

# Sining Chen, Ph.D.

## Contact information

615 North Wolfe St., W7041  
Dept. Environmental Health Sciences  
Johns Hopkins Bloomberg School of Public Health  
Baltimore, MD 21205  
Tel: (410) 502-4266  
Fax: (410) 955-1811  
Email: [sichen@jhsp.h.edu](mailto:sichen@jhsp.h.edu)

## Education

Ph.D. in Statistics and Decision Sciences, Duke University, September 2002  
M.S. in Statistics and Decision Sciences, Duke University, May 1999  
B.S. in Applied Mathematics, Tsinghua University, Beijing, P.R.China, July 1997

## Training and Workshops

Graduate Summer Institute of Epidemiology and Biostatistics, Johns Hopkins Bloomberg School of Public Health, June 2004  
Workshop on Writing a Biomedical Research Paper, Johns Hopkins University, 2004  
Workshop on Grant Writing, Johns Hopkins University, 2005

## Professional Experience

### Assistant Professor, August 2005 – present

Department of Environmental Health Sciences, Johns Hopkins Bloomberg School of Public Health

*Joint appointment*, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health (August 2005 – present)

*Joint appointment*, Department of Oncology, Johns Hopkins School of Medicine (August 2007 – present)

### Post-doctoral Fellow, September 2002 – August 2005

Division of Oncology Biostatistics, Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins

## Professional Associations

Active Member, the American Association for Cancer Research,  
Member, the American Statistical Association,  
Member, the International Biometry Society,  
Member, the International Society for Gastrointestinal Hereditary Tumors

## **Refereeing for Peer-reviewed Journals**

Journal of the National Cancer Institute,  
Journal of the American Statistical Association,  
Journal of Clinical Oncology,  
American Journal of Epidemiology,  
European Journal of Human Genetics,  
Computational Statistics & Data Analysis,  
Genetics in Medicine

## **Honors and Awards**

Johns Hopkins Breast SPORE Research Career Development Award, 2007-2008: \$50,000

Johns Hopkins School of Public Health Faculty Innovation Award, 2007-2008: \$35,000

Winner of the NSF Young Investigator's Award to attend the Latin America Probability and Mathematical Statistics Conference, Oct 2001

Duke University Graduate School Fellowship, 1997-1998 2000-2001

## **Research Grant Participation**

### Ongoing Research Grants

P30ES003819 Groopman/Chen (PI) NIEHS Center in Urban Environmental Health  
Pilot Project: Studying Associations in Neuroimages: An Empirical Bayes Approach.  
\$20,000 04/01/2006-03/31/2007.  
Statistical methodology for analyzing structure-function associations from neuroimages.  
Role: Principal Investigator

R01CA105090-01A1 Parmigiani (PI) 09/30/04 - 11/30/08 NIH/NCI  
Statistical Methods for Cancer Susceptibility Genes The major goal of this project is to contribute novel statistical methods and software for familial cancer risk prediction.  
Role: co-Investigator

R01 AG10785 -09-11 Schwartz (PI) 10/01/05-9/30/08 NIH/NIA 20% \$500,000 annually  
Age, lead exposure, and neurobehavioral decline. The major goal of this project is to examine longitudinal relations among tibia lead levels, volumetric measures by MRI of specific brain structures, white matter lesions as assessed by DTI and FLAIR imaging, and neurobehavioral function in a longitudinal study of former organolead manufacturing workers and matched community controls. Role: Statistician

5P30 CA06973, Abeloff/Parmigiani(PI) 05/01/2006 – NIH/NCI 10% \$200,000 for year 1 for the Bioinformatics core  
Regional Oncology Research Center/Bioinformatics Shared Resources Core  
Under the Oncology center grant, the Bioinformatics core provides statistical support to genetics and genomics-related projects. Role: co-Investigator

### Completed Research Support

P50CA62924 Parmigiani (PI) 07/01/02 -06/30/07 NIH SPORE in gastrointestinal Cancer: Biostatistics SPORE The major goals of this project are to develop areas of basic science with potential impact on colorectal and pancreatic cancer and to move promising areas into clinical evaluation including clinical trials. Role: Statistician

DK-58757 Germino (PI) 09/01/01 -08/31/03 NIDDK-Biotechnology Center The Hopkins DK Center for the Analysis of Gene Expression The major goals of this research are to utilize the cDNA microarray technology to perform genome-wide patterning of gene expression for the projects listed in D. Research and Design and Methods. Role: Statistician

