
GA Operators

선택

Generate initial solutions (say, p solutions);

do {

for ($i=0$; $i < k$; $i++$){

 Select two parent solutions;

 Crossover;

 Mutation;

 }

 Replace;

} **while** (not stopping condition);

Report the best solution;

Roulette-Wheel Selection, 가장 흔한 선택

- 각 해는 fitness 값 F_i 에 비례하는 선택 기회를 갖는다
- $F_i = (C_w - C_i) + (C_w - C_b)/(k-1), k > 1$

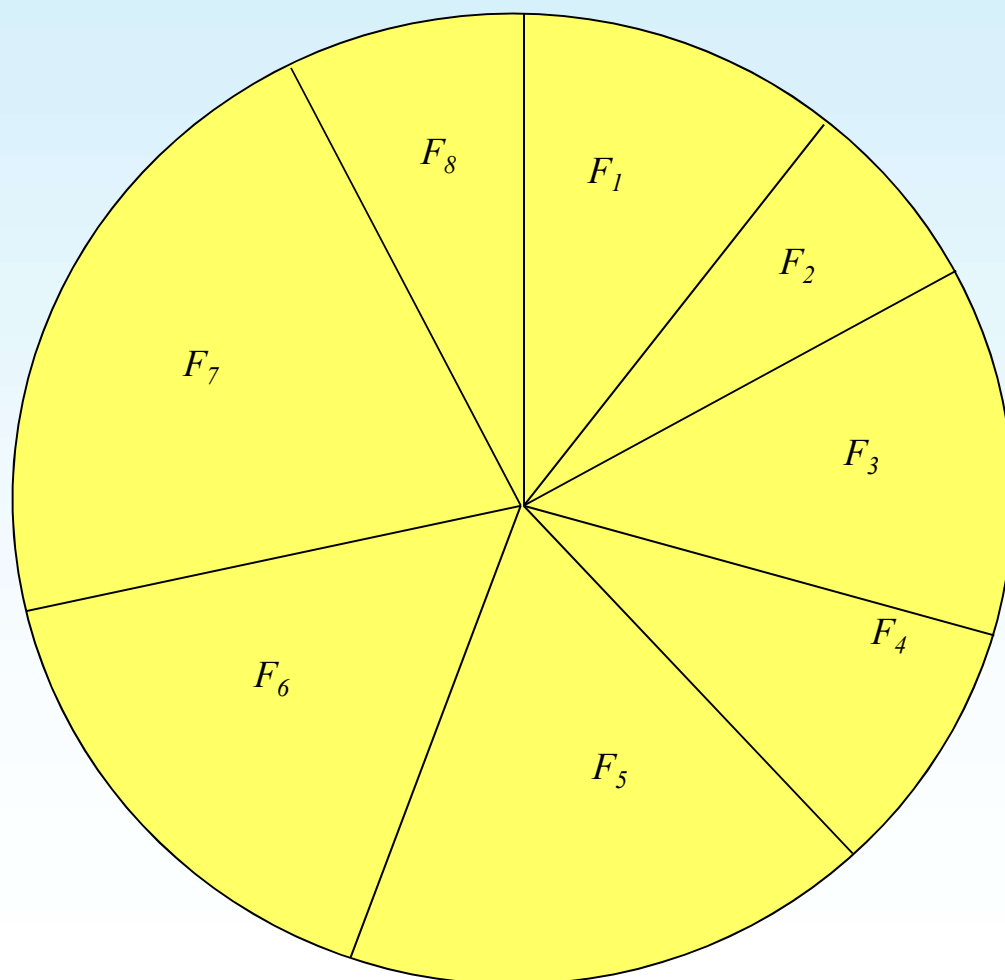
Where

C_w : population 내에서 가장 나쁜 해의 비용

C_b : population 내에서 가장 좋은 해의 비용

C_i : 해 i 의 비용

사회에서 실패한 사람도 훌륭한 자식을 낳을 수 있다
단, 확률은 아무래도 낮다



구현은 간단하다

Selection

```
point ← random( ) % SumOfFitness;  
sum ← 0;  
for  $i \leftarrow 0$  to  $P-1$  {  
    sum ← sum +  $f_i$  ;  
    if (point < sum) then return  $i$  ;  
}  
Report error ; // shouldn't be here
```

Tournament Selection

- 변형들이 많음
- 대표적인 tournament selection

tSelect(t) {

 Choose two chromosomes x_1 and x_2 ; // Assume WLOG x_1 is better

$r \leftarrow$ random number in $[0, 1)$;

if ($t > r$) **then** select x_1 ;

else select x_2 ;

}

- 다른 예

 Choose 2^k chromosomes ;

 Select a final one by tournament competition with the rule above ;

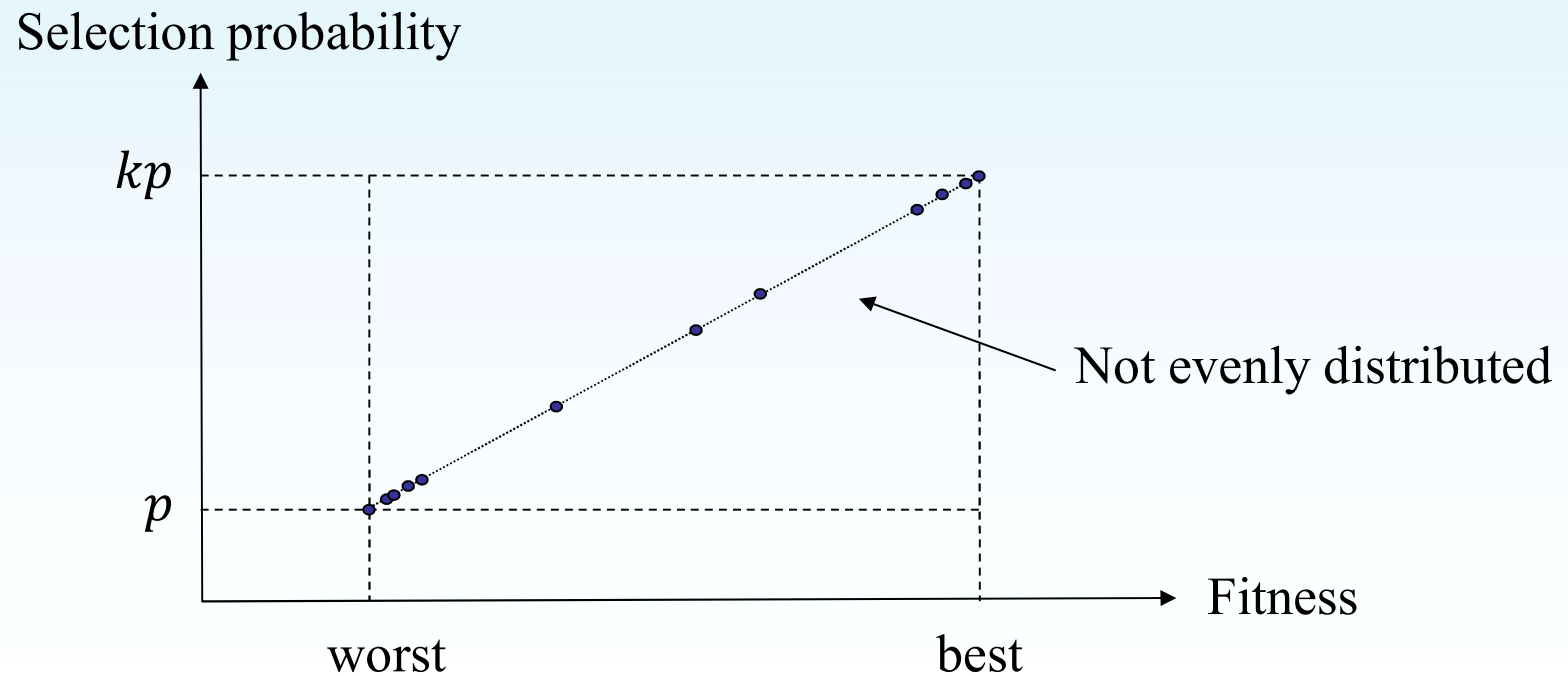
- What if $t = 1$?

