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CURRICULUM VITAE

HONGKAI JI

PERSONAL DATA

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EDUCATION AND TRAINING

Ph.D.	2007	Harvard University, Cambridge, MA, USA	Statistics
M.A.	2004	Harvard University, Cambridge, MA, USA	Statistics
M.E.	2002	Tsinghua University, Beijing, P.R. China	Pattern Recognition
B.E.	1999	Tsinghua University, Beijing, P.R. China	Automation

PROFESSIONAL EXPERIENCE

09/2007 – present Assistant Professor, Department of Biostatistics, Johns Hopkins
Bloomberg School of Public Health

07/01/2009-07/29/2009 Visiting Scholar, Beijing Institute of Genomics Chinese Academy
of Sciences, Beijing, China

PROFESSIONAL ACTIVITIES

Society Membership

American Statistical Association
Institute of Mathematical Statistics

Program Development

Session Organizer, ENAR 2009
Session Organizer, ICSA 2010

EDITORIAL ACTIVITIES

Peer Review Activities

Served as referee for:

Annals of Applied Statistics
Bioinformatics
Biometrics
Biostatistics
BMC Genomics
Computational Statistics and Data Analysis
Genome Biology
IEEE/ACM Transactions on Computational Biology and Bioinformatics
ISMB
Journal of Computational Biology
Journal of the Royal Statistical Society (Series B)
Nature Biotechnology
Pacific Symposium on Biocomputing
Proceedings of the National Academy of Sciences of the United States of America
Statistical Analysis and Data Mining
Statistical Applications in Genetics and Molecular Biology
Wiley Interdisciplinary Reviews: Systems Biology and Medicine

Ad Hoc Review of Proposals

BBSRC Grant Review, August 2007.

HONORS AND AWARDS

Honors

- 2004 Certificate of Distinction in Teaching, Harvard University
- 2002 Outstanding Master's Thesis, Tsinghua University
- 2000 Outstanding Graduate of Tsinghua University
- 1999 First Place of "Challenge Cup" Student Extra-Curricular Science and Technology Project Competition, Tsinghua University
- 1999 Third Place of NHK Robocon' 99 (Robosoccer) International Robotics Design Contest for Students, Japan

Awards

- 2007 Faculty Innovation Award, Johns Hopkins Bloomberg School of Public Health
- 2005 Chinese Medical Science and Technology Award (No. 20050319P0802), Chinese Medical Association
- 2005 Beijing Science and Technology Award (No. 2005Med-2-024-02), Beijing Municipal People's Government
- 2002-2004 Student Fellowship, Harvard University
- 1995-2002 Tsinghua University Excellent Student Scholarship

PUBLICATIONS

Peer Reviewed Journal Articles

(* corresponding author)

Judy JT and **Ji HK*** (2009) TileProbe: modeling tiling array probe effects using publicly available data. *Bioinformatics*. doi: 10.1093/bioinformatics/btp425.

Nishi Y, **Ji HK**, Wong WH, McMahon AP and Vokes SA (2009) Modeling the spatio-temporal network that drives patterning in the vertebrate central nervous system. *BBA - Gene Regulatory Mechanisms*. 1789: 299-305.

Ji HK, Jiang H, Ma W, Johnson DS, Myers RM and Wong WH (2008) An integrated software system for analyzing ChIP-chip and ChIP-seq data. *Nature Biotechnology*. 26: 1293-1300.

Vokes SA, **Ji HK**, Wong WH and McMahon AP (2008) A genome-scale analysis of the cis-regulatory circuitry underlying sonic hedgehog mediated patterning of the mammalian limb. *Genes & Development*, 22: 2651-2663.

Vokes SA, **Ji HK**, McCuine S, Tenzen T, Giles S, Zhong S, Longabaugh WJ, Davidson EH, Wong WH and McMahon AP (2007) Genomic characterization of Gli-activator targets in sonic hedgehog-mediated neural patterning. *Development*, 134: 1977-1989.

Paik JH, Kollipara R, Chu G, **Ji HK**, Xiao Y, Ding Z, Miao L, Tothova Z, Horner JW, Carrasco DR, Jiang S, Gilliland DG, Chin L, Wong WH, Castrillon DH and DePinho RA (2007) FoxOs are lineage-restricted redundant tumor suppressors and critical regulators of endothelial cell homeostasis. *Cell*, 128 (2): 309-323.

Ji HK, Vokes SA and Wong WH (2006) A comparative analysis of genome-wide chromatin immunoprecipitation data for mammalian transcription factors. *Nucleic Acids Research*, 34: e146. doi:10.1093/nar/gkl803.

Ji HK and Wong WH (2006) Computational biology: toward deciphering gene regulatory information in mammalian genomes. *Biometrics*, 62: 645-663.

Kim RS, **Ji HK** and Wong WH (2006) An improved distance measure between the expression profiles linking co-expression and co-regulation in mouse. *BMC Bioinformatics*, 7:44. doi:10.1186/1471-2105-7-44.

