When all genes have the same global space, specify their values as a `list`/`tuple`/`range`/`numpy.ndarray`. For example, `gene_space = [0.3, 5.2, -4, 8]` restricts the gene values to the 4 specified values. If each gene has its own space, then the `gene_space` parameter can be nested like `[[0.4, -5], [0.5, -3.2, 8.2, -9], ...]` where the first sublist determines the values for the first gene, the second sublist for the second gene, and so on. If the nested list/tuple has a `None` value, then the gene's initial value is selected randomly from the range specified by the 2 parameters `init_range_low` and `init_range_high` and its mutation value is selected randomly from the range specified by the 2 parameters `random_mutation_min_val` and `random_mutation_max_val`. `gene_space` is added in PyGAD 2.5.0. Check the Release History of PyGAD 2.5.0 section of the documentation for more details. In PyGAD 2.9.0, NumPy arrays can be assigned to the `gene_space` parameter. In PyGAD 2.11.0, the `gene_space` parameter itself or any of its elements can be assigned to a dictionary to specify the lower and upper limits of the genes. For example, `{'low': 2, 'high': 4}` means the minimum and maximum values are 2 and 4, respectively. In PyGAD 2.15.0, a new key called `"step"` is supported to specify the step of moving from the start to the end of the range specified by the 2 existing keys `"low"` and `"high"`.
- `on_start=None`: Accepts a function to be called only once before the genetic algorithm starts its evolution. This function must accept a single parameter representing the instance of the genetic algorithm. Added in PyGAD 2.6.0.
- `on_fitness=None`: Accepts a function to be called after calculating the fitness values of all solutions in the population. This function must accept 2 parameters: the first one represents the instance of the genetic algorithm and the second one is a list of all solutions' fitness values. Added in PyGAD 2.6.0.
- `on_parents=None`: Accepts a function to be called after selecting the parents that mates. This function must accept 2 parameters: the first one represents the instance of the genetic algorithm and the second one represents the selected parents. Added in PyGAD 2.6.0.
- `on_crossover=None`: Accepts a function to be called each time the crossover operation is applied. This function must accept 2 parameters: the first one represents the instance of the genetic algorithm and the second one represents the offspring generated using crossover. Added in PyGAD 2.6.0.
- `on_mutation=None`: Accepts a function to be called each time the mutation operation is applied. This function must accept 2 parameters: the first one represents the instance of the genetic algorithm and the second one represents the offspring after applying the mutation. Added in PyGAD 2.6.0.
- `callback_generation=None`: Accepts a function to be called after each generation. This function must accept a single parameter representing the instance of the genetic algorithm. Supported in PyGAD 2.0.0 and higher. In PyGAD 2.4.0, if this function returned the string `stop`, then the `run()` method stops at the current generation without completing the remaining generations. Check the **Release History** section of the documentation for an example. Starting from PyGAD 2.6.0, the `callback_generation` parameter is deprecated and should be replaced by the `on_generation` parameter. The `callback_generation` parameter will be removed in a later version.
- `on_generation=None`: Accepts a function to be called after each generation. This function must accept a single parameter representing the instance of the genetic algorithm. If the function returned the string `stop`, then the `run()` method stops without completing the other generations. Added in PyGAD 2.6.0.
- `on_stop=None`: Accepts a function to be called only once exactly before the genetic algorithm stops or when it completes all the generations. This function must accept 2 parameters: the first one represents the instance of the genetic algorithm and the second one is a list of fitness values of the last population's solutions. Added in PyGAD 2.6.0.
- `delay_after_gen=0.0`: It accepts a non-negative number specifying the time in seconds to wait after a generation completes and before going to the next generation. It defaults to `0.0` which means no delay after the generation. Available in PyGAD 2.4.0 and higher.
- `save_best_solutions=False`: When `True`, then the best solution after each generation is saved into an attribute named `best_solutions`. If `False` (default), then no solutions are saved and the

`best_solutions` attribute will be empty. Supported in PyGAD 2.9.0.
- `save_solutions=False`: If `True`, then all solutions in each generation are appended into an attribute called `solutions` which is NumPy array. Supported in PyGAD 2.15.0.
- `suppress_warnings=False`: A bool parameter to control whether the warning messages are printed or not. It defaults to `False`.
- `allow_duplicate_genes=True`: Added in PyGAD 2.13.0. If `True`, then a solution/chromosome may have duplicate gene values. If `False`, then each gene will have a unique value in its solution.
- `stop_criteria=None`: Some criteria to stop the evolution. Added in PyGAD 2.15.0. Each criterion is passed as `str` which has a stop word. The current 2 supported words are `reach` and `saturate`. `reach` stops the `run()` method if the fitness value is equal to or greater than a given fitness value. An example for `reach` is `"reach_40"` which stops the evolution if the fitness is >= 40. `saturate` means stop the evolution if the fitness saturates for a given number of consecutive generations. An example for `saturate` is `"saturate_7"` which means stop the `run()` method if the fitness does not change for 7 consecutive generations.
- `parallel_processing=None`: Added in PyGAD 2.17.0. If `None` (Default), this means no parallel processing is applied. It can accept a list/tuple of 2 elements **[**1) Can be either `'process'` or `'thread'` to indicate whether processes or threads are used, respectively.**,** 2) The number of processes or threads to use.**]**. For example, `parallel_processing=['process', 10]` applies parallel processing with 10 processes. If a positive integer is assigned, then it is used as the number of threads. For example, `parallel_processing=5` uses 5 threads which is equivalent to `parallel_processing=["thread", 5]`. For more information, check the Parallel Processing in PyGAD section.

The user doesn't have to specify all of such parameters while creating an instance of the GA class. A very important parameter you must care about is `fitness_func` which defines the fitness function.

It is OK to set the value of any of the 2 parameters `init_range_low` and `init_range_high` to be equal, higher, or lower than the other parameter (i.e. `init_range_low` is not needed to be lower than `init_range_high`). The same holds for the `random_mutation_min_val` and `random_mutation_max_val` parameters.

If the 2 parameters `mutation_type` and `crossover_type` are `None`, this disables any type of evolution the genetic algorithm can make. As a result, the genetic algorithm cannot find a better solution that the best solution in the initial population.

The parameters are validated within the constructor. If at least a parameter is not correct, an exception is thrown.

## Plotting Methods in `pygad.GA` Class

- `plot_fitness()`: Shows how the fitness evolves by generation.
- `plot_genes()`: Shows how the gene value changes for each generation.
- `plot_new_solution_rate()`: Shows the number of new solutions explored in each solution.

## Class Attributes

- `supported_int_types`: A list of the supported types for the integer numbers.
- `supported_float_types`: A list of the supported types for the floating-point numbers.
- `supported_int_float_types`: A list of the supported types for all numbers. It just concatenates the previous 2 lists.

## Other Instance Attributes & Methods

All the parameters and functions passed to the **pygad.GA** class constructor are used as class attributes and methods in the instances of the **pygad.GA** class. In addition to such attributes, there are other attributes and methods added to the instances of the **pygad.GA** class:



The next 2 subsections list such attributes and methods.

## Other Attributes

- `generations_completed`: Holds the number of the last completed generation.
- `population`: A NumPy array holding the initial population.
- `valid_parameters`: Set to `True` when all the parameters passed in the `GA` class constructor are valid.
- `run_completed`: Set to `True` only after the `run()` method completes gracefully.
- `pop_size`: The population size.
- `best_solutions_fitness`: A list holding the fitness values of the best solutions for all generations.
- `best_solution_generation`: The generation number at which the best fitness value is reached. It is only assigned the generation number after the `run()` method completes. Otherwise, its value is -1.
- `best_solutions`: A NumPy array holding the best solution per each generation. It only exists when the `save_best_solutions` parameter in the `pygad.GA` class constructor is set to `True`.
- `last_generation_fitness`: The fitness values of the solutions in the last generation. Added in PyGAD 2.12.0.
- `last_generation_parents`: The parents selected from the last generation. Added in PyGAD 2.12.0.
- `last_generation_offspring_crossover`: The offspring generated after applying the crossover in the last generation. Added in PyGAD 2.12.0.
- `last_generation_offspring_mutation`: The offspring generated after applying the mutation in the last generation. Added in PyGAD 2.12.0.
- `gene_type_single`: A flag that is set to `True` if the `gene_type` parameter is assigned to a single data type that is applied to all genes. If `gene_type` is assigned a `list`, `tuple`, or `numpy.ndarray`, then the value of `gene_type_single` will be `False`. Added in PyGAD 2.14.0.
- `last_generation_parents_indices`: This attribute holds the indices of the selected parents in the last generation. Supported in PyGAD 2.15.0.

Note that the attributes with its name start with `last_generation_` are updated after each generation.

## Other Methods

- `cal_pop_fitness`: A method that calculates the fitness values for all solutions within the population by calling the function passed to the `fitness_func` parameter for each solution.
- `crossover`: Refers to the method that applies the crossover operator based on the selected type of crossover in the `crossover_type` property.
- `mutation`: Refers to the method that applies the mutation operator based on the selected type of mutation in the `mutation_type` property.
- `select_parents`: Refers to a method that selects the parents based on the parent selection type specified in the `parent_selection_type` attribute.
- `adaptive_mutation_population_fitness`: Returns the average fitness value used in the adaptive mutation to filter the solutions.
- `solve_duplicate_genes_randomly`: Solves the duplicates in a solution by randomly selecting new values for the duplicating genes.
- `solve_duplicate_genes_by_space`: Solves the duplicates in a solution by selecting values for the duplicating genes from the gene space
- `unique_int_gene_from_range`: Finds a unique integer value for the gene.
- `unique_genes_by_space`: Loops through all the duplicating genes to find unique values that from their gene spaces to solve the duplicates. For each duplicating gene, a call to the `unique_gene_by_space()` is made.
- `unique_gene_by_space`: Returns a unique gene value for a single gene based on its value space to solve the duplicates.

The next sections discuss the methods available in the **pygad.GA** class.

# `initialize_population()`

It creates an initial population randomly as a NumPy array. The array is saved in the instance attribute named `population`.

Accepts the following parameters:

- `low`: The lower value of the random range from which the gene values in the initial population are selected. It defaults to -4. Available in PyGAD 1.0.20 and higher.
- `high`: The upper value of the random range from which the gene values in the initial population are selected. It defaults to -4. Available in PyGAD 1.0.20.

This method assigns the values of the following 3 instance attributes:

1. `pop_size`: Size of the population.
2. `population`: Initially, it holds the initial population and later updated after each generation.
3. `initial_population`: Keeping the initial population.

# `cal_pop_fitness()`

Calculating the fitness values of all solutions in the current population.

It works by iterating through the solutions and calling the function assigned to the `fitness_func` parameter in the **pygad.GA** class constructor for each solution.

It returns an array of the solutions' fitness values.

# `run()`

Runs the genetic algorithm. This is the main method in which the genetic algorithm is evolved through some generations. It accepts no parameters as it uses the instance to access all of its requirements.

For each generation, the fitness values of all solutions within the population are calculated according to the `cal_pop_fitness()` method which internally just calls the function assigned to the `fitness_func` parameter in the **pygad.GA** class constructor for each solution.

According to the fitness values of all solutions, the parents are selected using the `select_parents()` method. This method behavior is determined according to the parent selection type in the `parent_selection_type` parameter in the **pygad.GA** class constructor

Based on the selected parents, offspring are generated by applying the crossover and mutation operations using the `crossover()` and `mutation()` methods. The behavior of such 2 methods is defined according to the `crossover_type` and `mutation_type` parameters in the **pygad.GA** class constructor.

After the generation completes, the following takes place:

- The `population` attribute is updated by the new population.
- The `generations_completed` attribute is assigned by the number of the last completed generation.
- If there is a callback function assigned to the `callback_generation` attribute, then it will be called.

After the `run()` method completes, the following takes place:

- The `best_solution_generation` is assigned the generation number at which the best fitness value is reached.
- The `run_completed` attribute is set to `True`.

# Parent Selection Methods

The **pygad.GA** class has several methods for selecting the parents that will mate to produce the offspring. All of such methods accept the same parameters which are:

- `fitness`: The fitness values of the solutions in the current population.
- `num_parents`: The number of parents to be selected.

All of such methods return an array of the selected parents.

The next subsections list the supported methods for parent selection.

### `steady_state_selection()`

Selects the parents using the steady-state selection technique.

### `rank_selection()`

Selects the parents using the rank selection technique.

### `random_selection()`

Selects the parents randomly.

### `tournament_selection()`

Selects the parents using the tournament selection technique.

### `roulette_wheel_selection()`

Selects the parents using the roulette wheel selection technique.

### `stochastic_universal_selection()`

Selects the parents using the stochastic universal selection technique.

