Phytoplankton response to an intense dust storm in the Tasman Sea in September-October, 2009

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ABOUT ISB 2014

THEME AND SCOPE

The 8th International Conference on Systems Biology (ISB 2014), organized by Chinese Academy of Sciences and Qingdao University was co-held with and the 4th Translational Bioinformatics Conference (TBC 2014), in Qingdao, China, October 24–27, 2014. The conference is sponsored by National Natural Science Foundation of China (NSFC), Academy of Mathematics and Systems Sciences of CAS (AMSS), Shanghai Institutes for Biological Sciences of CAS (SIBS), Qingdao Institute of Bioenergy and Bioprocess Technology of CAS (QIBEBT), Qingdao University, Computational Systems Biology Society of ORSC, Functional Genome Informaics and Systems Biology Society of CSCB, Systems Biology Technical Committee of IEEE SMC Society, Korean Society for Bioinformatics and Systems Biology (KSBSB), The Korean Society of Medical Informatics (KOSMI), Korean Genome Organization (KOGO).

Systems Biology and Bioinformatics have become intensive research topics in the recent past decade and attracted great many leading scientists working in Biology, Physics, Mathematics and Computer Science. Optimization, Statistics, and many other mathematical methods have been widely used in the field. Following the successful ISB conferences series from 2007, the purpose of ISB/TBC 2014 is to extend the international forum for scientists, researchers, educators, and practitioners to exchange ideas and approaches, to present research findings and state-of-the-art solutions in this interdisciplinary field, including mathematical methods and its applications in biosciences and researches on various aspects of Systems Biology, such as integration of genome-wide microarray, proteomic, and metabolomic data, inference and comparison of biological networks, and model testing through design of experiments.

The purpose of ISB/TBC 2014 is to provide an international forum for scientists, researchers to exchange ideas and approaches, including theoretical methodology development and its applications in biosciences and researches on various aspects of Computational Systems Biology and Translational Bioinformatics. Themes of the ISB/TBC 2014 will be interdisciplinary by its nature and focus on bridging opportunities between mathematical methods and Systems Biology/Translational Bioinformtics studies. We are particularly interested in submissions that report on theoretical, experimental and applied research motivated by systems biology and translational bioinformatics problems. Typical, but not exclusive, topics of interest are:

- Gene Regulatory Networks
- Protein Interaction Networks
- Metabolic Networks
- Signaling Networks
- Comparative Genomics
- Functional Genomics
- Metagenomics
- Genome-Wide Association Study
- Promoter Analysis and Discovery
- Biomarker Identification and Drug Discovery
- Evolution and Phylogenetics
- Non-coding RNAs
- Proteomics
- Protein Structures and Functions
- Microbial Community Analysis
- Qualitative Analysis of Biological Systems
- Quantitative Models of Cellular and Multi-Cellular Systems
- Designing and Modeling Synthetic Biological Systems
- Nonlinear Dynamics and Analysis of Biological Systems
- Designing Synthetic Biological Circuits
- High Performance Computing for Biological Data Analysis
- Data Mining and Machine Learning for Biological Data
- Information Theory and Statistical Analysis
- Systems Biology of Cancer and Metastasis
- Brain Systems Biology
- Systems Neuro-Informatics
- Systems Biology of Development
- Next Generation Sequencing for Personal Genomics, Cancer Genomics and Metagenomics
- Rare and common variants of human genome
- Epigenomics, non-coding RNAs, and DNA methylation analyses

- Genome-Phenome-Envirome Network Analysis
- Microarray analysis and functional genomics for disease
- Biomarkers, Drug Discovery and Pharmacogenomics
- Biomedical Text/Data Mining and Visualization
- Network Biology/Medicine and Pathway/Regulation Analysis
- Biomedical Intelligence, Clinical Informatics, and Health Record
- Semantic Biology/Medicine and Biomedical Ontologies

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PROCEEDING PAPERS AND CONTRIBUTING AUTHORS

Forty-three papers selected for special issues of journals and forty full papers in this volume cover wide range of computational systems biology. Authors of these papers come from China mainland, Hong Kong, Taiwan, Australia, Canada, Czech, Germany, Greece, Italy, Japan, Korea, Netherlands, Pakistan, Thailand, United Kingdom, and United States. Many active researchers in various areas contributed their overview and introduction in their fields besides specific deep research achievements.

