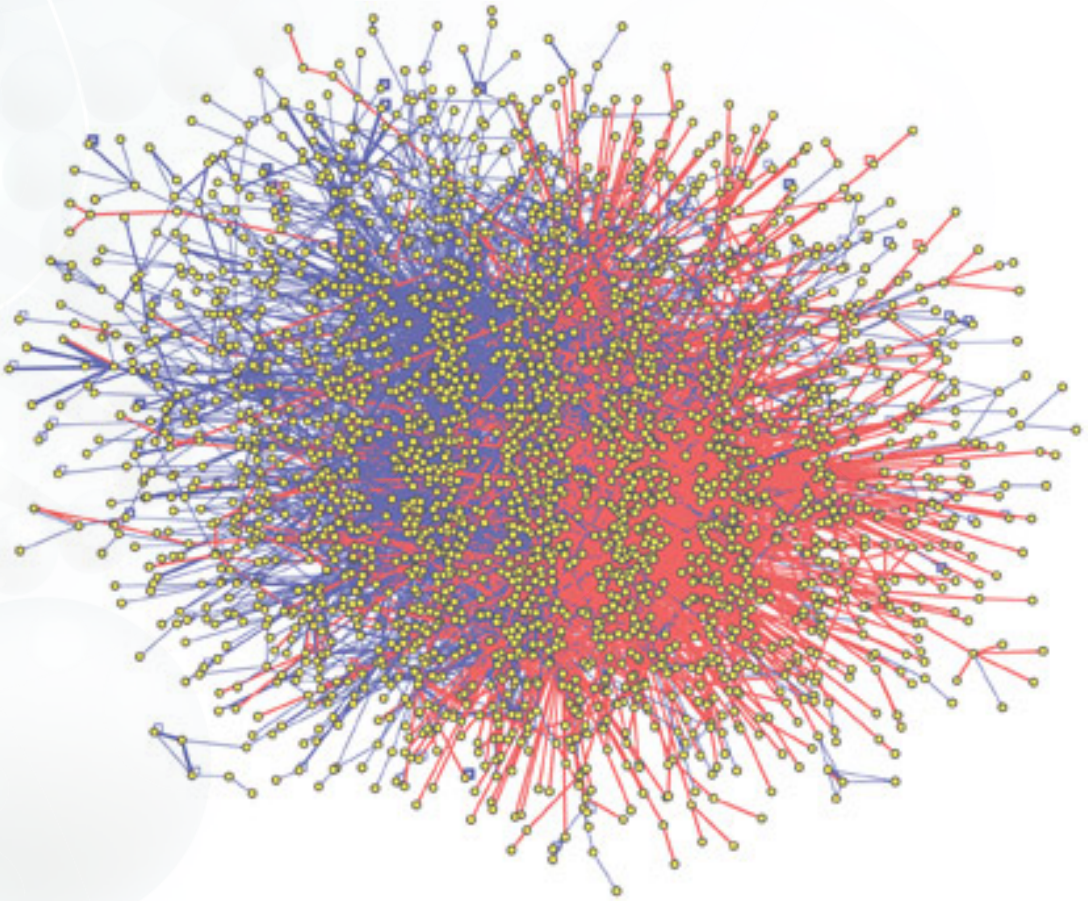
Network Biology / Integromics Bioinformatics:

Applications Towards Medicine

NORBIS



August 23-25 2017, Bergen, Norway

Illustration:

Centre for Cancer Biomarkers
Norwegian Centre of Excellence – University of Bergen

CENTRE FOR DIGITAL LIFE NORWAY

The Research Council of Norway

Contents **Page**

Program

Network Biology/Integromics Bioinformatics – Applications Towards Medicine

Grand Hotel Terminus, Bergen, 23-25 August 2017

Wednesday 23 August

09:00	09:15	**Inge Jonassen:** Welcome
09:15	10:45	**Konstantina Dimitrakopoulou:** Introduction to biological networks
10:45	11:00	*COFFEE BREAK*
11:00	12:00	**Christos Ouzounis:** Developing computational biology: From comparative genomics to systems biomedicine
12:00	13:00	*LUNCH*
13:00	14:30	**Eileen Marie Hanna:** Introduction to Cytoscape *Note:hands-on tutorial, for all participants*
14:30	14:45	*COFFEE BREAK*
14:45	16:45	**Pablo Porras Millan:** Protein interaction data (databases and analysis) *Note: Cytoscape hands-on session, for selected participants*
16:45	17:00	*COFFEE BREAK*
17:00	18:00	**Pablo Porras Millan:** Protein interaction data (databases and analysis) *Note: Cytoscape hands-on session, for selected participants*

