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## ViBioM 2025



What an unforgettable week in Lisbon! After months of preparation, we finally held **ViBioM 2025** – the International Virus Bioinformatics Meeting – hosted at **IHMT NOVA** with the support of the *European Virus Bioinformatics Center* in the vibrant city of Lisbon. And it was nothing short of amazing.

This dynamic and diverse community of virus bioinformaticians, ecologists, computational biologists, and virologists brought together **150+ participants from over 34 countries**. The energy, openness, and sheer brilliance of this field were on full display.

### Highlights included:

- Viral biodiversity from ancient retroviruses to urban viromes.
- Advances in machine learning, long-read metaviromics, and DNA virus recombination.
- Debates on ICTV taxonomy and virus classification.
- Insights into single-virus genomics, **CRISPR** detection, and **SARS-CoV-2**.
- Emerging tools and trends, including **VIRUS-MV** and **INSaFLU-TELEVIR+**.

**Sustainability matters:** A special thank-you to **Desafio Vegetariano** for their fully plant-based catering and carbon footprint challenge – delicious and climate-conscious!

**In 3 days, we saved more than 4000 kg of CO<sub>2</sub> emissions and more than 2,000,000 L of water. This is also Global Health!**

With deep appreciation to the organizing and program committees and on-site team: **Ana B. Abecasis MD, PhD, Inês Alves, Joana Abrantes, Manja Marz, Paula Istvan, Sofia Seabra, Sofia Rodrigues, Marta Pinharilho, Paula Pacheco, Victor Pimentel**.

Award Winners (generously supported by **MDPI** and **Seqera**):

- **Best Poster:** **Kieran Lamb** – “Predicting viral evolution and epistatic effects with protein language models”
- **Best Talk:** **João Dourado** – “INSaFLU-TELEVIR+: An open web-based bioinformatics platform for metagenomic pathogen detection”

We left inspired, full of ideas, and more connected than ever. The conversations sparked at **ViBioM 2025** will no doubt continue to shape the field in exciting ways.

## Announcements

### ✳ Call for Papers – MDPI Special Issues

- **“Virus Bioinformatics 2025” (Viruses)** – Open to topics from ViBioM 2025. APC: 2600 CHF. ViBioM attendees and EVBC members receive 20% off. [Details and Submission](#)
- **“Climate-Driven Effects on the Human Microbiome and Public Health” (Microorganisms)** – Guest Edited by [Anna Onisiforou, Ph.D.](#). [Details and Submission](#)

### ✳ Job Opportunity – PhD in Virome Studies

The National Institute of Biology (NIB), Ljubljana, Slovenia, offers a fully funded PhD position focused on virome research in invertebrates and related samples. [Application Details](#)

### ✳ Expression of Interest – Endogenous Viral Element Meeting

We are planning to organise a special interest meeting on endogenous viral elements, including RNA viral, retroviral and DNA viral elements, and looking to gauge interest. If you are interested in potentially attending such a meeting, please add your details to the form here: [Expression of Interest Form](#). For suggestions or questions, please contact Katy Brown at [kab84@cam.ac.uk](mailto:kab84@cam.ac.uk), University of Cambridge.

## Tools and Resources

### 🔑 Virus tools website

Tools developed by EVBC members are marked ✳.

- ✳ **StructMAN 2.0 Web:** A web server for structural annotation of protein sequences and mutations, providing insights into the structural impact of variants.
- ✳ **CoVFit:** A protein language model adapted from ESM-2, designed to predict variant fitness based solely on spike protein sequences.
- ✳ **Vclust:** An approach that determines average nucleotide identity by Lempel-Ziv parsing and clusters viral genomes with thresholds endorsed by authoritative viral genomics and taxonomy consortia.
- ✳ **CAMI Benchmarking Portal:** A community-led initiative promoting standards and best practices for benchmarking metagenomic software, providing comprehensive datasets and guidelines.
- ✳ **Physics-Informed Neural Networks for Omicron:** A study employing Physics-Informed Neural Networks to estimate temporal parameters influencing the spread of the Omicron variant.
- ✳ **EMitool:** An explainable multi-omics integration tool for disease subtyping, enhancing personalized medicine through comprehensive data analysis.
- ✳ **EVEs Detection Tool:** A method for the fast, sensitive, and precise detection of endogenous viral elements in host genomes, aiding in the study of viral evolution.

## Upcoming Events

 [Subscribe to Calendar](#)

We do not endorse any of the listings and do not take any responsibility for the accuracy of the information.

