EBI Roadshow
Databases, Sequence Alignment, ArrayExpress & Ensembl

AMC, Amsterdam
9-10 April 2013

Venue: Amsterdam Medical Centre, Amsterdam
Dates: 9-10 April 2013
Target audience: This course is aimed at researchers across the Netherlands who wish to develop their understanding of the data resources and tools available from EMBL-EBI.
Organizers: Antoine van Kampen (AMC), Aldo Jongejan (AMC), Tom Hancocks (EBI), Johanna Langrish (EBI), Celia van Gelder (NBIC).
Trainers: Andrew Cowley (External Services), Amy Tang (Functional Genomics), Emily Pritchard (Ensembl).
Registration: Please look at www.nbic.nl -> Education -> NBIC PhD School -> Enrolment.
More information: You can also contact Celia van Gelder at education@nbic.nl for information.

Description

This course is aimed at researchers across the Netherlands who wish to develop their understanding of the data resources and tools available from EMBL-EBI. The programme provides an overview of commonly-used EBI public resources for the analysis of nucleotide, protein and microarray data. Delegates will learn about these data resources in short lectures and then gain hands-on experience in using them to analyse data. The practical exercises use web-browser-based tools and assume no previous training in bioinformatics programming.

Programme

Time	Subject	Trainer
Day 1 – April 9 2013		
09:00-09:30	**Welcome and registration**	
09:30-10:30	Introduction to the databases at the EBI	Andrew Cowley
10:30-11:00	**Break**	
11:00-12:30	Introduction to the databases at the EBI	Andrew Cowley
12:30-13:30	**Lunch**	
13:30-15:00	Sequence Searching and Alignment	Andrew Cowley
15:00-15:30	**Break**	
15:30-17:00	Sequence Searching and Alignment	Andrew Cowley

Day 2, April 10 2013		
09:00-09:30	**Welcome and registration**	
09:30-10:30	ArrayExpress: Public database for transcriptomics data & Gene Expression Atlas	Amy Tang
10:30-11:00	**Break**	
11:00-12:30	ArrayExpress: Public database for transcriptomics data & Gene Expression Atlas	Amy Tang
12:30-13:30	**Lunch**	
13:30-15:00	Ensembl for new Ensembl users	Emily Pritchard
15:00-15:30	**Break**	
15:30-17:00	Ensembl for new Ensembl users	Emily Pritchard

What will I learn?

After this course you should be able to:

- Navigate the EBI website and the different ways to access and retrieve data
- Understand the depth and variety of tools and databases available at the EBI
- Recognize the major databases at EBI
- Understand the principles of nucleotide and protein sequence searching
- Use the different sequence searching tools available at the EBI (including BLAST, FASTA and iterative searches), and which ones are appropriate for different applications
- Use the different sequence alignment tools available
- Browse and retrieve data from the ArrayExpress public repository of transcriptomics data
- Browse and retrieve data from the Gene Expression Atlas
- Conduct a query for condition-specific gene expression patterns as well as broader exploratory searches for biologically interesting genes/samples correlations
- Understand the process of genome annotation with a focus on vertebrates and other eukaryotes
- Use data mining approaches based on BioMart
- Understand how to look at comparative genomics data (gene trees and homologies) and sequence variation (including structural variation)