Cologne Evolution Colloquium

SFB 680 Molecular Basis of Evolutionary Innovations

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Decoding the regulatory genome in Escherichia coli with base pair resolution

Organisms across all domains of life must make regulatory decisions in response to a changing environment. The decision about when and where to turn on transcription is largely controlled through the binding of transcription factors to regulatory regions of DNA. However, even for the organism Escherichia coli, whose regulation is arguably best understood, the details of the regulatory code are unknown for nearly half of its genes. Even in those cases where the regulatory features are known, a quantitative understanding of input-output response in terms of elementary protein-DNA and protein-protein interactions is almost always lacking. I will present an approach using Sort-Seq to identify and quantitatively model regulatory architectures. Sort-Seq combines flow cytometry and deep sequencing in order to measure the transcriptional activity of thousands to millions of a partially mutagenized E. coli promoter within a single experiment. This provides base pair resolved information about a promoter's regulatory landscape and enables inference of quantitative energy models that describe the different protein-DNA interactions. I will discuss work using this approach to probe several promoters in E. coli.

Thursday, June 22, 2017, 11:00

University of Cologne, Institute for Theoretical Physics

Conference Room 2, Ground Floor

Hosted by Michael Lässig