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## SÉMINAIRE

# Spatio-temporal mapping of pathogen epidemics

**Jean-Philippe RASIGADE**

HCL

Infectious diseases account for one fourth of human deaths worldwide. With pathogen collections of ever-increasing sizes, it becomes possible in theory to reconstruct past epidemic events on continental or worldwide scales and to gain actionable insights into the driving forces of pathogen dispersal and evolution. Current population genetics methods excel at this task, however their computational cost hampers their application on massive ( $n > 1,000$ ) genomic datasets. Here we introduce a novel approach, ancestral state interpolation (AncSI), to reconstruct epidemics through space and time in a computationally efficient fashion. AncSI infers past information (including location, resistance or transmission success) relative to all isolates in the study population in a given time period. By computing series of fine-grained time period, AncSI allows for the visualization of epidemic dispersal in the form of video files. We reconstruct the epidemic progression across Eurasia and Africa of two deadly bacterial pathogens, namely the *Mycobacterium tuberculosis* Beijing family ( $n = 4,000$  isolates with an evolution on the millennial scale) and the *Salmonella* Typhi H58 clone ( $n = 2,000$  isolates with an evolution on the decade scale). In both cases, AncSI-inferred epidemic dynamics exhibited a near-perfect match with the conclusions of previous studies based on hypothesis-driven population genetics analyses. Furthermore, AncSI results highlighted previously unreported features of the epidemics such as a Korean (rather than Chinese) emergence of *M.tuberculosis* Beijing. Our results indicate that an accurate reconstruction of past epidemics can be obtained efficiently from genomic datasets, potentially leading to novel discoveries by leveraging the fast growing collections of pathogen genomes.