Thursday 24 August

09:00	09:55	**João Pedro de Magalhães:** Bioinformatics, systems biology and ageing: Navigating the new oceans of data to discover the Fountain of Youth
10:00	11:00	**Albert-László Barabási:** Network Medicine: From Cellular Networks to the Human Diseasome
11:00	11:15	*COFFEE BREAK*
11:15	12:15	**Benno Schwikowski:** LEAN discovery of hot spots in networks
12:15	13:15	*LUNCH*
13:15	14:15	**Leonidas Alexopoulos:** Pathway-based approaches for early drug and biomarker discovery. Research and Industrial applications in osteoarthritis, liver cancer, non-alcoholic fat liver disease, multiple sclerosis, melanoma, chronic kidney disease, and liver toxicity.
14:15	15:15	**Eivind Almaas:** Differential co-expression network analysis: from pathways to disease
15:15	15:30	*COFFEE BREAK*
15:30	17:30	**Aristidis Vrahatis:** Integrative pathway analysis *Note: R/Bioconductor hands-on session, for selected participants*
19:00		*DINNER at Kalfaret Brygghus*

Friday 25 August

09:00	10:00	**Alfonso Valencia:** Networks based approaches for the study of epigenomics
10:00	11:00	**Ruth Barshir:** Using network approaches towards understanding tissue-specificity of hereditary diseases
11:00	11:15	*COFFEE BREAK*
11:15	12:15	**Laura Furlong:** DisGeNET discovery platform 5.0: Illuminating the study of human diseases
12:15	13:00	*LUNCH*
13:00	13:45	**Marc Vaudel:** Networks as a roadmap for clinical data
13:45	13:55	**Christine Stansberg:** Closing remarks and NORBIS announcements
14:00	14:30	Refreshments served before the Horizon lecture Auditorium 1 in the UiB building for Natural Sciences, see map
14:30	15:45	**Albert-László Barabási,** Horizon lecture: Network Science - From structure to control

Abstracts of invited lectures

Christos Ouzounis, CERTH, Centre for Research and Technology Hellas, Thessaloniki, Greece

Developing computational biology: From comparative genomics to systems biomedicine

Modern biology is experiencing a deep transformation by the expansion of molecular level measurements at all scales, using omics technologies. A key element in this transformation is the field of bioinformatics, that has -in the meanwhile- permeated pretty much all of biological and biomedical research and is now emerging as a key inter-disciplinary area that connects the natural sciences, advanced engineering, science education and policy. While omics information provides the elements for research & development in the life sciences, network biology has indeed provided a language with which meaning can be extracted from complex datasets. I will briefly review our earlier efforts in comparative genomics, the transition to systems biomedicine and discuss recent research activities in this area as well as initiatives to develop the field in the wider region and the lessons learned, regarding such efforts away from the major epicentres.

Pablo Porras Millan, European Molecular Biology Laboratory (EMBL) – European Bioinformatics Institute (EBI), UK

Protein interaction data (databases and analysis)

Protein-protein interaction (PPI) data has become an essential resource to build interaction maps that provide the funding steps for our understanding of cellular pathways. PPI datasets are recorded in a number of databases that manually curate or text-mine it from the literature or even generate PPI predictions using literature-derived datasets as a basis. This situation results in great variability both in how the data is represented and which datasets are recorded, making the generation of comprehensive, internally cohesive interactomes an often challenging, sometimes impossible task. In this session, we will provide an overview of the most commonly used resources for PPI data representation, discussing curation policies and their effect on the way the data is provided to the users. We will also address the problem of PPI data integration and present different strategies to solve it. We will finally use the popular networks representation and analysis tool Cytoscape to obtain and integrate PPI data from different resources, presenting its basic visualization and analysis features.

João Pedro de Magalhães, University of Liverpool, UK

Bioinformatics, systems biology and ageing: Navigating the new oceans of data to discover the Fountain of Youth

Ageing is the major biomedical challenge of the 21^st century, yet it remains largely mysterious, partly because the ageing process involves multiple genes and their interactions with each other and with the environment that remain poorly understood. In this talk, I will present genomic and computational approaches aimed at deciphering the genome and increasing our knowledge about how genes and pathways impact on ageing. We have also been employing whole transcriptome profiling (RNA-seq) to gather insights on ageing and its manipulation by diet. Moreover, I will present our work of integrating gene expression profiles with age-related changes at other biological levels and new online resources for integrative and systems biology of ageing.Lastly, I will discuss our recent work in sequencing and analyzing the genome of the longest-lived mammal, the bowhead whale, to identify longevity assurance mechanisms.

