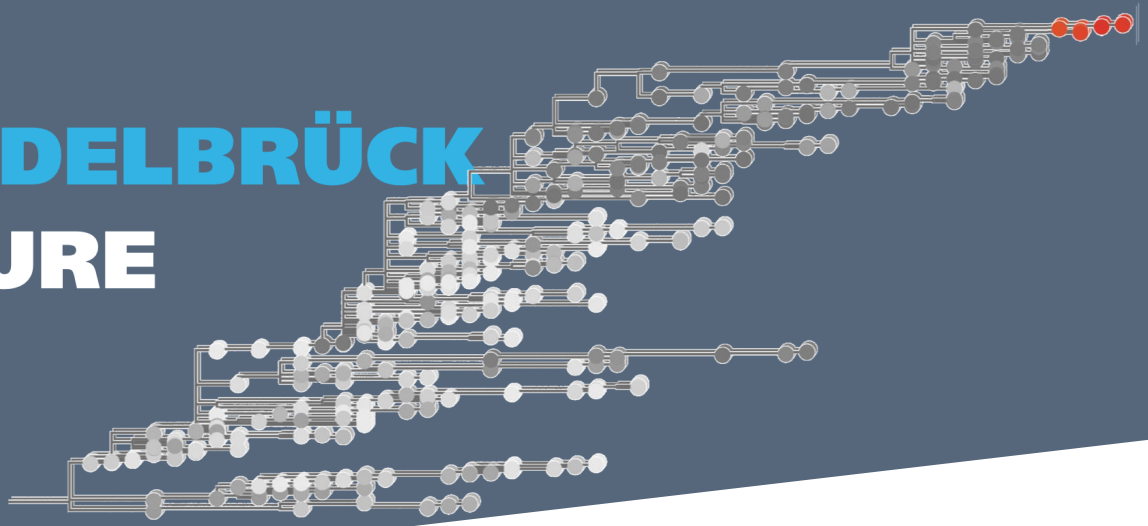


MAX DELBRÜCK LECTURE



Understanding the evolution and epidemiology of modern and ancient infectious disease agents using phylogenomics and machine learning.

Denise Kühnert
MPI of Geoanthropology Jena



Comprehending the evolution and epidemiology of infectious diseases is of vital importance to public health. In this talk I delve into the evolution and epidemiology of infectious diseases over vast timeframes - encompassing months, years, and even millennia. I examine the relatively short-term evolutionary developments and dispersion patterns of prevalent diseases, with an emphasis on concerns such as variant-driven transmission advantages. I further discuss the evolution and geographic dispersal of Lassa virus, and demonstrate our use of machine learning in rapid categorization of viral lineages that identifies important lineage-specific virus substitutions in the Lassa virus genome. Lastly, we trace the evolutionary history of the Hepatitis B virus across thousands of years. This talk emphasizes the benefit of computational methods to enhance our understanding of infectious diseases.

Wednesday, 20.11.2024, 17:00

University of Cologne

Institute for Biological Physics

Seminar Room S0.02, Zülpicher Str. 77a

Hosted by V. Kovacova & M. Lässig