✓ t 로 selection pressure를 조절할 수도 있다

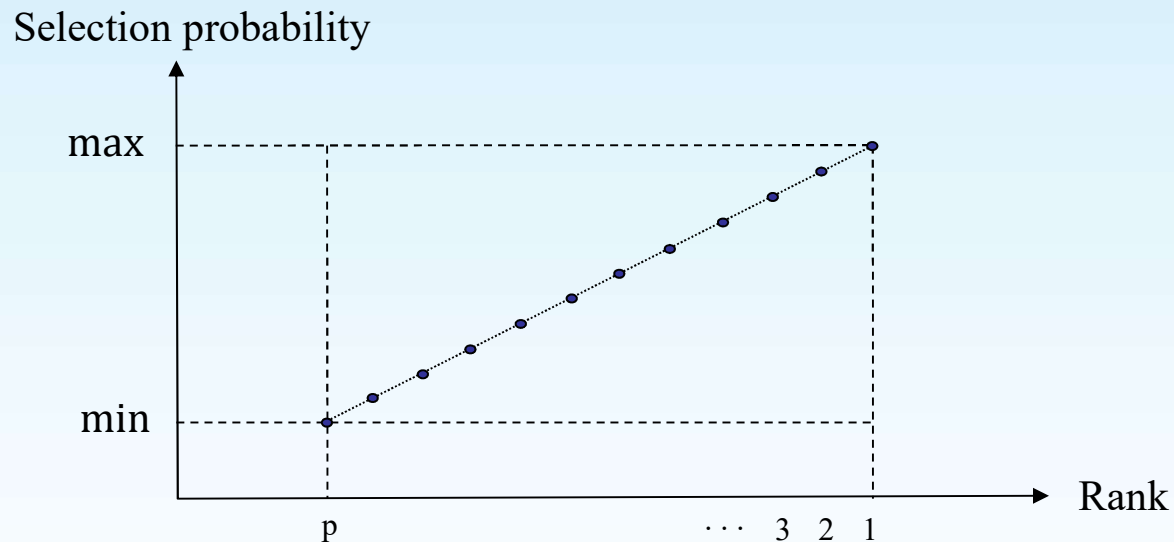
Rank-Based Selection

Roulette-wheel selection은 각 chromosome의 fitness에 비례하는 확률로 선택된다

- Roulette-wheel-based proportional selection이라고도 한다



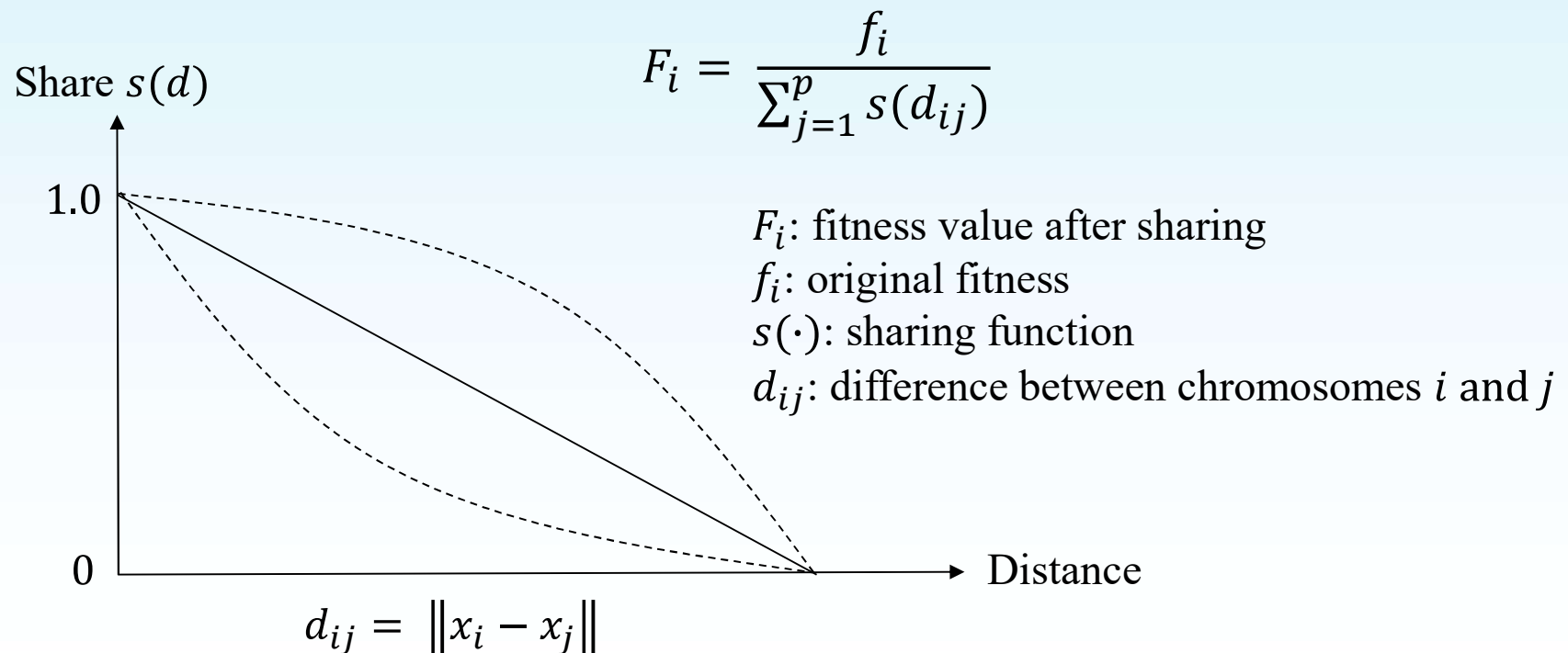
If we use "ranks" instead of fitness values, we can make the selection probabilities evenly distributed



- Rank i chromosome의 선택확률
 - $F_i = \max + (i - 1)(\min - \max)/(P - 1)$
- "min – max" can control the selection pressure
- But, even distribution is not a necessary property. We cannot say either of the two is better than the other.

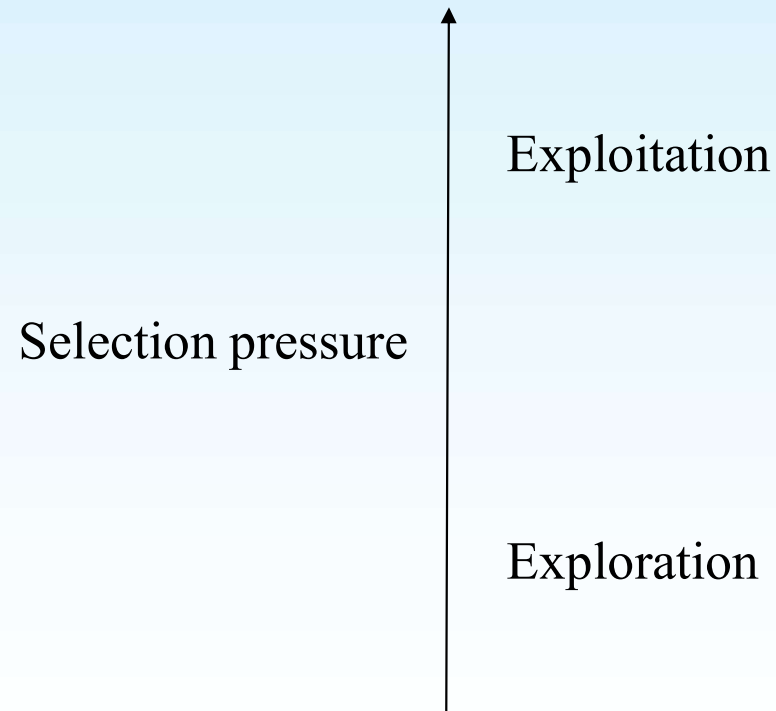
Sharing

- Gives penalties to the chromosomes w/ many similar ones in the population
- Helpful to maintain population diversity



Population Diversity & Selection Pressure

The increase of selection pressure decreases population diversity.



교차

Generate initial solutions (say, p solutions);

do {

for ($i=0$; $i < k$; $i++$){

 Select two parent solutions;

 Crossover;

 Mutation;

 }

 Replace;

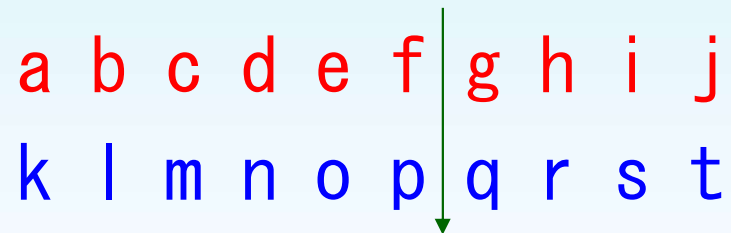
} **while** (not stopping condition);

Report the best solution;

1-Point Crossover

✓ GA의 대표 연산자

1-point crossover

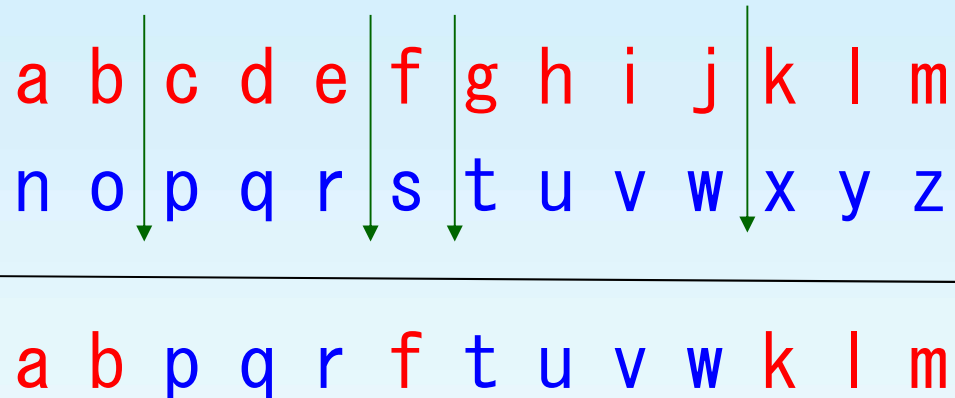


The diagram illustrates a 1-point crossover operation on two parent chromosomes. The first parent chromosome is represented by the sequence of letters 'a b c d e f g h i j' in red. The second parent chromosome is represented by the sequence 'k l m n o p q r s t' in blue. A vertical green line with a downward-pointing arrow is positioned between the 'f' and 'g' of the first chromosome and between the 'p' and 'q' of the second chromosome, indicating the crossover point. Below this, a horizontal line separates the parent chromosomes from the resulting offspring.