## Crossover Methods

The **pygad.GA** class supports several methods for applying crossover between the selected parents. All of these methods accept the same parameters which are:

- `parents`: The parents to mate for producing the offspring.
- `offspring_size`: The size of the offspring to produce.

All of such methods return an array of the produced offspring.

The next subsections list the supported methods for crossover.

### `single_point_crossover()`

Applies the single-point crossover. It selects a point randomly at which crossover takes place between the pairs of parents.

### `two_points_crossover()`

Applies the 2 points crossover. It selects the 2 points randomly at which crossover takes place between the pairs of parents.

### `uniform_crossover()`

Applies the uniform crossover. For each gene, a parent out of the 2 mating parents is selected randomly and the gene is copied from it.



### `scattered_crossover()`

Applies the scattered crossover. It randomly selects the gene from one of the 2 parents.

## Mutation Methods

The **pygad.GA** class supports several methods for applying mutation. All of these methods accept the same parameter which is:

- `offspring`: The offspring to mutate.

All of such methods return an array of the mutated offspring.

The next subsections list the supported methods for mutation.

### `random_mutation()`

Applies the random mutation which changes the values of some genes randomly. The number of genes is specified according to either the `mutation_num_genes` or the `mutation_percent_genes` attributes.

For each gene, a random value is selected according to the range specified by the 2 attributes `random_mutation_min_val` and `random_mutation_max_val`. The random value is added to the selected gene.

### `swap_mutation()`

Applies the swap mutation which interchanges the values of 2 randomly selected genes.

### `inversion_mutation()`

Applies the inversion mutation which selects a subset of genes and inverts them.

### `scramble_mutation()`

Applies the scramble mutation which selects a subset of genes and shuffles their order randomly.

### `adaptive_mutation()`

Applies the adaptive mutation which selects a subset of genes and shuffles their order randomly.

## `best_solution()`

Returns information about the best solution found by the genetic algorithm.

It accepts the following parameters:

- `pop_fitness=None`: An optional parameter that accepts a list of the fitness values of the solutions in the population. If `None`, then the `cal_pop_fitness()` method is called to calculate the fitness values of the population.

It returns the following:

- `best_solution`: Best solution in the current population.
- `best_solution_fitness`: Fitness value of the best solution.
- `best_match_idx`: Index of the best solution in the current population.

## `plot_fitness()`

Previously named `plot_result()`, this method creates, shows, and returns a figure that summarizes how the fitness value evolves by generation. It works only after completing at least 1 generation.

If no generation is completed (at least 1), an exception is raised.

Starting from PyGAD 2.15.0 and higher, this method accepts the following parameters:

1. `title`: Title of the figure.
2. `xlabel`: X-axis label.
3. `ylabel`: Y-axis label.
4. `linewidth`: Line width of the plot. Defaults to `3`.
5. `font_size`: Font size for the labels and title. Defaults to `14`.
6. `plot_type`: Type of the plot which can be either `"plot"` (default), `"scatter"`, or `"bar"`.
7. `color`: Color of the plot which defaults to `"#3870FF"`.
8. `save_dir`: Directory to save the figure.

# `plot_new_solution_rate()`

The `plot_new_solution_rate()` method creates, shows, and returns a figure that shows the number of new solutions explored in each generation. This method works only when `save_solutions=True` in the constructor of the `pygad.GA` class. It also works only after completing at least 1 generation.

If no generation is completed (at least 1), an exception is raised.

This method accepts the following parameters:

1. `title`: Title of the figure.
2. `xlabel`: X-axis label.
3. `ylabel`: Y-axis label.
4. `linewidth`: Line width of the plot. Defaults to `3`.
5. `font_size`: Font size for the labels and title. Defaults to `14`.
6. `plot_type`: Type of the plot which can be either `"plot"` (default), `"scatter"`, or `"bar"`.
7. `color`: Color of the plot which defaults to `"#3870FF"`.
8. `save_dir`: Directory to save the figure.

# `plot_genes()`

The `plot_genes()` method creates, shows, and returns a figure that describes each gene. It has different options to create the figures which helps to:

1. Explore the gene value for each generation by creating a normal plot.
2. Create a histogram for each gene.
3. Create a boxplot.

This is controlled by the `graph_type` parameter.

It works only after completing at least 1 generation. If no generation is completed, an exception is raised. If no generation is completed (at least 1), an exception is raised.

This method accepts the following parameters:

1. `title`: Title of the figure.
2. `xlabel`: X-axis label.
3. `ylabel`: Y-axis label.
4. `linewidth`: Line width of the plot. Defaults to `3`.
5. `font_size`: Font size for the labels and title. Defaults to `14`.
6. `plot_type`: Type of the plot which can be either `"plot"` (default), `"scatter"`, or `"bar"`.
7. `graph_type`: Type of the graph which can be either `"plot"` (default), `"boxplot"`, or `"histogram"`.

8. `fill_color`: Fill color of the graph which defaults to `"#3870FF"`. This has no effect if `graph_type="plot"`.
9. `color`: Color of the plot which defaults to `"#3870FF"`.
10. `solutions`: Defaults to `"all"` which means use all solutions. If `"best"` then only the best solutions are used.
11. `save_dir`: Directory to save the figure.

An exception is raised if:

- `solutions="all"` while `save_solutions=False` in the constructor of the `pygad.GA` class. .
- `solutions="best"` while `save_best_solutions=False` in the constructor of the `pygad.GA` class. .

## `save()`

Saves the genetic algorithm instance

Accepts the following parameter:

- `filename`: Name of the file to save the instance. No extension is needed.

# Functions in `pygad`

Besides the methods available in the **pygad.GA** class, this section discusses the functions available in pygad. Up to this time, there is only a single function named `load()`.

## `pygad.load()`

Reads a saved instance of the genetic algorithm. This is **not a method** but a **function** that is indented under the `pygad` module. So, it could be called by the **pygad** module as follows: `pygad.load(filename)`.

Accepts the following parameter:

- `filename`: Name of the file holding the saved instance of the genetic algorithm. No extension is needed.

Returns the genetic algorithm instance.

# Steps to Use `pygad`

To use the `pygad` module, here is a summary of the required steps:

1. Preparing the `fitness_func` parameter.
2. Preparing Other Parameters.
3. Import `pygad`.
4. Create an Instance of the **pygad.GA** Class.
5. Run the Genetic Algorithm.
6. Plotting Results.
7. Information about the Best Solution.
8. Saving & Loading the Results.

Let's discuss how to do each of these steps.

## Preparing the `fitness_func` Parameter

Even there are some steps in the genetic algorithm pipeline that can work the same regardless of the problem being solved, one critical step is the calculation of the fitness value. There is no unique way of calculating the fitness value and it changes from one problem to another.

On ``**15 April 2020**``, a new argument named `fitness_func` is added to PyGAD 1.0.17 that allows the user to specify a custom function to be used as a fitness function. This function must be a **maximization function** so that a solution with a high fitness value returned is selected compared to a solution with a low value. Doing that allows the user to freely use PyGAD to solve any problem by passing the appropriate fitness function. It is very important to understand the problem well for creating this function.

Let's discuss an example:

> Given the following function:
> y = f(w1:w6) = w1x1 + w2x2 + w3x3 + w4x4 + w5x5 + 6wx6
> where (x1,x2,x3,x4,x5,x6)=(4, -2, 3.5, 5, -11, -4.7) and y=44
> What are the best values for the 6 weights (w1 to w6)? We are going to use the genetic algorithm to optimize this function.

So, the task is about using the genetic algorithm to find the best values for the 6 weight `W1` to `W6`. Thinking of the problem, it is clear that the best solution is that returning an output that is close to the desired output `y=44`. So, the fitness function should return a value that gets higher when the solution's output is closer to `y=44`. Here is a function that does that:

```
function_inputs = [4, -2, 3.5, 5, -11, -4.7] # Function inputs.
desired_output = 44 # Function output.

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution*function_inputs)
    fitness = 1.0 / numpy.abs(output - desired_output)
    return fitness
```

Such a user-defined function must accept 2 parameters:

1. 1D vector representing a single solution. Introduced in PyGAD 1.0.17.
2. Solution index within the population. Introduced in PyGAD 2.0.0 and higher.

The `__code__` object is used to check if this function accepts the required number of parameters. If more or fewer parameters are passed, an exception is thrown.

By creating this function, you almost did an awesome step towards using PyGAD.

## Preparing Other Parameters

Here is an example for preparing the other parameters:

```
num_generations = 50
num_parents_mating = 4

fitness_function = fitness_func

sol_per_pop = 8
num_genes = len(function_inputs)

init_range_low = -2
init_range_high = 5

parent_selection_type = "sss"
keep_parents = 1

crossover_type = "single_point"

mutation_type = "random"
mutation_percent_genes = 10
```

## The `callback_generation` Parameter



This parameter should be replaced by `on_generation`. The `callback_generation` parameter will be removed in a later release of PyGAD.

In PyGAD 2.0.0 and higher, an optional parameter named `callback_generation` is supported which allows the user to call a function (with a single parameter) after each generation. Here is a simple function that just prints the current generation number and the fitness value of the best solution in the current generation. The `generations_completed` attribute of the GA class returns the number of the last completed generation.

```
def callback_gen(ga_instance):
    print("Generation : ", ga_instance.generations_completed)
    print("Fitness of the best solution :", ga_instance.best_solution()[1])
```

After being defined, the function is assigned to the `callback_generation` parameter of the GA class constructor. By doing that, the `callback_gen()` function will be called after each generation.

```
ga_instance = pygad.GA(...,
                       callback_generation=callback_gen,
                       ...)
```

After the parameters are prepared, we can import PyGAD and build an instance of the **pygad.GA** class.

## Import the `pygad`

The next step is to import PyGAD as follows:

```
import pygad
```

The **pygad.GA** class holds the implementation of all methods for running the genetic algorithm.

## Create an Instance of the `pygad.GA` Class

The **pygad.GA** class is instantiated where the previously prepared parameters are fed to its constructor. The constructor is responsible for creating the initial population.

```
ga_instance = pygad.GA(num_generations=num_generations,
                       num_parents_mating=num_parents_mating,
                       fitness_func=fitness_function,
                       sol_per_pop=sol_per_pop,
                       num_genes=num_genes,
                       init_range_low=init_range_low,
                       init_range_high=init_range_high,
                       parent_selection_type=parent_selection_type,
                       keep_parents=keep_parents,
                       crossover_type=crossover_type,
                       mutation_type=mutation_type,
                       mutation_percent_genes=mutation_percent_genes)
```

## Run the Genetic Algorithm

After an instance of the **pygad.GA** class is created, the next step is to call the `run()` method as follows:

```
ga_instance.run()
```

Inside this method, the genetic algorithm evolves over some generations by doing the following tasks:

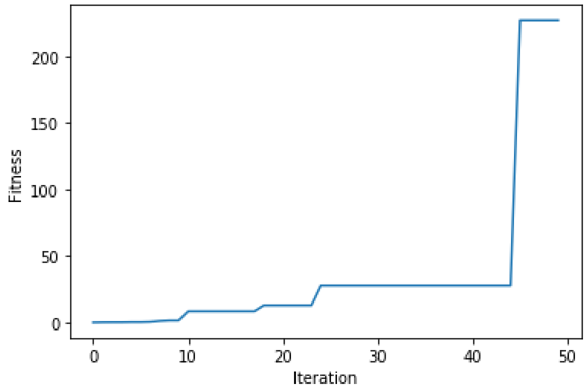
1. Calculating the fitness values of the solutions within the current population.
2. Select the best solutions as parents in the mating pool.
3. Apply the crossover & mutation operation
4. Repeat the process for the specified number of generations.



## Plotting Results

There is a method named `plot_fitness()` which creates a figure summarizing how the fitness values of the solutions change with the generations.

```
ga_instance.plot_fitness()
```




# Information about the Best Solution

The following information about the best solution in the last population is returned using the `best_solution()` method.

- Solution
- Fitness value of the solution
- Index of the solution within the population

```
solution, solution_fitness, solution_idx = ga_instance.best_solution()
print("Parameters of the best solution : {solution}".format(solution=solution))
print("Fitness value of the best solution = {solution_fitness}".format(solution_fitr
print("Index of the best solution : {solution_idx}".format(solution_idx=solution_idx
```

Using the `best_solution_generation` attribute of the instance from the **pygad.GA** class, the generation number at which the **best fitness** is reached could be fetched.

```
if ga_instance.best_solution_generation != -1:
    print("Best fitness value reached after {best_solution_generation} generations."
```

# Saving & Loading the Results

After the `run()` method completes, it is possible to save the current instance of the genetic algorithm to avoid losing the progress made. The `save()` method is available for that purpose. Just pass the file name to it without an extension. According to the next code, a file named `genetic.pkl` will be created and saved in the current directory.

```
filename = 'genetic'
ga_instance.save(filename=filename)
```

You can also load the saved model using the `load()` function and continue using it. For example, you might run the genetic algorithm for some generations, save its current state using the `save()` method, load the model using the `load()` function, and then call the `run()` method again.

```
loaded_ga_instance = pygad.load(filename=filename)
```

After the instance is loaded, you can use it to run any method or access any property.



```
print(loaded_ga_instance.best_solution())
```

# Crossover, Mutation, and Parent Selection

PyGAD supports different types for selecting the parents and applying the crossover & mutation operators. More features will be added in the future. To ask for a new feature, please check the **Ask for Feature** section.

