

## **CURRICULUM VITAE**

Ingo Ruczinski

Part I

### **PERSONAL DATA**

Department of Biostatistics  
Johns Hopkins Bloomberg School of Public Health  
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Baltimore, MD 21205-2179.

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### **EDUCATION AND TRAINING**

#### **Degrees**

- PhD, University of Washington, Seattle, WA, Statistics (2000).
- MA, University of Würzburg, Germany, Mathematics and Computer Science (1995).
- MA, State University of New York, Albany, NY, Mathematics and Statistics (1994).

#### **Postdoctoral Training**

- Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA (2000-2001).
- Department of Biochemistry, University of Washington, Seattle, WA (2000-2001).

#### **Visiting**

- Department of Statistics, University of Dortmund, Germany (2009).
- Department of Chemistry, University of California at Santa Barbara (2003,2004,2005,2006,2007,2008).
- Centre National de Genotypage, Paris-Evry, France (2005).
- Department of Statistics, University of Umeå, Sweden (1994).
- Department of Mathematics, University of Caen, France (1993).

## **PROFESSIONAL EXPERIENCE**

- Associate Professor, Department of Biostatistics, Johns Hopkins University (2007-present).
- Member, Johns Hopkins Institute for Multiscale Modeling of Biological Interactions (2006-present).
- Assistant Professor, Department of Biostatistics, Johns Hopkins University (2001-2007).
- Postdoctoral Fellow, Department of Biochemistry, University of Washington (2000-2001).
- Research Associate, Publ. Health Sciences, Fred Hutchinson Cancer Research Center (2000-2001).
- Consultant, Department of Statistics, University of Washington (1998-1999).
- Research Assistant, Publ. Health Sciences, Fred Hutchinson Cancer Research Center (1998-2000).
- Research Assistant, Department of Biochemistry, University of Washington (1996-2000).
- Teaching Assistant, Department of Statistics, University of Washington (1995-1996).

## **PROFESSIONAL ACTIVITIES**

### **Professional Memberships**

- American Statistical Association
- American Society of Human Genetics
- International Biometric Society
- Institute of Mathematical Statistics
- R Foundation for Statistical Computing
- International Genetic Epidemiology Society

### **Participation on Advisory Panels and Committees**

- Protein Folding Consortium (2004-present).
- CLUE serology advisory committee (2005-present).
- GAIN alternative allele calling working group (2008-present).
- STAMPEED steering/analysis committee (2008-present).
- GENEVA steering/analysis committee (2008-present).

### **Program Development**

- Program Chair, American Statistical Association, Section on Risk Analysis (2005-2006).
- Program Committee, Joint Statistical Meetings (2006).
- Program Committee, Eastern North Atlantic Region (2006,2011).
- Organizing Committee, Conference on Statistical Methods for Very Large Data Sets (2011).
- Session Chair, Joint Statistical Meetings (2001,2004,2005).
- Session Chair, Eastern North Atlantic Region Meeting (2003).
- Session Chair, American Society of Human Genetics Meeting (2009).

- Session Organizer, Joint Statistical Meetings (2002,2005,2006).
- Session Organizer, Eastern North Atlantic Region Meeting (2006,2007).
- Session Organizer, International Biometric Conference (2010).

## **EDITORIAL ACTIVITIES**

### **Peer Review Activities**

Algorithms for Molecular Biology, American Journal of Human Genetics, AMS-Dimacs Volume on Epidemiology and Data Mining, Australian and New Zealand Journal of Statistics, Bioinformatics, BioMed Central Bioinformatics, BioMed Central Genomics, Biometrical Journal, Biometrics, Biophysical Reviews and Letters, Biostatistics, Biotechnology Progress, Breast Cancer Research, Computational Statistics and Data Analysis, Genetic Epidemiology, Human Mutation, International Journal of Biostatistics, Journal of the American Statistical Association, Journal of Computational and Graphical Statistics, Journal of Heuristics, Journal of Statistical Software, Journal of the Royal Statistical Society (Series B), Mammalian Genome, Protein Science, Proteins: Structure, Function and Genetics, Proteins: Structure, Function and Bioinformatics, Public Library of Science (PLoS), Springer Verlag (New York), Statistical Applications in Genetics and Molecular Biology, Statistics in Medicine.

### **Editorial Board Membership**

- Editorial Board, *Cancer Prevention Research*, American Assoc. for Cancer Research (2008-present).
- Associate Editor, *Biometrics*, International Biometric Society (2008-present).
- Associate Editor, *Biometrical Journal*, International Biometric Society / Germany (2009-present).