Albert-László Barabási, Center of Complex Networks Research, Northeastern University and Division of Network Medicine, Harvard University, Boston, US
Network Medicine: From Cellular Networks to the Human Diseasome

Given the functional interdependencies between the molecular components in a human cell, a disease is rarely a consequence of an abnormality in a single gene, but reflects the perturbations of the complex intracellular network. The emerging tools of network medicine offer a platform to explore systematically not only the molecular complexity of a particular disease, leading to the identification of disease modules and pathways, but also the molecular relationships between apparently distinct (patho) phenotypes. Advances in this direction are essential to identify new disease genes, to uncover the biological significance of disease-associated mutations identified by genome-wide association studies and full genome sequencing, and to identify drug targets and biomarkers for complex diseases.

Benno Schwikowski, Institut Pasteur, Paris, France
LEAN discovery of hot spots in networks

“Everything should be made as simple as possible but not simpler,” said Einstein. But what does this mean for new computational models that link complex disease ‘omics data with relevant phenotypes? To be useful in practice, new models need to be simple enough to be computationally tractable, and yield biologically interpretable outcomes. Yet, models also need to be complex enough to allow the discovery of new, non-classical relationships between molecular and clinical measurements and disease phenotypes.

In my talk, I will discuss a simple subnetwork model for identifying ‘hot spots’ in interaction networks. Methods based on the classical subnetwork model tend to have long running times, provide single or partial, often heuristic, solutions, contain user-tuneable parameters, or lead to solutions that are difficult to interpret. An alternate approach (termed Local enrichment analysis, or LEAN) substitutes the general model by simpler model. The simpler model is more constrained, but, in return, allows exact,

parameter-free, efficient, and exhaustive identification of local subnetworks that are statistically dysregulated, and directly implicates single genes for follow-up experiments.

A first empirical evaluation on simulated and biological data suggests that LEAN detects dysregulated subnetworks, and reflects biological similarity between experiments better than standard approaches. A strong signal for the local subnetwork around Von Willebrand Factor (VWF), a gene which showed no change on the mRNA level, was identified by LEAN in transcriptome data in the context of a genetic disorder, Cerebral Cavernous Malformations (CCM). Targeted follow-up experiments revealed an unexpected strong cellular phenomenon around VFW. The LEAN method can be used to pinpoint statistically significant local subnetworks in any genome-scale data set.

Leonidas Alexopoulos, National Technical University of Athens, Greece
Pathway-based approaches for early drug and biomarker discovery. Research and Industrial applications in osteoarthritis, liver cancer, non-alcoholic fat liver disease, multiple sclerosis, melanoma, chronic kidney disease, and liver toxicity.

A major challenge for bringing safe and effective new treatment to patients is the deep understanding of a disease. Here, we describe high throughput proteomic technologies and systems biology algorithms for tackling major questions in the drug discovery and development pipeline: (i) construction of pathways and comparison between normal or diseased cells, (ii) identification of drug mode of action (MoA), and (iii) prediction of drug toxicity and efficacy. Our network based approach is able to predict the drugs' main target and uncover off-target effects. Subsequently, machine learning algorithms can select MoAs with reduced toxicity, increased efficacy and tailor drugs to specific disease mechanisms. So far, we have applied our approach in liver cancer, osteoarthritis, multiple sclerosis, non-alcoholic fat liver disease, chronic kidney disease and more recently in melanoma. Our pathway analysis algorithms and high throughput multiplex platform paves the road for new solutions in early drug discovery.

Eivind Almaas, Norwegian University of Science and Technology, Trondheim, Norway
Differential co-expression network analysis: from pathways to disease

Biological systems are built from many interlocking layers of molecular parts, forming a wide variety of pathways with complex function and control. When biological functions fail or their control systems are interrupted, we typically identify the emerging states as disease. Many human diseases are caused by microbial activity, and in this presentation, I will first discuss recent insights in the computational identification of possible antibiotic targets. Changing the focus to responses in humans, I will discuss system-level adjustments in gene activity-patterns to rheumatoid arthritis and infection by M. tuberculosis.

Aristidis Vrahatis, University of Patras, Greece
Integrative pathway analysis (R)

In the recent years pathway-based approaches have become prevalent in the modeling and analysis of biological systems. Towards this direction, the research community has been lately focusing on the analysis of subpathways, i.e., subnetworks within the pathway topology. Subpathways represent the underlying biological phenomena more accurately and have emerged as even more targeted and context-specific molecular candidate communities for the analysis of complex diseases. In this context, we will present indicative subpathway-based R/Bioconductor software packages and offer practical advices for "Pathway Analysis in R".

