Title: **Interface between bioinformatics and virology**

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Abstract: In the last years we have witnessed both the emergence of new viral diseases (e.g. MERS, SARS) and the re-emergence of known diseases in new geographical areas (e.g. Zika, Dengue and Chikungunya). Virologists have traditionally concentrated on studying viruses that cause disease in humans, animals or plants. However, there has been estimated around 10^{31} viruses in the biosphere and only a minuscule fraction has been identified, yet. On the other hand, the power of new genome sequencing technologies, associated with new tools to handle "big data", provide unprecedented opportunities to address fundamental questions in virology. We would like to emphasize that many of the common questions raised in virology require specific bioinformatics support and for the need to bring together the expertise of bioinformaticians and virologists.
For this mission, the European Virus Bioinformatics Center (EVBC) was founded on 8$^{\text{th}}$ March 2017 in Jena, Germany. The EVBC has about 100 founding members from over 50 research institutions distributed across 13 European countries. The EVBC is intended to bring together virologists and bioinformaticians across Europe and provide a platform for the implementation of interdisciplinary collaborative projects at local and international scales. I will present first attempts to tackle with virus-specific programs open questions in (co-)phylogeny, high-throughput sequencing data analysis, virus detection, virus-host interaction, and host barriers .

About the Author

since 07/2015	Full Professorship for "High Throughput Sequencing Analysis" at Friedrich Schiller University Jena
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