Cologne Evolution Colloquium

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Evolving complex promoters for complex phenotypes

To predict long-term patterns of evolution, knowledge of global genotype-phenotype map is required. Traditionally, such maps were postulated theoretically to provide qualitative insights into plausible evolutionary trajectories and speed of adaptation, based on a few controllable parameters, e.g., the strength and type of epistasis. Unfortunately, it is difficult to connect such toy model landscapes to empirical data. In contrast, empirically measured genotype-phenotype maps suffer from a curse of dimensionality and sample only a tiny region of genotype space. I will introduce past work and present our recent efforts to construct a good approximation to global genotype-phenotype maps for promoter sequences. The central claim is that biophysical laws on how transcription factors bind promoters — which we understand reasonably well — provide strong constraints on the form of genotype-phenotype maps. It is therefore possible to derive the global genotype-phenotype maps and calibrate them to either precision or high-throughput measurements of promoter mutant libraries, which I will illustrate for constitutive and regulated promoters in E. coli. As a result, we can try to answer fundamental evolutionary questions such as “How long would it take to evolve a strong promoter from a random sequence?”, “How many possible strong promoter sequences are out there?”, and others.

Wednesday, January 20, 2021, 17:00
Institute for Biological Physics
Online via Zoom

Hosted by Michael Lässig

CRC 1310 Predictability in Evolution