Abstract: To study the complex diseases, a major challenge is how to identify disease-relevant networks/functions, e.g. phenotypic functions of particular disease. From the viewpoints of systems biology, it is to capture significantly differentially expressed molecules in active signaling pathways, modules, or functions in phenotype-specific molecular networks. But, many genes, gene networks, or gene modules actually have slight but important changes on their expressions or functions among different phenotypes, e.g. the phenotypic change of expression of transcriptional factor. They are known as implicit factors to determine particular phenotypes; however, there are few systematical studies on them. In this article, we purpose a computational framework as network alteration analysis (NAA) to identify the classification-defined explicit and implicit function-networks in a genome-wide way, i.e. all known biological functions in gene ontology database or the corresponding to sub-networks. By NAA, we can recognize two different patterns of biological functions and its corresponding sub-networks associated with particular disease simultaneously, which can be divided into explicit and implicit functions/sub-networks related to disease development and progression. We used NAA to investigate the diabetes preliminarily, and mainly found: (1) the quantified scores of sub-networks corresponding to explicit or implicit functions/sub-networks can be used as markers to distinguish the non-diabetic samples and diabetic samples, although the similarity distance of scores of implicit functions/sub-networks were too close; (2) disease-associated genes have different locations on the sub-networks corresponding to explicit and implicit functions, so that, they (especially implicit functions) are key phenotypic functions and would play different roles (e.g. causes of diseases) in the disease development and progression.

Poster04: *Predicting Disease Genes based on Consistently Differential Interactions for Complex Diseases*

Qianqian Shi, Xiaoping Liu, Luonan Chen
Key Laboratory of Systems Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai 200031, China
Paper ID: 106

Abstract: A complex disease is generally caused by genetic alterations or disorder of biological processes. Systematic identification of causal disease genes can shed light on the mechanisms underlying complex diseases, and provide new ideas to develop efficient diagnosed biomarkers or therapies. In this paper, we proposed a novel approach to predict potential disease genes for complex diseases, based on a consistency-detection scheme for molecular interactions from normal and disease samples using heterogeneous datasets, rather than single dataset. In particular, we can determine reliable differential interactions between normal and disease states by identifying the consistent interactions on a protein-protein interaction network, from which the disease genes are further decided based on those consistent interactions and also their topological structure on the network. For validating the method, the breast cancer data is used to identify the consistently differential interactions from normal to breast cancer onset, and the results well agree with the known information, thereby implying predictive power of our method. Our method also provides superior and meaningful results by compared with some typical methods. In addition, we demonstrated that the differential interactions are informative in complex disease study, in particular for detecting novel disease genes, and actually those interactions can be used as new edgetic targets from the network viewpoint.

Poster05: *Detecting Biomarkers and Disease Pathways for Nonalcoholic Fatty Liver Disease in Mouse*

Xiaoping Liu, Luonan Chen
Key Laboratory of Systems Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai 200031, China
Paper ID: 117

Abstract: Nonalcoholic fatty liver disease (NAFLD) is a kind of common disease in the world, and is the most common liver disease. NAFLD is also regarded as causing by fat accumulation in the liver and associating with obesity and insulin resistance. Although, there are a few researches about disease mechanism of fatty liver due to non-lethal disease, it harms human health without treatment. So it would benefit to treat the NAFLD in human if we can understand the mechanism of NAFLD onset in mouse model. In this paper, we identified some biomarkers which can be used to test the disease development of NAFLD by differential expression of genes, and some potential disease pathways to attempt to depict the onset progress of NAFLD by detecting the differential interactions in different time points. By the KEGG and GO enrichment analysis, we can see these potential disease pathways of NAFLD can significantly enriched to some liver disease progress and fatty metabolism.

