Universidad del País Vasco / Euskal Herriko Unibertsitatea

ZTF-FCT
Zientzia eta Teknologia Fakultatea
Facultad de Ciencia y Tecnología

Genetic Algorithms and Genetic Programming on Comparison Sorting

Final Degree Dissertation
Degree in Mathematics

Etor Arza Gonzalez

Supervisor:
Francisco de la Hoz Mendez (Patxi)

Leioa, 1 May 2018

Contents

Introduction **v**

1 Theory background **1**
- 1.1 First definitions . . . 1
- 1.2 Classic Genetic Algorithms . . . 3

2 GA on function maximization **8**
- 2.1 Description of the algorithm . . . 8
- 2.2 Algorithm's performance . . . 10
  - 2.2.1 Uniparametric test function . . . 10
  - 2.2.2 Inverted Rastrigin's function . . . 11
  - 2.2.3 Inverted Himmelblau's function . . . 12

3 GA on interpolation **13**
- 3.1 Description of the algorithm . . . 13

4 GA on sorting **16**
- 4.1 First attempt: Hollands Broadcast Language . . . 16
  - 4.1.1 Theory introduction . . . 16
  - 4.1.2 Our approach . . . 18
- 4.2 Our second attempt: Linear Genetic Programming . . . 24
  - 4.2.1 Our Linear Programs Explained . . . 24
  - 4.2.2 Results . . . 26

5 Methodology and Coding Challenges **28**
- 5.1 Max Search . . . 28
- 5.2 Polynomial Interpolation . . . 29
- 5.3 List Sorting . . . 29

6 Future Work **31**

Appendix A Implemented Code **32**
- A.1 Matlab and Python Code for Max Search . . . 33
  - A.1.1 Main Functions and Classes . . . 33
  - A.1.2 Utility Functions . . . 50
  - A.1.3 Python Code . . . 53
- A.2 Matlab and Python Code for Polynomial Interpolation . . . 55
  - A.2.1 Main Functions and Classes . . . 55
  - A.2.2 Utility Functions . . . 60
  - A.2.3 Python Code . . . 61
- A.3 Code of List Sorting . . . 61
  - A.3.1 1^{st} original approach . . . 61

A.3.2 1^{st} restricted approach, with r as new operator 75
A.3.3 2^{nd} approach, final version 90

Introduction

A **Genetic Algorithm (GA)** is guided random search algorithm, more precisely, an **evolutionary algorithm** [4]. The fundamental idea behind evolutionary algorithms is simple: a random **population** (sample of solution candidates, represented as a set of strings) is drawn uniformly at random, then, the performance (**fitness**) of these solutions is measured, and based on this information, we sample a new population, whose fitness is expected to improve the one of the previous population.

Each of this pairs {*measure* and *sample*} is called a generation. Specifically, on genetic algorithms, the sampling is performed in an special way: first we select the best **individuals** (each {*string* , *fitness*} tuple) of the population, then we combine them and finally, we mutate them (apply small changes to promote diversity). We repeat {*measure* and *sample*} until a desired solution is found, the number of maximum iterations is reached or other stopping criteria are met. Throughout the whole algorithm, the individual with the highest fitness value is saved. Each time an individuals fitness is calculated, we compare it with the found best fitness, and if it exceeds it, we save the corresponding individual. When the algorithm terminates, this best fitted individual's string is the found solution.

Unlike other search algorithms such as hill climbing, gradient descent and greedy algorithms, GAs are very good global search techniques, but they may miss local optima, and most of the times, they are only capable of finding suboptimal solutions. An advantage of GAs is that they do not need specific domain knowledge, thus making them very versatile. However, this is sometimes a disadvantage, since they can not exploit this domain specific knowledge, and therefore, when this information is available, other techniques that exploit it usually perform better than GAs (gradient descent, for example). To some extent, GAs can be combined with other search techniques, obtaining the so called hybrid algorithms, capable of exploiting local information but without loosing the global scoop.

The versatility of GAs, makes them a nice optimization technique when no other problem specific algorithms are available. This versatility, however, has its limits, and for very complex problems, there may be encoding problems. For the GA to be able to work, our problem's solutions (**search space**) need to be represented as strings, which is not always possible. Moreover, being able to represent the solutions like a strings is not enough to ensure convergence on a reasonable time, since the quality of the encoding of these solutions also influences the success of the GA search, and the time it takes to converge. On a good encoding, for most of the individuals, a small change on the string has to make little change on the fitness, in other words, the fitness landscape across the solution space has to be as smooth as possible. In addition, if we intend to use classic genetic operators, the encoding needs to be as tight as possible, this means, related features should be placed one next to another. This is necessary because classic genetic operators are more likely to preserve parts of strings that are near each other, and so meaningful feature combinations should be close to one another if they are to make it to the next generation.

Regarding our project, our initial idea for this project was to create sorting algorithms using genetic algorithms, and on the way to our goal, we tried simpler examples to learn about the field, following Thomson's Rule: *'It is faster to make a four-inch mirror then a six-inch mirror than to make a six-inch mirror.'*
First we created a simple GA that tries to find the global maximum of an uniparametric or biparametric function on a given interval or rectangle. Then based on this example, we created a function that optimizes the interpolating points of a n degree polynomial. Finally, and after plenty trial and error, we created small sorting algorithms with the use of GA.
In this document, we briefly discuss the theory of Genetic Algorithms (GA) on chapter 1. We implemented a GA that tries to find the global maximum of an uniparametric or biparametric function, and tested its performance with different classical test functions. We show our work on the matter on chapter 2. Then, we show our implementation of a GA that tries to find the optimal interpolating points for a given function and interval on chapter 3. On chapter 4, we discuss our attempts at sorting lists using genetic algorithms and genetic programming. Finally, on chapter 5, we address some of the programming challenges we encountered while implementing the algorithms.

Chapter 1

Theory background

On this chapter we introduce the foundations of Genetic Algorithms, and some of the most important classical operators.

1.1 First definitions

These notions are based on [7] and [11].

Definition 1. *(alphabet):*

We say that a finite set of unique symbols Ω is an alphabet.

Definition 2. *(string and character):*

*We say that $S = s_1 s_2 ... s_n \in \Omega \times \Omega \times ... n\ times ... \times \Omega$ is a **string** of length n over the alphabet Ω. In this case, we say Ω^n is the set of strings of length n over the alphabet Ω. The s_i elements of a string are said to be **characters**.*

Definition 3. *(genetic operator):*

*Let P and Q be subsets of $\bigcup_{i=0}^{\infty} \Omega^i$. We say that a function α is a **genetic operator**,*

$$\alpha : P \xrightarrow{\alpha} \mathcal{P}(Q)$$
$$S \longmapsto \alpha(S)$$

where $\mathcal{P}(Q)$ is the set of all probability distributions over Q

Note: when $\alpha(P)$ is a degenerate probability distribution, we say the genetic operator to be **deterministic**. In this case, we may identify $\alpha(P)$ with a corresponding subset of Q .

Example 1. *(identity operator):*
Let $\Omega = \{0, 1\}$ be our alphabet, and Ω^n our set of strings. We define α as follows:

$$\alpha : (\Omega^n) \xrightarrow{\alpha} \Omega^n$$
$$S = s_1 s_2 ... s_n \longmapsto \alpha(S) = S$$

Example 2. *(permutation):*
Let Ω be an arbitrary alphabet, and Ω^n our set of strings. We define α as follows:

$$\alpha : (\Omega^n) \xrightarrow{\quad\alpha\quad} \Omega^n$$
$$S = s_1 s_2 ... s_n \longmapsto \alpha(S) = \sigma(S)$$

where σ is a permutation $\in S_n$.

Definition 4. *(search space):*

Let Ω be an alphabet.
*A **search space** is a finite subset of $\bigcup_{i=0}^{\infty} \Omega^i$*

When running a search algorithm, our goal is to find the optimal string from the search space given a fitness function.

Note: Sometimes, we may want our search space to be a subset of Ω^n.

Definition 5. *(deterministic fitness function):*

Let V be a search space. A fitness function μ maps strings on V to positive values:

$$\mu : V \longrightarrow \mathbb{R}^+ \bigcup \{0\}$$
$$S \longmapsto \mu(S)$$

Actually, this is a simplified definition of a more general fitness function. A more general definition would consider μ to be a function that maps each individual to a random variable on $\mathbb{R}^+ \bigcup \{0\}$.

Definition 6. *(stochastic fitness function):*

Let V be a search space. A fitness function μ maps strings on V to a random variable over the positive numbers.

$$\mu : V \longrightarrow \mathcal{P}(\mathbb{R}^+ \bigcup \{0\})$$
$$S \longmapsto \mu(S) = X$$

This second point of view may be useful when, for example, the computation of the fitness function is costly, but it can be approximated by using montecarlo sampling. The fitness function, in this case, can also be viewed as a nosy function, as seen in [13] and [14].

Example 3. *Let $\Omega = \{0, 1\}$ be our alphabet, and Ω^n our search space.*
We can define μ as follows:

$$\mu : V \longrightarrow \mathbb{R}^+ \bigcup \{0\}$$
$$S = s_1 s_2 ... s_n \longmapsto \mu(S) = \sum_{i=0}^{n} s_i$$

In this case, the best individual would be $S_{best} = 11...1$ and it's fitness value would be n.

1.2 Classic Genetic Algorithms

In the early era of genetic algorithms, the presence of operators observed in nature was dominant in the area. These first algorithms were based on three operators: selection, crossover and mutation.

Selection

Selection is a generic term used to define a family of operators, whose purpose is to discard the unfit and promote the fit, thus improving the overall fitness of the new population.
We now show the most natural way to define a selection operator.

Operator 1. *(simple selection):*

Given a search space V, a population P of size m and μ a fitness function, we define β our simple selection operator as follows:

$$\beta : V \longrightarrow \mathcal{P}(V)$$
$$P = \{S_1, S_2, ..., S_m\} \longmapsto \beta(S) = \{X_1, X_2, ..., X_q\}$$

Where $X_i \equiv \{P(X_i^{obs} = S_j) = \frac{\mu(S_j)}{\sum_{k=1}^{m} \mu(S_k)}\} \quad \forall i \in \{1, 2, ..., q\}$

Using this selection operator, often leads to premature convergence, if most individuals are almost null fitted, or, if an early great individual is discovered, the population reaches uniformness very quickly. To avoid this, we can use a similar operator:

Operator 2. *(simple selection with sigma truncation):*

Given a search space V, a non fitness-uniform population P of size m and μ a fitness function, we define β_{st} our selection operator as follows:

$$\beta_{st} : V \longrightarrow \mathcal{P}(V)$$
$$P = \{S_1, S_2, ..., S_m\} \longmapsto \beta_{st}(S) = \{X_1, X_2, ..., X_q\}$$

Where $X_i \equiv \{P(X_i^{obs} = S_j) = \frac{r \circ \mu(S_j)}{\sum_{k=0}^{m} r \circ \mu(S_k)}\} \quad \forall i \in \{1, 2, ..., q\}$ *and r is defined as follows:*

$$r : \mathbb{R} \cup \{0\} \longrightarrow \mathbb{R} \cup \{0\}$$
$$t \longmapsto r(t)$$

$$\tilde{r}(t) = 1 + \frac{t - \text{mean}(\{\mu(S_1), \mu(S_2), ..., \mu(S_m)\})}{c \ \text{std}(\{\mu(S_1), \mu(S_2), ..., \mu(S_m)\})}$$

$$r(t) = \begin{cases} 0 & \tilde{r}(t) \leq 0 \\ \tilde{r}(t) & \tilde{r}(t) > 0 \end{cases}$$

This operator is correctly defined, as we have stated that the population is not fitness-uniform. In the case of fitness-uniformness, we can extend the definition of this operator by stating that in an fitness-uniform situation, the result after applying the operator is a uniform distribution or even an identity operator.

Note1: c is a parameter that measures how separated is the sigma-truncated distribution of fitness, a bigger c means a less sparse distribution. Usually, we want to set c = 2.

Note2: This operator also adds pressure on the late stage of convergence, enhancing the differences between individuals so that small improvements are taken into account.

Note3: This operator is known as the roulette wheel selection with sigma truncation. This is the selection operator we used on our implementations.

Crossover

Crossover is an operator that mixes two individuals into two new individuals, potentially mixing two valuable string pieces and making an even better one. The classic crossover operator, crosses two individuals by choosing two cut points and exchanging the middle piece with one another.

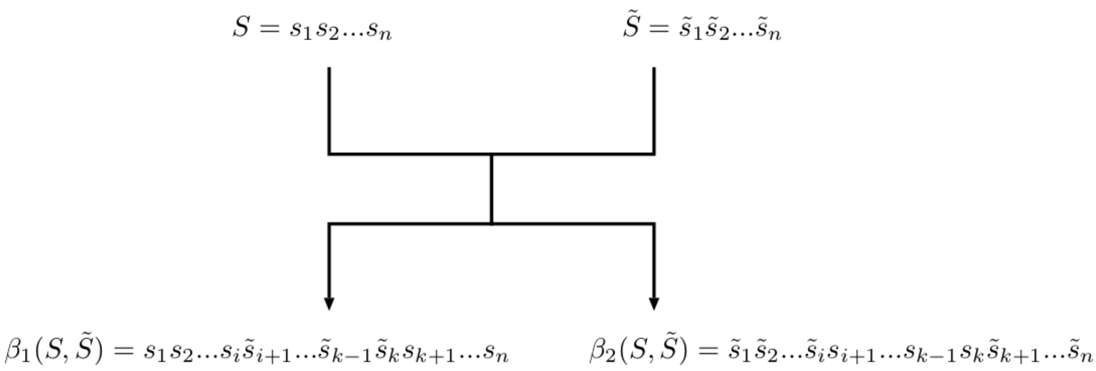


Figure 1.1: two point crossover illustration

Operator 3. *(two point crossover)*

Let Ω^n be our search space. We define the two point crossover operator as follows:

$$\beta : \Omega^n \times \Omega^n \longrightarrow \Omega^n \times \Omega^n$$

$$\{S, \tilde{S}\} \longmapsto \beta(\{S, \tilde{S}\}) = \{\beta_1(S, \tilde{S}), \beta_2(S, \tilde{S})\} = \{X_1, X_2\}$$

We can represent X_1 as (i, k) where i represents the first crossover cut point and k represents the second crossover cut point. X_1 and X_2 are probability distributions that completely depend on each other, thus, $P(X_2|X_1 \equiv (i, k))$ is a degenerate probability distribution:

$$P(X_2|X_1 \equiv (i,k)) = \begin{cases} 0 & X_2 \neq (i,k) \\ 1 & X_2 = (i,k) \end{cases}$$

There is a bijection between the free X_1 (or X_2) distribution and $\mathcal{P}$, the following probability distribution over $\{1, 2, ..., n\} \times \{1, 2, ..., n\}$:

$$\mathcal{P} \equiv (\mathcal{U}_1(\{1,2,...,n-2\}), \mathcal{U}_2(\{k+1,k+2,...,n-1\}|k=\mathcal{U}_1^{obs}))$$

Where $\mathcal{U}_i$ represents a random uniform distribution.
The bijection actually represents each pair of cut-points of the crossover operator as (i,k).

With this kind of crossover operator, we may destroy important information on the middle of the individuals string. To better illustrate this point, we introduce a new concept.

Definition 7. *(schema/schemata):*

Let Ω be our alphabet. Let our search space be Ω^n.
*We expand our alphabet to $\Omega^* = \Omega \cup \{\#\}$, where # represents a symbol $\# \notin \Omega$. In this way, we obtain an expanded search space: $(\Omega^*)^n$. We may also call the expanded search space **schemata space**. We say that any string of our expanded search space is a **schema**.*

Let $S = s_1 s_2 ... s_n \in \Omega^n$ be a string, and let $H = h_1 h_2 ... h_n \in (\Omega^*)^n$ be an schema.

*We say **string S follows schema H** $\Leftrightarrow \forall i \in \{1,2,...,n\}$, $s_i = h_i \lor h_i = \#$*
From an intuitive point of view, we may think that # is a wild card symbol, a symbol that matches any other symbol.

Note: We may denote $string\ S\ follows\ schema\ H\ as\ S \hookrightarrow H$.

Proposition 1. *Let Ω^n be our search space and let $(\Omega^*)^n$ be our schemata space. Let $\mathscr{P}(\Omega^n)$ be the set of all subsets of Ω^n. There exists a subset $\mathcal{H} \subset \mathscr{P}(\Omega^n)$ and a bijective application:*

$$\varphi : (\Omega^*)^n \longrightarrow \varphi((\Omega^*)^n) = \mathcal{H}$$
$$H \longmapsto \varphi(H) = \{S \in \Omega^n | S \hookrightarrow H\}$$

The idea of schemata arises from a need to represent useful parts of a string, for a particular purpose or fitness niche. Let's see some examples to better understand this point:

Example 4. *Let $\Omega^n = \{0,1\}^n$ be our search space, with $n > 2$. Let $\mu_1(S) = s_1 + s_2$ be our fitness function. Consider the schema $H_1 = 11\#...\#$.*

Observe that $\forall S \hookrightarrow H_1,\ \mu_1(S) = 2 = \max_{S \in \Omega^n} \mu_1(S)$.
In fact, $\mu_1(S) = 2 \Leftrightarrow S \hookrightarrow H_1$

Therefore, H_1 is the schema that contains the best strings with respect to fitness function μ_1.

Example 5. *Let* $\Omega^n = \{0,1\}^n$ *be our search space, with* $n > 4$*. Let* $\mu_2(S) = s_1 + s_n$ *be our fitness function and let* $H_2 = 1\#...\#...\#1$ *be our schema.*

Observe that $\forall S \hookrightarrow H_2,\ \mu_2(S) = 2 = \max_{S \in \Omega^n} \mu_2(S)$.
In fact, $\mu_2(S) = 2 \Leftrightarrow S \hookrightarrow H_2$

Therefore, H_2 *is the schema that contains the best strings with respect to fitness function* μ_2*.*

Example 6. *Now consider the strings* $S_0 = 0000...00$*,* $S_1 = 1100...0$ *and* $S_2 = 10...0000...1$ *of length n. Let* β *be our two point crossover operator.*

$$P(\beta_1(S_0, S1) \hookrightarrow H_1) = \frac{n-2}{n-1}$$

$$P(\beta_2(S_0, S1) \hookrightarrow H_1) = 0$$

On the other hand,

$$P(\beta_1(S_0, S2) \hookrightarrow H_2 = 0$$

$$P(\beta_2(S_0, S2) \hookrightarrow H_2 = 0$$

Therefore, we see that it is more likely that H_2 *schema is disrupted during a two point crossover operation. This simple example illustrates how the two point crossover operator disrupts sparse schemata more often than it disrupts tight schemata. Therefore, the representation we use with this operator, should depend on tight schemata, this is, related valuable information should be encoded on the string in the shortest way possible.*

To solve this problem, we may draw a string distribution from the selected space, based on a distance (i.e. hamming distance), and sample from that distribution [18], [1]. With this new combination method, the population itself decides which string positions are important, and which are not.

Mutation

Mutation is the last one of the classic genetic operators. Mutation ensures new variability enters the population, because genetic material on an initial population tends to disappear with selection and crossover alone. We present the mutation operator as follows:

Operator 4. *(simple mutation):*

Let Ω *be our alphabet,* Ω^n *our search space. We define* β_c*, our simple mutation operator as follows:*

$$\begin{aligned} \beta_c : \Omega^n &\longrightarrow \mathcal{P}(\Omega^n) \\ S &\longmapsto \beta_c(S) = X \end{aligned}$$

where $X = x_1x_2...x_n$ *and:*

$$x_i \equiv \begin{cases} s_i & \textit{with probability } c \\ s \in \Omega - \{s_i\} & \textit{with probability } \dfrac{1-c}{\text{card}(\Omega)-1} \end{cases}$$

Note1: Usually, $c < 0.05$, since higher values c values tend to slow down or even prevent convergence. For high c values, the GA is essentially a random walk.

There are other mutation operators, based on distances between strings (such as Hamming distance for an arbitrary search space, or Cayley and Spearman distances if $\Omega^n = S_n$, where S_n is the set of all permutations of length n) The simple mutation operator can be represented as a Hamming distance based distribution. In fact, the combination of crossover and mutation can be substituted by sampling from a distribution, with the so called EDAs, as seen in [18], [1].

Chapter 2

GA on function maximization

One of the advantages of Genetic Algorithms is it's capability to optimize non differentiable or even non continuous functions. They are also a good at finding global minimum at functions with several local minima. However, they are not good at finding the actual minimum, as we will illustrate in this section, by using GA to try to find a global optima of different functions. Therefore, GA can be combined with other local search techniques to ensure local optimality, avoid premature convergence and sometimes, even speed up the search, as seen in [9], [6], [24].

2.1 Description of the algorithm

The Algorithm tries to find the maximum on the given closed n dimensional rectangle (K) using the classical genetic operators, and given the multivariate function f. K can be represented by two of it's corners, $K \equiv (a_1, a_2, ..., a_n, b_1, b_2, ..., b_n)$, where $a = a_1...a_n$ is one of the corners, and $b = b_1...b_n$ the opposite corner.

If we denote *length_of_representation* by l, the search space is a discretization of K, discretized in $(2^l)^n = |K_{disc}|$ points. We encoded the search space in binary alphabet $\Omega = \{0, 1\}$ using a bijective function ϕ_K defined as follows:

$$\begin{aligned} \phi_K : K_{disc} &\longrightarrow (\Omega^l)^n \\ X = (x_1, ..., x_n) &\longmapsto \phi(X) = ((bin \circ \theta_1)(x_1), ..., (bin \circ \theta_n)(x_n)) \end{aligned}$$

Where $\theta_i(x_i, a_i, b_i) = \dfrac{(x_i - a_i)2^l}{b_i - a_i}$ and

$$\begin{aligned} \text{bin} : \{1, 2, ..., 2^l\} &\longrightarrow \Omega^l \\ t_{dec} &\longmapsto \text{bin}(t) = t_{bin} \end{aligned}$$

A sketch of the algorithm is shown below. For more on the implementation of the algorithm, refer to chapter 5.

Algorithm 1: search_max

Input:
$K = (a_1, a_2, ..., a_n, b_1, b_2, ..., b_n)$: a tuple containing the upper a_i and lower b_i bounds of the components of the search space, it represents two of the opposite corners of K.
$f(x_{1,2}, ..., x_n)$: function to be maximized. The function has to have n input arguments (corresponding to the i indexes above).

Output:
(max_x,max_f(x)): a tuple containing found maximum and the point at which the maximum was found.

Parameters:
popsize: The size of the population used by de GA.
max_iterations: The maximun number of generations to be computed.
length_of_representation: The length of the binary vector used to encode each x_i component.

```
pop ← initialize_population(popsize, length_of_representation)
i ← 1
best_fitness ← −∞
pop.calculate_fitness(f, K)
if max_{x∈pop}(x.fitness) > best_fitness then
    best_fitness ← max_{x∈pop}(x.fitness)
    best_individual ← argmax_{x∈pop}(x.fitness)
end
while i < max_iterations do
    pop ← select(pop)
    pop ← crossover(pop)
    pop ← mutation(pop)
    pop.calculate_fitness(f, K)
    if max_{x∈pop}(x.fitness) > best_fitness then
        best_fitness ← max_{x∈pop}(x.fitness)
        best_individual ← argmax_{x∈pop}(x.fitness)
    end
    i ← i + 1
end
search_max ← (best_individual.decode(), best_fitness)
```

2.2 Algorithm's performance

We only implemented the algorithm for functions with one and two variables, but the code can easily be extended to more dimensions. However, visualization on higher dimensions may be difficult.

To tested the performance of the algorithm, we used three test functions:

1) An uniparametric, multiple local maxima test function of our choice.
$f_1(x) = \cos(3x)(\frac{1}{4}x^2 + x + 5 + 5\sin^3(\cos(45x)) + 4\cos(45x) - 2x$

2) Inverted Rastrigin's function, A = 10.
$f_2(x, y) = 40 - (x^2 + y^2) - 10\cos(2\pi x) + 10\cos(2\pi y)$

3) Inverted Himmelblau's function.
$f_3(x, y) = 30 + 14x + 21x^2 - x^4 + 22y - 2x^2y + 13y^2 - 2xy^2 - y^4$

f_2 and f_3 are popular choices when it comes to benchmarking of search algorithms, for further reading, refer to [20], [10].

