

Genetic Example:

Problem: find X^2 over $[0...31]$

- Data presentation: binary code
- Fixed population size: 4
- Evolution: roulette wheel selection, 1-point crossover, bitwise mutation
- Run 1 one circle

Initialization			Selection		
Initial Population	Value x	Fitness $f(x) = x^2$	Probability	Expected Count	Actual Count
0 1 1 0 1	13	169	0.14	0.58	1
1 1 0 0 0	24	576	0.49	1.97	2
0 1 0 0 0	8	64	0.06	0.22	0
1 0 0 1 1	19	361	0.31	1.23	1
Max	576	Average	293		

Crossover				
Population after selection	Cross-over point	Offsprings	Value x	Fitness $f(x) = x^2$
0 1 1 0 1	4	0 1 1 0 0	12	144
1 1 0 0 0		1 1 0 0 1	25	625
1 1 0 0 0	2	1 1 0 1 1	27	729
0 1 0 0 0		1 0 0 0 0	16	256
Max	729	Average	439	

Mutation with probability p_m			
Population after crossover	Offsprings	Value x	Fitness $f(x) = x^2$
0 1 1 0 0	0 1 1 0 0	12	144
1 1 0 0 1	1 1 1 0 1	29	841
1 1 0 1 1	0 1 0 1 1	11	121
1 0 0 0 0	1 0 0 0 0	16	256
Max	841	Average	340

Comment: Cross-over or mutation can both give better or worse offsprings but it give us a chance to find best elitism. Even in last mutation, our average population decrease and we obtain better result, it shows that loss of good population is possible and bigger population means lower chances to degenerate it.

Hamming Cliff problem

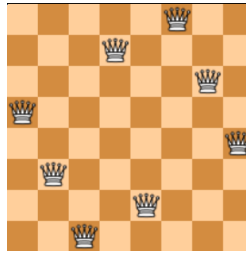
- Problem Statemetn: $\begin{cases} 256 - x^2 & \text{if } x \leq 0 \\ 0 & \text{else} \end{cases}$ for $x = [-16,16]$
- Data presentation: $b_{-16} = 00000 \dots b_{15} = 11111$
- **Optimum point $b_0 = 10000$, second best $b_{-1} = 01111$
 - o Cross-over: cannot generate b_0 from good parent b_1
 - o Mutation: cannot flip all positions
- ** Neighbour:

$b_{-16} = 00000$	$f(-16) = 0$
$b_8 = 11000$	$f(8) = 0$
$b_4 = 10100$	$f(4) = 0$
$b_2 = 10010$	$f(2) = 0$
$b_1 = 10001$	$f(1) = 0$

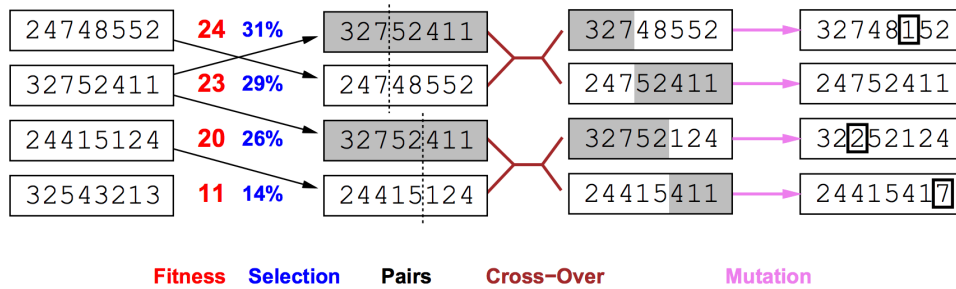
 - o Neighbours have poor performance
- Problem solve by using new data presentation $g(i) = b(i)$ or $b(\frac{i}{2})$ then $g(i)$ and $g(i+1)$ only differ 1 bit
 - o $g(0) = 11000$ and $g(-1) = 01000$

8-Queen problem

- Problem: place 8 queens on a chessboard such that no queen attacks any others



- Data presentation: State/Position is position of each queen in each column
 - o Ex: [46827135] represent a case in image above
- Fitness function: number of non-attacking queens (min=0, max=28)
 - o Higher value better result



- Cross-over: swap segment
- Mutation: invert random segment (choose segment and permutation), switch 2 random positions or change it

