### v) Crossover

- Crossover operation forms children chromosomes for next generation by using parent chromosomes from the mating pool of the current generation
- N/2 mating pairs are selected at random

- With some crossover probability ( $p_c$  close to 1.0), the parent chromosomes swap some portions of themselves to produce two children chromosomes
- In single-point crossover a crossover site is chosen at random and the portions on the right side of the crossover site are interchanged

### • Single-point Crossover

## •Two-point Crossover

#### • <u>Uniform Crossover</u>

- ✓ At each bit position a coin is tossed to decide whether there will be interchange of the bits.
- ✓ If 'head' appears then there will be a swapping else not

Let us assume that 2-nd, 4-th, 5-th, 8-th, 9-th, 12-th, 18-th and 20-th bit positions are selected for swapping

Found to perform better for large search spaces

• Crossover operation introduces randomness into the current population to help avoid getting trapped in local minima

• Crossover operation may result in better or worse strings. If a few worse offspring are formed, they will not survive for long since upcoming generations are likely to eliminate them

• What if all the new offspring are worse? To avoid such situations, go for an ELITIST selection

#### vi) Mutation

• After crossover, a small fraction (decided by a small mutation probability  $p_m$ ) of the N members are made to undergo Mutation.

A mutation site is chosen at random and the corresponding bit is flipped (single point mutation)

• Each bit of all the N chromosomes are flipped with the mutation probability  $p_m$  (bit-wise mutation)

- 1) 0101101011100110101
- 2) 00110100101110100101
- 3) 0101101011 1110100101
- 4) 0011010010 1001101001
- 5) 10101110011010010100
- **6)** 0 1 0 0 1 0 1 1 1 0 1 0 0 0 1 1 0 0 1 1
- 7) 10101111101010010100
- 8) 0100101001100011

• Helps a great deal to avoid getting stuck in local minima

• Too low  $p_m \longrightarrow local minima problem$ 

Too high  $p_m \longrightarrow$  too much randomization

#### **Termination criteria**

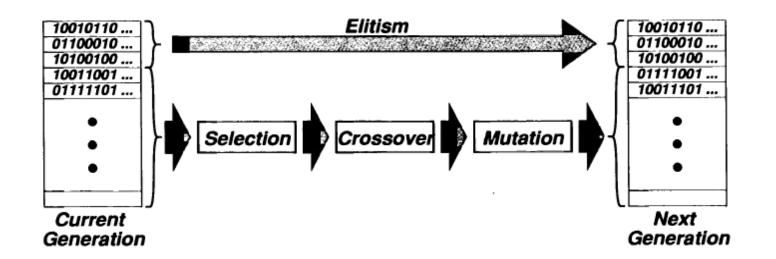
- Maximum number of Generations, say G = 100

- At least  $n_2$  generations are complete and at least over the last  $n_1$  generations, the best solution is not changing by more than a small  $\epsilon$ 

➤ Best solution of each generation is saved

#### **Elitism**

- Objective is to speed up convergence (best solutions are not lost from the population)
- A few best chromosomes of the present generation (Elite Count (EC) = 2, say) are directly sent to the next generation; others go through the normal process of selection, crossover and mutation



## **Example:**

maximize 
$$f(x_1, x_2) = x_1x_2$$
 where  $1.0 \le x_1, x_2 \le 10.0$ 

Initial population is randomly chosen as,

$$(2,8); (5,5); (9.5,7.5); (3,2); (10,3); (4,7)$$

Random numbers generated for Roulette wheel selection are,

Compute the next generation with the fitness values. Assume the following:

string length of each variable is 4

single point crossover with site 3 and 5 alternately

mating pairs as 1st and 4th members; 2nd and 5th members etc.

$$P_c = 1.0$$
;  $P_m = 0.0$  and EC=0.

