

Real coded Genetic Algorithms

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□ Disadvantage of binary coded GA

- more computation
- lower accuracy
- longer computing time
- solution space discontinuity
- hamming cliff

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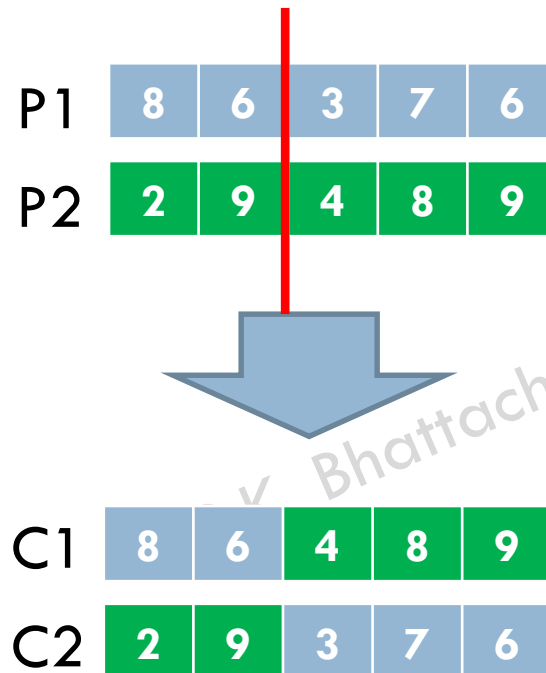
- The standard genetic algorithms has the following steps
 1. Choose initial population
 2. Assign a fitness function
 3. Perform elitism
 4. Perform selection
 5. Perform crossover
 6. Perform mutation
- In case of standard Genetic Algorithms, steps 5 and 6 require bitwise manipulation.

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Simple crossover: similar to binary crossover



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Linear Crossover

- Parents: (x_1, \dots, x_n) and (y_1, \dots, y_n)
- Select a single gene (k) at random
- Three children are created as,

$$(x_1, \dots, x_k, 0.5 \cdot y_k + 0.5 \cdot x_k, \dots, x_n)$$

$$(x_1, \dots, x_k, 1.5 \cdot y_k - 0.5 \cdot x_k, \dots, x_n)$$

$$(x_1, \dots, x_k, -0.5 \cdot y_k + 1.5 \cdot x_k, \dots, x_n)$$

- From the three children, best two are selected for the next generation

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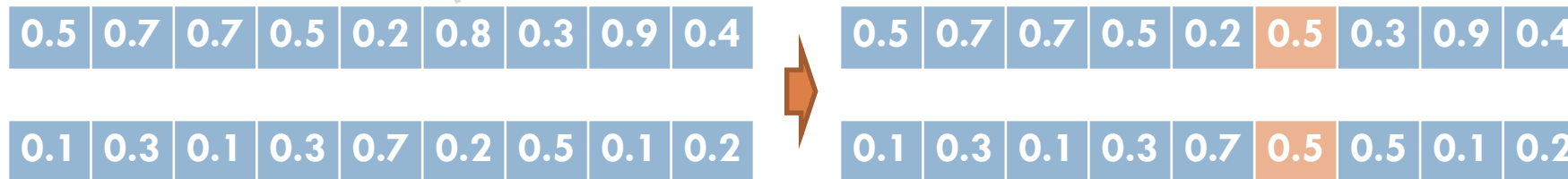
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Single arithmetic crossover

- Parents: (x_1, \dots, x_n) and (y_1, \dots, y_n)
- Select a single gene (k) at random
- child₁ is created as,