2.2.1 Uniparametric test function

This function has many local optima, but only one global optimum, as it can be seen in figure 2.1. Running the algorithm 300 times with parameters:

$popsize = 100$
$length\_of\_representation = 15$
$max\_iterations = 30$

The algorithm converged to a point near the global maxima on an average of 92.7% . We considered that the algorithm converged when:
$|x_{output} - x_{max}| < 0.1$, which is represented by the area between the green lines in figure 2.1.

The algorithm, therefore, does not get stuck in local optima very often with this particular function.

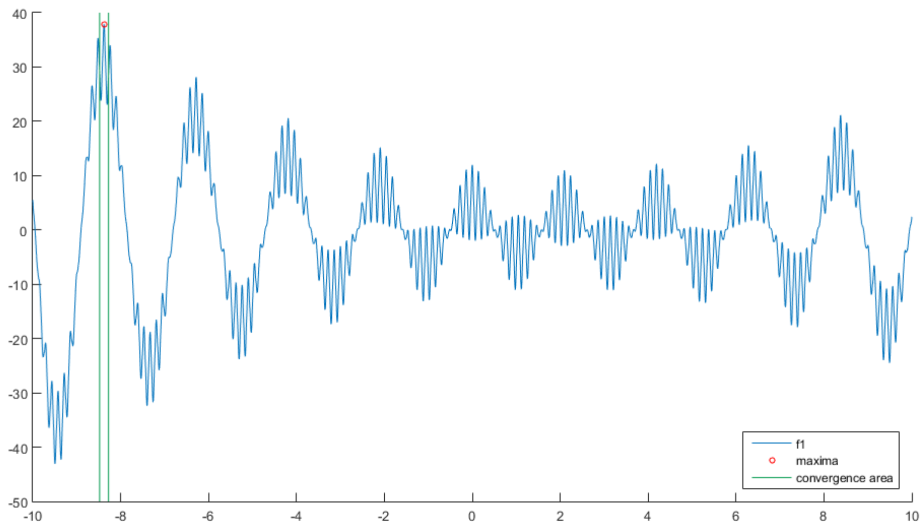


Figure 2.1: plot of f_1 , its global maximum, and the considered interval of convergence.

2.2.2 Inverted Rastrigin's function

This function, as can be seen in figure 2.3, has also many local optima, but only one global maximum, at (x,y) = (0,0).

The red dots in these figures represent the output from the algorithm, after 300 runs, using the same parameters we used on f_1. In this case, we can see the algorithm was not able to find the global optima most of the times. However, there are some options to improve the effectiveness, such as random restarts [22], [21], hybrid approaches with simulated annealing [19] or with particle swarm optimization [16]. The increase of the population size, and among other benefits, 'the accuracy of the genetic algorithm approaches, but does not reach, 100%. The greater the population size the greater the chance that the initial state of the population will contain a chromosome representing the optimal solution' [8] , but with an increased computation time. We estimated (see figure 2.2) the time complexity of the algorithm as a function of popsize to be $O(popsize)$, with fixed parameters:

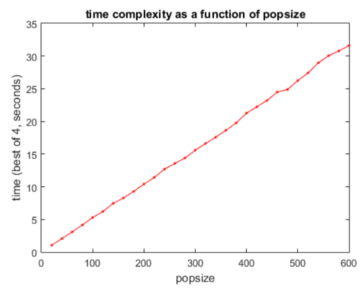
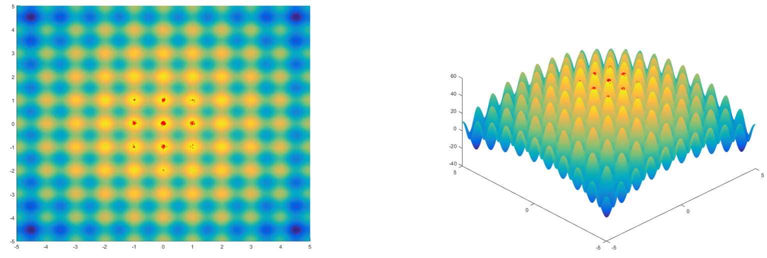


Figure 2.2: Experimental time complexity of GA with *popsize* as variable.

$length\_of\_representation = 15$
$max\_iterations = 30$

However, the population increase is not always beneficial, as can be seen in [2].



(a) Heat map (b) 3d plot

Figure 2.3: Heat map and 3d plot of f_2 and the output points of the algorithm over 300 runs.

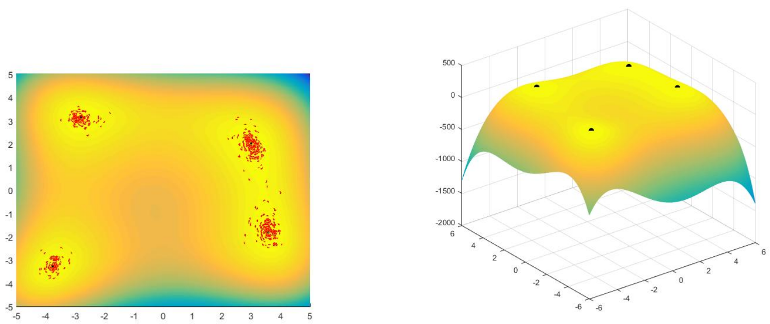
2.2.3 Inverted Himmelblau's function

Himmelblau's function is intended to test an algorithm's ability to find multiple optima, since this function has 4 global optima, represented by black dots in figure 2.4. The red dots represent the output obtained after 300 runs with parameters:

$popsize = 100$
$length\_of\_representation = 15$
$max\_iterations = 30$
We estimated the probability of the algorithm outputting near each of the nodes with 300 runs, and we found the probabilities to be:

$p(x_{out} > 0 \text{ } and \text{ } y_{out} > 0) = 0.497$
$p(x_{out} > 0 \text{ } and \text{ } y_{out} < 0) = 0.237$
$p(x_{out} < 0 \text{ } and \text{ } y_{out} > 0) = 0.167$
$p(x_{out} < 0 \text{ } and \text{ } y_{out} < 0) = 0.100$

This suggests the GA results depend on the starting individuals, and the way individuals are chosen to crossover and mutate. It also shows how GA are a powerful tool to find different good answers to a problem.



(a) Heat map (b) 3d plot

Figure 2.4: Heat map and 3d plot of f_3 and the output points of the algorithm over 300 runs.

Chapter 3

GA on interpolation

3.1 Description of the algorithm

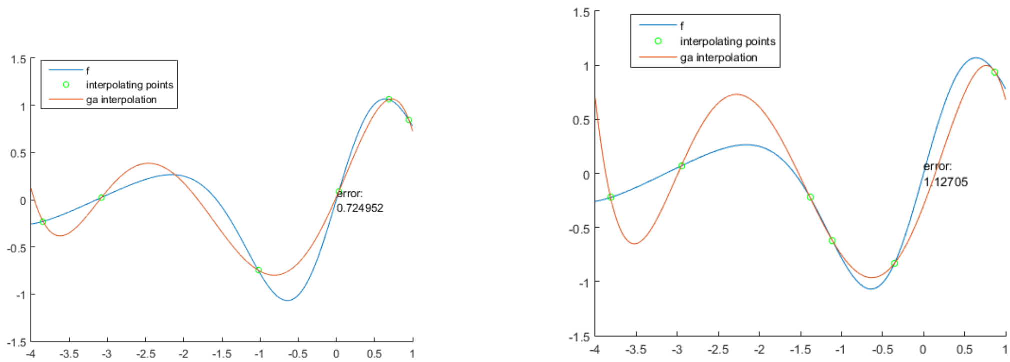
Given a closed interval $[a, b]$, the functions $f(x)$, $H(x)$, where $\frac{dH}{dx} \equiv f$ and an integer n, the algorithm tries to choose the optimal interpolating points for a n degree polynomial, to interpolate f by minimizing $\int_a^b \text{abs}(f(x) - \text{pol}(x))dx$.
Let V be the set of all closed intervals over $\mathbb{R}$, let $\mathcal{F}(\mathbb{R})$ be the set of all integrable functions on $\mathbb{R}$ and let $\mathcal{P}$ be the set of all polynomials over $\mathbb{R}$ Without further encoding details, the fitness function μ the algorithm uses is defined as follows:

$$\mu : \mathcal{F}(\mathbb{R}) \times V \times \mathcal{P} \longrightarrow \mathbb{R}$$
$$(f, [a, b], \text{pol}) \longmapsto \mu(f, [a, b], \text{pol}) = 100 - \log(\textstyle\int_a^b \text{abs}(f(x) - \text{pol}(x))dx)$$

However, for high degree polynomials, due to the Runge's phenomenon [23] it is difficult to estimate the value of the integral using numerical values or even analytically, due to the oscillator behavior of the polynomial. That is why we decided to consider an alternative fitness function, for any n $>$ 10:

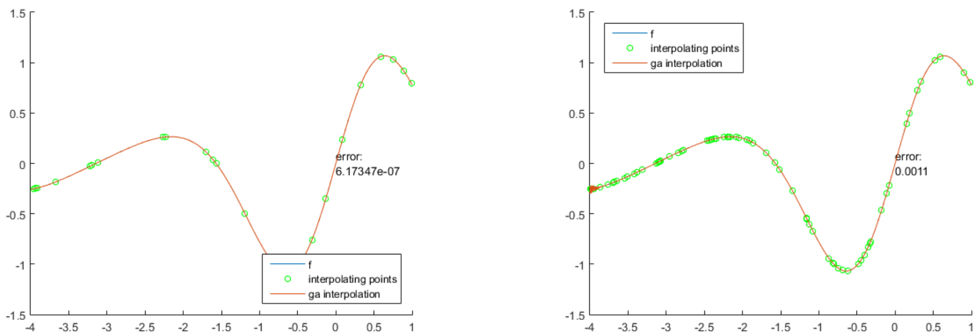
$$\mu_{n>10} : \mathcal{F}(\mathbb{R}) \times V \times \mathcal{P} \longrightarrow \mathbb{R}$$
$$(f, [a, b], pol) \longmapsto \mu(f, [a, b], \text{pol}) = 100 - \log(\text{abs}(\textstyle\int_a^b f(x)dx - \int_a^b \text{pol}(x)dx))$$

With this fitness function, the algorithm is trying to minimize $\text{abs}(\int_a^b f(x)dx - \int_a^b \text{pol}(x)dx)$ instead of $\int_a^b \text{abs}(f(x) - \text{pol}(x))dx$. However, in small n instances, this second fitness function is not as effective, as can be seen in figure 3.1. It does work on higher number of interpolating points, as we can see in figure 3.2 (a). For very high degree polynomials, however, the oscillations on the edges of the interval get more intense, increasing the error, 3.2 (b). All the tests on this section were done considering the following parameters:
$popsize = 100$
$length\_of\_representation = 50$
$max\_iterations = 30$



(a) $\int_a^b \text{abs}(f(x) - \text{pol}(x))dx$ as loss function (b) $\text{abs}(\int_a^b f(x)dx - \int_a^b \text{pol}(x)dx)$ as loss function

Figure 3.1: Comparison of the two fitness functions on a 6 point interpolation on the function. Error is measured as the loss of the first fitness function.



(a) n = 25 (b) n = 70

Figure 3.2: Interpolation is quite successful in medium valued n's, but it gets unstable for higher degree polynomials. Once again, error is measured with the loss function $\int_a^b \text{abs}(f(x) - \text{pol}(x))dx$.

Algorithm 2: interpolate

Input:

(a, b): a tuple containing the upper a and lower b bounds of the interpolating interval.

μ: fitness function, depends on the function to be interpolated, it's indefinite integral and the considered (a, b) interval.

Output:

$pol = (x_1, ..., x_n)$: a n sized tuple, containing the interpolating x values. The interpolating points, therefore are $(x_1, f(x_1)), ..., (x_2, f(x_2))$.

Parameters:

popsize: The size of the population used by de GA.

max_iterations: The maximun number of generations to be computed.

length_of_representation: The length of the binary vector used to encode each x_i component.

```
pop ← initialize_population(popsize, length_of_representation)
i ← 0
best_fitness ← −∞
pop.calculate_fitness((a, b), μ)
if max_{x∈pop}(x.fitness) > best_fitness then
    best_fitness ← max_{x∈pop}(x.fitness)
    best_individual ← argmax_{x∈pop}(x.fitness)
end
while i < max_iterations do
    pop ← select(pop)
    pop ← crossover(pop)
    pop ← mutation(pop)
    pop.calculate_fitness((a, b), μ)
    if max_{x∈pop}(x.fitness) > best_fitness then
        best_fitness ← max_{x∈pop}(x.fitness)
        best_individual ← argmax_{x∈pop}(x.fitness)
    end
    i ← i + 1
end
interpolate ← (best_individual.decode(), best_fitness)
```

Chapter 4

GA and Genetic Programming on list sorting

Genetic Programming (GP) is a branch of evolutionary algorithms that considers the search space as a set of programs, and the goal is to find the optimal program in the search space for a given task. One of the difficulties lies on the encoding of the programs. Some early attempts include Learning Classifier Systems [11], [12] , [17], and Holland's Broadcast Language (HBL), [11]. Other approaches, consider (GP) as computational trees, obtaining a Turing complete adaptable (through special genetic operators) programming languages [3] and GP with linear computation programs have also been tried [25].

4.1 First attempt: Hollands Broadcast Language

It has not yet been proven HBL is a Turing complete language, although Holland [11] suggested it to be. We chose to use HBL as our first implementation to our problem because it is a very natural extension of GA.

4.1.1 Theory introduction

In this section we briefly discuss the theory of HBL, and we give some examples. Most of this section has been taken from [11], [5] and [7]. We simplified the original approach to make it easier to implement and understand.

HBL is a message/action programming language, based on strings. Each 'instruction' of the program is of the form *condition* $\to$ *action*, where an action is performed $\iff$ the message received matches the *condition* field on the BU.

From [5] (adapted):
'We first describe the different structures constituting the language: the symbols, the broadcast units and broadcast devices. The interpretation of the symbols, broadcast units and broadcast devices will then follow. The broadcast language alphabet Ω is finite and contains ten different characters. We consider the set of strings over $\bigcup_{n=1}^{\infty} \Omega^n = S$.

$$\Omega = \{0, 1, *, :, \Diamond, \triangledown, \blacktriangledown, \triangle, p, '\}$$

Let I be an arbitrary string from Ω. In I, a character is said to be quoted if it is preceded by the character $'$. A broadcast unit I_n is an arbitrary string from B, which only contains a unquoted $*$, and it is on the first position of the string. A set of broadcast units may be concatenated to form a broadcast device. A broadcast device I may contain $0 \le n \le \infty$

broadcast units $I_1...I_n$ if $n = 0$ then, I does not contain any broadcast unit and I is then called a null device. A null device does not broadcast a signal under any circumstances. A broadcast device which is not null is said to be active and it may broadcast an output upon the detection of appropriate signals.'

First, we need to process BD into several BU. We begin by uncommenting all BD by removing each $'$ symbol and the symbol immediately next to it. Then, the resulting string is divided so that every resulting BU begins with the symbol $*$ and only contains that symbol once. Then, each BU is classified into one of five categories depending of the position of the first 3 : symbols (any subsequent : symbol is ignored).

0. any BU that does not fit on the other types. These are considered null BU.
1. $*I1 : I2$
2. $* : I1 : I2$
3. $*I1 :: I2$
4. $*I1 : I2 : I3$

We call any I_i a piece of BU. Each of the bu types has a different effect. We here give a very brief summary of how the BU processed.

1. If $I1$ message is on the environment, cast $I2$ to the environment.
2. If $I1$ message is not on the environment, cast $I2$ to the environment.
3. If $I1$ and $I2$ messages are on the environment, delete $I2$ from the environment.
4. If $I1$ and $I2$ messages are on the environment, cast $I3$ to the environment.

We first process **type 4** BU, and then the others. Various ways of execution order can be considered, (Randomized, by type or by the order in which they appear on the BD). In the original BU design, if several messages match the same BU, one of them is chosen at random uniformly. This is done in order for the BD to be able to simulate any distribution (given enough length and computing power). We decided to consider a ordered environment, so that the oldest messages are processed first. This way, we ensure the execution of the BD is consistent on each run.

Although in the original approach all characters were allowed on environmental messages, on our approach, we restricted them to binary sequences, in order to reduce the number of BD that do nothing. In addition to this, our interpretation of the special characters is not the same as on the original paper and we did not use the symbol p on our project to simplify the implementation.

$\lozenge$: If this symbol is found on a action piece, it is ignored. If $I = s_1 s_2 ... s_n$ is our condition piece and $M = m_1 ... m_r$ our environmental message, with $r \geq m$. Then $\lozenge$ can appear on three positions:

1. position $s_1 = \lozenge$
-If $s_2 s_3 ... s_n$ matches $m_{r-s} ... m_{r-1} m_r \longrightarrow I$ matches M.

2. position $s_i = \lozenge, i \notin \{1, n\}$
-If $s_1 ... s_{i-1} s_{i+1} ... s_n$ matches $m_1 ... m_{i-1} m_{i+1} ... m_{r-1} m_r \longrightarrow I$ matches M.

3. position $s_n = \lozenge$
-If $s_1 \in \{\lozenge, \triangledown, \blacktriangledown\} \longrightarrow s_n$ is ignored.
-ElseIf: $s_1 ... s_{n-1}$ matches $m_1 ... m_{n-1} \longrightarrow I$ matches M.

Notice that due to the restriction in **3. position**, $s_1 = \lozenge \wedge s_n = \lozenge$ is not possible.

$\triangledown, \blacktriangledown$: These symbols have a similar effect as $\lozenge$ symbol, but if found at **2. position**, they are ignored. They also save the exceeding part of the environmental message, and 'inject' it on the action piece, if the symbol is repeated at the action string. I.e.
Let $BU_1 = *\triangledown 11 : 00\triangledown 0$ be our BU and $\{0111, 000\}$ be the set of our environmental messages. Notice the following:

- 000 does not match $\triangledown 11$
- 0111 matches $\triangledown 11$, therefore, 01 is saved in memory, and since $\triangledown$ appears on the action piece, message 00010 is broadcast to the environment.

$\vartriangle$: This symbol acts as a single position copier. It will match any one character, and if the $\vartriangle$ also appears in the action message, it will inject the copied character. Only one first $\vartriangle$ instance is considered in the condition pieces and on the action piece, any subsequent occurrences are discarded. If there is no $\vartriangle$ in the condition piece, any occurrences of this symbol in the action piece are discarded.

4.1.2 Our approach

Our first attempt only considers lists of size 8. We now introduce the major algorithms used in this first attempt.

The algorithms used

To define the interaction between the messages and the environment, we introduce a procedure called *process_messages*:

Algorithm 3: process_messages

Input:
sl: The list to be ordered.
M: A list containing all environmental messages. All messages are binary arrays.
Output:
M_new: New environmental messages.
sl: The list to be ordered, after it has been modified.

```
new_M ← ∅
forall message ∈ M do
    if length(message) != 8 then
        continue
    else
        identifier ← message[0]message[1]
        pointer0 ← binary_to_decimal(message[2]message[3]message[4])
        pointer1 ← binary_to_decimal(message[5]message[6]message[7])
        pointer0, pointer1 ← min(pointer0, pointer1), max(pointer0, pointer1)
        switch identifier do
            case 00 or 11 do
                if sl[pointer0] > sl[pointer1] then
                    M_new ← M_new ∪ {11 ∪ decimal_to_binary(pointer0)}
                else
                    M_new ← M_new ∪ {00 ∪ decimal_to_binary(pointer0)}
                end
            end
            case 10 do
                sl ← sl[pointer1 : end] ∪ sl[pointer0 : pointer1] ∪ sl[pointer1]
            end
            case 01 do
                sl[pointer0], sl[pointer1] ← sl[pointer1], sl[pointer0]
            end
        end
    end
end
return sl, M_new
```

We also define the procedure *process_BD*, which interacts with the environmental messages.

Algorithm 4: process_BD

Input:
M: A list containing all environmental messages. All messages are binary arrays.
BD: The broadcast device to be processed.
Output:
M: Modified environmental messages.
Parameters:
max_env_messages: The number of maximun environmental messages.
max_env_message_length: Any environmental message containing more characters than this parameter, will be cropped to this length.

```
BU_list ← decompose(BD)
forall BU ∈ BU_list do
    forall message ∈ M do
        if match(BU, message) then
            reply ← answer(BU, message)
            M ← M − {message}
            M ← M ∪ reply
            break
        end
    end
end
M ← shorten_and_cut(M, max_env_messages, max_env_message_length)
return M
```

We define the algorithm that sorts a list given a list and a BD.

Algorithm 5: sort_list_with_BD

Input:
$\underline{BD}$: input BD.
$\underline{shuffled\_list}$: the list to be shuffled.

Output:
$\underline{shuffled\_list}$: shuffled list once it has been ordered.

Parameters:
start_env_message_list: The initial environmental message list. We used {11000111} to force the first comparison.
max_iterations: The maximum number of comparison rounds.

```
M ← start_env_message_list
i ← 0
while i < max_iterations do
    i ← i + 1
    shuffled_list, M ← process_messages(shuffled_list, M)
    M ← process_BD(M, BD)
end
return shuffled_list
```

We define the Fitness function, *calculate_fitness*.

Algorithm 6: Fitness_function

Input:
BD: BD whose fitness is evaluated.

Output:
calculate_fitness: the calculated fitness value.

Parameters:
number_of_lists_sampled: the number of lists on which the fitness is calculated.

```
i ← 0
fitness_value ← ∅
while i < number_of_lists_sampled do
    i ← i + 1
    sl ← generate_random_list(shuffled_list_length)
    sl_copy = copy(sl)
    sl ← sort_list_with_BD(BD, sl)
    fitness_hist ← calculate_entropy(sl_copy) − calculate_entropy(sl)
end
return mean(fitness_hist)
```

Finally, the algorithm we used to try to discover the best BD on the search space.

Algorithm 7: find_best_BD

Input:
void

Output:
$Best\_BD$: the best BD found.

Parameters:
popsize: The size of the population used by de GA.
max_ga_iterations: The maximun number of generations to be computed.
length_of_BD: The length of the BD considered in the search space.

$pop \leftarrow initialize\_random\_uniform\_population(popsize, length\_of\_BD)$
$best\_fitness \leftarrow -\infty$
$pop.calculate\_fitness()$
if $\max_{x \in pop}(x.fitness) > best\_fitness$ **then**
    $best\_fitness \leftarrow \max_{x \in pop}(x.fitness)$
    $best\_individual \leftarrow \operatorname{argmax}_{x \in pop}(x.fitness)$
end
$i \leftarrow 0$
while $i < max\_iterations$ **do**
    $pop \leftarrow select(pop)$
    $pop \leftarrow crossover(pop)$
    $pop \leftarrow mutation(pop)$
    $pop.calculate\_fitness()$
    if $\max_{x \in pop}(x.fitness) > best\_fitness$ **then**
        $best\_fitness \leftarrow \max_{x \in pop}(x.fitness)$
        $best\_individual \leftarrow \operatorname{argmax}_{x \in pop}(x.fitness)$
    end
    $i \leftarrow i + 1$
end
return $best\_individual$

The problems with this approach

On our first implementation, we found several problems:
- The fitness value was always 0 no matter what. This was caused by the fact that it is highly unlikely to randomly generate a BD that was able to make a change to the fitness list. To solve this, we classified all BD into two categories: null fitness BDs and BDs with non null fitness. We then initialized the population with only BD from the second category.

