Crossover Techniques in GAs

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Important GA Operations

1. Encoding
2. Fitness Evaluation and Selection
3. Mating pool
4. Crossover
5. Mutation
6. Inversion
7. Convergence test

Important GA Operations

1. Encoding
2. Fitness evaluation and Selection
3. Mating pool
4. **Crossover**
5. Mutation
6. Inversion
7. Convergence test

Reproduction in Genetic Algorithm

Reproduction:

- **Crossover**
- Mutation
- Inversion

These genetic operators varies from one encoding scheme to another.

- Binary coded GAs
- Real-coded GAs
- Tree-coded GAs

Mating Pool: Prior to crossover operation

- A mating pair (each pair consists of two strings) are selected at random. Thus, if the size of mating pool is N, then $\frac{N}{2}$ mating pairs are formed.[Random Mating]
- The pairs are checked, whether they will participate in reproduction or not by tossing a coin, whose probability being p_c. If p_c is head, then the parent will participate in reproduction. Otherwise, they will remain intact in the population. [Monte Carlo Simulation]

Note :
Generally, $p_c = 1.0$, so that almost all the parents can participate in production.

Crossover operation

Once, a pool of mating pair are selected, they undergo through crossover operations.

1. In crossover, there is an exchange of properties between two parents and as a result of which **two** offspring solutions are produced.
2. The crossover point(s) (also called k-point(s)) **is(are)** decided using a random number generator generating integer(s) in between 1 and L, where L is the length of the chromosome.
3. Then we perform exchange of gene values with respect to the k-point(s)

There are many exchange mechanisms and hence crossover strategies.

Crossover Techniques in Binary Coded GA

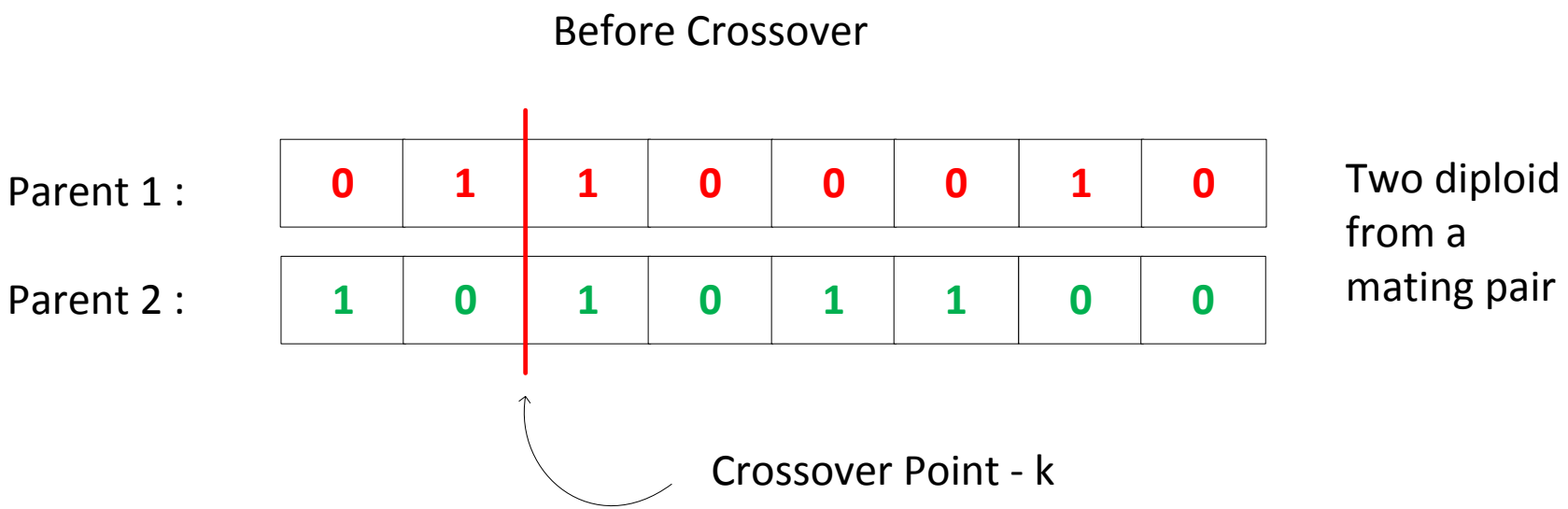
Crossover operations in Binary-coded GAs

- There exists a large number of crossover schemes, few important of them are listed in the following.
  1. Single point crossover
  2. Two-point crossover
  3. Multi-point crossover (also called n-point crossover)
  4. Uniform crossover (UX)
  5. Half-uniform crossover (HUX)
  6. Shuffle crossover
  7. Matrix crossover (Tow-dimensional crossover)
  8. Three parent crossover

Single point crossover

1. Here, we select the K-point lying between 1 and L. Let it be k.
2. A single crossover point at k on both parent's strings is selected.
3. All data beyond that point in either string is swapped between the two parents.
4. The resulting strings are the chromosomes of the offsprings produced.

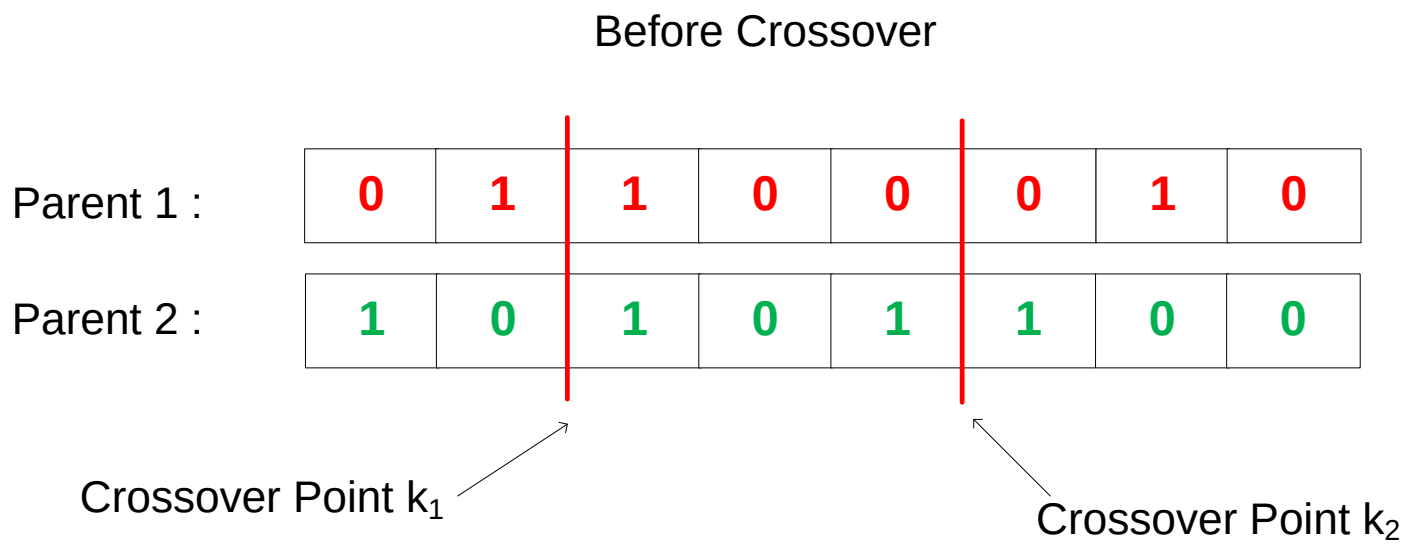
Single point crossover: Illustration



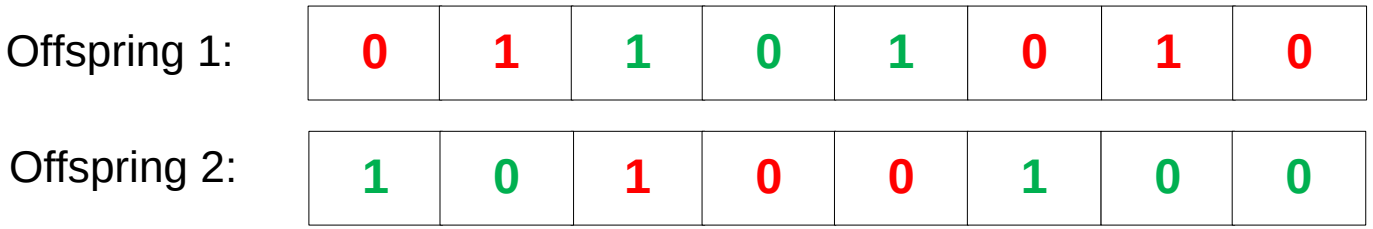
Two-point crossover

1. In this scheme, we select two different crossover points k_1 and k_2 lying between 1 and L at random such that $k_1 \neq k_2$.
2. The middle parts are swapped between the two strings.
3. Alternatively, left and right parts also can be swapped.