### **Ad-hoc Review of Proposals**

- Research and Development Program, Louisiana Board of Regents (2004).
- Cancer Research UK Bioinformatics Programme (2007).
- National Science Foundation, Biological Database and Informatics Program (2007).
- Johns Hopkins NIEHS Center in Urban Environmental Health (2008).
- Science Unbound Foundation (2008).
- National Institutes of Health, Cancer Biomarker Study Section (2006-2008).
- National Institutes of Health, ARRA RC1 Challenge Grant Review (2009).

## **HONORS AND AWARDS**

- ZW Birnbaum Award for Excellence in Teaching, University of Washington (1996).
- Faculty Innovation Award, Johns Hopkins University (2002).
- Research Grant, Maryland Cigarette Restitution Fund, Johns Hopkins Medical Institutions (2002).
- Travel Award, International Federation of Classification Societies, Cracow, Poland (2002).

- Best Contributed Paper Award, Joint Statistical Meetings, ASA Section on Risk Analysis (2003).
- NSF Young Researchers Travel Award, University of Florida (2003).
- NSF Young Researchers Travel Award (University of California at Los Angeles (2004).
- Johns Hopkins Bloomberg School of Public Health Faculty Research Initiative Award (2006).
- Advising, Mentoring, and Teaching Recognition Award, Johns Hopkins University (2007).

## PUBLICATIONS

### Peer-Reviewed Articles

- Louis TA, **Ruczinski I** (2009). *Efficient evaluation of ranking procedures when the number of units is large, with application to SNP identification*. Biometrical Journal (to appear).
- Mathias RA, Grant AV, Rafaels R, Hand T, Gao L, Vergara C, Tsai YJ, Yang M, Campbell M, Foster C, Gao P, Toggias A, Hansel N, Diette G, Adkinson NF, Liu M, Faruque M, Dunston GM, Watson H, Bracken MB, Hoh J, Maul P, Maul T, Murray T, Hetmanski JB, Ashworth R, Ongaco C, Hendricks K, Doheney K, Pugh E, Scott AF, Kabesch M, Liang L, Abecasis G, Moffatt MF, Cookson WO, **Ruczinski I**, Beaty TH, Barnes KC (2009). *A genome-wide association study on african-ancestry populations identifies novel asthma genes*. Journal of Allergy and Clinical Immunology (to appear).
- Sleiman PM, Flory J, Imielinski M, Bradfield JP, Annaiah K, Willis-Owen SA, Wang K, Rafaels NM, Michel S, Bonnelykke K, Zhang H, Kim CE, Frackelton EC, Glessner JT, Hou C, Otieno FG, Santa E, Thomas K, Smith RM, Glaberson WR, Garris M, Chiavacci RM, Beaty TH, **Ruczinski I**, Orange J, Allen J, Spergel JM, Grundmeier R, Mathias RA, Christie JD, von Mutius E, Cookson WO, Kabesch M, Moffatt MF, Grunstein MM, Barnes KC, Devoto M, Magnusson M, Li H, Struan FA, Grant SF, Bisgaard H, Hakonarson H (2009). *Common variants in DENND1B associate with pediatric asthma*. New England Journal of Medicine (to appear).
- Gallicchio L, Chang H, Christo DK, Thuita L, Huang HY, Strickland P, **Ruczinski I**, Hoffman SC, Helzlsouer KJ (2009). *Single nucleotide polymorphisms in obesity-related genes and all-cause and cause-specific mortality: a prospective cohort study*. BMC Medical Genetics 10: 103.
- Jorgensen TJ, **Ruczinski I**, Kessing B, Smith MW, Shugart YY, Alberg AJ (2009). *Hypothesis-driven candidate gene association studies: practical design and analytical considerations*. American Journal of Epidemiology 170(8): 986-93.
- Wheless L, **Ruczinski I**, Alani R, Clipp S, Hoffman-Bolton J, Jorgensen TJ, Liégeois NJ, Strickland PT, Alberg AJ (2009). *The association between skin characteristics and skin cancer prevention behaviors*. Cancer Epidemiology, Biomarkers, and Prevention 18(10): 2613-9.
- Price AL, Tandon A, Patterson N, Barnes KC, Rafaels N, **Ruczinski I**, Beaty TH, Mathias R, Reich D, Myers S (2009). *Sensitive detection of chromosomal segments of distinct ancestry in admixed populations*. PLoS Genetics 5(6): e1000519.

