



EPIZONE Workshop on Next Generation Sequencing applications and Bioinformatics

Learn from *Epi-SEQ* and *EPIZONE* NGS experts.

Program:

- **Tuesday 5 April 2016**

Introduction to NGS & data structure

09:00-09:15 Welcome

09:15-09:30 Practical announcements

09:30-10:15 Get to know: participants and trainers briefly introduce their background and NGS interests.

10:15-10:45 coffee break

10:45-11:45 Introduction to Next Generation Sequencing Technologies (Fredrik Granberg)

11:45-12:45 DNA library preparation solutions for NGS (G. Freimanis)

12:45-13:45 Lunch Break

13:45-14:45 Introduction to NGS data formats and analysis. (R. Orton)

14:45-15:45 Introduction to data manipulation in Linux operating systems/to Linux command line (R.Orton)

15:45-17:45 Practical: Linux command line basics. PART1 (R. Orton)

- **Wednesday 6 April 2016**

Practical sessions (Linux & Galaxy)

09:00-12:00 Practical: QC of data, sequence assembly, ... in Linux. PART2 (R. Orton)

12:00-1300 Lunch Break

13:00-14:00 introduction to analysis integration solutions (Galaxy) (A. Bossers)

14:00-17:30 Practical: building an analysis pipeline in Galaxy (A. Bossers)

19:00: *Social event*

- **Thursday 7 April 2016**

Practical sessions, viral metagenomics, and applications

09:00-12:00 Open practical session on Linux and Galaxy (repetition or using additional datasets provided)
all trainers

12:00-1300 Lunch Break

13:00-14:00 viral metagenomics (D. Höper)

14:00-15:30 Practical: metagenomics data analysis using RIEMS (D. Höper)

15:30-15:45 Coffee break

15:45-16:45 Applications, lecture 1 ASFV (Fredrik Granberg)

16:45-17:45 Applications, lecture 2 De novo assembly of DNA virus genomes from Pacbio reads (E. Mathijs)

- **Friday 8 April 2016**

Applications of NGS in vet virology. Detailed presentations from experimental design to data analysis and interpretation.

09:00-09:45 Tracing avian influenza virus evolution using a deep sequencing approach (A. Fusaro)

09:45-10:30 High definition analysis of FMDV evolution (G. Freimanis)

10:30-10:45 *Quick coffee*

10:45-11:30 "Pox virus genome analysis" (D. Höper)

11:30-12:15 Quasispecies analysis of WNV host adaptation (S. Van Borm)

12:15-13:00 *Lunch*

13:00-14:00 Pestivirus population analyses (D. Höper)

14:00-15:00 "Coronavirus sequencing and genome constraint characterization" (Y. Blanchard)

15:00-15:30 Conclusions & closing of the workshop

Trainers:

- Steven Van Borm, CODA-CERVA, Belgium
- Elisabeth Mathijs, CODA-CERVA, Belgium
- Richard Orton, University of Glasgow, United Kingdom
- Dirk Höper, FLI, Riems, Germany
- Alice Fusaro, IZSve, Padova, Italy
- Fredrik Granberg, SLU, Upsala, Sweden
- Graham Freimanis, Pirbright Institute, UK
- Yannick Blanchard, ANSES, Ploufragan, France
- Alex Bossers, CVI, Lelystad, The Netherlands

Local organizer: Steven Van Borm, CODA-CERVA