**EMBL-EBI**

# Biological Networks: Reconstruction, Analysis and Modelling, 5th May 2009 – 6th May 2009

Dear associates and invited participants,

We would like to invite you to the EBI Industry Programme workshop on Biological Networks: Reconstruction, Analysis and Modelling, May 5th to 6th 2009 at the European Bioinformatics Institute, Hinxton, Cambridge, on May 5th to 6th 2009.

## Motivation

Reductionist approaches in molecular biology combined with the development of high throughput platforms have led to several large information resources documenting structures, functions and experimental data relating to sub cellular components. What is important now is to infer and understand how molecules function within systems in ways that are not predictable from their individual properties. Network based approaches are an important element of this analysis and modelling.

This workshop will bring together experts and key opinion leaders from the academic and industrial research groups to identify key challenges, opportunities and bottlenecks in the process of network reconstruction, network analysis and network based modelling.

The workshop is sponsored by the EMBL-EBI Industry programme and is positioned as one of a number of pre-competitive initiatives supported by the programme.

The workshop is dividing into three sections focussed on

- Reconstructing networks (afternoon of 5th May)
- Analysing Networks (morning of 6th May)
- Modelling networks (afternoon of 6th May)

The workshop will include presentations by industry partners on what are seen as challenges and opportunities in this area and close with a discussion around these themes. A short report will be written on the workshop and presentations will be made available in PDF format to all participants.
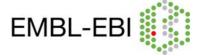
We are grateful to Bryn Williams-Jones (Pfizer), Andrew White (Unilever) and Cary O'Donnell (AstraZeneca) for advice on the construction of the agenda. Any questions about the agenda should be sent to Nicolas Le Novère (lenov@ebi.ac.uk) and Dominic Clark (clark@ebi.ac.uk). Any questions about logistics should be sent to Liz Ford (ford@ebi.ac.uk).

The link for registration for industry programme members is:

http://events.embl.org/iEBMS/reg/reg_p1_form.aspx?oc=20&ct=GBPNORMAL&eventid=5011

The link for registration for invited speakers is:

http://events.embl.org/iEBMS/reg/reg_p1_form.aspx?oc=20&ct=SPEAKER&eventid=5011

**AGENDA** (Speakers listed are tentative – except where in **Bold**. Titles are indicative)

## Tuesday 5th May 2009

| | |
|---|---|
| 12.30 | *Registration and buffet lunch* |
| 13.30 | Welcome and Introductions - **Dominic Clark** & Representative of the Industry Programme members |
| 13.40 | Overview of the Agenda - **Nicolas Le Novère** |
| | **Session 1: Reconstructing Networks** |
| 14.00 | • 14.00 Short presentations by members of the industry program involved in the analysis of biological networks, or needing to invest efforts in that direction <br> • 14.45 Primary data resource - Array-Express Atlas. „How to retrieve, download and process gene expression data in a form suitable to reconstruct gene networks and pathway-based data mining" **Misha Kapushesky** –(EMBL-EBI) <br> • 15.15 Primary data resource – IntAct. How to retrieve, download and process protein interaction data in a form suitable to reconstruct protein networks. **Sam Kerrien** (EMBL-EBI) <br> • 15.45 Discussion |
| 16.00 | • Tea/Coffee break |
| 16.30 | • Modelling and reconstruction of gene networks from expression data **Thomas Schlitt** (King's College London). <br> • Integrating protein-protein interactions and text mining for protein function prediction Ulf Leger, Humboldt-University Berlin, invited. <br> • Discussion: Which kind of data is missing in the current public repositories. Where should be the emphasis of ELIXIR? What sofware is missing in a usable form? |
| 18.00 | Close of first day |
| 18.30 | *Drinks reception* |
| 19:00 | Dinner |

EMBL-EBI

## Wednesday 6th May 2009

| 08.45 | *Tea/Coffee* |
|-------|--------------|
| 09.15 | Welcome and summary of Day 1 - Dominic Clark & Nicolas Le Novère |
| | **Session 2: Analysing Networks** |
| 09.30 | • 09.30 Introduction<br>• 09.45 Analysing transcriptional and metabolic networks - Nick Luscombe (EMBL-EBI, invited)<br>• 10.15 Data integration with Cytoscape **Samad Lotia** (Pasteur Institute, Paris, to be invited)<br>• 10.45 Discussion |
| 11.00 | Tea/Coffee |
| 11.30 | Tutorial: Linking Cytoscape and CellDesigner with BiNoM: from networks to models<br>**Laurence Calzone** (Curie Institute, Paris) |
| 12.30 | Lunch |
| | **Session 3: Modelling Networks** |
| 14.00 | • 14.00 Introduction (**Nicolas Le Novère**)<br>• 14.15 Encoding and annotating models with SBML - Nicolas Le Novère (EMBL-EBI)<br>• 14.45 Annotating and merging models with semanticSBML - **Wolfram Liebermeister** (Max Planck Institute for Molecular Genetics, Berlin) |
| 15.15 | *Tea/Coffee* |
| 15:45 | • Qualitative models of influence networks - **Ioannis Xenarios** (SIB, Geneva) |
| 16.30 | Wrap up discussion (chair **Dominic Clark**, discussant: **Nicolas Le Novère**) |
| 17.00 | *Close of meeting* |