

**Genetic programming types comparison**

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# Project description

Compare classic/normal genetic programming (GP) with the modified/enhanced GP starting from the Cella-Stefano reference code (possibly improving the code) on the ECG dataset by Arianna Cella:

The comparison should be made at the level of:

1. performance (e.g., MSE for a regression problem).

2. 'effective' size of the solution measured in number of equivalent nodes (i.e. transforming the added functions into the equivalent subtree using the basic functions defined at the beginning and measuring the number of nodes of that solution). (It is expected that equivalent performing solutions can be found with fewer nodes).

3. speed of convergence (by evolving smaller trees, the search space is reduced, and the search should be faster).

At the algorithmic/complexity and code level, it is interesting to evaluate what advantages can be obtained by using the classical representation through trees and the linear one that Francesca Stefano worked on.

Definitions:

"Normal GP" is a normal single run of GP (whatever its purpose) in which the parameters that regulate it, the function set and the terminal set remain constant throughout the execution.

"Modified GP" is the method implemented by Arianna Cella and subsequently modified by Francesca Stefano. In this method, trees of depth Pmax are evolved that are more limited than in the 'standard' case, thus limiting the size of the search space and therefore facilitating the search itself and limiting the generation of bloat.

To compensate for the limited depth, and therefore the limited expressiveness, of the trees that evolve, every X generations the subtrees of depth 2 or 3 at most that appear most frequently in the population are transformed into functions and inserted into the function set. In this way, the average depth of the trees of the current population is limited and it is possible to continue to evolve trees that continue to respect the constraint of the limited maximum depth (or, at most, slightly increasing the depth) with all the advantages that I have previously listed, but are actually equivalent to much deeper and therefore more 'expressive' trees.

The difference between Arianna Cella's version and Francesca Stefano's version consists in the use of a different representation for the trees, which can be found documented in the article to which Francesca Stefano's report refers and which should facilitate the generation of the histograms of the frequencies of the subtrees.

# Changes made to the reference codes

Here I report the most important changes made to both the reference codes.

General changes:

* Switch to English.
* Use of Python best practices.
* Switch to f strings, they are more efficient because avoid concatenation and calls to the *str* function.

## data\_loader.py

The original file was called “utils\_import\_data.py”. I removed the function *shuffle\_in\_union*. It is sufficient to use the shuffle=True parameter in “train\_test\_split” function already available from scikit-learn.

## utils.py

The original file was called “utils\_functions.py”. For clarity, I added the postfix *\_tree* to all the functions from the Cella’s reference code that works on a tree representation and *\_list* to all the functions from the Stefano’s reference code that works on a list representation (interested functions: *extraction* and *get\_modules*). Modified functions:

* **training\_rf**: Originally the mean F1 score was manually calculated after the call to “f1\_score” available from scikit-learn. Now it is directly calculated with the parameter average='macro' in the function f1\_score. I modified the usage of “LabelEncoder“ to directly encode all the labels, this avoid multiple encoding errors. I also removed the save and restore of the numpy random state that is useless/irrelevant because for repeatability is use the “random\_state” parameter of “RandomForestClassifier”. Both refence codes had these “errors”. I modified also the number of estimators from 50 to 100, 100 is the default value.
* **extraction\_tree**: I modified the last past of the function for a strong optimization trick, check the complexity section for more details.
* **extraction\_list**: I noticed the parsing of the tree was wrong, terminals were considered as internal nodes, this build an incorrect tree structure. In fact, commas separate children of the same parent, but the Stefano reference code nests subsequent nodes under the previous terminal. So, I had to rewrite it.
* **get\_modules\_list** and **get\_modules\_tree**: I generalized it in one function that take as argument the extraction mode (*extraction\_tree* or *extraction\_list*) because they do the same thing.
* **get\_modules\_individual\_tree** and **get\_modules\_individual\_list**: I removed these functions, they were unused.
* **depth\_tree** and **depth\_list**: I removed these functions because you can already obtain the individual depth with the tools provided by DEAP (individual.height), reducing the complexity.
* **view\_hist1** and **view\_hist2**: These two functions were different only in one print. So, I generalized them into one by passing the difference as parameter.
* **varAnd**: This function was exactly the same provided by DEAP then I simply imported it.

Unused library removed: “convolve” and “cross\_val\_score” from both the reference codes.

## gp\_types.py

The original file was called “GPmodular.py”. Unused library removed from both the reference codes: “collections”, “KMeans” and “PCA”.