a b c d e f q r s t

✓ There are $n - 1$ 1-pt xover operators for length- n chromosomes

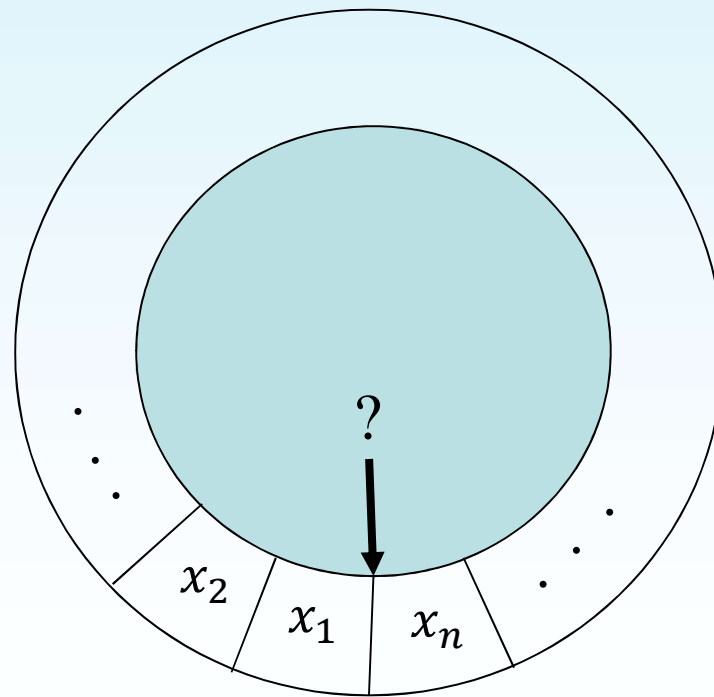
Multi-Point Crossover



For $x_1 x_2 \cdots x_n$, if $n - 1$ positions are allowed for cutting, x_1 and x_n always move **together** in an “**even**”-point xover.

... **apart** in an “**odd**”-point xover.

Therefore, it is also reasonable to allow cutting after x_n



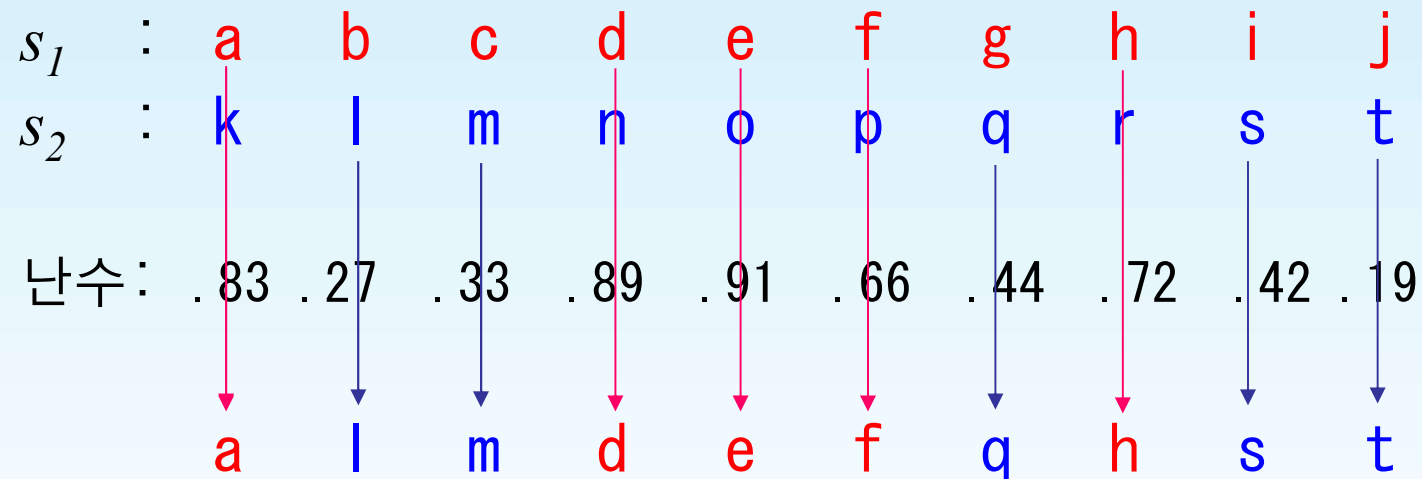
If we allow $n-1$ cutting positions,
there are $\binom{n-1}{k}$ k -point xover operators.

If we allow n cutting positions,
there are $\binom{n}{k}$ k -point xover operators.

- ✓ Multi-pt xovers are more useful in memetic GAs. (뒤에 소개함)