Alfonso Valencia, BSC-Barcelona Supercomputing Center, Spain
Networks based approaches for the study of epigenomics

In the context of the Blueprint epigenomic consortium (www.blueprint-epigenome.eu) we developed framework for the comparative analysis of DNA and histone modifications in terms chromatin states (EPICO http://blueprint-data.bsc.es/release_2016-08/) together with a set of Network Biology approaches for the analysis of epigenomic information.

As demonstration of these methodologies, we used Mouse Embryonic Stem Cells (mESC) data, since it represents the best-characterised biological system at the epigenenomics level, including basic components, i.e. Chromatin Related Proteins (CRPs), Histone modifications, DNA methylation modifications, as well as the genome mapping of a large collection of proteins and modifications (ChIP-Seq data) and data on the organization of the chromatin in the nucleus, determined with Chromatin Capture experiments, ChIA-PET in this case.

In a first study, we processed heterogeneous ChIP-Seq information to build a comprehensive genome co-localization network of Chromatin Related Proteins (CRPs), histone marks and DNA modifications. In this network, co-localization preferences can be translated into specific of "mESC Chromatin States", such as active regions or enhancers. The analysis of the properties of the "co-localization" network points to the 5hmC DNA modifications, as the key component in the organization of this network. The importance of 5hmC, as organizer of the epigenetic network, is reinforced by the evolutionary analysis of the protein components of the network. There, 5hmC acts as a mediator in the co-evolution of the CRPs protein components of the mESC network.
In the second network based approach, We explored the functional significance of the mESC Epigenetic Properties and Chromatin States, by analysing them in the context of the structure of the nucleus that might offer an additional layer of genes expression control. The results revealed interesting properties of the organization of the mESC epigenetic control system, in line with the emerging models of gene expression control and chromatin organization, and again support the role of 5hmC as a factor present in a

significant number of interactions related with active transcription in mouse embryonic stems cells.

The Blueprint analysis portal. Fernandez et al., 2016 Cell Systems
http://dx.doi.org/10.1016/j.cels.2016.10.021
Epigenomic Co-localization and Co-evolution Reveal a Key Role for 5hmC as a Communication Hub in the Chromatin Network of ESCs. Perner et al., (2016) Cell Rep. http://www.cell.com/cell-reports/pdf/S2211-1247(16)00028-0.pdf
Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. Pancaldi et al., (2016) Genome Biol. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4939006/
Parts of this work were developed in collaboration with: Vingron's (MPIMG, Berlin), Fraser's (Babraham Institute) labs and BSC, EBI-EMBL.

Ruth Barshir, Ben-Gurion University of the Negev, Beer-Sheva, Israel

Using network approaches towards understanding tissue-specificity of hereditary diseases

Using comparative analysis of tissue-specific molecular interaction networks we aim to solve a long-standing puzzle in human genetics: what limits the clinical manifestation of hereditary diseases to certain tissues or cell types, while their causal genes are expressed across the human body? Previously, we integrated data of gene and protein expression across human tissues with data of protein-protein interactions (PPIs) to create tissue-specific interactomes. Upon comparing these interactomes we found that they shared a common core sub-network while only a small fraction of their proteins and PPIs were tissue specific. We used these tissue interactomes to analyze the factors contributing to the tissue-specific manifestation of hereditary diseases. We found that in addition to elevated transcript levels, disease-causing genes tend to have increased number of tissue-specific PPIs in their disease tissue. These tissue-specific PPIs can highlight disease mechanisms and provide a powerful filter for interrogating disease etiologies.

An additional compelling mechanism that may contribute to tissue-specific disease manifestation is partial compensation by paralogous genes. It has been shown across organisms and recently in humans that paralogs can compensate for the loss of each other. This compensation may lead to masking of the harmful effects of the causal mutation across most tissues. However, in the disease tissue, this masking may become insufficient and thus disease phenotypes emerge. While this mechanism has been postulated previously to explain the tissue-selectivity of hereditary disease, the relevance of paralogs was never assessed at large-scale. We analyzed 120 tissue-specific hereditary diseases that manifest either in brain, skeletal muscle, heart, skin, liver, thyroid or testis and their causal genes had paralogs that shared high sequence identity, correlated expression across tissues, and significant overlap in their interactome neighborhoods. To test whether insufficient compensation occurs specifically in the disease tissue, we compared the expression levels of causal genes and their paralogs across tens of human tissues. We found strong evidence for insufficient compensation in the disease tissues for most hereditary diseases. Moreover, in 20% of the cases,

insufficient compensation arose due to the paralog being significantly under-expressed in the disease tissue.

