Genetic Programming



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The reasonable man adapts himself to the world; the unreason-able one persists in trying to adapt the world to himself. There-fore all progress depends on the unreasonable man.

- George Bernard Shaw, Maxims for Revolutionists

Search and Optimization

Some real-world problems are hard to solve:

- There are many possible solutions, we cannot enumerate them all
- We cannot formalize the problem description, thus requiring simplifications
- The evaluation criteria can be noisy, or change with time
- There are many constraints associated with the main problem

A problem can be formalized as either a **search problem** or an **optimization problem**.

A **search problem** is when given a set of candidate solutions *S* and a property $P : S \rightarrow \{T, F\}$, we have to find *s* such that $s \in S, P(s)$.

The Boolean Satisfability problem (SAT) is described as:



Given a boolean function f(x), assign **true** or **false** values to each x_i such that the function evaluates to **true**.

For example:

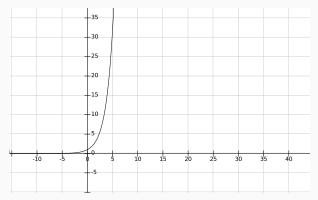
$$f(x) = (x_1 \lor x_3 \lor \neg x_4) \land (x_2 \lor \neg x_3)$$

To make things simpler, we can use 0 and 1 to represent false and true, respectivelly.

With 4 variables, our set S has $|S| = 2^4 = 16$ candidate solutions.

x_1	x_2	x_3	x_4
0	0	0	0
0	0	0	1
0	0	1	0
0	0	1	1

As the number of variables grow, the cardinality of ${\cal S}$ grows quite fast:



n	2^n	
1	2	
5	32	
10	1024	
100	1.2e30	
1000	1.1e301	

An **optimization problem** is when you have a set of candidate solutions X and a criteria function $F : X \to \mathbb{R}$ and you want to find $x \in X, x \in argmax_{y \in X}f(y)$, for maximization problems and $x \in X, x \in argmin_{y \in X}f(y)$ for minimization problems.



maximization problems have the objective of finding one of possibly many solutions that has a maximum value for the criteria function.



minimization problems have the objective of finding one of possibly many solutions that has a minimum value for the criteria function.

Nonlinear Optimization

$$G2(x) = \left| \frac{\sum_{i=1}^{n} \cos^4(x_i) - \prod_{i=1}^{n} \cos^2(x_i)}{\sqrt{\sum_{i=1}^{n} ix_i^2}} \right|$$

subject to
$$\prod_{i=1}^{n} x_i \ge 0.75$$
$$\sum_{i=1}^{n} x_i \le 7.5n$$
$$0 \le x_i \le 10, 1 \le i \le n$$

Conceptually there are an unlimited number of candidate solutions. But, when solving using floating point numbers in a computer, we have a (large but) finite number of solutions.

Assuming we can represent up till 6 decimal places, we would have 10.000.000 distinct values for each variable x_i .

So we have $10.000.000^n = 10^{7n}$ candidate solutions.

The main difference between search and optimization problem is that when you find a solution s, P(s), we can stop the search and return the solution. With an optimization problem, we have to check all possible solutions to be sure it is the best solution.

Basic Concepts



search space is the set of all candidate solutions.





an **objective-function** is a function that maps a candidate solution to a (usually real) value measuring the quality of that solution. It can be a maximization or minimization function.



the **neighborhood** of a solution *s* is the set of all solutions close to *s*.

The neighborhood can be defined using a distance measure or a function that projects a solution to a power set.

For example, for the nonlinear optimization problem, the representation is a vector $x \in \mathbb{R}^d$ and the neighborhood can be defined through a distance measure d:

$$d(x^{(1)}, x^{(2)}) = \sqrt{\sum_{i=1}^{d} (x_i^{(1)} - x_i^{(2)})^2}$$
$$\mathcal{N}(X) = \{y \in S \mid d(x, y) \le \epsilon\}$$

For the SAT problem, we can represent the solution as a binary vector and the neighborhood set is the function $\mathcal{N}: S \to 2^S$ that enumerates all set of solutions that swaps the value of two elements of the current solution.

Fundamentally, a function $f: S \to 2^S$ is equivalent to $f: S \to S \to 2$. That, uncurrying, is the same as $f: S \times S \to 2$.