- We now had the initial population full of non null fitness BDs since we had initialized them discarding any null fitness BD. Bear in mind that for a population size of 20, it took about 30 minutes to initialize our population, so it was a highly inefficient solution. In addition, once initialized, the first two iterations destroyed any valuable schemata on the population and fitness was once again null every time.
To solve this, we tried to reduce the search space: the BU contained on each BD were set to be type1 and have the following structure:

$$*XXXXXXXX : YYYYYYYY$$

Where $X \in \{0, 1, \Diamond, \triangledown, \vartriangle\}$ and $Y \in \{0, 1\}$

- With this we were able to get BDs that on average, improved any given lists entropy. Nonetheless, we still were not able to converge to a BD that was able to completely sort any given list.
We tried a new selection method, based on EDAs, truncating the population (selecting the best k individuals) and then sampling each position of the BD as an independent probability distribution. This did not improve the obtained solution.
We also tried introducing a new operator, r which would be randomly (fair coin toss) set to 0 or 1 each time it was read. This new operator improved our best found solution, but it depended too much on randomness, since the solutions we obtained were not deterministic programs. Each time they were executed, the outcome was different, and this is a undesirable property when it comes to list sorting.

Finally we decided to start from scratch with a smaller search space, and a new approach.

4.2 Our second attempt: Linear Genetic Programming

Based on the Turing Machine idea, we created a linear program with several commands and we evolved it using classic genetic operators.

4.2.1 Our Linear Programs Explained

We have two pointers, p0 and p1, and they represent a position (an index) on the list, p1 is initialized to 0, and p1 is initialized to floor($\frac{length\_of\_list}{2}$).

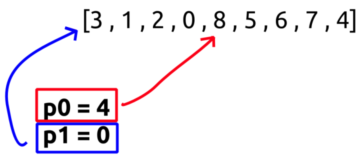


Figure 4.1: Example of pointer initialization for list length 9

We then defined the following operators: $s, i, 0+, 1+, 0-, 1-, 0++, 0--, 1++, 1--, c$.

s : when this symbol is found, the following is executed:

If p0 != p1

$compare\_and\_swap(p0, p1, shuffled\_list)$

Where *compare_and_swap* compares the elements of the list corresponding to p1 and p0 and swaps the elements if it makes the list more ordered.

i : when this symbol is found, the following is executed:

If p0 != p1

$compare\_and\_insert(p0, p1, shuffled\_list)$

Where *compare_and_insert* compares the elements of the list corresponding to p1 and p0 and inserts the element corresponding to p0 in the place it belongs: next or before the element corresponding to p1.

k+ and k- : k can be either 0 or 1. If 0+ is found we execute:

$p0 \leftarrow p0 + 1 \mod (list\_length)$

Likewise, if we find 1− :

$p1 \leftarrow p1 - 1 \mod (list\_length)$ is executed.

k++ and k– : k++ is equivalent to executing the command k+, floor($\frac{list\_size}{8}$) times consecutively. The homologous happens with $k--$.

c: When this command is found, it is ignored.

The optimization algorithm is the same as the one used on the first approach, so we won't be repeating it here. It should be noted that for list sizes 4 and 5, a brute force search was used, since it was more efficient than our algorithm.

4.2.2 Results

This time we were able to find algorithms that sorted any given list. We compared the obtained algorithms with two well known algorithms: insertion sort and quicksort. Bear in mind that when the list is ordered, the algorithm is terminated and the number of comparisons is measured. This is not normally the case, since the algorithm normally knows when to terminate. However, we measured the maximum number of comparisons needed to sort any list, and thus when trying to sort any list, if we execute the GP with the maximum number of comparisons needed for all lists, we know the list will be sorted.

To make the comparison between different algorithms fairer, on the insertion sort, after each insertion, we checked if the list is ordered, and if so, we terminated the algorithm, just like on the GP.

We did not do this on quicksort, due to the recursive nature of the algorithm. Therefore, the value that must be taken into account is the worst case for the obtained genetic program, since this program cannot by itself terminate, the only way to ensure any list can be sorted by this algorithm, is to let it make all the comparisons it makes on the worst case scenario.

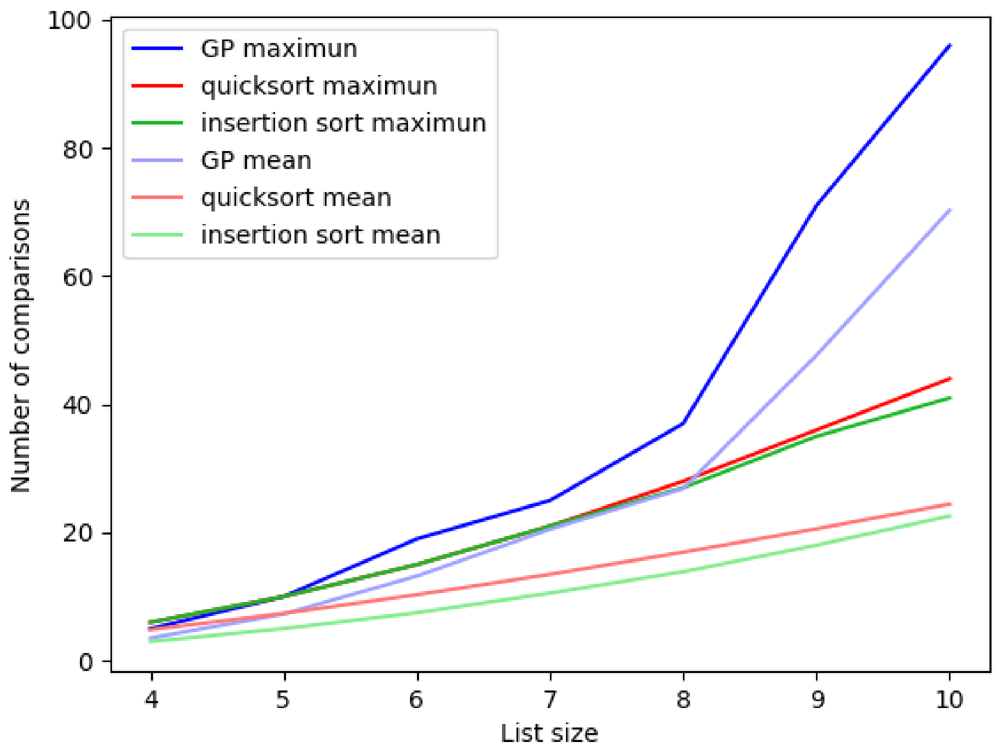


Figure 4.2: The number of comparisons required to sort a list given its size. Lighter colors represent the mean of the number of comparisons needed, and the darker colors represent the maximun required comparisons. (Smaller is better)

We only computed the GP for lists of size 4 to 10, since for bigger list the computation time required to obtain a reasonable solution on our machine would exceed 6 hours. In figure 4.2 we can see a comparative chart. The obtained best algorithm is worse than this two well known algorithms.

Chapter 5

Methodology and Coding Challenges

On this last chapter we will talk about some of the difficulties we faced when implementing the code. There where various different unsuccessful attempts which where not included on this document, because of the lack of space, and the obtained unexciting results.

5.1 Max Search

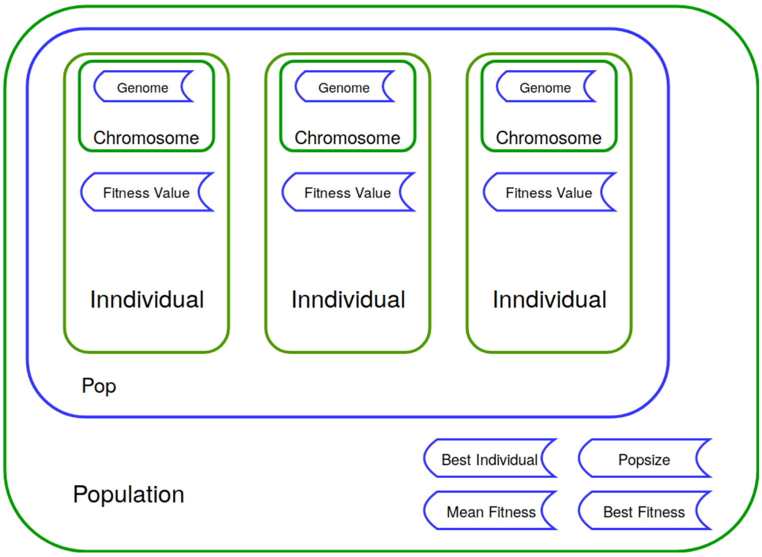


Figure 5.1: General structure of our GA implementation. Blue quadrilaterals represent properties, and green quadrilaterals represent classes.

We decided to structure the code using Matlab's OOP capabilities. Our main object is a Population type object, which contains the methods needed to run the GA. This structure was used both in Max Search and Polynomial Interpolation.

Some of the major challenges we faced while implementing this algorithm:

- Sometimes, selection function would crash. It was caused because very occasionally, specially with small population sizes, all individuals would have the same fitness, and therefore, there would be an 0 division error while calculating the probability of any individual on the roulette wheel selection. To solve this, we applied a small normal noise, before the selection function (line 17 of **select_ga.m**).

- While encoding and encoding and decoding between binary and real numbers, we had numerical problems because of the limit of integer size on Matlab. That is why we introduced a small python script (**Bigint.py**), since python has unlimited precision integers. Matlab has also got a third party package that supports unlimited sized integers, called Variable Precision Integer Arithmetic, but it was not easy to use and it had some limitations, so we figured out it would be easier to leave the big integer part to python. We see the call the python script on line 31 of **code_ab.m** and line 19 of **decode_ab.m**. Python returns to Matlab a string that first needs to be converted to a Matlab string, and then it can be evaluated with the *eval()* command.

5.2 Polynomial Interpolation

- The major problem we faced is the numerical error when integrating the L1 distance of two functions on Matlab. To avoid numerical errors, we introduced another loss function, which worked surprisingly well for big degree polynomials (n > 10). More details on section 3.1.

5.3 List Sorting

- The Broadcast Device approach turned to be a big waste of time. We only considered type 1 , 2 and 4 BUs, since type 3 BUs would not change much anyway. This approach had many problems, such as infinite loops, out of memory errors (caused by unlimited message lengths). After correcting all these problems, we did obtain a BD that seemed to improve a list's entropy *on average*. On figure 5.2 we see that the distribution of fitness values is slightly off to the right, and the mean fitness value is 0.0902. There is still much to improve, since it can barely be called a sorting algorithm.

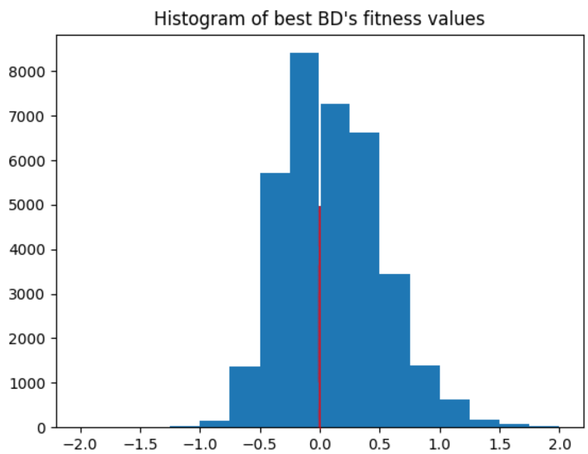


Figure 5.2: Histogram of the found best solution's fitness values over all lists of size 8 (there are 8! different lists of this size.) The red line represents the number of instances with null fitness. Positive fitness values represent the list's entropy was improved, and negative values represent it was worsened.

To improve the obtained result, we restricted our search space as stated in 20. We also introduced 'r' the random operator. With these changes, we were able to find a better solution, ***lwlwllww:11rrr00r*wlwl0w11:10111010**. With this BD, we obtained a average fitness value of 0.142. The distribution of the fitness values over all possible lists can be seen in figure 5.3. The obtained result depends on the used random seed, since the ’r’ operator is not deterministic (more about the ’r’ operator on 20).

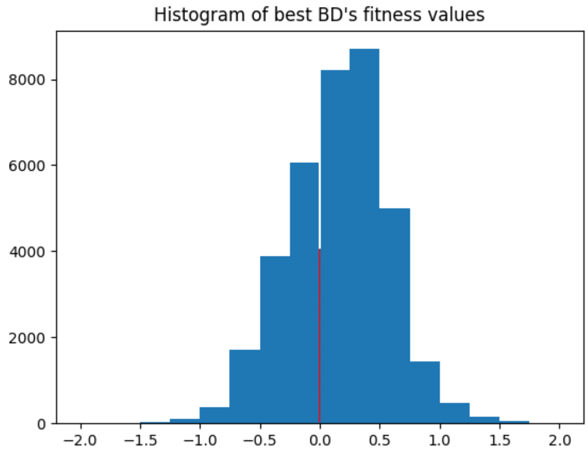


Figure 5.3: Histogram of the found best solution’s fitness values over all lists of size 8 (there are 8! different lists of this size.) The red line represents the number of instances with null fitness. Positive fitness values represent the list’s entropy was improved, and negative values mean it was worsened.

Chapter 6

Future Work

Our final approach for list sorting can still be improved, since it is a very simple algorithm. Whenever a number is inserted, we know that the element corresponding to the inserted index is correctly arranged with the inserted element. If we again insert on the same location this information can be exploited, which is what insertion sort does. For reasonable sized GPs, however, there is no solution on the search space that can exploit this information. It would not take much to adapt our second approach to take advantage of this information.

The idea would be to obtain small groups of 'linked' elements, and these groups would be arranged subsets. These linked groups would be created or extended whenever an insertion happened. The insertion operator can be changed to binary insertion. In regard to swaps, whenever a swap between two elements of the same group happens, this could be ignored. If a swap occurs between two different groups, these could be combined like mergesort does, obtaining a single bigger group.

When it comes to optimization methods, EDAs [18], [1] could be implemented. Also, other crossover operators could be used [15].

Appendix A

Implemented Code

A.1 Matlab and Python Code for Max Search

A.1.1 Main Functions and Classes

main.m

```
function [ population ] = main( txtfile , rep_len , pop_size , i_max )

% use nextline.m to read the txtfile
clear nextline
mode           = nextline(txtfile);
fitness_opts = nextline(txtfile);
fitness_opts = eval(fitness_opts);
fitness_mode_opts = {mode,fitness_opts{:}};
len                = eval(nextline(txtfile));
popsize            = eval(nextline(txtfile));
imax               = eval(nextline(txtfile));

% uncoment these lines to override data.txt values with input values
%len = rep_len;
%popsize = pop_size;
%imax = i_max;

switch mode

    %Uniparametric function mode
    case 'function_max'
        C = zeros(1,len);

        %Initialize population with randpop, and write mode_fitness_opts on popultion
        population = randpop(C,popsize,fitness_mode_opts);

        close all % close all previous figures
        hold all

        %we create two points to name the legends, make room for legends, and preallocate x axis
        scatter(0,0,'.','red')
        scatter(0,imax,'.','blue')
        legend('Max. fitness','Mean fitness','Location','southeast')

        for i = 1:imax
            matingpool = select_ga(population);
            matedpool = crossover(matingpool);
            population.pop = mutate(matedpool);
            scatter(i,population.bestfitness,'.','MarkerEdgeColor','red')
            scatter(i,population.meanfitness,'.','MarkerEdgeColor','blue')
            drawnow
        end

        %plot function and found maxima
        figure
        a = fitness_mode_opts{2};
        b = fitness_mode_opts{3};
        f = fitness_mode_opts{4};
        x = decode_ab(population.bestpopindividual.chrompack.genome,length(C),a,b);
        hold all


        mindist = min([x-a,b-x]);
        xmax = fminbnd(@(x) -f(x),x - (mindist/1000),x + (mindist/1000));
        %xmax = -8.3778;

        plot(a:(b-a)/100000:b,f(a:(b-a)/100000:b))
        %ga maximun
        plot(xmax, f(xmax), 'ro', 'markersize', 4)
        plot([xmax-0.1, xmax-0.1], ylim,'color',[0 0.6 0.3])
        plot([xmax+0.1, xmax+0.1], ylim,'color',[0 0.6 0.3])
        legend('f1','maxima','convergence area','Location','southeast')

        disp('error: ')
        disp( abs(f(xmax) - f(x)) )

```

```
        % code below used to measure the probability of terminating the algorithm on the conv area
        %if  0.1 > abs(x - xmax)
        %    population = 1;
        %else
        %    population = 0;
        %end
        %hold off
        %fclose all;
        population = {x, f(x)}


    %Biparametric function mode
    case 'multiparam_max'
        C = zeros(2,len);
        %Initialize population with randpop, and write mode_fitness_opts on popultion
        population = randpop(C,popsize,fitness_mode_opts);
        hold all

        %we create two points to name the legends, make room for legends, and
        %preallocate x axis

        scatter(0,0,'.','red')
        scatter(0,imax,'.','blue')
        legend('Max. fitness','Mean fitness','Location','southeast')
        for i = 1:imax
            matingpool = select_ga(population);
            matedpool = crossover(matingpool);
            population.pop = mutate(matedpool);
            scatter(i,population.bestfitness,'.','MarkerEdgeColor','red')
            scatter(i,population.meanfitness,'.','MarkerEdgeColor','blue')
            drawnow

        end
        hold off
        figure
        a1 = fitness_mode_opts{2};
        b1 = fitness_mode_opts{3};
        a2 = fitness_mode_opts{4};
        b2 = fitness_mode_opts{5};
        f  = fitness_mode_opts{6};
        x  = decode_ab(population.bestpopindividual.chrompack.genome(1,:),length(C(1,:)),a1,b1);
        y  = decode_ab(population.bestpopindividual.chrompack.genome(2,:),length(C(2,:)),a2,b2);

        % uncomment to plot found best solution
        disp({x,y,f(x,y)})

        x_vect = linspace(a1,b1,1000);
        y_vect = linspace(a2,b2,1000);

        [x_mesh, y_mesh] = meshgrid(x_vect, y_vect);

        z_mesh = f(x_mesh,y_mesh);

        mesh(x_mesh, y_mesh, z_mesh)
        hold all

        %uncomment to plot inverted himmelblau's maxima
        %plot3( 3.5804, -1.8200, 200, 'k.','MarkerSize', 25)
        %plot3(-2.8077, 3.1340, 200,'k.','MarkerSize', 25)
        %plot3(2.9905, 2.0118 ,200,'k.','MarkerSize', 25)
        %plot3(-3.7767, -3.2761,200,'k.','MarkerSize', 25)

        %we return the found best point
        population = {x,y,f(x,y)};


        %hold off
        %fclose all;


end
```

calculatefitness.m

```
function [ fitness ] = calculatefitness( genome , fitness_opts )

    mode = fitness_opts{1};


    switch mode
        case 'function_max'
            fitness  = function_max(genome,fitness_opts);
        case 'multiparam_max'
            fitness = function_max_multipar(genome, fitness_opts);

    end
end

function [fitness] = function_max(genome,fitness_opts)

    %mode = 'function_max'
    %fitness_opts = {'function_max', a , b , @(x) f(x)}


    f = fitness_opts{4};
    x = decode_ab(genome , length(genome) , fitness_opts{2} , fitness_opts{3});
    fitness = f(x);
end




function [fitness] = function_max_multipar(genome,fitness_opts)

    %mode = 'multiparam_max'
    %fitness_opts = {'multiparam_max', a1 ,b1 ,a2 ,b2 , f}


    f = fitness_opts{6};
    x = decode_ab(genome(1,:), length(genome(1,:)), fitness_opts{2}, fitness_opts{3});
    y = decode_ab(genome(2,:), length(genome(2,:)), fitness_opts{4}, fitness_opts{5});
    fitness = f(x,y);


end
```

Chrompack.m

```
classdef Chrompack


    properties
        genome
    end

    methods
        function r  = individualize(chrompacks)
            individuals = (arrayfun(@(x)Individual(x), chrompacks , 'UniformOutput',false));
            r = [individuals{:}];

        end
        function obj = Chrompack(gen)
            if nargin
                obj.genome = gen;
            end

         end
         function r=fitness(obj,fitness_mode_opts)
             r = calculatefitness(obj.genome,fitness_mode_opts);
        end
    end

end
```

code_ab.m

```
function [ C ] = code_ab(x ,n , a ,b)
    %CODE_AB returns the binary code of the entered number. Number of digits
    %and ab interval is also taken into account
    % x-->char / int       ---> value to be coded to binary, xĂ[a,b] is a must
    % n-->int     OPTIONAL ---> number of digits of the binary code
    % a-->numeric OPTIONAL ---> lower bound of interval
    % b-->numeric OPTIONAL ---> upper bound of interval
    %IMPORTANT: function has to be called with 4 arguments at least once
    %before calling it with only one argument, as persistent values need to
    %be set.


    persistent per_abd;
    persistent persistent_n;


    %NARGIN 1
    if nargin == 1

        %if x is not an string
        if not(ischar(x))

            %if x is not a string nor a number ---> error
            if not(isnumeric(x))
                error('x is not numeric nor string')
            end
            %check if x Ă [a,b] , else --> error
            if per_abd(1) <= x && per_abd(2) >= x
                %code with phyton module, output is phyton string.
                %we then convert phyton string to matlab string
                C_string = char(py.phyton.bigint.code(x,persistent_n,per_abd(1),per_abd(2)));
                %finally, we evaluate function
                C = eval(C_string);
            else
                error(' xĂ[a,b] is not true ')
            end

        else
            %try to call code_ab with a converted string
            C = code_ab(num2str(x,'%100.30f'));


        end







    %NARGIN 4
    %set persistent values for ab and n
    elseif nargin == 4

        %error check a > b
        if a > b
            error(' b > a on [a,b] interval')
        end

        per_abd = [a, b , b-a] ;
        persistent_n = n;

        C = code_ab(x);
    end

end
```

crossover.m

```
function [ matedpool ] = crossover( matingpool )
%    Input --> array of Individuals
%    Output --> array of Individuals

chrompackarray = [matingpool.chrompack]; %we obtain the chrompacks from individuals
outputchroms = simplecrossover(chrompackarray); %perform crossover
matedpool = individualize(outputchroms); %transform obtained chroms to individuals
end

function [crossedchrompacks] = simplecrossover (chrompacks)
        %SIMPLECROSSOVER
        %    Input --> array of Chrompack
        %    Output --> array of Chrompack %  since array of genomes may be problematic
        %     crossover inside each chromosome.
        %     [a a a a b b c c c] & [t t t t e e f f f] ----> [a a a a e e c c c] & [t t t t b b f f f]
        %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
        % control ---> logical variable 0 when pop even, 1 when pop odd
        control = 0;

        %check if population is multiple of 2
        len=length(chrompacks);
        if mod(len,2)
                control = 1;
                warning('population size is odd, an individual will not be crossed')
        end

        %we shuffle input
        chrompacks = shuffle(chrompacks);

        %preallocate output for speed
        crossedchrompacks(1:len) = Chrompack();

        %crossing

        for index=1:floor(len/2)
                parents = chrompacks(1,[index*2-1 , index*2]);
                crossedchrompacks([index*2 - 1 ,  index*2]) = couplemate(parents(1),parents(2));
        end

        if control %if population is odd, last individual is not crossed and kept
                crossedchrompacks(end) = chrompacks(end);
        end

        function [child1,child2] = couplemate(parent1,parent2) %we mate a couple of chrompacks
                %Input  --> Chrompack , Chrompack
                %Output --> Chrompack , Chrompack
                %we first convert input into genome
                parent1 = parent1.genome;
                parent2 = parent2.genome;

                %get nchrom and chromsize
                [nchrom , chromsize] = size(parent1);

                %get random positions
                randomindex = sort(randi(chromsize-1,2,nchrom));

                child1gen = parent1;
                child2gen = parent2;
                for i = 1:nchrom
                    child1gen(i,(randomindex(1,i)+1):randomindex(2,i)) = ...
                      parent2(i,(randomindex(1,i)+1):randomindex(2,i));
                    child2gen(i,(randomindex(1,i)+1):randomindex(2,i)) = ...
                      parent1(i,(randomindex(1,i)+1):randomindex(2,i));
                end
                child1 = Chrompack(child1gen);
                child2 = Chrompack(child2gen);
        end
end
```

data.txt

```
%mode ——> tell the main file what mode wil e be operating on
function_max

%Fitness function options. For 'function_max' mode , a cell containing:
%  {'funtion_max', a , b , f}

{−10 , 10 , @(x) cos(3∗x) .∗ (0.25∗x.^2+x+5+5∗sin(cos(45∗x)).^3+4∗cos(x∗45)−2∗x)}


%The sample Individual's genome (C)
15

%Popultion size (popsize)
100

%Number of iterations (imax)
20

%93



END
```

