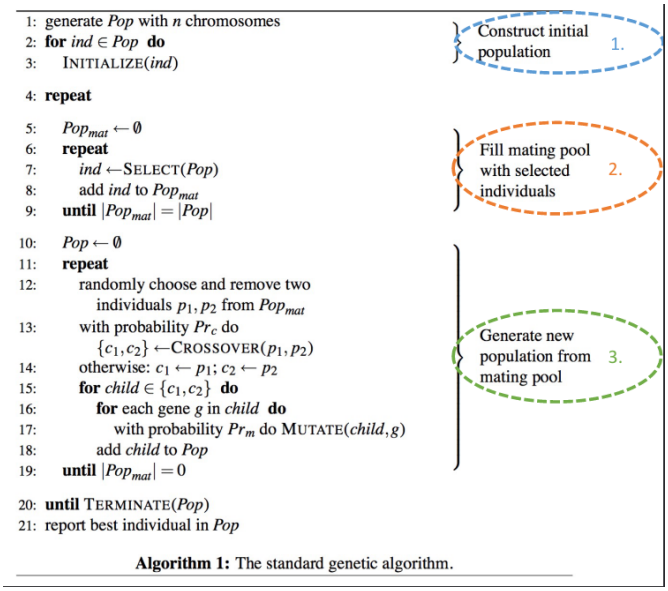
evolutionary_algorithms

What

- Evolutionary computation is a way to solve an optimization problem using a population and of candidate solutions and the dynamics of genetic evolution (selection, reproduction, and mutation)
  - Any-time algorithm
  - Iterative process
  - Stochastic process

Outline



Algorithm 1: The standard genetic algorithm.

Population of Candidate Solutions

- Randomly generated set of possible solutions
  - Usually low quality
  - Needs to be sufficiently diverse and large
  - Basic for better solutions
- Evolves through each generation

Genotype vs Phenotype

- Each encoding leads to a **solution** for the problem
  - Non-trivial translation
- Genotype gives rise to phenotype
  - Phenotype is tested for performance
- Genotype -> Encoding
- Phenotype -> The actual solution

Fitness

- Criterion to be optimized
- Complexity
  - Limit number of individuals making up the population
  - Limit number of generations that can be computed

Fitness Based Survival and Reproduction

- Performance of candidate solutions is used to steer:
  - Selection probabilities for survival
  - Reproduction probabilities to generate offspring and survival (parts of) the genotype.

Roulette Wheel Selection

- Fitness proportional selection

- Only works if you have positive fitnesses
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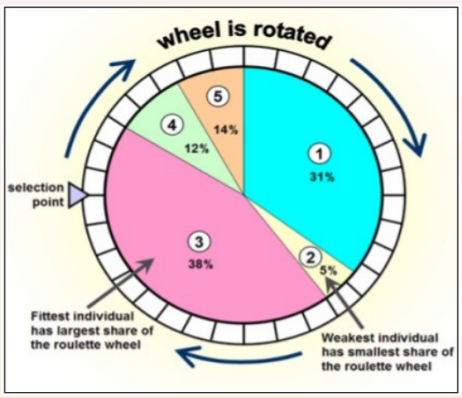
Fitness proportional selection

$$p_i = \frac{f_i}{\sum_{j=1}^{N} f_j}$$



Tuning

- Boltzmann or Gibbs distribution

$$p_i = \frac{e^{f_i/T}}{\sum_{j=1}^{N} e^{f_j/T}}$$

- Temperature-parameter (T)
  - Allows tuning of selection pressure
  - High values of T -> more randomness
  - Low values of T -> Deterministic according to fitness rank