## Supported Crossover Operations

The supported crossover operations at this time are:

1. Single point: Implemented using the `single_point_crossover()` method.
2. Two points: Implemented using the `two_points_crossover()` method.
3. Uniform: Implemented using the `uniform_crossover()` method.

## Supported Mutation Operations

The supported mutation operations at this time are:

1. Random: Implemented using the `random_mutation()` method.
2. Swap: Implemented using the `swap_mutation()` method.
3. Inversion: Implemented using the `inversion_mutation()` method.
4. Scramble: Implemented using the `scramble_mutation()` method.

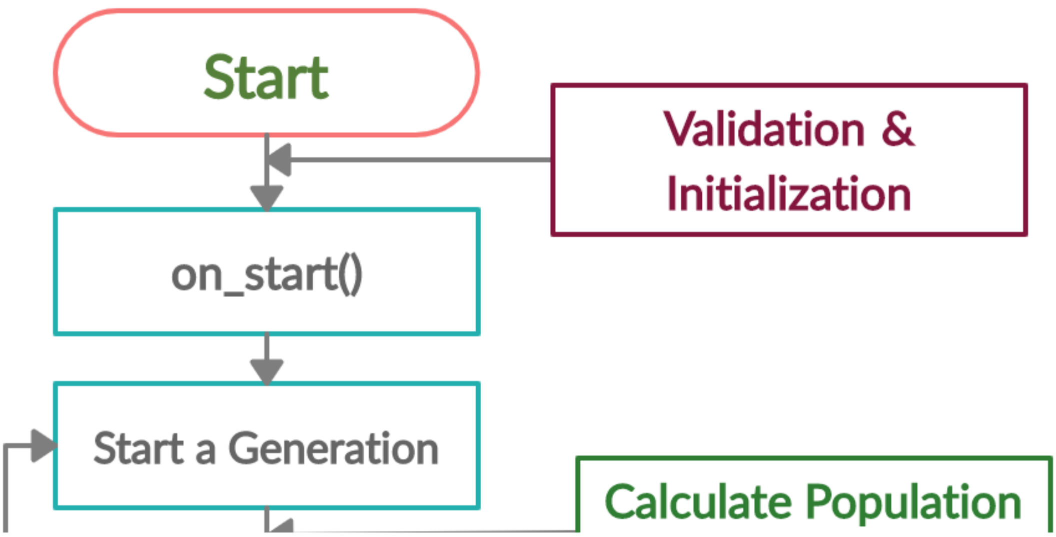
## Supported Parent Selection Operations

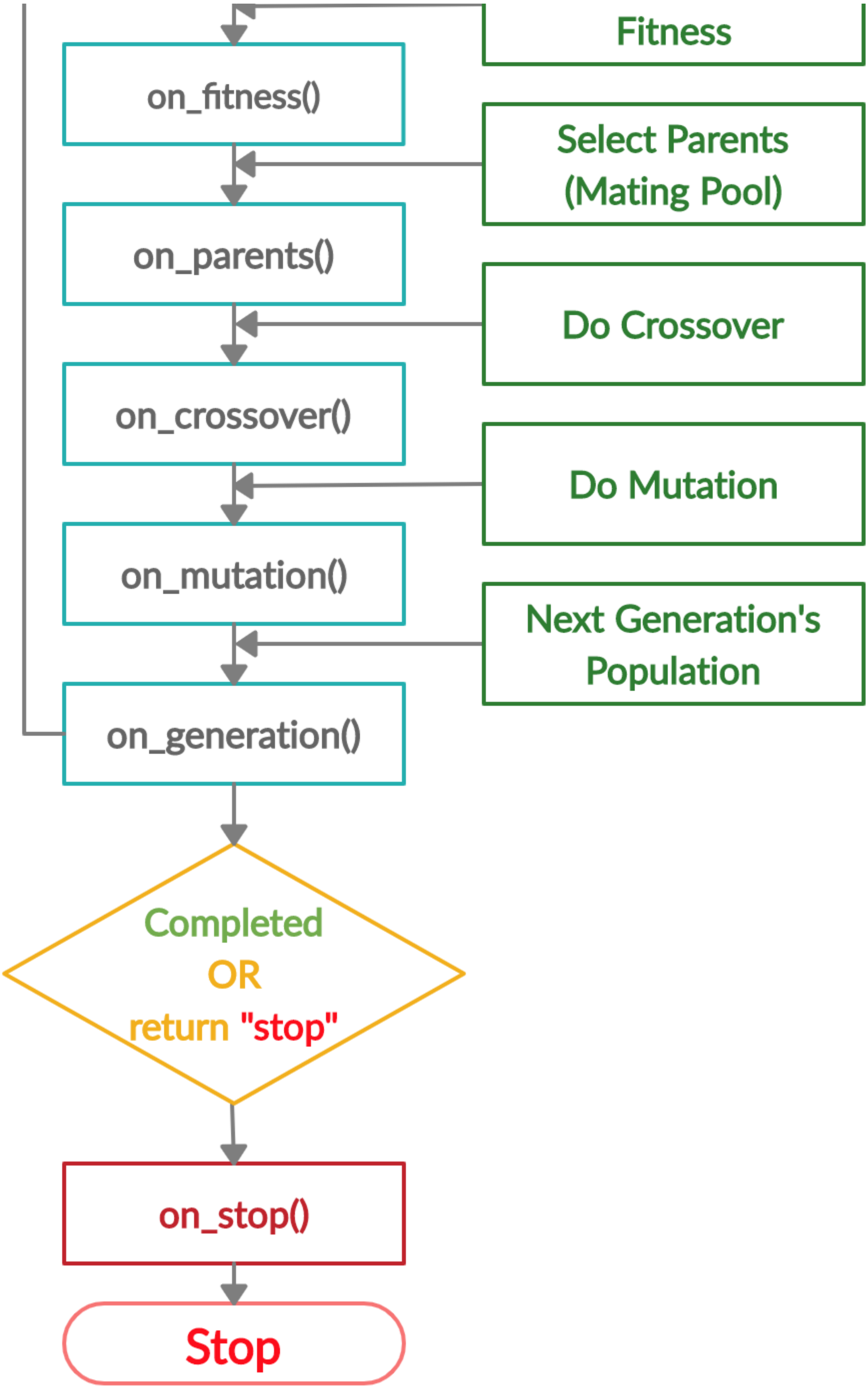
The supported parent selection techniques at this time are:

1. Steady-state: Implemented using the `steady_state_selection()` method.
2. Roulette wheel: Implemented using the `roulette_wheel_selection()` method.
3. Stochastic universal: Implemented using the `stochastic_universal_selection()`method.
4. Rank: Implemented using the `rank_selection()` method.
5. Random: Implemented using the `random_selection()` method.
6. Tournament: Implemented using the `tournament_selection()` method.

# Life Cycle of PyGAD

The next figure lists the different stages in the lifecycle of an instance of the `pygad.GA` class. Note that PyGAD stops when either all generations are completed or when the function passed to the `on_generation` parameter returns the string `stop`.






The next code implements all the callback functions to trace the execution of the genetic algorithm. Each callback function prints its name.

```
import pygad
import numpy

function_inputs = [4,-2,3.5,5,-11,-4.7]
desired_output = 44
```

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```python
def fitness_func(solution, solution_idx):
    output = numpy.sum(solution*function_inputs)
    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
    return fitness

fitness_function = fitness_func

def on_start(ga_instance):
    print("on_start()")

def on_fitness(ga_instance, population_fitness):
    print("on_fitness()")

def on_parents(ga_instance, selected_parents):
    print("on_parents()")

def on_crossover(ga_instance, offspring_crossover):
    print("on_crossover()")

def on_mutation(ga_instance, offspring_mutation):
    print("on_mutation()")

def on_generation(ga_instance):
    print("on_generation()")

def on_stop(ga_instance, last_population_fitness):
    print("on_stop()")

ga_instance = pygad.GA(num_generations=3,
                       num_parents_mating=5,
                       fitness_func=fitness_function,
                       sol_per_pop=10,
                       num_genes=len(function_inputs),
                       on_start=on_start,
                       on_fitness=on_fitness,
                       on_parents=on_parents,
                       on_crossover=on_crossover,
                       on_mutation=on_mutation,
                       on_generation=on_generation,
                       on_stop=on_stop)

ga_instance.run()
```

Based on the used 3 generations as assigned to the `num_generations` argument, here is the output.

```
on_start()

on_fitness()
on_parents()
on_crossover()
on_mutation()
on_generation()

on_fitness()
on_parents()
on_crossover()
on_mutation()
on_generation()

on_fitness()
on_parents()
on_crossover()
on_mutation()
on_generation()

on_stop()
```



# Adaptive Mutation

In the regular genetic algorithm, the mutation works by selecting a single fixed mutation rate for all solutions regardless of their fitness values. So, regardless on whether this solution has high or low quality, the same number of genes are mutated all the time.

The pitfalls of using a constant mutation rate for all solutions are summarized in this paper Libelli, S. Marsili, and P. Alba. "Adaptive mutation in genetic algorithms." Soft computing 4.2 (2000): 76-80 as follows:

> The weak point of "classical" GAs is the total randomness of mutation, which is applied equally to all chromosomes, irrespective of their fitness. Thus a very good chromosome is equally likely to be disrupted by mutation as a bad one.
>
> On the other hand, bad chromosomes are less likely to produce good ones through crossover, because of their lack of building blocks, until they remain unchanged. They would benefit the most from mutation and could be used to spread throughout the parameter space to increase the search thoroughness. So there are two conflicting needs in determining the best probability of mutation.
>
> Usually, a reasonable compromise in the case of a constant mutation is to keep the probability low to avoid disruption of good chromosomes, but this would prevent a high mutation rate of low-fitness chromosomes. Thus a constant probability of mutation would probably miss both goals and result in a slow improvement of the population.

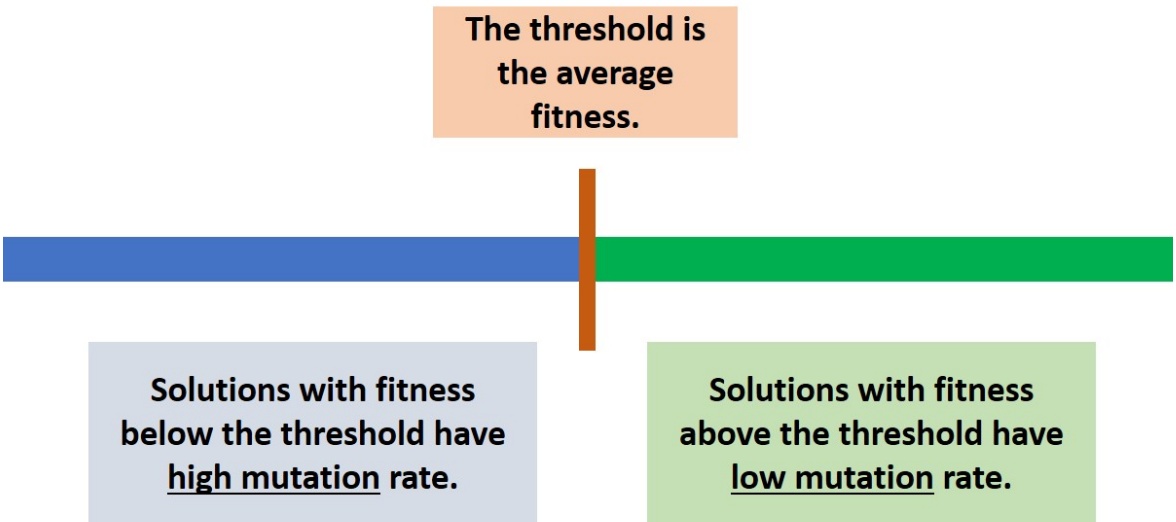
According to Libelli, S. Marsili, and P. Alba. work, the adaptive mutation solves the problems of constant mutation.

Adaptive mutation works as follows:

1. Calculate the average fitness value of the population (`f_avg`).
2. For each chromosome, calculate its fitness value (`f`).
3. If `f<f_avg`, then this solution is regarded as a **low-quality** solution and thus the mutation rate should be kept high because this would increase the quality of this solution.
4. If `f>f_avg`, then this solution is regarded as a **high-quality** solution and thus the mutation rate should be kept low to avoid disrupting this high quality solution.

In PyGAD, if `f=f_avg`, then the solution is regarded of high quality.

The next figure summarizes the previous steps.




This strategy is applied in PyGAD.

## Use Adaptive Mutation in PyGAD



In PyGAD 2.10.0, adaptive mutation is supported. To use it, just follow the following 2 simple steps:

1. In the constructor of the `pygad.GA` class, set `mutation_type="adaptive"` to specify that the type of mutation is adaptive.
2. Specify the mutation rates for the low and high quality solutions using one of these 3 parameters according to your preference: `mutation_probability`, `mutation_num_genes`, and `mutation_percent_genes`. Please check the [documentation of each of these parameters](#) for more information.

When adaptive mutation is used, then the value assigned to any of the 3 parameters can be of any of these data types:

1. `list`
2. `tuple`
3. `numpy.ndarray`

Whatever the data type used, the length of the `list`, `tuple`, or the `numpy.ndarray` must be exactly 2. That is there are just 2 values:

1. The first value is the mutation rate for the low-quality solutions.
2. The second value is the mutation rate for the low-quality solutions.

PyGAD expects that the first value is higher than the second value and thus a warning is printed in case the first value is lower than the second one.

Here are some examples to feed the mutation rates:

```
# mutation_probability
mutation_probability = [0.25, 0.1]
mutation_probability = (0.35, 0.17)
mutation_probability = numpy.array([0.15, 0.05])

# mutation_num_genes
mutation_num_genes = [4, 2]
mutation_num_genes = (3, 1)
mutation_num_genes = numpy.array([7, 2])

# mutation_percent_genes
mutation_percent_genes = [25, 12]
mutation_percent_genes = (15, 8)
mutation_percent_genes = numpy.array([21, 13])
```

Assume that the average fitness is 12 and the fitness values of 2 solutions are 15 and 7. If the mutation probabilities are specified as follows:

```
mutation_probability = [0.25, 0.1]
```

Then the mutation probability of the first solution is 0.1 because its fitness is 15 which is higher than the average fitness 12. The mutation probability of the second solution is 0.25 because its fitness is 7 which is lower than the average fitness 12.

Here is an example that uses adaptive mutation.

```
import pygad
import numpy

function_inputs = [4,-2,3.5,5,-11,-4.7] # Function inputs.
desired_output = 44 # Function output.

def fitness_func(solution, solution_idx):
    # The fitness function calulates the sum of products between each input and its
    output = numpy.sum(solution*function_inputs)
    # The value 0.000001 is used to avoid the Inf value when the denominator numpy.a
    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
    return fitness
```

```python
# Creating an instance of the GA class inside the ga module. Some parameters are ini
ga_instance = pygad.GA(num_generations=200,
                       fitness_func=fitness_func,
                       num_parents_mating=10,
                       sol_per_pop=20,
                       num_genes=len(function_inputs),
                       mutation_type="adaptive",
                       mutation_num_genes=(3, 1))

# Running the GA to optimize the parameters of the function.
ga_instance.run()

ga_instance.plot_fitness(title="PyGAD with Adaptive Mutation", linewidth=5)
```

# Limit the Gene Value Range

In PyGAD 2.11.0, the `gene_space` parameter supported a new feature to allow customizing the range of accepted values for each gene. Let's take a quick review of the `gene_space` parameter to build over it.

The `gene_space` parameter allows the user to feed the space of values of each gene. This way the accepted values for each gene is retracted to the user-defined values. Assume there is a problem that has 3 genes where each gene has different set of values as follows:

1. Gene 1: `[0.4, 12, -5, 21.2]`
2. Gene 2: `[-2, 0.3]`
3. Gene 3: `[1.2, 63.2, 7.4]`

Then, the `gene_space` for this problem is as given below. Note that the order is very important.

```python
gene_space = [[0.4, 12, -5, 21.2],
              [-2, 0.3],
              [1.2, 63.2, 7.4]]
```

In case all genes share the same set of values, then simply feed a single list to the `gene_space` parameter as follows. In this case, all genes can only take values from this list of 6 values.

```python
gene_space = [33, 7, 0.5, 95. 6.3, 0.74]
```

The previous example restricts the gene values to just a set of fixed number of discrete values. In case you want to use a range of discrete values to the gene, then you can use the `range()` function. For example, `range(1, 7)` means the set of allowed values for the gene are `1, 2, 3, 4, 5, and 6`. You can also use the `numpy.arange()` or `numpy.linspace()` functions for the same purpose.

The previous discussion only works with a range of discrete values not continuous values. In PyGAD 2.11.0, the `gene_space` parameter can be assigned a dictionary that allows the gene to have values from a continuous range.

Assuming you want to restrict the gene within this half-open range [1 to 5) where 1 is included and 5 is not. Then simply create a dictionary with 2 items where the keys of the 2 items are:

1. `'low'`: The minimum value in the range which is 1 in the example.
2. `'high'`: The maximum value in the range which is 5 in the example.

The dictionary will look like that:

```python
{'low': 1,
 'high': 5}
```

It is not acceptable to add more than 2 items in the dictionary or use other keys than `'low'` and `'high'`.

For a 3-gene problem, the next code creates a dictionary for each gene to restrict its values in a continuous range. For the first gene, it can take any floating-point value from the range that starts from 1 (inclusive) and ends at 5 (exclusive).

```
gene_space = [{'low': 1, 'high': 5}, {'low': 0.3, 'high': 1.4}, {'low': -0.2, 'high'
```

# Stop at Any Generation

In PyGAD 2.4.0, it is possible to stop the genetic algorithm after any generation. All you need to do it to return the string `"stop"` in the callback function `callback_generation`. When this callback function is implemented and assigned to the `callback_generation` parameter in the constructor of the `pygad.GA` class, then the algorithm immediately stops after completing its current generation. Let's discuss an example.

Assume that the user wants to stop algorithm either after the 100 generations or if a condition is met. The user may assign a value of 100 to the `num_generations` parameter of the `pygad.GA` class constructor.

The condition that stops the algorithm is written in a callback function like the one in the next code. If the fitness value of the best solution exceeds 70, then the string `"stop"` is returned.

```
def func_generation(ga_instance):
    if ga_instance.best_solution()[1] >= 70:
        return "stop"
```

# Stop Criteria

In PyGAD 2.15.0, a new parameter named `stop_criteria` is added to the constructor of the `pygad.GA` class. It helps to stop the evolution based on some criteria. It can be assigned to one or more criterion.

Each criterion is passed as `str` that consists of 2 parts:

1. Stop word.
2. Number.

It takes this form:

```
"word_num"
```

The current 2 supported words are `reach` and `saturate`.

The `reach` word stops the `run()` method if the fitness value is equal to or greater than a given fitness value. An example for `reach` is `"reach_40"` which stops the evolution if the fitness is >= 40.

`saturate` stops the evolution if the fitness saturates for a given number of consecutive generations. An example for `saturate` is `"saturate_7"` which means stop the `run()` method if the fitness does not change for 7 consecutive generations.

Here is an example that stops the evolution if either the fitness value reached `127.4` or if the fitness saturates for `15` generations.

```
import pygad
import numpy

equation_inputs = [4, -2, 3.5, 8, 9, 4]
desired_output = 44

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution * equation_inputs)

    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
```

v: latest

```
    return fitness

ga_instance = pygad.GA(num_generations=200,
                       sol_per_pop=10,
                       num_parents_mating=4,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       stop_criteria=["reach_127.4", "saturate_15"])

ga_instance.run()
print("Number of generations passed is {generations_completed}".format(generations_c
```

# Prevent Duplicates in Gene Values

In PyGAD 2.13.0, a new bool parameter called `allow_duplicate_genes` is supported to control whether duplicates are supported in the chromosome or not. In other words, whether 2 or more genes might have the same exact value.

If `allow_duplicate_genes=True` (which is the default case), genes may have the same value. If `allow_duplicate_genes=False`, then no 2 genes will have the same value given that there are enough unique values for the genes.

The next code gives an example to use the `allow_duplicate_genes` parameter. A callback generation function is implemented to print the population after each generation.

```
import pygad

def fitness_func(solution, solution_idx):
    return 0

def on_generation(ga):
    print("Generation", ga.generations_completed)
    print(ga.population)

ga_instance = pygad.GA(num_generations=5,
                       sol_per_pop=5,
                       num_genes=4,
                       mutation_num_genes=3,
                       random_mutation_min_val=-5,
                       random_mutation_max_val=5,
                       num_parents_mating=2,
                       fitness_func=fitness_func,
                       gene_type=int,
                       on_generation=on_generation,
                       allow_duplicate_genes=False)
ga_instance.run()
```

Here are the population after the 5 generations. Note how there are no duplicate values.

```
Generation 1
[[ 2 -2 -3  3]
 [ 0  1  2  3]
 [ 5 -3  6  3]
 [-3  1 -2  4]
 [-1  0 -2  3]]
Generation 2
[[-1  0 -2  3]
 [-3  1 -2  4]
 [ 0 -3 -2  6]
 [-3  0 -2  3]
 [ 1 -4  2  4]]
Generation 3
[[ 1 -4  2  4]
 [-3  0 -2  3]
 [ 4  0 -2  1]
 [-4  0 -2 -3]
```

```
 [-4  2  0  3]]
Generation 4
[[-4  2  0  3]
 [-4  0 -2 -3]
 [-2  5  4 -3]
 [-1  2 -4  4]
 [-4  2  0 -3]]
Generation 5
[[-4  2  0 -3]
 [-1  2 -4  4]
 [ 3  4 -4  0]
 [-1  0  2 -2]
 [-4  2 -1  1]]
```

The `allow_duplicate_genes` parameter is configured with use with the `gene_space` parameter. Here is an example where each of the 4 genes has the same space of values that consists of 4 values (1, 2, 3, and 4).

```python
import pygad

def fitness_func(solution, solution_idx):
    return 0

def on_generation(ga):
    print("Generation", ga.generations_completed)
    print(ga.population)

ga_instance = pygad.GA(num_generations=1,
                       sol_per_pop=5,
                       num_genes=4,
                       num_parents_mating=2,
                       fitness_func=fitness_func,
                       gene_type=int,
                       gene_space=[[1, 2, 3, 4], [1, 2, 3, 4], [1, 2, 3, 4], [1, 2,
                       on_generation=on_generation,
                       allow_duplicate_genes=False)
ga_instance.run()
```

Even that all the genes share the same space of values, no 2 genes duplicate their values as provided by the next output.

```
Generation 1
[[2 3 1 4]
 [2 3 1 4]
 [2 4 1 3]
 [2 3 1 4]
 [1 3 2 4]]
Generation 2
[[1 3 2 4]
 [2 3 1 4]
 [1 3 2 4]
 [2 3 4 1]
 [1 3 4 2]]
Generation 3
[[1 3 4 2]
 [2 3 4 1]
 [1 3 4 2]
 [3 1 4 2]
 [3 2 4 1]]
Generation 4
[[3 2 4 1]
 [3 1 4 2]
 [3 2 4 1]
 [1 2 4 3]
 [1 3 4 2]]
Generation 5
[[1 3 4 2]
 [1 2 4 3]
 [2 1 4 3]
```

```
 [1 2 4 3]
 [1 2 4 3]]
```

You should care of giving enough values for the genes so that PyGAD is able to find alternatives for the gene value in case it duplicates with another gene.

There might be 2 duplicate genes where changing either of the 2 duplicating genes will not solve the problem. For example, if `gene_space=[[3, 0, 1], [4, 1, 2], [0, 2], [3, 2, 0]]` and the solution is `[3 2 0 0]`, then the values of the last 2 genes duplicate. There are no possible changes in the last 2 genes to solve the problem.

This problem can be solved by randomly changing one of the non-duplicating genes that may make a room for a unique value in one the 2 duplicating genes. For example, by changing the second gene from 2 to 4, then any of the last 2 genes can take the value 2 and solve the duplicates. The resultant gene is then `[3 4 2 0]`. **But this option is not yet supported in PyGAD.**

# User-Defined Crossover, Mutation, and Parent Selection Operators

Previously, the user can select the the type of the crossover, mutation, and parent selection operators by assigning the name of the operator to the following parameters of the `pygad.GA` class's constructor:

1. `crossover_type`
2. `mutation_type`
3. `parent_selection_type`

This way, the user can only use the built-in functions for each of these operators.

Starting from PyGAD 2.16.0, the user can create a custom crossover, mutation, and parent selection operators and assign these functions to the above parameters. Thus, a new operator can be plugged easily into the PyGAD Lifecycle.

This is a sample code that does not use any custom function.

