

Genetic Algorithms

Chapter 3-1

Source: Eiben & Smith

Edited by: Hosein Alizadeh

<http://webpages.iust.ac.ir/halizadeh/>

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Computer Engineering Department, Iran University of Science & Technology
HA-EC, CE dept, IUST

GA Quick Overview

- Developed: USA in the 1970's
- Early names: J. Holland, K. DeJong, D. Goldberg
- Typically applied to:
 - discrete optimization
- Attributed features:
 - not too fast
 - good heuristic for combinatorial problems
- Special Features:
 - Traditionally emphasizes combining information from good parents (crossover)
 - many variants, e.g., reproduction models, operators

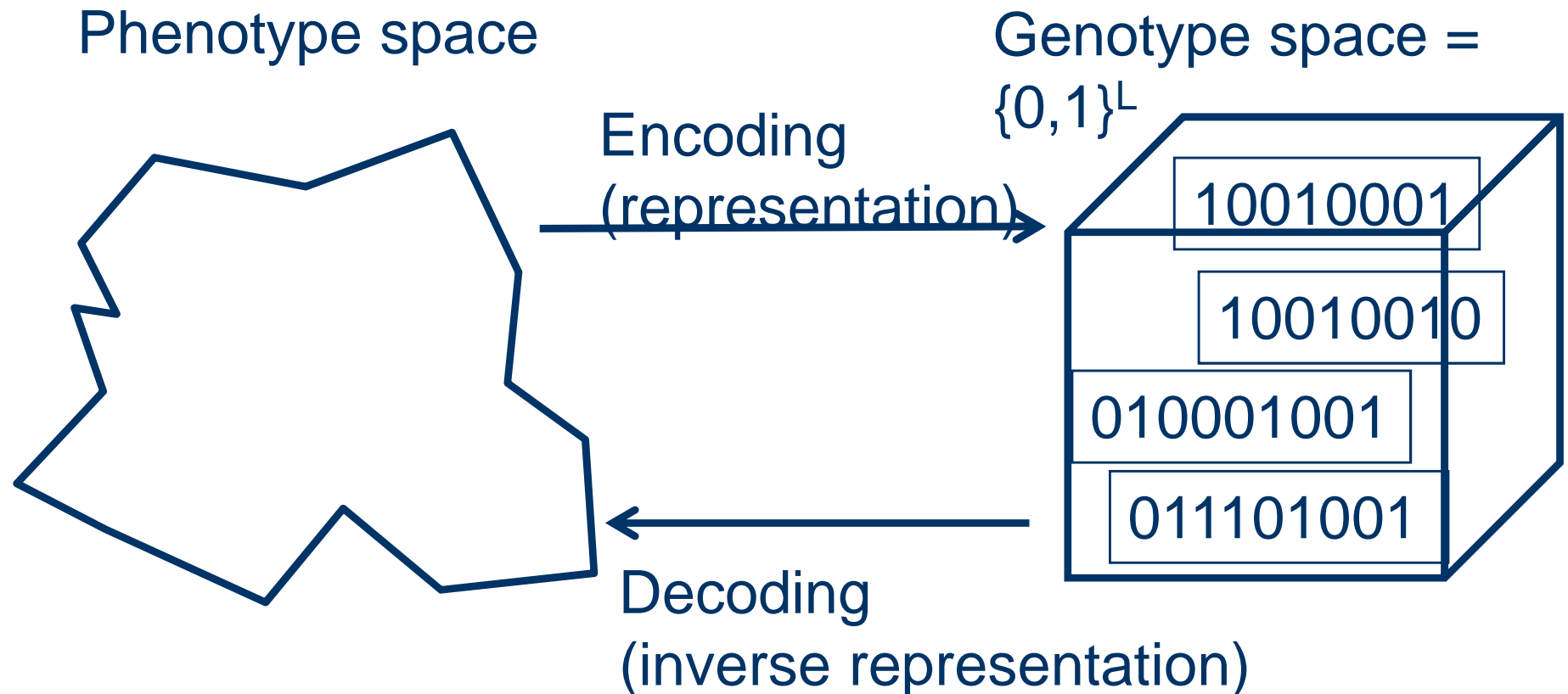
Genetic algorithms

- Holland's original GA: **Simple GA (SGA)**
- Other GAs use different:
 - Representations
 - Mutations
 - Crossovers
 - Selection mechanisms

