

Send us your news to evbc@uni-jena.de.

For more frequent updates, please follow us on Twitter  [EVirusBioinfC](https://twitter.com/EVirusBioinfC).

Selected Publications by EVBC Members (part 1)

 [All publications on Pubmed](#)

Viromics

📄 Study of the Teltow Canal in Berlin reveals a highly diverse and largely unexplored virome, adding 513 picorna-like viruses to over 2000 unassigned ones, with a predominance of marna-like and dicistro-like viruses, and includes unique viral sequences and novel features, while caliciviruses and secoviruses were notably absent. (Viruses: [10.3390/v16071020](#))

📄 The 'Platinum Age of Virus Discovery', driven by metagenomics and computational analysis, reveals complex host-microbe-virus interactions, exemplified by the identification of *Apocryptovirus odysseus* infecting *Toxoplasma gondii*, potentially a hypervirulence factor in toxoplasmosis. (Virus Evolution: [10.1093/ve/veae040](#))

Bioengineering

Engineered viruses, successfully used in veterinary and human medicine for delivering nucleic acids, peptides, and proteins, can similarly be applied in agriculture for the transient or heritable reprogramming of plant traits to enhance crop performance and sustainability. (Nat Rev Bioeng: [0.1038/s44222-024-00197-y](#))

Epidemiology

📄 Complete genome annotation, phylogeny, and mutational profile of a novel and sustained Clade I Mpox outbreak in Kamituga, DRC, identifying unique genetic characteristics and proposing the outbreak as a new subgroup (subgroup VI) of Clade I MPXV. (J Infect Dev Ctries: [10.3855/jidc.20136](#))

Phages


📄 The study discovered that automatic prediction of stop codon reassignment in phage genomes significantly improves the quality of annotations, leading to better functional annotation and increased coding capacity, particularly demonstrated with the modified tools Pharokka-gv and Prokka-gv. (ISME Communications: [10.1093/ismeco/ycae079](#))

Virus surveillance

📄 ViralFlow v1.0 is a versatile computational workflow for viral genomic surveillance, offering virus-agnostic genome assembly and mutation analysis across diverse computational platforms. (NAR Genomics and Bioinformatics: [10.1093/nargab/lqae056](#))

Tools and Resources

 [Virus tools website](#)

Tools that have been added to our [collection](#) this month have been newly released or updated. Tools developed by EVBC members are marked .

- 🌟 **Viralgenie**: metagenomic analysis pipeline for eukaryotic viruses
- 🌟 **NAGATA**: Nanopore Augmented Genome and Transcriptome Annotation
- 🌟 **Leaf**: Ultra-fast SV filter for population-scale long-read SV detection
- 🌟 **spread.gl**: Visualising pathogen dispersal in a high-performance browser application
- 🌟 **RAIN**: Rapid Automatic Identification of bNAbs (RAIN) to identify bNAbs from antibody immune repertoire
- 🌟 **Entourage**: All-in-One Sequence Analysis Software for Genome Assembly, Virus Detection, Virus Discovery, and Intrasample Variation Profiling
- 🌟 **Panacus**: Computing statistics for GFA-formatted pangenome graphs
- 🌟 **ViralFlow**: Viral genomic surveillance based on reference genome assembly
- 🌟 **SimRNAweb v2.0**: Web server for RNA folding simulations and 3D structure modeling
- 🌟 **vAMPirus**: Automated virus amplicon sequencing analysis program integrated with Nextflow pipeline manager

News and Announcements

After 7 years as Scientific Coordinator of the EVBC, I would like to announce that I have decided to step down from my role within the next months.

It has been an honor to shape the EVBC into what it is today, to see the community grow and come together, to gain so many insights into viral bioinformatics, and most of all to get to know all of our amazing members and their research! Together, we have built a vibrant community dedicated to scientific excellence in virus bioinformatics.

I am immensely proud of what we have accomplished and deeply grateful for the support and enthusiasm each of you has brought to the EVBC.

Thank you everyone, for being part of this journey!

If you have any questions or would like to stay in touch, please do not hesitate to reach out to me.

– Franziska –

We are committed to ensuring a smooth transition over the next months, and the search for a new coordinator is already underway.

If you are interested in either

- coordinating the EVBC,
- taking over individual tasks of the EVBC coordination,
- being part of the ViBioM organizing team

please [reach out to us](#).