datamultimodal.txt

```
%mode ——> tell the main file what mode wil e be operating on
multiparam_max

%Fitness function options. For 'multiparam_max' mode , a cell containing:
%  {'multiparam_max', a1 ,b1 ,a2 ,b2 , f}

% demo1
%{-10 , 10 , -10, 10, @(x,y) cos(0.05.*x.*y) .* (0.25.*x.^2+y)}

% Rastrigin A = 10
% Rastrigin, L. A. "Systems of extremal control." Mir, Moscow (1974).
%{-5 , 5 , -5, 5, @(x,y) 40 - (x.^2 + y.^2)  +  10.*cos(2.*pi.*x) + 10.*cos(2.*pi.*y)}

%Himmelblau's function
% Himmelblau, D. (1972). Applied Nonlinear Programming. McGraw-Hill. ISBN 0-07-028921-2.

{-6 , 6 , -6, 6, @(x,y) 200 - (x.^4 + 2.*x.^2.*y - 22.*x.^2 + y.^2 - 22.*y +121) - (x.^2 + 2.*x.*y
    .^2 - 14.*x + y.^4 - 14.*y.^2 + 49)}




%The sample Individual's genome (C)
15

%Popultion size (popsize)
100


%Number of iterations (imax)
30




END
```

decode_ab.m

```
function [ x ] = decode_ab( C ,n , a , b )
    %DECODE_AB returns the binary code of the entered number. Number of digits
    %and ab interval is also taken into account
    % C-->char / mat of doubles ---> value to be decoded to decimal
    % n-->int      OPTIONAL        ---> number of digits of the binary code
    % a-->numeric OPTIONAL         ---> lower bound of interval
    % b-->numeric OPTIONAL         ---> upper bound of interval
    %IMPORTANT: function has to be called with 4 arguments at least once
    %before calling it with only one argument, as persistent values need to
    %be set.

     persistent per_abd;
     persistent persistent_n;

    %Nargin1
    %decode C
     if nargin  == 1
         if ischar(C)
             x = eval(char(py.phyton.bigint.decode( C ,persistent_n,per_abd(1),per_abd(2))));
         elseif isnumeric(C)
             a = mat2str(C); %vector ----> str [1 2 3] --->str [1,2,3]
             x =  decode_ab(strrep(a,' ',','));

         end



    %NARGIN 4
    %set persistent values for ab and n
     elseif nargin == 4


         if a > b
             error(' b > a on [a,b] interval')
         end
         per_abd = [a , b] ;
         persistent_n = n;
         x = decode_ab(C);

    end



end
```

getdata_mutimodal.m

```
%get probabilities of Himmelblau's function maxima

close all
memory = [0 0 0 0];
% hold all
% x_vect = linspace(-5,5,1000);
% y_vect = linspace(-5,5,1000);
% [x_mesh, y_mesh] = meshgrid(x_vect, y_vect);
%
% %f = @(x,y) 200 - (x.^4 + 2.*x.^2.*y - 22.*x.^2 + y.^2 - 22.*y +121) - (x.^2 + 2.*x.*y.^2 - 14.*x
    + y.^4 - 14.*y.^2 + 49);
% f = @(x,y) 40 - (x.^2 + y.^2)  +  10.*cos(2.*pi.*x) + 10.*cos(2.*pi.*y);
% z_mesh = f(x_mesh,y_mesh);
% mesh(x_mesh, y_mesh, z_mesh)
% %plot3( 3.5804, -1.8200, 200, 'k.','MarkerSize', 7)
% %plot3(-2.8077, 3.1340, 200,'k.','MarkerSize', 7)
% %plot3(2.9905, 2.0118 ,200,'k.','MarkerSize', 7)
% %plot3(-3.7767, -3.2761,200,'k.','MarkerSize', 7)

for i = 1:300
    dat =  main('datamultimodal.txt',15,100,30);

    if dat{1}> 0 && dat{2}>0
        memory = memory + [1 0 0 0];
    elseif dat{1}> 0 && dat{2}<0
        memory = memory + [0 1 0 0];
    elseif dat{1}< 0 && dat{2}>0
        memory = memory + [0 0 1 0];
    elseif dat{1}< 0 && dat{2}<0
        memory = memory + [0 0 0 1];
    end

    disp(i)

    %     scatter3(dat{1},dat{2},dat{3},'r.')
%     drawnow
%     clear main

end



disp(memory)

%  149     71     50     30
```

getdata_unimodal.m

```
%get probabilities of Himmelblau's function maxima

close all
memory = [0 0];
% hold all
% x_vect = linspace(-5,5,1000);
% y_vect = linspace(-5,5,1000);
% [x_mesh, y_mesh] = meshgrid(x_vect, y_vect);
%
% f = @(x,y) 200 - (x.^4 + 2.*x.^2.*y - 22.*x.^2 + y.^2 - 22.*y +121) - (x.^2 + 2.*x.*y.^2 - 14.*x +
    y.^4 - 14.*y.^2 + 49);
%
% z_mesh = f(x_mesh,y_mesh);
% mesh(x_mesh, y_mesh, z_mesh)
% plot3( 3.5804, -1.8200, 200, 'k.','MarkerSize', 7)
% plot3(-2.8077, 3.1340, 200,'k.','MarkerSize', 7)
% plot3(2.9905, 2.0118 ,200,'k.','MarkerSize', 7)
% plot3(-3.7767, -3.2761,200,'k.','MarkerSize', 7)

for i = 1:100
    dat = main('data.txt');

%    [not_found_maxima, found_maxima]

    memory(dat + 1) = memory(dat + 1) + 1;
    disp('----------')
    disp(memory)
    clear main
end
```

Individual.m

```
classdef Individual < handle
    %INDIVIDUAL an individual of the population


    properties
        chrompack
        fitnessval = nan;


    end

    methods

        %fitness(obj) calculates the fitness value of the individual

        function r=fitness(obj,fitness_mode_opts)
             if isnan(obj.fitnessval)
                 obj.fitnessval=fitness(obj.chrompack,fitness_mode_opts);
             end
                 r=obj.fitnessval;
        end


        %constructor checks if genome provided in which case creates obj,
        %constructor checks if given argument is a genome (matrix) or a
        %chrompack (Chrompack object) and creates individual accordingly


        function obj = Individual(information)
            if nargin == 0
            elseif nargin == 1
                len = length(information);
                if isa(information,'Chrompack')
                    if len == 1;
                        obj.chrompack = information;
                    else
                        warning('use individualize method from Chrompack class instead')
                    end
                elseif isa(information,'double')
                    obj.chrompack = Chrompack(information);
                end
            end
        end
    end
end
```

measure_time.m

```
list = zeros(1,4);
speedvect = [];
for i = 20:20:600
    for j = 1:4
        tic()
        % repr length i = 15:30:615
        % [1.0682    1.7389    2.4093    3.0609    3.8373    4.3579    5.0001    5.7808    6.3701
            7.0363    7.7069    8.5390    9.0517    9.7044    10.4194    11.2592    11.7374    12.3754
            13.0258    13.7616    14.4588]
        % main('datamultimodal.txt',i,20,30);


        % popsize i = 20:20:600
        % [     1.0492    2.0691    3.0920    4.1568    5.2992    6.219
        % 7.4522    8.2882    9.2925    10.4069    11.4237    12.6933
        %13.5604    14.4098    15.5961    16.6138    17.5885    18.6490
        %19.7808    21.2651    22.2311    23.2110    24.4957    24.8846
        %26.2526    27.4251    28.9737    30.0530    30.7897    31.6119]



        main('datamultimodal.txt',15,i,30);
        list(j) = toc();
    end
    speedvect = [speedvect, min(list)];
    disp(i)
end

disp(speedvect)
```

mutate.m

```
function [ mutated_Individual_array ] = mutate( Individual_array , p )
%MUTATE mutate single character



%set default p mutation if not given by user

if nargin == 1
    p = 0.2;
end

chrompack_array= [Individual_array.chrompack];

preallocated_chroms(1,length(Individual_array)) = Chrompack();

for i = 1:length(chrompack_array)

preallocated_chroms(i) = mutate_chrom(chrompack_array(i),p);

end

mutated_Individual_array = individualize(preallocated_chroms);

end





function [ mutated_chrompack ] = mutate_chrom( chrompack , p )



%MUTATE mutate single character

%input --> chrompack
%output --> chrompack


%mutate single bit only if favorable biased coin toss
if not(randi([0,floor(1/p)]))
    genome = chrompack.genome;
    randompos = randi(numel(genome));
    genome(randompos) = not(genome(randompos));
    mutated_chrompack = Chrompack(genome);
else
    mutated_chrompack = chrompack;


end
end
```

Population.m

```
classdef Population < handle

    properties
        pop
        popsize = 0;
        bestpopindividual
        bestfitness = 0;
        meanfitness = 0 ;
        fitness_mode_opts

    end

    methods

        %after checking an Individual is given, adds it to the population
        function addindividual(obj,indiv)
            if not(isa(indiv,'Individual'))
                error('addindividual method can only add Individual objects to Population.pop')
            end
            obj.pop=[obj.pop , indiv];        %add indiv to pop
            obj.popsize = obj.popsize + 1; %increment by 1 popsize
            %fitness(obj.pop);              %fitnnes can be calculated upon
                                           %addition, sacrificing speed


        end


        %constructor checks type of input and creates obj
        %acepted inputs ---> Individual / Individual array

        function obj=Population(Individual_array , fitness_mode_opts)
            if nargin > 0
                if isa(Individual_array(1),'Individual')
                    obj.pop=Individual_array;
                else
                    error('Pupulation constructor can only get Individual arrays as input')
                end
                obj.popsize = obj.popsize + length(Individual_array);
                obj.fitness_mode_opts  = fitness_mode_opts;
                %fitness(obj);
            end
        end

        %we calculate the the fitness of the entire population and save the
        %best individual, and its fitness. We also calculate the mean
        %fitness and the number of individuals

        function fitvector = fitness(obj)
            %calculate fitness only if not previously calculated
            fitvector=arrayfun(@(x)x.fitness(obj.fitness_mode_opts), obj.pop);
            [maxf,maxindex]=max(fitvector);
            obj.meanfitness=sum(fitvector)/obj.popsize;

            if  obj.bestfitness < maxf
                obj.bestfitness=maxf;
                obj.bestpopindividual=obj.pop(maxindex);
            end


        end



    end




end
```

randpop.m

```
function [ pop ] = randpop( C , popsize , mode )
%RANDPOP generate random population drom a given individual example
%Input--->
%   C       ---> binary code, as an example of the individuals to generate
%   popsize ---> the number of individuals to be created
%
%Output--->
%   pop_of_individuals ---> randomly initialized population


%we extract examples size
[nchrom,chromlength] = size(C);

%- we create a matrix of random genomes, concatenated one next to the other
%- using mat2cell, we slice this concatenation of genomes to cells with one
%genome each

cell_of_genomes = mat2cell(randi([0,1],nchrom,chromlength * popsize),nchrom,ones(1,popsize)*
    chromlength);

%convert genomes to chromosomes,and chromosomes to individuals
cell_of_individuals = (cellfun(@(x) Individual(Chrompack(x)), cell_of_genomes,'UniformOutput',false)
    );

%convert cell aray to normal array
array_of_individuals = [cell_of_individuals{:}];

pop = Population(array_of_individuals , mode);

end
```

select_ga.m

```
function [ matingpool ] = select_ga( population )

%Selection with sigma trunc. and SRSWR
    %             sigma truncation
    %This is how sigma truncation works:
    %   A) fit'=fit - {mean(fit) - c * stdeviation(fit)}
    %   B) negative values set to 0
    %
    %
    %           stochastic remainder sampling without replacement
    %A) Expected individual count values calculated, and integer values
    %calculated and assigned
    %B) Treat fractional parts as biased coin tosses untill population is
    %full

    fitvector = fitness(population);  %we calculate fitness
    fitvector = fitvector + normrnd(0,0.01,1,length(fitvector)); %we add small noise to ensure non uniformity
    fitvector = sigmatruncation(fitvector,population.meanfitness); % apply sigma truncation
    %SRSWR selection method
    choicevector = fitvector.* population.popsize ./ sum(fitvector);
    selectedquantity = floor(choicevector); %calculate the integer parts
    remainder = choicevector - selectedquantity; %calculate non-integer parts
    sumselectedquantity = sum(selectedquantity); %calculate sum of integer parts
    if sumselectedquantity > population.popsize % check if new pop wil be too big
        error('new population popsize will exceed pop popsize')
    end

    P = remainder/sum(remainder); %we make the sum of remainders be 1, thus calculate the probabilities
    C = cumsum(P); %we calculate the cumulative probabilities

    for ind=1:(population.popsize - sumselectedquantity) %iterate untill population full
        randomposition=(1+sum(C(end)*rand>C));  % + 1 on a random position to selectedquantity
        selectedquantity(randomposition) = selectedquantity(randomposition) + 1 ;
    end

    if sum(selectedquantity) ~= population.popsize
        %disp(selectedquantity)
        %disp(population.popsize)
        %check if poppopsize == selectedquantity
        error('pop popsize and selectedquantity mismatch')
    end




   matingpool=repelem(population.pop,selectedquantity);


end

function [scalledfitvector] = sigmatruncation(fitvect,meanfitness)
    c=2;
    scalledfitvector = fitvect - (meanfitness - c*std(fitvect));
    scalledfitvector(scalledfitvector<0) = 0;
end
```

A.1.2 Utility Functions

Gbundle.m

```
classdef Gbundle < handle
    %MATEDPOOLINFO an auxiliary class to be able to do A(1,3) = Individual([chrompack1 chrompack2 chrompack3])
    %
    %
    %   setgetnext(input)---->  set chrompack array
    %   setgetnext()---------->  get next chrompack
    properties

    end

    methods (Static)

        function r = setgetnext(input)
            persistent sharedchrompacks;
            persistent index;
            if not(nargin)
                index = index + 1;
                r = sharedchrompacks(index);
            else
                index = 0;
                sharedchrompacks = input;
                r = 0;
            end
        end
    end
end
```

nextline.m

```
function [ text_line ] = nextline( textfile )
%NEXTLINE read next line of a file, ignores comment lines , blank lines or
%lines starting with an space. terminate read wen END is found


persistent textID;
persistent control;
persistent per_textfile;


% If textID is empty ---> open textfile to set textID
%                   ---> set per_textfile as textfile
if isempty(textID)
    textID = fopen(textfile);
    per_textfile = textfile;
end

%detect changes in textfile
if per_textfile ~= textfile
    error('data file changed')
end


control = '%';
%read until non void line or non coment line found and only if no 'END' read
while (strcmp(control, '%') || strcmp(control, '') || strcmp(control, ' ')) && not(strcmp(control, 'END'))

    %read line
     text_line = fgetl(textID);

     %if line void, control = ''
     %        else , control = text_line's first character (to detect
     %        comment lines)
     if isempty(text_line)
         control  = '';
     else
         control = text_line(1);
     end

end

%check if last line 'END', if so close file

if strcmp(text_line , 'END')
    disp(' END line found. Text file will be closed.')
    fclose(textID);
    clear textID
    clear control
    clear per_textfile
end


end
```

shuffle.m

```
function [ outarray ] = shuffle( inarray )
%SHUFFLE shuffles given array
index = randperm(length(inarray));
outarray = inarray(index);

end
```

A.1.3 Python Code

bigint.py

```python
from decimal import *  #we need this module so that we can reduce the numerical error in code/decode functions
from math import floor
getcontext().prec = 100 #we set default precision to 100 (which is very high)


##################################################################################
###################           CODE                    ##############################
##################################################################################


#return the binary code of an integer string (decimal integer)



def code(*args):

    ####code(x)####
    # x      ---> integer
    # output ---> list of 0 and 1 integers

    if len(args) == 1:

        #calculate binary string
        binary_string = bin(int(args[0]))
        #return an integer list
        return [int(x) for x in binary_string.split('b')[1]]



    ####code(x,n)####
    # x      ---> integer
    # n      ---> integer [number of digits we want on binary code]
    # output ---> list of 0 and 1 integers

    elif len(args) == 2:



        #calculate code(x)
        C = code(int(args[0]))

        #convert n to int to avoid problems
        n = int(args[1])

        #check if n too small, if not return C with zeroes at the begining
        if len(C) > n:
            print('len(c): '+str(len(C)))
            print('n: '+str(n))

            raise ValueError("len(C) > n , n is too small")
        else:
            dif = n - len(C)
            return  [0]*dif + C








    ####code(x,n,a,b)####
    # x      ---> float     ,  xâĆň[a,b]]
    # n      ---> integer   ,  number of digits we want on binary code
    # a      ---> float     ,  lower bound of interval
    # b      ---> float     ,  upper bound of interval
    # output ---> list of 0 and 1 integers

```

```
    elif len(args) == 4:

        getcontext().prec = int(floor(args[1]/4)) + 100
        x = Decimal(args[0])
        #convert n to int to avoid problems
        n = int(args[1])
        a = Decimal(args[2])
        b = Decimal(args[3])

        #set precision
        #10**n is a upper bound of (2**4)**n = 8**n

        getcontext().prec = int(floor(n/4)) + 100


        return str(code(int((Decimal(x) - Decimal(a))  /  (Decimal(b) - Decimal(a))  *  Decimal(2 **
            n - 1)) , n ))




############################################################################################
####################              DECODE                    #################################
############################################################################################


def decode(*args):

    #### decode(C)####
    # C       ---> binary list
    # output ---> integer

    if len(args) == 1:
        C = args[0]
        n = len(C)
        # [1,1,0,1] = sum([ 2^3 , 2^2 , 2^0]
        return   int(sum([2**(n - j - 1) for j in range(n) if C[j]]))






    #### decode(C,n,a,b)####
    # C       ---> binary list string ,  so that we can easily import an array from matlab
    # n       ---> integer              ,  number of digits we have on binary code
    # a       ---> float                ,  lower bound of interval
    # b       ---> float                ,  upper bound of interval
    # output ---> string(Decimal)

    if len(args) == 4: #n  = len(C) , however, we add it as an input argument for consistency with
        code calls

        getcontext().prec = int(floor(args[1]/4)) + 100
        C = eval(str(args[0]))
        n = int(args[1])
        a = Decimal(args[2])
        b = Decimal(args[3])

        if not(len(C) == n):
            raise ValueError("len(C) and n missmatch ")

        x = Decimal(decode(C))

        # return value on string format, without scientific notation
        return format(  Decimal(a + ( x  / (2**n - 1) * (b - a))) , 'f')
```

A.2 Matlab and Python Code for Polynomial Interpolation

Note: This code is the same on some modules.

A.2.1 Main Functions and Classes

main.m

```
function [ population ] = main( txtfile )

%we want no warnings on badly conditioned polinomials
warning('off','MATLAB:polyfit:RepeatedPointsOrRescale')


%Read sample Individual's genome
clear nextline
mode         = nextline(txtfile);
fitness_opts = eval(nextline(txtfile));


%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%create fitness_mode_opts --> {'mode',%fitnessopts%}
fitness_mode_opts = {mode,fitness_opts{:}};
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%

C_data            = eval(nextline(txtfile));
popsize           = eval(nextline(txtfile));
imax              = eval(nextline(txtfile));

a = fitness_mode_opts{2};
b = fitness_mode_opts{3};
f = fitness_mode_opts{4};
n = fitness_mode_opts{5};



%Initialize population with randpop, and write mode_fitness_opts on popultion
population = randpop(C_data,popsize,fitness_mode_opts);

hold all

%we create two points to name the legends, make room for legends, and
%preallocate x axis


legend('Max. fitness','Mean fitness','Location','southeast')
for i = 1:imax

    matingpool = select_ga(population);
    matedpool = crossover(matingpool);
    population.pop = mutate(matedpool);
    scatter(i,population.bestfitness,'.','MarkerEdgeColor','red')
    scatter(i,population.meanfitness,'.','MarkerEdgeColor','blue')
    drawnow


end
%plot function and found maxima
figure
%preallocate vector of positions of interpolating points
x = zeros(1,n);
%get best interpolating points
for i=1:n
    x(i) = decode_ab(population.bestpopindividual.chrompack.genome(i,:),size(C_data,2),a,b);
end
hold all


%plot f function
plot(a:(b-a)/1000:b,f(a:(b-a)/1000:b))

```

```
%plot interpolating polinomial
%get the polinomial coefficients
 p = polyfit(x,f(x),n-1);
%define polinomial handle
pol =  @(y) evalpol(p,y);

[~,error] = calculatefitness(population.bestpopindividual.chrompack.genome,fitness_mode_opts,true);



plot(x,f(x),'go', 'markersize', 5);

text(0,0,{'error: ',error});

plot(a:(b-a)/100000:b, pol(a:(b-a)/100000:b))





legend('f','interpolating points','ga interpolation','Location','southeast')

hold off
end
```

calculatefitness.m

```
function [ fitness , error ] = calculatefitness( genome , fitness_mode_opts, calc_error )



    if ~exist('calc_error','var')
     % third parameter does not exist, so default it to something
      calc_error = false;
    end

    mode = fitness_mode_opts{1};


    switch mode
        case 'function_max'
            fitness  = function_max(genome,fitness_mode_opts);
        case 'pol_interp'
            [fitness ,error] = pol_interp(genome,fitness_mode_opts, calc_error);


    end
end


%mode = 'function_max'
function [fitness] = function_max(genome,fitness_mode_opts)

    %fitness_opts = {'function_max', a , b , @(x) f(x)}


    f = fitness_mode_opts{4};
    x = decode_ab(genome , length(genome) , fitness_mode_opts{2} , fitness_mode_opts{3});
    fitness = f(x);


end


%mode = 'pol_interp'%
function [fitness , error] = pol_interp(genome,fitness_mode_opts,calc_error)
    %fitness_opts = {'pol_interp',a,b,f,n};
    %%%NEED TO ADD IF ROW OF GENOME REPEATED, FITNESS = 0%%%

%     if rank(genome) < size(genome,1)
%         fitness = 0;
%         return;
%     end

    f = fitness_mode_opts{4};
    n = fitness_mode_opts{5};
    %preallocation
    x = zeros(1,n);

    %length of each chromosome
    len = length(genome(1,:));

    for i=1:n
    x(i) = decode_ab(genome(i,:) , len , fitness_mode_opts{2} , fitness_mode_opts{3});
    end


    %get the polinomial coefficients
    p = polyfit(x,f(x),n-1);


    %define polinomial handle
    pol =  @(y) evalpol(p,y);

    f_integral = @(y)  -exp(cos(y)).*(-1 + cos(y));


    %define function to be integrated
```

```
    h = @(y) abs(f(y) - pol(y));

    %for fitness to be positive and positively oriented, we apply - log(x  + 0.00001)

    pol_int = polyint(p);


    if n > 2
        pol_int_value = abs(f_integral(fitness_mode_opts{3})-evalpol(pol_int,fitness_mode_opts{3}) - f_integral(fitness_mode_opts{2}) + evalpol(pol_int,fitness_mode_opts{2}));
        fitness = pol_int_value;
        if calc_error == true;
            L1_norm = integral(h,fitness_mode_opts{2} , fitness_mode_opts{3}, 'RelTol',0,'AbsTol',1e-12);
            error = L1_norm;
        else
            error = 'unknown';
        end
    else
        L1_norm = integral(h,fitness_mode_opts{2} , fitness_mode_opts{3}, 'RelTol',0,'AbsTol',1e-12);
        fitness = L1_norm + 0.00001;
        if calc_error == true;
            error = L1_norm;
        else
            error = 'unknown';
        end

    end

    fitness =100 - log(fitness);
    %disp(fitness)

%   we set fitness to 0 for negative fitness values
%      if fitness < 0
%          fitness = 0;
%      end


end
```

Chrompack.m

The same file as the one defined in Max Search.

code_ab.m

The same file as the one defined in Max Search.

crossover.m

The same file as the one defined in Max Search.

data.txt

```
%mode ---> tell the main file what mode will e be operating on
pol_interp

%Fitness function options. For 'pol_interp' mode , a cell containing:
%  {a , b , f ,n} where n is the number of interpolating points
%                                                           1 --> horizontal line
%                                                           2 --> inclined line
%                                                           3 --> parabola ...

{-4 , 1 , @(x) sin(x) .* cos(x) .* exp(cos(x)) , 70 }


%The sample Individual's genome (C) chrom length will be decided based on n 50
[0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0]



%Population size (popsize)100
100

%Number of iterations (imax) 30
30






END
```

decode_ab.m

The same file as the one defined in Max Search.

