

Send us your news to [evbc@uni-jena.de](mailto:evbc@uni-jena.de).

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

### Selected Publications by EVBC Members

 [All publications on Pubmed](#)

Virome characterization of game animals in China.: transmission of Bat coronavirus from bats to civets, and cross-species jumps of coronaviruses from bats to hedgehogs, from birds to porcupines, and from dogs to raccoon dogs. (Cell: [10.1016/j.cell.2022.02.014](#))

Helical assemblies can vary their diameters, becoming nearly spherical to package a larger genome suggesting how spindle-shaped viruses have evolved from archaeal rod-like viruses. (Cell: [10.1016/j.cell.2022.02.019](#))

MetaPop is an open-source bioinformatic pipeline that provides a single interface to analyze and visualize microbial and viral community metagenomes at both the macro- and microdiversity levels. (Microbiome: [10.1186/s40168-022-01231-0](#))

Evolutionary arms-race and impact of the innate immune system on viral population diversity and evolution of *Drosophila melanogaster* and *Drosophila C* virus. (Nat Ecol Evol: [10.1038/s41559-022-01697-z](#))

Very high temporal resolution on how the different members of the infant gut microbiota, and especially the virome, develop over time in the gut of healthy infants. (PNAS: [10.1073/pnas.2114619119](#))

Ribosome profiling of porcine reproductive and respiratory syndrome virus reveals novel features of viral gene expression. (eLife: [10.7554/eLife.75668](#))

Equine hepatitis virus infection of horses could represent a powerful surrogate animal model to gain insights into hepatitis B virus evolution and HCVs HVR1-mediated immune evasion strategy. (Virus Evol: [10.1093/ve/veac007](#))

Comparison of three strategies for data augmentation of DNA microarray and RNA-seq data from two selected studies on respiratory diseases of viral origin. (Int J Mol Sci: [10.3390/ijms23052481](#))

Systematic framework to assemble, identify, and measure the proportion of unknown sequences present in distinct human microbiomes. (mSystems: [10.1128/msystems.01468-21](#))

PhyCovA: web-based application allowing users to rapidly explore the association between candidate covariates and the number of phylogenetically informed transition events among locations. (Virus Evol: [10.1093/ve/veac015](#))

Origins, zoonotic potential, and impact of vaccination on the molecular evolution of Moroccan H9N2 Avian Influenza viruses. (Viruses: [10.3390/v14030509](#))

Non-canonical Peptides in Virus-Induced Autoimmunity: perspective on how these mechanisms can explain several autoimmune disorders in the wake of the COVID-19 pandemic. (Front Microbiol: [10.3389/fmicb.2022.840911](#))

Network meta-analysis of transcriptome expression changes in different manifestations of dengue virus infection. (BMC Genomics: [10.1186/s12864-022-08390-2](#))

CIAlign: A highly customisable command line tool to clean, interpret and visualize multiple sequence alignments. (PeerJ: [10.7717/peerj.12983](#))

#### Reviews / Commentaries / Editorials

Phylogenetic Analysis of Spread of Hepatitis C Virus Identified during HIV Outbreak Investigation, Unnao, India. (Emerg Infect Dis: [10.3201/eid2804.211845](#))

### Tools and Resources

 [Virus tools website](#)

**CIAlign**: clean and analyse multiple sequence alignments.

**MetaPop**: macro- and micro-diversity analyses and visualization of metagenomic-derived populations.

**PhyCovA**: exploring covariates of pathogen spread.

**serratus**: Explore the raw sequencing virome of millions of samples collected by the world biological community.

### Vacancies

 [Find a job](#)

**Post-doc position (Institute for Sustainable Plant Protection, National Research Council of Italy, Torino)** for the analysis of geminiviruses.

### ViBioM 2022

We thank all speakers, all presenters, and all participants for the updates and insights into their virus bioinformatics research and for making ViBioM 2022 such a wonderful experience! **Congrats to Spyros Lytras for winning the Best ECR Talk Award and to Luca Nishimura, Celia Pas and Gabriel Lenconi Lovate for winning the Best Poster Award.**

### EVBC Special Issues

 [Special issue list](#)

**Virus Bioinformatics 2022 in Viruses**: We remind you to submit to our Special Issue covering computational approaches in virology. Deadline: **30 April 2022**

**Bioinformatics for Plant Health in Life**: Edited by L. Miozzi | G. Bubic | S. Ghignone. Deadline: **30 September 2022**

**Molecular Epidemiology, Host Genetic Factors, and Viral Hepatitis Related Liver Diseases in Pathogens**: Edited by C. Thomas Bock | D. Todt. Deadline extended: **31 December 2022**

### viruses *in silico* | EVBC Lectures

 [Register](#)

**Open Virome: Foundations for discovery of the first 100 million RNA viruses**

25. April 2022 | 04–05pm CEST online  
Artem Babaian, Ph.D., University of Cambridge, UK

Artem Babaian will share an overview of how to navigate and use Open Virome project data to aid in RNA virus discovery, and open a (opinionated) discussion on what RNA virus discovery will mean in the exabase era.