### ISMB/ECCB Conference 2025

**20–27 July 2025 | Liverpool, UK**

Organized by the International Society for Computational Biology (ISCB), this 33rd annual ISMB meeting, in conjunction with the 24th ECCB, will feature over 500 scientific talks, training workshops, and networking opportunities, available both in-person and virtually.

### First Symposium of the Danish Viruses of Microbes Network

**11–13 June 2025 | Copenhagen, Denmark**

This inaugural symposium brings together researchers studying viruses of microbes, including bacteriophages and archaeal viruses, for three days of scientific talks, discussions, and community building. Poster submission deadlines: **30 May 2025**

### 8th Annual Training Course on Viral Bioinformatics and Genomics

**16–20 June 2025 | Garscube Campus, University of Glasgow, UK**

This course provides hands-on training in viral genome assembly, annotation, and analysis of next-generation sequencing data, designed for researchers studying virus genomics.

### International Symposium on Bioinformatics Research and Applications (ISBRA 2025)

**3–5 August 2025 | Helsinki, Finland**

ISBRA 2025 brings together academic and industry researchers in bioinformatics, computational biology, systems biology, and related fields to share their latest research and innovations.

### 29th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME)

**3–8 August 2025 | Dakar, Senegal**

Organized by the VEME, this internationally renowned workshop offers intensive training in virus evolution and molecular epidemiology, featuring hands-on modules tailored for different levels of expertise.

### Phage Therapy Congress 2025

**7–9 October 2025 | Porto, Portugal**


A congress dedicated to the latest advancements in phage therapy, featuring global experts discussing therapeutic applications and regulatory frameworks.


Conference details: [Phage Therapy 2025 website](#).


## Selected Publications by EVBC Members

 [All publications on PubMed](#)


### Virome and Microbiome Diversity

 This study investigates the virome drift in ulcerative colitis patients, revealing minimal phage engraftment dominated by microviruses following fecal microbiota transplantation. (Gut Microbes: [10.1080/19490976.2025.2499575](#))


 This research explores the untapped potential of wastewater for animal and potentially zoonotic virus surveillance, demonstrating the detection of non-human animal viruses in urban settings. (Environ Int: [10.1016/j.envint.2025.109500](#))


 This study investigates how type II-C CRISPR-Cas systems in bacteria mitigate the production of extraneous CRISPR RNAs (ecrRNAs), which can interfere with the immune response. The authors identify three distinct mechanisms: formation of upstream Rho-independent terminators, hairpin structures that sequester ecrRNA guides, and mutations in repeat sequences that disrupt ecrRNA formation. These findings enhance our understanding of the regulatory strategies employed by CRISPR-Cas systems to maintain immune efficiency. (microLife: [10.1093/femsml/uqaf007](#))


### Viral Taxonomy and Classification


 This publication discusses the standardization of virus species names, ensuring consistency in viral taxonomy while maintaining existing virus nomenclature. (mSphere: [10.1128/msphere.00020-25](#))





### Virology Studies

 This study examines the differential effect of acute versus persistent insect-specific flavivirus infection on superinfection exclusion of West Nile, Zika, and chikungunya viruses in RNAi-competent and -deficient mosquito cells. (One Health: [10.1016/j.onehlt.2024.100960](#))

 This research investigates the codon usage patterns of Ross River virus genomes from Australia and the Pacific, revealing coincidental and antagonistic patterns with common vertebrate hosts and a principal vector. (Virology: [10.1016/j.virol.2025.110530](#))

 This review discusses phages and phage-borne enzymes as new antibacterial agents, highlighting their potential in combating antibiotic-resistant bacteria. (Clin Microbiol Infect: [10.1016/j.cmi.2023.10.018](#))

 This study provides insights into the epidemiological and genomic evolution of the ongoing outbreak of clade Ib mpox virus in the eastern Democratic Republic of the Congo. (Nat Med: [10.1038/s41591-025-03582-1](#))

 – [open access](#)    – [preprints](#)    – [reviews, meta analyses](#)    – [tools](#)

## Call for workflows

 [Contribute](#)

### Calling all virus bioinformatics developers!

Add your Nextflow tools to **CLoWM** and help expand the **VJDB** – the central virus database of **NFDI4Microbiota** and **EVBC**.

Join a growing community working to make viral bioinformatics more interoperable, scalable, and FAIR.

***Collaborate. Integrate. Accelerate virus research.***

## Be part of the Newsletter

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We want to know about your **publications, tools, workshops and other events, vacancies** or anything important you would like to share with the EVBC community.

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