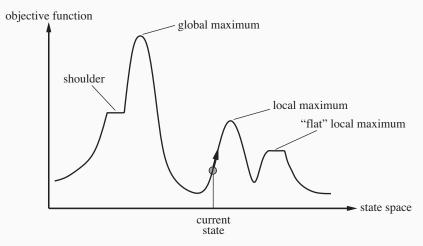
In other words, it is a function that takes two solutions and returns 0 or 1 depending whether they are neighbors or not.

Local search algorithms start from an initial solution and iteratively walks through the neighborhood until it reaches a point without a better neighbor. This point is called **local optimum**.

In some situations, we can guarantee that the **local optimum** is the best solution (or, **global optimum**).

For example, when maximizing $f(x) = -x^2$, iteratively walking through the neighborhood will always reach the global optima (under certain conditions).

But in many problems, depending on the amount of local optima, this procedure can get stuck at a subpar solution.



2

3

4

5

The **hill-climbing** algorithm or **steepest ascent**, repeats iteratively:

```
hill-climbing solution =
   best-neighbor = best (neighbors solution)
   if best-neighbor `better-than` solution
     then hill-climbing best-neighbor
     else return solution
```

Consider now an algorithm that keeps generating and evaluating random solutions.

This is called a random search:

```
1 random-search =
2 solution = random-solution
3 return solution : random-search
4
5 get-best random-search
```

A search algorithm is called **complete** if it guarantees to return a feasible solution (i.e., any s, P(s)).

A search algorithm is called **optimal** if it always return the global optimum.

The Hill-climbing is neither complete nor optimal since it cannot guarantee any of these properties.

A random search is both complete and optimal since, given an infinite amount of time, it will eventually find the best solution. Since we don't want to wait an infinite amount of time, we may try something in between Hill-climbing and random search.

Simulated annealing is one of such algorithm. It is essentially a hillclimbing algorithm but the decision of whether to replace the current solution with one of the neighbors is not deterministic.

```
simulated-annealing solution T =
      T <= eps = return solution
2
       otherwise =
3
       neighbor = random-neighbor solution
4
       next-solution =
        if neighbor `isBetterThan` solution
6
          || random <= exp (eval neighbor - eval solution)/T</pre>
7
          then neighbor
8
          else solution
9
        return simulated-annealing next-solution (shrink T)
10
```

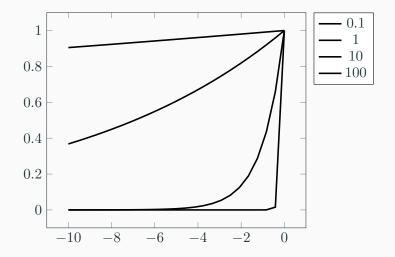
The main idea of SA is to pick a random neighbor s' and accept it (i.e., replace current solution) if:

- This neighbor is better than the current solution or
- Accept with a probability of $e^{\frac{f(s')-f(s)}{T}}$

Assuming maximization, if f(s') = f(s) it will always replace as it has the same objective-function value.

If f(s') < f(s) it will make the probability goes toward zero the higher the difference between both solutions. The value of T will determine how much worse we are willing to accept.

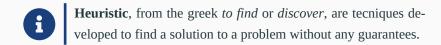
Simulated Annealing



Starting with a large value of T, SA will behave similarly to a random search, accepting almost any solution.

As the value of T is reduced at every iteration, it will start to behave more like a hill climbing, as it will be less likely to accept a worse soluion.

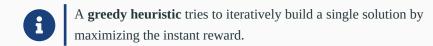
Heuristic



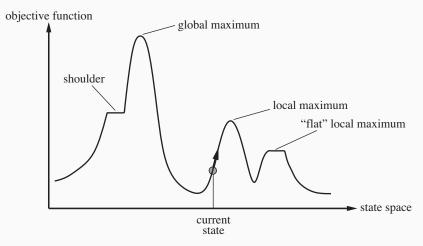
The main goal of a heuristic method is to find an approximate solution as efficiently as possible.

George Pólya¹ enumerates some tips to create a heuristic to solve a problem:

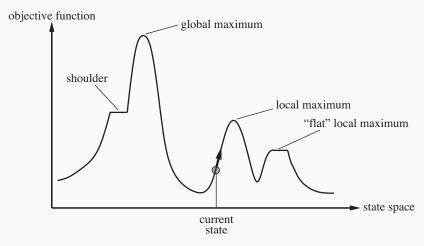
- If you cannot understand the problem, draw a diagram representing it.
- If you cannot reach a solution from an initial state, try reaching the initial state from the solution.
- If the problem is abstract, try creating a concrete example.
- Try to solve a less restrictive problem first.