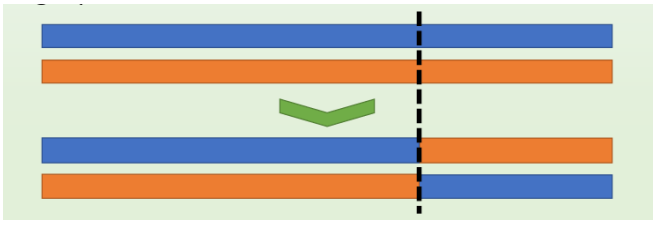
Tournament Selection

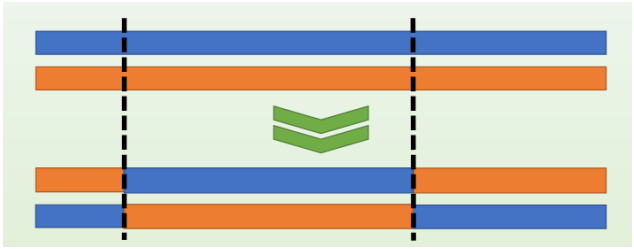
- Hold several limited size tournaments
  - Select set of individuals randomly
  - Use the fittest two for reproduction
- Smaller tournaments reduce selection pressure
  - More diversity in population
  - Slower convergence

Tuning

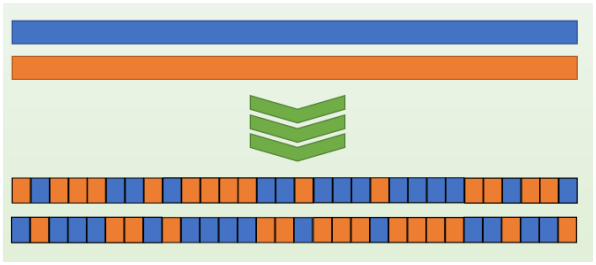
- Tournament size k
- Stochastic tournament outcomes
  - Fitter individuals only win with probability p

Reproduction

- Two parents share their genetic code and generate offspring
- Assume string-like genotypes
  - **Single point cross-over**
    
  - **Double point cross-over**



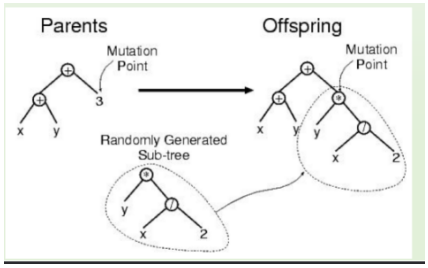
- **Uniform cross-over**



- **Other Possibilities**
  - Depending on genome-structure, not all re-combinations are possible
  - Complexity of cross-over operator grows with complexity of genotype

Mutation

- Random changes in the genotype
  - Low probability operator
  - Search regions uncovered by the initial population
  - Increase and restore population diversity
- **Bit flipping mutation**
  - Randomly selected bit gets flipped
  - Genome gets flipped completely
- **Real value mutation**
  - Boundary values
  - Uniform random
  - Non-uniform (reduce number of changes over-time)
  - Guassian noise addition
- **Headless Chicken Crossover**



Schemata

- Rules of GA behaviour are relatively simple
- Resulting dynamics are difficult to understand
- **Schema** theory offers insight into why good solutons survive and get combiend into better solutions

Definition

Consider binary genotypes:

0111 1111 1101 0101

All these instances belong to the schema

*1*1

- binary numbers indicate fixed value positions
- * indicates positions for which the value *does not matter*

$*1*1$

01 2 3

defining length = 3-1 = 2

Concepts

Consider fixed-length (n) schemata (s) of the form

$$s \in \{0, 1, *\}^n$$

The *order* of s is the number of fixed positions

$$o(s) = ||\{\forall i \in \{1 \dots n\}, s_i \neq *\}||$$

The *defining length* is the longest distance between fixed positions

$$d(s) = max(|i-j|, \forall i, j \in \{1 \dots n\}, s_i \neq * \wedge s_j \neq *)$$

Theory

Schemas can be used to reason about the disruptive properties of mutation and crossover.

The probability of a schemata to survive mutation is

$$(1 - p_m)^{o(s)}$$

where p_m is the mutation probability of a single bit

=> Schemata with higher order have a lower probability of surviving mutation

Order is the number of fixed positions in the template

- $o(s)$ is the order of the schemata

  $1 * 10 * 1$ is 4 and its defining length is 5

The probability of a schemata surviving crossover is

$$(1 - p_c \frac{d(s)}{n-1})$$

where p_c is the crossover probability

=> Schemata of longer defining lengths have a lower probability of survival after crossover

- n-1 says that considering all cutting points (except the last)

Schema Theorem

Of those schemata with above average fitness
those with
1. short defining lengths
and
2. low order
are more likely to survive and increase their proportion in the population

