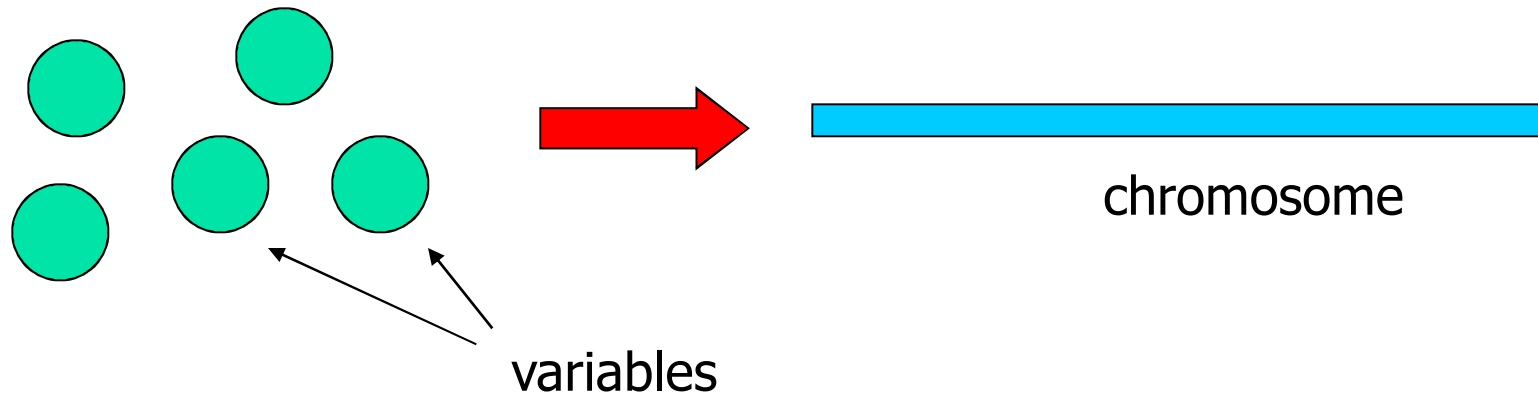


Artificial Intelligence 2, Lecture 2, 20101111

Basics of evolutionary algorithms

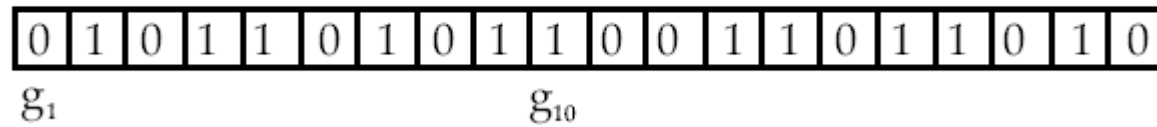
Encoding: the variables of the problem are encoded in strings of digits known as *chromosomes*.



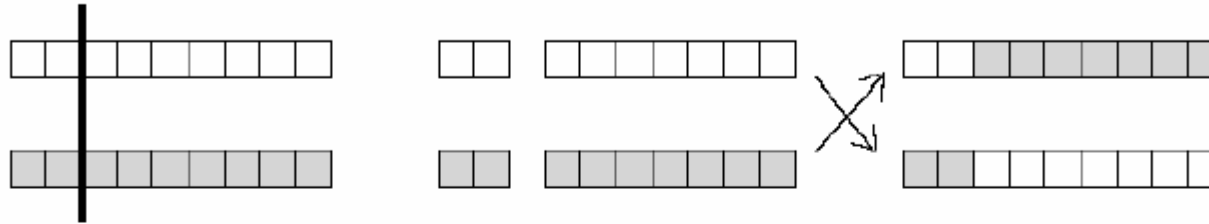
The exact encoding procedure varies from problem to problem – in the simple case of optimization of a function $f(x_1, x_2, x_3, \dots, x_n)$ the variables x_i , $i = 1, \dots, n$ should be encoded. In more complex problems (e.g. optimization of artificial brains for robots or optimization of neural networks), the specification of the encoding procedure can be much more complicated.