- Miller CL, Murakami P, **Ruczinski I**, Ross RG, Sinkus M, Sullivan B, Leonard S (2009). *The risk for schizophrenia and bipolar disorder conveyed by two complex genotypes incorporating loci relevant to the kynurenine pathway and melanotropin function*. Schizophrenia Research 113(2-3): 259-67.
- Lam TK, **Ruczinski I**, Helzlsouer K, Shugart YY, Li KE, Clipp S, Alberg AJ (2009). *Copy number variants of GSTM1 and GSTT1 in relation to lung cancer risk in a prospective cohort study*. Annals of Epidemiology 19(8): 546-52.
- Köttgen A, Glazer NL, Dehghan A, Hwang SJ, Katz R, Li M, Yang Q, Gudnason V, Launer LJ, Harris TB, Smith AV, Arking DE, Astor BC, Boerwinkle E, Ehret GB, **Ruczinski I**, Scharpf RB, Chen YI, de Boer IH, Haritunians T, Lumley T, Sarnak M, Siscovick D, Benjamin EJ, Levy D, Upadhyay A, Aulchenko YS, Hofman A, Rivadeneira F, Uitterlinden AG, van Duijn CM, Chasman DI, Paré P, Ridker PM, Kao WH, Witteman JC, Coresh J, Shlipak MG, Fox CS (2009). *Multiple loci associated with indices of renal function and chronic kidney disease*. Nature Genetics 41(6): 712-717.
- Himes BE, Hunninghake GM, Baurley JW, Rafaels NM, Sleiman P, Strachan DP, Wilk JB, Willis-Owen SA, Klanderma B, Lasky-Su J, Lazarus R, Murphy AJ, Soto-Quiros ME, Avila L, Beaty T, Mathias RA, **Ruczinski I**, Barnes KC, Celedn JC, Cookson WO, Gauderman WJ, Gilliland FD, Hakonarson H, Lange C, Moffatt MF, O'Connor GT, Raby BA, Silverman EK, Weiss ST (2009). *Genome-wide association analysis identifies PDE4D as an asthma-susceptibility gene*. American Journal of Human Genetics 84: 581-93.
- **Ruczinski I**, Plaxco KW (2009). *Some recommendations for the practitioner to improve the precision of experimentally determined protein folding rates and  $\Phi$  values*. Proteins: Structure, Function and Bioinformatics 74(2): 461-74.
- Schulze KJ, Christian P, **Ruczinski I**, Ray AL, Nath A, Wu LS, Semba RD (2008). *Hepcidin and iron status among pregnant women in Bangladesh*. Asia Pacific Journal of Clinical Nutrition 17(3): 451-6.
- Pattaro C, **Ruczinski I**, Fallin DM, Parmigiani G (2008). *Haplotype block partitioning as a tool for dimensionality reduction in SNP association studies*. BMC Genomics 9(1): 405.
- Chen J, **Ruczinski I**, Jorgensen TJ, Yenokyan G, Yao Y, Alani R, Liegeois NJ, Hoffman SC, Hoffman-Bolton J, Strickland PT, Helzlsouer KJ, Alberg AJ (2008). *Nonmelanoma skin cancer as a marker of risk for subsequent malignancy: a community-based prospective cohort study*. Journal of the National Cancer Institute 100(17): 1215-22.
- Sull JW, Liang KY, Hetmanski JB, Fallin MD, Ingersoll RG, Park J, Wu-Chou YH, Chen PK, Chong SS, Cheah F, Yeow V, Park BY, Jee SH, Jabs EW, Redett R, Jung E, **Ruczinski I**, Scott AF, Beaty TH (2008). *Differential parental transmission of markers in RUNX2 among cleft case-parent trios from four populations*. Genetic Epidemiology 32(6): 505-12.
- Scharpf R, Parmigiani G, Pevsner J, **Ruczinski I** (2008). *Hidden Markov models for the assessment of chromosomal alterations using high-throughput SNP arrays*. Annals of Applied Statistics

2(2): 687-713.

