

NANCY RUONAN ZHANG

SEPTEMBER 26, 2011

CONTACT INFORMATION

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EMPLOYMENT HISTORY

Assistant Professor 9/2006 Dept. of Statistics
- 6/2011 Stanford University, CA.
Post-doctoral Fellow 10/2005 Depts. of Statistics and Plant Biology
- 7/2006 University of California at Berkeley

EDUCATION

Doctor of Philosophy 9/2005 Dept. of Statistics
Stanford University, CA.
Master of Science 6/2001 Dept. of Computer Science
Stanford University, CA.
Bachelor of Science 6/2001 Dept. of Mathematics
Stanford University, CA

PUBLICATIONS

Articles in refereed Journals (excluding consulting publications):

- (1) Zhang, N.R. and Siegmund, D.O., 2007, A modified Bayes information criterion with applications to the analysis of comparative genomic hybridization data. *Biometrics* 63, 22–32.
- (2) Chan, H.P. and Zhang, N.R., 2007, Scan statistics with weighted observations. *JASA Theory and Methods*, 102, 595–602.*
- (3) The Encode Consortium, 2007, Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature* 447, 799–816.
- (4) Lai T.L., Xing, H and Zhang, N.R., 2008, Stochastic segmentation models for array-based comparative genomic hybridization data analysis. *Biostatistics*, 9, 290-307.*
- (5) Zhang, N.R., Wildermuth, M.C. and Speed, T.P., 2008, Transcription factor binding site prediction with multivariate gene expression data. *Annals of Applied Statistics*, 2, 332–365.

- (6) Zhang, N.R., Senbabaoglu, Y. and Li, J., 2010, Joint estimation of DNA copy number from multiple platforms. *Bioinformatics*, 26, 153–160.
- (7) Siegmund, D.O., Yakir, B. and Zhang, N.R., 2010, Tail approximations for maxima of random fields by likelihood ratio transformations. *Sequential Analysis*, 29, 245–262.*
- (8) Zhang, N.R., Siegmund, D.O., Ji, H., and Li, J., 2010, Detecting simultaneous change-points in multiple sequences. *Biometrika*, 97, 631–645.
- (9) Li, F. and Zhang, N., 2010, Bayesian variable selection in structured high-dimensional covariate spaces with applications in genomics. *Journal of the American Statistical Association – Theory and Methods*, 105, 1202-1214.*
- (10) Bickel, P., Boley, N., Brown, B., Huang, H. and Zhang, N.R., 2010, Subsampling methods for genomic inference. *Annals of Applied Statistics*, 4, 1660-1697.*
- (11) Chan, H.P.[‡], Zhang, N.R.[‡], and Chen, L.H.S., 2010, Importance sampling of word patterns in DNA and protein sequences. *Journal of Computational Biology*, 17, 1697-1709.
- (12) Chen, H., Xing, H., and Zhang, N.R.[†], 2011, Estimation of parent specific DNA copy number in tumors using high-density genotyping arrays, *PLoS Computational Biology*, 7, e1001060.
- (13) Siegmund, D.O., Yakir, B. and Zhang, N.R., 2011, Detecting simultaneous variant intervals in aligned sequences. *Annals of Applied Statistics*, 5, 645-668.*
- (14) Efron, B. and Zhang, N.R., 2011, False Discovery Rates and Copy Number Variation, *Biometrika*, 98, 251-271.*
- (15) Siegmund, D., Yakir, B. and Zhang, N.R., 2011, The false discovery rate for scan statistics, *Biometrika*, *in press*.*
- (16) Zhang, N.R. and Siegmund, D., 2011, Model Selection for High Dimensional, Multi-sequence Change-point Problems, *Statistica Sinica*, *in press*.
- (17) Muralidharan, O., Natsoulis, G., Bell, J., Newburger, D., Xu, H., Keta, I., Ji, H. and Zhang, N.[†], 2011, A Cross-Sample Statistical Model for SNP Detection in Short-Read Sequencing Data, *Nucleic Acids Research*, *in press*.[†]

Published book chapters:

- (18) Chan, H.P., Tu, I.P. and Zhang, N.R., 2009, Boundary crossing probability computations in the analysis of scan statistics. in *Scan Statistics - Methods and Applications*. Birkhauser, Boston.*
- (19) Zhang, N.R., 2010, DNA copy number profiling in normal and tumor genomes. *Frontiers in Computational and Systems Biology*, ed. Jianfeng Feng, Wenjiang Fu and Fengzhu Sun. pp. 259–281.

Submitted preprints:

- (20) Shen, J. and Zhang, N.R.[†], 2011, Change-point model on nonhomogeneous Poisson processes with application in copy number profiling by next-generation DNA sequencing. (*2nd round review for Annals of Applied Statistics.*)
- (21) Natsoulis, G., Bell, J.M., Xu, H., Buenrostro, J.D., Ordonez, H., Grimes, S., Newburger, D., Jensen, M., Zahn, J.M., Zhang, N. and Hanlee P. Ji, 2011, A Flexible Approach for Highly Multiplexed Candidate Gene Targeted Resequencing. (*2nd round review for PLoS One.*)
- (22) Muralidharan, O., Natsoulis, G. and Zhang, N.[†], 2011, Detecting mutations in mixed sample sequencing data using empirical Bayes. (*Submitted to Annals of Applied Statistics.*)
- (23) Sun, Y., Zhang, N. and Owen, A. Multiple hypothesis testing, adjusting for latent variables. (*Submitted to Annals of Applied Statistics.*)

* Authors are listed in alphabetical order.

† Corresponding author.