```python
import pygad
import numpy

equation_inputs = [4,-2,3.5]
desired_output = 44

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution * equation_inputs)
    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
    return fitness

ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=5,
                       num_parents_mating=2,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func)

ga_instance.run()
ga_instance.plot_fitness()
```

This section describes the expected input parameters and outputs. For simplicity, all of these custom functions all accept the instance of the `pygad.GA` class as the last parameter.

## User-Defined Crossover Operator



The user-defined crossover function is a Python function that accepts 3 parameters:

1. The selected parents.
2. The size of the offspring as a tuple of 2 numbers: (the offspring size, number of genes).
3. The instance from the `pygad.GA` class. This instance helps to retrieve any property like `population`, `gene_type`, `gene_space`, etc.

This function should return a NumPy array of shape equal to the value passed to the second parameter.

The next code creates a template for the user-defined crossover operator. You can use any names for the parameters. Note how a NumPy array is returned.

```
def crossover_func(parents, offspring_size, ga_instance):
    offspring = ...
    ...
    return numpy.array(offspring)
```

As an example, the next code creates a single-point crossover function. By randomly generating a random point (i.e. index of a gene), the function simply uses 2 parents to produce an offspring by copying the genes before the point from the first parent and the remaining from the second parent.

```
def crossover_func(parents, offspring_size, ga_instance):
    offspring = []
    idx = 0
    while len(offspring) != offspring_size[0]:
        parent1 = parents[idx % parents.shape[0], :].copy()
        parent2 = parents[(idx + 1) % parents.shape[0], :].copy()

        random_split_point = numpy.random.choice(range(offspring_size[1]))

        parent1[random_split_point:] = parent2[random_split_point:]

        offspring.append(parent1)

        idx += 1

    return numpy.array(offspring)
```

To use this user-defined function, simply assign its name to the `crossover_type` parameter in the constructor of the `pygad.GA` class. The next code gives an example. In this case, the custom function will be called in each generation rather than calling the built-in crossover functions defined in PyGAD.

```
ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=5,
                       num_parents_mating=2,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       crossover_type=crossover_func)
```

# User-Defined Mutation Operator

A user-defined mutation function/operator can be created the same way a custom crossover operator/function is created. Simply, it is a Python function that accepts 2 parameters:

1. The offspring to be mutated.
2. The instance from the `pygad.GA` class. This instance helps to retrieve any property like `population`, `gene_type`, `gene_space`, etc.

The template for the user-defined mutation function is given in the next code. According to the user preference, the function should make some random changes to the genes.

```
def mutation_func(offspring, ga_instance):
    ...
    return offspring
```

The next code builds the random mutation where a single gene from each chromosome is mutated by adding a random number between 0 and 1 to the gene's value.

```
def mutation_func(offspring, ga_instance):

    for chromosome_idx in range(offspring.shape[0]):
        random_gene_idx = numpy.random.choice(range(offspring.shape[0]))

        offspring[chromosome_idx, random_gene_idx] += numpy.random.random()

    return offspring
```

Here is how this function is assigned to the `mutation_type` parameter.

```
ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=5,
                       num_parents_mating=2,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       crossover_type=crossover_func,
                       mutation_type=mutation_func)
```

Note that there are other things to take into consideration like:

- Making sure that each gene conforms to the data type(s) listed in the `gene_type` parameter.
- If the `gene_space` parameter is used, then the new value for the gene should conform to the values/ranges listed.
- Mutating a number of genes that conforms to the parameters `mutation_percent_genes`, `mutation_probability`, and `mutation_num_genes`.
- Whether mutation happens with or without replacement based on the `mutation_by_replacement` parameter.
- The minimum and maximum values from which a random value is generated based on the `random_mutation_min_val` and `random_mutation_max_val` parameters.
- Whether duplicates are allowed or not in the chromosome based on the `allow_duplicate_genes` parameter.

and more.

It all depends on your objective from building the mutation function. You may neglect or consider some of the considerations according to your objective.

# User-Defined Parent Selection Operator

No much to mention about building a user-defined parent selection function as things are similar to building a crossover or mutation function. Just create a Python function that accepts 3 parameters:

1. The fitness values of the current population.
2. The number of parents needed.
3. The instance from the `pygad.GA` class. This instance helps to retrieve any property like `population`, `gene_type`, `gene_space`, etc.

The function should return 2 outputs:

1. The selected parents as a NumPy array. Its shape is equal to (the number of selected parents, `num_genes`). Note that the number of selected parents is equal to the value assigned to the second input parameter.
2. The indices of the selected parents inside the population. It is a 1D list with length equal to the number of selected parents.



Here is a template for building a custom parent selection function.

```
def parent_selection_func(fitness, num_parents, ga_instance):
    ...
    return parents, fitness_sorted[:num_parents]
```

The next code builds the steady-state parent selection where the best parents are selected. The number of parents is equal to the value in the `num_parents` parameter.

```
def parent_selection_func(fitness, num_parents, ga_instance):

    fitness_sorted = sorted(range(len(fitness)), key=lambda k: fitness[k])
    fitness_sorted.reverse()

    parents = numpy.empty((num_parents, ga_instance.population.shape[1]))

    for parent_num in range(num_parents):
        parents[parent_num, :] = ga_instance.population[fitness_sorted[parent_num],

    return parents, fitness_sorted[:num_parents]
```

Finally, the defined function is assigned to the `parent_selection_type` parameter as in the next code.

```
ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=5,
                       num_parents_mating=2,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       crossover_type=crossover_func,
                       mutation_type=mutation_func,
                       parent_selection_type=parent_selection_func)
```

# Example

By discussing how to customize the 3 operators, the next code uses the previous 3 user-defined functions instead of the built-in functions.

```
import pygad
import numpy

equation_inputs = [4,-2,3.5]
desired_output = 44

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution * equation_inputs)

    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)

    return fitness

def parent_selection_func(fitness, num_parents, ga_instance):

    fitness_sorted = sorted(range(len(fitness)), key=lambda k: fitness[k])
    fitness_sorted.reverse()

    parents = numpy.empty((num_parents, ga_instance.population.shape[1]))

    for parent_num in range(num_parents):
        parents[parent_num, :] = ga_instance.population[fitness_sorted[parent_num],

    return parents, fitness_sorted[:num_parents]

def crossover_func(parents, offspring_size, ga_instance):

    offspring = []
    idx = 0
    while len(offspring) != offspring_size[0]:
        parent1 = parents[idx % parents.shape[0], :].copy()
```

```
        parent2 = parents[(idx + 1) % parents.shape[0], :].copy()

        random_split_point = numpy.random.choice(range(offspring_size[1]))

        parent1[random_split_point:] = parent2[random_split_point:]

        offspring.append(parent1)

        idx += 1

    return numpy.array(offspring)

def mutation_func(offspring, ga_instance):

    for chromosome_idx in range(offspring.shape[0]):
        random_gene_idx = numpy.random.choice(range(offspring.shape[0]))

        offspring[chromosome_idx, random_gene_idx] += numpy.random.random()

    return offspring

ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=5,
                       num_parents_mating=2,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       crossover_type=crossover_func,
                       mutation_type=mutation_func,
                       parent_selection_type=parent_selection_func)

ga_instance.run()
ga_instance.plot_fitness()
```

# More about the `gene_space` Parameter

The `gene_space` parameter customizes the space of values of each gene.

Assuming that all genes have the same global space which include the values 0.3, 5.2, -4, and 8, then those values can be assigned to the `gene_space` parameter as a list, tuple, or range. Here is a list assigned to this parameter. By doing that, then the gene values are restricted to those assigned to the `gene_space` parameter.

```
gene_space = [0.3, 5.2, -4, 8]
```

If some genes have different spaces, then `gene_space` should accept a nested list or tuple. In this case, the elements could be:

1. Number (of `int`, `float`, or `NumPy` data types): A single value to be assigned to the gene. This means this gene will have the same value across all generations.
2. `list`, `tuple`, `numpy.ndarray`, or any range like `range`, `numpy.arange()`, or `numpy.linspace`: It holds the space for each individual gene. But this space is usually discrete. That is there is a set of finite values to select from.
3. `dict`: To sample a value for a gene from a continuous range. The dictionary must have 2 mandatory keys which are `"low"` and `"high"` in addition to an optional key which is `"step"`. A random value is returned between the values assigned to the items with `"low"` and `"high"` keys. If the `"step"` exists, then this works as the previous options (i.e. discrete set of values).
4. `None`: A gene with its space set to `None` is initialized randomly from the range specified by the 2 parameters `init_range_low` and `init_range_high`. For mutation, its value is mutated based on a random value from the range specified by the 2 parameters `random_mutation_min_val` and `random_mutation_max_val`. If all elements in the `gene_space` parameter are `None`, the parameter will not have any effect.

Assuming that a chromosome has 2 genes and each gene has a different value space. Then the gene_space could be assigned a nested list/tuple where each element determines the space of a gene.

According to the next code, the space of the first gene is [0.4, -5] which has 2 values and the space for the second gene is [0.5, -3.2, 8.8, -9] which has 4 values.

```
gene_space = [[0.4, -5], [0.5, -3.2, 8.2, -9]]
```

For a 2 gene chromosome, if the first gene space is restricted to the discrete values from 0 to 4 and the second gene is restricted to the values from 10 to 19, then it could be specified according to the next code.

```
gene_space = [range(5), range(10, 20)]
```

The gene_space can also be assigned to a single range, as given below, where the values of all genes are sampled from the same range.

```
gene_space = numpy.arange(15)
```

The gene_space can be assigned a dictionary to sample a value from a continuous range.

```
gene_space = {"low": 4, "high": 30}
```

A step also can be assigned to the dictionary. This works as if a range is used.

```
gene_space = {"low": 4, "high": 30, "step": 2.5}
```

If a None is assigned to only a single gene, then its value will be randomly generated initially using the init_range_low and init_range_high parameters in the pygad.GA class's constructor. During mutation, the value are sampled from the range defined by the 2 parameters random_mutation_min_val and random_mutation_max_val. This is an example where the second gene is given a None value.

```
gene_space = [range(5), None, numpy.linspace(10, 20, 300)]
```

If the user did not assign the initial population to the initial_population parameter, the initial population is created randomly based on the gene_space parameter. Moreover, the mutation is applied based on this parameter.

# More about the gene_type Parameter

The gene_type parameter allows the user to control the data type for all genes at once or each individual gene. In PyGAD 2.15.0, the gene_type parameter also supports customizing the precision for float data types. As a result, the gene_type parameter helps to:

1. Select a data type for all genes with or without precision.
2. Select a data type for each individual gene with or without precision.

Let's discuss things by examples.

## Data Type for All Genes without Precision

The data type for all genes can be specified by assigning the numeric data type directly to the gene_type parameter. This is an example to make all genes of int data types.

```
gene_type=int
```

Given that the supported numeric data types of PyGAD include Python's int and float in addition to all numeric types of NumPy, then any of these types can be assigned to the gene_type parameter.

If no precision is specified for a `float` data type, then the complete floating-point number is kept.

The next code uses an `int` data type for all genes where the genes in the initial and final population are only integers.

```
import pygad
import numpy

equation_inputs = [4, -2, 3.5, 8, -2]
desired_output = 2671.1234

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution * equation_inputs)
    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
    return fitness

ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=5,
                       num_parents_mating=2,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       gene_type=int)

print("Initial Population")
print(ga_instance.initial_population)

ga_instance.run()

print("Final Population")
print(ga_instance.population)
```

```
Initial Population
[[ 1 -1  2  0 -3]
 [ 0 -2  0 -3 -1]
 [ 0 -1 -1  2  0]
 [-2  3 -2  3  3]
 [ 0  0  2 -2 -2]]

Final Population
[[ 1 -1  2  2  0]
 [ 1 -1  2  2  0]
 [ 1 -1  2  2  0]
 [ 1 -1  2  2  0]
 [ 1 -1  2  2  0]]
```

# Data Type for All Genes with Precision

A precision can only be specified for a `float` data type and cannot be specified for integers. Here is an example to use a precision of 3 for the `numpy.float` data type. In this case, all genes are of type `numpy.float` and their maximum precision is 3.

```
gene_type=[numpy.float, 3]
```

The next code uses prints the initial and final population where the genes are of type `float` with precision 3.

