

Neural networks

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– Genetic Algorithms –

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Genetic Algorithms (GA)

◆ Lawrence Fogel

- studied *recombination and mutating* of populations
- *L. Fogel et al.: Artificial Intelligence Through Simulated Evolution, John Wiley and Sons, New York, 1966*

◆ John Holland

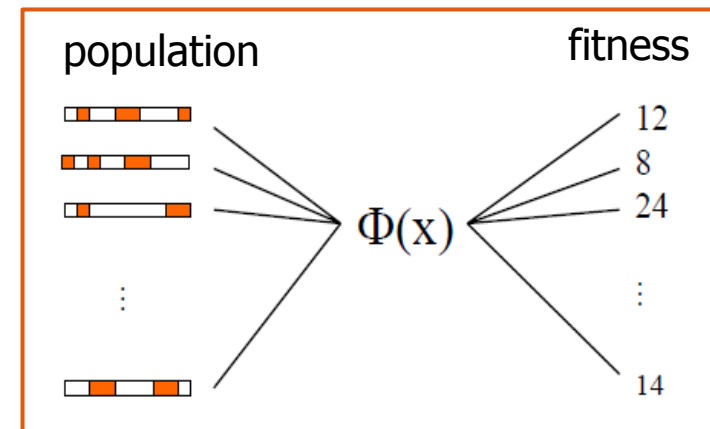
- proposed the *concept of schemata* and studied their diffusion dynamics
- *J. Holland: Adaptation in Natural and Artificial Systems: An Introductory Analysis with Applications to Biology, Control and Artificial Systems, The University of Michigan Press, Ann Arbor, MI, 1975*

◆ David Goldberg

- summarized *evolutionary methods* for the solution of optimization problems
- *D. Goldberg: Genetic Algorithms in Search, Optimization, and Machine Learning, Addison-Wesley, Reading, MA, 1989*

Genetic Algorithms (GA)

- ◆ **Artificial chromosome (genotype)**
 - ~ a string of symbols that code the properties of the individual (phenotype)
 - e.g., a binary value of a variable or their sequence
 - many types of coding – binary, Grey, real values, ...
 - alphabets – binary, ternary, ...
- ◆ **Population**
 - ~ a set of artificial chromosomes that cyclically undergo selective reproduction with random changes
 - more efficient individuals are favoured
- ◆ **Fitness function (performance criterion)**
 - ~ a mapping Φ : genotype $\rightarrow \mathbb{R}$
 - better individuals yield higher values



Genetic Algorithms (GA)

- ◆ **A general genetic algorithm (Goldberg, 1989)**
 - create a population of N randomly generated chromosomes
 x_1, x_2, \dots, x_N
 - repeat
 - decode all the chromosomes and evaluate their fitness, $f_i = \Phi(x_i)$
 - form a new population by means of selective reproduction
 - recombine the chromosomes - crossover
 - mutate the chromosomes
 - until the wanted individual has been found or the fitness of the so-far best individual does not improve

GA: Simple Selection

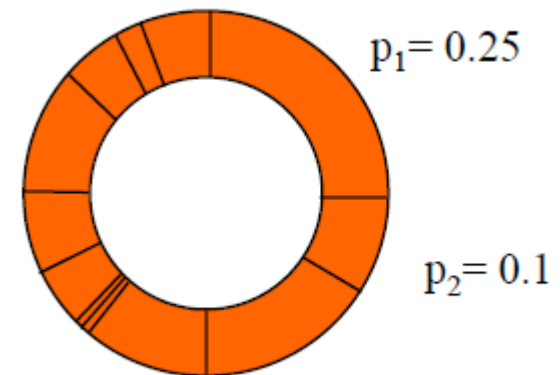
- ◆ a new population is created by copying the chromosomes from the previous population
 - the better is the copied individual, the more copies should be contained in the new population

- ◆ **Roulette wheel selection:**

- the chance of an individual's being selected is proportional to its fitness:

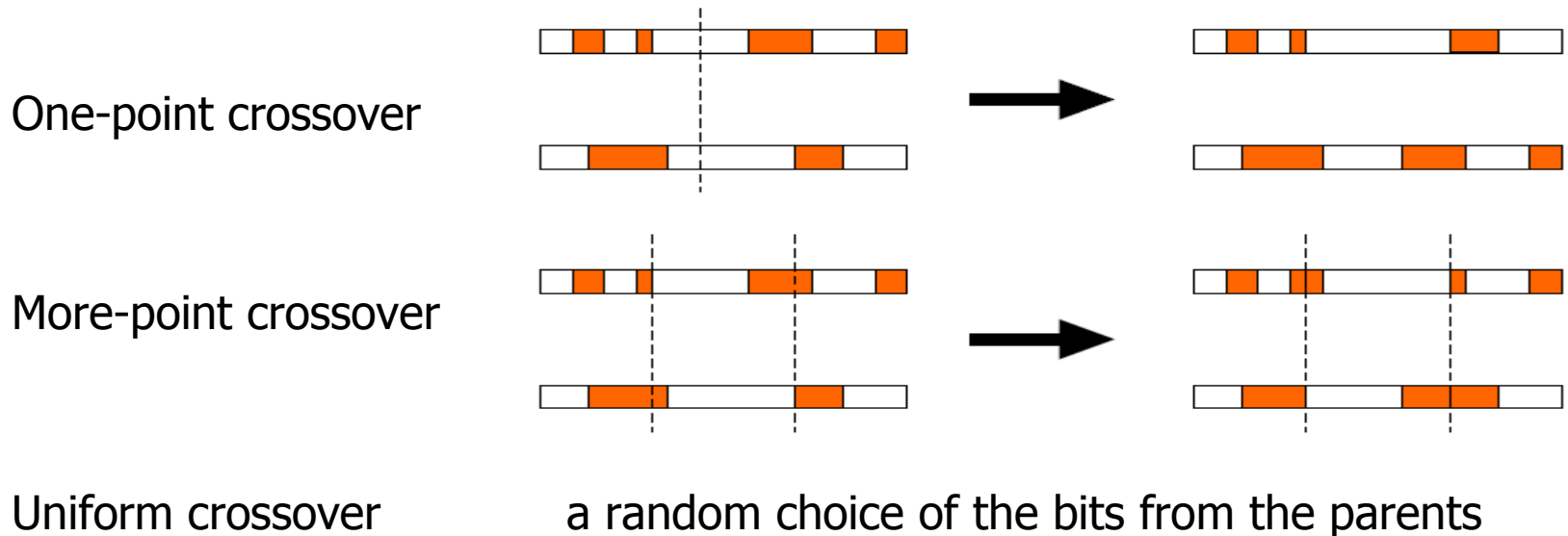
$$P_i = \frac{f_i}{\sum_{j=1}^N f_j}$$

- for a population of N individuals, the roulette wheel will be spun N -times



GA: Crossover

- ◆ individuals are randomly paired
- ◆ each pair of individuals will be „crossed over“ with a given probability



Mutation and distributed GA

◆ Mutation:

- alter each element of the chromosome with a given probability
 - (binary-valued) bits will be negated
 - in the case of other ranges, a randomly chosen value can be used directly or in addition to the original value

◆ Distributed genetic algorithms:

- the individuals of a population are arranged, e.g., into a 2D- space
- selection and crossover proceed only locally, yet individual sub-populations overlap
- this allows to propagate „advantageous“ properties over the entire population

GA: Non-determinism

- ◆ The whole GA is non-deterministic and uses random variables
- ◆ Typically, we are interested in the average and maximum fitness
- ◆ GA stops after the desired fitness value has been achieved, a preset number of generations has been completed or if the fitness did not change during several past generations
- ◆ Afterwards, GA can be run again with other parameters
- ◆ The result represents the best individual selected from final generations over all the GA-runs

GA: Schemata

- ◆ a schema is a mask describing a certain group of strings / chromosomes
 - $1**1 = \{ 1001, 1011, 1101, 1111 \}$; * stands for any allowed value
- ◆ binary strings of length l allow for at most 3^l different schemata
- ◆ a population of N individuals represented by strings of length k yields between 2^k and $N2^k$ schemata
- ◆ a schema may define a property that guarantees high fitness
- ◆ potentially allows to investigate more strings than actually contained within the population
- ◆ GA processes at most N^3 schemata in each step, even if it contains only N strings (an implicit parallelism in GA - Holland, 1975)

GA: Schemata (continued)

