



HILGENDORF LECTURE

Friday, 22 November 2024, 17:15
Alte Aula, Münzgasse 30, 72070 Tübingen



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Host: Cosimo Posth & the Archaeo- and Palaeogenetics Working Group

Tracking the evolution and epidemiology of infectious disease agents over months, years and millennia

Understanding the dynamics of infectious diseases is of profound significance to public health. This talk explores the evolution and epidemiology of infectious disease agents over broad timescales - ranging from months and years to millennia. It begins with a discussion of the short-term evolutionary dynamics and spreading patterns of diseases, focusing on phenomena such as variant-based transmission advantages. Shifting to a longer perspective, we zoom in on the evolution and population dynamics of Lassa virus and demonstrate how machine learning enables rapid classification of viral lineages and identification of lineage-defining virus substitutions. Lastly, we examine the evolutionary history of Hepatitis B virus over millennia. Throughout, the talk highlights the strength of integrating evolutionary insights with epidemiological studies to enhance our understanding of infectious diseases.



The Hilgendorf Lecture series aims at promoting evolutionary thinking across disciplines. The lecture is named after Franz M. Hilgendorf (1834-1904), a palaeontologist from Tübingen who, in 1863, constructed the first empirical phylogenetic tree of fossil organisms using snail shells. He thus provided the first fossil proof of gradual evolution and speciation as proposed by Darwin's theory of evolution.