SGA technical summary tableau

Representation	Binary strings
Recombination	N-point or uniform
Mutation	Bitwise bit-flipping with fixed probability
Parent selection	Fitness-Proportionate
Survivor selection	All children replace parents
Speciality	Emphasis on crossover

Representation

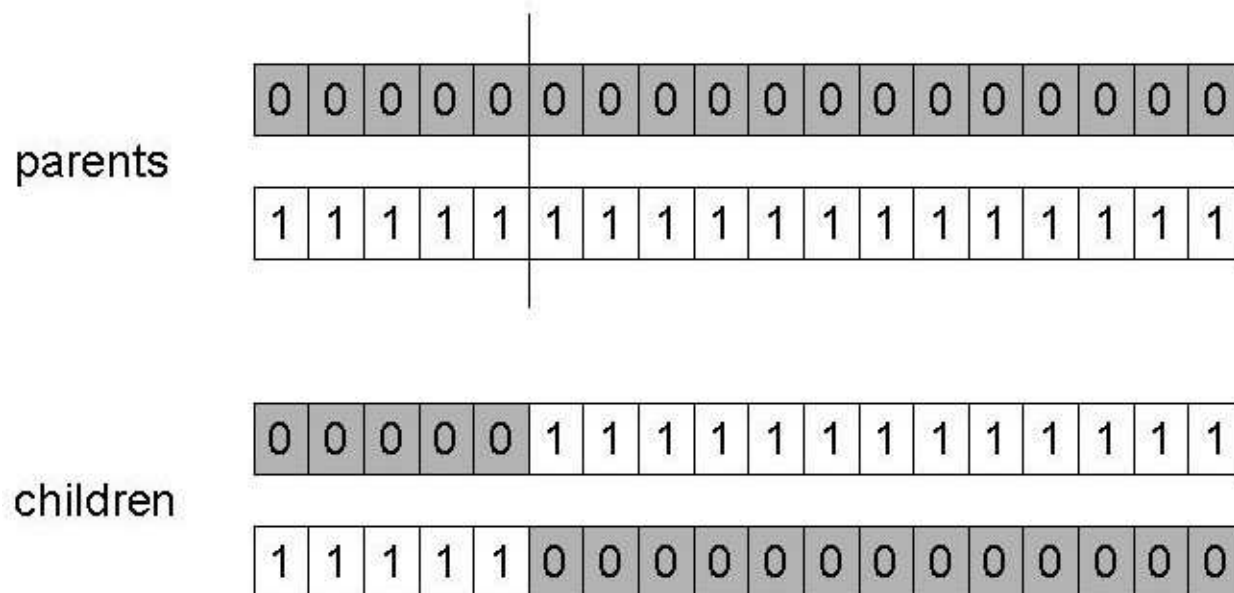


SGA reproduction cycle

1. Select parents for the mating pool
(size of mating pool = population size)
2. Shuffle the mating pool
3. Apply crossover with probability p_c , otherwise copy parents
4. For each offspring apply mutation (bit-flip with probability p_m independently for each bit)
5. Replace the whole population with the offsprings

SGA operators: 1-point crossover

- Choose a random point
- Split parents
- Create children by exchanging tails
- P_c typically in range (0.6, 0.9)



SGA operators: mutation

- Alter each gene independently with p_m
- p_m : mutation rate
 - Typically between $1/\text{pop_size}$ and $1/\text{chromosome_length}$