Random initialization of a population containing N chromosomes

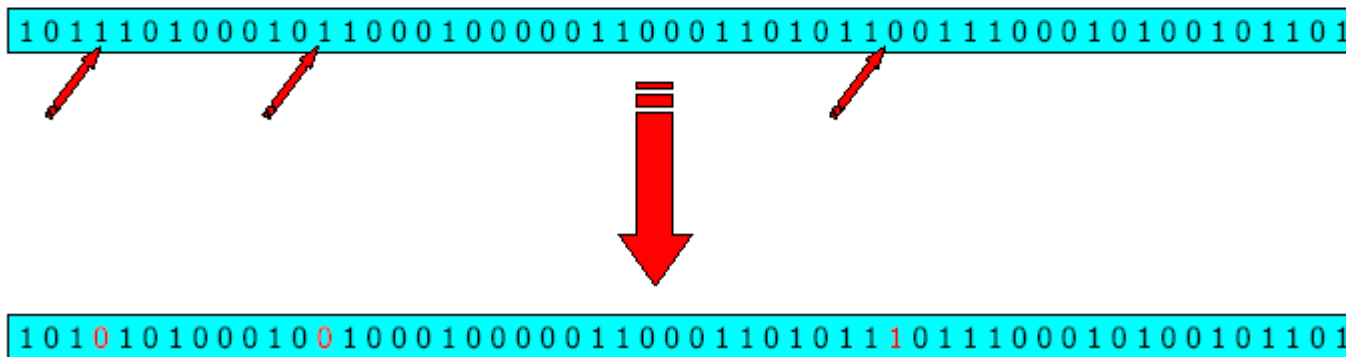
1	0 1 0 1 1 0 1 1 1 0 1 0 1 1 1 0 1 1 0 0 0 1 0 1 0 1 1 0 1 0 0 1 1 0 1 0 1 1 1 1 0 0 0 1 0 1 0 0 1 0 1 1 0 1
2	1 0 1 1 1 0 1 0 0 0 1 0 1 1 0 0 0 1 0 0 0 0 0 1 1 0 0 0 1 1 0 1 0 1 1 0 0 1 0 1 0 0 0 0 1 0 1 1 0 0 0 1 1 0
3	0 1 0 1 1 1 0 1 1 1 1 1 0 0 1 0 1 1 0 0 0 0 1 0 0 1 1 0 1 0 0 1 1 0 1 0 1 0 0 0 1 1 1 0 1 0 1 1 0 0 0 1 0 1
	...
N	0 1 0 1 1 0 1 1 1 0 1 0 0 0 1 1 1 0 1 1 1 0 1 1 0 1 0 0 1 0 0 1 1 0 1 0 1 1 1 1 0 0 0 1 1 1 0 0 0 0 0 0 0 1