## **Publications**

### Journal Articles

Caffo BS, **Chen S**, Stewart W, Bolla K, Yousem D, Davatzikos C, and Schwartz BS. “Are MRI-based brain volumes mediators of the associations of cumulative lead dose with cognitive function?”, *American Journal of Epidemiology*, forthcoming

Iversen ES, Parmigiani G, and **Chen S**. “Multiple Model Evaluation Absent the Gold Standard via Model Combination”, *Journal of the American Statistical Association*, forthcoming

Tai YC, Domcheck S, Parmigiani G and **Chen, S**, “Risk of Male Breast Cancer among BRCA1/2 Mutation Carriers”, *Journal of National Cancer Institute*, forthcoming

Parmigiani G, **Chen S**, and Velculescu V. “TRAB, Testing Whether Mutation Frequencies Are Above an Unknown Background. Statistical Applications in Genetics and Molecular Biology, forthcoming

**Chen S**, Euhus DM, and Parmigiani G (2007), “Quantitative models for predicting mutations in Lynch syndrome genes”, *Current Colorectal Cancer Reports* 3 (4)

Parmigiani G, **Chen S**, Iversen ES Jr, Friebel TM, Finkelstein DM, Anton-Culver H, Ziogas A, Weber BL, Eisen A, Malone KE, Daling JR, Hsu L, Ostrander EA, Peterson LE, Schildkraut JM, Isaacs C, Corio C, Leondaridis L, Tomlinson G, Amos CI, Strong LC, Berry DA, Weitzel JN, Sand S, Dutson D, Kerber R, Peshkin BN, and Euhus DM (2007) “Validity of models for predicting BRCA1 and BRCA2 mutations”, *Ann Intern Med* 147(7):441-50.

Schwartz BS, **Chen S**, Caffo B, Stewart WF, Bolla KI, Yousem D, and Davatzikos C, (2007) “Relations of brain volumes with cognitive function in males 45 years and older with past lead exposure”, *NeuroImage* 37(2):633-41

**Chen S** and Parmigiani G (2007) “A Comprehensive Analysis of *BRCA1* and *BRCA2* Penetrance”, *Journal of Clinical Oncology*, 25(11): 1329-1333

Wang W, **Chen S**, Brune KA, Hruban, RH, Parmigiani G and Klein, AP (2007), “Accurate Risk Assessment in Individuals with a Family History of Pancreatic Cancer”, *Journal of Clinical Oncology*, 25(11): 1417-1422.

**Chen S**, Wang W, Lee S, Nafa K, Lee J, Romans K, Watson P, Gruber SB, Euhus DM, Kinzler KW, Jass J, Gallinger S, Lindor N, Casey G, Ellis N, Giardiello FM, the Colon Cancer Family Registry, Offit K, and Parmigiani G (2006) “Prediction of Germline Mutations and Cancer Risk in the Lynch Syndrome”, *Journal of American Medical Association*, 296 (12)

**Chen S**, Iversen ES, Friebel T, Finkelstein D, Weber BL, Eisen A, Peterson LE, Schildkraut JM, Isaacs C, Corio C, Leondaridis L, Tomlinson G, Amos CI, Strong LC, Berry DA, Weitzel JN, Sand S, Dutson D, Kerber R, Peshkin BN, Euhus DM, and Parmigiani G (2006), “Characterization of BRCA1 and BRCA2 Mutations in a Large United States Sample”, *Journal of Clinical Oncology*, 24 (6)

**Chen S**, Watson P, and Parmigiani G (2005), “Accuracy of MSI Testing in Predicting Germline Mutations of MSH2 and MLH1: a Case Study in Bayesian Meta-Analysis of Diagnostic Tests without a Gold Standard,” *Biostatistics*, 6 (3)

Iversen ES and **Chen S** (2005), “Population-Calibrated Gene Characterization: Estimating Age at Onset Distributions Associated with Cancer Genes,” *Journal of the American Statistical Association*, 100, No. 470

**Chen S**, Wang W, Broman KW, Katki H A, and Parmigiani G(2004), “BayesMendel: an R Environment for Mendelian Risk Prediction”, *Statistical Applications in Genetics and Molecular Biology*, 3 (1).

