



## Sequence Analysis in Molecular Epidemiology of Pathogens

January 17 - 20, 2016

### Course description

<b>Faculty</b>	<p><b>Dr. Iñaki Comas, PhD</b> Genomics and Health Unit, FISABIO Public Health, Foundation for the Promotion of Health and Biomedical Research of Valencian Region (Valencia, Spain)</p> <p><b>Leonor Sánchez-Busó, PhD</b> Pathogen Genomics, Wellcome Trust Sanger Institute (Cambridge, UK)</p>
<b>Place</b>	<p><b>CH – 3823 Wengen   SWITZERLAND</b> <del>Room-Bühlstube</del> <b>Hotel Falken</b> (see map on <a href="http://www.epi-winterschool.org/hotels">http://www.epi-winterschool.org/hotels</a>)</p>
<b>Introduction</b>	<p>Molecular techniques can be of great aid to epidemiological investigations. However, classical and molecular epidemiology does not interact many times, which can translate in limited success of public health interventions. Currently, recent developments in massive genome sequencing are leading the performance of epidemiological inferences up to a resolution not possible before. Therefore, it is time to increase the crosstalk between the traditional and molecular epidemiology approaches. This course will help epidemiologists to understand the theoretical basis and the practical consequences of molecular epidemiology analyses. It will use two model pathogens (HIV and Mycobacterium tuberculosis) to illustrate the role of molecular epidemiology during epidemiological investigations. This course is aimed for epidemiologists working or interested in the state-of-the-art molecular epidemiology and typing of infectious diseases agents.</p>
<b>Course objectives</b>	<p>By the end of this short-course participants will have:</p> <ul style="list-style-type: none"><li>• An in-depth theoretical basis to interpret molecular epidemiology results.</li><li>• An understanding of the next generation sequencing technologies and their application to epidemiological investigations.</li><li>• Practical data analysis experience with Sanger sequencing and next generation sequencing data.</li></ul>

**Contact:**

University of Bern | Institute of Social and Preventive Medicine  
Finkenhubelweg 11  
3012 Bern | Switzerland  
[www.epi-winterschool.org](http://www.epi-winterschool.org) | [winterschool@ispm.unibe.ch](mailto:winterschool@ispm.unibe.ch)

<b>What you have to bring</b>	Students will need to bring their own laptops. Prior to the course, we will provide instructions regarding the installation of the software packages that will be used during the course. The operative system used in the practical sessions will be Windows and Linux (provided in a virtual machine).
<b>Outline of course</b>	<p>The course will run over three days and consists of a mixture of lectures and computer practicals. During the extended break in the afternoon, participants can review course materials, catch up on emails or go skiing.</p> <p><i>Sunday, January 17th (15.00 – 18.00)</i></p> <ul style="list-style-type: none"> <li>• Introduction to software and installation.</li> </ul> <p><i>Monday, January 18 (8:30 – 12:00   17:00 – 19:00)</i></p> <ul style="list-style-type: none"> <li>• Introduction to sequence analysis in epidemiology.</li> <li>• Basic concepts in phylogenetics.</li> <li>• Models of molecular evolution and statistical testing.</li> <li>• Phylogenetics and network approaches applied to the epidemiology of infectious diseases.</li> <li>• Practical session:             <ul style="list-style-type: none"> <li>○ Detecting HCV transmission cases: from Sanger sequencing to preliminary detection of transmission clusters.</li> </ul> </li> <li>• Additional information: Recommended packages for phylogenetic and phylodynamic reconstruction of epidemiological patterns.</li> </ul> <p><i>Tuesday, January 19 (8:30 – 12:00   17:00 – 19:00)</i></p> <ul style="list-style-type: none"> <li>• Introduction to next generation sequencing (NGS) technologies.</li> <li>• Processing of raw NGS data.</li> <li>• Analysis pipelines for NGS data in the context of infectious diseases.</li> <li>• Practical session:             <ul style="list-style-type: none"> <li>○ Test run of raw NGS data: from sequencing to SNP detection.</li> </ul> </li> <li>• Additional information: Recommended packages for NGS data processing and analysis.</li> </ul> <p><i>Wednesday, January 20 (8:30 – 12:00   17:00 – 19:00)</i></p> <ul style="list-style-type: none"> <li>• NGS in infectious diseases I. Inferring the global evolution of pathogens.</li> <li>• NGS in infectious diseases II. Genome sequence as an epidemiological marker.</li> <li>• NGS in infectious diseases III. Tuberculosis as an example.</li> <li>• Practical session:             <ul style="list-style-type: none"> <li>○ Inferring a tuberculosis transmission network: from raw data to networks of transmission.</li> </ul> </li> </ul>
<b>Credit</b>	1.5 ECTS
<b>Maximum number of participants</b>	The maximum number of participants on this course will be 18.
<b>Course fee</b>	Academic: CHF 900 Industry: CHF 1800
<b>Registration</b>	Registration on the Winter School website <a href="http://www.epi-winterschool.org">www.epi-winterschool.org</a> .
<b>Course hotels</b>	The participants have to book their accommodation themselves (see map and recommendation on <a href="http://www.epi-winterschool.org/hotels">www.epi-winterschool.org/hotels</a> ).