Ji HK and Wong WH (2005) TileMap: create chromosomal map of tiling array hybridizations. *Bioinformatics*, 21: 3629-3636.

The Chimpanzee Sequencing and Analysis Consortium (2005) Initial sequence of the chimpanzee genome and comparison with the human genome. *Nature*, 437: 69-87.

Hellmann I, Prüfer K, **Ji HK**, Zody MC, Pääbo S and Ptak SE (2005) Why do human diversity levels vary at a megabase scale? *Genome Research*, 15: 1222-1231.

Chinese Schizophrenia Consortium (2004) Association study of an SNP combination pattern in the dopaminergic pathway in paranoid schizophrenia: a novel strategy for complex disorders. *Molecular Psychiatry*, 9: 510-521. (**Joint First Author with Xu Q, Yuan YB and Yu YQ**)

Ji HK, Zhou Q, Wen F, Xia HY, Lu X and Li YD (2001) AsMamDB: an alternative splice database of mammals. *Nucleic Acids Research*, 29: 260-263.

Ji HK, Zhou Q, Wen F and Ji L (2001) Research on multiple alignments for alternative splicing. *Journal of Tsinghua University (Science and Technology)*, 41(9): 111-114.

Others

Ji HK (2007) Decoding mammalian gene regulatory programs through efficient microarray, ChIP-chip and sequence analysis. PhD thesis, Harvard University

Ji HK and Wong WH (2005) Increasing power of microarray gene selection: an empirical Bayes approach. (Harvard Qualifying Paper)

Ji HK (2002) Analysis of alternative splicing and complex disease based on population comparisons. Master's Dissertation. Tsinghua University.

CURRICULUM VITAE

HONGKAI JI

PART II

TEACHING

Advisees

Hao Wu, PhD candidate, Department of Biostatistics, 2007-present (Joint with Rafael Irizarry)

George Wu, PhD candidate, Department of Biostatistics, 2007-present

Students Working on Projects

Thai Le, College, Biomedical Engineering and Mathematics, 2007-2008

Jennifer A. Toolan, Department of Mental Health, 2008-present

Xueying Ji, Department of Geography and Environmental Engineering, 2009-present

Preliminary Oral Participation

Hao Wu, Department of Biostatistics, 01/10/2008

Ji Li, Department of International Health, 06/09/2008

Simina Boca, Department of Biostatistics, 12/10/2008

Classroom Instruction – Instructor

2008 Advanced Statistical Computing (140.778)

2008 Special Topics in Genetics and Genomics (140.668)

Classroom Instruction – Co-Instructor

2007 Introduction to Statistical Theory II (140.674)

Center Scholar Interns, Center for Talented Youth

Rachel Napthal, Weston High School, MA, 06/29/2009-08/04/2009

Other Significant Teaching

Introduction to CisGenome. *Affymetrix Workshop at EMBL*. Nov 2007

RESEARCH GRANT PARTICIPATION

Current and Past Grants

Title of Grant: Decoding transcriptional regulatory programs in tumors dependent on hedgehog signaling

Dates: 08/01/2007-08/01/2008

Sponsoring Agency: The Richard L. Gelb Cancer Research Fund, Johns Hopkins Bloomberg School of Public Health.

Principal Investigator: Hongkai Ji

Funding Level: \$10,000

Main Grant Objective: Identify genes that are direct targets of Gli proteins in Hh induced medulloblastoma, BCC and RMS, by utilizing genome-wide chromatin immunoprecipitation (ChIP) analysis coupled with genomic tiling (chip) arrays in a novel mouse model of Hh-related tumors. Develop statistical methods to analyze tiling array data and to compare TF-DNA binding activities across tumor samples.

Principal Responsibilities of Individual: PI

Title of Grant: Center for the Epigenetics of Common Human Diseases

Dates: 11/01/2007-04/30/2009

Sponsoring Agency: NHGRI

Principal Investigator: Andrew Feinberg

Funding Level: 20%

Main Grant Objective: Develop high throughput tools for epigenome analysis. Develop statistical methods to analyze allele specific expression data.

Principal Responsibilities of Individual: Co-Investigator

Title of Grant: Bioinformatics and Resequencing in Mood Disorders

Dates: 08/01/2008-07/31/2011

Sponsoring Agency: Gift Fund

Principal Investigator: James Potash

Funding Level: 25%

Main Grant Objective: Develop bioinformatics tools for analyzing massively parallel sequencing data for mood disorders.

Principal Responsibilities of Individual: Co-Investigator

Title of Grant: Preprocessing and Analysis Tools for Contemporary Microarray Applications

Dates: 08/01/2008-07/31/2010

Sponsoring Agency: NIH

Principal Investigator: Rafael Irizarry

Funding Level: 10%

Main Grant Objective: Develop statistical methods and bioinformatics tools for analyzing high-density tiling array data.

Principal Responsibilities of Individual: Co-Investigator

Title of Grant: Genomic Analysis of Active L1 Transposon Element in Human

Dates: 09/22/2008-09/21/2010

Sponsoring Agency:

Principal Investigator: Jef Boeke

Funding Level: 10%

Main Grant Objective: Develop statistical models for detecting active L1 transposon elements in human genome.

