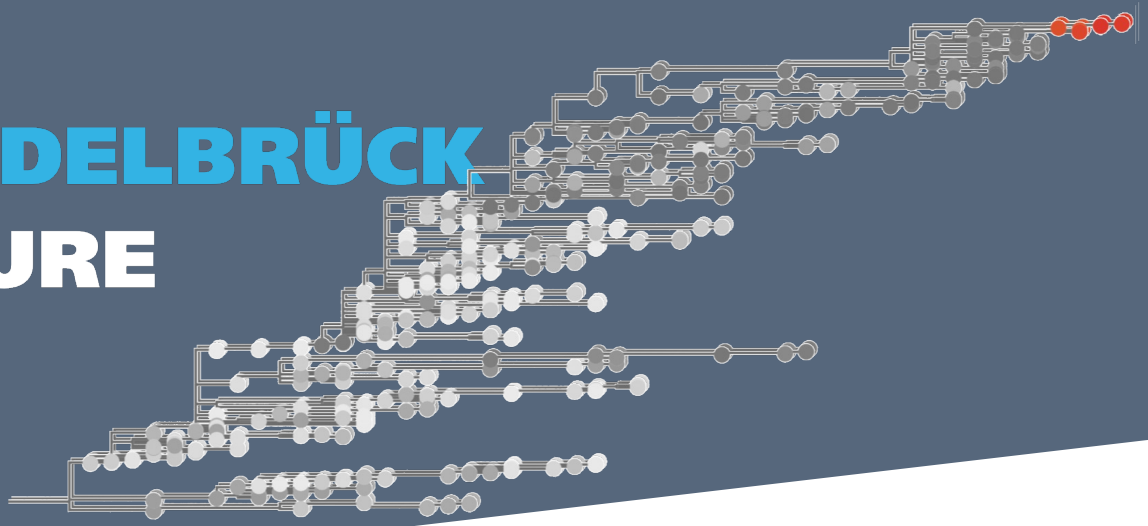


# MAX DELBRÜCK LECTURE



## A molecular odyssey: Blind searches in genotype spaces and efficient adaptation of viral populations

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The exploration of vast genotype spaces poses a major challenge to evolving populations. As the number of genotype sequences representing viable phenotypes grows exponentially with genome length, understanding how populations navigate and adapt within such spaces becomes paramount. In this contribution, we delve into the dynamics of populations within genotype spaces using data from the environmental adaptation of populations of a small phage infecting *E. coli* (Qbeta phage) and SARS-CoV-2 genomes. Despite the vastness of the spaces they have in principle access to, even the largest realizable viral populations cover only a tiny fraction of possible sequences, constrained by a local, blind exploration of the nearest attainable. We explore how these populations achieve phenotypic improvements and evolutionary innovations, presenting data-driven insights from extensive datasets. Our analysis reveals crucial features of empirical populations that challenge established theoretical expectations, shedding light on the dynamic interplay between genotype and phenotype in the evolutionary process.

Wednesday, 21.05.2025, 17:00

University of Cologne

Institute for Biological Physics

Seminar Room S0.03, Zùlpicher Str. 77a

Hosted by G. Petrunaro & M. Lässig