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SFB 680
Molecular Basis of
Evolutionary Innovations

Mapping chromatin organisation in 4D

I discuss the current picture of chromosome spatial organization emerging from HiC or our recent GAM technology in mouse and human cells and tissues. We mapped chromatin contacts, in particular, during neuronal differentiation. We found that the genome is folded in a hierarchy of domains-withindomains. The higherorder organization extends across genomic scales and correlates with epigenomic features, highlighting a functional role of the spatial organization. Next, I discuss how architecture data and folding mechanisms can be understood by basic polymer physic (PRISMR). Using the EPHA4 locus as a model, I show that the effects of pathogenic mutations can be predicted. PRISMR accurately predicts the alterations of architecture and the rewiring of enhancer-promoter interactions, causing disease by gene misexpression. That opens the way to novel diagnostic methods.

Tuesday, January 09, 2018, 12:00
University of Cologne, Institute for Genetics
Lecture hall 4th floor
Hosted by Thomas Wiehe