A possible greedy heuristic for the optimization problem is to fix every variable to a starting value, and optimize a single variable at every iteration. The local search and greedy heuristics so far worked with a single solution. Their main limitation was to reach the closest optima to the starting point.



What if we start at multiple points in parallel?

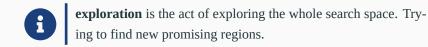


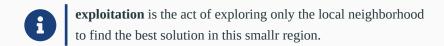
By doing so we can reach multiple local optima at once, increasing our chances of finding the global optima.

We can explore this idea even further by creating a competition among the different solutions and focus the search only on the promising regions.

Also, we can try to combine parts of different good solutions with the expectation of creating a better solution.

The main idea of a populational heuristic is to find a balance between **exploration** and **exploitation**.





Both are equally important as we need to find promising regions while extracting the best from the current best regions. Let us suppose we create 30 random solutions for the SAT problem. We can do that by sampling random bits with a probability p = 0.5 of sampling a 1. Next, we randomly select with replacement 30 solutions from this population with a probability proportional to the objective-function. From this selection, we will apply a random perturbation and repeat these procedures with this new population.

For a SAT problem with 91 terms and 20 variables, in 30 executions with 200 solutions and a maximum of 1000 iterations, this simple procedure will

- Reach the goal in 24 of the executions
- Reach a solution on average after 272 iterations

An abstract description of this algorithm is:

	<pre>population-heurisitc =</pre>
2	pop = random-population
3	f = eval pop
Ļ	while not done
;	<pre>selection = selectWithReplacement pop f</pre>
6	pop = perturb selection
7	return pop

One example of populational heuristic is the **evolutionary algorithm**.

Evolutionary Algorithms

Evolution is a natural process in which a species adapts itself successively with the objective of:

- survival
- ecological balance
- diversity

Natural Selection was proposed by Charles Darwin to explain why some characteristics become very common while others disappear.

- 1. More offsprings are produced than necessary
- 2. Characteristics of an individual defines its probability of survival
- 3. Characteristics are hereditary

Let's illustrate with the constant fight for survivor of rabbits in a territory filled with foxes.

In a population of rabbits, some are more clever and some are faster than others.

Those have more chance of survival and produce **more rabbits**.

With fast rabbits reproducing with clever rabbits, new variants of rabbits appear:

- fast and dumb
- slow and clever
- slow and dumb
- fast and clever

Evolution

Nature sometimes throw a *crazy rabbit* in this population with some variation in the genes.

The offsprings are not exact copy of their parents, but random variations (remember the regression to the mean).



Throughout the generations, hopefully the population of rabbits become faster and more clever than the initial population.

But the foxes also evolve...

1	<pre>p = initial-population</pre>							
2	while not do	ne						
3	parents	<pre>= select-from p</pre>						
4	offsprings	= recombine-from parents						
5	xmen	= mutate offsprings						
6	р	= replace-from (p + xmen)						
7	return p							

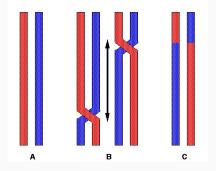
Each individual of the population represents a solution represented as seen fit.

In evolutionary algorithms this representation is called **chromosome**.

At this stage, the soon-to-be parents are selected from the population with a probability proportional to their fitness.

The idea is that the fittest have a higher chance of reproducing and passing their characteristics to their offsprings.

Recombination simulates the reproduction of individuals of the same species where the exchange of genetic material happens.



Assuming a vectorial representation:											
parent1 =	[3	0	2	5	2	1]					
<pre>parent2 =</pre>	[5	1	2	5	0	3]					
child1 =	[3	0 2	5	03	3]						
child2 =	[5	1 2	5	2 1]						

Mutation promotes novelty in our current population.

It prevents that every individual is the same.

Mutation in this algorithm is a random perturbation in the solution representation:

child = [3 0 *2* 5 2 1] xman = [3 0 *4* 5 2 1] Once we have a population of offsprings, we will replace the current population with either the offsprings or a mix of the current population and their offsprings. Whenever we need to make a decision based on how fit an individual is, we use the objective-function or an adaptation of that to calculate the **fitness** of an individual.