parent

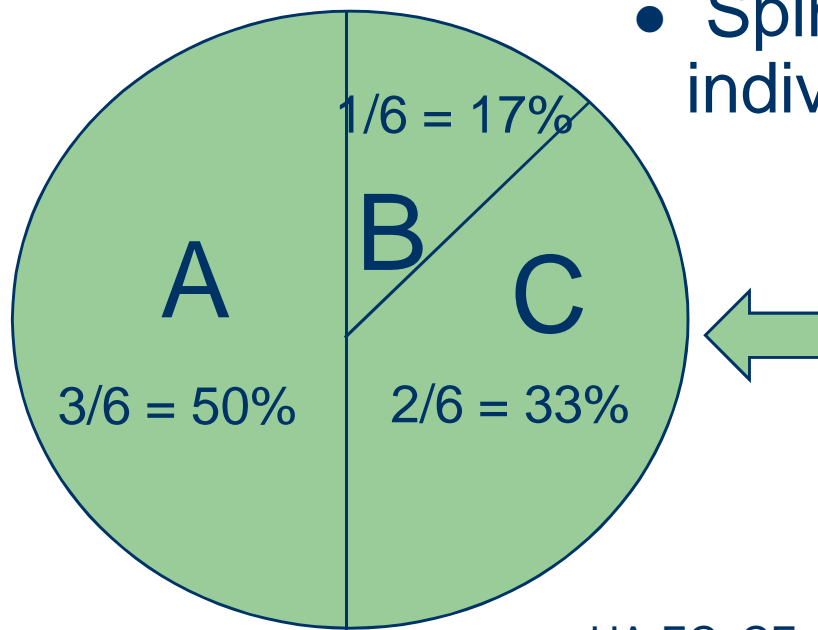
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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child

0	1	0	0	1	0	1	1	0	0	0	1	0	1	1	0	0	1
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SGA operators: Selection

- Main idea: better individuals get higher chance
 - Chances proportional to fitness
 - Implementation: roulette wheel technique
 - Assign a part of the roulette wheel to each individual
 - Spin the wheel n times to select n individuals



$$\text{fitness}(A) = 3$$

$$\text{fitness}(B) = 1$$

$$\text{fitness}(C) = 2$$

An example after Goldberg '89 (1)

- Simple problem: $\max x^2$ over $\{0,1,\dots,31\}$
- GA approach:
 - Representation: binary code, e.g. $01101 \leftrightarrow 13$
 - Population size: 4
 - 1-point crossover, bitwise mutation
 - Roulette wheel selection
 - Random initialisation
- We show one generational cycle done by hand

X² example: selection

String no.	Initial population	x Value	Fitness $f(x) = x^2$	$Prob_i$	Expected count	Actual count
1	0 1 1 0 1	13	169	0.14	0.58	1
2	1 1 0 0 0	24	576	0.49	1.97	2
3	0 1 0 0 0	8	64	0.06	0.22	0
4	1 0 0 1 1	19	361	0.31	1.23	1
Sum			1170	1.00	4.00	4
Average			293	0.25	1.00	1
Max			576	0.49	1.97	2

X² example: crossover

String no.	Mating pool	Crossover point	Offspring after xover	x Value	Fitness $f(x) = x^2$
1	0 1 1 0 1	4	0 1 1 0 0	12	144
2	1 1 0 0 0	4	1 1 0 0 1	25	625
2	1 1 0 0 0	2	1 1 0 1 1	27	729
4	1 0 0 1 1	2	1 0 0 0 0	16	256
Sum					1754
Average					439
Max					729

X² example: mutation

String no.	Offspring after xover	Offspring after mutation	x Value	Fitness $f(x) = x^2$
1	0 1 1 0 0	1 1 1 0 0	26	676
2	1 1 0 0 1	1 1 0 0 1	25	625
2	1 1 0 1 1	1 1 0 1 1	27	729
4	1 0 0 0 0	1 0 1 0 0	18	324
Sum				2354
Average				588.5
Max				729