Two-point crossover: Illustration



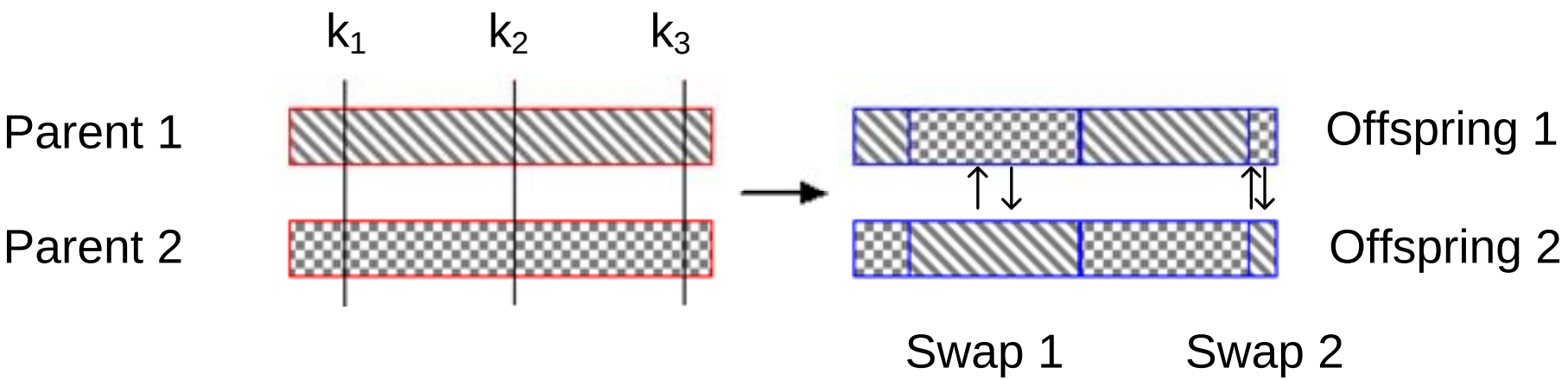
Select two crossover points randomly



After Crossver

Multi-point crossover

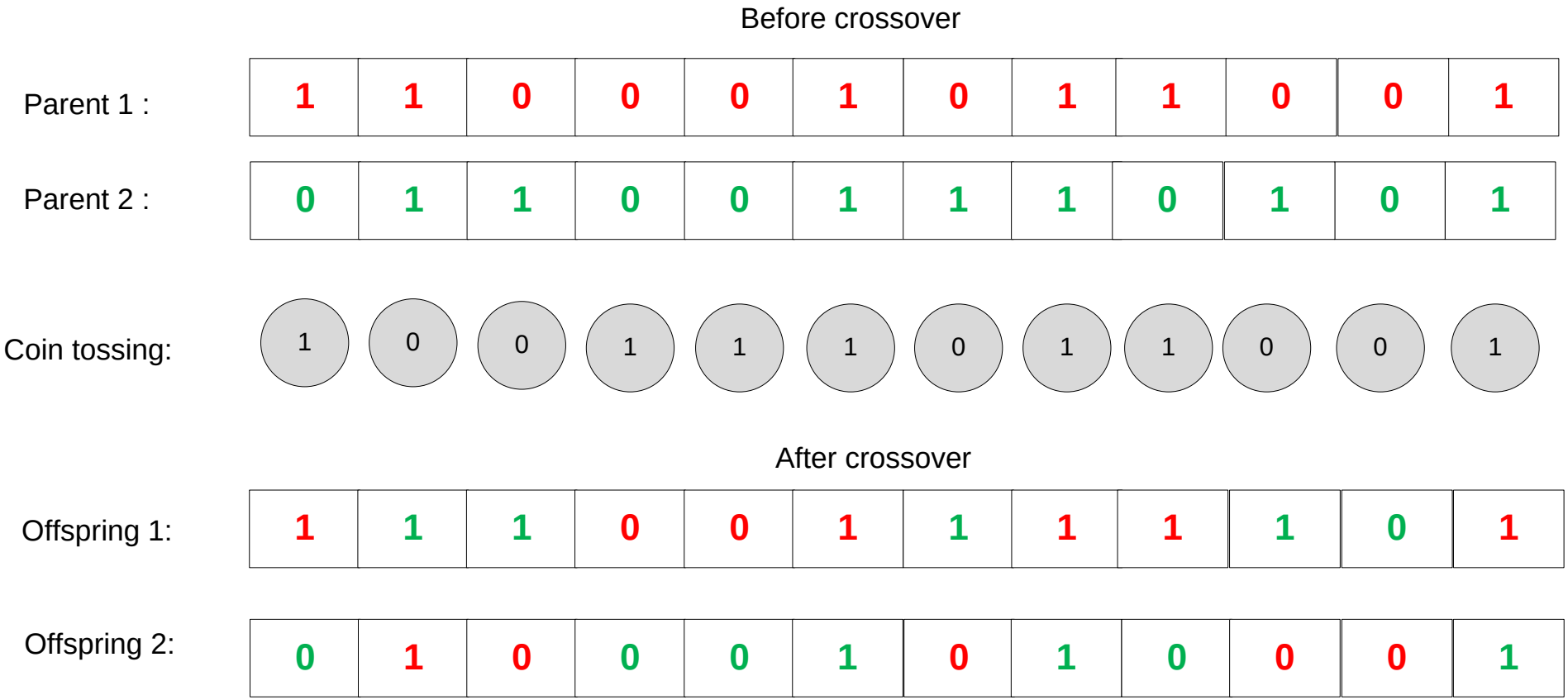
1. In case of multi-point crossover, a number of crossover points are selected along the length of the string, at random.
2. The bits lying between alternate pairs of sites are then swapped.



Uniform Crossover (UX)

- Uniform crossover is a more general version of the multi-point crossover.
- In this scheme, at each bit position of the parent string, we toss a coin (with a certain probability p_s) to determine whether there will be swap of the bits or not.
- The two bits are then swapped or remain unaltered, accordingly.

Uniform crossover (UX): Illustration



Rule: If the toss is 0 than swap the bits between P1 and P2

Uniform crossover with crossover mask

- Here, each gene is created in the offspring by copying the corresponding gene from one or the other parent chosen according to a random generated binary crossover mask of the same length as the chromosome.
- Where there is a 1 in the mask, the gene is copied from the first parent
- Where there is a 0 in the mask, the gene is copied from the second parent.
- The reverse is followed to create another offsprings.