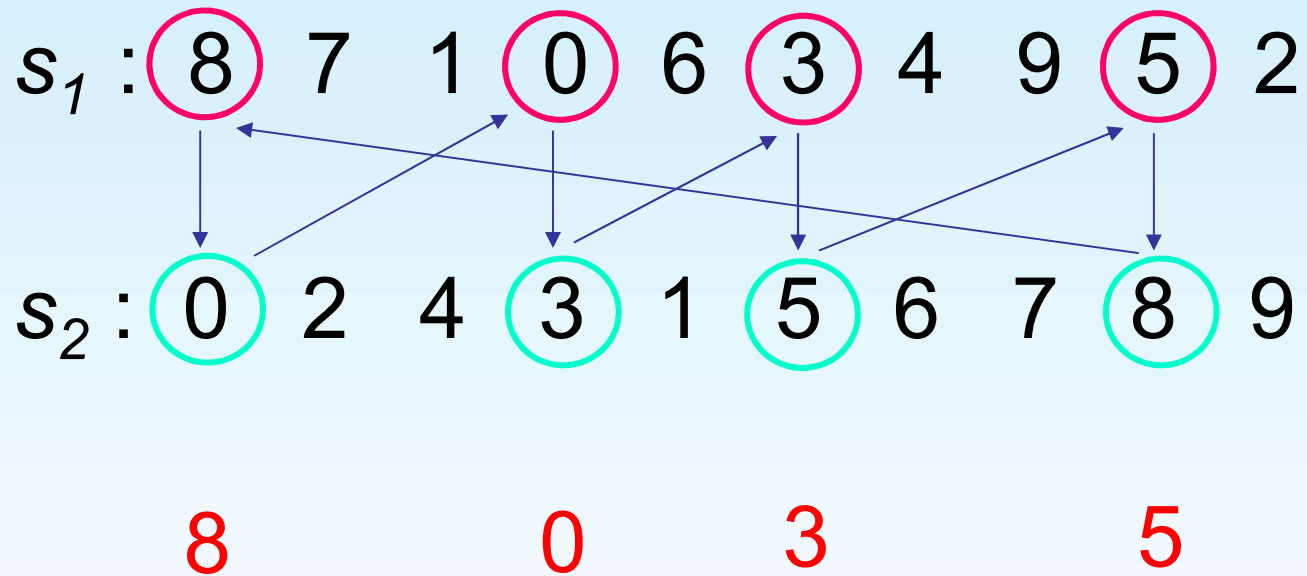
Uniform Crossover

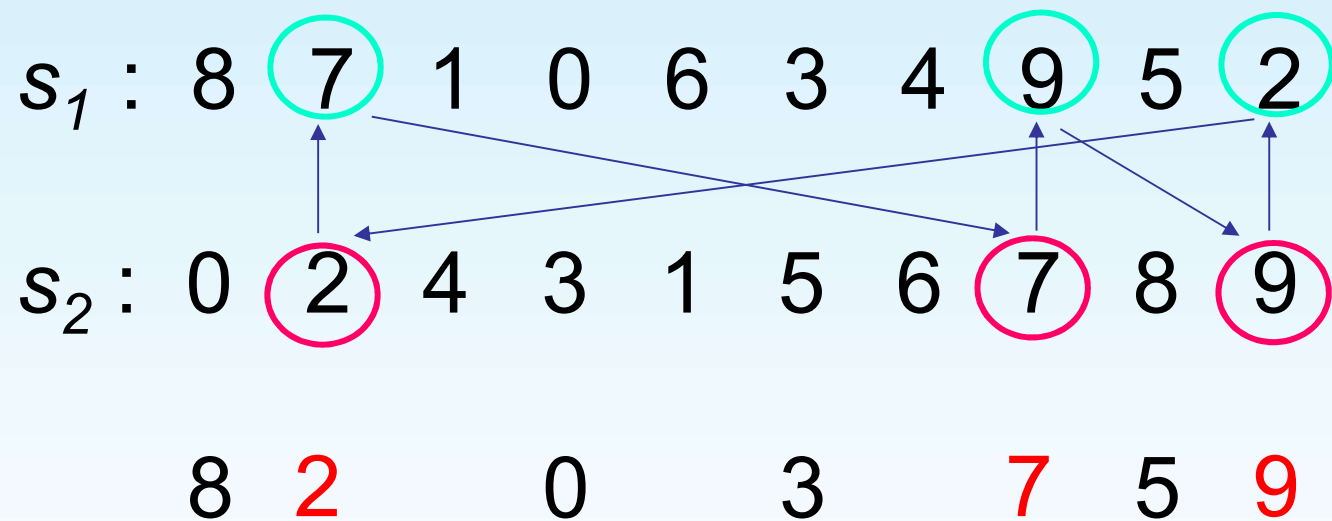
$$P_0 = 0.6$$

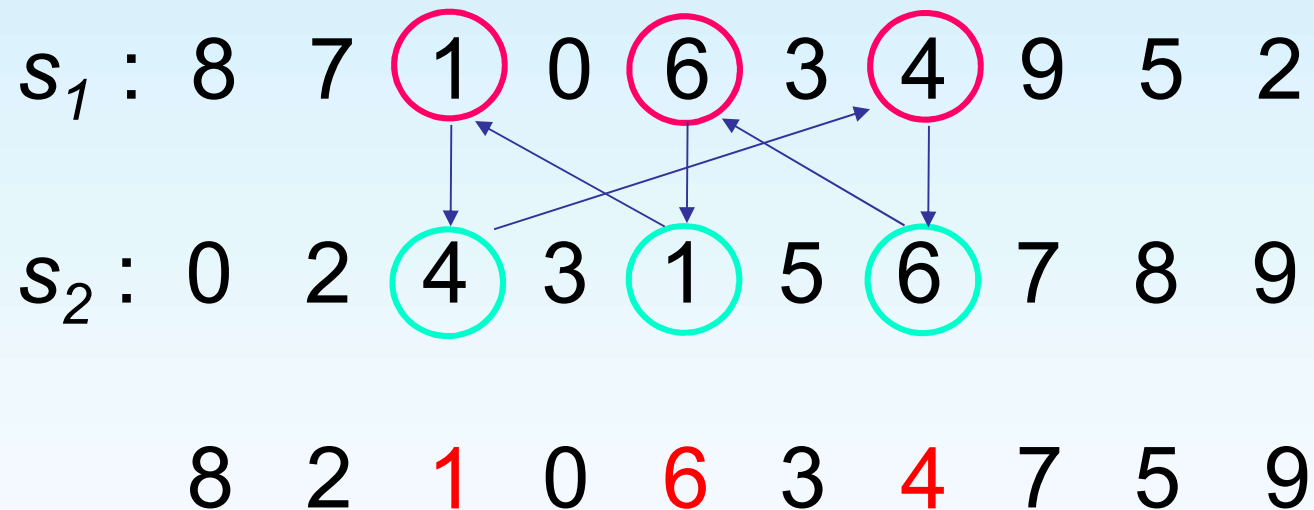


- Uses no cutting points
- Generates a binary mask where 1's are uniformly distributed on the n positions
- $\exists 2^n$ masks (operators) $\gg \binom{n}{k}$
- Maximum perturbation occurs at $P_0 = 0.5$

Cycle Crossover



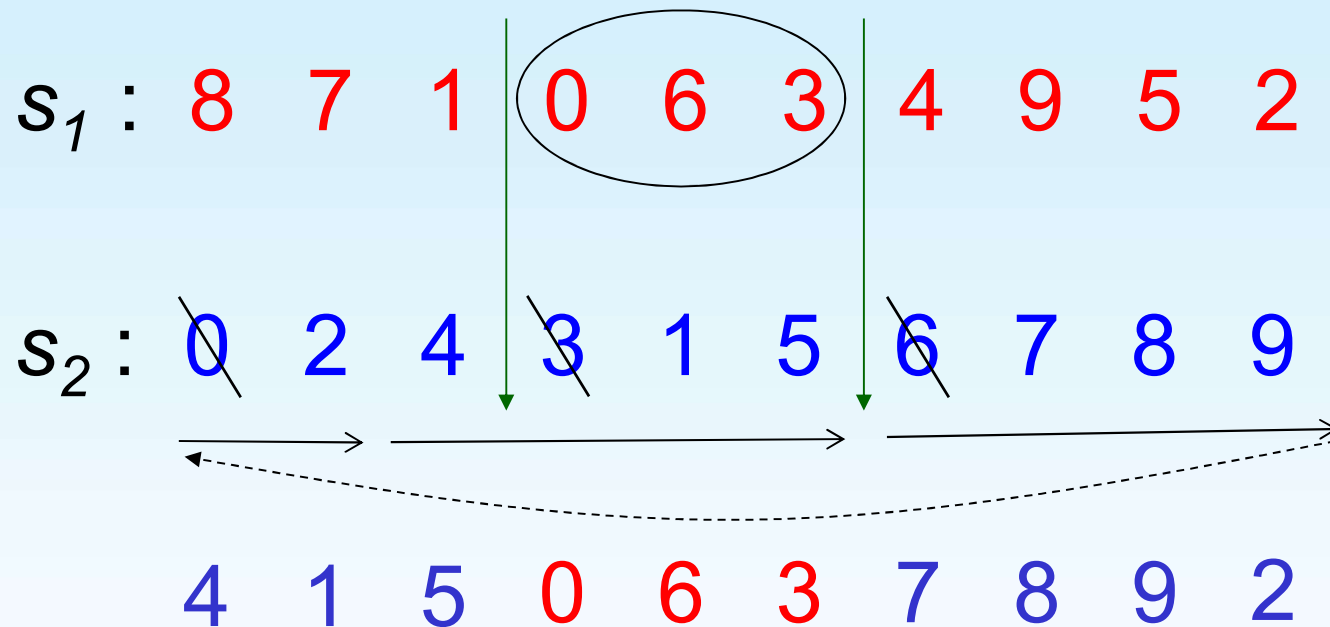




An important property of cycle crossovers

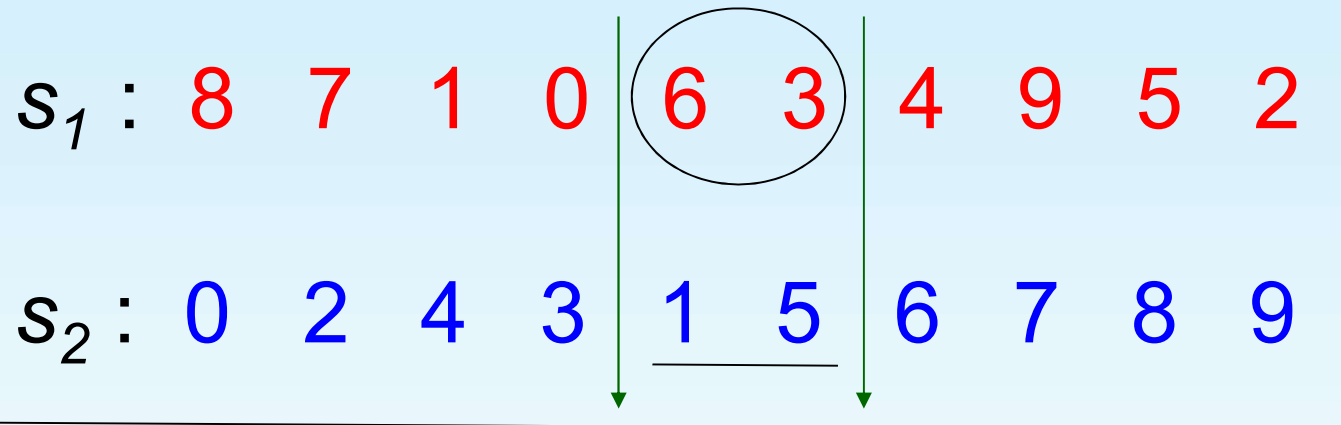
- Every gene value in the offspring is from the same position of a parent
- cf: PMX, Order crossover

Order Crossover



1. 임의로 2개의 cutting point를 정한다
2. 가운데 부분을 한 parent 1로부터 복사한다
3. parent 2에서 두번째 cutting point 다음부터 시작해서 중복을 피하면서 채워나간다

PMX (Partially Matched Crossover)