```
import pygad
import numpy

equation_inputs = [4, -2, 3.5, 8, -2]
desired_output = 2671.1234

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution * equation_inputs)
    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
```

```
    return fitness

ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=5,
                       num_parents_mating=2,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       gene_type=[float, 3])

print("Initial Population")
print(ga_instance.initial_population)

ga_instance.run()

print("Final Population")
print(ga_instance.population)
```

```
Initial Population
[[-2.417 -0.487  3.623  2.457 -2.362]
 [-1.231  0.079 -1.63   1.629 -2.637]
 [ 0.692 -2.098  0.705  0.914 -3.633]
 [ 2.637 -1.339 -1.107 -0.781 -3.896]
 [-1.495  1.378 -1.026  3.522  2.379]]

Final Population
[[ 1.714 -1.024  3.623  3.185 -2.362]
 [ 0.692 -1.024  3.623  3.185 -2.362]
 [ 0.692 -1.024  3.623  3.375 -2.362]
 [ 0.692 -1.024  4.041  3.185 -2.362]
 [ 1.714 -0.644  3.623  3.185 -2.362]]
```

# Data Type for each Individual Gene without Precision

In PyGAD 2.14.0, the `gene_type` parameter allows customizing the gene type for each individual gene. This is by using a `list`/`tuple`/`numpy.ndarray` with number of elements equal to the number of genes. For each element, a type is specified for the corresponding gene.

This is an example for a 5-gene problem where different types are assigned to the genes.

```
gene_type=[int, float, numpy.float16, numpy.int8, numpy.float]
```

This is a complete code that prints the initial and final population for a custom-gene data type.

```
import pygad
import numpy

equation_inputs = [4, -2, 3.5, 8, -2]
desired_output = 2671.1234

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution * equation_inputs)
    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
    return fitness

ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=5,
                       num_parents_mating=2,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       gene_type=[int, float, numpy.float16, numpy.int8, numpy.float

print("Initial Population")
print(ga_instance.initial_population)

ga_instance.run()
```

```
print("Final Population")
print(ga_instance.population)
```

```
Initial Population
[[0 0.8615522360026828 0.7021484375 -2 3.5301821368185866]
 [-3 2.648189378595294 -3.830078125 1 -0.9586271572917742]
 [3 3.7729827570110714 1.2529296875 -3 1.395741994211889]
 [0 1.0490687178053282 1.51953125 -2 0.7243617940450235]
 [0 -0.6550158436937226 -2.861328125 -2 1.8212734549263097]]

Final Population
[[3 3.7729827570110714 2.055 0 0.7243617940450235]
 [3 3.7729827570110714 1.458 0 -0.14638754050305036]
 [3 3.7729827570110714 1.458 0 0.0869406120516778]
 [3 3.7729827570110714 1.458 0 0.7243617940450235]
 [3 3.7729827570110714 1.458 0 -0.14638754050305036]]
```

# Data Type for each Individual Gene with Precision

The precision can also be specified for the `float` data types as in the next line where the second gene precision is 2 and last gene precision is 1.

```
gene_type=[int, [float, 2], numpy.float16, numpy.int8, [numpy.float, 1]]
```

This is a complete example where the initial and final populations are printed where the genes comply with the data types and precisions specified.

```
import pygad
import numpy

equation_inputs = [4, -2, 3.5, 8, -2]
desired_output = 2671.1234

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution * equation_inputs)
    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
    return fitness

ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=5,
                       num_parents_mating=2,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       gene_type=[int, [float, 2], numpy.float16, numpy.int8, [numpy

print("Initial Population")
print(ga_instance.initial_population)

ga_instance.run()

print("Final Population")
print(ga_instance.population)
```

```
Initial Population
[[-2 -1.22 1.716796875 -1 0.2]
 [-1 -1.58 -3.091796875 0 -1.3]
 [3 3.35 -0.107421875 1 -3.3]
 [-2 -3.58 -1.779296875 0 0.6]
 [2 -3.73 2.65234375 3 -0.5]]

Final Population
[[2 -4.22 3.47 3 -1.3]
 [2 -3.73 3.47 3 -1.3]
 [2 -4.22 3.47 2 -1.3]
```

```
    [2 -4.58 3.47 3 -1.3]
    [2 -3.73 3.47 3 -1.3]]
```

# Visualization in PyGAD

This section discusses the different options to visualize the results in PyGAD through these methods:

1. `plot_fitness()`
2. `plot_genes()`
3. `plot_new_solution_rate()`

In the following code, the `save_solutions` flag is set to `True` which means all solutions are saved in the `solutions` attribute. The code runs for only 10 generations.

```
import pygad
import numpy

equation_inputs = [4, -2, 3.5, 8, -2, 3.5, 8]
desired_output = 2671.1234

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution * equation_inputs)
    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
    return fitness

ga_instance = pygad.GA(num_generations=10,
                       sol_per_pop=10,
                       num_parents_mating=5,
                       num_genes=len(equation_inputs),
                       fitness_func=fitness_func,
                       gene_space=[range(1, 10), range(10, 20), range(15, 30), range
                       gene_type=int,
                       save_solutions=True)

ga_instance.run()
```

Let's explore how to visualize the results by the above mentioned methods.

## `plot_fitness()`

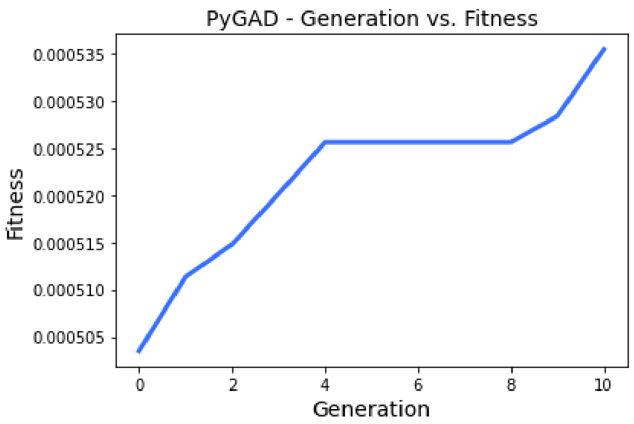
The `plot_fitness()` method shows the fitness value for each generation.

### `plot_type="plot"`

The simplest way to call this method is as follows leaving the `plot_type` with its default value `"plot"` to create a continuous line connecting the fitness values across all generations:

```
ga_instance.plot_fitness()
# ga_instance.plot_fitness(plot_type="plot")
```

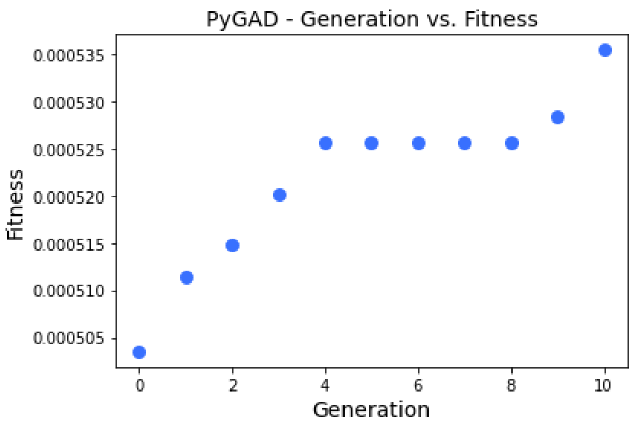
v: latest




## plot_type="scatter"

The `plot_type` can also be set to `"scatter"` to create a scatter graph with each individual fitness represented as a dot. The size of these dots can be changed using the `linewidth` parameter.

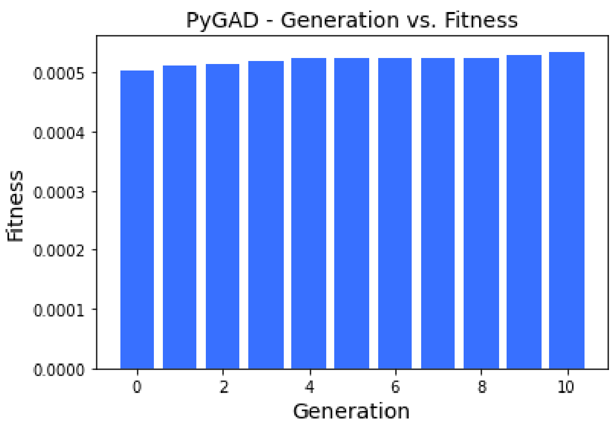
```
ga_instance.plot_fitness(plot_type="scatter")
```




## plot_type="bar"

The third value for the `plot_type` parameter is `"bar"` to create a bar graph with each individual fitness represented as a bar.

```
ga_instance.plot_fitness(plot_type="bar")
```




v: latest

# plot_new_solution_rate()

The `plot_new_solution_rate()` method presents the number of new solutions explored in each generation. This helps to figure out if the genetic algorithm is able to find new solutions as an indication of more possible evolution. If no new solutions are explored, this is an indication that no further evolution is possible.

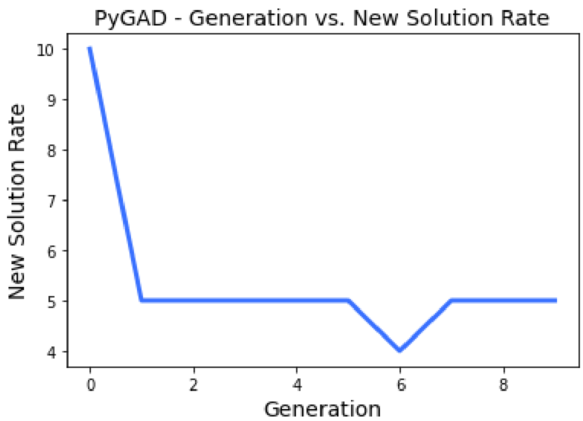
The `plot_new_solution_rate()` method accepts the same parameters as in the `plot_fitness()` method with 3 possible values for `plot_type` parameter.

## `plot_type="plot"`

The default value for the `plot_type` parameter is `"plot"`.

```
ga_instance.plot_new_solution_rate()
# ga_instance.plot_new_solution_rate(plot_type="plot")
```

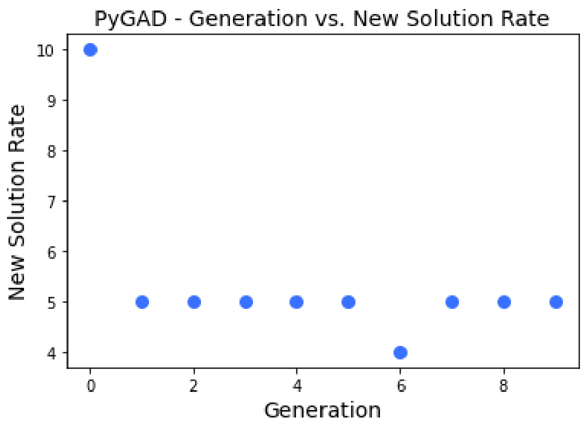
The next figure shows that, for example, generation 6 has the least number of new solutions which is 4. The number of new solutions in the first generation is always equal to the number of solutions in the population (i.e. the value assigned to the `sol_per_pop` parameter in the constructor of the `pygad.GA` class) which is 10 in this example.




## `plot_type="scatter"`

The previous graph can be represented as scattered points by setting `plot_type="scatter"`.

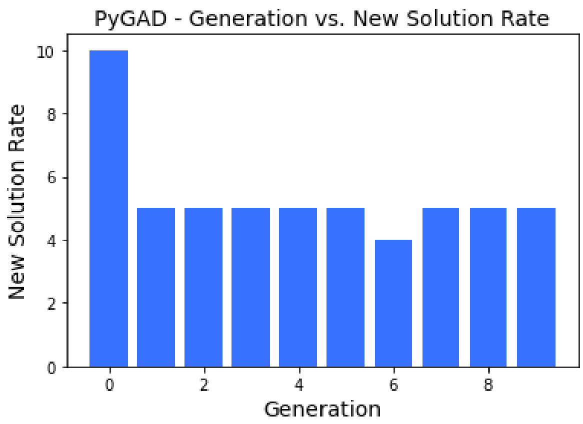
```
ga_instance.plot_new_solution_rate(plot_type="scatter")
```




## `plot_type="bar"`

By setting `plot_type="scatter"`, each value is represented as a vertical bar.

