Workshop

Organizators: J. Hesser, C. Cremer

Topic:

Computational Methods in the Nanoscopy of Supramolecular Biological Complexes

Program

Part A: Molecular Level

9:00-9:30 Introduction and Bioinformatics in Mannheim, J. Hesser, ICM, Univ. Mannheim & Heidelberg
9:30-10:00 Computer Simulation of Protein Dynamics and Function, J. Smith, Univ. Heidelberg
10:00-10:30 Improving Protein Structure Prediction with Additional Experimental Data, Mario Albrecht, MPI Saarbrücken

10:30-11:00 Coffee-Break

Part B: Supramolecular Level

11:00-11:10 Introduction, C. Cremer, KIP Univ. Heidelberg
11:10-11:30 Chromosome territory arrangements and dynamics on large scales: a computer model approach, Gregor Kreth, KIP Univ. Heidelberg
11:30-12:00 Chromatin Complexes, Tobias Knoch, DKFZ Heidelberg
12:00-12:30 Brownian Dynamics Simulation of human nuclei using the Spherical 1-Mbp Chromatin Domain model, Nick Kepper, KIP Univ. Heidelberg

12:30-14:00 Lunch

Part C: Computational Methods

14:00-14:05 Introduction. G. Steidl, Univ. Mannheim
14:05-14:30 Deconvolution for Microscopy Images, O. Krivonos, ICM, Univ. Mannheim & Heidelberg
14:30-15:00 Volume Graphics, J. Hesser, ICM, Univ. Mannheim & Heidelberg
15:00-15:30 Boundary conditions and fast deblurring algorithms, G. Steidl, Univ. Mannheim
15:30-15:35 Conclusions (J. Hesser, C. Cremer)

15:35-16:00 Coffee-Break

16:00-17:00 Laboratory visit