

Assignment 44

Since the position where the cross-over points may vary, the number of possible offsprings varies with the length L of the genome. We have:

| L | Offspring |
|---|-----------|
| 1 | 2 |
| 2 | 4 |
| 3 | 8 |
| 4 | 14 |
| 5 | 22 |

Table 1: number of legal offsprings with varying length of genome

This is expressed via the following formula: $Z = L^2 - L + 2$. For $L = 64$: $Z = 4034$. ■

Assignment 45

A binary genome of length L can be represented by a hypercube of dimension L of unit edge length. Every bit of the genome corresponds to an axis of the hypercube. Since the hypercube has unit edge length and the genome is binary, a genome corresponds to a specific corner of the hypercube. This is depicted for the three-bit-genomes $(0,0,1)$, $(1,1,0)$, $(1,0,1)$ in figure (1). ■

Assignment 46

Generating all possible sequences of L is equivalent to finding all permutations of L . Since every permutation can be expressed as a product of transpositions (the swapping of two elements), the algorithm can generate all sequences. ■

Assignment 47

$$Pr[\text{"a specific bit is not flipped"}] = 1 - p$$

$$Pr[\text{"L bits are not flipped"}] = (1 - p)^L$$

$$Pr[\text{"at least one of L bits is flipped - change in genome"}] = 1 - (1 - p)^L$$

$$Pr[\text{"at least one of L bits in N individuals are flipped"}] =$$

$$Pr[\text{"none are identical to parent"}] = (1 - (1 - p)^L)^N$$

$$Q = (1 - (1 - 0.01)^{100})^{20}$$

$$= 0,00011$$

■

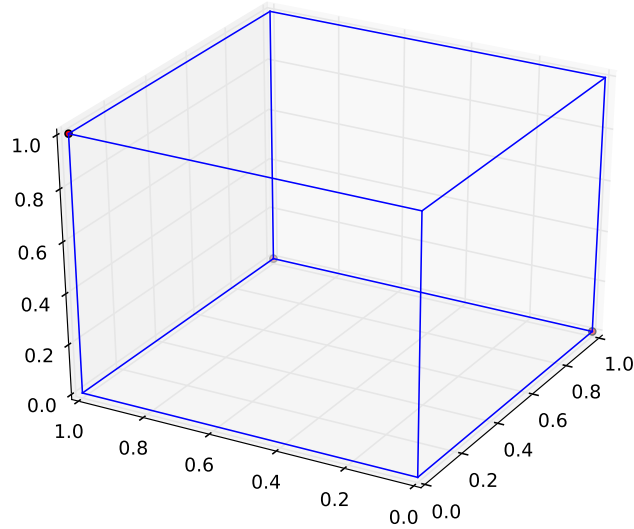


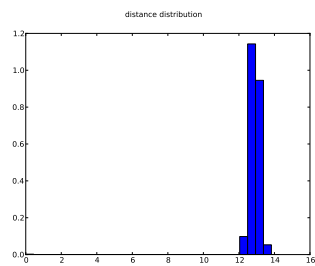
Figure 1: representation of three-bit-genomes by an three dimensional hypercube

Assignment 48

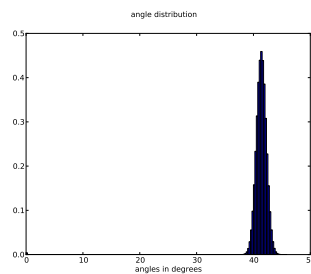
External selection selects the individuals to "survive", while the rest of the population is discarded. *Parent selection* selects those "survivors" which will generate new offspring to replenish the population. ■

Assignment 49

For an experimental run, we find a mean distance of: 12.8903802695 and the following distributions for angles and distances. Maximal hamming distance: 1000. Maximal distance $\sqrt{1000} \approx 31.623$.



(a) distance distribution



(b) angle distribution