```python
ga_instance.plot_new_solution_rate(plot_type="bar")
```




# `plot_genes()`

The `plot_genes()` method is the third option to visualize the PyGAD results. This method has 3 control variables:

1. `graph_type="plot"`: Can be `"plot"` (default), `"boxplot"`, or `"histogram"`.
2. `plot_type="plot"`: Identical to the `plot_type` parameter explored in the `plot_fitness()` and `plot_new_solution_rate()` methods.
3. `solutions="all"`: Can be `"all"` (default) or `"best"`.

These 3 parameters controls the style of the output figure.

The `graph_type` parameter selects the type of the graph which helps to explore the gene values as:

1. A normal plot.
2. A histogram.
3. A box and whisker plot.

The `plot_type` parameter works only when the type of the graph is set to `"plot"`.

The `solutions` parameter selects whether the genes come from **all** solutions in the population or from just the **best** solutions.

## `graph_type="plot"`

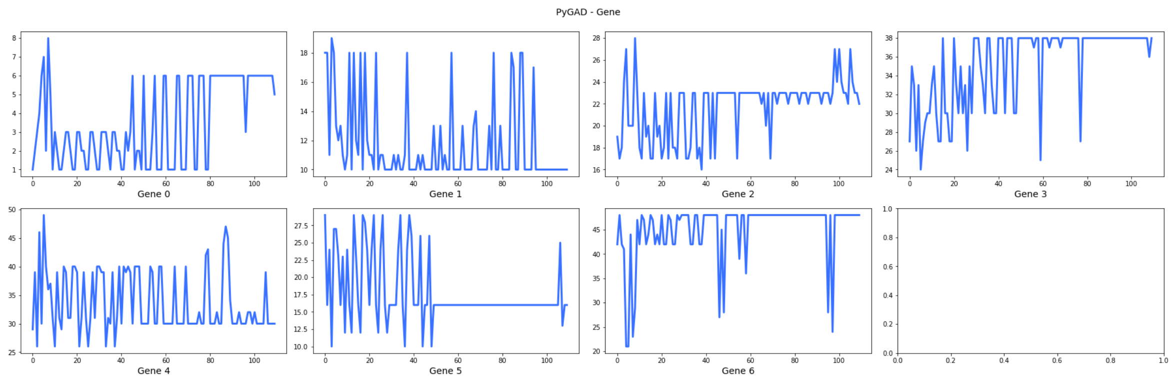
When `graph_type="plot"`, then the figure creates a normal graph where the relationship between the gene values and the generation numbers is represented as a continuous plot, scattered points, or bars.

### `plot_type="plot"`

Because the default value for both `graph_type` and `plot_type` is `"plot"`, then all of the lines below creates the same figure. This figure is helpful to know whether a gene value lasts for more generations as an indication of the best value for this gene. For example, the value 16 for the gene with index 5 (at column 2 and row 2 of the next graph) lasted for 83 generations.

```python
ga_instance.plot_genes()

ga_instance.plot_genes(graph_type="plot")

ga_instance.plot_genes(plot_type="plot")

ga_instance.plot_genes(graph_type="plot",
                       plot_type="plot")
```

v: latest



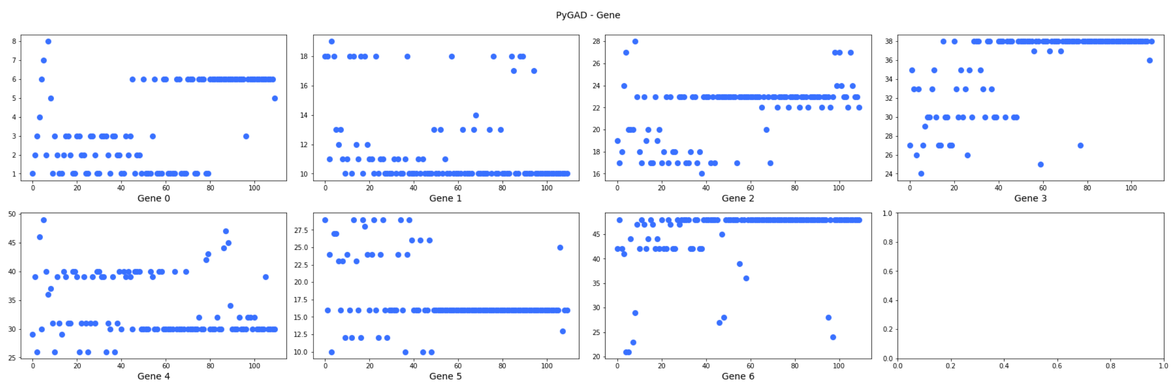

As the default value for the `solutions` parameter is `"all"`, then the following method calls generate the same plot.

```
ga_instance.plot_genes(solutions="all")

ga_instance.plot_genes(graph_type="plot",
                       solutions="all")

ga_instance.plot_genes(plot_type="plot",
                       solutions="all")

ga_instance.plot_genes(graph_type="plot",
                       plot_type="plot",
                       solutions="all")
```

## `plot_type="scatter"`

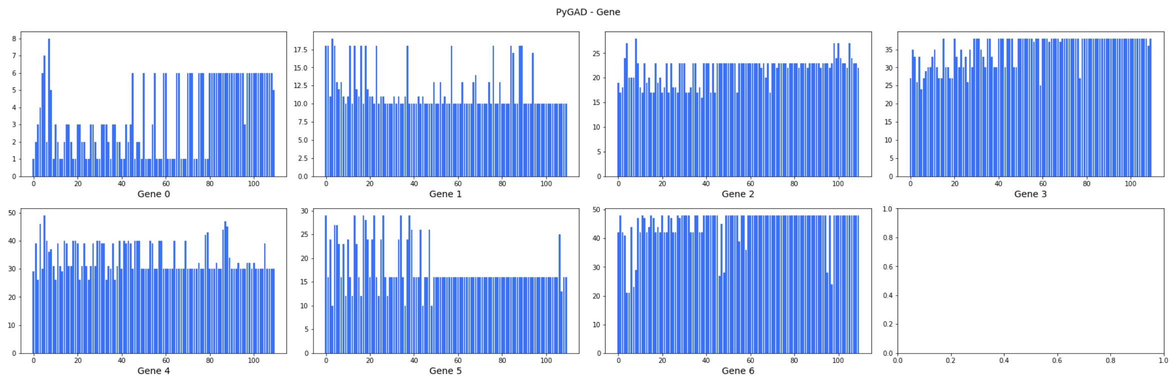
The following calls of the `plot_genes()` method create the same scatter plot.

```
ga_instance.plot_genes(plot_type="scatter")

ga_instance.plot_genes(graph_type="plot",
                       plot_type="scatter",
                       solutions='all')
```




## `plot_type="bar"`

```
ga_instance.plot_genes(plot_type="bar")

ga_instance.plot_genes(graph_type="plot",
                       plot_type="bar",
                       solutions='all')
```

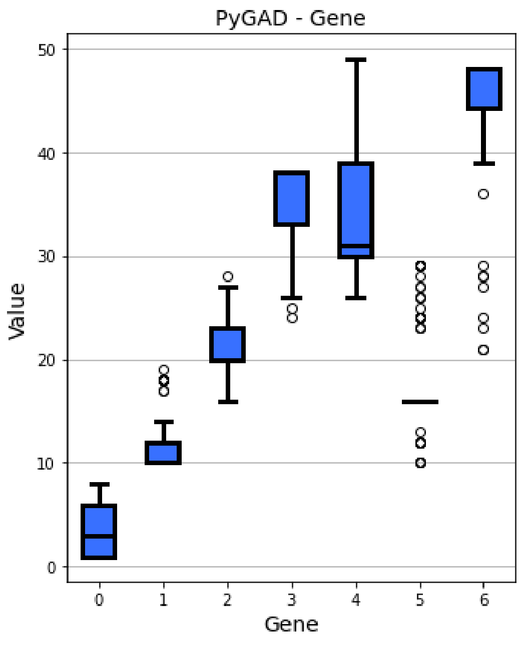



## graph_type="boxplot"

By setting `graph_type` to `"boxplot"`, then a box and whisker graph is created. Now, the `plot_type` parameter has no effect.

The following 2 calls of the `plot_genes()` method create the same figure as the default value for the `solutions` parameter is `"all"`.

```
ga_instance.plot_genes(graph_type="boxplot")

ga_instance.plot_genes(graph_type="boxplot",
                       solutions='all')
```



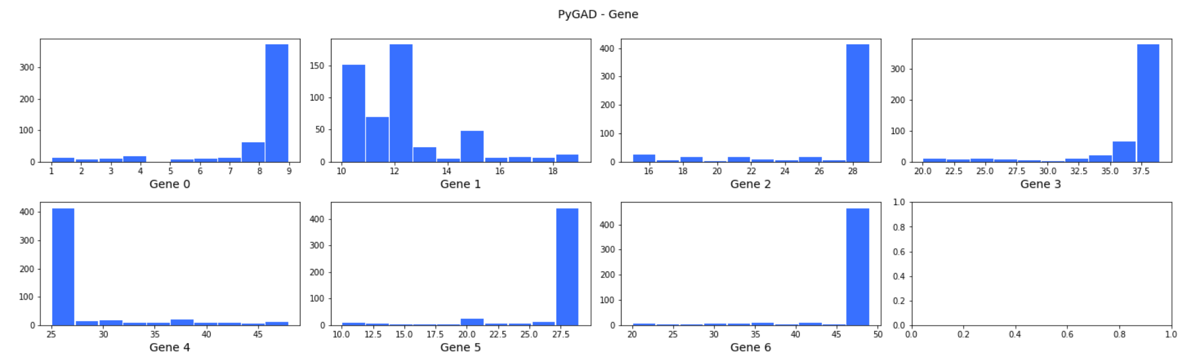

## graph_type="histogram"

For `graph_type="boxplot"`, then a histogram is created for each gene. Similar to `graph_type="boxplot"`, the `plot_type` parameter has no effect.

The following 2 calls of the `plot_genes()` method create the same figure as the default value for the `solutions` parameter is `"all"`.

```
ga_instance.plot_genes(graph_type="histogram")

ga_instance.plot_genes(graph_type="histogram",
                       solutions='all')
```

v: latest




All the previous figures can be created for only the best solutions by setting `solutions="best"`.

# Parallel Processing in PyGAD

Starting from PyGAD 2.17.0, parallel processing becomes supported. This section explains how to use parallel processing in PyGAD.

According to the PyGAD lifecycle, parallel processing can be parallelized in only 2 operations:

1. Population fitness calculation.
2. Mutation.

The reason is that the calculations in these 2 operations are independent (i.e. each solution/chromosome is handled independently from the others) and can be distributed across different processes or threads.

For the mutation operation, it does not do intensive calculations on the CPU. Its calculations are simple like flipping the values of some genes from 0 to 1 or adding a random value to some genes. So, it does not take much CPU processing time. Experiments proved that parallelizing the mutation operation across the solutions increases the time instead of reducing it. This is because running multiple processes or threads adds overhead to manage them. Thus, parallel processing cannot be applied on the mutation operation.

For the population fitness calculation, parallel processing can help make a difference and reduce the processing time. But this is **conditional** on the type of calculations done in the fitness function. If the fitness function makes intensive calculations and takes much processing time from the CPU, then it is probably that parallel processing will help to cut down the overall time.

This section explains how parallel processing works in PyGAD and how to use parallel processing in PyGAD

## How to Use Parallel Processing in PyGAD

Starting from PyGAD 2.17.0, a new parameter called `parallel_processing` added to the constructor of the `pygad.GA` class.

```
import pygad
...
ga_instance = pygad.GA(...,
                       parallel_processing=...)
...
```

This parameter allows the user to do the following:

1. Enable parallel processing.
2. Select whether processes or threads are used.
3. Specify the number of processes or threads to be used.

These are 3 possible values for the `parallel_processing` parameter:

1. ``None``: (Default) It means no parallel processing is used.
2. A positive integer referring to the number of **threads** to be used (i.e. threads, not processes, are used.
3. `list`/`tuple`: If a list or a tuple of exactly 2 elements is assigned, then:
    1. The first element can be either `'process'` or `'thread'` to specify whether processes or threads are used, respectively.
    2. The second element can be:
        1. A positive integer to select the maximum number of processes or threads to be used
        2. ``0`` to indicate that 0 processes or threads are used. It means no parallel processing. This is identical to setting `parallel_processing=None`.
        3. ``None`` to use the default value as calculated by the `concurrent.futures module`.

These are examples of the values assigned to the `parallel_processing` parameter:

- `parallel_processing=4`: Because the parameter is assigned a positive integer, this means parallel processing is activated where 4 threads are used.
- `parallel_processing=["thread", 5]`: Use parallel processing with 5 threads. This is identical to `parallel_processing=5`.
- `parallel_processing=["process", 8]`: Use parallel processing with 8 processes.
- `parallel_processing=["process", 0]`: As the second element is given the value 0, this means do not use parallel processing. This is identical to `parallel_processing=None`.

# Examples

The examples will help you know the difference between using processes and threads. Moreover, it will give an idea when parallel processing would make a difference and reduce the time. These are dummy examples where the fitness function is made to always return 0.

The first example uses 10 genes, 5 solutions in the population where only 3 solutions mate, and 9999 generations. The fitness function uses a `for` loop with 100 iterations just to have some calculations. In the constructor of the `pygad.GA` class, `parallel_processing=None` means no parallel processing is used.

