



UNIVERSITÀ
di VERONA

Scuola di Dottorato
di SCIENZE NATURALI
ED INGEGNERISTICHE

LECTIO MAGISTRALIS

“Genome Rearrangement by Double Cut and Join”

May 14, 2018 - h. 15.00

Jens Stoye

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Abstract:

Genome evolution on the basis of gene order has been modeled by a variety of rearrangement operations such as inversions, translocations, transpositions, block interchanges, fusions and fissions. The double cut and join (DCJ) operation, introduced by Yancopoulos et al. (2005), allows to model all these classical operations while allowing for very simple algorithms, compared to earlier ones for more restricted models.

We will present several algorithmic results related to genome rearrangement based on the DCJ model: calculation of the distance between two genomes, construction of an optimal scenario transforming one genome into another one, and counting and sampling from the set of all optimal rearrangement scenarios. We will also show how, by small adaptations, other rearrangement distances can be computed easily based on the DCJ model. Finally, we will discuss generalizations for cases where the genomes under study do not have the same gene content. This setting also raises some interesting mathematical modeling questions about the weight of insertions and deletions in genomic distances.

This is joint work with Anne Bergeron, Marília D. V. Braga, Paul Medvedev, Julia Mixtacki, and Eyla Willing.

The lecture will take place **at 15.00 – Sala Verde – Cà Vignal 3 – Strada Le Grazie, 15**

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Students attending this lecture are entitled to 1 CFR valid for the specific activities of the Graduate School.

Short bio

Jens Stoye received his PhD in Computer Science from University of Bielefeld in 1997, defending a thesis on multiple sequence alignment. After postdoctoral positions at the University of California at Davis and the German Cancer Research Center in Heidelberg, he became the head of the Algorithmic Bioinformatics Group at the Max Planck Institute for Molecular Genetics in Berlin. In 2002, he returned to Bielefeld University as professor of Genome Informatics at the Faculty of Technology, serving twice as Dean of the Faculty of Technology (2007-09 and 2010-13). His current research interests are algorithmic bioinformatics and the development of computational methods for biological sequence analysis and comparative genomics. He has published more than 150 papers (receiving about 7000 citations, more than 700 for the most cited article), which appeared in the top venues in computational biology, bioinformatics, computer science, and stringology. He is on the steering committee of WABI and has served as programme committee member (including as chair) of the main conferences in algorithmic stringology (CPM, SPIRE), computational biology and bioinformatics (WABI, RECOMB, ISMB, ECCB, RECOMB-CG), as well as theory and algorithms (LATA, ESA, ALENEX). He is associate editor of IEEE/ACM Transactions on Computational Biology and Bioinformatics and BMC Bioinformatics. He has supervised more than 30 PhD theses.