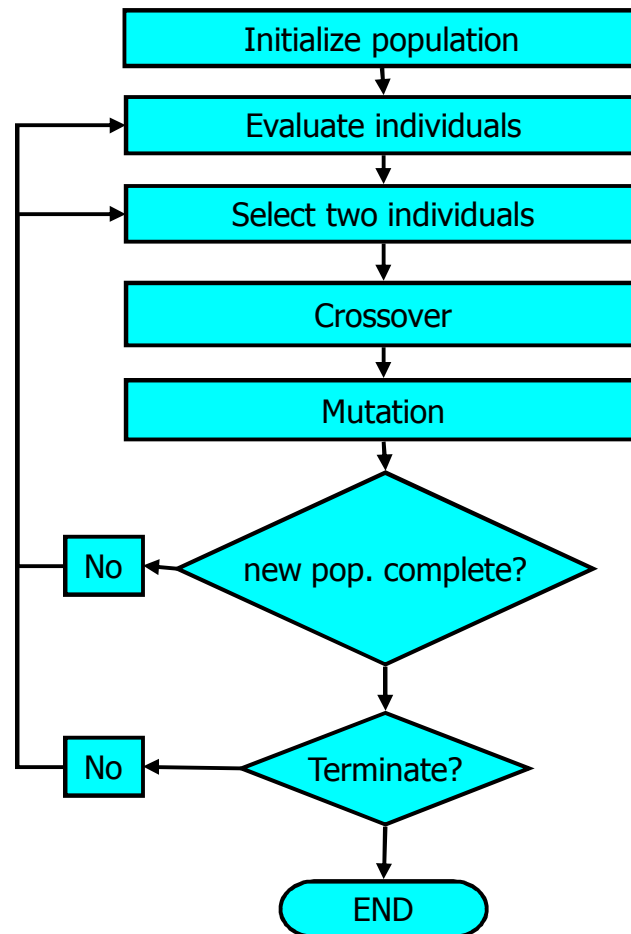


Crossover



Mutation





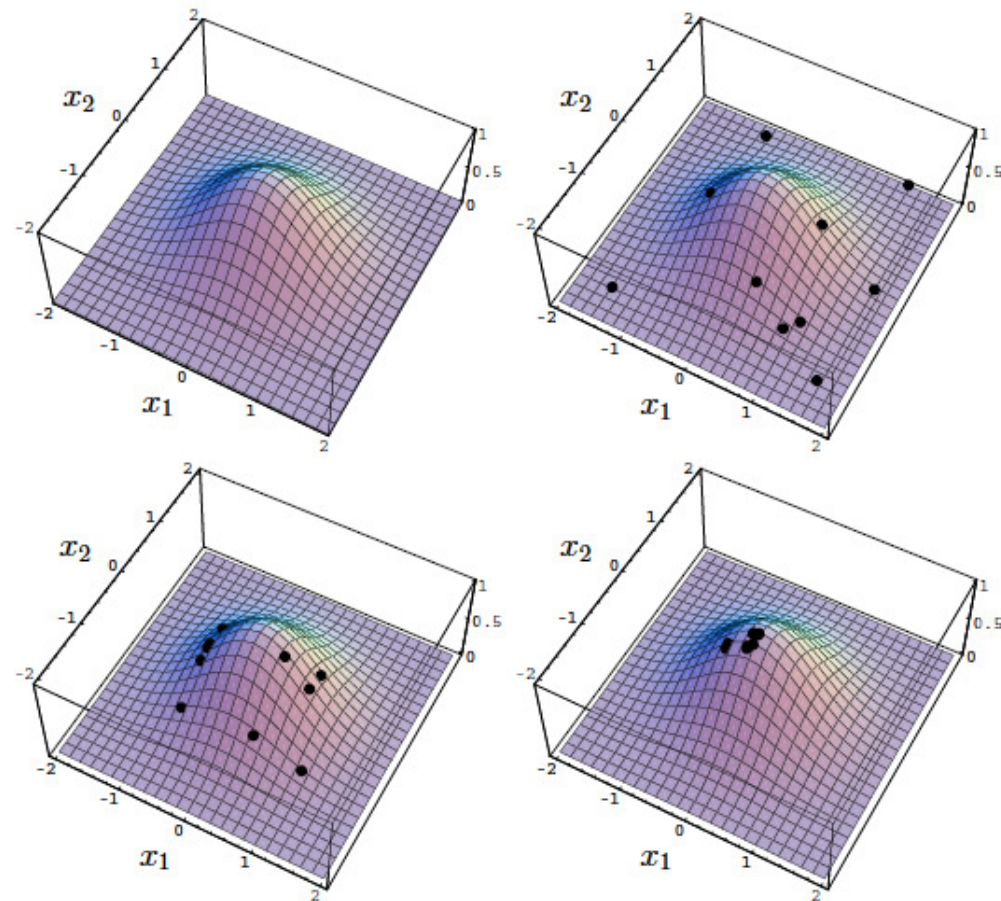
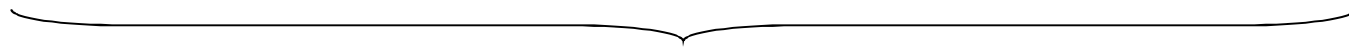


Figure 3.7: The progress of a GA searching for the maximum of the function $f(x_1, x_2) = e^{-x_1^2 - x_2^2}$. The upper right panel shows the initial population, whereas the lower left and lower right panels show the population after two and 25 generations, respectively.