### Changes to both methods

* I generalized the two functions *evalTestSet* and *evalValidationSet* into a sigle one, *evalSet*, by passing the type of test set as parameter.
* The functions *mul* and *protectedDiv* were not necessary as defined, this because if the situation NaN happen for them should happen also for the other operators. So, I used the *mul* operator provided by the “operator” library as is done for the other operators. The unique real risk is the division by zero, so I maintained the *protectedDiv* (fixed), and I renamed it to *div* this because the regexes search for *div*.
* the definition of the ephemeral constant was done via a *lambda* function, this prevented the serialization of the individual in the final wild of the best individual. I replaced the *lambda* with *functools.partial*.
* I rewrite the function *sostituisci* (now called *replace*), to cycle the index efficiently by exploiting the mathematical operation of the module.
* I avoided the possible risk of overwriting between best individual and identity at the beginning of the iteration.
* At each iteration the MAX\_DEPTH variable was increased by two, but this operation has no effect. The maximum depth is defined with the "resister" on the toolbox and therefore the variable is considered at that moment. Furthermore, a control limit is added to the toolbox to not exceed this depth. I therefore removed this operation also because it is contrary to the methodology of keeping the depth limited to work on the submodules. Check the code for more details.
* At the end of the iteratio, the individuals to be kept were added to the psets. The operation was done in two cycles, it could be done with just one reducing the complexity. I fixed it.
* I added the function *count\_nodes* to count the number of equivalent nodes of an individual by expanding the submodules.

### Changes to Cella’s method

I moved the *replace* function definition out of the loop on iterations to avoid the overhead of continuous redefinition.

### Changes to Stefano’s method

* I removed the library “warnings” because warnings must be resolved not ignored.
* In the individual evaluation function (*evalTrainingSet*) the number of nodes was defined as the depth of the individual. Also, as k-value (in the parsimony pressure formula to avoid bloat) 1e-2 was used which is too high. In fact, the best individual was practically always a terminal. I corrected these things and brought the k-value back to the same one used in Cella’s method (1e-4) also to have the fairest comparison possible between the two methods.
* In the function *get\_individuals\_to\_keep* the fitness normalization formula was incorrect, I brought it back to the formula originally used by Cella.
* I fixed the *adjust\_probabilities* function to dynamically calculate the *cxpb* and *mutpb* probabilities (what it should do), originally it was swapping the mutation operators.
* An identity individual was inserted into the population in all iterations. This should only be done at the first iteration (as Cella's method does), in subsequent iterations the population must evolve with the operators (elitism aside). I fixed it.
* The evolutionary algorithm originally started with varAnd, then evaluated fitness, made a selection, and repeated the process for all generations. This is not in line with the general evolutionary algorithm (already implemented by eaSimple) where before starting the generations the fitness is evaluated, and then a selection is made at the beginning of the generation, etc. So, I switched it back to using *eaSimple\_elite* also for as fair a comparison as possible with the Cella’s method, maintaining the function *adjust\_probabilities*.

## user\_interface.py

The original UI relied on just one process (the graphics one) that had to handle the graphics and run the program when launched, so if it ran the program, the graphics would get stuck and become unresponsive.

I used multiprocessing to run the program through a dedicated process. So now it is possible to launch in parallel different configurations that run at the same time (if the hardware supports). You can launch all three types of GP at the same time (classic, Cella and Stefano’s methods).

I modified the “run\_script” function to measure the running time and to save all the run data in a more compact and structured mode avoiding unnecessary cycles that save the same information multiple times. I improved the efficiency of calculating the mean F1 by calculating it with "map" and "sum" functions rather than manually scrolling the list with a for loop.

I also added support for the “verbose” choice in the graphics.

A screenshot of a computer

AI-generated content may be incorrect.

I removed the function “graph” because no longer useful, I did a dedicate UI to see results.

## user\_interface\_charts.py

I created this “extra” UI to parse and show the run results saved. With this UI is possible to plot in multiple windows results of different runs to compare them. It shows the parameters configurations, the F1 performance on test and validation set along the iterations for each run, the number of equivalent nodes of the best individual, the run time and average F1 on the test set. Finally, it shows average F1 on all runs and total time.

## best\_ind\_f1.py

The original file was called “script.py”. This file loads a dataset, a best individual with its kernel size and its pset.

I used the functions already defined in the other files (before they were redefined), and removed useless operations (e.g., the pset was set from the saved parameters but then read from the file in which it is saved).

# Representation complexity analysis

The “representation functions” are in *utils.py*. For the following analysis, “n” is the general length of a string (individual).

