

32nd International Dynamics & Evolution of Human Viruses



Tuesday, May 6, 2025 - Friday, May 9, 2025

Abbaye de Royaumont, Asnières-sur-Oise, France

Scientific Program

Genomics & bioinformatics

New sequencing technologies and methods, and their application to the analysis of virus genomes.

Innovations and improvements to bioinformatic pipelines for processing virus sequence data.

Environmental metagenomics, including wastewater sequencing.

Note: new computational methods that could be incorporated into a pipeline may be more suitable for the Software track.

Zoonoses & emerging infections

Using phylogenetic analysis to reconstruct host-switch events associated with the origin of novel human viruses.

Estimating the time of origin for a virus species using molecular clock methods.

Dynamics and evolution of emerging viruses.

Transmission dynamics & clusters

Characterizing transmission risk factors: transmission cluster analysis, transmission pair studies.

Genomic epidemiology, outbreak detection by tracking genetic clusters.

Molecular source attribution.

Multi-scale dynamics and evolution.

Phylodynamics & phylogeography

Reconstructing the evolving spatial distribution of virus populations over time (phylogeography)

Phylodynamic and model-based estimation of transmission rates (basic/effective reproduction numbers) and related parameters.

Software, tools & methods

Development and validation of new software for studying human viruses.

Method comparison and benchmarking.

Database / web application announcements.

Advances in statistical and mathematical modeling methods.

Within-host dynamics & adaptation

Viral dynamics in primary infection, transmission bottlenecks.

Viral latency.

Within-host genetic diversity and compartmentalization.

Models of within-host viral and immune dynamics.

Drug resistance and effects of therapy on virus populations.

Vaccines & immune escape

Vaccine-driven virus evolution and predictive vaccine design.

Dynamics of adaptive immunity.

Antigenic and epitope evolution in viral proteins.