```
import pygad
import time

def fitness_func(solution, solution_idx):
    for _ in range(99):
        pass
    return 0

ga_instance = pygad.GA(num_generations=9999,
                       num_parents_mating=3,
                       sol_per_pop=5,
                       num_genes=10,
                       fitness_func=fitness_func,
                       suppress_warnings=True,
                       parallel_processing=None)

if __name__ == '__main__':
    t1 = time.time()

    ga_instance.run()

    t2 = time.time()
    print("Time is", t2-t1)
```

When parallel processing is not used, the time it takes to run the genetic algorithm is `1.5` seconds.

In the comparison, let's do a second experiment where parallel processing is used with 5 threads. In this case, it take `5` seconds.

```
...
ga_instance = pygad.GA(...,
                       parallel_processing=5)
...
```

For the third experiment, processes instead of threads are used. Also, only 99 generations are used instead of 9999. The time it takes is `99` seconds.

```
...
ga_instance = pygad.GA(num_generations=99,
                       ...,
                       parallel_processing=["process", 5])
...
```

This is the summary of the 3 experiments:

1. No parallel processing & 9999 generations: 1.5 seconds.
2. Parallel processing with 5 threads & 9999 generations: 5 seconds
3. Parallel processing with 5 processes & 99 generations: 99 seconds

Because the fitness function does not need much CPU time, the normal processing takes the least time. Running processes for this simple problem takes 99 compared to only 5 seconds for threads because managing processes is much heavier than managing threads. Thus, most of the CPU time is for swapping the processes instead of executing the code.

In the second example, the loop makes 99999999 iterations and only 5 generations are used. With no parallelization, it takes 22 seconds.

```
import pygad
import time

def fitness_func(solution, solution_idx):
    for _ in range(99999999):
        pass
    return 0

ga_instance = pygad.GA(num_generations=5,
                       num_parents_mating=3,
                       sol_per_pop=5,
                       num_genes=10,
                       fitness_func=fitness_func,
                       suppress_warnings=True,
                       parallel_processing=None)

if __name__ == '__main__':
    t1 = time.time()
    ga_instance.run()
    t2 = time.time()
    print("Time is", t2-t1)
```

It takes 15 seconds when 10 processes are used.

```
...
ga_instance = pygad.GA(...,
                       parallel_processing=["process", 10])
...
```

This is compared to 20 seconds when 10 threads are used.

```
...
ga_instance = pygad.GA(...,
                       parallel_processing=["thread", 10])
...
```

Based on the second example, using parallel processing with 10 processes takes the least time because there is much CPU work done. Generally, processes are preferred over threads when most of the work in on the CPU. Threads are preferred over processes in some situations like doing input/output operations.

*Before releasing*PyGAD 2.17.0,László Fazekas*wrote an article to parallelize the fitness function with PyGAD. Check it:* How Genetic Algorithms Can Compete with Gradient Descent and Backprop.

# Examples

This section gives the complete code of some examples that use `pygad`. Each subsection builds a different example.

## Linear Model Optimization

This example is discussed in the Steps to Use PyGAD section which optimizes a linear model. Its complete code is listed below.

```
import pygad
import numpy

"""
Given the following function:
    y = f(w1:w6) = w1x1 + w2x2 + w3x3 + w4x4 + w5x5 + 6wx6
    where (x1,x2,x3,x4,x5,x6)=(4,-2,3.5,5,-11,-4.7) and y=44
What are the best values for the 6 weights (w1 to w6)? We are going to use the genet
"""

function_inputs = [4,-2,3.5,5,-11,-4.7] # Function inputs.
desired_output = 44 # Function output.

def fitness_func(solution, solution_idx):
    output = numpy.sum(solution*function_inputs)
    fitness = 1.0 / (numpy.abs(output - desired_output) + 0.000001)
    return fitness

num_generations = 100 # Number of generations.
num_parents_mating = 10 # Number of solutions to be selected as parents in the matin

sol_per_pop = 20 # Number of solutions in the population.
num_genes = len(function_inputs)

last_fitness = 0
def on_generation(ga_instance):
    global last_fitness
    print("Generation = {generation}".format(generation=ga_instance.generations_comp
    print("Fitness    = {fitness}".format(fitness=ga_instance.best_solution(pop_fitn
    print("Change     = {change}".format(change=ga_instance.best_solution(pop_fitnes
    last_fitness = ga_instance.best_solution(pop_fitness=ga_instance.last_generation

ga_instance = pygad.GA(num_generations=num_generations,
                       num_parents_mating=num_parents_mating,
                       sol_per_pop=sol_per_pop,
                       num_genes=num_genes,
                       fitness_func=fitness_func,
                       on_generation=on_generation)

# Running the GA to optimize the parameters of the function.
ga_instance.run()

ga_instance.plot_fitness()

# Returning the details of the best solution.
solution, solution_fitness, solution_idx = ga_instance.best_solution(ga_instance.las
print("Parameters of the best solution : {solution}".format(solution=solution))
print("Fitness value of the best solution = {solution_fitness}".format(solution_fitn
print("Index of the best solution : {solution_idx}".format(solution_idx=solution_idx
```

```
prediction = numpy.sum(numpy.array(function_inputs)*solution)
print("Predicted output based on the best solution : {prediction}".format(predictior

if ga_instance.best_solution_generation != -1:
    print("Best fitness value reached after {best_solution_generation} generations."

# Saving the GA instance.
filename = 'genetic' # The filename to which the instance is saved. The name is witł
ga_instance.save(filename=filename)

# Loading the saved GA instance.
loaded_ga_instance = pygad.load(filename=filename)
loaded_ga_instance.plot_fitness()
```

# Reproducing Images

This project reproduces a single image using PyGAD by evolving pixel values. This project works with both color and gray images. Check this project at GitHub: https://github.com/ahmedfgad/GARI.

For more information about this project, read this tutorial titled Reproducing Images using a Genetic Algorithm with Python available at these links:

- Heartbeat: https://heartbeat.fritz.ai/reproducing-images-using-a-genetic-algorithm-with-python-91fc701ff84
- LinkedIn: https://www.linkedin.com/pulse/reproducing-images-using-genetic-algorithm-python-ahmed-gad

## Project Steps

The steps to follow in order to reproduce an image are as follows:

- Read an image
- Prepare the fitness function
- Create an instance of the pygad.GA class with the appropriate parameters
- Run PyGAD
- Plot results
- Calculate some statistics

The next sections discusses the code of each of these steps.

## Read an Image

There is an image named `fruit.jpg` in the GARI project which is read according to the next code.

```
import imageio
import numpy

target_im = imageio.imread('fruit.jpg')
target_im = numpy.asarray(target_im/255, dtype=numpy.float)
```

Here is the read image.

Based on the chromosome representation used in the example, the pixel values can be either in the 0-255, 0-1, or any other ranges.

Note that the range of pixel values affect other parameters like the range from which the random values are selected during mutation and also the range of the values used in the initial population. So, be consistent.

## Prepare the Fitness Function

The next code creates a function that will be used as a fitness function for calculating the fitness value for each solution in the population. This function must be a maximization function that accepts 2 parameters representing a solution and its index. It returns a value representing the fitness value.

```
import gari

target_chromosome = gari.img2chromosome(target_im)

def fitness_fun(solution, solution_idx):
    fitness = numpy.sum(numpy.abs(target_chromosome-solution))

    # Negating the fitness value to make it increasing rather than decreasing.
    fitness = numpy.sum(target_chromosome) - fitness
    return fitness
```

The fitness value is calculated using the sum of absolute difference between genes values in the original and reproduced chromosomes. The `gari.img2chromosome()` function is called before the fitness function to represent the image as a vector because the genetic algorithm can work with 1D chromosomes.

The implementation of the `gari` module is available at the GARI GitHub project and its code is listed below.

```
import numpy
import functools
import operator

def img2chromosome(img_arr):
    return numpy.reshape(a=img_arr, newshape=(functools.reduce(operator.mul, img_arr

def chromosome2img(vector, shape):
    if len(vector) != functools.reduce(operator.mul, shape):
        raise ValueError("A vector of length {vector_length} into an array of shape

    return numpy.reshape(a=vector, newshape=shape)
```

## Create an Instance of the `pygad.GA` Class

It is very important to use random mutation and set the `mutation_by_replacement` to `True`. Based on the range of pixel values, the values assigned to the `init_range_low`, `init_range_high`, `random_mutation_min_val`, and `random_mutation_max_val` parameters should be changed.

If the image pixel values range from 0 to 255, then set `init_range_low` and `random_mutation_min_val` to 0 as they are but change `init_range_high` and `random_mutation_max_val` to 255.

Feel free to change the other parameters or add other parameters. Please check the PyGAD's documentation for the full list of parameters.

```
import pygad

ga_instance = pygad.GA(num_generations=20000,
                       num_parents_mating=10,
                       fitness_func=fitness_fun,
                       sol_per_pop=20,
```

```python
                            num_genes=target_im.size,
                            init_range_low=0.0,
                            init_range_high=1.0,
                            mutation_percent_genes=0.01,
                            mutation_type="random",
                            mutation_by_replacement=True,
                            random_mutation_min_val=0.0,
                            random_mutation_max_val=1.0)
```

## Run PyGAD

Simply, call the `run()` method to run PyGAD.

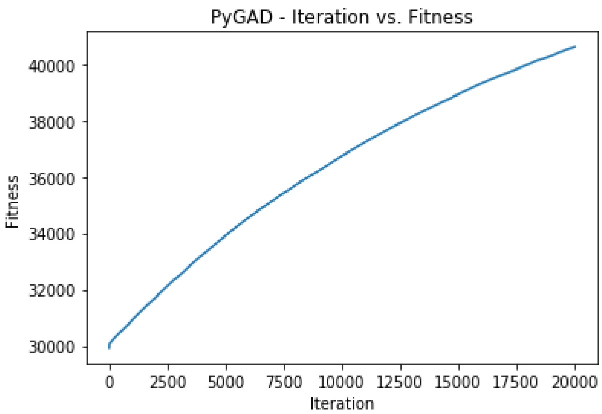
```python
ga_instance.run()
```

## Plot Results

After the `run()` method completes, the fitness values of all generations can be viewed in a plot using the `plot_fitness()` method.

```python
ga_instance.plot_fitness()
```

Here is the plot after 20,000 generations.




## Calculate Some Statistics

Here is some information about the best solution.

```python
# Returning the details of the best solution.
solution, solution_fitness, solution_idx = ga_instance.best_solution()
print("Fitness value of the best solution = {solution_fitness}".format(solution_fitr
print("Index of the best solution : {solution_idx}".format(solution_idx=solution_idx

if ga_instance.best_solution_generation != -1:
    print("Best fitness value reached after {best_solution_generation} generations."

result = gari.chromosome2img(solution, target_im.shape)
matplotlib.pyplot.imshow(result)
matplotlib.pyplot.title("PyGAD & GARI for Reproducing Images")
matplotlib.pyplot.show()
```

## Evolution by Generation

The solution reached after the 20,000 generations is shown below.

v: latest

After more generations, the result can be enhanced like what shown below.

The results can also be enhanced by changing the parameters passed to the constructor of the `pygad.GA` class.

Here is how the image is evolved from generation 0 to generation 20,000s.

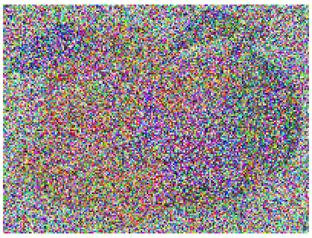
**Generation 0**

**Generation 1,000**

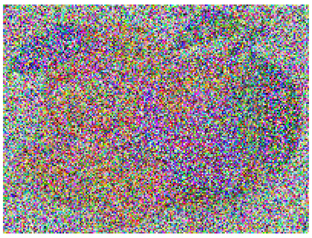
**Generation 2,500**

**Generation 4,500**

**Generation 7,000**



**Generation 8,000**



**Generation 20,000**

## Clustering

For a 2-cluster problem, the code is available here. For a 3-cluster problem, the code is here. The 2 examples are using artificial samples.

Soon a tutorial will be published at Paperspace to explain how clustering works using the genetic algorithm with examples in PyGAD.

## CoinTex Game Playing using PyGAD

The code is available the CoinTex GitHub project. CoinTex is an Android game written in Python using the Kivy framework. Find CoinTex at Google Play: https://play.google.com/store/apps/details?id=coin.tex.cointexreactfast

Check this Paperspace tutorial for how the genetic algorithm plays CoinTex: https://blog.paperspace.com/building-agent-for-cointex-using-genetic-algorithm. Check also this YouTube video showing the genetic algorithm while playing CoinTex.