## Complexity of *extraction\_tree*

The “replace” function have a complexity of O(n).

*regex\_depth1* complexity: *(?:add|sub|neg|mul|div|execTree\d+)* is a direct comparison so it is O(1), the part *\((...)\)* is a series of alternatives:

* -?\d+ search for a positive/negative number, worst case O(n)
* [A-Za-z0-9\_]+ search one or more objects in the specified ranges, worst case O(n)
* \([^()]+\) search for something between parenthesis but not parenthesis, worst case o(n)
* -?\d+,-?\d+ search for a pair of integer, worst case O(n)
* [-A-Za-z0-9\_]+,-?\d+ search for a pair “string” in the range and a number, worst case O(n)
* [-A-Za-z0-9\_]+,[A-Za-z0-9\_]+ search for a pair of “strings” in the range, worst case O(n)

All the other regex are combinations of these or similar objects like “(?:-?\d+|ARG\d+|[A-Za-z0-9\_]+)”, “(?:,-?\d+|,ARG\d+|,[A-Za-z0-9\_]+){0,3}” this is O(3n) but it is always O(n), etc. So, all these have a complexity of O(n). As consequence the re.findall(str\_a, str\_b) has a complexity O(m\*n) where m is the number of matches but it is always O(n). We know that O(n) + O(n) + … + O(n) = O(n). For the last part of the function is better to see the code with comments.

A computer screen with text

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The original code was the one with worst case complexity O(n3), with my optimization the final complexity of this function is O(n).

## Complexity of *get\_modules*

This function is composed by a for loop (on the population of size p) with a call to *extraction\_*tree and two for loop (one for module with size m1 and m2) nested at the same level, so the complexity is O(p)\*(O(n)+O(m1)+O(m2)) = O(p\*n). It could be considered as O(n) with n → ∞ and a limited population or O(p) with p → ∞ and a limitation on the size of the individuals.

## Complexity of *extraction\_list*

The complexity analysis is done always for the worst case. It starts with a “replace” that is O(n), after there some calls to support functions, all of these are bounded by O(n):

* parse\_expr: entirely scan the individual to build a representation (‘func’, [(‘func2’, [‘arg0’, ‘arg1’]), ‘arg1’]), so it is O(n)
* extract\_nodes: entirely scan the previous representation (so the nodes) to build the submodules depth lists, so it is O(b) with b the number of nodes

Support functions used:

* is\_operator: it directly checks for “mul”, “add”, etc. It is O(1)
* is\_flat: it checks if a node is a terminal and return it, if not return the operator and its arguments. Then, it is O(k) with k the number of arguments for a node.
* node\_to\_str: rebuild the submodule as a single string by joining the node and its children. It is O(m) with m the total number of characters involved.

Since all of these are bounded by O(n) the final complexity is O(n).

## Final complexity comparison

Both the representations use the *get\_modules*, so they are different only in the “extraction” (*extraction\_tree* and *extraction\_list*). I showed the two extraction modes have the same complexity O(n), then they are practically comparable or equal.

Overall, the Stefano’s method can be a bit slower than Cella’s method because it dynamically calculates the crossover and mutation probabilities at every iteration.

# Results comparison

For the classical/normal GP the number of runs and iterations are always 1. While individuals to keep (number of submodules) is not applicable, it is 0. So, the classical GP will obviously take less time when the other methods have more runs or iterations.

Note: results are subject to variation due to probabilities and hardware.

Here some experiments and comparison:

Number of runs = 1. Max depth = 4. Generations = 10. Population = 100. Iterations = 2. Individuals to keep = 5. Kernel size = 3. Dataset = arrhythmias\_data\_balanced\_3000elements.

|  |  |  |  |
| --- | --- | --- | --- |
| **Method** | **Mean F1 (test set)** | **Eq. nodes** | **Time (minutes)** |
| modularGP\_Cella |  |  |  |
| modularGP\_Stefano |  |  |  |
| classicalGP | 0.9014 | 14 | 28.1061 |

|  |  |  |  |
| --- | --- | --- | --- |
| **Method** | **Mean F1 (test set)** | **Eq. nodes** | **Time (minutes)** |
| modularGP\_Cella |  |  |  |
| modularGP\_Stefano |  |  |  |
| classicalGP |  |  |  |

|  |  |  |  |
| --- | --- | --- | --- |
| **Method** | **Mean F1 (test set)** | **Eq. nodes** | **Time (minutes)** |
| modularGP\_Cella |  |  |  |
| modularGP\_Stefano |  |  |  |
| classicalGP |  |  |  |