6: Integer and Real-Valued Representations

- Integer representations
 - mutation (random resetting and creep mutation)
 - crossover (*n*-point and uniform crossover)
- Real-valued representation
 - mutation (uniform and nonuniform mutation)
 - crossover (discrete and arithmetic crossover)
- Textbook Chapter 4.3, 4.4

Integer representations

- Some problems naturally have integer variables
- Ordinal vs. cardinal attributes
- Examples
 - graph k-coloring problem
 - function optimization with integer variables
 - path finding on a square grid
 - combinatorial optimizations

Integer representations - mutation

Random resetting

- randomly choose a permissible new value to replace
- all alleles are equally likely to be chosen

Creep mutation

- adding a small value to each gene with a probability p
- sampled from a distribution symmetric about zero
- more likely to generate small changes than larger ones
- parameter mutation_step_size

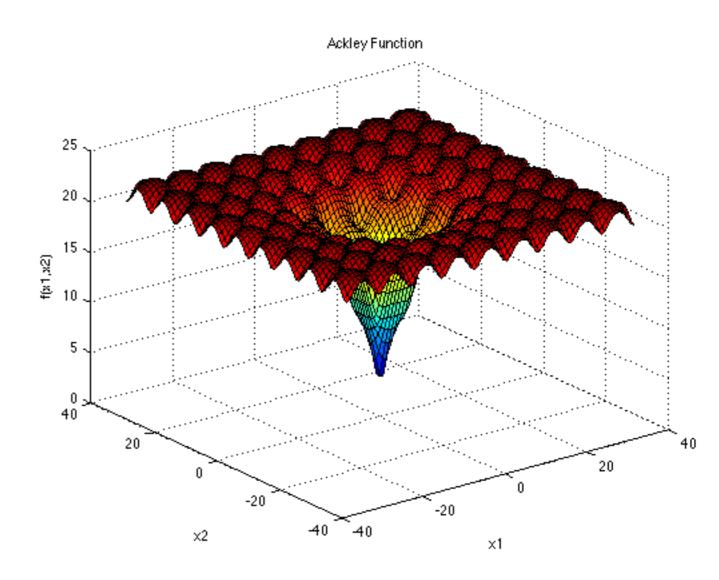
Integer representations - crossover

- Similar to binary representations
- *n*-point crossover
 - positional bias
- Uniform crossover
 - distributional bias

Real-valued representations

- Many problems occur as real-valued, e.g. continuous parameter optimization
- Example: Ackley's function

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



Floating-point representations - mutation I

General scheme of floating point mutations

$$\langle x_1, \dots, x_n \rangle \to \langle x'_1, \dots, x'_n \rangle$$
, where $x_i, x'_i \in [L_i, U_i]$

- Uniform mutation
 - x_i' are drawn uniformly randomly from $[L_i, U_i]$
 - Analogous to bit-flipping (binary) or random resetting (integers)

Floating-point representations - mutation 2

• Non-uniform mutations:

- Most schemes are probabilistic but usually only make a small change to value
- Most common method is to add random deviate to each variable separately, taken from
 - a Gaussian distribution (with zero mean)
- Standard deviation (mutation_step_size) controls the magnitude of change
- Other distributions, e.g., Cauchy, power-law

Floating-point representations - crossover

• Discrete:

- each allele value in offspring z comes from one of its parents (x,y) with equal probability:

$$z_i = x_i$$
 or y_i

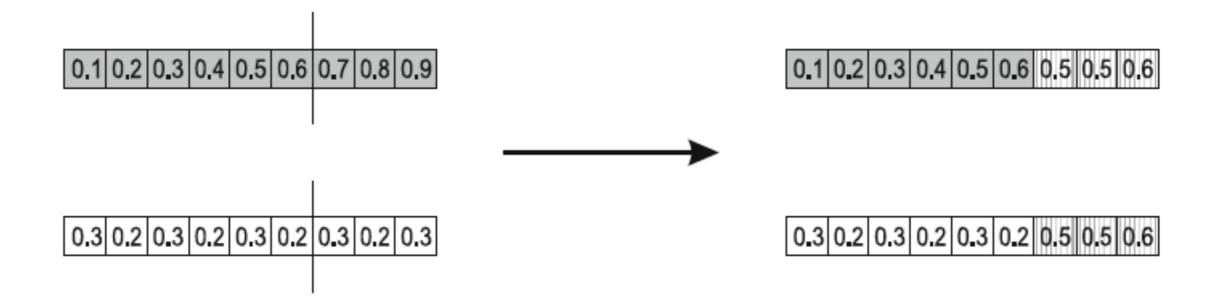
- could use *n*-point or uniform

• Arithmetic (intermediate):

- exploits idea of creating children "between" parents
- $z_i = \alpha x_i + (1 \alpha)y_i$, where α is between 0 and 1
- The parameter α can be:
 - constant
 - variable (e.g. depend on the age of the population)
 - picked at random every time

One-point arithmetic crossover

- Pick a recombination point *k*
- Child I: $\langle x_1, \ldots, x_k, \alpha \cdot y_{k+1} + (1-\alpha) \cdot x_{k+1}, \ldots, \alpha \cdot y_n + (1-\alpha) \cdot x_n \rangle$



Single arithmetic crossover

- Pick a random locus k
- At that position, take the arithmetic average of the two parents
- Child I: $\langle x_1, \dots, x_{k-1}, \alpha \cdot y_k + (1-\alpha) \cdot x_k, x_{k+1}, \dots, x_n \rangle$

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

 \longrightarrow

0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.2 0.3

0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.5 0.3

Whole arithmetic crossover

- Most commonly used operator
- Taking the weighted sum of the two parental allele for each gene
- Child I: $\alpha \cdot \bar{x} + (1-\alpha) \cdot \bar{y}$
- Chile 2: $\alpha \cdot \bar{y} + (1 \alpha) \cdot \bar{x}$

0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9

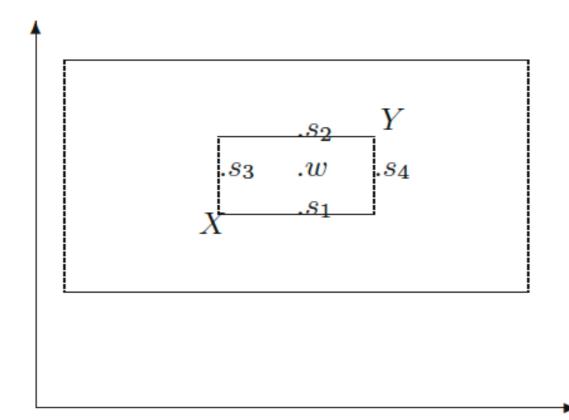
0.2 0.2 0.3 0.3 0.4 0.4 0.5 0.5 0.6

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

Blend crossover

- Create offspring in a region that is bigger than the (n-dimensional) rectangle spanned by the parents
- Two parents x and y and assume that $x_i < y_i$ at position i , $d_i = y_i x_i$
- The *i*-th value in the child z is in the range $[x_i \alpha \times d_i, y_i + \alpha \times d_i]$



Multi-parent recombination

- Not constricted by the practicalities of nature
- Been around since 1960s, still rare but shown useful
- Three main types:
 - Based on allele frequencies, e.g. voting uniform crossover
 - Based on segmentation and recombination of the parents, e.g. generalizing *n*-point crossover
 - Based on numerical operations on real-valued alleles, e.g., center of mass crossover, generalizing arithmetic recombination operators