



28
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🕒 de 13h à 14h

📍 Salle de formation du PRABI

SÉMINAIRE

Towards understanding and forecasting evolution of pathogenic viruses

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Once a purely basic field of science, evolutionary biology is now learning to predict the origin and spread of infectious disease. Viral evolution is largely defined by the fitness of novel variants of the virus. This fitness, and therefore future evolution, is in principle predictable. However, to make such predictions, we need to address two properties of the viral fitness landscape: mutlidimensionality and variability. Using my work on human pathogenic viruses including HIV-1, influenza virus and SARS-CoV-2, I will illustrate how analysis of big genomic data allows to address these challenges, revealing interactions between sites and alternating modes of selection. I will show how this approach allowed to understand emergence of drug resistance in influenza, and describe previously uncharacterized escape from T-cell immune pressure in SARS-CoV-2.