Individual.m

The same file as the one defined in Max Search.

mutate.m

The same file as the one defined in Max Search.

Population.m

The same file as the one defined in Max Search, except line 7 is set to:
$bestfitness = -10^{30}$;

randpop.m

```
function [ pop ] = randpop( C , popsize , mode )
%RANDPOP generate random population drom a given individual example
%Input-->
%   C        ---> binary code, as an example of the individuals to generate
%   popsize  ---> the number of individuals to be created
%
%Output-->
%   pop_of_individuals ---> randomly initialized population


%we extract examples size
nchrom = mode{5};
chromlength = size(C,2);

%- we create a matrix of random genomes, concatenated one next to the other
%- using mat2cell, we slice this concatenation of genomes to cells with one
%genome each

cell_of_genomes = mat2cell(randi([0,1],nchrom,chromlength * popsize),nchrom,ones(1,popsize)*
    chromlength);

%convert genomes to chromosomes,and chromosomes to individuals
cell_of_individuals = (cellfun(@(x) Individual(Chrompack(x)), cell_of_genomes,'UniformOutput',false)
    );

%convert cell aray to normal array
array_of_individuals = [cell_of_individuals{:}];

pop = Population(array_of_individuals , mode);

end
```

select.m

The same file as the one defined in Max Search.

A.2.2 Utility Functions

Gbundle.m

The same file as the one defined in Max Search.

nextline.m

The same file as the one defined in Max Search.

shuffle.m

The same file as the one defined in Max Search.

evalpol.m

```
%Evaluate pol, utility function to define handle interpolating polinomial
function [ k ] = evalpol( P,x )
k=zeros(1,length(x));
for s=1:length(P)
    k=k+P(s).*x.^(length(P)-s);
end
```

A.2.3 Python Code

bigint.py

The same file as the one defined in Max Search.

A.3 Code of List Sorting

A.3.1 1^{st} original approach

main.py

```
import modules_ga as mo
import random
import copy
from matplotlib import pyplot as plt
from tqdm import tqdm
from statistics import stdev, mean




def consecutive_list_generator():
    for i1 in range(8):
        for i2 in range(7):
            option_list = list(range(8))
            option_list.remove(i1)
            i2 = option_list[i2]
            for i3 in range(6):
                option_list = list(range(8))
                option_list.remove(i1)
                option_list.remove(i2)
                i3 = option_list[i3]
                for i4 in range(5):
                    option_list = list(range(8))
                    option_list.remove(i1)
                    option_list.remove(i2)
                    option_list.remove(i3)
                    i4 = option_list[i4]
                    for i5 in range(4):
                        option_list = list(range(8))
                        option_list.remove(i1)
                        option_list.remove(i2)
                        option_list.remove(i3)

                        option_list.remove(i4)
                        i5 = option_list[i5]
                        for i6 in range(3):
                            option_list = list(range(8))
                            option_list.remove(i1)
                            option_list.remove(i2)
                            option_list.remove(i3)
                            option_list.remove(i4)
                            option_list.remove(i5)
                            i6 = option_list[i6]
```

```
                                for i7 in range(2):
                                    option_list = list(range(8))
                                    option_list.remove(i1)
                                    option_list.remove(i2)
                                    option_list.remove(i3)
                                    option_list.remove(i4)
                                    option_list.remove(i5)
                                    option_list.remove(i6)
                                    i7, i8 = option_list[i7] , option_list[(i7 + 1)%2]
                                    yield [i1, i2, i3, i4, i5, i6, i7, i8]


random.seed(4)
a = mo.broadcast_device(sr = '1w:ww:w00wc::l1c::01w01cc010wc10w1100c1w0*01*0:0w0w00:11ccw00l00B0001c1:c1101101ww1wc0'
                                 '::11:l:101101*01cc1::*:c0111c:10cw1c01:1011cb1w10cww0w:0011w10c0w111ccc11:w0B:11w0w*wc*'
                                 '::10w00:10www:1w11c1::0c::110w:c10:1ccw:w0:10:cw1**::1w*1w:1w:00cw0cwwl001*:c00c*0:00*1'
                                 'w0w1000011:wc0*c110c0wcc01ww:11l:*::Bc01c0B1cl1ww101:wc:0100cww0*ww*cw1w10:::0w11:11:11'
                                 'cw1w:0w:wwc:c*1wc100111w010:cw1cc0100c1c01ccw1::101::wc11c0www:wb*10::c*c0111c1w00w1w0c1'
                                 '1:1110101100:11:0c0c0c1::::110:c011101:01110:w:0cw100*:0c:1w:010:')

fitness_value = mo.fitness_function(a,
                                number_of_shuffled_lists_measured=100,
                                comparision_rounds=20,
                                max_nullfit_on_10=10)



ed = []
i = 0
for sl in consecutive_list_generator():
    i += 1
    if i%100 == 0:
        print(i)
    random.seed(5+i)
    sl_copy = copy.copy(sl)
    mo.sort_list_with_bd(a, sl_copy, 20)
    ed.append(mo._measure_order(sl) - mo._measure_order(sl_copy))

    '''
    print(f'fitness value: {fitness_value}')
    print('-----')
    print(sl)
    print(sl_copy)
    print('-----')
    print(f'entropy diference: {mo._measure_order(sl) - mo._measure_order(sl_copy)}')
    '''

print(ed)
print(mean(ed))

plt.hist(ed, bins = [-2,-1.75,-1.5,-1.25,-1,-0.75,-0.5,-0.25,-0.01,0.01,0.25,0.5,0.75,1,1.25,1.5,1.75,2])
plt.show()
#mo.fit()
```

modules_ga.py

```python
import math
import random
from statistics import stdev, mean
import numpy as np
from tqdm import tqdm
#from pympler import summary, muppy
#import multiprocessing.pool
import functools


# region finess and list modules

# argmax returns index of highest value
def argmax(iterable):
    return max(enumerate(iterable), key=lambda x: x[1])[0]



# measure list's entropy on logarithmic scale
def _measure_order(input_list):
    """
     calculate the level of disorder of the input list. It is measured on a logarithmic scale

    :param input_list: the list to be measured
    :return: positive float
    """

    #  sum( |input_list - ordered list| )
    sum_of_difference = sum([abs(input_list[i] - i) for i in range(len(input_list))])
    return math.log1p(sum_of_difference)


# binaryze and debinarize
def _decimal(list_of_binary_strings):
    return sum((2**i for i in range(len(list_of_binary_strings))
                if list_of_binary_strings[len(list_of_binary_strings) -1 -i] =='1'))


# get binary list of strings '1' and '0' of size bin_len.
def _binary(decimal_number, bin_len):
    if decimal_number < 0:
        raise ValueError('Negative numbers have no binary')
    c = str(bin(decimal_number))
    c = c[2:]
    c = [char for char in c]
    return (bin_len - len(c))*['0'] + c


#  return n sized shuffled list
def _generate_random_list(n):
    return_list = list(range(n))
    random.shuffle(return_list)
    return return_list


#  interprets messages by updating the list to be ordered and updating the message list.
#  Only one comparison per iteration
def _process_messages(shuffled_list, env_messages):
    max_messages = 8
    max_message_length = 8
    list_size = len(shuffled_list)
    advaliable_comparation = True # This variable makes sure only 1 comparation per iteration is done
    return_messages = []
    message_size = int(2*(math.log2(list_size)) + 2)
    piece_length = int((message_size - 2) / 2)
    for i in range(len(env_messages)):
        current_message  = env_messages[i]
        if len(current_message) == message_size:
            # ignore message
            # compare elements (only once per iteration)
```

```
            if env_messages[i][0:2] == ['1', '1'] or env_messages[i][0:2] == ['0', '0']:
                # advaliable_comparation = False
                first_piece = _decimal(env_messages[i][2:2 + piece_length])
                second_piece = _decimal(env_messages[i][2 + piece_length:2 + piece_length * 2])

                # if change is benefitial
                if (
                        shuffled_list[first_piece] < shuffled_list[second_piece]
                    and first_piece > second_piece
                ) or (
                        shuffled_list[first_piece] > shuffled_list[second_piece]
                    and first_piece < second_piece
                ):
                    # if first piece < second piece, just change the prefix
                    if first_piece < second_piece:
                        env_messages.insert(0, ['1', '1'] + env_messages[i][2:])
                        env_messages.pop(i+1) #delete compared message
                    # else, swap places and change prefix
                    else:
                        env_messages.insert(0, ['1', '1'] +
                                        env_messages[i][2 + piece_length:2 + piece_length * 2] +
                                        env_messages[i][2:2 + piece_length])
                        env_messages.pop(i+1)

                # if change is NOT benefitial
                else:
                    if first_piece < second_piece: #pieces in order
                        env_messages.insert(0, ['0', '0'] + env_messages[i][2:])
                        env_messages.pop(i+1)
                    else:
                        env_messages.insert(0, ['0', '0'] +
                                        env_messages[i][2 + piece_length:2 + piece_length * 2] +
                                        env_messages[i][2:2 + piece_length])
                        env_messages.pop(i+1)


            # swap pieces
            elif env_messages[i][0:2] == ['1','0']:
                index0 = _decimal(env_messages[i][2:2+piece_length])
                index1 = _decimal(env_messages[i][2+piece_length:2 + 2*(piece_length)])
                index0, index1 = sorted([index0,index1])[0], sorted([index0,index1])[1]
                shuffled_list[:] = (shuffled_list[index1:] +
                                    shuffled_list[index0:index1] +
                                    shuffled_list[:index0])

            # swap elements
            elif env_messages[i][0:2] == ['0', '1']:
                index0 = _decimal(env_messages[i][2:2 + piece_length])
                index1 = _decimal(env_messages[i][2 + piece_length:2 + 2 * (piece_length)])
                if index0 != index1:
                    shuffled_list[index0], shuffled_list[index1] = shuffled_list[index1],
                        shuffled_list[index0]

        else:
            return_messages.append(env_messages[i])
    env_messages = env_messages[0:max_messages]
    for i in range(len(env_messages)):
        env_messages[i] = env_messages[i][0:max_message_length]
    return return_messages


# sorts list with broadcast_device

def sort_list_with_bd(b_device,shuffled_list,max_iterations):
    i = 0
    env_messages = [['1','1','0','0','0','1','1','1']]
    _process_messages(shuffled_list, env_messages)
    while i < max_iterations and env_messages:
        i = i + 1
        process_broadcast_device(b_device, env_messages)
        _process_messages(shuffled_list,env_messages)
```

```
#  return broadcast device's fitness on a single list
def fitness_function(b_device,
                     number_of_shuffled_lists_measured,
                     comparision_rounds=150,
                     max_nullfit_on_10 = 10,
                     fast_0_fitness = False,
                     list_size=8
                     ):
    if number_of_shuffled_lists_measured != 1:
        number_of_nullfit = 0
        fit_list = []
        for i in range(number_of_shuffled_lists_measured):
            #print each individual once
            #if i  == 0:
                #print(b_device)
            fit = fitness_function(b_device,
                     number_of_shuffled_lists_measured = 1,
                     max_nullfit_on_10 = max_nullfit_on_10,
                     comparision_rounds = comparision_rounds,
                     fast_0_fitness = fast_0_fitness,
                     list_size=list_size
                     )
            fit_list.append(fit)
            if fit == 0:
                # we get rid of bd if no response in first iteration
                if i == 1 and fast_0_fitness:
                    return 0.0
                number_of_nullfit += 1
                # we get rid of bd if too many null fitness on first 10 iterations
                if number_of_nullfit == max_nullfit_on_10 and i < 10:
                    return 0.0
            if i == number_of_shuffled_lists_measured-1:

                # percentage of improved lists - 0.5

                #return (sum((1 for i  in fit_list if i > 0.00001))/
                    number_of_shuffled_lists_measured) - 0.5
                # the mean of improvement
                return mean(fit_list)
    shuffled_list = _generate_random_list(list_size)
    shuffled_entropy = _measure_order(shuffled_list)
    sort_list_with_bd(b_device, shuffled_list,comparision_rounds)
    return (shuffled_entropy - _measure_order(shuffled_list))


# endregion


# region genetic algorithm operators


#initializes bd of length bd_length and initializes random characters based on given
#prob_dist = [0, 1, *, :, w, b, B, l, c]
def initialize_random_bd(bd_length, prob_dist):
    random.seed()
    return broadcast_device(sr = [_get_char(prob_dist) for i in range(bd_length)])

#auxiliar function for initialize_random_bd
def _get_char(prob_dist, posible_chars = ('0', '1', '*', ':', 'w', 'b', 'B', 'l', 'c')):

    return random.choices(posible_chars,weights = prob_dist, k=1)[0]


#initializes random bd with no nule fitness
def initialize_random_bd_no_0_fitness(bd_length,
                                      comparision_rounds,
                                      number_of_shuffled_lists_measured,
                                      fast_0_fitness,
                                      max_nullfit_on_10
                                      ):
```

```
    prob_dist = (0.25, 0.25, 0.05, 0.15, 0.15, 0.01, 0.01, 0.01, 0.12)
    #           [ '0', '1' , '*' , ':' , 'w' , 'b'  , 'B'  , 'l'  , 'c' ]
    bd = initialize_random_bd(bd_length=bd_length, prob_dist=prob_dist)
    fitness = fitness_function(bd, number_of_shuffled_lists_measured=number_of_shuffled_lists_measured,
                               fast_0_fitness=fast_0_fitness, comparision_rounds=comparision_rounds,
                               max_nullfit_on_10=max_nullfit_on_10)

    it = 0
    while fitness == 0:
        it +=1
        if it%50 == 0:
            print(str(it) + ' iterations without bd initialization')
        bd = initialize_random_bd(bd_length, prob_dist=prob_dist)
        fitness = fitness_function(bd, number_of_shuffled_lists_measured=number_of_shuffled_lists_measured,
                                   fast_0_fitness=fast_0_fitness, comparision_rounds=comparision_rounds,
                                   max_nullfit_on_10=max_nullfit_on_10)

    return bd

# get bd list of fitness. If fitness on first list is 0, set bd's fitness to 0
# without further operations
def _bd_list_fitness(bd_list,number_of_lists_sampled,comparision_rounds,max_nullfit_on_10):
    fitness_list = []
    for i in range(len(bd_list)):
        random.seed(4)
        fitness_list.append(
            fitness_function(
                            b_device=bd_list[i],
                            number_of_shuffled_lists_measured=number_of_lists_sampled,
                            comparision_rounds=comparision_rounds,
                            max_nullfit_on_10=max_nullfit_on_10
                             )
                            )
    return fitness_list

# scale fitness with sigma truncation
def _sigma_truncation(list_of_fitness):
    c = 2
    sigma = stdev(list_of_fitness)
    mu = mean(list_of_fitness)
    return [(list_of_fitness[i] - (mu - c*sigma)) for i in range(len(list_of_fitness))]


# returns list with number of offspring using roulette wheel selection
# https://stackoverflow.com/questions/10324015/fitness-proportionate-selection-roulette-wheel-selection-in-python
def _roulette_selection(weights):
    '''performs weighted selection or roulette wheel selection on a list
    and returns the index selected from the list'''

    # sort the weights in ascending order
    sorted_indexed_weights = sorted(enumerate(weights));
    indices, sorted_weights = zip(*sorted_indexed_weights);
    # calculate the cumulative probability
    tot_sum = sum(sorted_weights)
    if tot_sum == 0:
        prob = [1/len(sorted_indexed_weights) for i in range(len(sorted_indexed_weights))]
    else:
        prob = [x / tot_sum for x in sorted_weights]
    cum_prob = np.cumsum(prob)
    # select a random a number in the range [0,1]
    random_num = random.random()

    for index_value, cum_prob_value in zip(indices, cum_prob):
        if random_num < cum_prob_value:
            return index_value


# mates using two point crossover
def crossover(mate0,mate1):
```

```python
    sr0 = mate0.sr
    sr1 = mate1.sr

    mating_indexes = [random.randint(0,len(sr1)-1),random.randint(0,len(sr1)-1)]
    mating_indexes.sort()

    return [
        broadcast_device(
        sr = sr0[:mating_indexes[0]] +
             sr1[mating_indexes[0]:mating_indexes[1]] +
             sr0[mating_indexes[1]:]),
        broadcast_device(
        sr = sr1[:mating_indexes[0]] +
             sr0[mating_indexes[0]:mating_indexes[1]] +
             sr1[mating_indexes[1]:])
    ]


# mutation anywhere, taking into account prob mutation and prob_dist
def simple_mutation(bd,prob_mutation = 0.02,**kwargs):
    n_mutations = math.floor(len(bd.sr)* prob_mutation )
    if 'prob_dist' in kwargs:
        prob_dist = kwargs['prob_dist']
    else:
        prob_dist = (0.20,0.20,0.10,0.10,0.03,0.2  ,0.03,0.03,0.11)
    pass

    partial_sum = [sum(prob_dist[0:i]) for i in range(1, len(prob_dist) + 1)]

    while n_mutations > 0:
        n_mutations += -1
        bd.sr[random.randint(0,len(bd.sr)-1)] = _get_char(partial_sum)


# endregion


#region broadcast device modules

class broadcast_device:

    sr = []
    _active_sr = []
    type = -2

    # kwargs --> sr or string_representation: initializes with sr (it can be a string or a list)
    def __init__(self,**kwargs):

        '''


        :param kwargs: sr / string_representation: list or string to initialize broadcast
        '''

        #set sr if input sr given
        if 'string_representation' or 'sr' in kwargs: #check if sr is given
            if 'string_representation' in kwargs:
                input_sr = kwargs['string_representation']
            else:
                input_sr = kwargs['sr']

            if isinstance(input_sr,str):
                self.sr = list(input_sr)
            elif isinstance(input_sr,list):
                self.sr = input_sr
            else:
                raise TypeError('unsupported type: {} for sr initialization. '.format(type(input_sr)))


    #returns the list sr as a string
    def __str__(self):
        return str(''.join(self.sr))
```

```
    #returns the length of sr
    def __len__(self):
        return len(self.sr)


    #removes all quotes and quoted elements from sr and returns the list (it does not change sr)
    def _unquote(self): # return unquoted list of chars
        if self.sr:
            if self.sr[0] == "c":
                return [self.sr[i] for i in range(1,len(self)) if self.sr[i-1] != "c" and self.sr[i] != "c"]
            else:
                return [self.sr[i] for i in range(0,len(self)) if i ==0 or (self.sr[i-1] != "c" and self.sr[i] != "c")]


    #retuns list of broadcast units, splitting them by *. It automatically uncoments sr
    def piecewise(self):
        self_unquoted = self._unquote()
        if not self_unquoted:
            return []
        unquoted_string = ''.join(self_unquoted)
        piecewise_strings = unquoted_string.split('*')
        return [broadcast_device(sr = i) for i in piecewise_strings if i != '']


    #sets _active_sr and returns the length of the set list. If retun the numbe of ':' found
    def _decompose_and_set_active_sr(self):
        b = []  # in this list we save de indexes at wich instances of ':' were found
        count = 0 #number of ':' instances found
        for i in range(len(self)):
            if self.sr[i] == ':': # when ':' instance found, apend it to b
                b.append(i)
                count += 1
                if count == 3: # when third instance of ':' found, ignore rest
                    self._active_sr = [self.sr[0:b[0]], self.sr[b[0] + 1:b[1]], self.sr[b[1] + 1:b[2]]]
                    return count
        if count == 2: # if only two instances found, return appropiate list of sr pieces
            self._active_sr = [self.sr[0:b[0]], self.sr[b[0] + 1:b[1]], self.sr[b[1] + 1:]]
            return count
        elif count == 1: # if only one instance of ':' found, return appropiate list
            self._active_sr = [self.sr[0:b[0]], self.sr[b[0] + 1:]]
            return count
        return 0 #if no ':' found, return 0


    #set type, and while doing so modify self.sr to try to convert it to a unit
    #it also sets the active string representation
    def set_type(self):

        if self.type == -2:
            if not self.sr:
                self.type = 0
                return
            ### we need to make sure c is not on self.sr before setting type ###
            #self.sr = self.piecewise()[0].sr  # Make sure that the bc device is a bc unit, or just take the first bu
            count = self._decompose_and_set_active_sr()
            if count == 0:
                self.type = 0
            elif count == 1: #it could be type 1 bu
                if  self._active_sr[0] and self._active_sr[1]: #[1 , 1] --> type 1
                    self.type = 1
            else:  # in this case, we have found our two valid ':' , it could be type 2,3,4
                if not self._active_sr[0]: #if first component is empty [ - , ? , ? ]
                    # 2nd and 3rd components are non empty --> type 2 [- , 1 , 1]
                    if self._active_sr[1] and self._active_sr[2]:
                        self.type = 2
                else: #if first component is non empty [ 1 , ? , ? ]
                    if not self._active_sr[1]: #if second component empty [1 , - , ? ]
```

```
                        if self._active_sr[2]: # if third component non-empty [1 , - , 1]
                            self.type = 3
                    elif self._active_sr[2]: #[1,1,1]
                        self.type = 4
        if self.type == -2:
            self.type = 0 #when no other type mach, set type to 0



# splits the bd into b units, activates their ASR and calls _process_broadcast_units
def process_broadcast_device(bd, env_mes_list,max_mes = 5, max_message_len = 8):
    bu_list = bd.piecewise()
    for bu in bu_list:
        bu.set_type()
    _process_broadcast_units(bu_list,env_mes_list,max_mes, max_message_len)




def _process_broadcast_units(array_of_active_units, env_mes_list,max_mes, max_message_len):

     # max_mes maximum number of messages to be outputted

    new_env_mes_list = []

    # we first process type 4 units
    t4_ind = [i for i in range(len(array_of_active_units))
                if array_of_active_units[i].type == 4]  # select type 4 units
    for current_bu_ind in t4_ind:
        # process type 4 units in order
        ASR = array_of_active_units[current_bu_ind]._active_sr  # get the bu's active string representation
        if not ASR[0] or not ASR[1] or not ASR[2]:
            continue
        i,replay_from_bu = 0,False
        while i < len(env_mes_list) and not replay_from_bu:
            b_B_l = [[], [], []]
            if _match4_I1(ASR[0],env_mes_list[i], b_B_l):
                j = 0
                while j < len(env_mes_list) and not replay_from_bu:
                    if _match4_I2(ASR[1], env_mes_list[j], b_B_l):
                        replay_from_bu = True
                    j += 1
            i += 1
        if replay_from_bu:
            _write_reply(ASR[2], env_mes_list, b_B_l)
            if len(env_mes_list) > max_mes:
                del env_mes_list[-max_mes:]

    # we then process type 1 ,
    t12_ind = [i for i in range(len(array_of_active_units))
                if array_of_active_units[i].type in {1,2}]
    for current_bu_ind in t12_ind:
        if array_of_active_units[current_bu_ind].type == 1: #  for type 1 b units
            ASR = array_of_active_units[current_bu_ind]._active_sr  # get the bu's active string representation
            i, replay_from_bu = 0, False
            b_B_l = [[], [], []]
            while i < len(env_mes_list) and not replay_from_bu:
                if _match1_I1(ASR[0], env_mes_list[i], b_B_l):
                    replay_from_bu = True
                    _write_reply(ASR[1],env_mes_list,b_B_l)
                i+=1
        elif array_of_active_units[current_bu_ind].type == 2: #  for type 1 b units
            ASR = array_of_active_units[current_bu_ind]._active_sr  # get the bu's active string representation
            i, replay_from_bu = 0, False
            b_B_l = [[], [], []]
            while i < len(env_mes_list) and not replay_from_bu:
                if _match1_I1(ASR[1], env_mes_list[i], b_B_l):
                    replay_from_bu = True
                i+=1
            if not replay_from_bu:
```

```
                b_B_l = [[],[],[]]
                _write_reply(ASR[2], env_mes_list, b_B_l)

    # shorten too lengthy messages and select only first max_mes messages
    while len(env_mes_list) > max_mes:
        env_mes_list.pop()
    for i in range(len(env_mes_list)):
        while len(env_mes_list[i]) > max_message_len:
            env_mes_list[i].pop()


    # return True if match. Update b_B_l in that case. Else, return False and flush b_B_l
# kwargs only for internal recursive calls
def _match4_I1(ASR0,current_mes,b_B_l,**kwargs):

    # The case where 'b' or 'B' is at the first position, do_not_validate = False
    # In any other call, (recursive), do_not_validate = True
    # We only validate if it's the non recursive call of _match4_I1

###########################################################################

    if 'do_not_validate' in kwargs:
        do_not_validate = kwargs['do_not_validate']
    else:
        do_not_validate = False

    if not do_not_validate:
        if len(ASR0) == 0:
            return False
        validated_ASR0 = _validate_ASRi(ASR0)
    else:
        validated_ASR0 = ASR0

###########################################################################

    if validated_ASR0[0] in {'b','B'}:
        if len(validated_ASR0) > len(current_mes): #  if bu length too large, return False
            return False

        #len( validated ASR0 ) = 0 , 1 cases
        elif len(validated_ASR0) == 0:
            return False
        elif len(validated_ASR0) == 1:  #  len current message = 1 or 0
            if validated_ASR0[0] == 'b':
                b_B_l[0] = current_mes[:]
                return True
            else:
                b_B_l[1] = current_mes[:]
                return True


        #  len( validated ASR0 ) > 1 cases
        #  comparing message and bu length, where to start reading env_mes,
        #  if bu[0] = 'b' or 'B' i + i0 is the first one to read
        i_0 = len(current_mes) - len(validated_ASR0)
        i = 1
        #  update b_B_l
        if validated_ASR0[0] == 'b':
            b_B_l[0] = current_mes[0:i_0+1]
        else: # validated_ASR0[0] = 'B'
            b_B_l[1] = current_mes[0:i_0+1]


        while i + i_0 < len(current_mes) and _match_char(validated_ASR0[i],current_mes[i+i_0],b_B_l):
            i = i+1
        if i + i_0 == len(current_mes):
            return True
        else:
            b_B_l[0],b_B_l[1],b_B_l[2] = [],[],[] #we do it this way to change b_B_l and not
            #  the object it references on this particular function
            return False
    elif validated_ASR0[-1] in {'b','B'}:
```

```
        # Move 'b' or 'B' to first position, change current_message in similar fashion, and solve recursively
        return _match4_I1(

                                [validated_ASR0[len(validated_ASR0)-1]]
                                + validated_ASR0[:len(validated_ASR0)-1],

                                current_mes[len(validated_ASR0)-1:] + current_mes[0:len(validated_ASR0)-1],

                                b_B_l,

                                do_not_validate = True


                                )
    # 'w' at the first or last position only processed as 'multiple' wild cards if no 'b' or
    # 'B' found at first and last position. Else, 'w'
    elif validated_ASR0[0] == 'w':
        # Recursive call for validated_ASR0[0] = 'b'. 'b' saved in temporal storage
        # and 'w' replaced with 'b'. After recursive excecution,
        # --> if match True , restore original 'b' on b_B_l
        # --> if match False , b_B_l is reset by recursive call
        temp_b_stored = b_B_l[0]
        b_B_l[0] = []
        validated_ASR0[0] = 'b'
        if _match4_I1(validated_ASR0,current_mes,b_B_l,do_not_validate = True):
            b_B_l[0] = temp_b_stored
            return True
        else:
            return False
    elif validated_ASR0[-1] == 'w':
        #the same as last elif, but considering the last position instead
        temp_b_stored = b_B_l[0]
        b_B_l[0] = []
        validated_ASR0[-1] = 'b'
        if _match4_I1(validated_ASR0,current_mes,b_B_l,do_not_validate = True):
            b_B_l[0] = temp_b_stored
            return True
        else:
            return False
    else:
        if len(validated_ASR0) != len(current_mes):
            b_B_l[0], b_B_l[1], b_B_l[2] = [], [], []
            return False
        else:
            for i in range(len(current_mes)):
                if not _match_char(validated_ASR0[i],current_mes[i],b_B_l):
                    b_B_l[0], b_B_l[1], b_B_l[2] = [], [], []
                    return False
            return True

# to be called after _match4_I1. It works the same, but in case of no match, b_B_l
# remains unchanged.
def _match4_I2(ASR1,current_mes,b_B_l,**kwargs):
    backup_b_B_l = [b_B_l[0][:],b_B_l[1][:],b_B_l[2][:]]

    #this approach does not work for ['b','B',0,1...] case if 'b' and 'B' present on b_B_l,
    #but such thing cannot happen if on I1 we only allow either 'B' or 'b'

    if not ASR1: #if not element found in ASR1
        return False

    if ASR1[0] == 'b': #check for duplicate 'b' , 'B' and 'l' in b_B_l and ASR1
        if b_B_l[0]: #if b_B_l['b'] not empty,
            while ASR1 and ASR1[0]=='b': #while ASR1 not empty and it's first element = 'b'
                ASR1.pop(0)
    elif ASR1[0] == 'B':
        if b_B_l[1]: #if b_B_l['B'] not empty,
            while ASR1 and ASR1[0]=='B': #while ASR1 not empty and it's first element = 'B'
                ASR1.pop(0)

    if not ASR1: #if not element found in ASR1
```

```
        return False

    #  we do the same with the last element
    if ASR1[-1] == 'b':
        if b_B_l[0]:
            while ASR1 and ASR1[-1]=='b':
                ASR1.pop()
    elif ASR1[-1] == 'B':
        if b_B_l[1]:
            while ASR1 and ASR1[-1]=='B':
                ASR1.pop()

    if not ASR1: #if not element found in ASR1
        return False
    #  we handle the case when l is already used and finally, we validate.
    if b_B_l[2]: #  if b_B_l['l'] not empty,
        ASR1.insert(1,'l')
        validated_ASR1 = _validate_ASRi(ASR1)
        if 'l' in validated_ASR1:
            validated_ASR1.remove('l')


    if not 'validated_ASR1' in locals():
        validated_ASR1 = _validate_ASRi(ASR1)
    if _match4_I1(validated_ASR1,current_mes,backup_b_B_l):
        b_B_l[0], b_B_l[1], b_B_l[2] = backup_b_B_l[0], backup_b_B_l[1], backup_b_B_l[2]
        return True
    else:
        return False

#calls _match4_I1
def _match1_I1(ASR0,current_mes,b_B_l,**kwargs):
    return _match4_I1(ASR0,current_mes,b_B_l,**kwargs)

# return ASRi with valid b , B and l instances
# return error if ASRi is empty
def _validate_ASRi(ASRi):
    if len(ASRi) > 1:
        return_ASRi = []
        b_0 = ASRi[0] == 'b'
        B_0 = ASRi[0] == 'B'
        first_bB_found = b_0 or  B_0
        first_l_found = False
        if first_bB_found: # if b or B found 2 at ASRi[0], append it to return_ASRi
            return_ASRi.append(ASRi[0])
        for i in range(len(ASRi)):
            if not first_bB_found and ASRi[i] in {'b','B'}: # if it's the first instance of 'b' or 'B', but not i=0
                if i == len(ASRi)-1: # if the first bB instance is the last element, append it to the list
                    return_ASRi.append(ASRi[i])
                first_bB_found = True
            elif not first_l_found and ASRi[i] == 'l':
                return_ASRi.append(ASRi[i])
                first_l_found = True
            else:
                if ASRi[i] not in {'b','B','l'}:
                    return_ASRi.append(ASRi[i])
    elif len(ASRi) == 1:
        return_ASRi = ASRi
    else:
        raise ValueError('Processed ASRi cannot be empty')
    return return_ASRi

# returns False if no match occurs,
# returns True if character or wild card match, or one time 'l' match
# updates b_B_l to include found l (if found)
def _match_char(char_bu, char_current_mes, b_B_l):
    if char_bu == char_current_mes:
        return True
    elif char_bu in {'0','1'}:
        return False
    elif char_bu == 'w':
```

```
            return True
        elif char_bu == 'l' :
                if b_B_l[2]:
                    raise ValueError("b_B_l[2] is not empty when trying to write 'l' ")
                b_B_l[2] = [char_current_mes]
                return True
        else:
            raise ValueError('{} not a valid character for _match_char'.format(char_current_mes))

# write reply considering broadcast unit's last component
def _write_reply(answer_ASRi,env_mes_list,b_B_l,max_mes_len = 9):
    reply_mes = []
    for j in range(len(answer_ASRi)):
        if len(reply_mes) > max_mes_len:
            del reply_mes[-max_mes_len:]
            env_mes_list.insert(0, reply_mes)
            return
        #  first three cases, for when b,B,or l is written (only once)
        #  last case, write 0 or 1
        if answer_ASRi[j] == 'b':
            if b_B_l[0] !=[]:
                reply_mes.extend(b_B_l[0])
                b_B_l[0] = []
        elif answer_ASRi[j] == 'B':
            if b_B_l[1] !=[]:
                reply_mes.extend(b_B_l[1])
                b_B_l[1] = []
        elif answer_ASRi[j] == 'l':
            if b_B_l[2] != []:
                reply_mes.extend(b_B_l[2])
                b_B_l[2] = []
        elif answer_ASRi[j] in {'1', '0'}:
            reply_mes.append(answer_ASRi[j])
        elif answer_ASRi[j] == 'w':
            pass
        else:
            raise ValueError('non valid character encountered, {}'.format(answer_ASRi[j]))
    env_mes_list.insert(0, reply_mes)

#endregion


def fit(max_iterations = 20,popsize = 20, bd_len = 500):
    population = [initialize_random_bd_no_0_fitness(bd_len,20,15,True,4) for i in tqdm(range(popsize))]
    print('-start-')
    max_fitness = -1e10
    current_max_fitness = -1e10
    for i in range(max_iterations):
        fitness_list = _bd_list_fitness(bd_list=population,
                                        number_of_lists_sampled=100,
                                        comparision_rounds=20,
                                        max_nullfit_on_10=10)
        current_max_fitness = max(fitness_list)
        current_max_index = argmax(fitness_list)

        # # population reinitialization
        # if current_max_fitness == 0: #if null fitness on all devices, reinitialize pop
        #     print('-reinitializing -')
        #     population = [initialize_random_bd_no_0_fitness(bd_len) for i in tqdm(range(popsize),desc='initializing')]
        #     print('iteration:{} / {} \nmax_fitness:{}\ncurrent_max_fitness:{}'.format(
        #         i, max_iterations, max_fitness, curretnt_max_fitness)
        #     )
        #     continue
        #

        if current_max_fitness > max_fitness:
            best_bd = population[current_max_index]
            max_fitness = max(fitness_list)

        fitness_list = _sigma_truncation(fitness_list)
        newpop = list()
```

```
        for j in range(math.floor(popsize/2)):
            bd_ind0 = _roulette_selection(fitness_list)
            bd_ind1 = _roulette_selection(fitness_list)
            children_bd = crossover(population[bd_ind0],population[bd_ind1])
            simple_mutation(children_bd[0],0.02)
            simple_mutation(children_bd[1],0.02)
            newpop.extend(children_bd)
        population = newpop
        print(f'-----\n{i/max_iterations}% done\nmax_fit:{max_fitness}\ncurrent_max_fit:{
            current_max_fitness}')
        print(f'best bd: {str(best_bd)}\n----')

'''
import cProfile
import re
bat = 1
cProfile.run('fit', 'restats')
import pstats
p = pstats.Stats('restats')
p.strip_dirs()
p.sort_stats('cumulative').print_stats(10)
'''
```