Uniform crossover with crossover mask: Illustration

Before Crossover

Parent 1 :	1	1	0	0	0	1	0	1
Parent 2 :	0	1	1	0	0	1	1	1
Mask	1	0	0	1	1	1	0	1
Offspring 1:	1	1	1	0	0	1	1	1
Offspring 2:	0	1	0	0	0	1	0	1

After Crossver

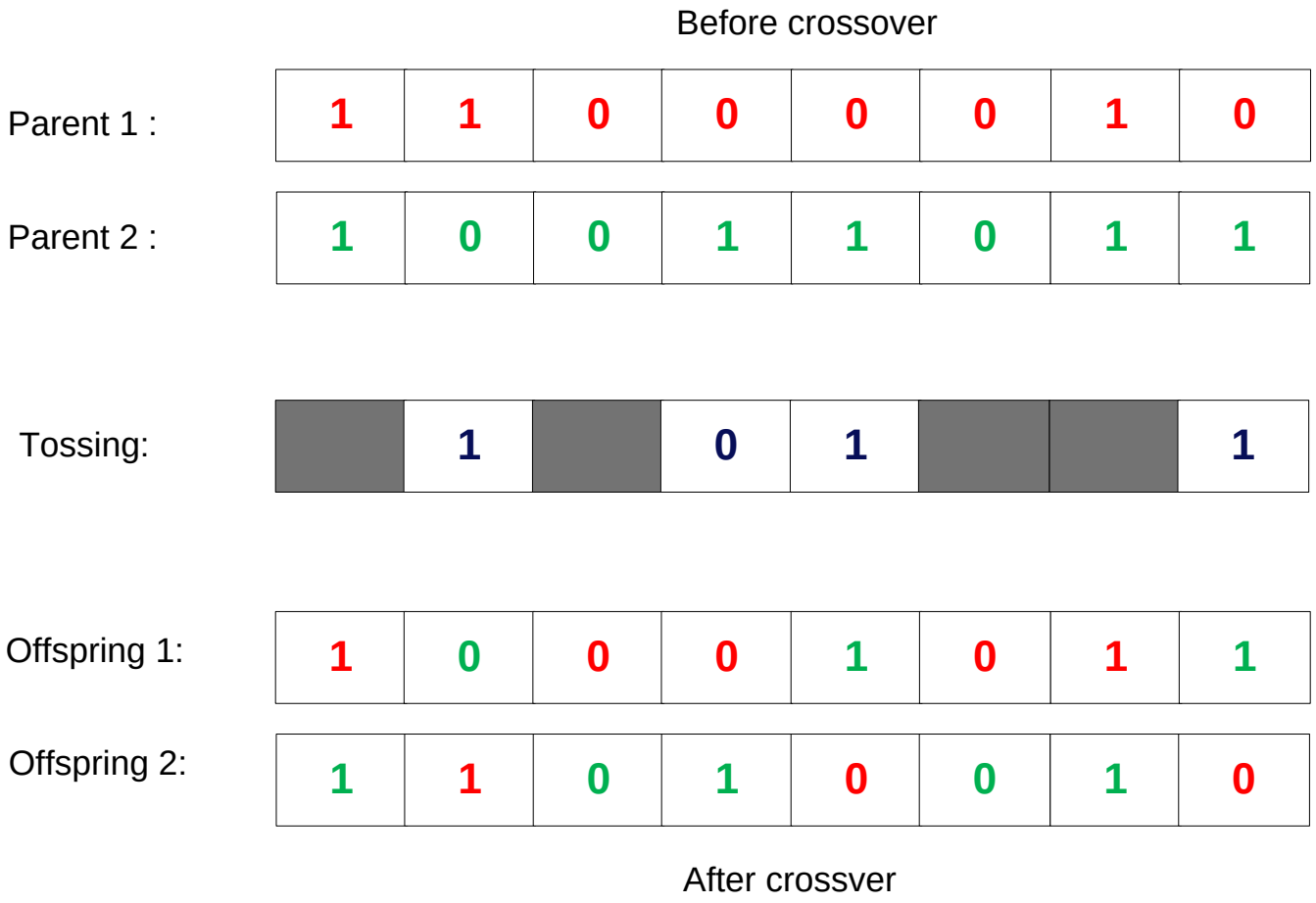
When there is a 1 in the mask, the gene is copied from Parent 1 else from Parent 2.

When there is a 1 in the mask, the gene is copied from Parent 2 else from Parent 1.

Half-uniform crossover (HUX)

- In the half uniform crossover scheme, exactly half of the non-matching bits are swapped.
  1. Calculate the Hamming distance (the number of differing bits) between the given parents.
  2. This number is then divided by two.
  3. The resulting number is how many of the bits that do not match between the two parents will be swapped but probabilistically.
  4. Choose the locations of these half numbers (with some strategies, say coin tossing) and swap them.