‡ Joint first authors.

TEACHING

I have taught the following courses at Stanford:

- 06-07 Winter, 07-08 Winter:** Applied Statistics (STAT191)
- 08-09 Winter, 09-10 Winter:** Introduction to ANOVA (STAT203)
- 06-07 Spring, 07-08 Spring:** Nonparametric Statistics (STAT205)
- 08-09 Winter, 09-10 Winter, 10 Fall:** Stochastic Processes with Applications in Biology (STAT215)
- 08-09 Spring:** Computational Algorithms in Statistical Genetics (STAT345/GEN245)
- 09-10 Spring:** Statistical Methods in Genetics (STAT166/STAT366)

HONORS AND AWARDS

- 2011:** Sloan Fellowship, Sloan Foundation
- 2011-2014:** NIH R01 HG006137-01, PI, Project title: “Statistical Models for Genome Sequencing and Association”.
- 2010-2013:** NSF DMS Grant ID 1043204, co-PI with David Siegmund, Project title: “Statistical Methods for Threat Detection”
- 2009-2012:** NSF DMS Grant ID 0906394, PI, Project title: “Change-point Problems in Genomic Profiling”
- 2006-current:** Terman Fellowship, Stanford University
- 2007:** New World Silver Medal for the Best PhD Thesis in the Mathematical Sciences
- 2002:** Honorary Stanford Graduate Fellow

2002: National Defense Science and Engineering Graduate Fellowship

OTHER CURRENT AND PENDING FUNDING SOURCES

2011-2016: NIH U01 CA151920-01A1, Co-PI with Hanlee Ji, Project title: “Integrated Genomic Discovery and Functional Validation of Colorectal Cancer Loci”. Pending IRG review.

2008-2013: NIH R01 GM082802 , Investigator, Project title: Statistical Methods for Integrative Analysis of Genomics and Proteomics Data. PI: Pei Wang.

STUDENTS I AM CURRENTLY ADVISING

- (1) Hao Chen, doctoral candidate, Department of Statistics, Stanford University.
- (2) Jeremy Shen, doctoral candidate, Department of Statistics, Stanford University.
- (3) Yi Liu (joint with David Siegmund), doctoral candidate, Department of Statistics, Stanford University.
- (4) Yunting Sun (joint with Art Owen), doctoral candidate, Department of Statistics, Stanford University.
- (5) Sonya Marie Schuh-Huerta, Postdoctoral Researcher, Institute for Stem Cell Biology & Regenerative Medicine, Stanford University.

SERVICE AND SYNERGISTIC ACTIVITIES

2010 fall: Masters student advisor for Stanford statistics department.

2007-current: Faculty advisor for the Computational Mathematics Undergraduate major at Stanford University.

2006-current: Part of the development team for the statistical analysis portal for ENCODE data.

2009 spring: Organized the workshop titled “Mathematical Genomics” during April 13, 2009 to April 15, 2009 at the Mathematical Sciences Research Institute in Berkeley.

2007 summer: Coordinated the Stanford VPUE Undergraduate Research Program, advised undergraduates in their research projects.

INVITED TALKS

2006/01: IPAM Workshop in Mathematical Biology, UCLA

2006/01: Statistics Department, Stanford University

2006/02: Statistics Department, UC Berkeley

2006/07: Statistica Sinica, Taiwan

2006/07: National Health Research Institute, Taiwan

2006/11: Department of Epidemiology and Biostatistics, UC San Francisco

2007/04: Biostatistics Workshop, Stanford University

- 2007/05:** Bayesian Statistics Conference, Harvard University
2007/06: Graybill Conference, Fort Collins, Colorado
2007/06: Taipei International Statistical Symposium, Taiwan
2007/08: International Conference on the Frontiers of Statistics: High Dimensional Data Analysis, Kunming, China
2007/09: Department of Statistics, Duke University
2007/10: Department of Biomathematics, UCLA
2008/01: Computational Biology Seminar, Carnegie Mellon University
2008/04: Biostatistics Workshop, Stanford University
2008/06: WNAR, Davis, CA
2008/07: International Workshop on Applied Probability, Campiegne, France
2008/08: Joint Statistical Meetings, Denver
2008/09: Workshop Change-Point Detection Methods and Applications, Paris
2008/10: Department of Statistics, UC Berkeley
2008/11: Department of Epidemiology and Biostatistics, UC San Francisco
2009/04: Department of Statistics, University of Chicago
2009/04: Mathematical Biology Workshop, Mathematical Sciences Research Institute, Berkeley
2009/06: Conference in Honor of 70-th Birthday of Minping Qian
2009/06: ICSA Applied Statistics Symposium, San Francisco, CA
2009/06: IMS Asian Pacific Rim Meeting, Seoul, Korea
2009/06: Statistical Genomics Workshop, Singapore
2009/07: Department of Mathematics, Nankai University, Tianjin, China
2009/07: IMS-China International Conference on Statistics and Probability
2009/10: Department of Statistics, UC Davis
2009/10: Seminar in Computational Biology, University of Southern California
2009/10: Department of Statistics, Stanford University
2010/01: Neyman Seminar, UC Berkeley
2010/02: Seminar in Computational Biology, Stanford University
2010/06: ICSA Applied Statistics Symposium, Indianapolis (Jeremy Shen gave the talk.)
2010/08: Joint Statistical Meetings, Vancouver, Canada
2010/12: Department of Statistics, University of Pennsylvania
2011/03: ENAR, Miami, FL (Jeremy Shen gave the talk.)

COUNTRY OF CITIZENSHIP

United States of America