A.3.2 1^{st} restricted approach, with r as new operator

main.py

```
import modules_ga as mo
import random
import copy
from matplotlib import pyplot as plt
from statistics import mean


def consecutive_list_generator():
    for i1 in range(8):
        for i2 in range(7):
            option_list = list(range(8))
            option_list.remove(i1)
            i2 = option_list[i2]
            for i3 in range(6):
                option_list = list(range(8))
                option_list.remove(i1)
                option_list.remove(i2)
                i3 = option_list[i3]
                for i4 in range(5):
                    option_list = list(range(8))
                    option_list.remove(i1)
                    option_list.remove(i2)
                    option_list.remove(i3)
                    i4 = option_list[i4]
                    for i5 in range(4):
                        option_list = list(range(8))
                        option_list.remove(i1)
                        option_list.remove(i2)
                        option_list.remove(i3)

                        option_list.remove(i4)
                        i5 = option_list[i5]
                        for i6 in range(3):
                            option_list = list(range(8))
                            option_list.remove(i1)
                            option_list.remove(i2)
                            option_list.remove(i3)
                            option_list.remove(i4)
                            option_list.remove(i5)
                            i6 = option_list[i6]
                            for i7 in range(2):
                                option_list = list(range(8))
                                option_list.remove(i1)
                                option_list.remove(i2)
                                option_list.remove(i3)
                                option_list.remove(i4)
                                option_list.remove(i5)
                                option_list.remove(i6)
                                i7, i8 = option_list[i7] , option_list[(i7 + 1)%2]
                                yield [i1, i2, i3, i4, i5, i6, i7, i8]



good_sr = '*00llllll:01000000*wwwwwwww:11rrrrrr'
sr= '*lwlwllww:11rrr00r*wlwl0w11:10111010'
a = mo.broadcast_device(sr=sr)
print(mo.fitness_function(a))
shuffled_list = [6,2,3,4,1,5,7,0]
mo.sort_list_with_bd(a,shuffled_list,20)

print('----------------')

ed = []
i = 0
for sl in consecutive_list_generator():
    i += 1
    if i%100 == 0:
        print(i)
    random.seed(5+i)
```

```
    sl_copy = copy.copy(sl)
    mo.sort_list_with_bd(a, sl_copy, 20)
    ed.append(mo._measure_order(sl) - mo._measure_order(sl_copy))

    '''
    print(f'fitness value: {fitness_value}')
    print('-----')
    print(sl)
    print(sl_copy)
    print('-----')
    print(f'entropy diference: {mo._measure_order(sl) - mo._measure_order(sl_copy)}')
    '''

print(ed)
# 0.14154995352778119
print(mean(ed))

plt.hist(ed, bins = [-2,-1.75,-1.5,-1.25,-1,-0.75,-0.5,-0.25,-0.01,0.01,0.25,0.5,0.75,1,1.25,1.5,1.75,2])
plt.title("Histogram of best BD's fitness values")
plt.show()


#mo.fit()
```

modules_ga.py

```
import math
import random
from statistics import stdev, mean
import numpy as np
from tqdm import tqdm
import multiprocessing.pool
import functools
from matplotlib import pyplot as plt
import time
#from memory_profiler import profile


#region tools

def argmax(iterable):
    return max(enumerate(iterable), key=lambda x: x[1])[0]

#  https://stackoverflow.com/questions/492519/timeout-on-a-function-call
def timeout(max_timeout):
    """Timeout decorator, parameter in seconds."""

    def timeout_decorator(item):
        """Wrap the original function."""

        @functools.wraps(item)
        def func_wrapper(*args, **kwargs):
            """Closure for function."""
            pool = multiprocessing.pool.ThreadPool(processes=1)
            async_result = pool.apply_async(item, args, kwargs)
            # raises a TimeoutError if execution exceeds max_timeout
            return async_result.get(max_timeout)

        return func_wrapper

    return timeout_decorator

#  dinamic ploting


def update_line(hl, new_data):
    hl.set_xdata(np.append(hl.get_xdata(), new_data))
    hl.set_ydata(np.append(hl.get_ydata(), new_data))
    plt.draw()

#endregion

#region finess and list modules

# measure list's entropy on logarithmic scale
def _measure_order(input_list):
    """
     calculate the level of disorder of the input list. It is measured on a logarithmic scale

    :param input_list: the list to be measured
    :return: positive float
    """

    #  sum( |input_list - ordered list| )
    sum_of_difference = sum((abs(input_list[i] - i) for i in range(len(input_list))))
    return math.log1p(sum_of_difference)


# binaryze and debinarize
def _decimal(list_of_binary_strings):
    return sum((2 ** i for i in range(len(list_of_binary_strings))
                if list_of_binary_strings[len(list_of_binary_strings) - 1 - i] == '1'))


# get binary list of strings '1' and '0' of size bin_len.
def _binary(decimal_number, bin_len):
    if decimal_number < 0:
```

```
        raise ValueError('Negative numbers have no binary')
    c = str(bin(decimal_number))
    c = c[2:]
    c = [char for char in c]  # convert from '0101' to ['0', '1', '0', '1']
    return (bin_len - len(c)) * ['0'] + c


#  return n sized shuffled list
def _generate_random_list(n):
    return_list = list(range(n))
    random.shuffle(return_list)
    return return_list


#  interprets messages by updating the list to be ordered and updating the message list.
#  Only one comparation per iteration
#  clean
def _process_messages(shuffled_list, env_messages):
    list_size = len(shuffled_list)
    advaliable_comparation = True  # This variable makes sure only 1 comparation per iteration is
        done
    piece_length = int(math.log2(list_size))
    message_size = int(piece_length * 2 + 2)
    i = 0
    while i < len(env_messages):
        if len(env_messages[i]) == message_size:
            # just delete message
            if env_messages[i][0:2] == ['0', '0']:
                env_messages.pop(i)
                i = i - 1
            # compare elements (only once per iteration)
            elif env_messages[i][0:2] == ['1', '1'] and advaliable_comparation:
                advaliable_comparation = False
                # if first piece < second piece, just change the prefix
                first_piece = _decimal(env_messages[i][2:2 + piece_length])
                second_piece = _decimal(env_messages[i][2 + piece_length:2 + piece_length * 2])
                if (
                        shuffled_list[first_piece] < shuffled_list[second_piece]
                    and first_piece > second_piece
                ) or (
                        shuffled_list[first_piece] > shuffled_list[second_piece]
                    and first_piece < second_piece
                ):

                    if first_piece < second_piece:
                        env_messages.insert(0, ['0', '0'] + env_messages[i][2:])
                        env_messages.pop(i + 1)
                    # else, swap places and change prefix
                    else:
                        env_messages.insert(0, ['0', '0'] +
                                                env_messages[i][2 + piece_length:2 + piece_length * 2] +
                                                env_messages[i][2:2 + piece_length])
                        env_messages.pop(i + 1)



            # swap pieces
            elif env_messages[i][0:2] == ['1', '0']:
                index0 = _decimal(env_messages[i][2:2 + piece_length])
                index1 = _decimal(env_messages[i][2 + piece_length:2 + 2 * (piece_length)])
                index0, index1 = sorted([index0, index1])[0], sorted([index0, index1])[1]
                shuffled_list[:] = (shuffled_list[index1:] +
                                    shuffled_list[index0:index1] +
                                    shuffled_list[:index0])
                env_messages.pop(i)
                i = i - 1
            # swap elements
            elif env_messages[i][0:2] == ['0', '1']:
                index0 = _decimal(env_messages[i][2:2 + piece_length])
                index1 = _decimal(env_messages[i][2 + piece_length:2 + 2 * (piece_length)])
                if index0 != index1:
                    shuffled_list[index0], shuffled_list[index1] = shuffled_list[index1],
                        shuffled_list[index0]
```

```
                env_messages.pop(i)
                i = i - 1
        i = i + 1


# sorts list with broadcast_device
def sort_list_with_bd(b_device, shuffled_list, max_iterations):
    env_messages = [['1', '1', '0', '0', '0', '1', '1', '1']]
    _process_messages(shuffled_list, env_messages)
    i = 0
    while i < max_iterations and env_messages:
        i = i + 1
        process_broadcast_device(b_device, env_messages)
        _process_messages(shuffled_list, env_messages)


#  return broadcast device's fitness on a single list
def fitness_function(b_device, number_of_shuffled_lists_measured = 100, max_nullfit_on_10 = 3, fast_0_fitness = False):
    if number_of_shuffled_lists_measured != 1:
        number_of_nullfit = 0
        fit_list = []
        for i in range(number_of_shuffled_lists_measured):
            fit = fitness_function(b_device,1)
            fit_list.append(fit)
            if fit == 0:
                if i == 1 and fast_0_fitness: #we get rid of bd if no response in first iteration
                    return 0.0
                number_of_nullfit += 1
                if number_of_nullfit == max_nullfit_on_10 and i <= 10:
                    return -0.5
            if i == number_of_shuffled_lists_measured-1:

                # percentage of improved lists - 0.5

                #return (sum((1 for i  in fit_list if i > 0.00001))/number_of_shuffled_lists_measured) - 0.5
                # the mean of improvement
                return mean(fit_list)
    list_size = 8
    max_iterations = 150
    shuffled_list = _generate_random_list(list_size)
    shuffled_entropy = _measure_order(shuffled_list)
    sort_list_with_bd(b_device, shuffled_list, max_iterations)
    return (shuffled_entropy - _measure_order(shuffled_list))


# endregion


# region genetic algorithm operators and initialization


# initializes bd of length bd_length and initializes random characters based on given
# prob_dist = [0, 1, *, :, w, b, B, l, c,r]
def initialize_random_bd(bd_length, **kwargs):
    random.seed()
    if 'prob_dist' in kwargs:
        prob_dist = kwargs['prob_dist']
    else:  # ['0', '1', '*', ':', 'w', 'b', 'B', 'l', 'c','r']
        raise ValueError('No prob_dist introduced')
    pass

    if not 0.999 < sum(prob_dist) < 1.0001:
        raise ValueError("sum(prob_dist) = 1 is false")

    #partial_sum = [sum(prob_dist[0:i]) for i in range(1, len(prob_dist) + 1)]

    return broadcast_device(sr=
            ["*" if i % 18 == 0 else
            ":" if i % 18 == 9 else
            _get_char(prob_dist,['w','l']) if i % 18 > 9 else
            _get_char(prob_dist,['r']) for i in range(bd_length)])
```

```python


# auxiliary function for initialize_random_bd
# --> do_not_generate = list[str] , reroll _get_char if generated char in do
def _get_char(prob_dist, do_not_generate=[]):
    random_number = random.random()
    index = 0
    index_selected = False
    while index < len(prob_dist) and not index_selected:
        if random_number < sum(prob_dist[0:index+1]):
            if (['0', '1', '*', ':', 'w', 'b', 'B', 'l', 'c','r'][index]
                    in do_not_generate):
                # if undesirable char selected, call function recursively
                return _get_char(prob_dist,do_not_generate=do_not_generate)
            else:
                return ['0', '1', '*', ':', 'w', 'b', 'B', 'l', 'c','r'][index]
        index = index + 1


# initializes random bd with no nule fitness
def initialize_random_bd_no_0_fitness(bd_length,prob_dist):
    bd = initialize_random_bd(bd_length, prob_dist=prob_dist)
    fitness = fitness_function(bd)
    it = 0
    while fitness < 0:
        it += 1
        if it % 500 == 0:
            print(str(it) + ' iterations without valid bd creation.')
        del bd
        bd = initialize_random_bd(bd_length, prob_dist=prob_dist)
        fitness = fitness_function(bd,fast_0_fitness=True)
    return bd
    #               ['0', '1', '*', ':', 'w', 'b', 'B', 'l', 'c','r']


# get bd list of fitness. If fitness on first list is 0, set bd's fitness to 0
# without further operations
def _bd_list_fitness(bd_list):
    fitness_list = []
    state = random.getstate()
    for i in range(len(bd_list)):
        random.setstate(state)
        fitness_list.append(fitness_function(bd_list[i]))
    return fitness_list


# scale fitness with sigma truncation
def _sigma_truncation(list_of_fitness, **kwargs):
    if 'c' in kwargs:
        c = kwargs['c']
    else:
        c = 2
    sigma = stdev(list_of_fitness)
    mu = mean(list_of_fitness)
    return [(list_of_fitness[i] - (mu - c * sigma)) for i in range(len(list_of_fitness))]


# returns list with number of offspring using roulette wheel selection
# https://stackoverflow.com/questions/10324015/fitness-proportionate-selection-roulette-wheel-
    selection-in-python
def _roulette_selection(weights):
    '''performs weighted selection or roulette wheel selection on a list
    and returns the index selected from the list'''

    # sort the weights in ascending order
    sorted_indexed_weights = sorted(enumerate(weights));
    indices, sorted_weights = zip(*sorted_indexed_weights);
    # calculate the cumulative probability
    tot_sum = sum(sorted_weights)
    if tot_sum == 0:
        prob = [1 / len(sorted_indexed_weights) for i in range(len(sorted_indexed_weights))]
    else:
        prob = [x / tot_sum for x in sorted_weights]
```

```
    cum_prob = np.cumsum(prob)
    # select a random a number in the range [0,1]
    random_num = random.random()

    for index_value, cum_prob_value in zip(indices, cum_prob):
        if random_num < cum_prob_value:
            return index_value


# mates using two point crossover
def crossover(mate0, mate1):
    sr0 = mate0.sr
    sr1 = mate1.sr

    mating_indexes = [random.randint(0, len(sr1) - 1), random.randint(0, len(sr1) - 1)]
    mating_indexes.sort()

    return [
        broadcast_device(
            sr=sr0[:mating_indexes[0]] +
               sr1[mating_indexes[0]:mating_indexes[1]] +
               sr0[mating_indexes[1]:]),
        broadcast_device(
            sr=sr1[:mating_indexes[0]] +
               sr0[mating_indexes[0]:mating_indexes[1]] +
               sr1[mating_indexes[1]:])
    ]




# simple mutation, without destroying ':' and '*' instances and/or commenting them
# need to include non disruptant comments (not to comment : and * instances)
def simple_respectful_mutation(bd, prob_mutation=0.02, **kwargs):
    n_mutations = len(bd.sr) * prob_mutation
    n_mutations = int(n_mutations) + int(
        n_mutations - int(n_mutations) > random.random()
    )


    if 'prob_dist' in kwargs:
        prob_dist = kwargs['prob_dist']
    else:
        raise ValueError('no prob_dist introduced')
    pass

    while n_mutations > 0:
        ran_num = random.randint(0, len(bd.sr) - 1)
        if bd.sr[ran_num] not in {'*', ':'}:
            if ran_num % 18 > 9:
                bd.sr[ran_num] = _get_char(prob_dist,['w','l'])
            else:
                bd.sr[ran_num] = _get_char(prob_dist,['r'])

        n_mutations += -1


# endregion IN


# region broadcast device modules

class broadcast_device:
    sr = []
    _active_sr = []
    type = -2

    # kwargs --> sr or string_representation: initializes with sr (it can be a string or a list)
    def __init__(self, **kwargs):

        '''


