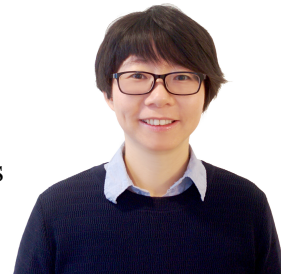


Chuan-Xing Li, born March 02, 1981
Respiratory Medicine Unit, Dept. of Medicine
Karolinska Institute, Sweden.
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RESEARCH INTEREST

Computational systems biology and multi-omics systems analysis
Network biology and modeling biomolecular networks
Bioinformatics and medical informatics
Genomics, complex disease and biomarker identification

EDUCATION

Ph.D. in Pharmacology, Harbin Medical University, China (2009/06)

Dissertation: Research on identification of disease-related miRNA and SNP module biomarkers by multi-omics network integration analysis.

Area of Specialization: Bioinformatics. Advisor: Prof. Xia Li.

M.S. and B.A. in Medicine, Harbin Medical University, China (2006/06)

Dissertation: Research on disease related single-nucleotide polymorphism (SNP) modules identification. Advisor: Prof. Xia Li.

Area of Specialization for M.S.: Bioinformatics,

Area of Specialization for B.A.: Basic Medicine Science

CURRENT POSITION

Assistant Professor, Karolinska Institutet, 2018/01-current [4 months sick leave]

PI: Assoc. prof. Åsa M. Wheelock, Pulmonomics group (www.pulmonomics.net)

Respiratory Medicine Unit, Dept. of Medicine Solna & Center for Molecular Medicine

PREVIOUS POSITIONS & RESEARCH EXPERIENCE

Senior post-doctoral researcher, Karolinska Institutet, 2014/10/15-2017/12 [6 months parental leave]

Pulmonomics group, Respiratory Medicine Unit, Dept of Medicine & Center for Molecular Medicine. Network-based approaches to sub-phenotyping of Chronic Obstructive Pulmonary Disease using a multi-molecular level OMICS data from the Karolinska COSMIC cohort. PI: Assoc. prof. Åsa M. Wheelock

Postdoctoral fellow & Research Scientist, Institute for Systems Biology, Seattle, USA, 2011/08 - 2014/06, PI: Prof. Ilya Shmulevich

- Probabilistic Boolean network inference by integrating expression with network data. Probabilistic Boolean networks (PBNs) were firstly introduced by Ilya Shmulevich in 2002, to be used as a rule-based uncertainty model for gene regulatory networks or cell signaling network. It is possible to perform model training, validation and model-based prediction to investigate the dynamic behavior of cells or tissues in response to a stimulus, and to understand the mechanism of a specific phenotype. We developed a new strategy and toolbox - PBNinfer, to infer PBNs by integrating the known gene regulatory network with time-course gene expression data. Based on the inferred PBN, we could answer four kinds of biological questions: 1) prediction of direct or indirect regulators of specific targets; 2) construction of sub-models and pathways of interesting processes or functions; 3) prediction of dynamic behavior of cell based on simulation analysis in response to a stimulus, perturbed gene or a specified initial state; and 4) identification of key regulators that drive conversion between PBN states.
- A logical model for retinoic acid (RA) signaling based on REF data and literature. Our goal was to understand the beneficial as well as the undesirable effects of treating mouse skin with tRA. We inferred a PBN for tRA-treated mouse skin with 243 genes, 518 transcriptional factor-target interactions, and 2,143 Boolean functions. It revealed multiple activation pathways for COL1A1 and COL1A2 via STAT3 consistent with

well-understood literature reports. We have tested the predictions of the model with different small molecule inhibitors of STAT3 as well as inhibitors directed against other pathways that regulate COL1A1. Reliable understanding of how tRA affects the skin will lead to more rational treatments to enhance skin health.

Assistant Professor, Harbin Medical University, Harbin, China, 06/07 - 11/07

- Prediction of ultrasound-related proteins by combining literature-mining and protein-protein interaction network
- Dissection the modularity organization principle of protein interaction network
- Development of disease miRNAs prioritization algorithm based on their topological features in the microRNA-target dysregulated network.
- Development of algorithm to identify inflammatory bowel disease related bacteria and genes by integration of microbial metagenomic and human transcriptomic data

Doctoral Research, Harbin Medical University, Harbin, China, 06/09 - 09/06

- Dissecting the organization of subcellular localizations in protein interaction network.
- Construction of miRNA-miRNA synergistic network and analysis of properties of disease miRNA.
- Further development of algorithm to identify disease risk single nucleotide polymorphisms (SNPs) by combining multiple genomic data.

PI: Prof. Xia Li

Masters Research, Harbin Medical University, Harbin, China, 03/07 - 06/08

- Development of algorithms to identify disease risk SNPs.
- Construction of gene regulatory network based on gene expression profiles.

PI: Prof. Xia Li

GRANTS

- **Mats Kleberg's Stiftelse**, *Multi-omics integration for sub-phenotyping of the spectrum diagnoses asthma and COPD*, 2019-09-28, 2020-09-27, Principal Investigator, SEK 100 000.
- **Swedish Heart-lung foundation**, *Molecular phenotyping of endemic lung diseases (MORPHEUS)*, 2019-01-25, 2022-01-25, co-applicant SEK 15 000 000.
- **Karolinska Institutet Research Grant**, 2016-2017, 2018-2019
- **National Natural Science Foundation of China** “*Research on disease related single-nucleotide polymorphism (SNP) modules identification*”. Principal Investigator. (2007-2009) € 25,934 (200,000 Chinese Yuan)
- **Basic research funds of Harbin Medical University**: Research on identification of disease related miRNA-mRNA bi-modules. Principal Investigator. (2009-2011) € 38,902 (300,000 Chinese Yuan)

FELLOWSHIP AND AWARDS

- ERS/EU RESPIRE Marie Curie Post-doctoral Research Fellowship, Europe, 2015
- Awarded “Excellent PhD graduates” of Heilongjiang Province, China, 2009
- Awarded “Excellent PhD graduates” of Harbin Medical University, China, 2009
- Awarded “First Rank Award for the excellent academic work and research achievement” by the educational committee of Heilongjiang Province, China, 2006
- Excellence Scholarships, Harbin Medical University, 2001-2006

TEACHING EXPERIENCE

Instructor, Genome Informatics, Harbin Medical University, 2007-2010

Graduated students, 5 weeks per year. Lectures and dry-lab experiments, emphasis on gene expression profiles analysis, gene function annotation and transcriptional regulation.

Instructor, Functional Genomics, Harbin Medical University, 2008-2010

Graduated students, 5 weeks per year. Lectures, emphasis on prediction of gene function and analysis of protein network and disease network.

Instructor, Medical Informatics, Harbin Medical University, 2007-2008

Undergraduate students, 6 weeks per year. Lectures, emphasis on the usage of biological databases and disease biomarker identification.