In summary, comparative network analyses can illuminate the etiology of hereditary diseases and effectively enhance our efforts to develop cures.

Laura Furlong, Universitat Pompeu Fabra, Barcelona, Spain
DisGeNET discovery platform 5.0: Illuminating the study of human diseases

In the last few decades, our knowledge about the genetic underpinnings of human diseases has grown at an unprecedented pace. Data resulting from GWAS studies, experiments in animal models of disease, and from exome sequencing pipelines are freely available, but scattered across several repositories. To enable translation of this wealth of knowledge into better disease biomarkers and drug therapies, this data should be made readily available to translational researchers and clinicians. I will present our work in this area exemplified by the DisGeNET and PsyGeNET knowledge platforms. The key role of text mining for extraction of relations between biomedical concepts will be discussed. I will present some of the hurdles we face in structuring the knowledge of human diseases, such as the prevalence of data silos in biomedicine, limitations of current ontologies and the need of data curation and prioritization strategies. In this regard I will share our experience for data curation leveraging on users' community. Finally, the importance of building an ecosystem of linked data in biomedicine to support translational research will be presented.

Marc Vaudel, KG Jebsen Center for Diabetes Research, Department of Clinical Science, University of Bergen
Networks as a roadmap for clinical data

Clinical teams benefit from a large palette of sample characterization techniques to refine diagnostic, prognostic, and treatment of patients. For example, genome sequencing is now routinely employed, often in combination with other high throughput analytical approaches like metabolite and protein assays. However, the datasets generated are often so vast that it becomes challenging to distinguish the patterns relevant to patient care.

Using the underlying network of interaction between the characterized compounds is currently seen as the most promising way to extract meaningful information on disease mechanisms. In this presentation, we show how networks of molecular interactions are used to refine patient care, and improve our understanding of complex diseases. We navigate such networks, highlighting some of the current limitations in their usage for clinical applications, and proposing solutions towards the creation of a roadmap for clinical data.

About the speakers

Konstantina Dimitrakopoulou
Computational Biology Unit, University of Bergen

Konstantina Dimitrakopoulou holds an M.S. in biomedical engineering (2007) and a PhD (2014), both from the University of Patras, Greece. Her doctoral thesis focused on complex disease analysis through systems biology approaches. She is now a postdoc in the group of Inge Jonassen at Computational Biology Unit (University of Bergen) and in collaboration with the group of Lars Akslen at Centre for Cancer Biomarkers CCBIO focuses on systems biology studies of the breast cancer microenvironment.

Christos Ouzounis
CERTH, Centre for Research and Technology Hellas, Thessaloniki, Greece

Christos A. Ouzounis is a Director of Research at CPERI-CERTH (Greece). He received his PhD from the University of York UK at EMBL (-1993), and was a Human Frontiers Science Program (HFSP) Fellow at the AI Center, SRI International in Menlo Park, CA (-1996). He led the Computational Genomics Group at EMBL's European Bioinformatics Institute (Cambridge UK) (-2005), the Computational Genomics Unit at CERTH (-2007) and the Centre for Bioinformatics at King's College London (-2010). He is an Associate Editor for PLoS Computational Biology, PLoS ONE, Biosystems and a Senior Editor for Microbial Genomics, has been an Associate Editor for Bioinformatics (now honourary Editor), as well as an editorial board member for a number of journals and the Faculty of 1000 (Sequence Analysis, Section co-Head). He is a founding officer of the International Society for Computational Biology (ISCB), the Mikrobiokosmos initiative (Greece), the Hellenic Society for Computational Biology & Bioinformatics (HSCBB) and Hellenic Bioinformatics (hbio.info). Since 2015, he is also an Affiliate Scientist at Berkeley National Lab (CA, USA).

Eileen Marie Hannah
Computational Biology Unit, University of Bergen

Eileen-Marie Hanna is a Postdoctoral Fellow at the Computational Biology Unit (CBU) - University of Bergen. She currently works on the "dCod 1.0: Decoding the systems toxicology of Atlantic cod" project. With a Computer Science background and an interest in the Bioinformatics field, she received an MS in Computer Science with a specialization in Bioinformatics from the University of Trento in 2008. She was then awarded a PhD in Computer Science from UAEU in 2015. Her PhD research mainly consisted of developing a method for the detection of protein complexes in protein-protein interaction (PPI) networks, in addition to modeling the dynamic aspect of PPI networks using gene expression data and adapting the developed approach accordingly. Her research interests include network biology, omics data integration and data mining.