$$(x_1, \dots, x_k, \alpha \cdot y_k + (1 - \alpha) \cdot x_k, \dots, x_n)$$

- reverse for other child. e.g. with $\alpha = 0.5$



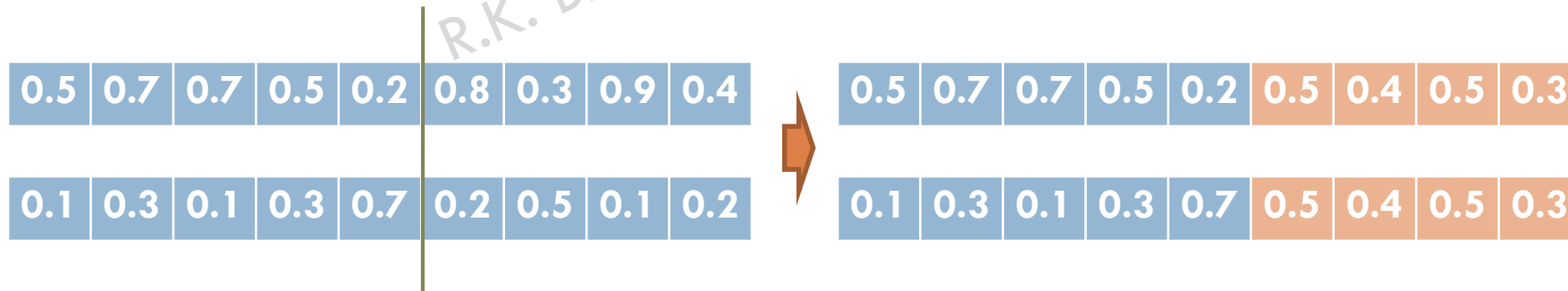
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Simple arithmetic crossover

- Parents: (x_1, \dots, x_n) and (y_1, \dots, y_n)
- Pick random gene (k) after this point mix values
- child₁ is created as:
 $(x_1, \dots, x_k, \alpha \cdot y_{k+1} + (1-\alpha) \cdot x_{k+1}, \dots, \alpha \cdot y_n + (1-\alpha) \cdot x_n)$
- reverse for other child. e.g. with $\alpha = 0.5$



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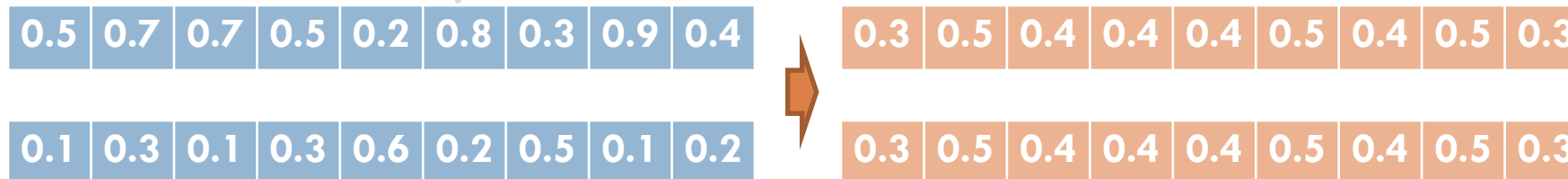
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Whole arithmetic crossover

- Most commonly used
- Parents: (x_1, \dots, x_n) and (y_1, \dots, y_n)
- child₁ is:

$$\alpha \cdot \bar{x} + (1 - \alpha) \cdot \bar{y}$$

- reverse for other child. e.g. with $\alpha = 0.5$



Simulated binary crossover

- Developed by Deb and Agrawal, 1995)

$$x_i^{(1,t+1)} = 0.5 \left[(1 + \beta_{qi}) x_i^{(1,t)} + (1 - \beta_{qi}) x_i^{(2,t)} \right]$$

$$x_i^{(2,t+1)} = 0.5 \left[(1 - \beta_{qi}) x_i^{(1,t)} + (1 + \beta_{qi}) x_i^{(2,t)} \right]$$

$$\beta_{qi} = \begin{cases} (2u_i)^{\frac{1}{n_c+1}}, & \text{if } u_i \leq 0.5 \\ \left(\frac{1}{2(1-u_i)} \right)^{\frac{1}{n_c+1}}, & \text{otherwise} \end{cases}$$

Where, u_i a random number

n_c is a parameter that controls the crossover process. A high value of the parameter will create near-parent solution

Random mutation

$$y_i^{(1,t+1)} = u_i(x_i^u - x_i^l)$$

Where u_i is a random number between $[0,1]$

$$y_i^{(1,t+1)} = x_i^{1,t+1} + (u_i - 0.5)\Delta_i$$

Where, Δ_i is the user defined maximum perturbation

Normally distributed mutation

A simple and popular method

$$y_i^{(1,t+1)} = x_i^{1,t+1} + N(0, \sigma_i)$$

Where $N(0, \sigma_i)$ is the Gaussian probability distribution with zero mean

Polynomial mutation

Deb and Goyal, 1996 proposed

$$y_i^{1,t+1} = x_i^{1,t+1} + (x_i^u - x_i^l)\delta_i$$

$$\delta_i = \begin{cases} (2u_i)^{1/(\eta_m+1)} - 1 & \text{If } u_i < 0.5 \\ 1 - (2(1 - u_i))^{1/(\eta_m+1)} & \text{If } u_i \geq 0.5 \end{cases}$$

THANKS

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