Coordinating tasks would be for example:

- Editing the monthly newsletter
- Maintaining social media channels
- Maintaining the tool collection
- Organizing EVBC lectures
- Organizing EVBC workshops
- Organizing ViBioM
- Editing special issues

Selected Publications by EVBC Members (part 2)

 [All publications on Pubmed](#)

RNA viruses and structures

📄 This study presents the first genome-wide multiple sequence alignment and RNA secondary structure predictions for the full-length HCV genome, identifying conserved RNA structures in the core coding region, C-terminal NS5A region, and NS5B region, suggesting functional importance beyond coding sequences. (Scientific Reports: [10.1038/s41598-024-62897-0](#))

📄 The discovery of Orsay virus in *C. elegans* has advanced viral immunity studies and shown promise as a model for virus evolution experiments. After 10 serial passages, slight infectivity changes and non-synonymous mutations were observed, laying the groundwork for future research in this pathosystem. (Infect Genet Evol: [10.1016/j.meegid.2024.105623](#))

📄 SimRNAweb v2.0 enhances RNA 3D structure prediction with new features for detailed analysis, flexible simulations, and incorporation of experimental data. (NAR: [10.1093/nar/gkac356](#))

Software and visualisation

📄 spread.gl is an open-source, feature-rich browser application for intuitive visualization and animation of phylogeographic inference results, aiding in the interpretation of pathogen dispersal patterns through multiple data layers. (medRxiv: [10.1101/2024.06.04.24308447](#))

📄 Panacus is a scalable tool for analyzing pangenome graphs, capable of quantifying core genome sequences and measuring pangenome growth, and can process a human pangenome graph with 110 million nodes in under one hour. (bioRxiv: [10.1101/2024.06.11.598418](#))

📄 A comprehensive tool for analyzing DNA and RNA virus amplicon sequencing data, offering features for sequence abundance, taxonomic classification, phylogeny, and diversity metrics, while promoting reproducibility and comparability in viral community studies. (Mol Ecol Resour: [10.1111/1755-0998.13978](#))

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. EVBC members are involved in events marked ✨.

7th International Viromics Workshop

23–25 October 2024 | Columbus, Ohio, USA

Deep dives on virus identification, virus taxonomy/classification, databases, ecogenomics pipeline, auxiliary metabolic gene analysis, virus-host linkages, and genome annotation.

Application deadline: **05 August 2024**

✨ Olivier Zablocki, Matt Sullivan (Organizers)

German Conference on Bioinformatics 2024

30 September - 2 October 2024 | Bielefeld, Germany

GCB is an annual, international conference devoted to all areas of bioinformatics, including data science, imaging, infrastructure & services, medical informatics, modeling, omics, single cell research, structural biology, and other fields.

Poster submission deadline: **07 August 2024**

✨ Bas Dutilh, Caroline Friedel (Keynote Speakers)

VEGA Symposium 2024

12–13 November 2024 | Berkeley, CA, USA

Bringing together the "Viral EcoGenomics" community to foster discussion on how to best capture and characterize uncultivated viruses, understand the role of viruses in natural ecosystems, and functionally explore viral genetic diversity toward innovative biotechnological and industrial applications.

Early bird deadline: **31 August 2024**

23rd European Conference on Computational Biology

16-20 September 2024 | Turku, Finland

ECCB 2024, will feature keynotes, talks, poster sessions, exhibitions, and social events focused on data and algorithms for health and science, welcoming scientists from diverse disciplines to address global challenges and enhance well-being through computational and multidisciplinary expertise.

Registration deadline: **01 September 2024**

Vacancies

 [Find a job](#)

Scientific Coordinator EVBC. The EVBC is looking for a new Scientific Coordinator. This is a half-time position that can be combined with a research position on e.g. viruses in the RNA bioinformatics lab at the Friedrich Schiller University Jena.

Junior Research Group Leader in (theoretical) computer science, statistics, and machine learning/AI. The RNA Bioinformatics lab at Friedrich Schiller University Jena is seeking for a talented junior research group leader to develop advanced algorithms and models that address complex problems to analyze large-scale datasets and uncover meaningful insights. Preferentially in the context of virus research.

[More information](#)

Application deadline: **31 July 2024**

Computational Biologist - Virology (Postdoc or equal). Join "The Laboratory for RNA-Based Lifeforms" in University of Toronto's Donnelly Centre. Together with Dr. Artem Babaian the work will develop the state of the art for the detection and sequence analysis of RNA viruses and virus-like agents.

[More information](#)

Postdoc in bioinformatics with a focus on RNA-seq. The RNA Bioinformatics lab at Friedrich Schiller University Jena is seeking a PostDoc engaging in cutting-edge research on gene expression and regulation through advanced bioinformatics analysis of high-throughput RNA-seq data to make impactful discoveries in virus immune response.