0 2 4 ~~3~~ 6 3 ~~6~~ 7 8 9

5 1

0 2 4 3 5 1 6 7 8 9

Arithmetic Crossover

s_1 : 8 7.6 4.1 0 1.6 3.8 42

s_2 : 0 2.6 4.2 3 1.8 5.0 60

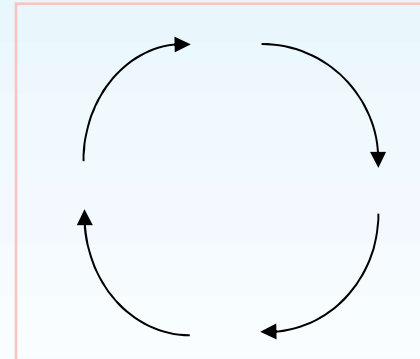
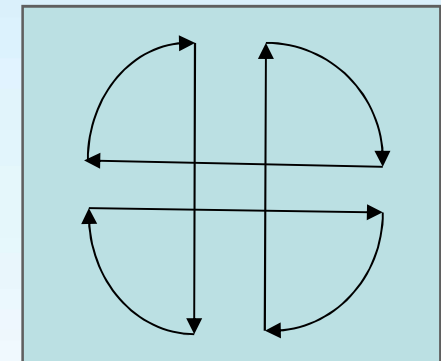
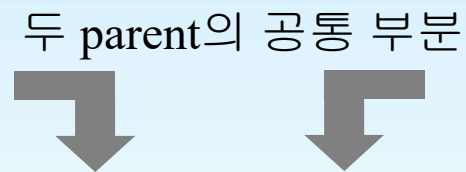
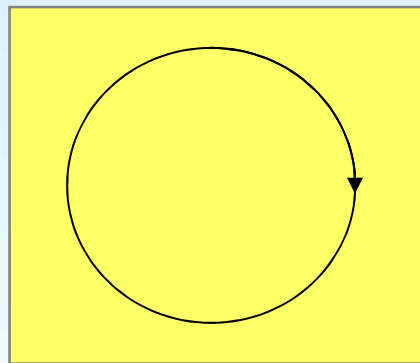
4 5.1 4.25 1.5 1.7 4.4 51

각 유전자별로 평균을 취한다

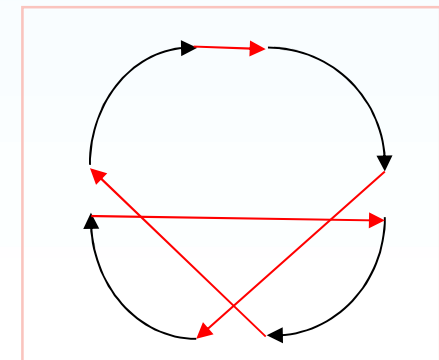
Heuristic Crossovers

Crossovers that use problem-specific knowledge

예: DPX for TSP



greedy repair



Edge Recombination for TSP

S_1 : 0 1 2 3 4 5 6 8 7 9

S_2 : 2 5 0 9 7 3 8 6 1 4



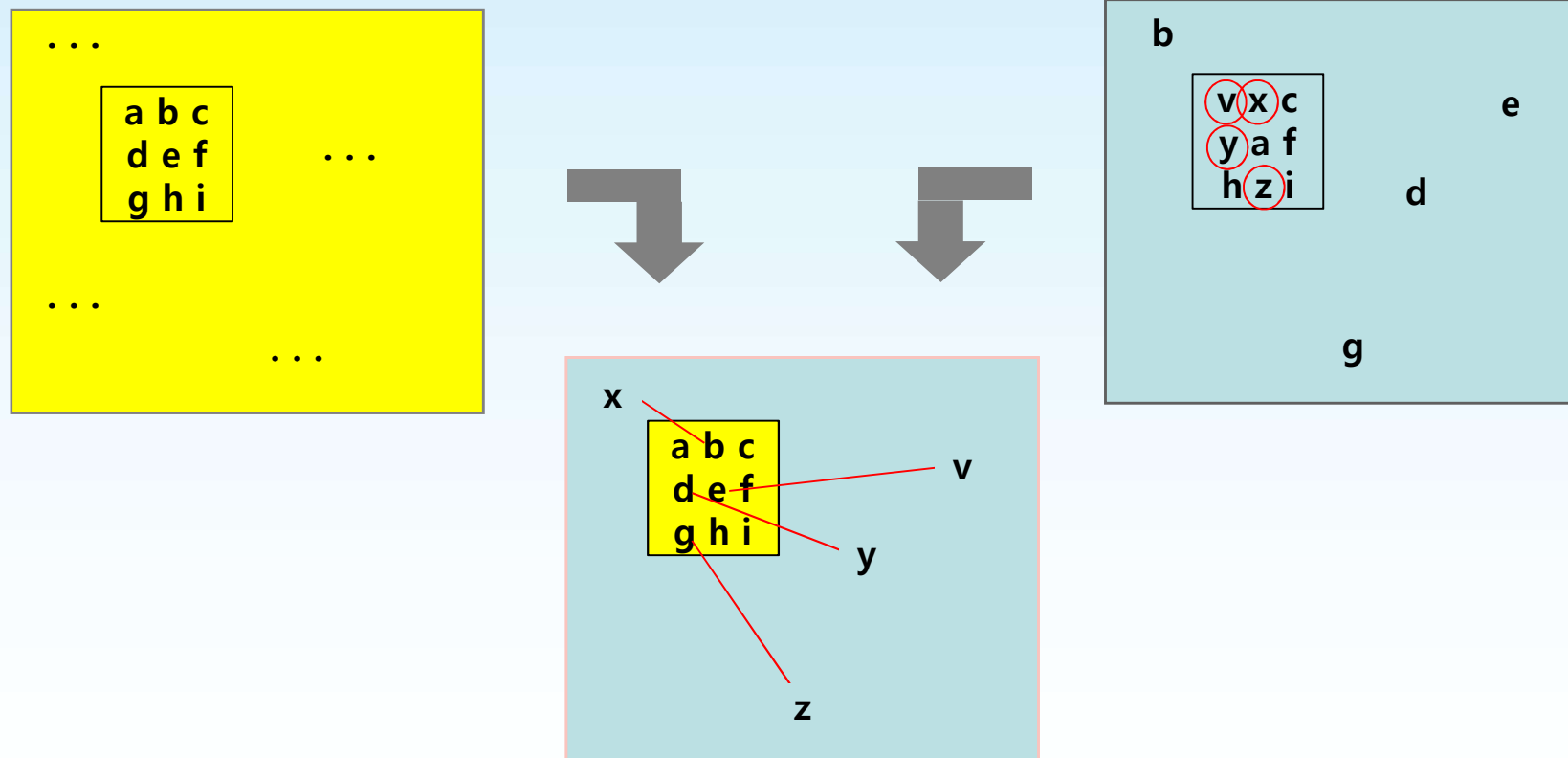
0 9 7 8 6 1 2 4 3 5



vertex	links
0	9 , 1, 5
1	0 , 2 , 6 , 4
2	1 , 3, 6 , 4
3	2 , 4 , 7 , 8 ⑤
4	③, 5, 1 , 2
5	4, 6, 2, 0
6	5, 8, ①
7	⑧, 9 , 3
8	⑥, 7 , 3
9	0 , ⑦