Notice that conceptually the fitness is a maximization objective, but it is sometimes used as minimization for some problems.

- **Genetic Algorithms** : proposed by Holland with the main goal of studying the adaptation phenomena.
- **Evolution Strategies**: introduced by Rechenberg to solve parameter optimization of nonlinear functions.
- **Evolutionary Programming**: represents a program as a finite state machine, proposed by Fogel at al.
- **Genetic Programming**: main goal of evolving computer programs, proposed by Koza.

Evolutionary Algorithms were proposed by different researchers in different forms, but with some common properties, they all

- Work with the idea of population of solutions
- Use selective pressure, with a likelihood of survival proportional to the fitness
- Measure the quality of each solution with a maximization objective-function
- Combine set of solutions thus expanding the local neighborhood
- Perturb selected solutions at random

This generates two fundamental forces in this class of algorithms:

- Variation Operators: promote diversity and search for new solutions (exploration).
- **Selective Pressure:** promote maintenance of good quality solutions (exploitation).

- Individual: a solution represented by a *chromosome*.
- **Chromosome:** the computational representation of a solution, also known as **genotype**.
- **Phenotype:** the decoded representation.
- **Fitness:** a maximization objective-function that measures the quality of an individual.
- **Population:** a bag of individuals.
- **Crossover:** or **recombination**, a function that combines the information of two or more individuals.
- Mutation: a function that randomly changes one individual.

Selection Strategies

In this strategy, assuming f_i the fitness of the *i*-th individual, the probability of selecting it as a parent is (assuming non-negative fitness):

$$p_i = \frac{f_i}{\sum_j f_j}$$

So the probability is proportional to the absolute value of the fitness.

This strategy has some drawbacks:

- Individuals with much higher fitness may end up dominating the selection causing a **premature convergence**.
- When the fitness values are too close to each other, there is no selective pressure and the choice is almost uniformly at random.
- The probability of choosing an individual may be sensitive to small variations in fitness.

Selection proportional to fitness

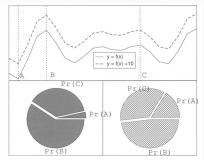


Fig. 3.19. Example of the susceptibility of fitness proportionate selection to function transposition. Top: the fitness of three points for fitness functions f(x) and f' = f(x) + 10. Bottom left: selection probabilities of the three points under f(x). Bottom right: selection probabilities of the three points under f(x)

Figure 1: Eiben, Agoston E., and James E. Smith. Introduction to evolutionary computing. Springer-Verlag Berlin Heidelberg, 2015.

We can alleviate some of these problems with the **sigma scaling** proposed by Goldberg:

$$f'_{i} = max(f_{i} - (\bar{f} - c\sigma_{f}), 0.0)$$
$$p_{i} = \frac{f'_{i}}{\sum_{j} f'_{j}}$$

where \bar{f} , σ_f are the mean and standard deviation fitness of the population and c is a scaling constant, usually set to 2.

Another strategy is to use the **rank** of the solutions instead of the fitness. For example, the fitness:

> [0.1, 19.3, 1.4, 0.05]Would be mapped to: [2, 4, 3, 1]

To calculate the selection probability based on rank, we can use a linear or exponential scale:

$$rank_{linear}(i) = \frac{2-s}{\mu} + \frac{2(i-1)(s-1)}{\mu(\mu-1)}$$
$$rank_{exp}(i) = \frac{1-e^{-i}}{\sum_{j} 1-e^{-j}}$$

where i is the rank value, 1 < s < 2 the scaling factor, μ is the highest observed rank.

The roulette selection assigns a region of a wheel to each individual, pick a random value, and returns the individual at that spot of the wheel.

$$P(x_i) = \frac{\text{fitness}(x_i)}{\sum_j \text{fitness}(x_j)}$$

1	<pre>spin fs = do</pre>
2	r = random (0, 1)
3	wheel = cumsum(probability fs)
4	return (firstOf (>r) wheel)

If the fitness of our individuals are [324, 1, 100, 289]

The probability for each individual is [0.454, 0.001, 0.140, 0.405].