```

```
        :param kwargs: sr / string_representation: list or string to initialize broadcast
        '''

        # set sr if input sr given
        if 'string_representation' or 'sr' in kwargs:  # check if sr is given
            if 'string_representation' in kwargs:
                input_sr = kwargs['string_representation']
            else:
                input_sr = kwargs['sr']

            if isinstance(input_sr, str):
                self.sr = list(input_sr)
            elif isinstance(input_sr, list):
                self.sr = input_sr
            else:
                raise TypeError('unsupported type: {} for sr initialization. '.format(type(input_sr)
                    ))

    # returns the list sr as a string
    def __str__(self):
        return str(''.join(self.sr))


    def __repr__(self):
        return str(self)

    # returns the length of sr
    def __len__(self):
        return len(self.sr)

    # removes all quotes and quoted elements from sr and returns the list (it does not change sr)
    def _unquote(self):  # return unquoted list of chars
        if self.sr:
            return [self.sr[i] for i in range(1, len(self)) if self.sr[i] != "c"]

    # retuns list of broadcast units, splitting them by *. It automatically uncoments sr
    def piecewise(self):
        self_unquoted = self._unquote()
        if not self_unquoted:
            return []
        unquoted_string = ''.join(self_unquoted)
        piecewise_strings = unquoted_string.split('*')
        return [broadcast_device(sr=i) for i in piecewise_strings if i != '']

    # sets _active_sr and returns the length of the set list. If retun the numbe of ':' found
    def _decompose_and_set_active_sr(self):
        b = []  # in this list we save de indexes at wich instances of ':' were found
        count = 0  # number of ':' instances found
        for i in range(len(self)):
            if self.sr[i] == ':':  # when ':' instance found, append it to b
                b.append(i)
                count += 1
                if count == 3:  # when third instance of ':' found, ignore rest
                    self._active_sr = [self.sr[0:b[0]], self.sr[b[0] + 1:b[1]], self.sr[b[1] + 1:b
                        [2]]]
                    return count
        if count == 2:  # if only two instances found, return appropiate list of sr pieces
            self._active_sr = [self.sr[0:b[0]], self.sr[b[0] + 1:b[1]], self.sr[b[1] + 1:]]
            return count
        elif count == 1:  # if only one instance of ':' found, return appropiate list
            self._active_sr = [self.sr[0:b[0]], self.sr[b[0] + 1:]]
            return count
        return 0  # if no ':' found, return 0




    # set type, and while doing so modify self.sr to try to convert it to a unit
    # it also sets the active string representation
    def set_type(self):

        if self.type == -2:
            if not self.sr:
```

```
                self.type = 0
                return
            ### we need to make sure c is not on self.sr before setting type ###
            # self.sr = self.piecewise()[0].sr  # Make sure that the bc device is a bc unit, or just
                take the first bu
            count = self._decompose_and_set_active_sr()
            if count == 0:
                self.type = 0
            elif count == 1:  # it could be type 1 bu
                if self._active_sr[0] and self._active_sr[1]:  # [1 , 1] --> type 1
                    self.type = 1
            else:  # in this case, we have found our two valid ':' , it could be type 2,3,4
                if not self._active_sr[0]:  # if first component is empty [ - , ? , ? ]
                    if self._active_sr[1] and self._active_sr[
                        2]:  # 2nd and 3rd components are non empty --> type 2 [- , 1 , 1]
                        self.type = 2
                else:  # if first component is non empty [ 1 , ? , ? ]
                    if not self._active_sr[1]:  # if second component empty [1 , - , ? ]
                        if self._active_sr[2]:  # if third component non-empty [1 , - , 1]
                            self.type = 3
                    elif self._active_sr[2]:  # [1,1,1]
                        self.type = 4
        if self.type == -2:
            self.type = 0  # when no other type mach, set type to 0


def process_broadcast_device(bd, env_mes_list, max_mes=5):
        _process_broadcast_device_with_timeout(bd, env_mes_list, max_mes)



# splits the bd into b units, activates their ASR and calls _process_broadcast_units

# timeout creates memory leak bug
# @profile()
def _process_broadcast_device_with_timeout(bd, env_mes_list, max_mes):
    bu_list = bd.piecewise()
    for bu in bu_list:
        bu.set_type()
    _process_broadcast_units(bu_list, env_mes_list, max_mes)


def _process_broadcast_units(array_of_active_units, env_mes_list, max_mes, max_message_len=8):
    # max_mes maximum number of messages to be outputted

    # we first process type 4 units
    '''
    t4_ind = [i for i in range(len(array_of_active_units))
              if array_of_active_units[i].type == 4]  # select type 4 units
    for current_bu_ind in t4_ind:
        # process type 4 units in order
        ASR = array_of_active_units[current_bu_ind]._active_sr  # get the bu's active string
            representation
        if not ASR[0] or not ASR[1] or not ASR[2]:
            continue
        i, replay_from_bu = 0, False
        while i < len(env_mes_list) and not replay_from_bu:
            b_B_l = [[], [], []]
            if _match4_I1(ASR[0], env_mes_list[i], b_B_l):
                j = 0
                while j < len(env_mes_list) and not replay_from_bu:
                    if _match4_I2(ASR[1], env_mes_list[j], b_B_l):
                        replay_from_bu = True
                    j += 1
            i += 1
        if replay_from_bu:
            _write_reply(ASR[2], env_mes_list, b_B_l)
            while len(env_mes_list) > max_mes:
                env_mes_list.pop()
    '''


    # we then process type 1 , 2 and 3 units
```

```
    t12_ind = [i for i in range(len(array_of_active_units))
               if array_of_active_units[i].type in {1, 2}]
    new_env_mes_list = []
    for current_bu_ind in t12_ind:
        if array_of_active_units[current_bu_ind].type == 1:  # for type 1 b units
            ASR = array_of_active_units[current_bu_ind]._active_sr  # get the bu's active string representation
            i, replay_from_bu = 0, False
            while i < len(env_mes_list) and not replay_from_bu:
                b_B_l = [[], [], [[]]]
                if _match1_I1(ASR[0], env_mes_list[i], b_B_l):
                    replay_from_bu = True
                    _write_reply(ASR[1], new_env_mes_list, b_B_l)
                i += 1
        '''
        elif array_of_active_units[current_bu_ind].type == 2:  # for type 1 b units
            ASR = array_of_active_units[current_bu_ind]._active_sr  # get the bu's active string representation
            i, replay_from_bu = 0, False
            b_B_l = [[], [], []]
            while i < len(env_mes_list) and not replay_from_bu:
                if _match1_I1(ASR[1], env_mes_list[i], b_B_l):
                    replay_from_bu = True
                i += 1
            if not replay_from_bu:
                b_B_l = [[], [], []]
                _write_reply(ASR[2], env_mes_list, b_B_l)
        '''



    # shorten too lengthy messages and select only first max_mes messages
    env_mes_list[:] = new_env_mes_list[:]
    while len(env_mes_list) > max_mes:
        env_mes_list.pop()
    for i in range(len(env_mes_list)):
        while len(env_mes_list[i]) > max_message_len:
            env_mes_list[i].pop()

    # return True if match. Update b_B_l in that case. Else, return False and flush b_B_l


# kwargs only for internal recursive calls
def _match4_I1(ASR0, current_mes, b_B_l, **kwargs):
    # The case where 'b' or 'B' is at the first position, do_not_validate = False
    # In any other call, (recursive) , do_not_validate = True
    # We only validate if it's the non recursive call of _match4_I1

    ###########################################################################

    if 'do_not_validate' in kwargs:
        do_not_validate = kwargs['do_not_validate']
    else:
        do_not_validate = False

    if not do_not_validate:
        if len(ASR0) == 0:
            return False
        validated_ASR0,found_l_positions = _validate_ASRi(ASR0)
    else:
        validated_ASR0 = ASR0

    ###########################################################################

    if validated_ASR0[0] in {'b', 'B'}:
        if len(validated_ASR0) > len(current_mes):  # if bu length too large, return False
            return False

        # len( validated ASR0 ) = 0 , 1 cases
        elif len(validated_ASR0) == 0:
            return False
        elif len(validated_ASR0) == 1:  # len current message = 1 or 0
            if validated_ASR0[0] == 'b':
```

```
                b_B_l[0] = current_mes[:]
                return True
            else:
                b_B_l[1] = current_mes[:]
                return True

        # len( validated ASR0 ) > 1 cases
        # comparing message and bu length, where to start reading env_mes,
        # if bu[0] = 'b' or 'B' i + i0 is the first one to read
        i_0 = len(current_mes) - len(validated_ASR0)
        i = 1
        # update b_B_l
        if validated_ASR0[0] == 'b':
            b_B_l[0] = current_mes[0:i_0 + 1]
        else:  # validated_ASR0[0] = 'B'
            b_B_l[1] = current_mes[0:i_0 + 1]

        while i + i_0 < len(current_mes) and _match_char(validated_ASR0[i], current_mes[i + i_0],
            b_B_l):
            i = i + 1
        if i + i_0 == len(current_mes):
            return True
        else:
            b_B_l[0], b_B_l[1], b_B_l[2] = [], [], []  # we do it this way to change b_B_l and not
            # the object it references on this particular function
            return False
    elif validated_ASR0[-1] in {'b', 'B'}:
        # Move 'b' or 'B' to first position, change current_message in similar fashion, and solve
            recursively
        return _match4_I1(

            [validated_ASR0[len(validated_ASR0) - 1]]
            + validated_ASR0[:len(validated_ASR0) - 1],

            current_mes[len(validated_ASR0) - 1:] + current_mes[0:len(validated_ASR0) - 1],

            b_B_l,

            do_not_validate=True

        )
    # 'w' at the first or last position only processed as 'multiple' wild cards if no 'b' or
    # 'B' found at first and last position. Else, 'w'
    elif validated_ASR0[0] == 'w':
        # Recursive call for validated_ASR0[0] = 'b'. 'b' saved in temporal storage
        # and 'w' replaced with 'b'. After recursive excecution,
        # --> if match True , restore original 'b' on b_B_l
        # --> if match False , b_B_l is reset by recursive call
        temp_b_stored = b_B_l[0]
        b_B_l[0] = []
        validated_ASR0[0] = 'b'
        if _match4_I1(validated_ASR0, current_mes, b_B_l, do_not_validate=True):
            b_B_l[0] = temp_b_stored
            return True
        else:
            return False
    elif validated_ASR0[-1] == 'w':
        # the same as last elif, but considering the last position instead
        temp_b_stored = b_B_l[0]
        b_B_l[0] = []
        validated_ASR0[-1] = 'b'
        if _match4_I1(validated_ASR0, current_mes, b_B_l, do_not_validate=True):
            b_B_l[0] = temp_b_stored
            return True
        else:
            return False
    else:
        if len(validated_ASR0) != len(current_mes):
            b_B_l[0], b_B_l[1], b_B_l[2] = [], [], []
            return False
        else:
            b_B_l[2] = [[]]
            for i in range(len(current_mes)):
```

```
                if not _match_char(validated_ASR0[i], current_mes[i], b_B_l,i):
                    b_B_l[0], b_B_l[1], b_B_l[2] = [], [], []
                    return False
            return True


# to be called after _match4_I1. It works the same, but in case of no match, b_B_l
# remains unchanged.
def _match4_I2(ASR1, current_mes, b_B_l, **kwargs):
    backup_b_B_l = [b_B_l[0][:], b_B_l[1][:], b_B_l[2][:]]

    # this approach does not work for ['b','B',0,1...] case if 'b' and 'B' present on b_B_l,
    # but such thing cannot happen if on I1 we only allow either 'B' or 'b'

    if not ASR1:  # if not element found in ASR1
        return False

    if ASR1[0] == 'b':  # check for duplicate 'b' , 'B' and 'l' in b_B_l and ASR1
        if b_B_l[0]:  # if b_B_l['b'] not empty,
            while ASR1 and ASR1[0] == 'b':  # while ASR1 not empty and it's first element = 'b'
                ASR1.pop(0)
    elif ASR1[0] == 'B':
        if b_B_l[1]:  # if b_B_l['B'] not empty,
            while ASR1 and ASR1[0] == 'B':  # while ASR1 not empty and it's first element = 'B'
                ASR1.pop(0)

    if not ASR1:  # if not element found in ASR1
        return False

    #  we do the same with the last element
    if ASR1[-1] == 'b':
        if b_B_l[0]:
            while ASR1 and ASR1[-1] == 'b':
                ASR1.pop()
    elif ASR1[-1] == 'B':
        if b_B_l[1]:
            while ASR1 and ASR1[-1] == 'B':
                ASR1.pop()

    if not ASR1:  # if not element found in ASR1
        return False
    #  we handle the case when l is already used and finally, we validate.
    if b_B_l[2]:  # if b_B_l['l'] not empty,
        ASR1.insert(1, 'l')
        validated_ASR1 = _validate_ASRi(ASR1)
        if 'l' in validated_ASR1:
            validated_ASR1.remove('l')

    if not 'validated_ASR1' in locals():
        validated_ASR1 = _validate_ASRi(ASR1)
    if _match4_I1(validated_ASR1, current_mes, backup_b_B_l):
        b_B_l[0], b_B_l[1], b_B_l[2] = backup_b_B_l[0], backup_b_B_l[1], backup_b_B_l[2]
        return True
    else:
        return False


# calls _match4_I1
def _match1_I1(ASR0, current_mes, b_B_l, **kwargs):
    return _match4_I1(ASR0, current_mes, b_B_l, **kwargs)


# return ASRi with valid b , B and l instances
# return error if ASRi is empty
# fills found_l_positions if necessary
def _validate_ASRi(ASRi):
    found_l_positions = []
    if len(ASRi) > 1:
        return_ASRi = []
        b_0 = ASRi[0] == 'b'
        B_0 = ASRi[0] == 'B'
        first_bB_found = b_0 or B_0
        if first_bB_found:  # if b or B found 2 at ASRi[0], append it to return_ASRi
```

```
            return_ASRi.append(ASRi[0])
        for i in range(len(ASRi)):
            if not first_bB_found and ASRi[i] in {'b', 'B'}:  # if it's the first instance of 'b' or 'B', but not i=0
                if i == len(ASRi) - 1:  # if the first bB instance is the last element, append it to the list
                    return_ASRi.append(ASRi[i])
                first_bB_found = True
            elif ASRi[i] == 'l':
                return_ASRi.append(ASRi[i])
                found_l_positions.append(len(return_ASRi)-1)
            else:
                if ASRi[i] not in {'b', 'B'}:
                    return_ASRi.append(ASRi[i])
    elif len(ASRi) == 1:
        return_ASRi = ASRi
    else:
        raise ValueError('Processed ASRi cannot be empty')

    return return_ASRi,found_l_positions

# returns False if no match occurs,
# returns True if character or wild card match, or one time 'l' match
# updates b_B_l to include found l (if found)
def _match_char(char_bu, char_current_mes, b_B_l,pos = None):
    if char_bu == char_current_mes:
        return True
    elif char_bu in {'0', '1'}:
        return False
    elif char_bu == 'w':
        return True
    elif char_bu == 'l':
        b_B_l[2][0].append(pos)
        b_B_l[2].append(char_current_mes)
        return True
    elif char_bu == 'r':
        return bool(random.randint(0,1))
    else:
        raise ValueError('{} not a valid character for _match_char'.format(char_current_mes))


# write reply considering broadcast unit's last component
def _write_reply(answer_ASRi, env_mes_list, b_B_l, max_mes_len=8):
    reply_mes = []
    for j in range(len(answer_ASRi)):
        if len(reply_mes) > max_mes_len:
            del reply_mes[-max_mes_len:]
            env_mes_list.insert(0, reply_mes)
            return
        #  first three cases, for when b,B,or l is written (only once)
        #  last case, write 0 or 1
        if answer_ASRi[j] == 'b':
            if b_B_l[0] != []:
                reply_mes.extend(b_B_l[0])
                b_B_l[0] = []
        elif answer_ASRi[j] == 'B':
            if b_B_l[1] != []:
                reply_mes.extend(b_B_l[1])
                b_B_l[1] = []
        elif answer_ASRi[j] == 'l':
            if b_B_l[2] != []:
                reply_mes.extend(b_B_l[2])
                b_B_l[2] = []
        elif answer_ASRi[j] in {'1', '0'}:
            if j in b_B_l[2][0]:
                b_B_l[2][0].pop(0)
                reply_mes.append(b_B_l[2].pop(1))
            else:
                reply_mes.append(answer_ASRi[j])
        elif answer_ASRi[j] == 'w':
            pass
        elif answer_ASRi[j] == 'r':
            reply_mes.append(str(random.randint(0,1)))
```

```python
        else:
            raise ValueError('non valid character encountered, {}'.format(answer_ASRi[j]))
    env_mes_list.insert(0, reply_mes)


# endregion


def fit(max_iterations=500,
        popsize=1200,
        bd_len=36,
        prob_dist=(0.20, 0.20, 0.00, 0.00, 0.20, 0.00, 0.00, 0.20, 0.00,0.20)
        #         [ '0', '1',   '*',  ':',  'w',  'b',  'B',  'l', 'c' , 'r']
        ):
    population = [initialize_random_bd_no_0_fitness(bd_len, prob_dist=prob_dist) for i in tqdm(range(popsize))]
    print('\n-start-\n')
    max_fitness = 0
    current_max_fitness = 0
    max_fitness_history = []
    for i in range(max_iterations):
        random.seed()
        fitness_list = _bd_list_fitness(population)
        current_max_fitness = max(fitness_list)
        max_fitness_history.append(current_max_fitness)
        if current_max_fitness > max_fitness:
            max_fitness = max(fitness_list)
            best_bd = population[argmax(fitness_list)]
            print(best_bd)
        average_fitness = mean((i for i in fitness_list if i != -0.5))
        fitness_list = _sigma_truncation(fitness_list, c=6)
        newpop = list()
        for j in range(int(math.floor(popsize / 2))):
            bd_ind0 = _roulette_selection(fitness_list)
            bd_ind1 = _roulette_selection(fitness_list)
            children_bd = crossover(population[bd_ind0], population[bd_ind1])
            simple_respectful_mutation(children_bd[0], 0.02, prob_dist=prob_dist)
            simple_respectful_mutation(children_bd[1], 0.02, prob_dist=prob_dist)
            newpop.extend(children_bd)
        population = newpop
        print('iteration:{:6f}/{} curr. max:{:4f} overall max:{:4f} current mean:{:4f}'.format(
            i, max_iterations, current_max_fitness, max_fitness,average_fitness)
        )
        '''
        #region dinamic ploting

        if i ==0:
            #ysample = random.sample(range(-50, 50), 100)

            xdata = []
            ydata = []
            plt.show()
            axes = plt.gca()
            axes.set_xlim(0, max_iterations)
            axes.set_ylim(0, 4)
            line, = axes.plot(xdata, ydata, 'r-')


        xdata.append(i)
        ydata.append(average_fitness)
        line.set_xdata(xdata)
        line.set_ydata(ydata)
        plt.draw()
        plt.pause(1e-17)
        time.sleep(0.1)
        # endregion
        '''

    #plt.show()
    print(best_bd)


'''
```

```
import cProfile
import re
bat = 1
cProfile.run('fit', 'restats')
import pstats
p = pstats.Stats('restats')
p.strip_dirs()
p.sort_stats('cumulative').print_stats(10)
'''
```