SGA

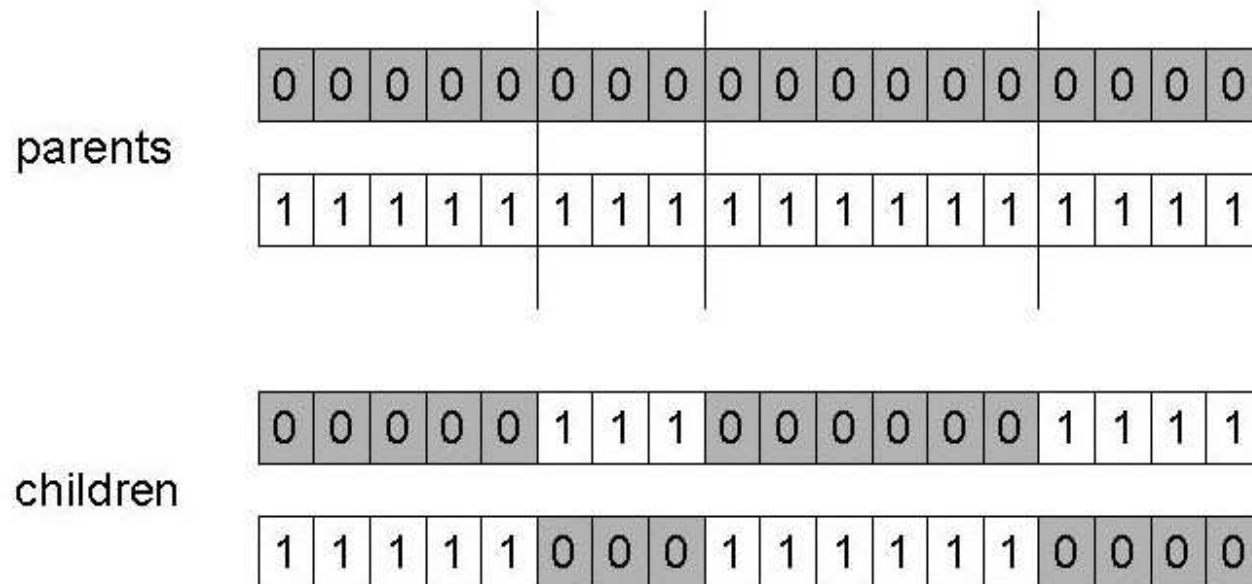
- Subject of many studies
- Shortcomings:
 - Representation: too restrictive
 - Mutation & crossovers: only applicable for bit-string & integer representations
 - Selection mechanism: converging populations with close fitness values
 - Next Generation model (step 5 in SGA): can be improved with better survivor selection

Alternative Crossover Operators

- Performance with 1 Point Crossover depends on the **order** of genes
- *Positional Bias*
 - more likely to keep together genes that are **near** each other
 - Can never keep together genes from **opposite ends**

