Seminario de Investigación

Curso 2017-18

Miércoles 28 de febrero, 16:00 – Sala de Grados.

“Computing Translocation Distances”

Ponente: Victor Mitrana (profesor de la UPM)

Exercise: tick the correct answer

1. Uniform translocation means
   - [ ] the two chromosomes exchanges prefixes with each other
   - [ ] the two chromosomes exchanges prefixes of the same length with each other
   - [ ] the two chromosomes exchanges suffixes with each other

2. The translocation distance between two genomes with chromosomes of the same length and without duplications is computed by an algorithm that is
   - [ ] exact and linear
   - [ ] exact and exponential
   - [ ] approximative

3. A contiguous sequence of translocations means that any translocation can be applied to:
   - [ ] any pair of chromosomes
   - [ ] one of the two chromosomes is an initial chromosome
   - [ ] two chromosomes such that each of them has an available copy
4. The translocation distance for a singleton target set is based on the:
   - greedy strategy
   - dynamical programming
   - heuristic strategy

5. What is the difference between the algorithms for computing the translocation distance for a singleton target set and a multiple target set:
   - both have polynomial time complexity
   - one is exact while the other is approximative
   - both are approximative

Enviar el cuestionario resuelto a jlacalle@etsisi.upm.es