



Editorial

Bioinformatics tools for the investigation of viral evolution and molecular epidemiology

The 14th edition of the International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology took place for the first time in Africa at the South African National Bioinformatics Institute Cape Town, South Africa, September 8–12, 2008. It was also the first time that so many African students could attend, along with students from all continents, receiving training in the analysis of their virus data.

Investigations on virus evolution, molecular epidemiology and control of viral diseases through drugs and vaccines requires extensive bioinformatics analyses. Phylogenetic analysis is the major tool to investigate virus molecular epidemiology by mapping genetic differences depicting their relationship similarly as in a pedigree. Where does the virus come from, and how did it spread? Data mining techniques allow the identification of mutations associated with particular evolutionary events such as escape from drug or vaccine selection pressure. All this information is crucial to design better public health and veterinary medicine practices, to design strategies to battle agricultural plagues or biodiversity threats. More detailed phylogenetic investigations can unravel the timeframe of viral evolution and allow dating particular events during virus history. Information on selection pressure, viral population dynamics and phylogeography requires increasingly complicated bioinformatic tools.

Many virologists want to learn to use these methods but lack the theoretical background, especially in mathematics, and practical training. This yearly workshop gives a thorough training in the scientific background of molecular evolution, and the application of the phylogenetic analysis and data mining methods (<http://www.rega.kuleuven.be/cev/workshop/>). The phylogenetic methods instructed during the classes are summarized in The Phylogenetic Handbook (<http://www.kuleuven.ac.be/aidslab/>

[phylogenybook/index.htm](http://www.kuleuven.ac.be/aidslab/phylogenybook/index.htm)), the second edition is now available. During the workshop, the sessions alternate between theoretical classes and practical computer classes, and we encourage the students to work on their own data, with help of the teachers. Contacts between participants and with the workshop teachers stimulate discussions on the application of bioinformatics tools to specific viral problems.

This special section is the result of this stimulating environment, and reflects the progress of the students in their work, following this 14th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology. The 15th workshop was in Rotterdam (Erasmus Medical Centre Rotterdam, The Netherlands, September 7–11, 2009) and participating students are now working hard to submit their work for the next proceedings. The 16th workshop is currently planned in Johns Hopkins University, Baltimore, 29 August–03 September 2010, Bethesda, USA. We are looking forward to train again new virologists and help them in their bioinformatics analysis of virus data.

Anne-Mieke Vandamme*
 Katholieke Universiteit Leuven, Laboratory for Clinical and
 Epidemiological Virology, AIDS Reference Laboratory,
 Rega Institute and University Hospitals,
 Minderbroedersstraat 10, 3000 Leuven, Belgium

*Tel.: +32 16332160; fax: +32 16332131
 E-mail address: annemie.vandamme@uz.kuleuven.ac.be
 URL: <http://www.rega.kuleuven.be/cev/workshop/>

Available online 19 February 2010