- ◆ some schemata yield a higher average fitness
- ◆ long schemata can be easily destroyed: 1*****1 vs. ***01**
- ◆ **short schemata yielding a high average fitness grow exponentially during GA**
- ◆ schemata are considered to be the **basic building blocks** of evolution; crossover represents its main operator as it allows to investigate the combinations of schemata. In this respect, however, appropriate coding is required with short building blocks
- ◆ Note: sometimes, crossover worsens the results – in such a case, its probability shall be set to very small values or zero

GA: Schemata Theorem

- ◆ The **order of the schema** H , $o(H)$, is the number of fixed positions in the schema H (i.e., with values 0 or 1 for a binary alphabet), e.g.:
 - $o(011*1**) = 4$
 - $o(1*****) = 1$
- ◆ The **length of the schema** H , $\delta(H)$, corresponds to the distance between the first and the last fixed position of H :
 - $\delta(011*1**) = 4$
 - $\delta(1*****) = 0$
- ◆ The **schemata theorem analyzes the influence of reproduction, crossover and mutation on the number of strings corresponding to a given schema**

GA - Convergence Analysis: the Influence of Reproduction

The influence of reproduction on the expected number of individuals with a given schema in the population:

- ◆ At time t , the population contains m strings of the schema H ($m=m(H,t)$)
- ◆ During reproduction, a string A_i is selected to the following population (according to its fitness $f_i=\Phi(A_i)$) with the probability: $p_i = \frac{f_i}{\sum_{j=1}^n f_j}$
- ◆ In the following population of the size n , the expected number of strings complying with the schema H ($m=m(H,t+1)$) can be estimated as:

$$m(H, t + 1) = m(H, t) \cdot n \cdot \frac{f(H)}{\sum_{j=1}^n f_j}$$

where $f(H)$ is the average fitness of strings complying with the schema H

GA - Convergence Analysis: the Influence of Reproduction (2)

The influence of reproduction on the expected number of individuals with a given schema in the population (cont.):

- ◆ For the average fitness $f(H)$ of strings complying with the schema H at time t and for the average fitness of the entire population of n strings:

$$\bar{f} = \frac{\sum_{j=1}^n f_j}{n}$$

we obtain: $m(H, t + 1) = m(H, t) \cdot \frac{f(H)}{\bar{f}}$

- **During the fitness-based reproduction, the number of strings complying with a given schema grows / drops in the population according to their average fitness**

GA - Convergence Analysis: the Influence of Crossover

The influence of crossover on the expected number of individuals with a given schema in the population:

- ♦ for each schema, we can assess the probability p_s of surviving crossover as:

$$p_s = 1 - \frac{\delta(H)}{l - 1}$$

- ♦ if crossover is performed randomly with probability p_c , the probability of surviving crossover corresponds to:

$$p_s = 1 - p_c \frac{\delta(H)}{l - 1}$$

- **During reproduction combined with crossover, the number of strings complying with a given schema grows / drops in the population according to the length of the schema and its average fitness:**

$$m(H, t + 1) \geq m(H, t) \cdot \frac{f(H)}{\bar{f}} \cdot \left[1 - p_c \frac{\delta(H)}{l - 1} \right]$$

GA - Convergence Analysis: the Influence of Mutation

The influence of mutation on the expected number of individuals with a given schema in the population:

- ♦ a random change occurs at each position with probability p_m
==> each position survives mutation with probability $1 - p_m$
- ♦ all the respective mutations are mutually independent
- ♦ for a schema, each of the $o(H)$ fixed positions has to survive
==> the probability of surviving mutation is for schema H :

$$(1 - p_m)^{o(H)}$$

- ♦ approximation for very small values of p_m ($\ll 1$):

$$(1 - p_m)^{o(H)} \sim 1 - o(H) p_m$$

GA - Convergence Analysis: the Influence of Mutation (2)

The influence of mutation on the expected number of individuals with a given schema in the population (cont.):

- ♦ The expected number of strings complying with schema H in the population after reproduction, crossover and mutation:

$$m(H, t + 1) \geq m(H, t) \cdot \frac{f(H)}{\bar{f}} \cdot \left[1 - p_c \frac{\delta(H)}{l - 1} - o(H) \cdot p_m \right]$$

- **During reproduction combined with crossover and mutation, the highest chance to survive possess short schemata with few fixed positions and above-average fitness**