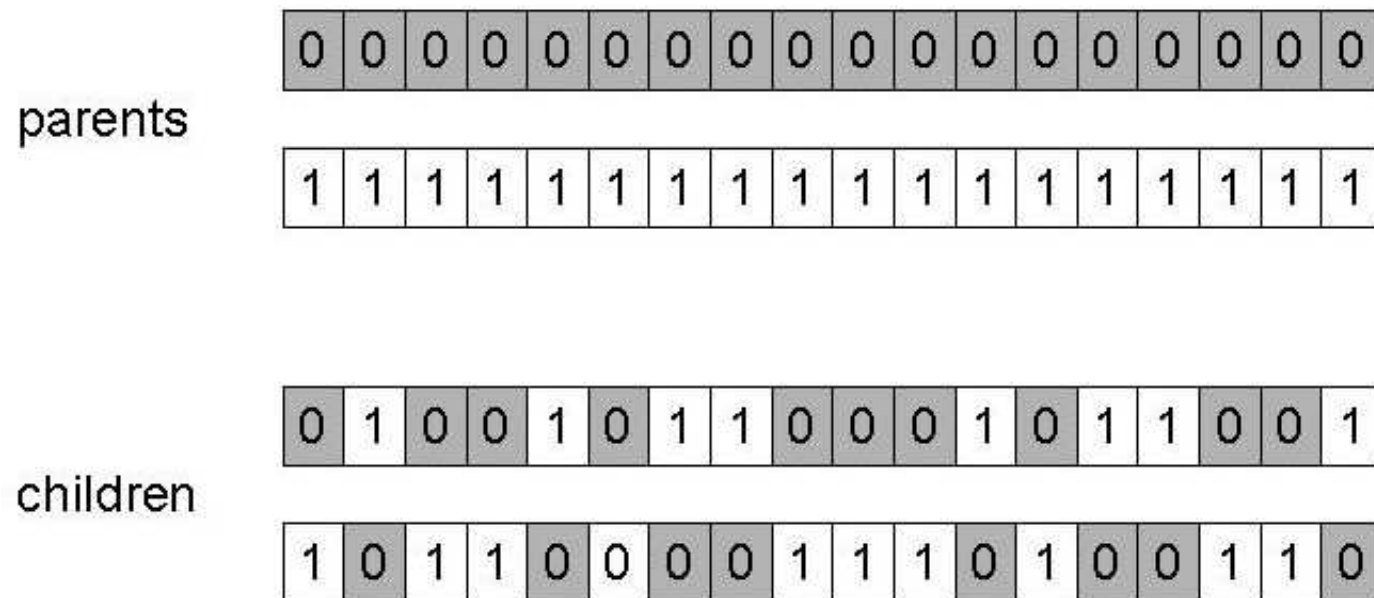
n-point crossover

- Choose n random crossover points
- Split along those points
- Exchange parts
- Generalisation of 1 point (still some positional bias)



Uniform crossover

- Assign 'heads' to one parent, 'tails' to the other
- Flip a coin for each gene
- Inheritance is independent of position (No Positional Bias)



Crossover OR mutation?

- which one is better / necessary?
- Answer (at least, rather wide agreement):
 - it depends on the problem, but
 - in general, it is good to have both
 - both have another role
 - mutation-only-EA is possible, crossover-only-EA would not work

Crossover OR mutation? (cont'd)

Exploration: Discovering promising areas in the search space (gaining information)

Exploitation: Optimizing within a promising area (using information)

- Crossover is explorative
 - makes a *big* jump to an area somewhere “between” parent areas
- Mutation is exploitative
 - creates random *small* diversions, staying near the parent

Crossover OR mutation? (cont'd)

- crossover only combine information from two parents
- mutation only introduce new information
- Crossover does not change the allele frequencies of the population (thought experiment: 50% 0's on first bit in the population, ?% after performing n crossovers)
- Often need a 'lucky' mutation to hit the optimum

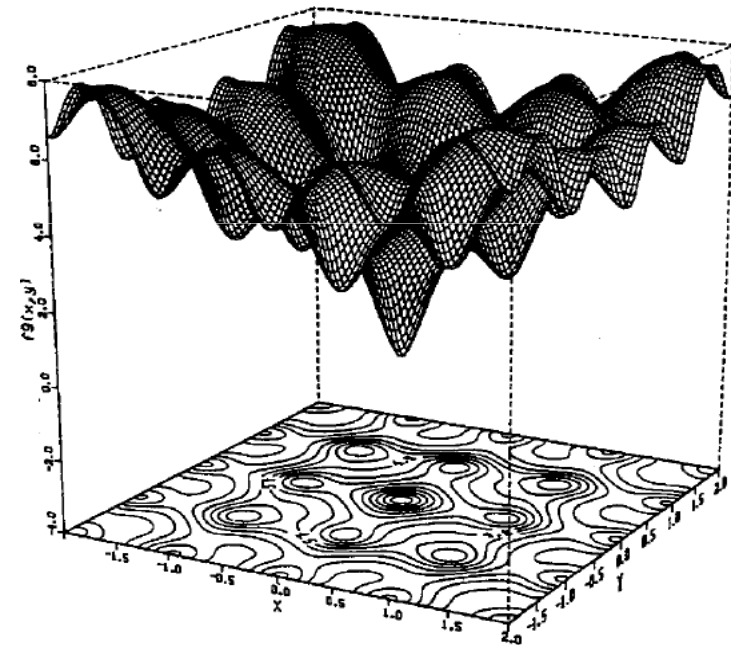
Integer representations

- Problems with integer variables
 - image processing parameters
 - *categorical* values {blue, green, yellow, pink}
- N-point / uniform crossover operators work
- Extend bit-flipping mutation to make
 - “creep” i.e. more likely to move to similar value
 - Random choice (esp. categorical variables)

Real valued problems

- Many problems occur as real valued problems
 - continuous parameter Optimization $f: \mathcal{R}^n \rightarrow \mathcal{R}$
- Ackley's function

$$f(\bar{x}) = -c_1 \cdot \exp \left(-c_2 \cdot \sqrt{\frac{1}{n} \sum_{i=1}^n x_i^2} \right) \\ - \exp \left(\frac{1}{n} \cdot \sum_{i=1}^n \cos(c_3 \cdot x_i) \right) + c_1 + 1 \\ c_1 = 20, c_2 = 0.2, c_3 = 2\pi$$



