

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

For more frequent updates, please follow us on Twitter [@EVirusBioinfC](#).

News and Announcements

This month we celebrate the 4th anniversary of the EVBC and on this occasion we have quite some exciting news to share:

- The **International Virus Bioinformatics Meeting 2022** is going to take place in Valencia. Thank you to Gloria, Walter and Alba! Details will follow soon.
- The EVBC is starting a monthly **lecture series** called **“viruses in silico”**.
- We revised and redesigned our **collection of virus bioinformatics tools**.
- We have set up a Discord Server for EVBC members.

For details, see below.

Tools and Resources

We are very happy to announce our revised and redesigned **collection of virus bioinformatics tools**. Don't hesitate to contact us if you want a tool to be added or require any further features for this collection. We strongly encourage you to leave comments and/or send us feedback on the tools.



[Virus tools website](#)

New tools:

COJAC is a set of command-line tools to analyse co-occurrence of mutations on amplicons.

MUFFIN is a hybrid assembly and differential binning workflow for metagenomics, transcriptomics and pathway analysis.

VIBRANT for automated recovery, annotation and curation of microbial viruses.

VirSorter2 is a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses.

Vacancies

PhD student virus bioinformatics – TWINCORE

Help to build a research group with fresh ideas and a lot of enthusiasm, and discover unknown viruses or study the effects of genetic variation in the human genome on the course of viral infections.

Application deadline:

10 March 2021

[Q Find a job](#)

New Members

We have invited outstanding scientists for membership and are happy to welcome our new members:

- **Isabella Eckerle**, University of Geneva, Switzerland
- **Shawna McCallin**, University of Zurich, Switzerland
- **Karin J. Metzner**, University of Zurich, Switzerland
- **José R Penadés**, Imperial College London, United Kingdom
- **Noam Stern-Ginossar**, Weizmann Institute of Science, Israel

[EVBC members website](#)

EVBC Discord Server

We have set up a Discord server for EVBC members to offer you the opportunity to

- easily get in touch with other EVBC members,
- discuss virus bioinformatics tools,
- get help with your research,
- stay up-to-date about new publications,
- ...

Joining this server is restricted to EVBC members for the time being. An invitation link will be sent in a separate message. Please let us know about features you would like us to add.

[Apply for membership](#)



Recent Selected Publications by EVBC Members

Recent African strains of Zika virus display higher transmissibility and fetal pathogenicity than Asian strains. Now published in *Nat Commun* [10.1038/s41467-021-21199-z](https://doi.org/10.1038/s41467-021-21199-z)

Relax, keep walking—a practical guide to continuous phylogeographic inference with BEAST. *Mol Biol Evol* [10.1093/molbev/msab031](https://doi.org/10.1093/molbev/msab031)

Efficient dilution-to-extinction isolation of novel virus-host model systems for fastidious heterotrophic bacteria. *ISME J* [10.1038/s41396-020-00872-z](https://doi.org/10.1038/s41396-020-00872-z)

Highly Pathogenic Avian Influenza A(H5N8) Virus Spread by Short- and Long-Range Transmission, France, 2016–17. *Emerg Infect Dis* [10.3201/eid2702.202920](https://doi.org/10.3201/eid2702.202920)

Efficient inference, potential, and limitations of site-specific substitution models. *Virus Evol* [10.1093/ve/veaa066](https://doi.org/10.1093/ve/veaa066)

A theoretical and generalized approach for the assessment of the sample-specific limit of detection for clinical metagenomics. *Comput Struct Biotechnol J* [10.1016/j.csbj.2020.12.040](https://doi.org/10.1016/j.csbj.2020.12.040)

Metagenomics workflow for hybrid assembly, differential coverage binning, metatranscriptomics and pathway analysis (MUFFIN). *PLoS Comput Biol* [10.1371/journal.pcbi.1008716](https://doi.org/10.1371/journal.pcbi.1008716)

Dynamic Molecular Epidemiology Reveals Lineage-Associated Single-Nucleotide Variants That Alter RNA Structure in Chikungunya Virus. *Genes* [10.3390/genes12020239](https://doi.org/10.3390/genes12020239)

A novel dicistrovirus in a captive red squirrel (*Sciurus vulgaris*). *J Gen Virol* [10.1099/jgv.0.001555](https://doi.org/10.1099/jgv.0.001555)

Characterization of Hepatitis B Virus Integrations Identified in Hepatocellular Carcinoma Genomes. *Viruses* [10.3390/v13020245](https://doi.org/10.3390/v13020245)

AnnapuRNA: A scoring function for predicting RNA-small molecule binding poses. Now published in *PLoS Comput Biol* [10.1371/journal.pcbi.1008309](https://doi.org/10.1371/journal.pcbi.1008309)

Application of spectral library prediction for parallel reaction monitoring of viral peptides. *Proteomics* [10.1002/pmic.202000226](https://doi.org/10.1002/pmic.202000226)

Interpretable detection of novel human viruses from genome sequencing data. *NAR Genom Bioinform* [10.1093/nargab/lqab004](https://doi.org/10.1093/nargab/lqab004)

Influenza virus infection induces widespread alterations of host cell splicing. *NAR Genom Bioinform* [10.1093/nargab/lqaa095](https://doi.org/10.1093/nargab/lqaa095)

Preprints

Prisoner of War dynamics explains the time-dependent pattern of substitution rates in viruses. *bioRxiv* [10.1101/2021.02.09.430479](https://doi.org/10.1101/2021.02.09.430479)

A deep learning framework for real-time detection of novel pathogens during sequencing. *bioRxiv* [10.1101/2021.01.26.428301](https://doi.org/10.1101/2021.01.26.428301)

Targeting the DEAD-box RNA Helicase eIF4A with Rocaglates - A Pan-Antiviral Strategy for Minimizing the Impact of Future RNA Virus Pandemics. *Preprints* [10.20944/preprints202102.0058.v1](https://doi.org/10.20944/preprints202102.0058.v1)

Mutation bias implicates RNA editing in a wide range of mammalian RNA viruses. *bioRxiv* [10.1101/2021.02.09.430395](https://doi.org/10.1101/2021.02.09.430395)

 [EVBC publications website](https://www.evbc.uni-jena.de)

viruses *in silico* | EVBC Lectures



To keep you up to date with the latest developments in virus bioinformatics, especially new tools that might help you in your research, we start a monthly lecture series entitled *viruses in silico*. The lectures will take place online. Participation is free. We are happy to receive your suggestions for interesting topics and speakers!

DeePaC-Live: Predicting pathogenic potentials of short DNA reads with reverse-complement deep neural networks.

22. March 2021 | 04–05pm

online

Jakub Bartoszewicz, Hasso-Plattner-Institut, GER

NGS is the state-of-the art in open-view pathogen detection, and one of the few methods available at the earliest stages of an epidemic, even when the biological threat is unknown. We show that deep neural architectures can accurately predict if raw, unassembled sequencing reads originate from novel, human-infecting agents and further detect virulence-related genes in novel agents. As analyzing the samples as the sequencer is running can greatly reduce the turnaround time, we extend the approach to classify incomplete Illumina and Nanopore reads in real-time.

 [Register](#)

Upcoming Events

EVBC does not endorse any of the listings and is only involved in events marked as **EVBC Events** ★.

Bioinformatics for Principal Investigators

15–17 June 2021

online

This course has been designed to provide Principal Investigators (PI's) working in the life sciences with an introduction to the challenges of working with biological data as a research leader.

Application deadline:

26 March 2021

 [Subscribe to EVBC Event Calendar](#)