

30th International Dynamics & Evolution of Human Viruses



Wednesday, April 19, 2023 - Saturday, April 22, 2023

German Cancer Research Center (DKFZ)

Scientific Program

Genome sequencing & 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. (Note, new computational methods for post-processing analysis of sequence data 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.

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

Reconstructing the rates of spread over time using phylodynamic methods.

Transmission dynamics & clusters

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

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

Genomic epidemiology, outbreak detection by tracking genetic clusters.

Molecular source attribution.

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.

Vaccines & immunology

Vaccine-driven virus evolution.

Dynamics of adaptive immunity.

Kinetics of the B and T cell repertoires.

Within host dynamics

Viral dynamics in primary infection.

Within-host genetic diversity and evolution.

Models of within-host viral and immune dynamics.

Drug resistance and effects of therapy on virus populations.

Antigenic evolution and immune escape

Identification of epitope sites.

Prediction of population-level spread of mutations.