Pablo Porras Millan
European Molecular Biology Laboratory (EMBL) – European Bioinformatics Institute (EBI), UK

Pablo Porras started his career in the University of Córdoba, Spain, doing research about trans-membrane protein translocation and redox homeostasis. After that, he moved to Berlin to work in the Neuroproteomics group of the Max Delbrueck Center, getting involved in projects dealing with interactomics and neurodegenerative diseases. During this postdoc, he faced the problem of how to represent and analyze molecular interactions data, an experience that led him to join the EBI to work as a scientific curator and bioinformatician in the molecular interactions database IntAct, where he deals with representation, integration and analysis of large interaction datasets. He has been heavily involved in training and research collaborations since arriving to the EBI in 2011 and has recently been appointed project leader for the Molecular Interactions Team.

João Pedro de Magalhães
University of Liverpool, UK

Dr de Magalhaes graduated in Microbiology in 1999 from the Escola Superior de Biotecnologia in his hometown of Porto, Portugal, and then obtained his PhD in 2004 from the University of Namur in Belgium. Following a postdoc with genomics pioneer Prof George Church at Harvard Medical School, in 2008 Dr de Magalhaes was recruited to the University of Liverpool. He is now a reader and leads the Integrative Genomics of Ageing Group (http://pcwww.liv.ac.uk/~aging/). The group's research focuses on understanding the genetic, cellular, and molecular mechanisms of ageing. Dr de Magalhaes has given over 100 invited talks, including a TEDx talk, and his research has been widely featured in the popular press (BBC, CNN, the Washington Post, the Financial Times and many others).

Albert-László Barabási,
Northeastern University and Harvard University, Boston, US

Professor Albert-László Barabási is the Robert Gray Dodge Professor of Network Science and a Distinguished University Professor at Northeastern University, where he directs the Center for Complex Network Research, and holds appointments in the Departments of Physics and College of Computer and Information Science, as well as in the Department of Medicine at Harvard Medical School and Brigham and Women Hospital in the Channing Division of Network Science, and is a member of the Center for Cancer Systems Biology at Dana Farber Cancer Institute.

A Hungarian born native of Transylvania, Romania, he received his Masters in Theoretical Physics at the Eötvös University in Budapest, Hungary and was awarded a

Ph.D. three years later at Boston University. Barabási latest book is Network Science (Cambridge University Press, 2016). He has also authored "Linked: The New Science of Networks" (Perseus, 2002), currently available in fifteen languages, "Bursts: The Hidden Pattern Behind Everything We Do" (Dutton, 2010) available in five languages, and is the co-editor of "The Structure and Dynamics of Networks" (Princeton, 2005). His work lead to the discovery of scale-free networks in 1999, and proposed the Barabási-Albert model to explain their widespread emergence in natural, technological and social systems, from the cellular telephone to the WWW or online communities.

Benno Schwikowski
Institut Pasteur, Paris, France

Trained as a mathematician and computer scientist, Dr. Schwikowski joined Richard M. Karp's group at the University of Washington in Seattle in 1998, creating algorithmic approaches to DNA sequence comparison (now called 'phylogenetic footprinting') and new combinatorial designs of DNA arrays. After joining the Institute for Systems Biology (ISB) in Seattle as its one of the first faculty members, he pioneered data analysis methods that employ large-scale interaction networks, such as function prediction and the identification of network modules from transcriptomic data. Confronted with the need to visually explore experimental data, and interpret computational results in the context of networks, Dr. Schwikowski co-created, with Trey Ideker, the Cytoscape platform for visualization and analysis. He contributed various algorithmic and statistical methods to the establishment of computational proteomics workflows. Today, Dr. Schwikowski and his team at the Systems Biology Lab at the Pasteur Institute in Paris focus on network biology- and machine learning-based approaches to advance our understanding of complex disease.

Leonidas Alexopoulos
National Technical University of Athens, Greece

Leonidas Alexopoulos is a assistant professor at National Technical University of Athens (Systems Bioengineering Lab (https://ntuabiolab.wikispaces.com) and founder of Protavio (http://www.protavio.com), a systems pharmacology SME. His research combines pathway analysis tools and novel multiplex assays for early drug discovery. Dr Alexopoulos received his PhD from the department of Biomedical Engineering at Duke University in 2004 and subsequently he attended MIT (Dept of Biological Eng) and Harvard Medical School (Dept of Systems Biology) for his postdoctoral research. He has has strong publication record and industrial experience with major pharmaceutical companies including Roche, Becton & Dickinson, Vertex, Pfizer, and Boehringer Ingelheim in the area of systems biology for drug and biomarker discovery & development.

