

# 31st International Dynamics & Evolution of Human Viruses



**Wednesday, June 19, 2024 - Saturday, June 22, 2024**

**Squamish, BC, Canada**

## **Scientific Programme**

## **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.

## **Phylogenetics & phylogeography**

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