Half-uniform crossover: Illustration



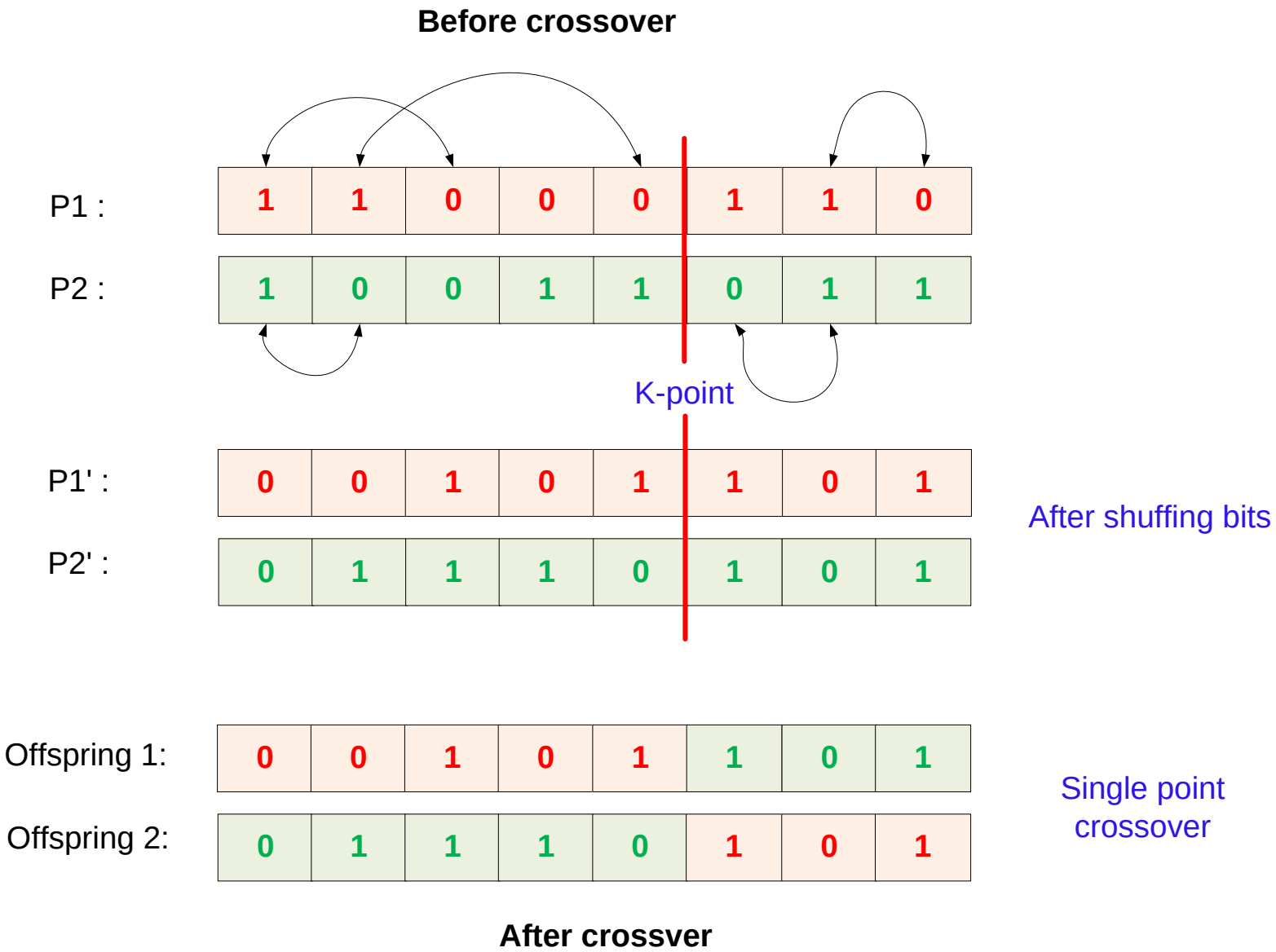
Here, Hamming distance is 4

If toss is 1, then swap the bits else remain as it is

Shuffle crossover

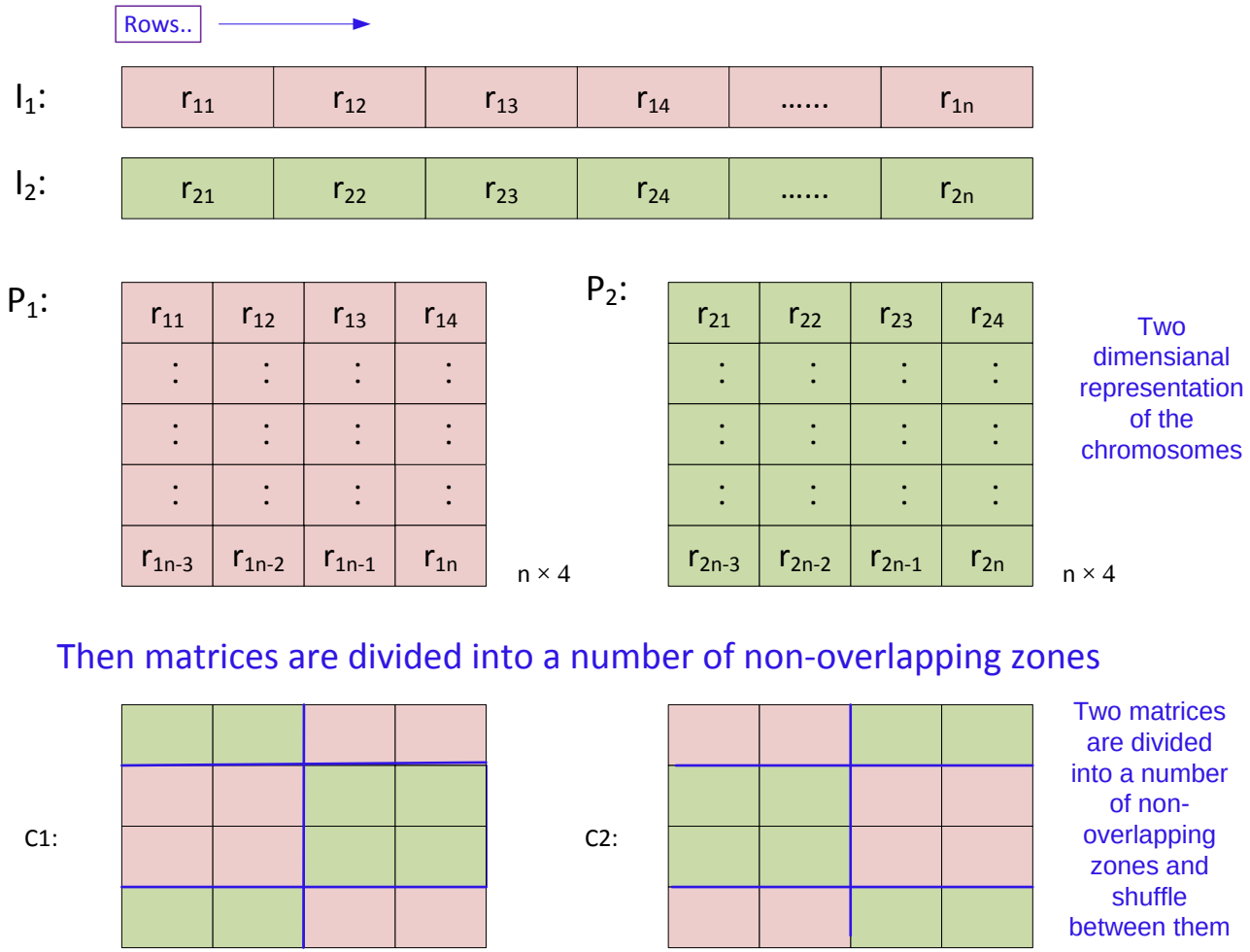
- A single crossover point is selected. It divides a chromosome into two parts called schema.
- In both parents, genes are shuffled in each schema. Follow some strategy for shuflling bits
- Schemas are exchanged to create offspring (as in single crossover)

Shuffle crossover: Illustration



Matrix crossover

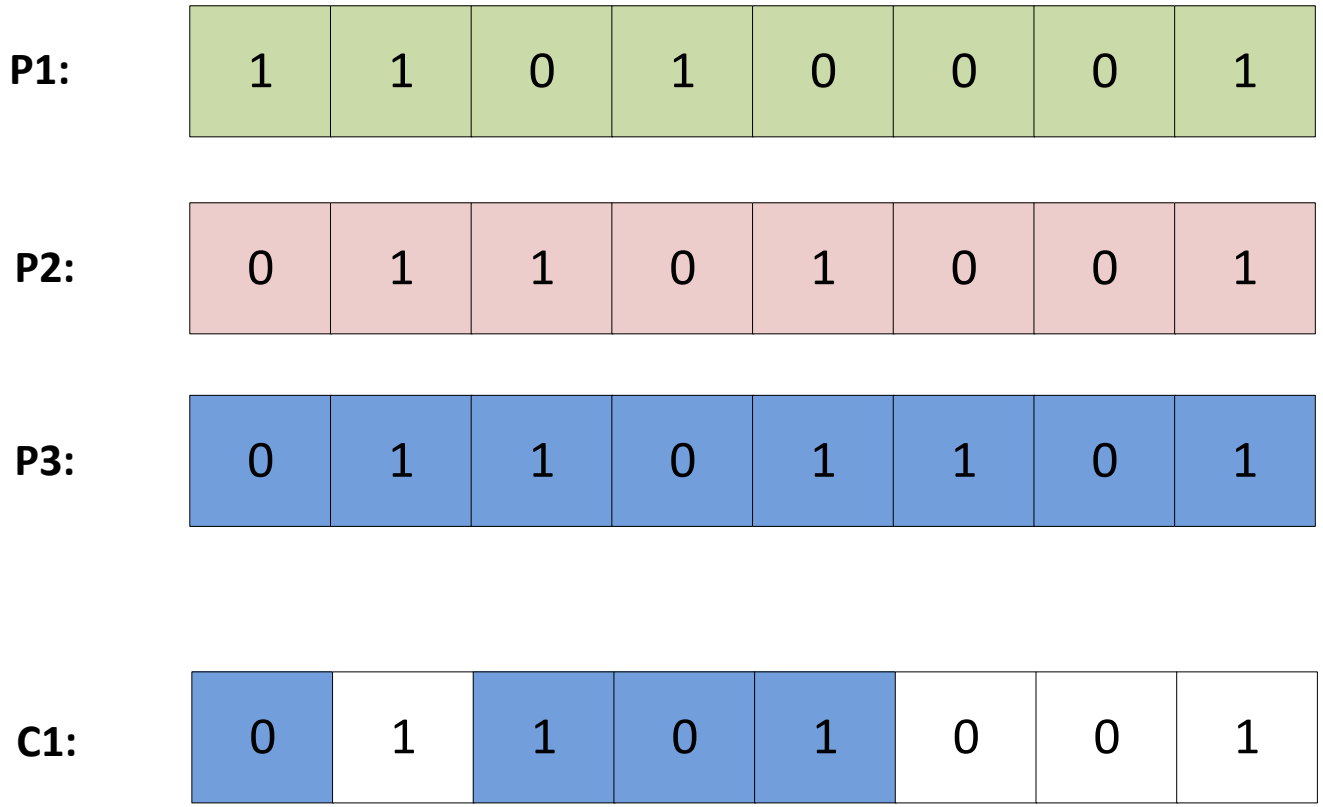
The matrix crossover strategy is expained with the following illustration.



Three parent crossover

- In this techniques, three parents are randomly chosen.
- Each bit of the first parent is compared with the bit of the second parent.
- If both are the same, the bit is taken for the offspring.
- Otherwise, the bit from the third parent is taken for the offspring.

Three parent crossover: Illustration



Note: Sometime, the third parent can be taken as the crossover mask.