Principal Responsibilities of Individual: Co-Investigator

Ongoing Applications

Title of Grant: Statistical methods for second-generation sequencing data analysis

Sponsoring Agency: NIH RO1

Principal Investigator: Irizarry RA

Principal Responsibilities of Individual: Co-investigator

ACADEMIC SERVICE

Department of Biostatistics

Member, Post Doctoral Fellow Committee (2007)

Member, Faculty Search Committee (2008)

PRESENTATIONS

Scientific Meetings

FlexModule: a flexible cis-regulatory module sampler. *IMS-China International Conference on Statistics and Probability, Weihai, Shandong, China, July 4, 2009*

A correlation motif based hidden Markov model for pooling information from multiple ChIP-chip experiments. *ENAR, San Antonio, TX, Mar 17, 2009*

CisGenome: an integrated tool for the analysis of ChIP-chip tiling array data. *The first North American ChIP-on-chip Scientific Meeting, Affymetrix, Boston, MA, Sept 14, 2007.*

Invited Seminars

Decoding gene regulatory Program using ChIP-chip and ChIP-seq. *Bioinformatics Division, Tsinghua National Lab of Information Science and Technology, Beijing, China, July 27, 2009.*

Decoding gene regulatory Program using ChIP-chip and ChIP-seq. *Beijing Institute of Genomics Chinese Academy of Sciences, Beijing, China, July 8, 2009.*

Decoding gene regulatory Program using ChIP-chip and ChIP-seq. *National Heart Lung and Blood Institute, NIH, Bethesda, MD, Feb 5, 2009.*

CisGenome: an integrated system for analyzing ChIP-chip and ChIP-seq data. *Department of Bioinformatics and Computational Biology, George Mason University, Manassas, VA, Oct 21, 2008.*

Detecting gene regulatory signals from genome-wide ChIP-chip and sequence data. *Department of Biostatistics & Epidemiology, University of Pennsylvania, Oct 23, 2007.*

Analysis of ChIP-chip tiling array data for mammalian transcription factors. *Affymetrix Northern California ChIP-on-chip Workshop, Berkeley, CA, Jul 24, 2007.*

Detecting gene regulatory signals from genome-wide ChIP-chip and sequence data. *Department of Statistics, Purdue University, Mar 7, 2007.*

Detecting gene regulatory signals from genome-wide ChIP-chip and sequence data. *Department of Biostatistics, University of North Carolina at Chapel Hill, Mar 5, 2007.*

Detecting gene regulatory signals from genome-wide ChIP-chip and sequence data. *Department of Statistics, North Carolina State University, Feb 23, 2007.*

Detecting gene regulatory signals from genome-wide ChIP-chip and sequence data. *Department of Biostatistics, Johns Hopkins University, Feb 19, 2007.*

Detecting gene regulatory signals from genome-wide ChIP-chip and sequence data. *Department of Biostatistics, University of Washington, Feb 15, 2007.*

Detecting gene regulatory signals from genome-wide ChIP-chip experiments and sequence data: towards developing a strategy with increased statistical power, *Department of Statistics, Pennsylvania State University, Feb 6, 2007.*

Detecting gene regulatory signals from genome-wide ChIP-chip and sequence data. *Department of Statistics, Texas A&M University, Jan 30, 2007.*

Statistical analysis of genome-wide chromatin immunoprecipitation data for mammalian transcription factors. *The Stanford Workshop in Biostatistics, Stanford, CA, Nov 16, 2006.*

CisGenome – an *in silico* lab for the analysis of ChIP-chip tiling array data. *The Affymetrix GeneChip Exon and Tiling Arrays Data Analysis Workshop, Cambridge, MA, Mar 23, 2006.*

ADDITIONAL INFORMATION

Personal statement of research and research objectives

My major research interest is computational biology. I am particularly interested in studying gene regulation and systems biology. My research involves developing statistical methods to decipher *cis*-regulatory information from mammalian genomes. These include statistical tools to detect genomic regions where protein-DNA interactions occur, to detect epigenetic marks, to discover transcription factor binding motifs, and to identify genes that function according to specific spatial and temporal patterns. By working together with collaborators, we have applied these methods to studying gene regulation in mouse Sonic Hedgehog (SHH) signaling pathway. Our long term goal is to establish effective and efficient statistical strategies that allow us to reconstruct mammalian gene regulatory networks through synthesizing information from gene expression, protein-DNA interactions, protein-protein interactions, genetic and epigenetic variations, transcription factor binding motifs and existing knowledge on signaling and metabolic pathways. Knowledge of these networks will serve as the basis for us to understand human development and disease.

Keywords

Gene regulation, Genomics, Epigenetics, ChIP-chip, Tiling Array, Massively Parallel Sequencing, Microarray, Motif, Bayesian/Empirical Bayes Methods, MCMC, Hierarchical Models