1	0	0	1	0	1	1	1	1	0	0	1
---	---	---	---	---	---	---	---	---	---	---	---



$$x = -d + \frac{2d}{1 - 2^{-k}}(2^{-1}g_1 + \dots + 2^{-k}g_k),$$

0.465148391133	0.953185830213	0.159105940423
----------------	----------------	----------------



$$x = -d + 2dg,$$

0 1 0 1 1 0 1 1 1 0 1 0 1 1 1 0 1 1 0 0 0 1 0 1 0 1 1 0 1 0 0 1 1 0 1 0 1 1 1 1 0 0 0 1 0 1 0 0 1 0 1 1 0 1

x

y

0.34215678 0.34767614 0.75636461 0.77663421 0.91893711 0.01375721 0.67485732

x_1

x_2

x_3

x_4

x_5

x_6

x_7

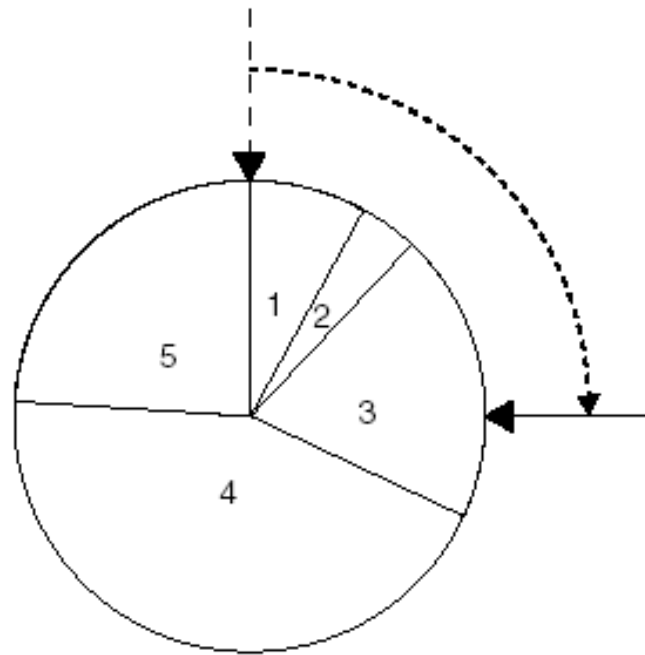


Figure 3.8: *Roulette-wheel selection in a population consisting of five individuals, described in detail in Example 3.3.*

Roulette wheel selection

Example 3.3 (p. 49)

- Individual 1: $F_1 = 2.0$
- Individual 2: $F_1 = 1.0$
- Individual 3: $F_1 = 5.0$
- Individual 4: $F_1 = 11.0$, etc.
- Individual 5: $F_1 = 6.0$

$$\sum_{i=1}^5 F_i = 25$$

- Example: $r = 0.25 \Rightarrow j = 3$ etc.

