

**Monday, 23 May 2022**

Format: Online via ZOOM, at 16:15

**Towards a quantitative understanding of long-range transcriptional regulation****Luca Giorgetti, PhD**Friedrich Miescher Institute for Biomedical  
Research, Basel, CH [www.fmi.ch](http://www.fmi.ch)

*In mammals, the control of gene expression relies on tens of thousands of enhancer sequences that are differentially active in every cell type. Enhancers engage with target promoters often from large genomic distances and govern their spatio-temporal and quantitative expression dynamics. Genetic variation within these noncoding regions is a major driver of evolution, but is also causal to developmental disorders and numerous human diseases. Despite their central role in gene regulation in health and disease, however, the principles by which enhancers select and control their target genes remain largely unknown. What are the molecular mechanisms that transmit regulatory information from an enhancer to a promoter? How are they related to chromosome structure and physical interactions between enhancers and promoters? Are these mechanisms universal or rather depend on locus- and tissue-specific contexts? My group addresses these fundamental questions at the interface of molecular biology and biophysics using a tight interplay of experimental and theoretical approaches. In my talk, I will present how using a combination of genomic engineering, physical modeling and live-cell imaging we recently discovered that a promoter's transcription level are a nonlinear function its contact probabilities with a cognate enhancer, and how this could arise from dynamic and unstable physical interactions between enhancers and promoters.*