Comments on the binary crossover techniques

1. **Non-uniform variation:**

   It can not combine all possible schemas (i.e. building blocks)

   For example : it can not in general combine instances of
   1 1 * * * * * 1
   and
   *** * * * 1 1 * ***
   to form an instance of
   1 1 * * 1 1 * 1.

2. **Positional bias:**

   The schemas that can be created or destroyed by a crossover depends strongly on the location of the bits in the chromosomes.

Comments on the binary crossover techniques

3. **End-point bias:**

   It is also observed that single-point crossover treats some loci preferentially, that is, the segments exchanged between the two parents always contain the end points of the strings.

4. **Hamming cliff problem:**

   A one-bit change can make a large (or a small) jump.
   A multi-bits can make a small (or a large gap).

   For example, **1000** $\Longrightarrow$ **0111**
   (Here, Hamming distance = 4, but distance between phenotype is 1)

   Similarly, **0000** $\Longrightarrow$ **1000**
   (Here, Hamming distance = 1, but distance between phenotype is 8)

Comments on the binary crossover techniques

- To reduce the positional bias and end-point bias, two-point crossover and multi-point crossover schemes have been evolved.
- In contrast, UX and HUX distribute the patterns in parent chromosomes largely resulting too much deflections in the offspring.
- To avoid binary code related problem, **gray coding** can be used.
- In summary, binary coding is the simplest encoding and its crossover techniques are fastest compared to the crossover techniques in other GA encoding schemes.

Crossover Techniques in Real Coded GA

Crossover techniques in Real coded GA

Following are the few well known crossover techniques for the real-coded GAs.

- Linear crossover
- Blend crossover
- Binary simulated crossover

Linear crossover in Real-coded GAs

- This scheme uses some linear functions of the parent chromosomes to produce the new children.
- **For example**

  Suppose P_1 and P_2 are the two parameter's values in two parents, then the corresponding offspring values in chromosomes can be obtained as

$$C_i = \alpha_i P_1 + \beta_i P_2$$

  where $i = 1, 2 \cdots n$ (number of children).
  α_i and β_i are some constants.

Linear crossover: An example

- Example :

  Suppose $P_1 = 15.65$ and $P_2 = 18.83$

  $\alpha_1 = 0.5 = \beta_1$

  $\alpha_2 = 1.5$ and $\beta_2 = -0.5$

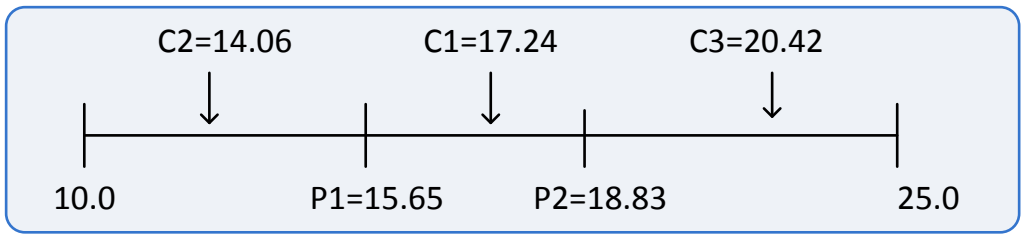
  $\alpha_3 = -0.5$ and $\beta_3 = 1.5$

- Answer :

  $C_1 = 0.5 \times (P_1 + P_2) = 17.24$

  $C_2 = 1.5 \times P_1 - 0.5 \times P_2 = 14.06$

  $C_3 = -0.5 \times P_1 + 1.5 \times P_2 = 20.24$



Advantages and limitations

Advantages

1. It is simple to calculate and hence faster in computation
2. Can allow to generate a large set of offspring from two parent values
3. Controls are possible to choose a wide-range of variations

Limitations

1. Needs to be decided the values of α_i and β_i
2. It is difficult for the inexperienced users to decide the right values for α_i and β_i
3. If α_i and β_i values are not chosen properly, the solution may stuck into a local optima.

Blend crossover in Real-coded GAs

This scheme can be stated as follows.

1. Let P_1 and P_2 are the two parameter's values in two parent's chromosomes, such that $P_1 < P_2$
2. Then the blend crossover scheme creates the children solution lying in the range

$$\langle \{P_1 - \alpha (P_2 - P_1)\} \cdots \{P_2 - \alpha (P_2 - P_1)\} \rangle$$

where α is a constant to be decided so that children solution do not come out of the range of domain of the said parameter.

Blend crossover in Real-coded GAs

3. Another parameter γ has to be identified by utilizing the α and a random number r in the range of (0.0, 1.0) both exclusive like the following:

$$\gamma = (1 + 2\alpha)\, r - \alpha$$

4. The children solutions C_1 and C_2 are determined from the parents as follows,

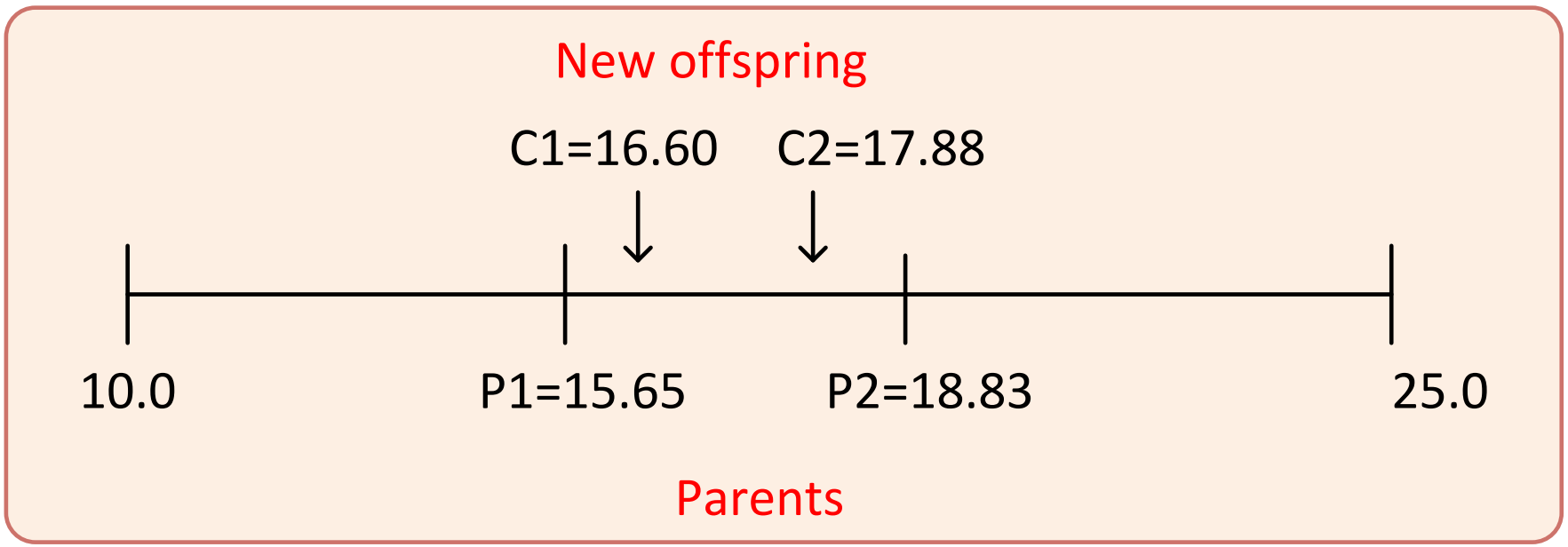
$$C_1 = (1 - \gamma)\, P_1 + \gamma P_2$$
$$C_2 = (1 - \gamma)\, P_2 + \gamma P_1$$

Blend crossover : An example

- Example :

  $P_1 = 15.65$ and $P_2 = 18.83$

  $\alpha = 0.5$ and $\gamma = 0.6$



Simulated binary crossover in Real-coded GAs

- This scheme is based on the probability distribution of generated children solution from the given parents.
- A spread factor α is used to represent the spread of the children solutions with respect to that of the parents, as given below.

$$\alpha = \left| \frac{C_1 - C_2}{P_1 - P_2} \right|$$

Here P_1 and P_2 are represent the parent points and C_1 and C_2 are two children solutions.

