

**Genetic programming types comparison**

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# Project description

Compare classic/normal genetic programming (GP) with the 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 code

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”.
* **extraction\_tree**: I modified the last past of the function for an 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**: As consequence
* **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).
* **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.

## gp\_types.py

The original file was called “GPmodular.py”.

## user\_interface.py

## user\_interface\_charts.py

# 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.

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AI-generated content may be incorrect.

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\_tree*

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 → ∞ or O(p) with p → ∞ and a limitation on the size of the individuals.

## Complexity of *extraction\_list*

The original complexity of this function wrote by Stefano was O(n) but there was some overhead due to the support structures (memory complexity) making it a lot slower than the optimized tree version. The function was also incorrect as I said before.

## Complexity of *get\_modules\_list*

The structure of this function is similar to the tree version, but it needs to do some more O(1) checks because the *exctraction\_list* does not return the individual already separated in submodules. The external loop is always O(p).

## Final complexity comparison

The regex version is better, it is intuitive because it avoids explicit tree traversal and directly identifies valid subtrees of depth 1 or 2 with a direct match, reducing overhead.

# Results comparison