Eivind Almaas
Norwegian University of Science and Technology, Trondheim, Norway

Professor Eivind Almaas is a professor of systems biology at Dept. of Biotechnology and a member of the K.G. Jebsen Center for Genetic Epidemiology at the Norwegian University of Science and Technology (NTNU). He received his M.Sc. in Theoretical Physics from the Norwegian Institute of Technology (NTH) and a Ph.D. from The Ohio State University. After a post doctoral position in the Barabasi lab, he lead a research group at Lawrence Livermore Natn'l Lab before moving to NTNU in 2009. He is the Chair of both the Program for Applied Ethics (PAE) and Program for Bioinformatics (PBI) at NTNU. Research in the Almaas Lab is focused on topics in network systems biology, with a main interest in co-expression networks and genome-scale metabolic modeling. Professor Almaas was the first to organize a Norwegian iGEM team, and this year's team is the 7th representing NTNU.

Aristidis Vrahatis
University of Patras, Greece

Aristidis G. Vrahatis received his Ph.D. in 2016 from the Department of Computer Science and Engineering, University of Patras, Greece. He is currently postdoctoral researcher at Biosignal Lab, Medical School at University of Patras. His research focuses on the fields of Computational Biology, Bioinformatics and Systems Biology. He is interested in developing novel computational methodologies for elucidating the mechanisms of complex diseases and biological processes based on biological networks and integration of heterogeneous omics data. He has developed Matlab and R/Bioconductor software packages with novel methodologies addressing network biology problems.

Alfonso Valencia
BSC-Barcelona Supercomputing Center, Spain

Alfonso Valencia is a Biologist by training with a Ph.D. in Biochemistry and Molecular Biology by the Universidad Autónoma, Madrid and a postdoc in Bioinformatics at the EMBL Heidelberg, in Chris Sander's lab. He started as group leader at National Centre for Biotechnology (CNB-CSIC) in 1995. He was made Research Professor in 2002. From 2006 o 2016 Valencia was Director Structural Biology and Biocomputing Programme of the Spanish National Cancer Research Center (CNIO) and ViceDirector for basic Research from 2014 to 2016.

In 2004 he was appointed as Director of Spanish Bioinformatics Institute INB. In 2002 the INB was organized as a technical platform of ISCIII and in 2013 Dr. Valencia was appointed as Head of the Spanish node of the European Infrastructure for Life-Science Information, ELIXIR. In 2017 Dr. Valencia moved to Barcelona as ICREA Professor and

Director of the Life Science Department of the Barcelona Supercomputing Centre – Centro Nacional de Supercomputación.

As Computational Biologist Dr. Valencia is interested in the analysis of large collection of genomic information with particular emphasis in the study of protein interaction networks applied to (epi)Genomics, Cancer Biology and Precision Medicine. His group is particularly interested in the application of Text Mining methodology to biomedical problems.

Alfonso Valencia has published more than 300 articles with an h-index of 94 (Google Scholar profile). His group participates in various international consortiums including GENCODE/ENCODE, BLUEPRINT/IHEC (epigenomics), RD-Connect/IRDiRC (rare diseases), CLL/ICGC/PCAWG (cancer genomics). Alfonso Valencia is a founder and current member of the steering committee of the BioCreative Text Mining challenge, where he has emphasized particularly the importance of text mining in the connection between Molecular Biology and Chemistry.

Prof. Valencia is a founder member and current President of the International Society for Computational Biology (ISCB), elected member of the European Molecular Biology Organization (EMBO). Prof. Valencia is Executive Editor of the main journal in the field since 2006 ("Bioinformatics" OUP) and editors of FEBS Letters, PeerJ and F1000Prime. He is also reviewing Editor of e-LIFE. He has been member of a number of advisor boards, including EMBO, BioZentrum U. Basel, Swiss Bioinformatics Institute, EMBL-EBI chemical and protein domain databases, Department of Biology UPF, Department of Bioinformatics Curie Institute, IRB-Barcelona, among others. Dr. Valencia is Professor Honoris Causa by the Danish Technical University - DTU.