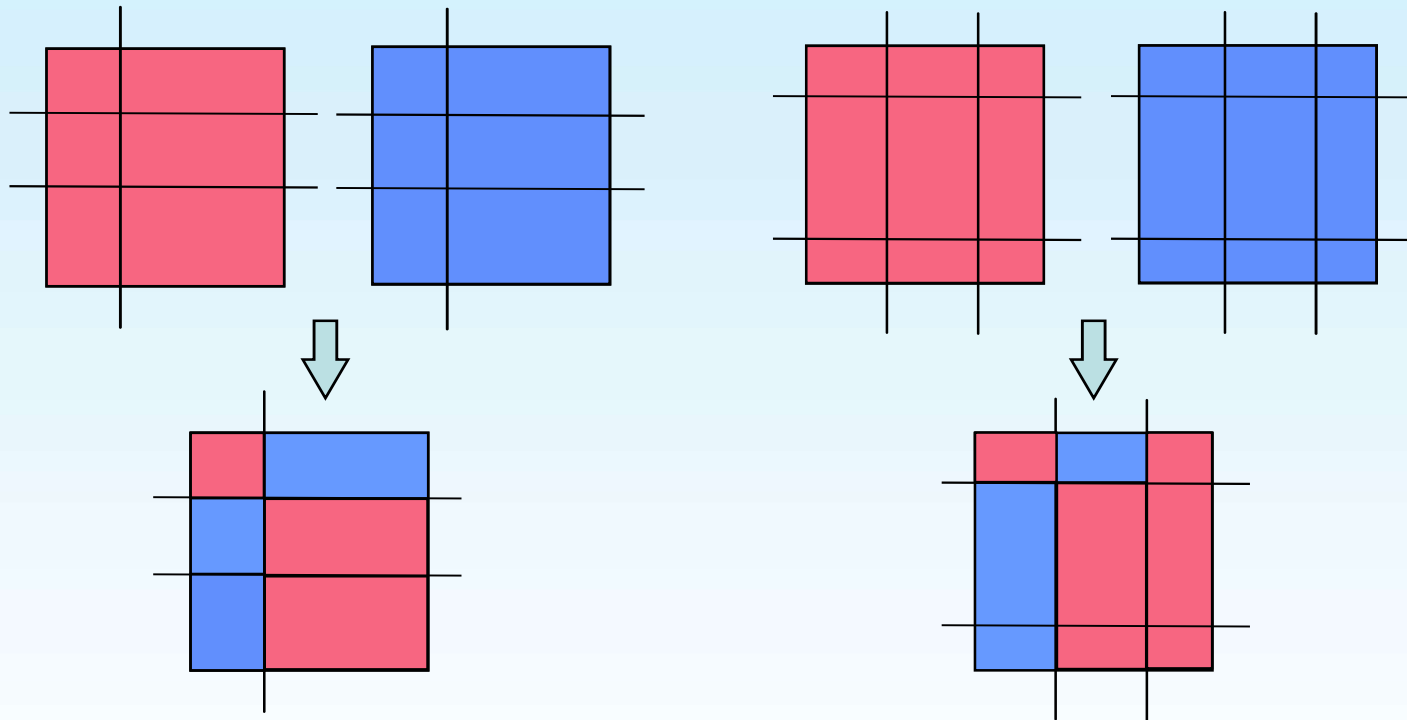
Cohon&Paris' Crossover

VLSI-CAD Placement를 위해 고안
최초의 multi-dimensional xover



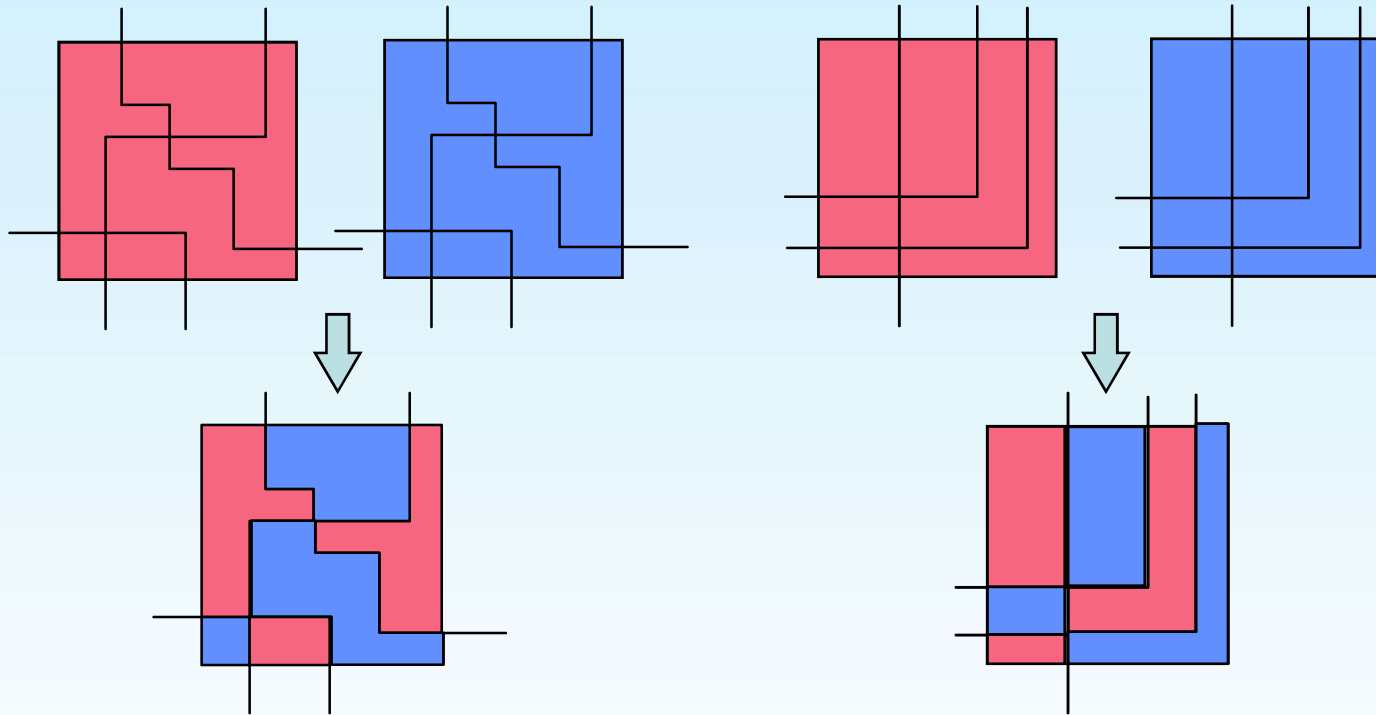
✓ 사실상 PMX를 2차원으로 확장한 것

Block-Uniform Crossover



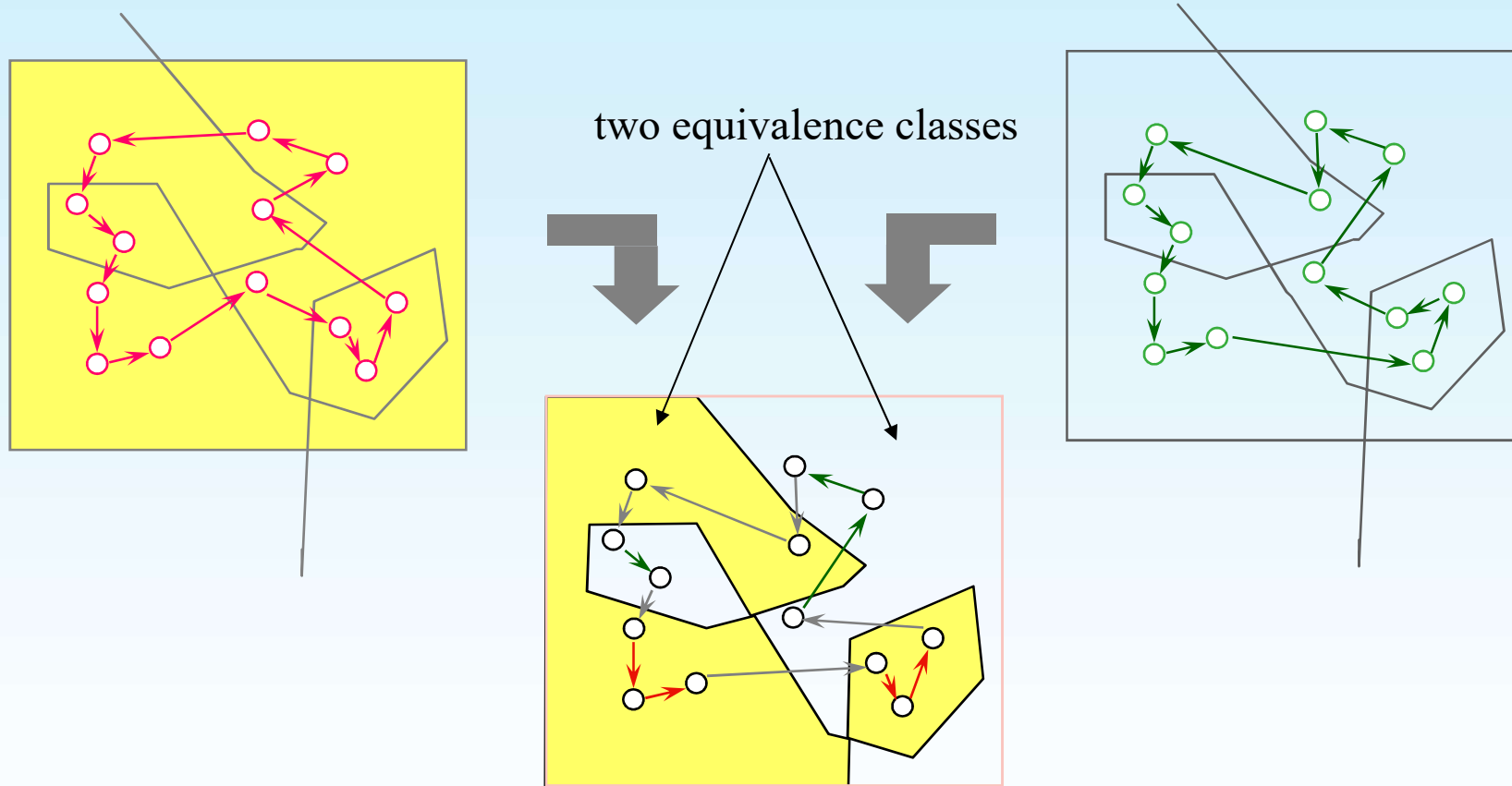
1. 직선을 사용하여 2차원 chromosome을 $i \times j$ 블록으로 분할한다
 2. 각 블록마다 0 또는 1을 임의 할당한다 (uniform xover처럼)
 3. 앞의 0 또는 1 값에 따라 각 블록을 각 parent로부터 복사한다
- ✓ 이것을 3차원 이상으로 확장하는 것은 어렵지 않다