Tao Y, **Chen S**, Hartl D L, and Laurie C C (2003),, “Genetic Dissection of Hybrid Incompatibilities between *Drosophila Simulans* and *Drosophila Mauritiana*. I. Differential accumulation of hybrid male sterility effects on the X and autosomes”, *Genetics* 164 (3)

#### Comments and Letter

Iversen ES, Katki H, **Chen S**, Berry DA, and Parmigiani G. Letter to the editor on “Limited family structure and BRCA gene mutation status in single cases of breast cancer.” by Weitzel JN, Lagos VI, Cullinane CA et al., *Journal of American Medical Association*, forthcoming

Wang W, **Chen S**, Parmigiani G, Brune KA, Hruban, RH and Klein, AP (2007), Reply to letter to the editor on “Accurate Risk Assessment in Individuals with a Family History of Pancreatic Cancer”, *Journal of Clinical Oncology*, 25(33)

Parmigiani G and **Chen S** (2007), Reply to “One risk fits all?” by De Bock GH, Mourits MJ, Oosterwijk JC. *Journal of Clinical Oncology*, 25(22): 3384

**Chen S**, Iversen ES, and Parmigiani G (2006), Reply to “Re: Characterization of BRCA1 and BRCA2 Mutations in a Large United States Sample.” by A Antoniou, PDP Pahroah, DF Easton, DG Evans, *Journal of Clinical Oncology*, 24 (20)

Peer-reviewed Abstracts

Caffo B, **Chen S**, and Schwartz BS, “Is MRI-based structure a mediator for cumulative lead exposure’s effect on cognitive function?”, Proceedings of the 2007 Human Brain Mapping conference, Chicago, IL

**Chen S**, Yin Y, Wang W, et al. “Cancer Risks for *MLH1* and *MSH2* Mutation Carriers: Findings from 15,704 Individuals in 65 U.S. Lynch Syndrome Families”, Proceedings of the Fifth American Association for Cancer Research International Conference, 2007

**Chen S**, Wang W, Lee S *et al.*, “A Mendelian Model and Software to Compute the Probability of Carrying *MLH1* and *MSH2* Mutations”, Proceedings of the Third American Association for Cancer Research International Conference, 2004

Manuscripts Under Review

Chu H, **Chen S**, and Louis, TA, “Random Effects Models in Meta-Analysis for Evaluating Accuracy of Diagnostic Tests in the Presence of Missing Data”

Katki H, **Chen S**, and Parmigiani G, “Competing Risks and Censoring in Mendelian Mutation Prediction Models”

Tai YC, **Chen S**, Parmigiani G, Klein A P, “Incorporating Tumor Immunohistochemical Markers in BRCA1 and BRCA2 Carrier Probability Prediction”,

**Chen S**, Wang C, Caffo B, Lynn E, and Schwartz BS, “Adaptive Control of False Discovery Rate in Voxel-Based Morphometry”

**Presentations**

Invited Talks

“Risk prediction and screening in colorectal cancer”, Johns Hopkins Center for Cancer Prevention and Control, September 2007

“Risk prediction in hereditary cancers”, Peking University Health Science Center School of Public Health, Beijing, China, April 2007

“Risk prediction in hereditary colorectal cancers”, Johns Hopkins School of Public Health, Department of Environmental Health Sciences, DOEH seminar, Baltimore, MD, October 2006

“Risk prediction in hereditary breast cancer”, Johns Hopkins Breast SPORE Research Seminar Series, Baltimore, MD, October 2006

“Risk Estimation in Persons at Genetic Risk of Cancer”,  
– Invited speaker in session “Using Genetics/Genomics to Advance Public Health”,  
Joint Statistical Meeting, Seattle, WA, August 2006

“Advancing Statistics in Environmental Health Sciences”,  
-- Faculty Retreat, Dept. Environmental Health Sciences, Johns Hopkins  
Bloomberg School of Public Health, Baltimore, MD, Jan 2006  
-- Division of Occupational Environmental Health, Dept. Environmental Health  
Sciences, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, December  
2005

“Design and Analysis of Studies of Cancer Risks from Major Genes”:  
– Department of Statistics, University of California, Riverside, CA, May 2005  
– Center for Statistical Sciences, Brown University, Providence, RI, May 2005  
– Department of Statistics, University of Pittsburgh, Pittsburgh, PA, April 2005  
– Department of Environmental Health Sciences and Department of Biostatistics,  
Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, April 2005