Poster06: *Phytoplankton response to an intense dust storm in the Tasman Sea in September-October, 2009.*

Albert Gabric, Roger Cropp, Grant McTainsh, Barbara Johnston Johnston, Harry Butler
Griffith University, Nathan Campus, Brisbane, Queensland, Australia

Paper ID: 118

Abstract: Here we present a detailed analysis of the marine biological response in the Tasman Sea (25-40ºS, 150-170°E) after the "Red Dawn" dust storm, which was one the largest recorded in SE Australia in the last 70 years. We examine the impact of dust-derived nutrients deposited to the ocean surface on satellite-derived estimates of phytoplankton biomass as indicated by surface chlorophyll-a. We have simulated contemporaneous atmospheric dust load and deposition over the adjacent ocean using a regional dust transport model that provides daily data from September to December 2009. The phytoplankton response was confined to the region south of 30ºS, with the greatest positive anomalies (>0.6 mgm-3) occurring south of 35ºS, even though deposition was recorded further north. Contrary to previous reports of little biological impacts from dust storms in the Tasman Sea, our results suggest the regional phytoplankton can respond strongly to inputs of aeolian nutrients during the austral spring if deposition is strong and ocean conditions are favourable.

Poster07: *Detecting Causality from Nonlinear Dynamics with Short-term Time Series*

Huanfei Ma, Luonan Chen
School of Mathematics, Soochow University, Suzhou 215006, China

Paper ID: 126

Abstract: Quantifying causality between variables from observed time series data is of great importance on various fields but also a challenging task, especially when the observed data are short. Unlike the conventional methods, we find it possible to detect causality only with very short time series data, based on embedding theory of an attractor for nonlinear dynamics. Specifically, we first show that measuring the smoothness of a cross map between two observed variables can be used to detect a causal relation. Then, we provide a very effective algorithm to computationally evaluate the smoothness of the cross map, or “Cross Map Smoothness” (CMS), and thus to infer the causality, which can achieve high accuracy even with very short time series data. Analysis of both mathematical models from various benchmarks and real data from biological systems validates our method.

Poster08: *Kinase-inhibitor family map for kinase inhibitor selectivity*

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National Chiao Tung University, Hsinchu 30013, Taiwan

Paper ID: 127

Abstract: Kinases play central roles in signaling pathways and are promising therapeutic targets for many diseases. Designing selective kinase inhibitors is an emergent and challenging task, because kinases share an evolutionary conserved ATP binding site. To understand kinase-inhibitor binding mechanisms, kinase inhibitor selectivity, and kinase-inhibitor-disease relationships are helpful to design selective kinase inhibitors for many diseases, such as cancers, neurological and metabolic diseases. Here, we propose kinase-inhibitor family (KIF) to address these issues. A KIF can be defined as follows: (i) the kinases in the KIF with significant sequence similarity, (ii) the inhibitors in the KIF with significant topology similarity and (iii) the kinase-inhibitor interactions (KIIs) in the KIF with significant interaction similarity. The KIIs within a KIF are often conserved on some consensus KIFMap anchors, which represent conserved interactions between the kinase subsites and consensus moieties of their inhibitors. Our experimental results reveal that the members of a KIF often possess similar inhibition profiles. The KIFMap anchors can reflect kinase conformations types, kinase functions and kinase inhibitor selectivity. Moreover, we construct KIFMap database, including 1208 KIFs, 962 KIDs, 55603 KIIs, 35788 kinase inhibitors, 399 human protein kinases, 339 diseases and 638 disease allelic variants, to explore kinase-inhibitor-disease relationships. We believe that KIFMap provides biological insights into kinase inhibitor selectivity, binding mechanisms and cancer network.

Poster09: *Molecular Features of Canine MAOA Gene: VNTR, Expression, and Methylation in Different Dog Breeds*

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Paper ID: 131

Abstract: Monoamine Oxidase A (MAOA), an enzyme that metabolizes serotonin and norepinephrine, has been known to be associated with some behavioral changes such as depression and antisocial/aggressive behavior. It has been reported that MAOA is expressed mostly in various parts of the dog brain. We previously analyzed canine MAOA gene such as genomic location, in silico expression, and interactions with other personality-related genes. However, genomic structures, expression patterns, and regulation of the MAOA gene in dogs are still not fully understood. To evaluate molecular features of the canine MAOA, we analysed genomic sequences including dog-specific VNTR, and the association between transcriptional levels and methylation status in promoter region of canine MAOA in brains of three dog breeds (Beagle, Sapsaree and Shepherd). We found the 7 dog breeds have the conserved dog-specific VNTR containing two blocks of 90bp and a truncated block in MAOA promoter region.