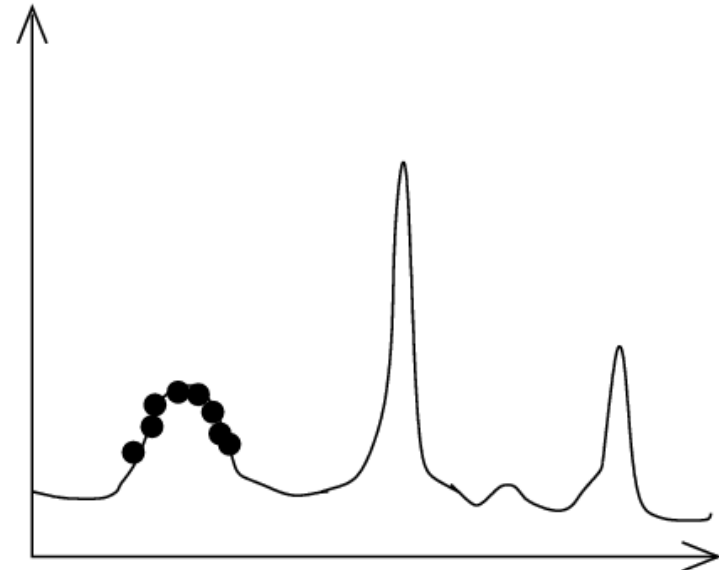
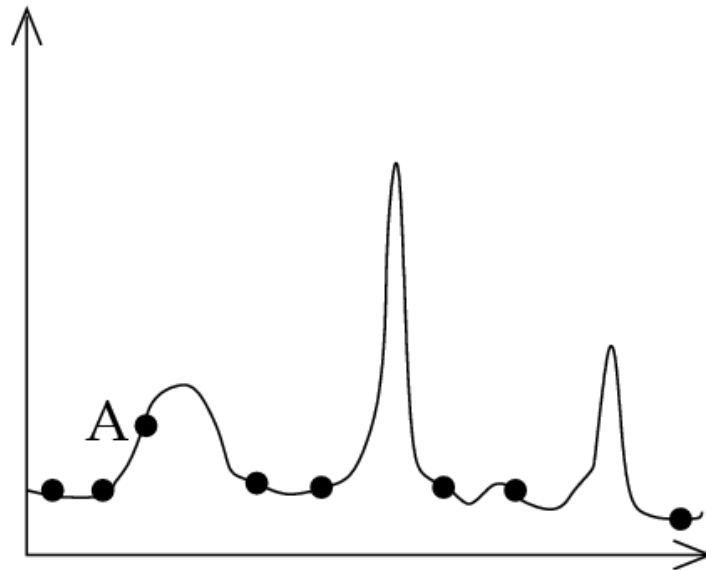
$$\begin{aligned} \phi_1 &= 0.08, & \swarrow & 2/25 \\ \phi_2 &= 0.08 + 0.04 = 0.12, \\ \phi_3 &= 0.32, & & (0.12 + 0.20) \end{aligned}$$

(1, 1)	(1, 2)	(1, 3)	(1, 4)	(1, 5)
(2, 1)	(2, 2)	(2, 3)	(2, 4)	(2, 5)
(3, 1)	(3, 2)	(3, 3)	(3, 4)	(3, 5)
(4, 1)	(4, 2)	(4, 3)	(4, 4)	(4, 5)
(5, 1)	(5, 2)	(5, 3)	(5, 4)	(5, 5)

Figure 3.9: *Tournament selection, with tournament size equal to two, in a population consisting of five individuals, described in detail in Example 3.4.*

$$p_1 = \frac{1}{25}(1 + 2p_{\text{tour}} + 6(1 - p_{\text{tour}})) = \frac{1}{25}(7 - 4p_{\text{tour}}) = 0.152.$$