Next we calculate the cummulative sum of these probabiilities, defining the slice of the wheel:

 $\left[0.454, 0.455, 0.595, 1.000\right]$

Now we choose a random value $0 \le r \le 1$ and check which slice this value belongs to. The individual within this slice is chosen as one of the parents for reproduction.

[0.454, 0.455, 0.595, 1.000]

For r = 0.3 we choose the first individual.

For r = 0.4541 we choose the second individual.

The main problem with this approach is that by spinning the wheel multiple times we may not generate a representative sample of our population.

We can expand this idea by spinning the wheel with multiple arrows and sample multiple individuals at once. This is known as **stochastic universal sampling** (SUS)

```
sus n fs = do
r = random(0, 1/n)
wheel = cumsum(probability(fs))
choices = for [1..n] (\i -> firstOf (>(r*i)) wheel)
return choices
```

This strategy guarantees that the number of times the *i*-th individual is selected is at least the integral part of $n \cdot P(i)$.

The tournament selection simply samples k individuals of the population and returns the best among them.

This is a local selection strategy, since it only uses the knowledge about the k sampled individuals as opposed to the roulette wheel that requires knowing the fitness of the entire population.

An important characteristic of this strategy is that it is invariant to translation and transposition. The choice of fitness does not affect the results of this method. The probability that an individual is selected depends of:

- Its rank in the population
- The size *k* of the tournament (the higher the size, the higher the bias to above average individuals)
- If the individuals are selected with or without replacement (without replacement, the k-1 worse will never be selected)

1	tournament k pop = do
2	competitors = sampleWithReplacement(k, pop)
3	return (best competitors)

Most selection strategies so far compare individuals using an aggregated score (i.e., the fitness).

In some situations, we can evaluate the individual locally.

For example, in regression we can calculate the squared residue for a single point or the sum of squared residues for a selection of the sample.

Evaluating the aggregated value we stimulate **generalists**. But during the evolution process we may want to combine two or more **specialists**.

Assuming maximization (fitness) and xy is the list of tuples (x, y) from our sample:

```
lexicase pop xy =
     pool = pop
     cases = shuffle xy
3
     return (while-loop pool cases)
4
   while-loop pool (case:cases)
6
       sizeOf pool == 1 = return (head pool)
7
      sizeOf cases == 0 = return (random pool)
8
       otherwise =
9
         best = max (partial-fit case) pool
10
        pool' = filter (==best . partial-fit case) pool
11
        while-loop pool' cases
12
```

When our fitness is continuous and we want some tolerance between two very similar individuals, we can use the ϵ -lexicase selection.

In this version, we simply replace the comparison with the best value with a comparison to whether the difference between the best value and the current value is within an ϵ radius.

Evolutionary Algorithms often works with one of two popular models: **generational** and **stationary**.



Generational model in a population of size μ we choose μ parents and generate $\lambda = \mu$ offsprings that entirely replace the parent population.



In the stationary model, we generate $\lambda < \mu$ offsprings to replace some of the current solutions in the population. A special case is when $\lambda = 1$.

When using the stationary model, we have to select which individuals will survive and which will be replaced.

In the fitness based replacement, we use one of the selection strategies to select the next generation.

In this strategy we pick n worse individuals of the current population and replace with the offsprings.

In this strategy, we keep the best n individuals in the population and use another strategy to select the remainders.

Sometimes we want to optimize more than one objective and they are conflicting with each other (if we improve one, we make the other worse). For these situations we can apply a Multi-objective version of the evolutionary algorithms. The main difference is in the selection and reproduction operators in which the comparison between individuals are made through the dominance operator instead of equality. In multi-objective optimization we evaluate the individuals using m > 1 objectives. As such, we have to redefine how we compare two solutions.

Instead of saying one solution is better than another, we say that one solution dominates another (denoted by $f(x_1) \prec f(x_2)$) if both:

$$\forall i \in \{1 \dots m\} : f_i(\mathbf{x_1}) \le f_i(\mathbf{x_2}), \\ \exists i \in \{1 \dots m\} : f_i(\mathbf{x_1}) \neq f_i(\mathbf{x_2}),$$

are true considering a minimization problem.

