IRTG - Advanced Method Course (January 2015):

Next Generation Sequencing

In 1990 started the human genome project (HGP) with the aim to identify all genes in the estimated $3x10^9$ base pairs of human DNA. The first draft of the human genome needed 11 years to completion and annotation of all approximately 20.500 human genes an additional 2 years. This international effort had a price tag of $3x10^9$ US$. A parallel project started by Celera in 1998, implementing the newest technologies, needed only 3 years to obtain the draft sequence for one tenth of the costs. One decade later, using Next Generation Sequencing Technologies the cost have plummeted even further and it is possible to sequence a whole human genome for roughly 1000 €. This opens many new opportunities for medical diagnostics. For example, monogenetic diseases caused by mutations in protein coding genes, are relatively easily to unveil by sequencing the Exomes of patients and healthy parents.
In this course we will isolate genomic DNA from the blood of one volunteer. Prepare a whole genome library using the NEBNext® Ultra Dual Index method from New England Biolabs. Sequence the genome on an Illumina NextSeq 500 overnight. In parallel, we will analyse the genomic DNA for mutations in the WAS gene using Sanger sequencing.

Literature

- International Human Genome Sequencing Consortium (2001) Initial sequencing and analysis of the human genome. *Nature*; **409**(6822):860-921
- Venter JC et al. (2001) The sequence of the human genome. *Science*; **291**(5507):1304-51
- Chakravarti A. (2001) To a future of genetic medicine. *Nature*; **409**(6822):822-3
- van Dijk EL et al. (2014) Ten years of next-generation sequencing technology. *Trends Genet*; **30**(9):418-426
- Conley ME and Casanova JL (2014) Discovery of single-gene inborn errors of immunity by next generation sequencing. *Current Opinion in Immunology*; **30**, 17–23