Simulated binary crossover in Real-coded GAs

Three different cases may occurs:

- Case 1: $\alpha < 1$ (Contracting Crossover)

  The spread of children is less than the parents.

- Case 2: $\alpha > 1$ (Expanding Crossover)

  The spread of children is more than the parents.

- Case 3: $\alpha = 1$ (Stationary Crossover)

  The spread of children is same as that of the parents.

Simulated Binary Crossover

Probability Distribution:

- Case 1: For Contracting Crossover

$$C(\alpha) = 0.5(q+1)\alpha^2$$

- Case 2: For Expanding Crossover

$$E(\alpha) = 0.5(q+1)\frac{1}{\alpha^{q+2}}$$

Simulated binary crossover in Real-coded GAs

Following steps are used to create two children solutions C_1 and C_2 from the parents P_1 and P_2.

1. Create a random number $r \in \{0.0 \cdots 1.0\}$
2. Determine α' such that

$$\int_0^{\alpha'} C(\alpha) d\alpha = r, \text{ if } r < 0.5$$

and

$$\int_1^{\alpha'} E(\alpha) d\alpha = r, \text{ if } r > 0.5$$

3. Using the value of α' obtain two children solution as follows
   - $C_1 = 0.5\,[(P_1 + P_2) - \alpha'\,|P_2 - P_1|]$
   - $C_2 = 0.5\,[(P_1 + P_2) + \alpha'\,|P_2 - P_1|]$

Simulated binary crossover in Real-coded GAs

Example:

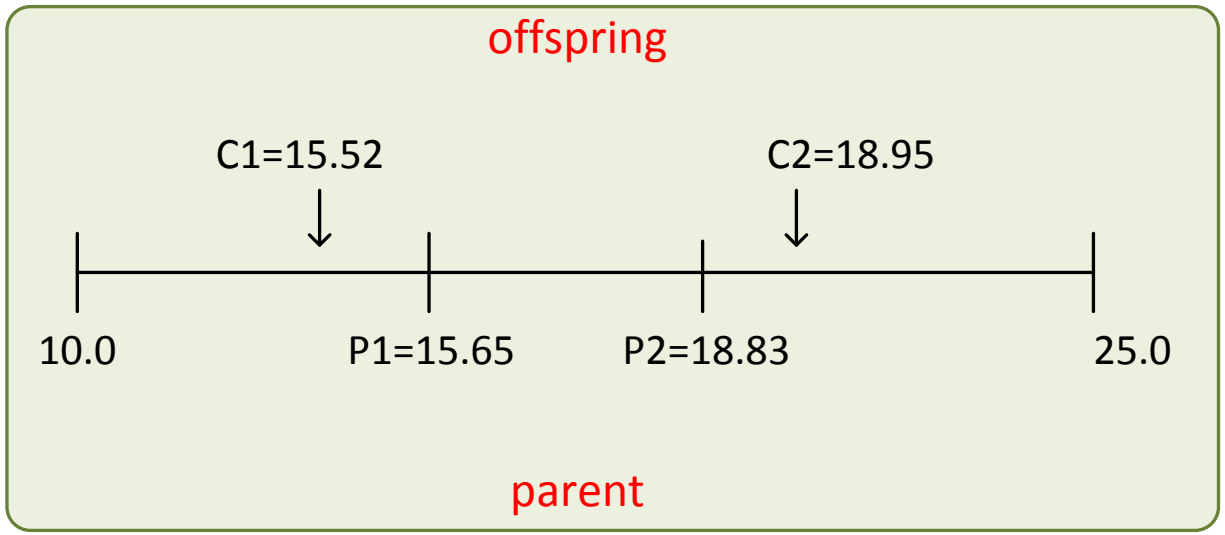
$P_1 = 15.65$

$P_2 = 18.83$

$q = 2$

$\alpha' = 1.0772$

Assuming expanding crossover with $r > 0.5$



Advantages and limitations

Advantages

1. We can generate a large number of offspring from two parents.
2. More explorations with diverse offspring.
3. Results are accurate and usually terminated with global optima.
4. Termination with a less number of iterations.
5. Crossover techniques are independent of the length of the chromosome.

Limitations

1. Computationally expensive compared to binary crossover.
2. If proper values of parameters involved in the crossover techniques are not chosen judiciously, then it may lead to premature convergence with not necessarily optimum solutions.

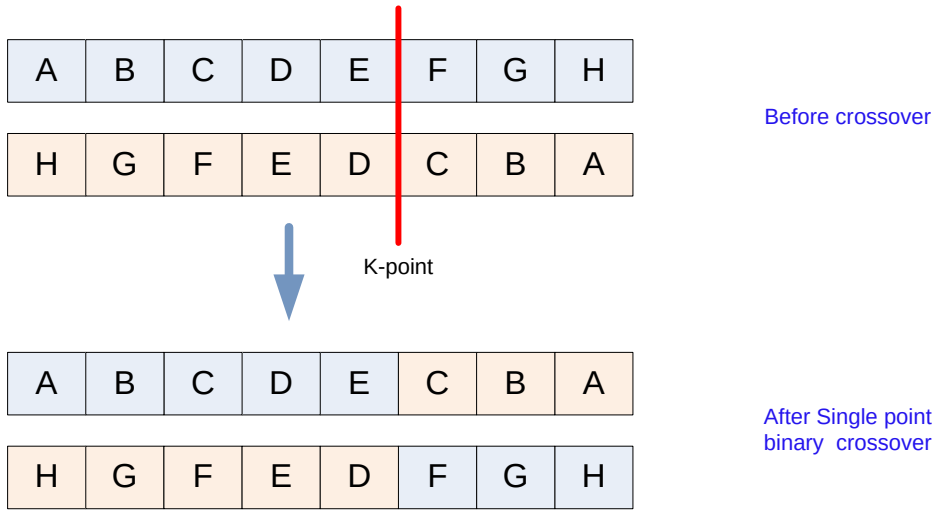
Crossover Techniques in Order GAs

Crossover techniques in order GA

- Any binary crossover techniques are not applicable to Order coded GAs

  Example

Reference: TSP
Consider any two chromosomes with Order-coded encoding scheme



Here, the offspring are not valid chromosomes

- Since, sequence of gene values are important, Real-coded crossover techniques, which are to produce real number from two given real numbers are also not applicable to Order-coded GAs.

Crossover techniques in order GA

Some important crossover techniques in Order-coded GAs are:

1. Single-point order crossover
2. Two-point order crossover
3. Partially mapped crossover (PMX)
4. Position based crossover
5. Precedence-preservation crossover (PPX)
6. Edge recombination crossover

Assumptions: For all crossover techniques, we assume the following:

- Let L be the length of the chromosome.
- P_1 and P_2 are two parents (are selected from the mating pool).
- C_1 and C_2 denote offspring (initially empty).