In short, this means that a certain solution dominates the other if it is equal or better in every objective and better in at least one of them. The Pareto optimal set is defined as the set of optimal solutions that are not dominated by any other:

$$\mathbb{P} = \{ \mathbf{x}^* \in \Omega \mid \nexists \mathbf{x} \in \Omega : \mathbf{f}(\mathbf{x}) \prec \mathbf{f}(\mathbf{x}^*) \}.$$

And the Pareto front is represented as the image of this set:

$$\mathcal{F} = \{\mathbf{f}(\mathbf{x}) : \mathbf{x} \in \mathbb{P}\}.$$

A Multi-objective approach for evolutionary algorithms is the Fast Nondominated sorting algorithm (NSGA-II)² together with the Crowding Distance.

The only changes in the algorithm is the replacement step that takes the dominance into consideration

²Deb, Kalyanmoy, et al. "A fast and elitist multiobjective genetic algorithm: NSGA-II." IEEE transactions on evolutionary computation 6.2 (2002): 182-197.

```
replacement pop =
S = [filter (dominatedBy i) pop | i <- pop]
n = [lengthIf (dominates i) pop | i <- pop]
pop' = [i | i, ni <- enumerate n, ni == 0]
case length pop'
a == length pop -> return pop'
> length pop -> crowding pop' (length pop)
< length pop -> return (pop' + replacement (pop / pop'))
```

```
crowding pop nPop =
dists = array 0 `ofSize` nPop
for j <- [0 .. nObjs]
    ixs = argsortByObj j pop
    for (prev, i, next) <- window ixs
    dists[i] = dists[i] + (dists[next] - dists[prev])
    dists[first ix] = inf
    dists[last ixs] = inf
    ixs = argsort (-dists)
    return (take nPop ixs)</pre>
```

Genetic Programming

Is it possible to evolve a computer program using just a sample of inputs and outputs?

A program can be thought as a function that gets one or more input arguments and return a value of a certain type. This function can be decomposed in elementa functions that belong to our grammar:

countElements [1, 2, 1, 3, 2, 1] = [(1,3), (2,2), (3,1)]

countElements = sort => group => map (head, length)

Depending of our context, the grammar can be reduced!

A classification problem has the following structure:

if predicate
 then class1
 else class2

And the predicate is simply a boolean function:

x1 > 3 && x2 <= 5

We only need to evolve the predicate function! We have >, >=, <, <=, ==, !=, number, var, &&, ||, not as part of our grammar.

A mathmatical expression is also a program:

f(x) = x[1]² - x[2]*x[3]*cos(pi*x[1])

To evolve a program we have first to define the set of functions and terminals:

Name	Set
Function	$\{+,-,*,/,^2\}$
Terminal	$\mathbb{R} \cup \{x1, x2, x3\}$

Each function requires a number of input arguments, this number is called **arity**.

The function + has arity 2, the partially applied function ² has arity 1.

The function if-then-else has arity 3.

These sets must obey the formal language rules:

- Every element of the terminal set T must be a valid and correct expression.
- If *f* ∈ *F* is a function with arity *n* and *e*₁, *e*₂, ..., *e*_n are valid and correct expressions, then *fe*₁...*e*_n is also a valid and correct expression.
- There are no other correct form besides these.

It is also possible that the expression contains the type information. A typed function must get the arguments of the correct type. The expression $e_1 \lor e_2$ requires that e_1, e_2 are booleans. The main evolutionary algorithm that evolves program is called **Genetic Programming** (GP).

```
gp =
      pop = randomPopulation
2
      until convergence do
3
        children = empty
4
        until length(children)==lambda do
          mut? = random(0,1)
6
          if mut?
7
            then ix = random(0, n)
8
                 child = mutate(pop[ix])
9
                 children = children <> child
10
            else (p1, p2) = randomParents(pop)
11
                 (c1, c2) = combine(p1, p2)
12
                 children = children <> [c1, c2]
13
       pop = replace pop children
14
15
   return pop
```

The fitness of a program is proportional to the amount of the test cases that passes within the training data.

If the output is a continuous value, we can measure the absolute or square difference between generated and expected outputs.

If the representation allows invalid programs, there is a need to apply some treatments to either fix the program or protect the output.

For example, it is common to use the analytical quotient instead of division:

$$aq(a,b) = \frac{a}{\sqrt{1+b^2}}$$

There are many ways to represent a program:

- Linear
- Tree
- Direct Acyclic Graph

With the linear representation, a program is reprenseted in its imperative form with state changes. In other words, a source code similar to an assembly language.