### Upcoming Events

 [Subscribe to Calendar](#)

#### 2022 Viromics Workshop

11–13 May 2022 | Ohio State University, Columbus, OH  
Pre-registration is now open. There will be a 'mini-symposium' that will be broadcasted live. The following two days will then be exclusively in-person workshop sessions.

[Pre-registration form](#) | [in-person application form](#) (deadline April 7)


### EVBC workshops

 [Submit your interests](#)

We are planning to set up a workshop program. Would you like to delve deeper into a specific topic?

Let us know your interests so we can shape our upcoming events accordingly.

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**Board of Directors**

Martin Beer, Li Deng, Bas E. Dutilh, Philippe Le Mercier, Manja Marz, Volker Thiel

### Member Profile: Elliot Lefkowitz



**Name:** Elliot Lefkowitz  
**Position:** Professor  
**Research focus:** Viral genomics, evolution, classification, and taxonomy



#### What do you love about viruses?

How they manage to do such magnificent things from such a small package

#### Who is your favourite scientist and why?

My own personal mentors. They helped me at different stages in my career and helped me find my own path.

#### On what topic could you give a 30-min talk without preparation?

Poxvirus evolution or virus classification

#### What is your favourite way to spend a day off?

Sitting on the deck of a boat, gin & tonic in hand, reading whatever science fiction novel comes up first on my iPad.

#### What are you currently learning?

PHP, Drupal, SQL (in depth). (I am having to take up the slack from not being able to find a developer to hire.)

#### What is the most interesting unanswered question in science?

Are we alone in the universe?

#### What is the coolest thing about your research?

I get to "touch" (figuratively, at least) essentially all known viruses on the planet since the International Committee on Taxonomy of Viruses (ICTV) classifies all viruses.

#### What do people think about you that isn't true?

That I don't have a soft spot.

#### For which project idea are you looking for a cooperation partner?

These days, it is difficult to find people to hire with the expertise needed to support any of the projects I work on. I need to hire Bioinformaticians and Software (Web) Developers (full-stack developers).

#### What was your biggest achievement / your biggest failure?

I'm not a boom and bust kind of a guy. Myself, and my work are fairly even keeled.

#### If you were completely free to choose a scientific topic to work on, which would it be?

None of us is completely free to choose a topic to work on. Someone or something is always needed to pay for what you are doing. Therefore, I don't waste time on such fanciful musings.

#### If you had the option to give advice to a younger version of yourself, what would that be?

Promote yourself.

### Member Profile: Emilio Mastriani



**Name:** Emilio Mastriani  
**Position:** Bioinformatician  
**Research focus:** Development of virus profiling pipelines based on 2nd and 3rd generation sequencers



#### What do you love about viruses?

Their ability to adapt and organize for surviving

#### Who is your favourite scientist and why?

L. Pasteur because of his determination and scientific discoveries

#### On what topic could you give a 30-min talk without preparation?

Using of computational resources like HPC (Unix based) for intensive calculation tasks

#### What is your favourite way to spend a day off?

Play music, walking on the nature and staying with my family

#### What are you currently learning?

Deep-learning strategies to identify cervix cells infected by HPV

#### If you could create a new invention, what would it be?

Something useful to poor people and to marginalized communities

#### What is the most interesting unanswered challenge in science?

Completely understand the reason why some viruses are transmitted among humans and not others belonging to the same family (e.g. Hantaviruses)

#### What is the coolest thing about your research?

Using appropriate computational approach to obtain the best results saving time

#### What do people think about you that isn't true?

Being rude

#### What was your most surprising scientific finding?

The suspected correlation between the CpG distribution on Andes hantavirus and their ability of human transmission

#### For which project idea are you looking for a cooperation partner?

To define a general rule linking the CpG distribution in viruses (Hantavirus) and their human-to-human transmission ability

#### What was your biggest achievement / your biggest failure?

My biggest achievement is my family, while my biggest failure was getting late my PhD

#### Which scientific topic (outside of your field of research) do you think should have more scientific attention?

The relationship between the ecological changes and the occurrence of new diseases

#### If you had the option to advise a younger version of yourself, what would that be?

The time is a really precious good, avoid of losing it

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