A.3.3 2^{nd} approach, final version

main_v10.py

```python
import modules_ga_v10 as mo
import time
import random
from matplotlib import pyplot as plt



print('\n \n ---------------- \n \n')

time.sleep(0.5)

random.seed(4)
# print(sum((mo.measure_order(mo.generate_random_list(mo.list_size)) for i in range(200)))/200)




computed_sizes = [4,5, 6, 7, 8, 9, 10]
# ['c', '1-', '1++', 'i', '1+', '0-', '1--', '1-', 'i', '0++']
# ['0-', '0-', 's', '1++', '1-', '1-', '1++', '1--', '1--', '0++']
# ['0--', '0++', '0--', 'c', 'i', '1--', '0++', '0+', '0--', '0-', 's', '1-', '1-', 'c', '0--', 'c', '1+', '0++', '1--', '0+']
# ['s', '0++', '1--', '0+', '1++', '1+', '1+', '1-', '0--', '0--', '0+', 's', '0+', 's', '1+', 's', '0+', '1+', 's', '0++', '0+', '0--', '1--']
# ['1+', '0-', '1-', 's', '1--', '1-', '0+', '1-', '1--', '0+', 's', '0+', '0-', 's', '1+', '0--', 'c', '1+', 'i', '1-', '0--', '0++', '0-', 's', '0-', '1++']
# ['c', '0--', 'c', '0-', '1-', 'c', '0++', '0+', '1+', 'c', '0--', '0-', '1+', '0--', '1+', '0-', '1++', '0-', '0--', '0++', 's', '0+', 'c', '1-', 'c', '1-', '0-',
#'0-', '1--', 's', '1--', '1++', 'i', '1++', '0--', '0--', '1--', '0++', '0--', '0+', '1--', '1--', '0--', '1--', '0--', '0--', '0--', '0--', '1+', '0--']
# ['1-', '1+', '1--', '0+', '1+', 'c', '1+', '0-', '1-', '1-', '0--', '0--', 's', 's', '1-', '0++', '0+', 'c', '1--', '0-', '0-', '1+', '1+', 'c', 's', '1++', '0++',
#'1-', '1--', '1--', '1-', '0++', 'c', '1-', '1--', 's', '1++', 's', '1-', '1++', '0+', 'c', '0++', '0--', 'c', '1-', '1--', '0+', '1-', '1--', '0--', '1--', '0++',
#'0-', '1--', 'c', '1--', '0-', '1++', '0--']
mean_pstep_count_hist = [3.526,  7.2835, 13.2014, 20.5113, 26.8551, 47.6345, 70.3024]
mean_qstep_count_hist = [4.8446, 7.3829, 10.2942, 13.4719, 16.9368, 20.5831, 24.4349]
mean_istep_count_hist = [2.9961, 5.0081, 7.4823,  10.5419, 13.8817, 18.0272, 22.5761]
max_pstep_count_hist =  [5,      10,     19,      25,      37,      71,      96]
max_qstep_count_hist =  [6,      10,     15,      21,      28,      36,      44]
max_istep_count_hist =  [6,      10,     15,      21,      27,      35,      41]


plt.plot(computed_sizes,max_pstep_count_hist, color = '#0004ff', label='GP maximun')

plt.plot(computed_sizes,max_qstep_count_hist, color = '#ff0505', label='quicksort maximun')

plt.plot(computed_sizes,max_istep_count_hist, color = '#1bb628', label='insertion sort maximun')

plt.plot(computed_sizes,mean_pstep_count_hist, color = '#9ea0ff', label='GP mean')

plt.plot(computed_sizes,mean_qstep_count_hist, color = '#ff7575', label='quicksort mean')

plt.plot(computed_sizes,mean_istep_count_hist, color = '#83ec8c', label='insertion sort mean')

plt.xticks(computed_sizes)

plt.legend()

plt.xlabel('List size')

plt.ylabel('Number of comparisons')



plt.show()
```

```

# uncomment to perform search
#mo.get_comp_number_data()
```

modules_ga_v10.py

```
import math
import random
from statistics import stdev, mean
import numpy as np
from tqdm import tqdm
import functools
from matplotlib import pyplot as plt
import os as sys
import time
import multiprocessing as mp
import copy


# declare global variables
global list_size
global max_comparisons
global program_size
global number_of_lists_sampled
global popsize



# region parameters
seed = 4
list_size = 9
test_prog = ['0++', '1+', '1+', '1+', '1+', '1-', 'c', '0+', '0--', '1-', '1-', '0++', 'i', '1--', 's', '0++', '0-', '1+', '1--', '0--', '0--', '1++', '1--', 'i', '0++', '0+', '1++', 's', '0-', '1--', 's', '1+', '0--', 'i', 'c', '1+', '1-', '0-', '0++', 'i', '1-', '1-', 'i', '0+', 's', '1-', '0+', '1-', '0++', '0++', '0+', '0++', '0--', '0++', 's', 's', '1+', '0++', '1+', '1++', '1--', '0--', 's', '0++', '1--', '1--', 's', '0++', 's', '1-', '0-', '1--', 'i', 'i', '0+', '1+', 'c', 'c', '0++', '1++', 's', '0--', '0++', '1+', '1++', '1+', '0-', '1--', '0-', 'i', '1++', 'i', 'i', '1--', '0+', '0+', '0-', '0--', '0+', '0+']

# program execution
max_comparisons = list_size * list_size * 10
max_program_iterations = 10 * list_size
program_size = 10


# fitness function parameters
number_of_lists_sampled = 500


# ga parameters
max_ga_iterations = 20
prob_mut = 0.02
popsize = 40
c = 2


#endregion


# region tools


def argmax(iterable):
    return max(enumerate(iterable), key=lambda x: x[1])[0]


# endregion


#region other sorting algos

# taken from https://stackoverflow.com/questions/18262306/quicksort-with-python
def qsort(l, first_call = True):
    if not l: return l , 0 # empty sequence case
    pivot = l[random.choice(range(0, len(l)))]
    head , count0 = qsort([elem for elem in l if elem < pivot], first_call=False)
    tail , count1 = qsort([elem for elem in l if elem > pivot], first_call=False)
```

```
    count = count0 + count1 + len(head) + len(tail)
    if first_call:
        l[:] = head + [pivot] + tail
        return count
    else:
        return head + [pivot] + tail , count

# http://interactivepython.org/courselib/static/pythonds/SortSearch/TheInsertionSort.html
def isort(l):
    comp_count = 0
    for index in range(1, len(l)):
        currentvalue = l[index]
        position = index
        while position > 0 and l[position - 1] > currentvalue:
            comp_count += 1
            l[position] = l[position - 1]
            position = position-1
            l[position] = currentvalue
            if l == list(range(len(l))):
                return comp_count
    return comp_count




#endregion


#region shuffled list


#  return n sized shuffled list
def generate_random_list(n):
    return_list = list(range(n))
    random.shuffle(return_list)
    return return_list

def measure_order(input_list):

    """
     calculate the level of disorder of the input list. It is measured on a logarithmic scale
    :param input_list: the list to be measured
    :return: positive float
    """

    #  sum( |input_list - ordered list| )
    sum_of_difference = sum((abs(input_list[i] - i) for i in range(len(input_list))))
    return math.log1p(sum_of_difference)





#endregion


#region program - commands


class ordering_program:

    prob_distr =     (1   , 1  , 1   , 1   , 1   , 1   , 1   , 1    , 1    ,  1   , 1 )
    possible_chars = ('s', 'i', '0+', '1+', '0-', '1-', '0++', '0--', '1++', '1--','c')

    def __init__(self,n = None,**kwargs):
        if 'command_list' in kwargs or 'command_string' in kwargs:
            initialize = False
        else:
            initialize = True
        if not initialize:
            if 'command_list' in kwargs:
                self.command_list = kwargs['command_list']
            elif 'command_string' in kwargs:
```

```python
                self.command_list = [command for command in kwargs['command_string']]

        else:
            if n is None:
                raise ValueError('no command list size given')
            self._initialize_random_command_list(n)

    def _initialize_random_command_list(self, n):
        state = random.getstate()
        random.seed()
        self.command_list = list(random.choices(self.possible_chars, weights=self.prob_distr, k=n))
        random.setstate(state)

    def __len__(self):
        return len(self.command_list)

    def __str__(self):
        return str(self.command_list)

    def order_list_with_program(self,
                                shuffled_list,
                                initial_pos = math.floor(list_size / 2),
                                plusplus_difference = math.floor(list_size/8)):

        plusplus_difference = math.floor(list_size / 8)
        initial_pos = math.floor(list_size / 2)
        comparison_counter_container = [0] # we make it a list to make it mutable
        p0 = initial_pos
        p1 = 0
        len_of_moves = (1,plusplus_difference)

        for i in range(max_program_iterations):
            for command_pos in range(len(self)):
                current_char = self.command_list[command_pos]

                if comparison_counter_container[0] >= max_comparisons:
                    return comparison_counter_container[0]
                if shuffled_list == list(range(list_size)):
                    return comparison_counter_container[0]

                elif current_char in {'s','i'}:
                        execute_command(current_char,shuffled_list,comparison_counter_container,p0,p1)
                        #print('{} : {} - {}'.format(comparison_counter_container, p0, p1))

                elif current_char == 'c':
                    pass
                else:  # movement command found
                    if current_char[0] == '0':
                        p0 += len_of_moves[len(current_char) - 2]
                        p0 = p0 % list_size
                    elif current_char[0] == '1':
                        p1 += len_of_moves[len(current_char) - 2]
                        p1 = p1 % list_size
        return comparison_counter_container[0]


    def mutate_k_position(self,k):
        self.command_list[k] = list(random.choices(self.possible_chars, weights=self.prob_distr, k=1))[0]



# order_list_with_program commands




# command swap 's'
def swap(shuffled_list, comparison_counter_container, p0, p1):
    if p0 == p1:
        return
    shuffled_list[min(p0,p1)],shuffled_list[max(p0,p1)] = sorted([shuffled_list[p0],shuffled_list[p1
```

```
        ]])
    comparison_counter_container[0] += 1


# command insert 'i'
def insert(shuffled_list, comparison_counter_container, p0, p1):
    if p0 == p1:
        pass
    else:
        if shuffled_list[p0] > shuffled_list[p1]:
            element_to_be_inserted = shuffled_list[p0]
            shuffled_list.insert(p1 + 1, element_to_be_inserted)
        else:
            element_to_be_inserted = shuffled_list[p0]
            shuffled_list.insert(p1, element_to_be_inserted)
        if shuffled_list[p0] == element_to_be_inserted:
            shuffled_list.pop(p0)
        elif shuffled_list[p0 + 1] == element_to_be_inserted:
            shuffled_list.pop(p0 + 1)
        else:
            raise ValueError('Second element not erased')
        comparison_counter_container[0] += 1


#
def execute_command(command, shuffled_list, comparison_counter_container, p0, p1):
    if command == 's':
        swap(shuffled_list, comparison_counter_container, p0, p1)
    elif command == 'i':
        insert(shuffled_list, comparison_counter_container, p0, p1)
    else:
        raise ValueError('The only valid commands are s and i, {} was found.'.format(command))

# endregion


#region ga operators

class individual:


    def __init__(self, program):
        if not isinstance(program,ordering_program):
            raise TypeError('The initialization requires an'+
                            ' ordering_program type object. {} type object was given'.format(type(program)))
        self.program = program

    def __str__(self):
        return str(self.program)

    def calc_fitness(self):
        random.seed(seed)
        all_fitness_values = []
        shuffled_lists = [generate_random_list(list_size) for i in range(number_of_lists_sampled)]
        for shuffled_list in shuffled_lists:
            all_fitness_values.append(fitness_function(self.program,shuffled_list))
        # Fitness value, penalize for worst n of comparisons
        self.fitness =  ( mean(all_fitness_values) + min(all_fitness_values) ) / 2

        return self.fitness

    def crossover(self, other):
        # mates using two point crossover

        ind_0_command_list = self.program.command_list
        ind_1_command_list = other.program.command_list



        mating_indexes = [random.randint(0, len(ind_0_command_list) - 1), random.randint(0, len(ind_0_command_list) - 1)]
        mating_indexes.sort()
```

```python

        new_individuals = [
            individual(
            ordering_program(
                command_list=ind_0_command_list[:mating_indexes[0]] +
                             ind_1_command_list[mating_indexes[0]:mating_indexes[1]] +
                             ind_0_command_list[mating_indexes[1]:]))),
            individual(
                ordering_program(
                command_list = ind_1_command_list[:mating_indexes[0]] +
                           ind_0_command_list[mating_indexes[0]:mating_indexes[1]] +
                           ind_1_command_list[mating_indexes[1]:]))

        ]

        # new_bds[0].message_spawner_set = spawn_mes0
        # new_bds[1].message_spawner_set = spawn_mes1

        return new_individuals


    def mutate(self):
        mut_index = np.random.binomial(2,prob_mut,len(self.program))
        for i in range(len(self.program)):
            if mut_index[i]:
                self.program.mutate_k_position(i)




class population:

    best_individual = None
    best_fitness = -1e10


    def __init__(self):
        self.pop = [individual(get_working_program(program_size, list_size)) for _ in range(popsize)]
        self.iterations_done = 0


    def ga_iteration(self, verbose = 1):

        if verbose:
            time.sleep(0.5)
            fitness_list = [self.pop[i].calc_fitness() for i in tqdm(range(popsize))]
            time.sleep(0.5)
        # keeping track of best individuals and iteration
        else:
            fitness_list = [self.pop[i].calc_fitness() for i in range(popsize)]
        best_index = argmax(fitness_list)
        best_iteration_fitness = fitness_list[best_index]
        best_iteration_individual = self.pop[best_index]
        mean_iteration_fitness = mean(fitness_list)
        self.iterations_done += 1


        if self.best_fitness < best_iteration_fitness:
            self.best_fitness  = best_iteration_fitness
            self.best_individual = best_iteration_individual
            if verbose:
                print('{:.4f} --> {}'.format(self.best_fitness, str(self.best_individual)))

        fitness_list = sigma_truncation(fitness_list)

        selected_pop = [self.pop[roulette_selection(fitness_list)] for _ in range(popsize)]

        if verbose:
            for indiv in self.pop:
                print('{:.4f} --> {}'.format(indiv.fitness, str(indiv)))

        newpop = []
```

```python
        for i in range(0,popsize,2):
            newpop.extend(selected_pop[i].crossover(self.pop[i+1]))
        self.pop = newpop
        for indiv in self.pop:
            indiv.mutate()
        if verbose:
            print('it: {:5}  overall best: {:.4f} -- current best: {:.4f} -- current mean: {:.4f}'.format(self.iterations_done,self.best_fitness,best_iteration_fitness,mean_iteration_fitness))




# fitness function
def fitness_function(program,shuffled_list):
    initial_entropy = measure_order(shuffled_list)
    n_comparisons = program.order_list_with_program(shuffled_list)
    bonus_well_ordered = 0
    if shuffled_list == list(range(list_size)):
        bonus_well_ordered  = max_comparisons - n_comparisons
    return initial_entropy - measure_order(shuffled_list) + bonus_well_ordered

# scale fitness with sigma truncation
def sigma_truncation(list_of_fitness):
    sigma = stdev(list_of_fitness)
    mu = mean(list_of_fitness)
    return [(list_of_fitness[i] - (mu - c * sigma)) for i in range(len(list_of_fitness))]


# returns list with number of offspring using roulette wheel selection
# https://stackoverflow.com/questions/10324015/fitness-proportionate-selection-roulette-wheel-selection-in-python
def roulette_selection(weights):
    '''performs weighted selection or roulette wheel selection on a list
    and returns the index selected from the list'''

    # sort the weights in ascending order
    sorted_indexed_weights = sorted(enumerate(weights))
    indices, sorted_weights = zip(*sorted_indexed_weights)
    # calculate the cumulative probability
    tot_sum = sum(sorted_weights)
    if tot_sum == 0:
        prob = [1 / len(sorted_indexed_weights) for i in range(len(sorted_indexed_weights))]
    else:
        prob = [x / tot_sum for x in sorted_weights]
    cum_prob = np.cumsum(prob)
    # select a random a number in the range [0,1]
    random_num = random.random()

    for index_value, cum_prob_value in zip(indices, cum_prob):
        if random_num < cum_prob_value:
            return index_value






#endregion


def fit(verbose = 1 , size = list_size):
    global list_size
    old_size, list_size = list_size , size

    global number_of_lists_sampled
    fit_population = population()
    best_hist = []
    for i in tqdm(range(max_ga_iterations), 'GA iteration'):
        fit_population.ga_iteration(verbose=verbose)
        if verbose == 1:
            print('-------')
            print('max_comparisons = {}'.format(max_comparisons))
```

```
            print('----------')
        best_hist.append(fit_population.best_individual.calc_fitness())

    time.sleep(0.5)
    print('Best individual:')
    print('----------')
    print(fit_population.best_individual)
    if verbose == 1:
        print(fit_population.best_individual.calc_fitness())
        plt.plot(list(range(1,1 + len(best_hist))),best_hist)
        plt.show()
    list_size = old_size

    return fit_population.best_individual.program


def test_ord_prog(test_prog):
    random.seed(5)
    global list_size
    ls = list_size
    pstep_count_hist, qstep_count_hist , istep_count_hist = [], [], []
    all_well_ordered = True
    for i in range(10000):
        shuffled_list0 = generate_random_list(ls)
        shuffled_list1 = copy.deepcopy(shuffled_list0)
        shuffled_list2 = copy.deepcopy(shuffled_list0)
        p = test_prog

        # sorting with different algorithms, and saving number of comparisons
        pstep_count_hist.append(p.order_list_with_program(shuffled_list0))
        qstep_count_hist.append(qsort(shuffled_list1))
        istep_count_hist.append(isort(shuffled_list2))
        if shuffled_list0 != list(range(len(shuffled_list0))):
            all_well_ordered = False

    print('#LS = {}'.format(list_size))
    print('#test_prog = {}'.format(test_prog))


    return all_well_ordered,\
           mean(pstep_count_hist), mean(qstep_count_hist), mean(istep_count_hist),\
           max(pstep_count_hist), max(qstep_count_hist), max(istep_count_hist)



def get_comp_number_data():
    mean_pstep_count_hist, mean_qstep_count_hist, mean_istep_count_hist, \
    max_pstep_count_hist, max_qstep_count_hist, max_istep_count_hist = [], [], [], [], [], []
    hists =[ mean_pstep_count_hist, mean_qstep_count_hist, mean_istep_count_hist,
    max_pstep_count_hist, max_qstep_count_hist, max_istep_count_hist ]
    for i in range(9,15):

        #variable parameters
        global list_size
        global max_comparisons
        global popsize
        global program_size
        global max_program_iterations

        list_size = i
        max_comparisons = list_size * list_size * 10
        program_size = 20 + 10 * (i - 6)
        max_program_iterations = list_size * 10


        test_prog = fit(verbose=0, size=i)
        all_well_ordered, \
        mean_pstep_count, mean_qstep_count, mean_istep_count,\
        max_pstep_count, max_qstep_count, max_istep_count = test_ord_prog(test_prog)

        obtained_results = (mean_pstep_count, mean_qstep_count, mean_istep_count,
                            max_pstep_count, max_qstep_count, max_istep_count)

```

```
        for hist_index in range(6):
            hists[hist_index].append(obtained_results[hist_index])


        if not all_well_ordered:
            print(f'Not all well ordered, failed iteration: {i} \n\n ------ \n\n')
            raise ValueError
        else:
            print(f'iteration {i}')
            print(
            f'\n mean_pstep_count_hist = {mean_pstep_count_hist} \n mean_qstep_count_hist = {
                mean_qstep_count_hist} \n mean_istep_count_hist = {mean_istep_count_hist} \n
                max_pstep_count_hist = {max_pstep_count_hist} \n max_qstep_count_hist = {
                max_qstep_count_hist} \n max_istep_count_hist = {max_istep_count_hist}'
            )



def get_working_program(ps, ls):

    # correct global parameters
    global list_size
    global max_comparisons
    global program_size

    #backup original global variables
    list_size_copy = copy.copy(list_size)
    max_comparisons_copy = copy.copy(max_comparisons)
    program_size_copy  = copy.copy(program_size)

    #set new global variables
    list_size = ls
    max_comparisons = ls * ls * 10
    program_size = ps
    #


    working_program = False
    n_of_programs_checked = 0
    while not working_program:
        n_of_programs_checked += 1
        op_to_be_checked = ordering_program(n = ps)
        i = 0
        list_has_been_ordered = True
        while list_has_been_ordered and i < 100:
            i += 1
            shuffled_list = generate_random_list(ls)
            op_to_be_checked.order_list_with_program(shuffled_list)
            if shuffled_list != list(range(len(shuffled_list))):
                list_has_been_ordered = False

        if list_has_been_ordered:
            working_program = True
        if n_of_programs_checked % 15000 == 0:
            print(f'n of iterations without valid op created: {n_of_programs_checked}. List size {
                list_size} and op size {program_size}')
            if n_of_programs_checked > 1500000:
                raise ValueError


    # restore original global variables
    list_size = list_size_copy
    max_comparisons = max_comparisons_copy
    program_size = program_size_copy
    #


    return op_to_be_checked



def local_search(n_iterations, start_string = '*w0llwlwwwwwwww:1001rr1r001111*llllw1llwlwwwl:
    r1100rr0rr1rrr'): # to be adapted to second approach
```

```
    random.seed()
    state = random.getstate
    string = start_string
    string_change = string
    new_fitness = -1e10
    print(start_string + ' --> ' + 'start string')
    print('--start--')
    for it in range(n_iterations):
        random.setstate = state
        fitness = fitness_function(broadcast_device(sr = string),10000, 10, 20,False,64)
        for new_string in dist_1_generator(string):
            random.setstate = state
            new_fitness = fitness_function(broadcast_device(sr = new_string),200, 10, 20,False,64)
            if new_fitness > fitness:
                random.setstate = state
                new_fitness = fitness_function(broadcast_device(sr=new_string), 1000, 10, 20, False, 64)
                if not new_fitness > fitness:
                    continue
                fitness = new_fitness
                string_change = new_string
        random.setstate = state
        if fitness_function(broadcast_device(sr = string_change),10000, 10, 20,False,64) > fitness:
            print(new_string + ' --> ' + str(new_fitness))
            string = string_change
        print('Iteration: '+ str(it))

def dist_1_generator(string):
    possible_chars = ('0', '1', 'w', 'l', 'r')
    for i in (i for i in range(len(string)) if i%30 != 0 and i%30 != 15):
        for char in possible_chars:
            if not (15 < i%30 < 30 and char == 'l'):
                yield '%s%s%s' % (string[:i],char,string[i+1:])




#list_size = 6

#print(test_ord_prog(test_prog=ordering_program(command_list=['c', '1-', '1++', 'i', '1+', '0-', '1--', '1-', 'i', '0++'])))


#steps = 1e9
#for j in range(1000):
#     p = get_working_program(20, list_size)
#     oldsteps = steps
#     steps = min(max( (p.order_list_with_program(generate_random_list(list_size)) for i in range(10000) )), steps)
#     if steps < oldsteps:
#         print('-----')
#         print(p)
 #        print(steps)
```

Bibliography

[1] Peter A.N. Bosman and Dirk Thierens. Expanding from discrete to continuous estimation of distribution algorithms: The idea. 2000.

[2] Tianshi Chen, Ke Tang, Guoliang Chen, and Xin Yao. A large population size can be unhelpful in evolutionary algorithms. *CoRR*, 2012.

[3] Nichael Lynn Cramer. A representation for the adaptive generation of simple sequential programs. 1985.

[4] Dilvan de Abreu Moreira. *Agents: A Distributed Client/Server System for Leaf Cell Generation*. PhD thesis, The University of Kent at Canterbury, 1995.

[5] James Decraene. The holland broadcast language. 2006.

[6] Tarek El-mihoub, Adrian Hopgood, Lars Nolle, and Battersby Alan. Hybrid genetic algorithms: A review. 3(2), 2006.

[7] David Edward Goldberg. *Genetic Algorithms in Search, Optimization, and Machine Learning*. Addison-Wesley Publishing Company, 1989.

[8] Stanley Gotshall and Bart Rylander. Optimal population size and the genetic algorithm. 2002.

[9] William Eugene Hart. Adaptive global optimization with local search. 1994.

[10] D. Himmelblau. *Applied Nonlinear Programming*. McGraw-Hill, 1972.

[11] John H. Holland. *Adaptation in Natural and Artificial Systems: An Introductory Analysis with Applications to Biology, Control, and Artificial Intelligence*. MIT Press, 1975.

[12] John H. Holland. *Hidden order: how adaptation builds complexity*. Helix book. Addison-Wesley, 1995.

[13] Hajime Kita and Yasuhito Sano. Optimization of noisy fitness functions by means of genetic algorithms using history of search. 2000.

[14] Hajime Kita and Yasuhito Sano. Genetic algorithms for optimization of noisy fitness functions and adaptation to changing environments. 2003.

[15] Padmavathi Kora and Priyanka Yadlapalli. Crossover operators in genetic algorithms: A review. *International Journal of Computer Applications*, 2017.

[16] Thiemo Krink and Morten Løvbjerg. *The LifeCycle Model: Combining Particle Swarm Optimisation, Genetic Algorithms and HillClimbers*. Springer Berlin Heidelberg, 2002.

[17] P.L. Lanzi, W. Stolzmann, and S.W. Wilson. *Learning Classifier Systems: From Foundations to Applications.* Lecture Notes in Computer Science. Springer Berlin Heidelberg, 2003.

[18] Pedro Larrañaga and Jose A Lozano. *Estimation of Distribution Algorithms: A New Tool for Evolutionary Computation.* Springer Science and Business Media, 2001.

[19] Xia Li, Xun-Guiand Wei. An improved genetic algorithm-simulated annealing hybrid algorithm for the optimization of multiple reservoirs. *Water Resources Management*, 2008.

[20] L. A. Rastrigin. Systems of extremal control. 1974.

[21] Y. Sakurai, K. Takada, N. Tsukamoto, T. Onoyama, R. Knauf, and S. Tsuruta. Backtrack and restart genetic algorithm to optimize delivery schedule. pages 85–92, Dec 2010.

[22] Y. Sakurai, Kouhei Takada, Natsuki Tsukamoto, T. Onoyama, Rainer Knauf, and S. Tsuruta. Inner random restart genetic algorithm to optimize delivery schedule. Oct 2010.

[23] O.X. Schlömilch, B. Witzschel, M. Cantor, E. Kahl, R. Mehmke, and C. Runge. *Zeitschrift für Mathematik und Physik.* Number v. 46. B. G. Teubner., 1901.

[24] Wen Wan and Jeffrey B. Birch. An improved hybrid genetic algorithm with a new local search procedure. 2013.

[25] Garnett Wilson and Wolfgang Banzhaf. *A Comparison of Cartesian Genetic Programming and Linear Genetic Programming.* Springer, 2008.