2 Support theorem and some example for this algorithm

Schema:

Definition: $s = s_1, s_2 \dots s_l$ with $s_i = 0, 1$ or *

- present a subset of D
- s contains $2^{l-o(s)}$ chromosomes. $o(s)$ = number of defined bit and l is length of schema
- each chromosome belong to 2^l schemas

Schema Theorem

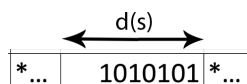
- provide estimate of number of schemas during evolution (selection, cross-over and mutation) to analyse how chromosomes vary in schema
- Definition:
 - o Population P , size n , at time t , schema s .
 - o $m(s, t)$ = number of chromosomes of s in P at time t

Selection:

- probabilistic selection: $p(x) = \frac{f(x)}{\sum_{y \in P} f(y)}$
 - o let $\bar{f}(t) = \frac{1}{n} \sum_{y \in P} f(y)$ and $\hat{u}(s, t) = \frac{1}{m(s, t)} \sum_{x \in s \cap P} f(x)$ (expect value of F over P and s)
 - o $p(x \in s) = \sum_{x \in s \cap P} p(x) = \sum_{x \in s \cap P} \frac{f(x)}{\sum_{y \in P} f(y)} = \frac{1}{n \bar{f}(t)} \hat{u}(s, t) m(s, t) = \alpha$
- Assume that we choose only 1 best chromosome. Our current population is P_0
 - o Expect value of number of chromosomes after 1 selection $E_1 = \sum_{k=0}^1 kp = 0(1 - \alpha) + 1\alpha = \alpha$
 - o Expect value of number of chromosomes after n selections $E_n = nE_1 = n\alpha$
 - o Expect value of number of chromosomes of s after n selections $E(m_1(s, t)) = n \frac{1}{n \bar{f}(t)} \hat{u}(s, t) m(s, t) = \frac{\hat{u}(s, t)}{\bar{f}(t)} m(s, t)$
 - o So if we have good schema, ratio $\frac{\hat{u}(s, t)}{\bar{f}(t)} > 1$ and then number of good chromosomes increases

Crossover:

- We only try applying 1 point crossover with probability p_c that means $(1 - p_c)$ population P_1 (after selection step) will be in P_2
 - o $d(s)$ **max distance** between defined binary values
 - o suppose $x \in P$ belongs to schema s:



- if i (a cross-over point) is outside $d(s)$: schema preserved
- if i is inside $d(s)$: possible that both offspring are not in s . Schema can be destroyed.
- We will find numbers of survive chromosomes after cross-over
 - Probability that a chromosome of s does not produce a chromosome of s is $\frac{p_c d(x)}{l-1}$
 - $E(\text{number of chromosomes of } s \text{ are destroyed}) \leq \frac{p_c d(x)}{l-1} m_1(s, t)$
 - Expect value of number of chromosomes of s after cross-over: $E(m_2(s, t)) = (1 - \frac{p_c d(x)}{l-1}) m_1(s, t)$

Mutation:

- Each chromosome will be mutated with probability p_m
 - Survival probability $s_m(s) = (1 - p_m)^{o(s)}$ (probability that each bits should not be mutated)
 - Expect value of number of chromosomes of s in new population $E(m(s, t + 1)) \geq m_2(s, t)(1 - p_m)^{o(s)}$

Conclusion:

- $$E(m(s, t + 1)) \geq (1 - \frac{p_c d(x)}{l-1})(1 - p_m)^{o(s)} \frac{\hat{u}(s, t)}{\bar{f}(t)} m(s, t)$$
- $(1 - \frac{p_c d(x)}{l-1})$ and $(1 - p_m)^{o(s)}$ are less than 1, so quality of schema at beginning is quite important so that $\frac{\hat{u}(s, t)}{\bar{f}(t)} \gg 1$

The N^3 Argument

- Theorem: Under reasonable assumptions, random population of size N sample N^3 schemas (100 chromo => 10^6 schemas)
- The proof: It is not very useful to understand this. You can look for it online
- Intuitive interpretation:
 - Increase a population, we also sample more schema so that we have greater chances to meet "good" schema
 - Since good schema is created during evolution, we have greater chance to get global maximum