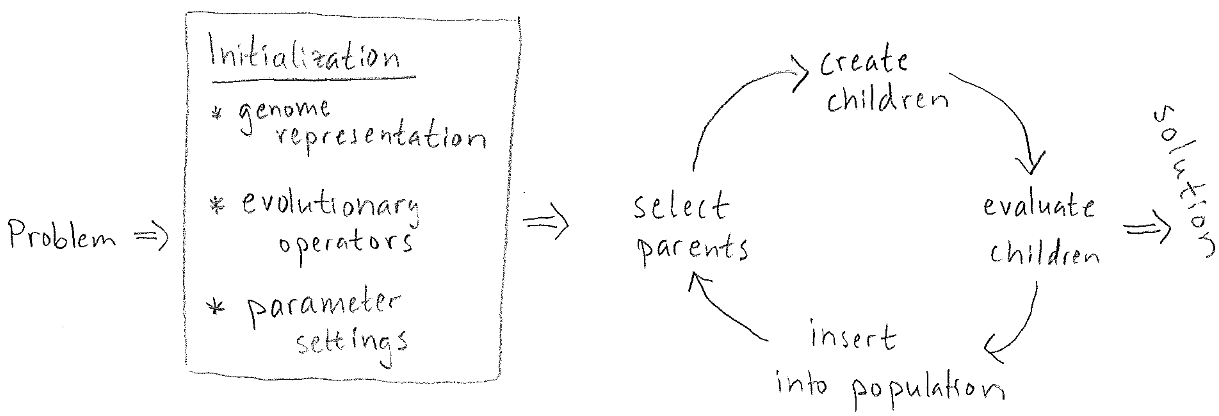
GENETIC ALGORITHMS

Pros	Cons
* Global optimizer - avoids local optima - creative search process	* Many function evaluations → Time consuming
* Handles many different types of problems	* Hard to prove that the optimum is found
* Lots of software available	* Rather complicated algorithm to implement and control
* active research field	



Hamburger Restaurant Problem

3 design variables:

1 - The price for the burger
  1 = $2.0
  0 = $20.0

2 - The drinks
  1 = Coke
  0 = wine

3 - The service
  1 = fast sloppy service
  0 = luxurious service

⇒ A restaurant that serves cheap burgers with coke and has fast sloppy service could be representated as

gene
price
$\boxed{1}\boxed{1}\boxed{1}$
drinks
service
chromosome

With 3 design variables that can take 2 values we have $2^3 = 8$ possible designs/restaurants

Imagine that the optimal restaurant serves cheap burgers with coke and has fast service: $\boxed{1}\boxed{1}\boxed{1}$: McDonalds is the best

Decode the binary string to give it a fitness value/objective score

Restaurang	Fitness
0 0 0	0
0 0 1	1
0 1 0	2
0 1 1	3
1 0 0	4
1 0 1	5
1 1 0	6
1 1 1	7

① Initialize the population

* Determine the representation
* Determine the population size
  Here = 4
* Determine evolutionary operators
* Create individuals
* Calculate their score / fitness

Generation 0				Mating Pool		Generation 1	
Individual	Chromosome	Fitness	P_{sel}	Chrome	Score	Chrome	Score
1	0 1 1	3	0.25	0 1 1	3	0 1 0	2
2	0 0 1	1	0.08	1 1 0	6	1 1 1	7
3	1 1 0	6	0.5	1 1 0	6	1 1 0	6
4	0 1 0	2	0.17	0 1 0	2	0 1 0	2
Total		12	1		17		17
Worst		1			2		2
Average		3			4.25		4.25
Best		6			6		7

② Selection

The probability of being selected for mating and reproduction is based on the fitness of the individual

selection probability $\quad P_{sel} = \dfrac{\text{individual fitness}}{\text{total fitness}}$

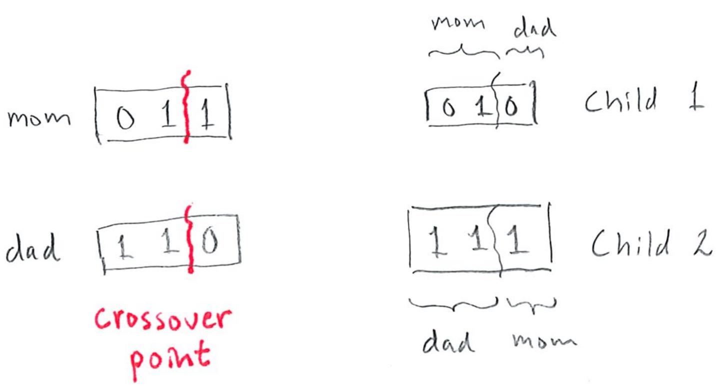
One common way of implementing selection is the Roulette wheel selection, where the slot size is proportional to the selection probability

Typically, the mating pool is more fit than the previous generation

③ Reproduction

Crossover: Children are created by combining genes from different parents

* Select parents from the mating pool, e.g. parent 1 & 2
* Do one-point crossover
  - pick a crossover point at random
  - combine segments from both parents



Usually there is a crossover probability (P_{cros}) in a GA for when crossover occurs
Otherwise, the children are exact copies of their parents

④ Mutation

Choose a random individual in a random fashion

* Choose an individual randomly
* Choose a mutation point
* Flip that bit

Let's say nr 4: 010

→ 011

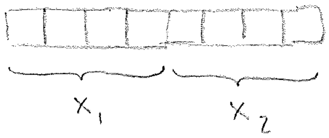
Ex: Binary Representation

$$\min f(\bar{x}) = 100(x_1^2 - x_2)^2 + (1 - x_1)^2$$

$$-2 \leq x_i \leq 1.75$$

Let's represent x_1 & x_2 with a binary representation with 4 bits per variable.

$\Rightarrow 2^4 = 16$ possible values for each variable



	x_1	x_2
0 0 0 0 | 0 0 0 0	-2	-2
0 0 0 1 | 0 0 0 1	-1.75	-1.75
0 0 1 0 | 0 0 1 0	-1.5	-1.5
⋮ ⋮	⋮	⋮
1 1 1 0 | 1 1 1 0	1.5	1.5
1 1 1 1 | 1 1 1 1	1.75	1.75

In the GA, an individual is represented by a chromosome like this $\begin{array}{|c|c|c|c|c|c|c|c|}\hline \ & \ & \ & \ & \ & \ & \ & \ \\ \hline\end{array}$ in what is called the genotype space

The chromosome is transformed to the optimization variable space (e.g. x_1 x_2) by decoding the string

To calculate the objective function value, the decoded variable values are sent to the objective function. That gives a value in the objective space

$$\begin{array}{|c|c|c|c|c|c|c|c|}\hline 0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 \\ \hline\end{array} \xRightarrow{\text{Decoding}} \begin{array}{l} x_1 = -2 \\ x_2 = 1.75 \end{array} \xRightarrow{\text{obj. fcn. evaluation}} f(x) = 100\left((-2)^2 - 1.75\right)^2 + (1+2)^2$$

Uniform crossover vs. one point crossover

Imagine a problem with two real optimization variables, and two different representations, one binary and one real.

Let the variables vary between $0 \leq x_i \leq 3.75$

0	0	0	0	0
0	0	0	1	0.25
0	0	1	0	0.5
0	0	1	1	0.75
0	1	0	0	1.0
0	1	0	1	1.25
0	1	1	0	1.5
0	1	1	1	1.75
1	0	0	0	2
1	0	0	1	2.25
1	0	1	0	2.5
1	0	1	1	2.75
1	1	0	0	3
1	1	0	1	3.25
1	1	1	0	3.5
1	1	1	1	3.75

Dad

$\underbrace{1|0|0|1}_{x_1}\underbrace{|0|1|1|0}_{x_2}$

$0|1|1|1|1|0|0|1$

Mom

$\boxed{2.25 \,|\, 1.5}$ $\Rightarrow$ $\boxed{1.75 \,|\, 2.25}$

$\xRightarrow{\text{one-point crossover}}$

$\boxed{2.25 \,|\, 2.25}$

$\boxed{1.75 \,|\, 1.5}$

Child 1

$\underbrace{1|0|0|1}_{2.25}\underbrace{|0|1|0|1}_{1.25}$

$\underbrace{0|1|1|1}_{1.75}\underbrace{|1|0|1|0}_{2.5}$

Child 2

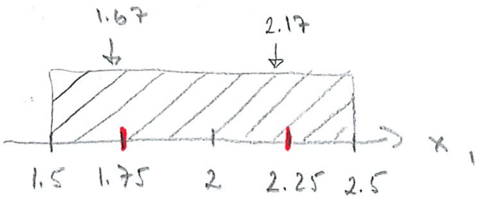
One point crossover works for binary genes but not for real valued genes.

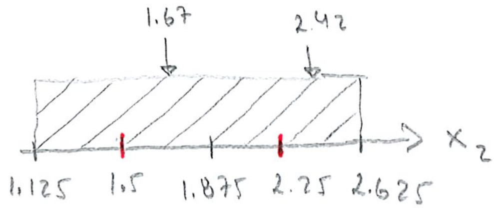
Blend Crossover

Study our two individuals again

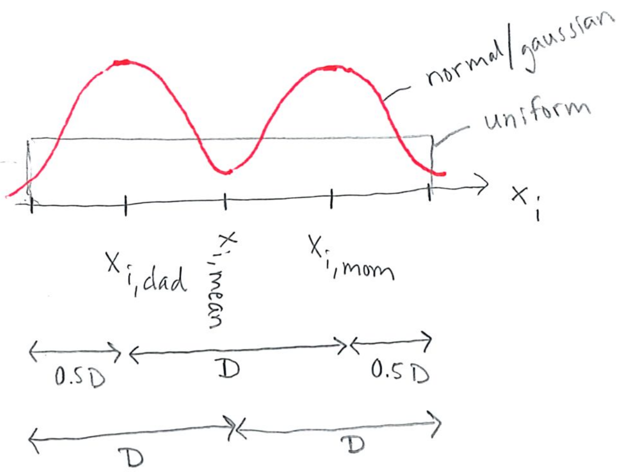
Dad	2.25	1.5	⇒	1.67	1.67
Mom	1.75	2.25		2.17	2.42

Two new children with new values in their genes

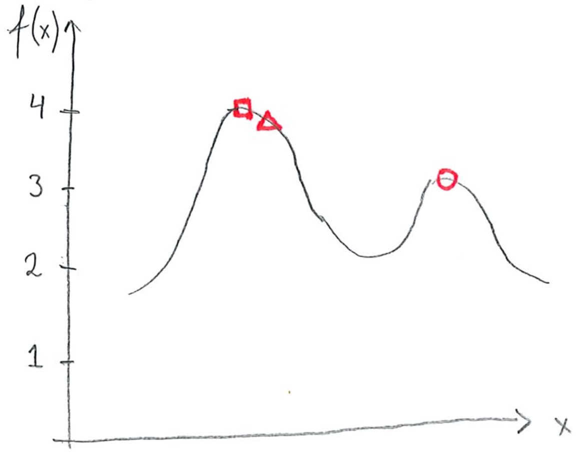




Above, we used uniform distributions. Others can be used as well, but uniform is most common



Fitness Sharing Example



$f(\square) = 4$

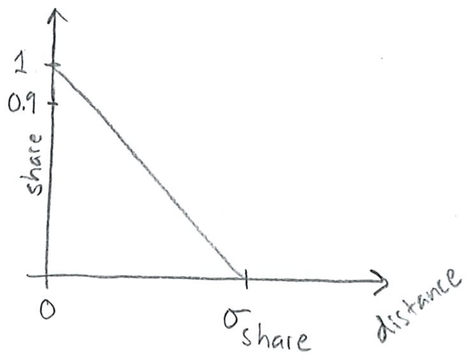
$f(\triangle) = 3.9$

$f(\circ) = 3$

$$f_{share}(x) = \frac{f(\bar{x}_i)}{\sum_{j=1}^{n} s(d(\bar{x}_i, \bar{x}_j))}$$

s: sharing function

d= distance function



$$f_{share}(\square) = \frac{4}{\Sigma\left(s(\underbrace{d(\square,\square)}_{=0}) + s(d(\square,\triangle)) + s(\underbrace{d(\square,\circ)}_{\text{large}})\right)}$$

$$f_{share}(\square) = \frac{4}{1+0.9+0} = \frac{4}{1.9} \approx 2$$

$$f_{share}(\circ) = \frac{3}{1+0+0} = 3$$

∴ It is better to be alone on a small top than to be many on the large top

Distance Functions

Genotype distance

- How many bits differ? $\left.\begin{array}{l}\boxed{1|1|0}\\ \boxed{0|1|0}\end{array}\right\}$ 1 bit

- Phenotype distance $\left.\begin{array}{r}0.75\\ -0.25\end{array}\right\}$ 1.0

- Attribute or objective distance

$$f(0.75) - f(-0.25) = 0.5$$

Ex: $f(x) = x^2$

$-0.75 \le x \le 1$

3 bit binary representation

	x	f
0 0 0	-0.75	
0 0 1	-0.5	
0 1 0	-0.25	1/16
0 1 1	0	
1 0 0	0.25	
1 0 1	0.5	
1 1 0	0.75	9/16
1 1 1	1	

The difference could be normalized to yield values between 0 and 1 by division of the maximum distance

$\Rightarrow$ 0 means that the individuals are identical

$\Rightarrow$ 1 means individuals are as far away as possible

Genotype: $\dfrac{1 \text{ bit}}{3 \text{ bits}} = \dfrac{1}{3} = 0.33$

Phenotype: $\dfrac{1.0}{1-(-0.75)} = \dfrac{1}{1.75} = \dfrac{4}{7} = 0.57$

Attribute: $\dfrac{0.5}{1-0} = 0.5$