



POLITÉCNICA



Universidad
Politécnica
de Madrid

ETSI SISTEMAS
INFORMÁTICOS

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