Ruth Barshir
Ben-Gurion University of the Negev, Beer-Sheva, Israel

Ruth Barshir has a B.Sc in biology from Hebrew university, Jerusalem, Israel and a M.Sc in Neuroscience from the University of Texas, Dallas, USA. She as worked as a database team leader and project manager at Compugen, a leading Israeli bioinformatics company. She got her PhD in bioinformatics under the Guidance of Dr. Esti Yeger-Lotem in Ben Gurion University, Israel on the subject 'Deciphering the etiology of hereditary diseases by using tissue-specific molecular networks'. She is currently doing a short post-doc at Esti Yeger-Lotem's lab.

Laura Furlong
Universitat Pompeu Fabra, Barcelona, Spain

Laura I. Furlong is head of the Integrative Biomedical Informatics Group, which belongs to the Research Programme on Biomedical Informatics (IMIM-UPF) and Associate

Professor at the Pompeu Fabra University (Spain). She holds a PhD in Biology from the University of Buenos Aires and an Msc in Bioinformatics by Pompeu Fabra University. She has a broad expertise covering molecular biology, computational systems biology and text mining. Her current research interests include: a) knowledge management and linked data; b) biomedical text mining; c) network medicine for the study of human diseases and drug toxicity; d) Real World Data analytics in health. Her group provides knowledge platforms to support translational research, such as DisGeNET (http://www.disgenet.org/) and PsyGeNET (http://www.psygenet.org/).
She has published 54 peer-reviewed articles, and acts as reviewer for the journals Bioinformatics, BMC Bioinformatics, BMC Systems Biology, Database and PLOS journals. She has participated in several FP7 and IMI projects (@neurist, EU- ADR, Open PHACTS) and is currently involved in eTOX, EMIF, IPiE, TransQST and MedBioinformatics projects.

Marc Vaudel
KG Jebsen Center for Diabetes Research, Department of Clinical Science, University of Bergen

I currently work as a scientist at the KG Jebsen Center for Diabetes Research, Department of Clinical Science, University of Bergen, and at the Center for Medical Genetics and Molecular Medicine, Haukeland University Hospital, both in Bergen, Norway. I am affiliated through active cooperation to the Bergen Stem Cell Consortium and the CompOmics group in Gent, Belgium. I am member of the European Bioinformatics Community (EuBIC) initiative, and of the educational committee of the European Proteomics Association (EuPA).
My main research focus is the improvement of diagnostic, prognostic, and treatment of diseases through the application of omics techniques. My field of expertise is the bioinformatic interpretation of clinical data. My research is primarily applied to projects at the biomedical and clinical departments of the University of Bergen, but the methods and tools produced can be applied in other contexts. I have strong interests in knowledge sharing and education, and therefore try to make my work open and documented.

Practical information

All addresses are indicated on the attached map

Venue

The workshop will take place at Grand Hotel Terminus (www.grandterminus.no), Zander Kaaes gate 6, Bergen, see attached map. The hotel is situated next door to Hotel Zander K, where many participants will stay, and also to the central train station. We will provide lunch, coffee, tea and snacks.

Transport

From Bergen Airport Flesland, you can travel by the airport bus or the city light rail called 'Bybane', both will take you to the city centre. Leave the bybane at the 'Nonneseter' stop, or the bus at the 'Bystasjonen' stop, to reach Grand Hotel Terminus, see attached map.

Hands-on practical sessions

The hands-on sessions will be organised between 14:45-17:45 on Wednesday 23 August and 15.30-17.30 on Thursday 24 August, tentatively. Please make sure that you have access to a laptop computer during the workshop, and that you install Cytoscape and R/Bioconductor software according to the instructions that can be found here: https://goo.gl/FnG3fW

Prior to the Cytoscape hands-on session on August 23, Eileen Marie Hannah will give an introduction to Cyoscape. This session will have a tutorial style and we recommend that you bring a laptop to follow this, even if you are not signed up for the following hands-on session.

Workshop dinner

The workshop dinner will take place at Kalfaret Brygghus, Kalfarveien 76 (www.kalfaretbrygghus.no) on Thursday August 24 at 19.00. Kalfaret Brygghus may be reached by a nice 10-15 min walk from Grand Hotel Terminus, see attached map, alternatively, a bus may take you approximately half of the distance.

Horizon lecture

In association with this workshop, Professor Albert-László Barabási will give a Horizon lecture at the UiB Science building on Friday 25 August at 14.30, a 10-15 min walk from Grand Hotel Terminus, see map. The Horizon lecture series targets staff and students of the UiB Faculty of Mathematics and Natural Sciences, and all others that are interested in major scientific questions and challenges across disciplinary borders, and is open for everyone. Refreshments and snacks will be served between 14.00 and 14.30. Read more about Barabási's Horizon lecture here: https://goo.gl/LL2nx5

How to find your way around during the Network Biology workshop: