Network Biology SIG 2013
July 19th, Berlin, Germany

Invited Keynotes

Benno Schwikowski – Head of Systems Biology Lab at Institut Pasteur, Paris, France
Natasa Przulj – Assoc. Prof. in Computational Network Biology at Imperial College, London, UK
Esti Yeger-Lotem – Senior Lecturer in Clinical Biochemistry at The National Institute for Biotechnology in the Negev, Israel
Stefan Schuster – Head of Dept. of Bioinformatics at Friedrich-Schiller University Jena, Germany
Michael Schroeder – Director of Biotechnology Center at Technical University Dresden, Germany

Accepted abstracts

David Amar – *"Algorithms for Mapping Modules in Pairs of Biological Networks"*
Tel-Aviv University, Israel

We study a fundamental problem in the analysis of pairs of biological networks. The goal is to detect gene sets that are strongly connected in one network and have dense connections between some of the sets in the other network. Hence, modules reflect association in the first network, and their relations reflect association in the other, represented as a map of modules, thereby providing a richer picture than is achievable by each network separately. We develop novel algorithms for module-map construction that analyze the two networks simultaneously. We show that they considerably outperform prior art on simulated and real data from two application domains: (1) differential correlation of disease gene expression data, and (2) protein-protein interactions and genetic interactions. In a third, novel application domain, we apply our method on two networks of Arabidopsis Thaliana data: a protein-protein interaction network, and a metabolic-dependency network. We show that the constructed module map of the networks can help in gene function prediction of Arabidopsis genes.

Robin Haw – *"Reactome Knowledgebase and Functional Interaction (FI) Cytoscape Plugin"*
Reactome, Canada

Reactome is an open-source, free access, manually curated and peer-reviewed biological pathway knowledgebase. Recent extensions of our data model accommodate the annotation of disease events, such as those associated with cancer. To support the graphical representation of cancer-related pathways, we have altered our Pathway Browser to display disease variants and events in a way that allows comparison with the wild type pathway, and displays connections between perturbations in cancer and other biological pathways. The curation of pathways associated with cancer, coupled with our efforts to create other disease-specific pathways, will interoperate with our existing pathway and network analysis tools. Previously, we have developed the Reactome FI Cytoscape plugin, which can construct a FI sub-network based on provided gene list, perform network clustering analysis using a very fast, in-house implemented, modularity-driver spectral partition clustering algorithm, and annotate individual network modules using pathway/Gene Ontology enrichment analysis. A recent extension of Reactome FI network, with updated protein-protein interactions and other pair-wise protein or gene relationships, genome-wide screening data sets, including interactions between transcription factors and their targets from the ENCODE project, and mouse protein-protein interactions has increased the FI network to covering just over half of

human proteins in SwissProt and almost 274,000 interactions. We have also implemented the HotNet algorithm, for finding significantly altered sub-networks by using a graph heat-kernel model. The HotNet algorithm, combined with the survival analysis function and other previously implemented features of the Reactome FI plugin should provide a powerful framework for molecular signature discovery.

Vuk Janjic – *"A Journey to the Core of Human Disease"*

Imperial College London, UK

We demonstrate that we can computationally isolate a sub-network of the human protein-protein interaction (PPI) network that is topologically and functionally homogeneous and statistically significantly enriched in disease genes and drug targets. It also contains "driver" genes, postulated to be involved in key mechanisms for disease onset and progression, which indicates that topology that "drives" disease formation may exists within our interactome. Hence, we call this network the Core Diseasome and highlight how it could be used in therapeutics. In addition, we use a similar approach to look "inside the core" of the new human G-protein coupled receptor PPI network from Stagljar Lab. We find the whole GPCR network to be a signal transduction "backbone" of the human PPI network, with its "core" proteins primarily expressed in brain, and involved in a range of personality and behavioural disorders.

Thomas Kelder – *"Functional Network Signatures Link Anti-diabetic Interventions with Disease Parameters"*

TNO, The Netherlands

To improve our understanding and ability to intervene with complex, multi-factorial diseases such as type 2 diabetes mellitus (T2DM) it is important to discover the molecular networks underlying the biological system and elucidate which and how interactions contribute to pathology. This study identifies hepatic network signatures that link effects of dietary and drug interventions with disease parameters for T2DM. A recent study [1] showed that Dietary Life Style Intervention (DLI) was successful in reverting nearly all T2DM risk factors and complications. Drug interventions improved hyperglycemia, however T2DM complications were not improved or were even aggravated. Here we identify gene co-expression modules that significantly correlate with T2DM disease parameters, extract intervention-specific subnetworks and prioritize the most relevant targets and interactions. This results in functional network signatures and mechanistic paths characteristic for both positive and negative effects of anti-diabetic interventions, holding promise for aiding an improved intervention design.

Martina Kutmon – *"Building Biological Regulatory Networks in Cytoscape Using CyTargetLinker"*

Maastricht University, The Netherlands

The regulation of gene expression and protein synthesis is still far from completely known because of its complexity, dynamic mechanisms and diversity in different settings. However, by deciphering the role of important regulators, like transcription factors and microRNAs, a better understanding of the regulatory processes can be obtained.

Our systems biology approach combines and analyzes regulatory interactions from different available resources together, which is essential in interpreting the regulation of biological processes. We developed CyTargetLinker, a Cytoscape app, for building regulatory networks in a user-friendly and flexible manner. Various interactions, like microRNA-target, transcription factor-gene and/or drug-target, can be added to genes, proteins, and/or microRNAs in a biological network.

CyTargetLinker provides a quick and extensive enrichment of biological networks in Cytoscape. The visualization options allow biological interpretation of complex regulatory networks in a graphical way. Importantly the incorporation of our tool into the Cytoscape framework allows the usage of CyTargetLinker in combination with a wide variety of other apps for further network analysis.

We will present the basic workflow of CyTargetLinker and two of our biological applications: (i) integrating ENCODE (Encyclopedia of DNA Elements) data, especially transcription factor-gene interactions, into our network approaches and (ii) using CyTargetLinker to study the influence of drugs on biological pathways.

Tijana Milenkovic – *"What Can Biological Networks Tell Us About Aging?"*

University of Notre Dame, Indiana, USA

Studying human aging is of societal importance. Since human aging is hard to study due to long lifespan and ethical constraints, analogous to sequence alignment, we use network alignment to transfer aging-related knowledge from model species to human. Also, we integrate static network data with aging-related gene expression data to construct dynamic, age-specific networks. Then, we predict genes whose network positions significantly change with age as aging-related.

Gang Su – *"CoolMap Cytoscape App: Flexible Multi-scale Heatmap-Driven Molecular Network Exploration"*

University of Michigan, Ann Arbor, USA

We developed the CoolMap Cytoscape App to offer data driven Cytoscape network exploration for large omics datasets. It is built on CoolMap, a flexible, versatile and multi-scale heatmap application. CoolMap is a dynamic heatmap with multiple levels of rows and columns. The relationships between the multi-level rows or columns can be defined by external data structures such as Gene Ontology, KEGG Pathway or from clustering results. As a result, overviews of the original data can be displayed at concept levels (e.g., different level of Gene ontology) using aggregation functions such as mean, quantile, variance, etc. If strong signals could be identified from an aggregated view, the corresponding ontology rows/columns can be further expanded to reveal underlying details while maintaining the aggregation level of the neighbor context. By using such a technique, big heatmaps can be explored in a much condensed, high-level format, arranged in pre-defined or generated groups. A custom rendering engine was developed to render heatmap on the base level (color, shape, etc.), or in aggregated level (sorted values, boxplot, etc.). The CoolMap view can be explored interactively using zoom, pan, per-cell-level-resize; rows and columns can be dragged-reordered for user-desired arrangements, and the Coolmap view can be searched and filtered.

Panelists

Gabrielle Sales – University of Padova, Italy
Daniela Boernigen – Harvard University, Boston, USA
Inna Kuperstein – Institut Curie-Inserm, France
Frank Kramer – University Medical Center Göttingen, Germany

Posters

George Acquaah-Mensah - *In Situ Hybridization Data and Brain Region-specific Transcriptional Regulatory Relationships*

Karthik Azhagesan - *'Joint' phylogenetic profiling of protein pairs reveals novel unique protein-protein associations and evolutionarily conserved protein interactions*

Sandhya Balasubramanian - *Reconstruction of gene networks from coding and non-coding genomic data*

Ruth Barshir - *Differential analysis of human tissues reveals major factors leading to the tissue-specific manifestation of hereditary diseases*

Ruth Barshir - *The TissueNet database of human tissue protein–protein interactions*

Omer Basha - *A network biology approach to decipher melanoma pathways*

Daniela Boernigen - *Predicting biomolecular mechanisms in pathway-specific functional relationship networks in prostate cancer*

Tobias Czauderna - *Visualising biological networks in SBGN using VANTED and its SBGN-ED add-on*

Natasa Djurdjevac - *Understanding biological networks using random-walk-based approaches*

Luis M Escudero - *Systems Biology methods for image analysis in development and disease*

Keywan Hassani-Pak - *QTLNetMiner - Using integrated plant and animal knowledge networks for candidate gene discovery*

Marcin Joachimiak - *Deep Surveys of Biological Modules: K-biclustering Gene Expression and Phenotype Data*

Tim Kacprowski - *NetworkPrioritizer facilitates the prioritization of genes and other molecules based on integrated biological networks*

Frank Kramer - *Integrating Prior Pathway Knowledge into Methods for Network Reconstruction*

Inna Kuperstein - *Signalling networks construction, analysis and modelling for explaining synthetic genetic interactions in cancer*

Victor Mireles - *Finding connected sub-networks consisting of similar nodes*

Suzanne Paquette - *BioTapestry: New Platform, New Directions*

Dexter Pratt - *NDEx - An Information Commons for Biological Networks*

Ilan Smoly - *The yeast phosphorylation network is composed of numerous, hierarchical and reactive kinases and a small set of robust, highly-abundant phosphatases*

Nyima Tenzin - *Linear and nonlinear transcriptomic response to dietary fat intake in PPI network communities*

Giorgio Valentini - *Network integration boosts disease gene prioritization*

Andra Waagmeester - *Visualizing Linked Open Data in Biological Pathways and Networks*