

Frontiers of Functional Genomics ESF program

European Meeting on Next Generation Sequencing

Hands-on Workshops August 29, 2010

Leiden University Medical Center, The Netherlands

In collaboration the EMBL's European Bioinformatics Institute (EMBL-EBI), we offer hands on activities where users (preferably PhD students or researchers doing lab work rather than PIs) can learn how to make the most of the data resources hosted at the EBI and get first-hand experience in next generation sequence data analysis.

Four concurrent hands on computer workshops will be organized on Sunday August 29 from 13:30-15:00 and from 15:30-17:00. Please indicate which two workshops you would like to attend. Due to space limitations, placement of your first choice may not be possible; please indicate whether you would accept another workshop instead. You will receive confirmation of placement.

Expression. This session will instruct participants on how to retrieve biologically meaningful information from microarray data using EBI resources. Participants will learn how to browse and retrieve data from the **ArrayExpress** public repository of functional genomics data and the **Atlas of Gene Expression**, a curated subset of gene expression. This tutorial also spells out which types of data should be submitted to **ArrayExpress** and the **European Genome-phenome Archive**, a permanent repository for all types of potentially identifiable genetic and phenotypic data. Teacher: Emma Hastings (EMBL-EBI).

Genomes. A session focusing on browsing genome sequences with **Ensembl** to explore variation and comparative genomics, and the **1000 Genome Browser**, a browser for the 1000 Genomes project, which aims to create the most detailed and medically useful picture of human genetic variation (<http://browser.1000genomes.org>). Teacher: Bert Overduin (EMBL-EBI).

Sequence. A session focusing on tools for similarity searches as well as retrieving information from **ENA**, the European Nucleotide Archive, using the **ENA Browser**. Search tools available for the nucleotide and protein sequence databases include **BLAST**, the Smith-Waterman-based methods **FASTA** and **SSEARCH**, as well as the iterative searches **PSI-BLAST** and **PSI-SEARCH**. Various tools enhance these algorithms, including sequence alignment programs, **InterPro** functional predictions, and links to various databases that provide a wide range of annotation. Teacher: Jennifer McDowall (EMBL-EBI).

Next generation sequence data analysis. Using a pipeline in Galaxy, you will learn how to process sequence reads to generate report files and browser tracks. Teacher: Matthew Hestand (Leiden University Medical Center).