Single point order crossover

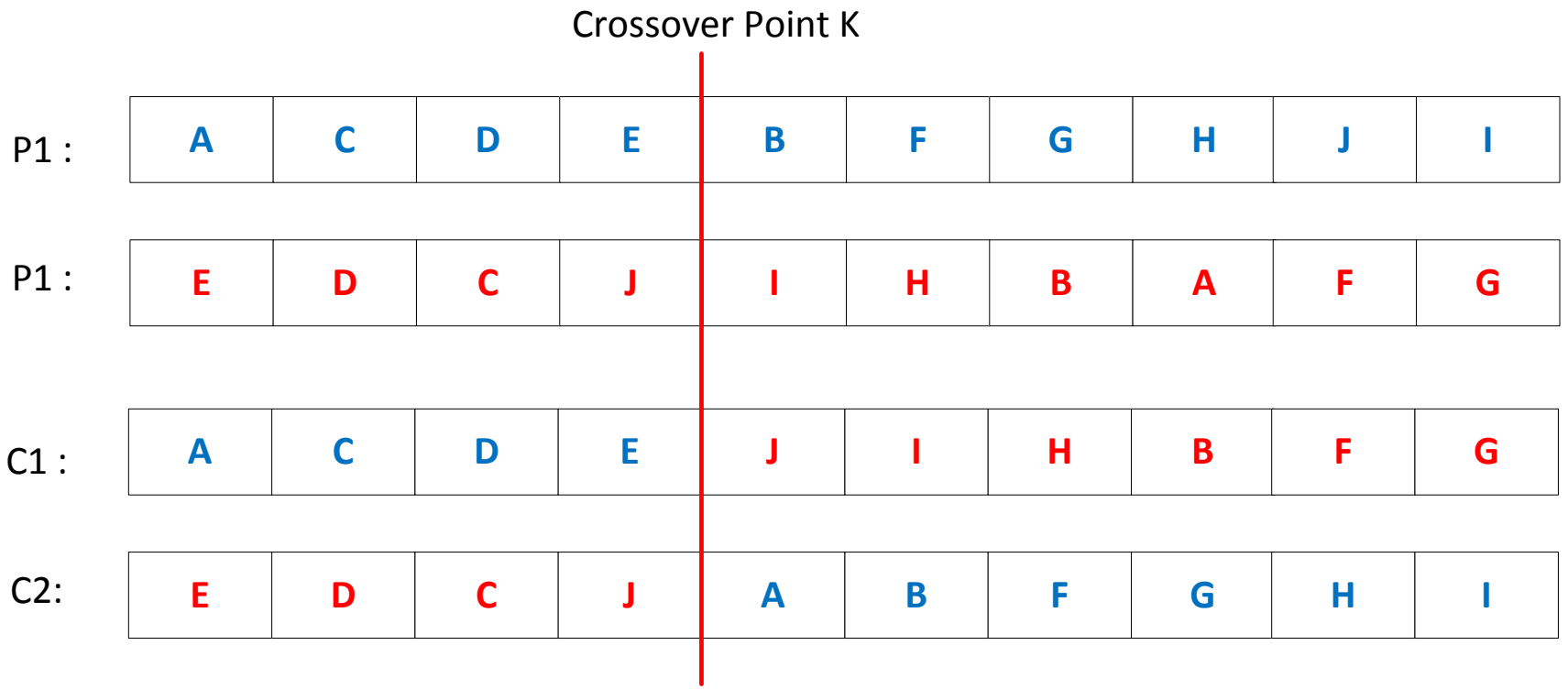
Given two parents P_1 and P_2 with chromosome length, say L.

Steps:

1. Randomly generate a crossover point K such that $(1 < K < L)$.
2. Copy the left schema of P_1 into C_1 (initially empty) and left schema of P_2 into C_2 (also initially empty).
3. For the schema in the right side of C_1, copy the gene value from P_2 in the same order as they appear but not already present in the left schema.
4. Repeat the same procedure to complete C_2 from P_1.

Single point order crossover: Illustration

Example :



Two-point order crossover

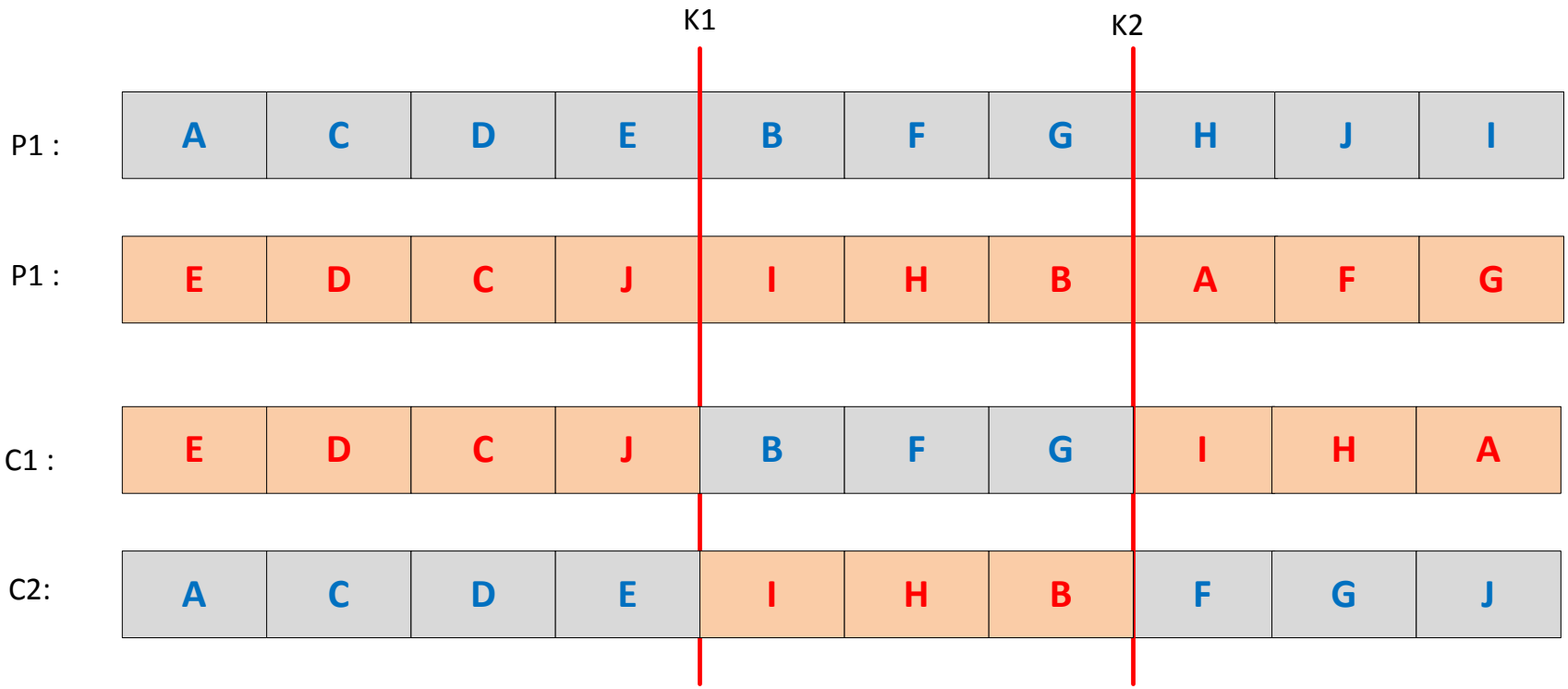
It is similar to the single-point order crossover, but with two $k-$points.

Steps:

1. Randomly generate two crossover points K_1 and K_2. $1 < K_1$, $K_2 < L$
2. The schema in middle of P_1 and P_2 are copied into C_1 and C_2 (initially both are empty), respectively in the same location as well as in the same order.
3. The remaining schema in C_1 and C_2 are copied from P_2 and P_1 respectively, so that an element already selected in child solution does not appear again.

Two-point order crossover: Illustration

Example :



Precedence preservation order crossover

Let the parent chromosomes be P_1 and P_2 and the length of chromosomes be L.

Steps:

(a) Create a vector V of length L randomly filled with elements from the set $\{1, 2\}$.

(b) This vector defines the order in which genes are successfully drawn from P_1 and P_2 as follows.

1. We scan the vector V from left to right.
2. Let the current position in the vector V be i (where $i = 1, 2, \cdots, L$).
3. Let j (where $j = 1, 2, \cdots, L$) and k (where $k = 1, 2, \cdots, L$) denotes the j^{th} and k^{th} gene of P_1 and P_2, respectively. Initially $j = k = 1$.

Precedence preservation order crossover

4. If i^{th} value is 1 then

   Delete j^{th} gene value from P_1 and as well as from P_2 and append it to the offspring (which is initially empty).

5. Else

   Delete k^{th} gene value from P_2 and as well as from P_1 and append it to the offspring.

