



POLITÉCNICA



Universidad
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**ETSI SISTEMAS
INFORMÁTICOS**

**Máster Universitario en
Ciencias y Tecnologías de la Computación
Curso 2017-18
Seminario de Investigación**

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

“Computing Translocation Distances”

Ponente: Victor Mitrana (*profesor de la UPM*)

Resumen:

A basic problem in the area of combinatorial algorithms for genome evolution is to determine the minimum number of large scale evolutionary events (genome rearrangements) that transform a genome into another. We consider two translocation operations suggested by the genome rearrangements. In this talk chromosomes are viewed as being linear strings that exchange each other prefixes in the translocation process. We define a distance between a pair of multichromosomal genomes and examine the complexity of computing this distance in the case of uniform translocation. Our work differs from previous approaches in several respects: the strings representing chromosomes may have multiple occurrences of the same symbol, they may have common symbols, the number of copies of all strings in the initial set is assumed arbitrarily large. One exact algorithm and one approximation algorithms, both of them based on greedy strategies, are discussed. We present an exact polynomial algorithm when the target set is a singleton while a 2-approximation algorithm is provided when considering arbitrary target sets. Some open problems are finally formulated.