



University
of Basel

Department
Biozentrum



Swiss Institute of
Bioinformatics

BIOZENTRUM

The Center for
Molecular Life Sciences

Basel Computational Biology Seminar

21563 Current research in Bioinformatics II



Mikhail Gelfand

Chromatin structure: from individual observations to a neural network

I will briefly start with several studies on model objects, including single-cell HiC in *Drosophila*, and developmental series of Dictyostelium and Danio rerio, and turn to a unified view of the chromatin structure based on a deep neural network representation. Chimaera is a convolutional neural network that predicts Hi-C maps from DNA sequences. Its latent representations yield an unsupervised atlas of key chromatin features (such as insulation, loops, fountains/jets) and allow one to quantify structural signatures in processes such as the cell cycle and embryogenesis. Targeted search in the latent space and other techniques link DNA sequence elements to specific chromatin structures. Applying Chimaera across multiple species confirmed the insulator roles of CTCF in vertebrates and BEAF-32 in *Drosophila melanogaster* and identified a previously unreported insulator motif in *D. melanogaster*. In Dictyostelium and other organisms, loop formation is influenced by gene orientation on the DNA strand.



Event Details

Date: Monday, March 23, 2026

Time: 16:15 – 17:15 h

Location: Biozentrum, U1.197

Host: Aleksei Mironov

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