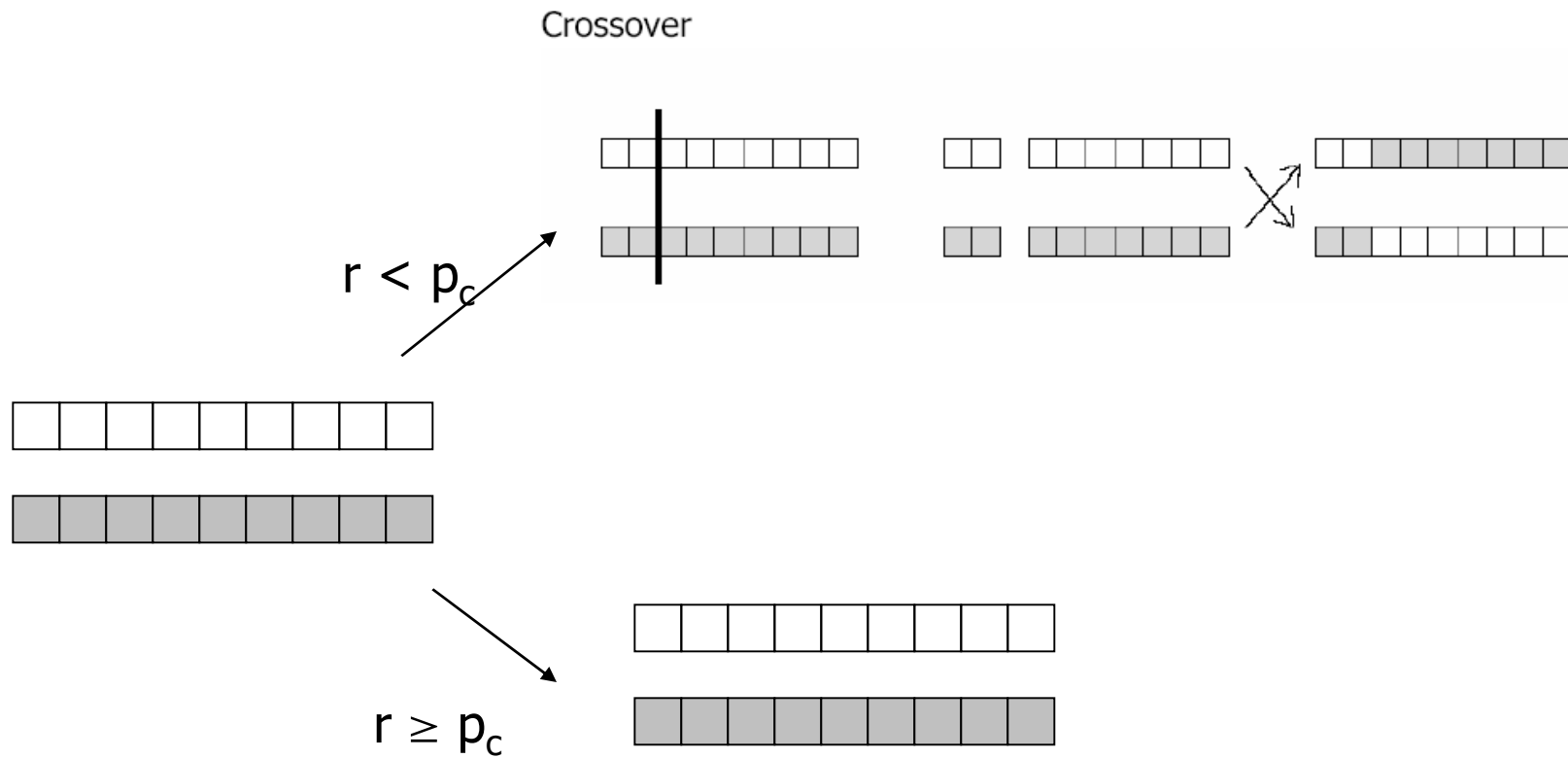
Premature convergence:



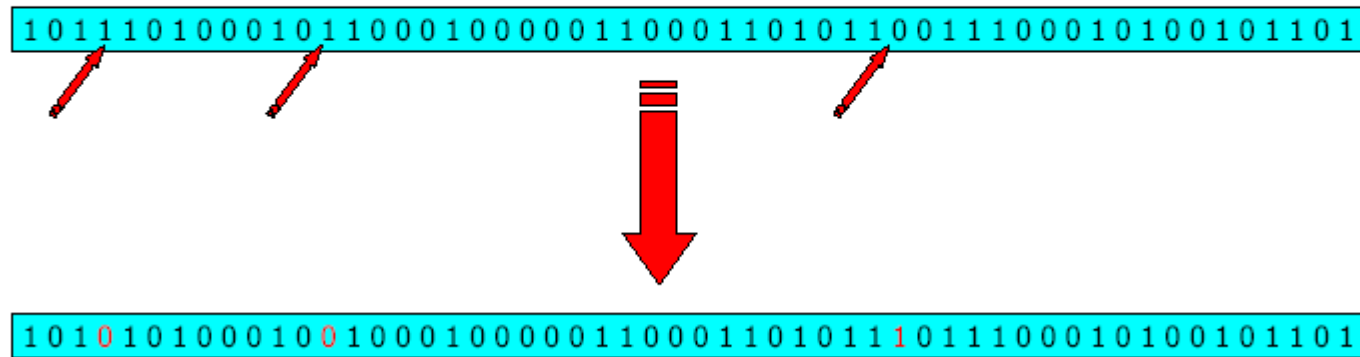
Fitness ranking:

$$f(i) = (N + 1 - R(i)).$$

$$f(i) = f_{\max} - (f_{\max} - f_{\min}) \left(\frac{R(i) - 1}{N - 1} \right).$$

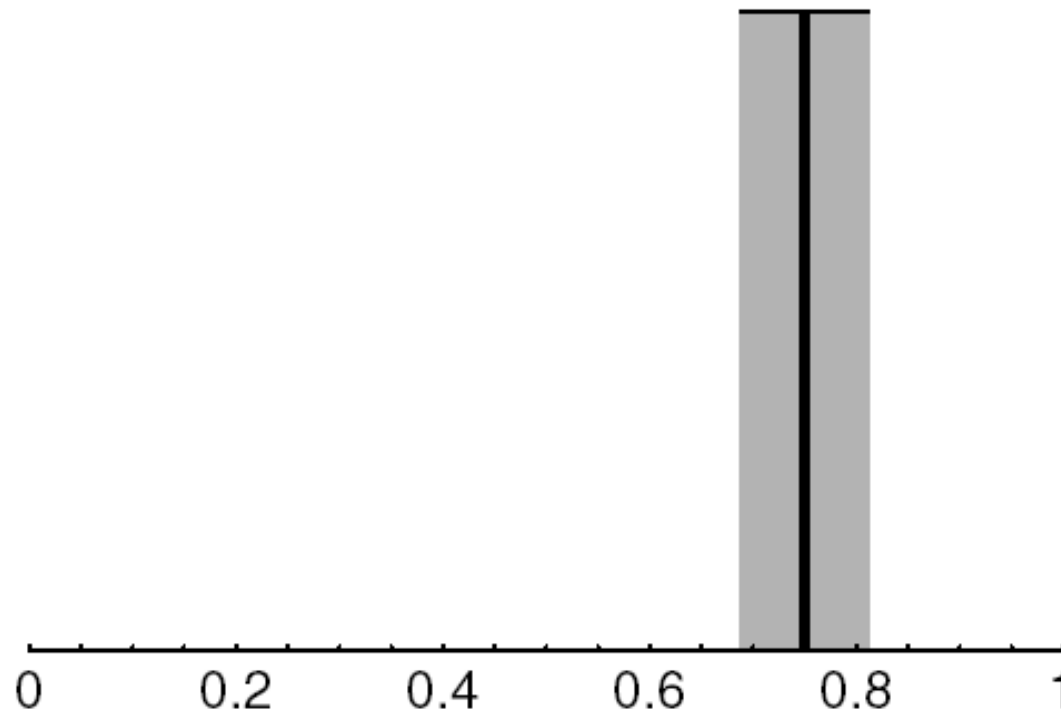


Mutation



Note: EVERY gene is checked. If, for a given gene, $r < p_{mut}$, the gene mutates ($r \in [0,1]$).

Typical value for p_{mut} : $\sim 1/m$, where m is the number of genes in the chromosome.



(Uniform) creep
mutation

Creep mutations: (example of implementation, in connection with real-number encoding)

0.23131541	0.59182321	0.98148176	0.01987612	0.59176192	0.19857612
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For each gene, check(as usual) whether or not the gene should be mutated (using p_{mut})

If the gene should be mutated, check whether or not creep mutations should be used (using p_{creep})

If yes, carry out a creep mutation:

$$g \rightarrow g' = g - C_r/2 + C_r r \quad (\text{example})$$

If no, carry out an ordinary mutation:

$$g \rightarrow g' = \text{rand}$$