

Open Symposium: Multi-scale simulation of living organisms: from genomes to entire human organs

Massive DNA sequencing, genomic transcription, and functional genomic transcription projects help us decipher the action mechanisms of human genes. Furthermore, proteomics, and molecular modeling tools are increasing the knowledge on protein functions within the cell. Finally the integration of medical data in biomechanical and neuroinformatic models allows us to make rational representations of organs which work for customized simulations. This dense knowledge at different scales is a major challenge in computing, which in turn opens the opportunity for innovation in future medical therapies.

In this open symposium several research leaders in the field of computing and life sciences will discuss multi-scale simulation in the computer models that allow us to study living organisms. They will discuss the current state and future expectations of human simulations and the technical aspects of simulation and genomics.

Date: Thursday, September 19 from 15:00 pm to 18:30 pm.

Location: CosmoCaixa. C / Isaac Newton, 26, of Barcelona.

Program

15:00 – 15.40 Henry Markram, École Polytechnique Fédérale de Lausanne

15:40 – 16.20 Jan Korbel, EMBL, Heidelberg

16:20 - 16:40 Coffee Break

16:40 – 17.20 Alfonso Valencia, CNIO, Madrid

17:20 – 18.00 Peter Coveney, University College London

18:00 - 18:30 Open debate, moderated by Dr. Orozco, director of the joint research program in computational biology IRB-BSC

Free registration is now open. The symposium will be held entirely in English.

The symposium, jointly organized by B- Debat and joint research program in computational biology IRB-BSC, is part of the B-Debate event "Towards in Silico Human. A Challenge for Exascale Computing Area", that will take place from 18th to 20th of September in CosmoCaixa.

Event Homepage:

<http://www.biocat.cat/agenda/open-symposium-multiscale-simulation-living-organisms-genomes-entire-human-organs>

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