

- |  | TRUE                     | FALSE                    |
|--|--------------------------|--------------------------|
| 1. It is important to make the right choice between binary and real-number encoding, for a given optimization problem.   | <input type="checkbox"/> | <input type="checkbox"/> |
| 2. In tournament selection, the number of individuals participating in a tournament is always equal to two.  | <input type="checkbox"/> | <input type="checkbox"/> |
| 3. In some cases, after selecting two individuals, one does not carry out crossover.   | <input type="checkbox"/> | <input type="checkbox"/> |
| 4. During mutations (in GAs) each gene is considered separately, so that the number of mutations can, in principle, be anything from 0 to $m$ (= the number of genes). | <input type="checkbox"/> | <input type="checkbox"/> |

1. Not really – There is no evidence that one encoding scheme provides (generally) faster convergence than the other. Often, real-number encoding is used for simplicity, at least if the number of variables is large enough (more than 10, say) to allow crossover to operate as it should.

2. This is FALSE. The size of the tournaments can be generalized to any positive integer  $\geq 2$  (up to the population size), even though two is the most common tournament size. See p. 50 for a description of how to implement tournament selection in cases where tournament size is larger than two.

3. This is TRUE. Crossover, which is a very efficient operator, is only carried out with a certain probability (the crossover probability), to avoid premature convergence; see p. 53 and pp. 68-69. In cases where crossover is not carried out, the two selected individuals are subjected only to mutation before being inserted in the new population.

4. Yes, this is TRUE. During mutation, one runs through each chromosome gene by gene, checking whether or not the current gene should be mutated. Thus, in principle, the number of mutations can be anything from 0 to  $m$ , even though, typically, the mutation rate is set to a small value (usually  $1/m$ ) so that, on average, only a few mutations (or zero) occur.