Resolution for each variable,

$$\epsilon' = \frac{10 - 1}{2^4 - 1} = 0.6$$

Now, 
$$x_1 = x_1^{min} + x_1^d \in '$$
$$2 = 1 + 0.6 * x_1^d$$
$$x_1^d = 1.66 \approx 2.0 = '0010'$$

Similarly, 
$$8 = 1 + 0.6 * x_2^d$$
$$x_2^d = 11.66 \approx 12.0 = '1100'$$

G	F	N	#	1
•	_			-

**GEN #1** 

(Phenotype Space) (Genotype Space)

1. (2, 8)

0010 1100

2. (5, 5)

0111 0111

3. (9.5, 7.5)

1110 1011

4. (3, 2)

0011 0010

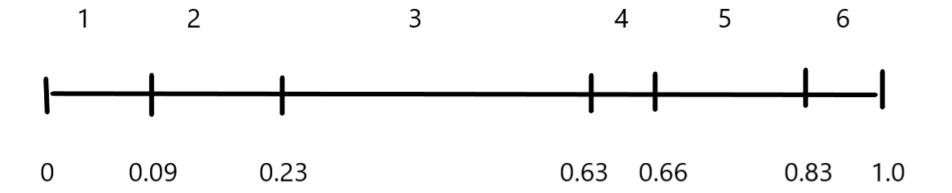
5. (10, 3)

1111 0011

6. (4, 7)

0101 1010

<b>GEN #1</b> (Phenotype Space)	<b>GEN #1</b> (Genotype Space)	Fitness Value (f=x1.x2)	Select. Prob.
1. (2, 8)	0010 1100	16.00	0.09
2. (5, 5)	0111 0111	25.00	0.14
3. (9.5, 7.5)	1110 1011	71.25	0.40
4. (3, 2)	0011 0010	06.00	0.03
5. (10, 3)	1111 0011	30.00	0.17
6. (4, 7)	0101 1010	28.00	0.17
		176.25	



<b>GEN #1</b> (Phenotype Space)	<b>GEN #1</b> (Genotype Space)	Fitness Value (f=x1.x2)	Select. Prob.	Mating Pool	
1. (2, 8)	0010 1100	16.00	0.09	1110 1011	(3)
2. (5, 5)	0111 0111	25.00	0.14	1111 0011	(5)
3. (9.5, 7.5)	1110 1011	71.25	0.40	0111 0111	(2)
4. (3, 2)	0011 0010	06.00	0.03	1111 0011	(5)
5. (10, 3)	1111 0011	30.00	0.17	0101 1010	(6)
6. (4, 7)	0101 1010	28.00	0.17	1110 1011	(3)
		176.25			

Mating Pool	<b>GEN #2</b> (Genotype Space)
1110 1011	1111 0011
1111 0011 —	1110 1011
011 0111	1111 0010
111 0011	0101 1011
0101 1010	0110 1011
1110 1011	1111 0111

Now, 
$$x_1 = x_1^{min} + x_1^d \in Y$$
  
= 1 + 15 \* 0.6

and 
$$x_2 = x_2^{min} + x_2^d \in Y$$
  
= 1 + 3 \* 0.6

Mating Pool	<b>GEN #2</b> (Genotype Space)	<b>GEN #2</b> (Phenotype Space)	Fitness Value (f=x1.x2)
111 <mark>0 1011 ——</mark>	1111 0011	(10, 2.8)	28.00
1111 0 <mark>011 —</mark>	1110 1011	(9.4, 7.6)	71.44
011 <mark>1 0111</mark>	1111 0010	(10, 2.2)	22.00
11111 0011	0101 1011	(4, 7.6)	30.40
0101 1010	0110 1011	(4.6, 7.6)	34.96
1110 1011	1111 0111	(10, 5.2)	52.00
			238.80

# **Example:**

$$f = -10\cos x_1\cos x_2 e^{-\left\{\frac{(x_1-1)^2}{4} + (x_2-2)^2\right\}}$$
$$-5.0 \le x_1 \le 5.0; \quad -5.0 \le x_2 \le 5.0$$

$$\underline{x}^* = \begin{bmatrix} 2.51 & (2.49) \\ 2.48 & (2.43) \end{bmatrix} \quad f^* = -2.8613 \quad (-2.8733)$$

- N=20 (40)
- Pc=0.9
- Pm=0.09
- EC=0
- Chromosome length= 10+10
- Uniform crossover