This representation allows the programs to be coded as *bytecodes* allowing us to use the common mutation and recombination of binary representation.

The Gene Expression Programming³ algorithm represents a program as an array of pre-fixed size:

$$Q * - + abcd$$

³Ferreira, Candida. "Gene expression programming: a new adaptive algorithm for solving problems." arXiv preprint cs/0102027 (2001).

We can also represent a function in polish notation:

$$* + x2y = (x+2) * y$$

The algorithm *Cartesian Genetic Programming*⁴ represents a program as a graph:

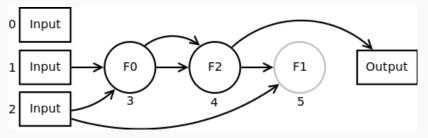


Figure 2: FONTE: http://www.cgplibrary.co.uk/files2/CartesianGeneticProgramming-txt.html

⁴Miller, Julian Francis, and Simon L. Harding. "Cartesian genetic programming." Proceedings of the 10th annual conference companion on Genetic and evolutionary computation. 2008.

Tree Representation

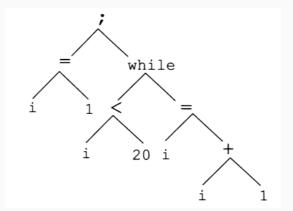


Figure 3: Fonte: Eiben, Agoston E., and James E. Smith. Introduction to evolutionary computing. Springer-Verlag Berlin Heidelberg, 2015.

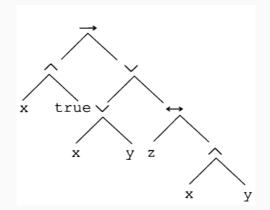


Figure 4: Fonte: Eiben, Agoston E., and James E. Smith. Introduction to evolutionary computing. Springer-Verlag Berlin Heidelberg, 2015.

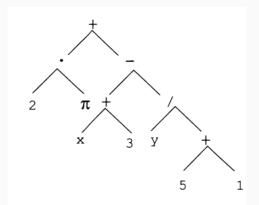


Figure 5: Fonte: Eiben, Agoston E., and James E. Smith. Introduction to evolutionary computing. Springer-Verlag Berlin Heidelberg, 2015.

When creating an initial solution, we must be careful that we create a correct expression (i.e., the leaves are terminals) and that the program is not too large.

In the **full** method, we create a complete tree with depth d. In other words, all of the branches of the tree must have the same depth.

1	<pre>full max-depth =</pre>
2	<pre>node = if max-depth == 0</pre>
3	then sampleTerm
4	else sampleNonTerm
5	children = [full (max-depth - 1) _ <- [1 arity(node)]]
6	return (Node node children)

The **grow** method freely generates a tree up to a maximum depth d, where it will sample only terminals.

Before reaching the maximum depth, the sample of a node is biased toward non-terminals to avoid short programs.

```
grow max-depth =
1
     ratio = n_terms / n_symbols
2
     r = random(0,1)
3
     node = if max-depth == 0 or r < ratio</pre>
4
               then sampleTerm
5
               else sampleNonTerm
6
     children = [grow (max-depth - 1) | _ <- [1 .. arity(node)]]
7
     return (Node node children)
8
```

In **Ramped Half-and-Half** we create a population of initial solutions by varying the application of the previous methods with different values of maximum depths.

If we want to create n individuals, we use full in half of them and grow to the other half. For each method, we choose a maximum depth from a range $[min_depth, max_depth]$ uniformly distributed.

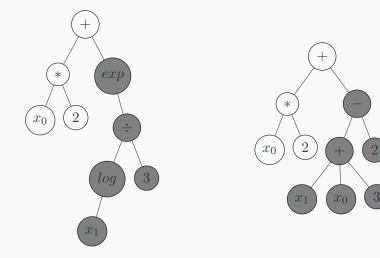
1	<pre>ramped min-depth max-depth n-pop =</pre>
2	
3	n = n-pop / 2 divisão inteira
4	(q, r) = (n / 2, n % 2)
5	treesFull = [full min-depth _ <-[1q]]
6	treesGrow = [grow min-depth _ <-[1q+r]]
7	<pre>trees = ramped(min-depth+1, max-depth, n-pop - n)</pre>
8	return (treesFull + treesGrow + trees)

Mutation

In this mutation operator we choose a subtree and replace it by a new randomly generated tree.

