

## Upcoming Events

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

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### International Conference on Research in Computational Molecular Biology (RECOMB) 2020

10–13 May 2020, Padua, Italy

*The conference aims at bridging the computational, mathematical, statistical, and biological sciences, and bringing together researchers, professionals, students and industrial practitioners from all over the world for interaction and exchange of new developments in all areas of bioinformatics and computational biology.*

Paper submission deadline: **01 November 2019**

### EVBC Event | International Virus Bioinformatics Meeting 2020

05–06 March 2020, Bern, Switzerland

*We are happy to announce Alexander Gorbalenya, Irmtraud Meyer, Daniel Blanco Melo, Simon Roux, Tulio de Oliveira and Marco Vignuzzi as invited speakers.*

[Registration now open](#)

### EVBC Event | Course on Theoretical and Practical Approaches to Metagenomics and Viral Discovery

21–25 October 2019, São Paulo, Brazil

*In this course, we intend to cover some innovative methods, such as Hidden-Markov-Models and Machine Learning, that can increase the sensitivity of detection of evolutionary remote viruses. We will teach conceptual aspects and offer practical sessions.*

Registration deadline: **07 October 2019**

### EVBC Event | Hands-on Workshop on Nanopore Sequencing: Adventures in Metagenomics and Antimicrobial Resistance

25–29 November 2019, Delhi, India

*This workshop is part of a project, where metagenomics assisted surveillance tools shall be developed for tracking antibiotic resistance. During the workshop, water and sediment samples will be analyzed using Nanopore sequencing to assess the effect of human settlement on the quality of water in terms of bacterial load.*

Registration deadline: **15 November 2019**

## Recent Selected Publications by EVBC Members

Stable distinct core eukaryotic viromes in different mosquito species from Guadeloupe, using single mosquito viral metagenomics. *Microbiome* [10.1186/s40168-019-0734-2](#)

Viral Metagenomics in the Clinical Realm: Lessons Learned from a Swiss-Wide Ring Trial. *Genes* [10.3390/genes10090655](#)

HIV Rebound Is Predominantly Fueled by Genetically Identical Viral Expansions from Diverse Reservoirs. *Cell Host Microbe* [10.1016/j.chom.2019.08.003](#)

NCBI's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. *Genes* [10.3390/genes10090714](#)

Viral metagenomic analysis of the cheese surface: A comparative study of rapid procedures for extracting viral particles. *Food Microbiol* [10.1016/j.fm.2019.103278](#)

A Deep-Sequencing Workflow for the Fast and Efficient Generation of High-Quality African Swine Fever Virus Whole-Genome Sequences. *Viruses* [10.3390/v11090846](#)

Bat influenza viruses transmit among bats but are poorly adapted to non-bat species. *Nat Microbiol* [10.1038/s41564-019-0556-9](#)

DisCVR: Rapid viral diagnosis from high-throughput sequencing data. *Virus Evol* [10.1093/ve/vez033](#)

Using phylogeographic approaches to analyse the dispersal history, velocity and direction of viral lineages. *Mol Ecol* [10.1111/mec.15222](#)

Metaviromics Reveals Unknown Viral Diversity in the Biting Midge *Culicoides impunctatus*. *Viruses* [10.3390/v11090865](#)

No evidence for viral small RNA production and antiviral function of Argonaute 2 in human cells. *Sci Rep* [10.1038/s41598-019-50287-w](#)

Zika Virus-Mediated Death of Hippocampal Neurons Is Independent From Maturation State. *Front Cell Neurosci* [10.3389/fncel.2019.00389](#)

A Phage Protein Aids Bacterial Symbionts in Eukaryote Immune Evasion. *Cell Host Microbe* [10.1016/j.chom.2019.08.019](#)

### Preprints

An updated genotype classification system for Zika viruses *bioRxiv* [10.1101/760066](#)

Phylogeographic and phylodynamic approaches to epidemiological hypothesis testing. *bioRxiv* [10.1101/788059](#)

## Vacancies

**Clinical Bioinformatician at National Virus Reference Laboratory, University College Dublin.** This position will involve development of analytical sequencing services in the laboratory including designing databases, generating programs to automate analysis, and creating next generation sequencing pipelines.

Application deadline: **14 October 2019**