Single arithmetic crossover

- Parents: $\langle x_1, \dots, x_n \rangle$ and $\langle y_1, \dots, y_n \rangle$
- Pick a single gene (k) at random,
- child₁ is: $\langle x_1, \dots, x_k, \alpha \cdot y_k + (1 - \alpha) \cdot x_k, \dots, x_n \rangle$
- reverse for other child. e.g. with $\alpha = 0.5$

0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
-----	-----	-----	-----	-----	-----	-----	-----	-----

0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.5	0.9
-----	-----	-----	-----	-----	-----	-----	-----	-----



0.3	0.2	0.3	0.2	0.3	0.2	0.3	0.2	0.3
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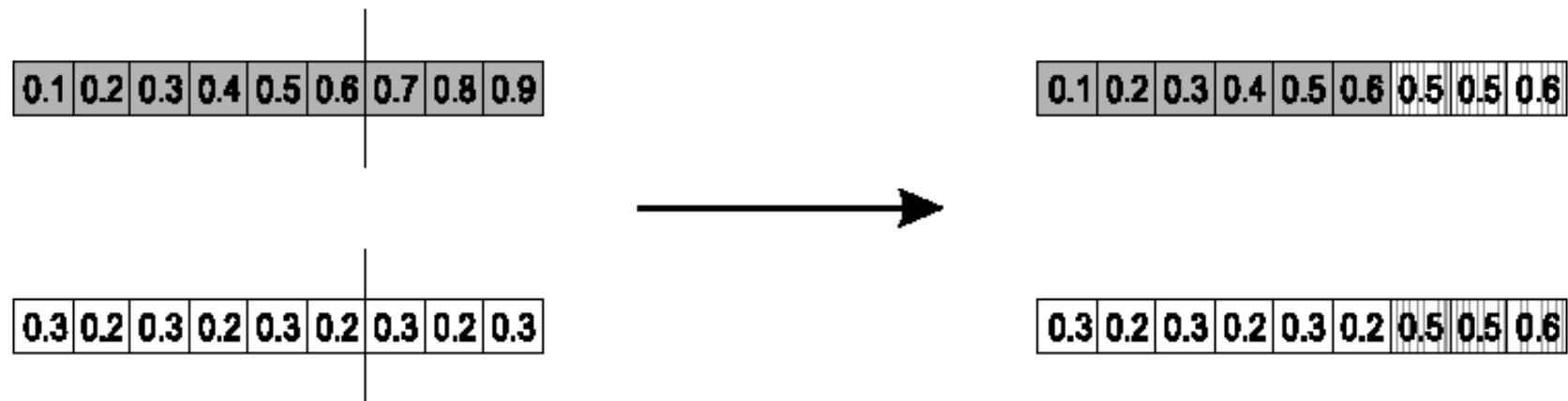
0.3	0.2	0.3	0.2	0.3	0.2	0.3	0.5	0.3
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Simple arithmetic crossover

- Parents: $\langle x_1, \dots, x_n \rangle$ and $\langle y_1, \dots, y_n \rangle$
- Pick random gene (k) after this point mix values
- child₁ is:

$$\left\langle x_1, \dots, x_k, \alpha \cdot y_{k+1} + (1 - \alpha) \cdot x_{k+1}, \dots, \alpha \cdot y_n + (1 - \alpha) \cdot x_n \right\rangle$$

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



Whole arithmetic crossover

- Most commonly used
- Parents: $\langle x_1, \dots, x_n \rangle$ and $\langle y_1, \dots, y_n \rangle$
- child₁ is:

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

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

0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
-----	-----	-----	-----	-----	-----	-----	-----	-----

0.2	0.2	0.3	0.3	0.4	0.4	0.5	0.5	0.6
-----	-----	-----	-----	-----	-----	-----	-----	-----



0.3	0.2	0.3	0.2	0.3	0.2	0.3	0.2	0.3
-----	-----	-----	-----	-----	-----	-----	-----	-----

0.2	0.2	0.3	0.3	0.4	0.4	0.5	0.5	0.6
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