[More information](#)

PhD position in spatiotemporal diversity of phages. Wageningen University is offering a PhD position focused on studying the evolutionary factors influencing the genome diversity of bacteriophages using bioinformatics and mathematical modeling. The project involves analyzing phage diversity in various environments, developing bioinformatics pipelines, and creating models to explain observed diversity patterns.

[More information](#)

Application deadline: **26 August 2024**

Postdoc in Genomics (Wet-Lab). The RNA Bioinformatics lab at FSU Jena is seeking a PostDoc to design and execute advanced genomic experiments, develop innovative methodologies, and contribute to high-impact scientific discoveries aimed at advancing genetic mechanisms related to virus research.

[More information](#)

Application deadline: **31 July 2024**

Selected Publications by EVBC Members (part 3)

 [All publications on Pubmed](#)

Immunity and pathogenicity

🔗 A new computational method, RAIN, using machine learning-based sequence features, enables the rapid and accurate identification of HIV-1 broadly neutralizing antibodies (bNAbs) from immune repertoires, demonstrated through successful antibody identification and structural analysis. (Nature Communications: [10.1038/s41467-024-49676-1](#))

🔗 Using single-cell RNA sequencing data, an artificial intelligence system was developed to differentiate and identify the severity of immune-dysregulated syndromes, successfully distinguishing between mild and severe sepsis and COVID-19 by identifying key gene expression changes in specific immune cells. (Int J Mol Sci: [10.3390/ijms25115920](#))

🔗 VZV glycoprotein C (gC) modulates IFN- γ activity to upregulate a subset of ISGs, enhancing lymphocyte adhesion and promoting VZV spread from skin keratinocytes to peripheral blood mononuclear cells. (Nature Communications: [10.1038/s41467-024-49657-4](#))

Long read data

🔗 The NAGATA software, utilizing nanopore direct RNA sequencing data, significantly improves the high-resolution annotation of transcriptomes in gene-dense viruses, outperforming existing tools and successfully identifying 77 distinct transcripts in the human adenovirus type F41. (mSystems: [10.1128/msystems.00505-24](#))

🔗 A new filter-based computational pipeline for population-scale long-read structural variant detection is presented. It captures SV signals more effectively and resolves intra-read rearrangements better than conventional pipelines, while also improving computational efficiency. (Genome Biology: [10.1186/s13059-024-03297-5](#))

Virus-host interactions

🔗 Generalized transduction plays a crucial role in bacterial evolution, and sequencing the transducing particle content of three Salmonella Typhimurium phages (Det7, ES18, and P22) revealed significant disparities, with P22 showing increased packaging and transduction frequencies due to conserved pac-like sequences in the host chromosome. (NAR: [10.1093/nar/gkae489](#))

🔗 Mosquito-specific viruses might modulate malaria transmission by Anopheles mosquitoes through immune pathways, describing interactions between viruses, parasites, and mosquitoes warrant further investigation. (Curr Opin Insect Sci: [10.1016/j.cois.2024.101222](#))

Evolution

🔗 This study reveals the protein structure similarities between the DNA polymerases of diverse Preplasmiviricota viruses and prokaryotic PRD1-like tectivirids, and outlines a comprehensive evolutionary scenario for the phylum's origin and development. (PNAS: [10.1073/pnas.2405771121](#))

🔗 This review contextualizes and compares theories of 'meaningful information' from natural language research with neo-Darwinian genetic information, focusing on molecular-level interpretations relevant to RNA virus evolution. (J Physiol: [10.1113/JP284415](#))

🔗 The DIGS approach uncovers approximately 1.1 million endogenous viral elements (EVEs) across 874 vertebrate genomes, revealing novel virus diversity and offering new insights into viral impact on vertebrate genome evolution. (Genome Biology: [10.1186/s13059-024-03258-y](#))

Virus detection and discovery

🔗 Entourage is a versatile, all-in-one bioinformatics tool for virome investigation, providing a streamlined, end-to-end workflow for virus sequence detection, assembly, and analysis from metagenomic data with demonstrated effectiveness in both synthetic and real-world datasets. (BMC Bioinformatics: [10.1186/s12859-024-05846-y](#))

🔗 This study identifies a novel class of small double-stranded DNA viruses named "Mriyaviricetes," which represent the closest relatives to the ancestors of the Nucleocytoviricota and exhibit a unique genome replication mechanism. (mBio: [10.1128/mbio.01035-24](#))

🔗 This review assesses electrochemical methods for virus detection, highlighting their high sensitivity, selectivity, and potential for point-of-care applications, with 77% of studies using nanotechnological modifications and finding that most research remains at a proof-of-concept stage. (Crit Rev Anal Chem: [10.1080/10408347.2024.2343853](#))