EUROPEAN SOCIETY OF HUMAN GENETICS

NGS Variant Interpretation 2020

To establish precision medicine in the health care service, there is a need for doctors and clinical laboratory geneticists to understand how to interpret and use genetic variant information from next generation sequencing technology, in the clinic.

This course focusses on the interpretation of single nucleotide variants and copy number variants from exome sequencing data for obtaining a genetic diagnosis. Lectures address topics like filtering strategies, population frequencies, ACMG guidelines, and HGVS nomenclature. During practical sessions you will apply the material from the lectures to obtain a genetic diagnosis for real-life exome cases. The course is intended for individuals that have beginning or intermediate experience with exome sequencing.

Workshop Instructors:

- *Christian Gilissen, bioinformatician, expert in WES analysis*
- *Rolph Pfundt, clinical molecular geneticist, expert in cytogenetics of WES*
- Helger Yntema, clinical molecular geneticist, expert in molecular interpretation of WES
- *Siddharth Banka, clinical geneticist*

Registration Fee: EUR 200,00 *Attendance limited to max. 40 participants.*

PROGRAMME

Day 1: Thursday, June 4, 2020

08:30-09:00	**Registration**
09:00-09:45	**Lecture: General background on WES sequencing and bioinformatics** • *What is WES and how does it work (sequencing techniques, WES captures)* • *What analysis steps are needed for WES (QC, mapping, calling, annotation)* • *Quality control of data + sequence coverage*
09:45-10:30	**Lecture: Exome data interpretation of SNVs** • *Filtering strategies: Panel analysis versus open exome* • *Variant classification / ACMG guidelines* • *Use of Phenotype for filtering* • *Commercial software for variant filtering* • *Use of external databases (gnomad / exac)* • *SNV nomenclature*
10:30-10:45	Coffee Break

10:45-12:15	**Workshop: Exome interpretation of SNVs with cases** • *Panel analysis* • *Full exome analysis* • *Inheritance patterns*
12:15-12:30	Q&A
12:30-13.30	Lunch
13:30-14:00	**Lecture: Technical challenges in SNV detection and interpretation** • *Potential pitfalls: mapping errors, SNV calling errors, CNV calling errors, annotation errors)*
14:00-14:45	**Lecture: Exome data interpretation of CNVs** • *CNVs from arrays compared to Exomes* • *CNV detection algorithms and their limitations* • *CNV reference cohorts* • *Use of external databases (Decipher)* • *Visualization* • *Nomenclature of CNVs*
14:45-15:00	Coffee Break
15:00-16:30	**Workshop: Exome interpretation CNVs with cases** • *Unbalanced translocations* • *Aneuploidies* • *Microdeletions* • *Normal copy number variation* • *Problematic genome regions*
16:30-17:00	Q&A, Wrap-up

Day 2: Friday, June 5, 2020

09:00-09:45	**Lecture: Complex WES cases** • *Reduced penetrance* • *Mosaicisms* • *Unconventional inheritance patterns* • *Combination of different variant types* • *Imprinting* • *Uniparental disomies* • *Incidental findings*
09:45-11:15	**Workshop: Exome data interpretation of complex cases** • *Cases based on the previous lecture*
11:15-11:30	Coffee Break
11:30-12:30	**Interesting cases by participants that they present**
12:30-13:30	Lunch
13:30-16:30	**TBA**
16:30-17:00	Q&A, Wrap-up