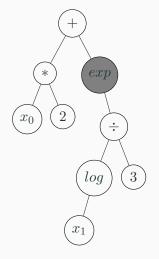
We can use either the grow or full method to create this random subtree.

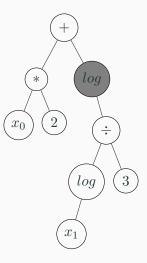
Subtree Replacement



With node mutation, we choose a node and change it with another token of the same arity.

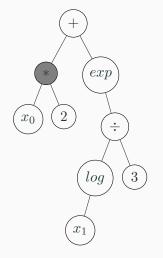
Node Mutation

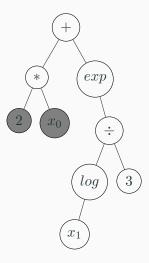




In swap mutation, a non-terminal node is chosen and its children are swapped (if they are of the same type).

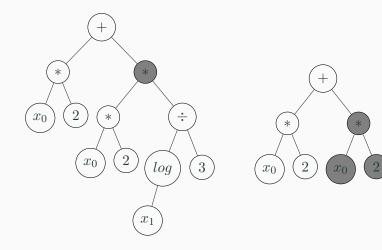
Swap Mutation





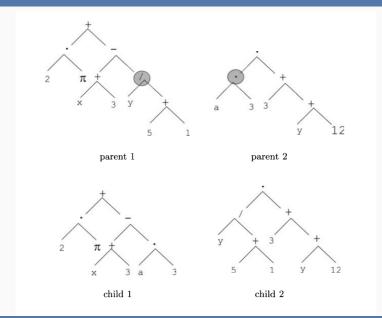
In shrink mutation, a random nonterminal node is replaced by one of its children.

Shrink Mutation



The recombination operator simply chooses a subtree of each parent and swap them.

Recombination



Bloat

In the initial generations, it is common to observe the increase of the average fitness of the population together with the increase of the size of the tree.

At a certain point, it is possible to observe the increase in size without any increase in the average fitness.

This phenomenon is known as **bloat** and it may be a problem since the computational cost to evaluate a larger program is higher.

Not only that, but the program loses its interpretability potential.

A hypothesis for this is the **replication of accuracy theory** which says the ability to generate a child solution that is functionally similar to its parents favors its replication in the population.

Bloated expressions favors this property.

In the **removal bias theory**, we notice that a tree can have inactive codes. When we apply reproduction and mutation in those inactive subtrees, there is a chance of increasing the size without any benefit to the fitness. The **programs search space theory** says that after a certain size, the average fitness will not change with size.

The reproduction of large programs tend to create even larger children which propagates throughout the generation favoring a population of large programs. One way to deal with bloat is to disallow the generation of programs of a certain size.

If a children is larger than the maximum allowed size, it is discarded.

The main problem of this solution is that those trees close to the maximum allowed size will have many copies in the population as their children will likely be discarded. Another solution is to return the children that violates such restrictions with a very small fitness such that it will be naturally discarded during replacement.

- search problem: find a valid solution from a set.
- optimization problem: find the best solution from a set.
- maximization problem: the best solution has the maximum value.
- minimization problem: the best solution has the minimum value.
- search space: set of all candidate solutions.
- solution representation: convenient representation of a solution.
- **objective-function:** functiona that maps a candidate to a value measuring the quality of the solution.
- **neighborhood:** set of candidate solutions close to a solution *s*.

- local optima: the best solution inside the neighborhood.
- global optima: the best solution of the search space.
- local search: searches for the nearest local optima.
- **heuristic:** technique to efficiently find a solution without any guarantees.
- **exploration:** act of exploring the search space.
- **exploitation:** act of exploring a promising neighborhood.

- Field Guide GP
- Livro Koza
- Livro 2 Koza
- Livro 3 Koza
- Livro 4 Koza

- Genetic Programming The Movie Part 1
- Genetic Programming The Movie Part 2
- Genetic Programming III: Human Competitive Machine Intelligence
- Genetic Programming IV Video: Human-Competitive Machine Intelligence
- Chapter 4 of Gabriel Kronberger, Bogdan Burlacu, Michael Kommenda, Stephan M. Winkler, Michael Affenzeller. Symbolic Regression. To be plubished.

• Nonlinear evolutionary symbolic regression