Building Blocks Theorem

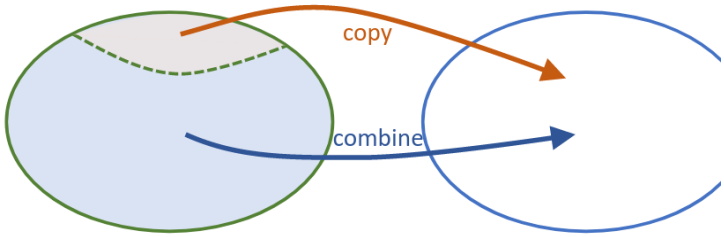
- GA's perform adaption by identifying and recombining so called **building blocks** of relatively high fitness to build entire solutions
- These building blocks take the form of schemata with low order and short defining length

Genotype Design

- Genotype guidlines
  - Put related genes close together so they can form schemas with low descriptive length.
  - Make each gene as independent from one another as possible
- Crossover operator
  - Crossover operator a low probability of destroying schemas

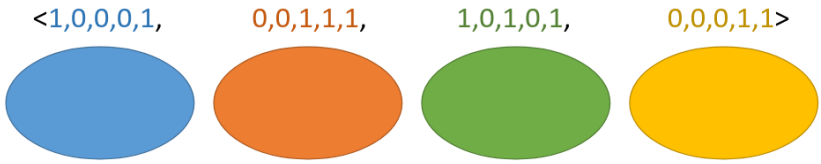
Destruction (Elitism)

- Crossover and mutation can have destructive consequences
- Having the k-best individuals transferred to the population of the next generation avoids loss of good solution



Cooperative Coevolution

- According to the bulding blocks theorem, the different blocks and their influence on performance should be independent
- If they are, they can be searched for independently



- Each pool is a sub-population

Optimal Genotype Encodings

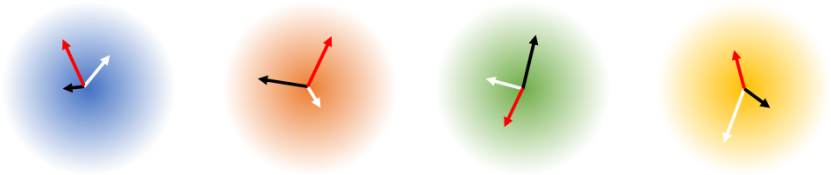
- Each gene in a genotype should be independent
  - Optimal encoding of the possible phenotypes
  - Each gene-population can be represented as a probability distribution
- **SNES** - Seperable Natural Evolution Strategy
  - Maintains a Natural distribution (Gaussian) (μ, σ) for each gene
  - An individual from the population is generated by sampling each gene seperately

SNES

- No standard selection, reproduction and mutation
- Means and standard deviations are updated according to a weighted sum of the genomes in the generated population (=similar to gradient)

    - Fit individuals have a stronger vote in the gradient
- Mutation is covered by sampling each generation
- This randomness of sampling ensures diversity and prevents sub-optimal convergence

☐ Understand the below figure better



- Sampling two numbers (white, black)
    - If the white does better than the black one, move the mean in direction of the white one.
    - End of arrows represents a gene
- There is no population any more. Everything we know is information in the distributions
- If values are approx equal, then can increase standard deviation
- Significant deviations means that you want a smaller standard deviation

Premature Convergence

- A niche solution can draw a lot of the population towards a sub-optimal solution
    - Too many individuals become similar. cross-over does not result in any more search
    - Only mutation can get the population out of the situation
- GA's given no assurances about the quality of the solution that will be reached
- Monitor by showing the finesses (bar graph) of the population's fitness

Niche Penalty

- Avoid over-production of similar individuals
- Any group of individuals of sufficient similarity (niche radius) can have a penalty added to their fitness evaluation.
    - Might not always work depending on fitness landscape)

Complex Problems -> Complex solutions

- Evolutionary algorithms don't scale well with problem complexity
- Building block theorem states that partial solutions should combine into a full solution
    - Problem is not always divisible into smaller sub-problems
    - Not the case for intrinsically complex problems

Fitness requirements/ limitations

- Fitness function needs to be able to seperate partial solutions from non-solutions
    - Spread of fitness values
- GA's can not solve tasks with a binary fitness value
    - Percentage success is a suitable fitness evaulation as an alternative
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