6. Repeat Step 2 until both P_1 and P_2 are empty and the offspring contains all gene values.

Precedence preservation order crossover : Example

Example :

Random Vector σ	2	1	1	2	1	1	2	2	1	2
P1 :	A	C	D	E	B	F	G	H	J	I
P2 :	E	D	C	J	I	H	B	A	F	G
C1 :	E	C	D	J	B	F	H	A	I	G
C2:	?									

Note : We can create another offspring following the alternative rule for 1 and 2.

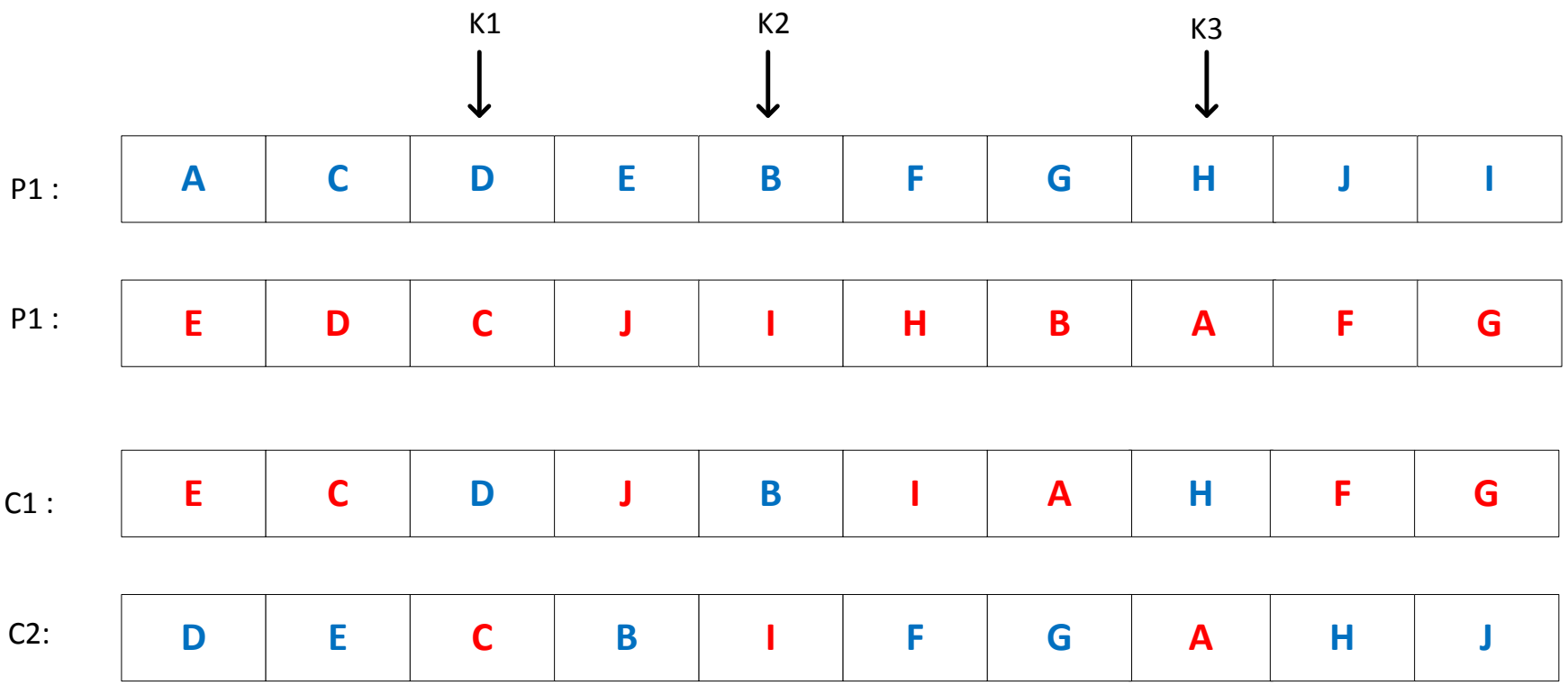
Position-based order crossover

Steps :

1. Choose n crossover points $K_1, K_2 \cdots K_n$ such that $n \ll L$, the length of chromosome.
2. The gene values at $K_1^{th}, K_2^{th} \cdots K_n^{th}$ positions in P_1 are directly copied into offspring C_1 (Keeping their position information intact).
3. The remaining gene values in C_1 will be obtained from P_2 in the same order as they appear there except they are already not copied from P_1.
4. We can reverse the role of P_1 and P_2 to get another offspring C_2.

Position-based order crossover : Example

Let su consider three $k-$points namely K_1, K_2 and k_3 in this example.



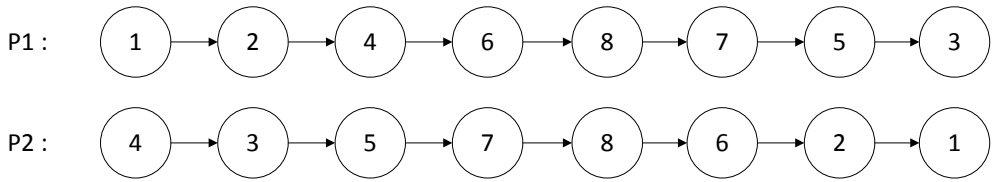
Edge recombination order crossover

- This crossover technique is used to solve TSP problem when the cities are not completely connected to each other.
- In this technique, an edge table which contains the adjacency information (but not the order).
- In the other words, edge table provides connectivity information.

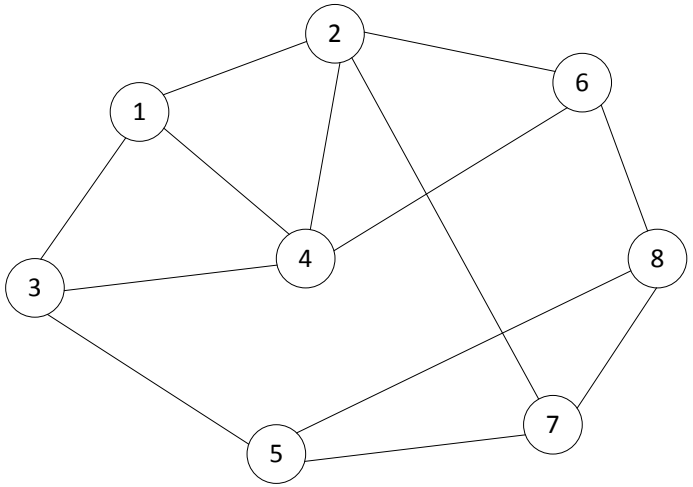
Edge recombination order crossover: Illustration

Example

- Let us consider a problem instance of a TSP with 9 cities.
- Assume any two chromosome P_1 and P_2 for the mating.

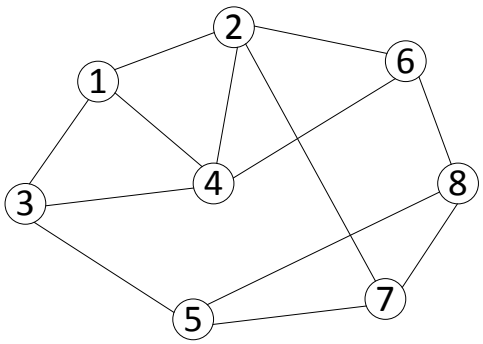


Connectivity graph:



Edge recombination order crossover: Illustration

Edge table for the connectivity graph:



City	Connectivity
1	2 4 3
2	1 4 7 6
3	1 4 5
4	1 2 3 6
5	3 7 8
6	2 4 8
7	2 5 8
8	5 6 7

Edge recombination order crossover: Illustration

Steps:

Let the child chromosome be C_1 (initially empty).

1. Start the child tour with the starting city of P_1. Let this city be X.
2. Append city X to C.
3. Delete all occurrences of X from the connectivity list of all cities (right-hand column).
4. From city X choose the next city say Y, which is in the list of minimum (or any one, if there is no choice) connectivity links.
5. Make $X = Y$ [i.e. new city Y becomes city X].
6. Repeat Steps 2-5 until the tour is complete.
7. End

Any questions??