







Small molecules, gene products and their interaction

Day 1-3: Relevant EBI resources: roadshow by EBI

Day 4-5: Pathway and network approaches: diXa Training & BiGCaT

General information

Date: July 1- 5, 2013

Location: Maastricht School of Management, Maastricht, the Netherlands

Website: http://www.nbic.nl/education/course-

overview/pages3/1/coursedetails/small-molecules-gene-products-and-

their-interaction/

Organisers: Chris Evelo (Maastricht University, www.bigcat.unimaas.nl), Egon

Willighagen (Maastricht University), Tom Hancocks (EMBL-EBI), Vera Matser (EMBL-EBI & diXa, www.dixa-fp7.eu), Celia van Gelder (NBIC,

www.nbic.nl)

Contact: Chris Evelo (chris.evelo at maastrichtuniversity.nl),

Celia van Gelder (education at nbic.nl)

Registration: http://www.nbic.nl/education/nbic-phd-school/enrolment/. The

registration deadline is June 27, 2013. After registration you will

receive further information about hotel accommodation.

Course description

This five day course introduces various databases and data analysis tools to get grips on the big data in the life sciences. The course consists of two parts:

Part 1 (day 1-3) introduces the advanced uses of the gene and genomes databases, small molecule resources, the protein sequence databases, and interaction and pathway databases at EBI (a.o. UniPROT, ENSEMBL, CHEMBL, IntAct and Reactome). This first part is an EBI Roadshow hosted by UM & NBIC.

Part 2 (day 4-5) focuses on real data analysis using pathway and network approaches with links to the databases covered in first part. Tools that will be used include WikiPathways, PathVisio and Cytoscape. Covered aspects include pathway creation, data preparation for analysis, pathway analysis, network analysis and network extension using target information. This second part is provided by the department of Bioinformatics-BiGCaT at Maastricht University in collaboration with the diXa FP7 project on systems biology approaches in toxicogenomics. The diXa project will provide examples about (re)use and (re)analysis of large genomics datasets.

Target audience

This course is intended for researchers in Life Sciences, Bioinformatics and Systems Biology, Pharmacology, Toxicology.









Programme

Time	Subject	Trainer
Day 1		
12:30-13:30	Welcome and registration	
13:30-14:00	Introduction to the EBI	Denise Carvalho-Silva
14:00-15:00	Browsing genes and genomes with Ensembl	Denise Carvalho-Silva
15:00-15:30	Break	
15:30-17:00	Browsing genes and genomes with Ensembl	Denise Carvalho-Silva
17:00	End of day 1	
Day 2	Description of the Control of the Co	Daving Consulting City
09:00-10:30	Browsing genes and genomes with Ensembl	Denise Carvalho-Silva
10:30-11:00	Break	
11:00-12:30	Browsing genes and genomes with Ensembl	Denise Carvalho-Silva
12:30-13:30	Lunch	
13:30-15:00	Small Molecule Resources	Louisa Bellis
15:00-15:30	Break	
15:30-17:00	Small Molecule Resources	Louisa Bellis
17:00	End of day 2	
Day 3		
09:00-10:30	Protein Sequence Databases	Sandra Orchard
10:30-11:00	Break	
11:00-12:30	Protein Sequence Databases	Sandra Orchard
12:30-13:30	Lunch	
13:30-15:00	Interactions and Pathways	Sandra Orchard
15:00-15:30	Break	
15:30-17:00	Interactions and Pathways	Sandra Orchard
17:00	End of day 3	
Day 4		
09:00-10:30	Pathway analysis with WikiPathways and PathVisio	Martina Kutmon & Egon Willighagen
10.30-11:00	Break	
11:00-12:30	Pathway analysis with WikiPathways and PathVisio	Martina Kutmon & Egon Willighagen
12:30-13:30	Lunch	
13:30-15:00	Introduction to the diXa project	Stathis Kanterakis
15:00-15:30	Break	
15:30-17:00	Introduction to ArrayAnalysis.org	Lars Eijssen
17:00	End of day 4	
Day 5		
09:00-10:30	Cytoscape tutorial - basic	Martina Kutmon & Anwesha Dutta
10.30-11:00	Break	
11:00-12:30	Cytoscape tutorial - advanced	Martina Kutmon & Anwesha Dutta
12:30-13:30	Lunch	
13:30-15:00	ConsensusPathDB	Christopher Hardt
15:00	End of course	,