“Mendelian Models for Cancer Susceptibility Genes”,  
–Department of Epidemiology and Biostatistics, Michigan State University  
–Division of Biostatistics, University of California at Davis School of Medicine  
–Division of Epidemiology and Biostatistics, Memorial Sloan Kettering Cancer  
Center  
–Division of Biostatistics, Fox Chase Cancer Center, Philadelphia, PA, Jan 2005

“Validation of Models for Prediction of BRCA1 and BRCA2 Mutations”  
– Biostatistics Branch, Division of Cancer Epidemiology and Genetics, National  
Institute of Health, Bethesda, MD, Jan 2004  
– (Poster) Cancer Risk Prediction Models Workshop, Washington, DC, May 2004

“Population-Calibrated Penetrance Estimation among BRCA1/2 Mutation Carriers”  
– Dept. of Epidemiology and Biostatistics, Memorial Sloan-Kettering Cancer  
Center, New York, NY, March 2002  
– Dept. of Biostatistics, MD Anderson Cancer Center, Houston, TX, March 2002  
– Johns Hopkins University, Baltimore, MD, Feb 2002  
– Biostatistics Branch, National Institute of Environmental Health Sciences, RTP,  
NC, Jan 2002

“A Hierarchical Deformation Model for Images”  
– Dept. of Statistics, Columbia University, New York, NY, March 2002  
– National Institute of Environmental Health Sciences, RTP, NC, Jan 2002

“On Informative Prior Models for Image Deformations”

– First SIAM (Society for Industrial and Applied Mathematics) Conference on Computational Science and Engineering, Washington, DC, Sept 2000

### Contributed Talks and Posters

Poster, “Cancer Risks for *MLH1* and *MSH2* Mutation Carriers: Findings from 15,704 Individuals in 65 U.S. Lynch Syndrome Families”, the Fifth American Association for Cancer Research International Conference, Los Angeles, CA April 2007

Poster, “Cancer Risks for *MLH1* and *MSH2* Mutation Carriers: Findings from 15,704 Individuals in 65 U.S. Lynch Syndrome Families”, the 2<sup>nd</sup> Biennial Scientific Meeting of the International Society for Gastrointestinal Hereditary Tumours, Yokohama, Japan, March 2007

Talk, “Comprehensive Evaluation of Breast and Ovarian Cancer Risks”, Joint Statistical Meeting, Minneapolis, MN, August 2005

Talk, “A Deformation Model for Images”, Eastern North American Region (ENAR) meeting, Austin, TX, March 2005

Poster, “A Mendelian Model and Software to Compute the Probability of Carrying *MLH1* and *MSH2* Mutations”, the Third American Association for Cancer Research International Conference, Seattle, WA, November 2004

Talk, “Penetrance Estimation of HNPCC Mutations from Family History Data”, Joint Statistical Meeting, San Francisco, CA, August 2003

Poster, “A Deformation Model for Images”, International Workshop on Bayesian Data Analysis, Santa Cruz, CA, August 2003

Session discussant, “Bayesian Robustness”, Joint Statistical Meeting, New York City, NY, August 2002

### Conference Participation

Joint Statistical Meeting, Baltimore, MD August 1998

International Biometry Society Eastern North American Region meeting, Washington, DC, March 2000

International Biometry Society Eastern North American Region meeting, Tampa, FL, March 2006

American Association for Cancer Research (AACR) Frontiers in Cancer Prevention Research, Boston, MA, November 2006

## **Teaching**

### Classroom Instruction

“Bayesian Methods”, 2007, Johns Hopkins School of Public Health

“Analysis of Biological Sequences”, 2003, 2004, 2005, Johns Hopkins School of Public Health.

*Recitations and Computer Labs*

“Introduction to Statistics for Mathematical Scientists”, 2002, Duke University

“Probability and Statistics for Engineers”, 1999, Duke University

“Introduction to Statistics for Economy Majors”, 1997, Duke University

**PhD Student Dissertation Committees**

Yue Yin, Shirley Van Zandt

**Master’s Thesis Reader**

Li-juan Deng

**Service**

Research Committee, Department of Environmental Health Sciences, Johns Hopkins  
School of Public Health, 2006--present