Geographic Crossover



1. 단조 직선을 사용하여 2차원 chromosome을 여러 블록으로 분할한다
 - 이렇게 분할된 블록들은 항상 2개의 equivalence class로 나눌 수 있다
 2. 각 블록이 속한 equivalence class에 따라
parent 1 또는 parent 2로부터 복사한다
- ✓ 교차 연산자의 다양성을 높인다

Natural Crossover for TSP



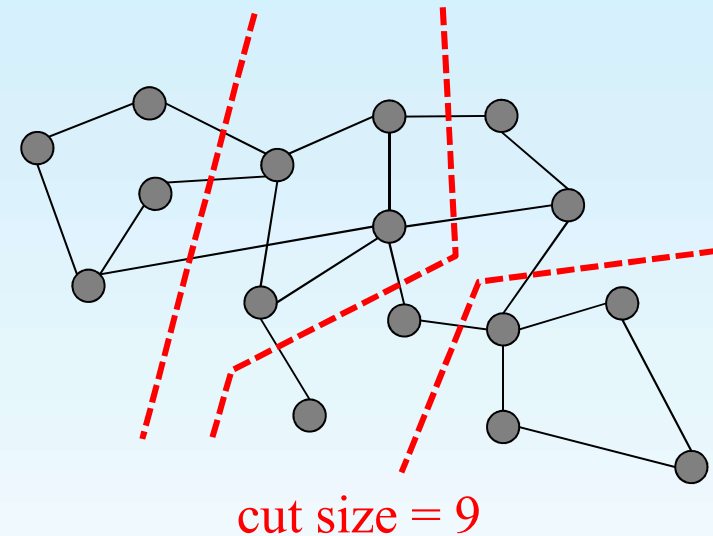
1. 2차원 chromosome에서 손의 궤적을 따라 k 개의 cutting line을 그린다
2. 1의 결과로 모든 폐공간이 2개의 equivalence class로 나뉜다
3. 각 parent에서 자신의 equivalence class에 속하는 vertex들을 연결하는 edge들을 복사한다
4. 적당히 나머지 edge들을 만들어 Hamiltonian cycle을 만든다

Normalization

e.g. 4-way partitioning problem

s_1 : 3 3 2 2 | 3 3 0 2 1 1 | 1 0 | 0 0 1 2
 s_2 : 2 2 0 0 | 2 2 1 0 3 3 | 1 1 | 3 3 1 0

 3 3 2 2 2 2 1 0 3 3 1 0 3 3 1 0



s'_1 → 2 2 0 0 | 2 2 3 0 1 1 | 1 3 | 3 3 1 0
 normalization ↗
 s_1 : 3 3 2 2 | 3 3 0 2 1 1 | 1 0 | 0 0 1 2
 s_2 : 2 2 0 0 | 2 2 1 0 3 3 | 1 1 | 3 3 1 0

 2 2 0 0 2 2 1 0 3 3 1 3 3 3 1 0

$\|s'_1 - s_2\| = 4$
 $\|s_1 - s_2\| = 14$

Phenotype의 의미를 훨씬 살렸다

Phenotype은 비슷한데 genotype은 전혀 다르다

Normalization이 유용한 예

- Sorting networks
- neural networks
- graph partitioning
- number partitioning
- ...

Proving Xovers' Validity

Alternate copy is clear in most cases.

But it is not clear in some cases particularly in multi-dimensional xovers.

Assume chromosomal domain space $D^n, D = \{0, 1, \dots, l - 1\}$.

(l -ary n -cube structure)

[Def. 1] A cutting surface in $R^n - D^n$ is a hypersurface
that divides the chromosomal domain space D^n
into exactly two disjoint subspaces

[Def. 2] For two points $x, y \in D^n$, $(x, y) \in R_e$ iff \exists a path from x to y
that makes an even # of intersections with cutting surfaces

[Fact] Relation R_e is an equivalence relation

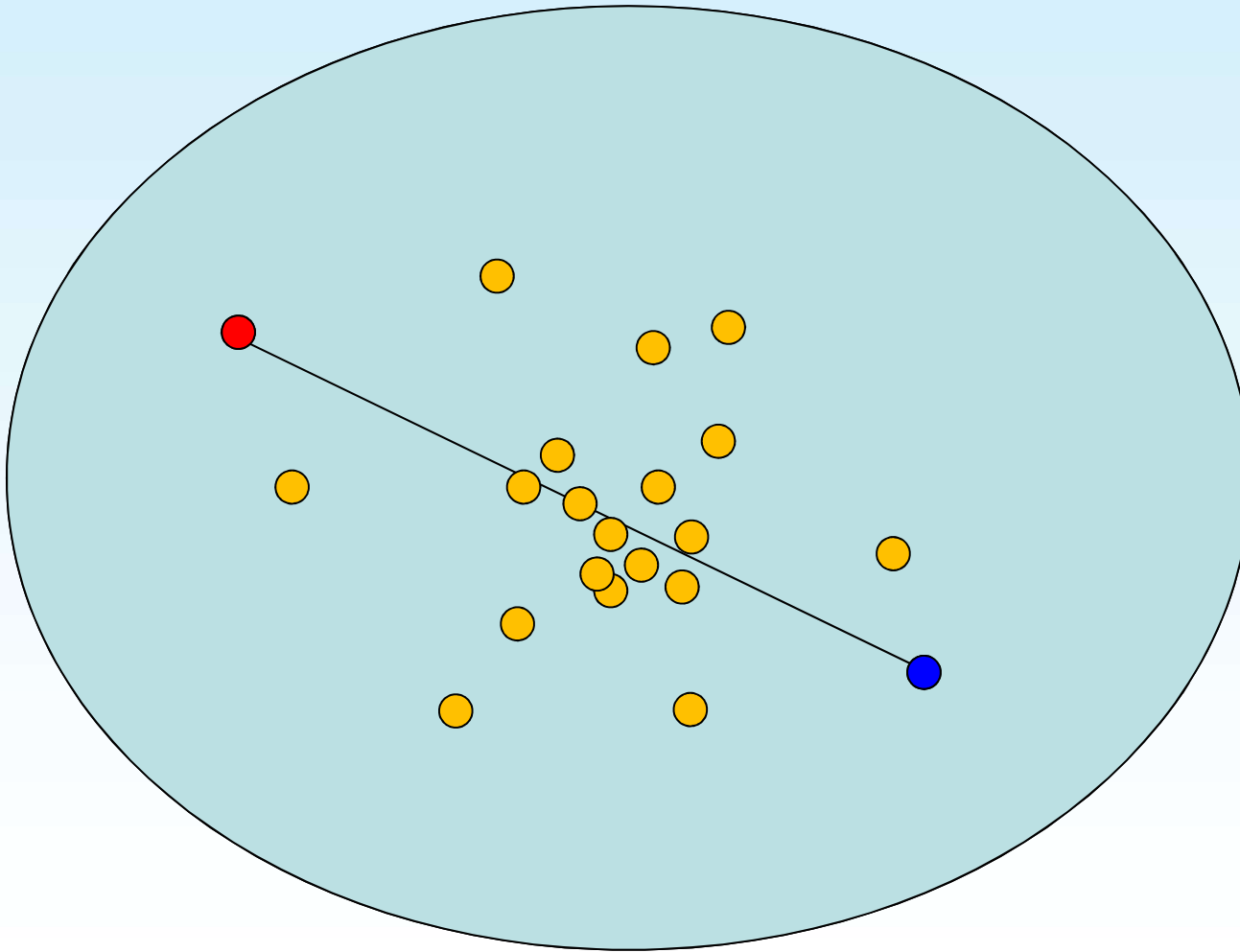
<Proof> $(x, x) \in R_e$ (reflexive)
 $(x, y) \in R_e$ iff $(y, x) \in R_e$ (commutative)
 $(x, y) \in R_e$ and $(y, z) \in R_e$ then $(x, z) \in R_e$ (transitive)

[Thm 1] If $(x, y) \in R_e$, then “any” path from x to y
also has an even # of intersections with cutting surfaces

[Thm 2] For any number k of cutting surfaces,
the equivalence relation R_e induces exactly two equivalence
classes of points in D^n

✓ Thm 2 guarantees a valid crossover

공간탐색에서 교차의 역할



대략 두 chromosome의 중앙 부근을 지향한다

변이

Generate initial solutions (say, p solutions);

do {

for ($i=0$; $i < k$; $i++$){

 Select two parent solutions;

 Crossover;

 Mutation;

 }

 Replace;

} **while** (not stopping condition);

Report the best solution;

Perturbs a small fraction of an offspring to introduce unexplored solution space

Typical form

	a	b	c	d	e	f	g	h	i	j	k	
random #s :	0.25	0.22	0.03	0.9	0.71	0.45	0.63	0.87	0.2	0.99	0.16	∈ [0,1]
e.g. $P_t = 0.05$	a	b	c'	d	e	f	g	h	i	j	k	

Non-Uniform Mutation

The degree of perturbation decreases over time

gene value $\rightarrow v = \begin{cases} v + \Delta(t, \text{UB} - v) & \text{if } r_1 = 0 \\ v + \Delta(t, v - \text{LB}) & \text{if } r_1 = 1 \end{cases}$

where $\begin{cases} r_1 \in \{0, 1\} \text{ (random)} \\ \Delta(t, y) = y \left(1 - r_2^{\left(1 - \frac{t}{T}\right)^b} \right) \end{cases}$

where $\begin{cases} r_2: \text{random number in } [0, 1] \\ T: \text{max generation} \\ b: \text{a parameter} \end{cases}$

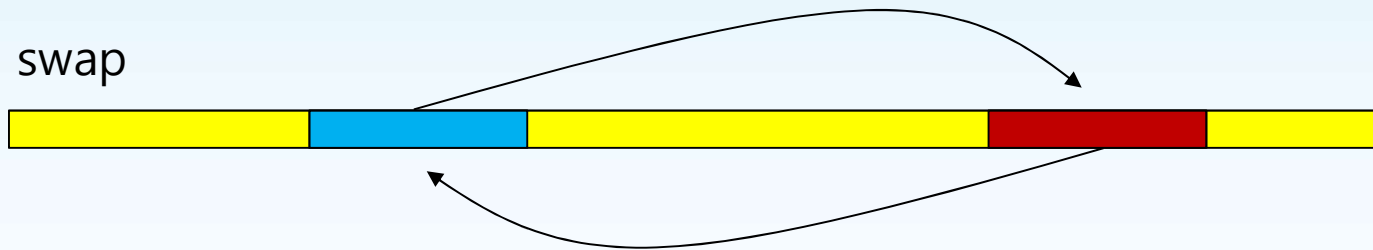
- ✓ Okay in a pure GA
- ✓ But may not be good in a memetic GA

다른 변이들

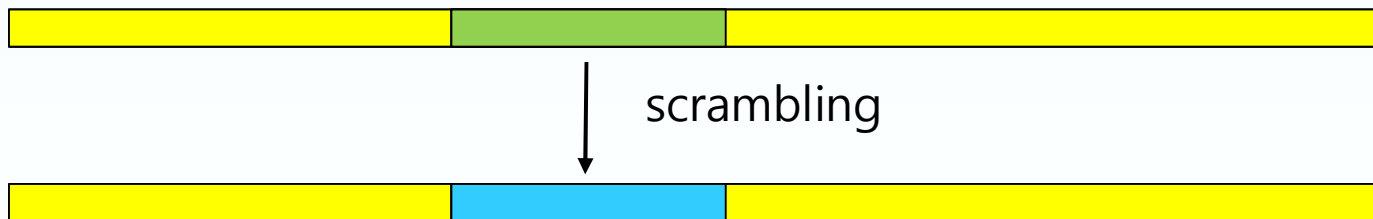
Interval inversion



Interval swap

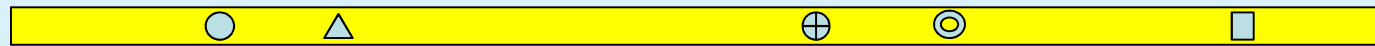


Interval scramble



다른 변이들

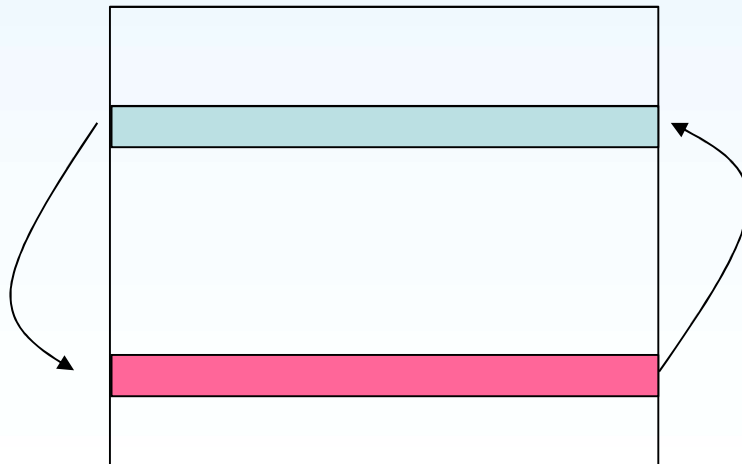
Pick & scramble



Select some positions and random scrambling



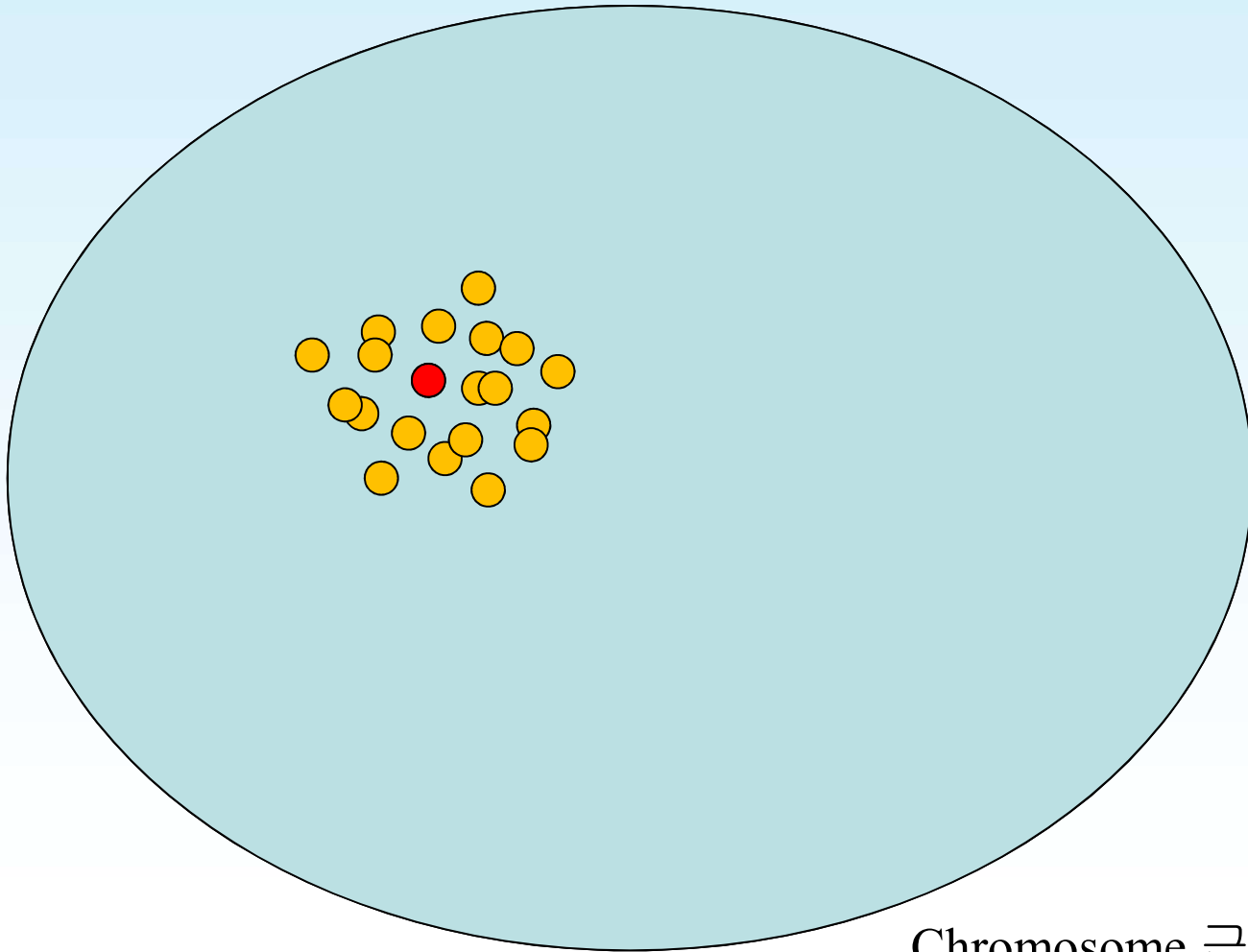
row swap



- Mutation can slow down the convergence.
- Mutation is a background operator in GA.
- But it is the main operator in ES and is the only operator in EP. (in the sense EP doesn't use xover)
- Usually, steady-state GAs converge faster than generational GAs. Steady-state GAs are more probable to premature convergence. Stronger mutation can alleviate steady-state GAs' premature convergence.

공간탐색에서 변이의 역할

대개, 해의 일부를 임의로 변형시킨다



Chromosome 근처에서 조금 옮긴다

대치

Generate initial solutions (say, p solutions);

do {

for ($i=0$; $i < k$; $i++$){

 Select two parent solutions;

 Crossover;

 Mutation;

 }

 Replace;

} **while** (not stopping condition);

Report the best solution;

Replacement Strategies

- ✓ Easy in generational GAs (usually)
- ✓ There are some choices in steady-state GAs
- Genitor-style
 - Replace the worst solution in the population
- Preselection
 - Replace one of the parents
- Crowding
 - Randomly choose k solutions at random in the population
 - Replace the most similar one to the offspring
- Combinations