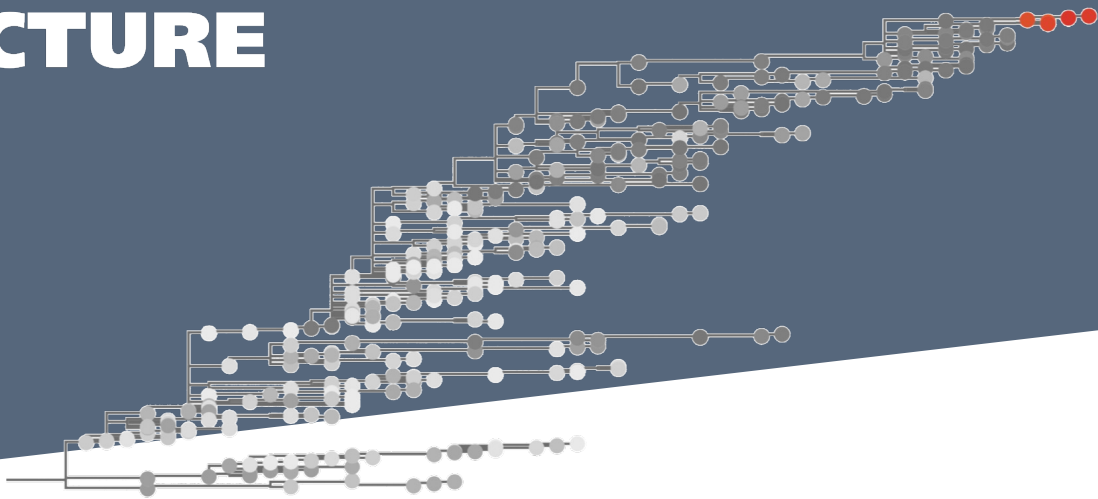


MAX DELBRÜCK LECTURE



Predicting ecological function: Insights from genetic landscapes

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Given a list of candidate microbial species, which community should one form to optimize a target function? To answer this question, we must develop predictive quantitative models of community function, but doing so has been difficult due to the complex web of interactions that take place in most communities. To address this challenge, we are drawing inspiration from the theory of quantitative genetics, in particular the concept of global epistasis on fitness landscapes. We find that similar to genetics, community function follows simple, predictable patterns as a result of widespread interactions. These simple patterns allow us to learn the quantitative map between community composition and function in synthetic consortia and rationally optimize their function. Our work seeks to place the goals of engineering biological function across scales, from the molecular to the organismal to the ecological, under a common theoretical and methodological framework that can lead to the flow of ideas and methodologies across fields.

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Institute for Biological Physics
Seminar Room S0.02, Zùlpicher Str. 77a

Hosted by G. Petrunaro & M. Lässig