- Gallicchio L, Chang H, Christo DK, Thuita L, Huang HY, Strickland P, **Ruczinski I**, Hoffman SC, Helzlsouer KJ (2008). *Single nucleotide polymorphisms in inflammation-related genes and mortality in a community-based cohort in Washington county, Maryland*. *American Journal of Epidemiology* 167(7): 807-13.
- Ting JC, Roberson ED, Miller N, Lysholm-Bernacchi A, Stephan DA, Capone GT, **Ruczinski I**, Thomas GH, Pevsner J (2007). *Visualization of uniparental inheritance, Mendelian inconsistencies, deletions and parent of origin effects in single nucleotide polymorphism trio data with SNP trio*. *Human Mutation* 28(12): 1225-35.
- Scharpf RB, Ting JC, Pevsner J, **Ruczinski I** (2007). *SNPchip: R classes and methods for SNP array data*. *Bioinformatics* 23(5): 627-8.
- Visvanathan K, Crum RM, Strickland PT, You X, **Ruczinski I**, Berndt S, Alberg AJ, Hoffman SC, Comstock GW, Bell DA, Helzlsouer KJ (2007). *Alcohol dehydrogenase genetic polymorphisms, low-to-moderate alcohol consumption and risk of breast cancer*. *Alcoholism: Clinical and Experimental Research* 31(3): 467-76.
- Jorgensen J, Visvanathan K, **Ruczinski I**, Thuita L, Helzlsouer KJ (2007). *Breast cancer risk is not associated with polymorphic forms of Xeroderma Pigmentosum genes in a cohort of women from Washington County, Maryland*. *Breast Cancer Research and Treatment* 101(1): 65-71.
- Dai J\*, **Ruczinski I**\*, LeBlanc M, Kooperberg C (2006). *Imputation methods to improve inference in SNP association studies*. *Genetic Epidemiology* 30(8): 690-702 \* contributed equally.
- **Ruczinski I**, Sosnick TR, Plaxco KW (2006). *Methods for the accurate estimation of confidence intervals on protein folding  $\Phi$ -values*. *Protein Science* 15(10): 2257-64.
- Brown EE, Fallin D, **Ruczinski I**, Hutchinson A, Staats B, Vitale F, Lauria C, Serraino D, Rezza G, Mbisa G, Whitby D, Messina A, Goedert JJ, Chanock SJ, and the Kaposi Sarcoma Working Group (2006). *Associations of classic kaposi sarcoma with common variants in genes that modulate host immunity*. *Cancer Epidemiology, Biomarkers and Prevention* 15(5): 926-34.
- De Los Rios MA, Muralidhara BK, Wildes D, Sosnick TR, Marqusee S, Wittung-Stafshede P, Plaxco KW, **Ruczinski I** (2006). *On the precision of experimentally determined protein folding rates and  $\Phi$ -values*. *Protein Science* 15(3): 553-63.
- Brewster AM, Jorgensen TJ, **Ruczinski I**, Huang HY, Hoffman S, Thuita L, Newschaffer C, Lunn RM, Bell D, Helzlsouer KJ (2006). *Polymorphisms of the DNA repair genes XPD (Lys751Gln) and XRCC1 (Arg399Gln and Arg194Trp): relationship to breast cancer risk and familial predisposition to breast cancer*. *Breast Cancer Research and Treatment* 95(1): 73-80.
- Ting JC, Ye Y, Thomas GH, **Ruczinski I**, Pevsner J (2006). *Analysis and visualization of chromosomal abnormalities in SNP data with SNPscan*. *BMC Bioinformatics*, 18:7(1): 25.
- Mao R, Wang X, Spitznagel Jr EL, Frelin LP, Ting JC, Ding H, Kim J, **Ruczinski I**, Downey TJ,

- Pevsner J (2005). *Primary and secondary transcriptional effects in the developing human Down syndrome brain and heart*. *Genome Biology*, 6(13): R107.
- McCarney ER, Werner JH, Bernstein SL, **Ruczinski I**, Makarov DE, Goodwin PM, Plaxco KW (2005). *Site-specific dimensions across a highly denatured protein: a single molecule study*. *Journal of Molecular Biology*, 352(3): 672-82.
  - Maxwell KL, Wildes D, Zarrine-Afsar A, De Los Rios MA, Brown AG, Friel CT, Hedberg L, Horng JC, Bona D, Miller EJ, Vallee-Belisle A, Main ER, Bemporad F, Qiu L, Teilum K, Vu ND, Edwards AM, **Ruczinski I**, Poulsen FM, Kragelund BB, Michnick SW, Chiti F, Bai Y, Hagen SJ, Serrano L, Oliveberg M, Raleigh DP, Wittung-Stafshede P, Radford SE, Jackson SE, Sosnick TR, Marqusee S, Davidson AR, Plaxco KW (2005). *Protein folding: defining a standard set of experimental conditions and a preliminary kinetic data set of two-state proteins*. *Protein Science* 14(3): 602-16.
  - Kooperberg C, **Ruczinski I** (2005). *Identifying interacting SNPs using monte carlo logic regression*. *Genetic Epidemiology* 28(2): 157-70.
  - **Ruczinski I**, Kooperberg C, LeBlanc M (2004). *Exploring interactions in high dimensional genomic data: an overview of logic regression, with applications*. *Journal of Multivariate Analysis* 90: 178-95.
  - Kohn JE, Millett IS, Jacob J, Zagrovic B, Dillon TM, Cingel N, Dothager RS, Seifert S, Thiagarajan P, Sosnick TR, Hasan MZ, Pande VS, **Ruczinski I**, Doniach S, Plaxco KW (2004). *Random-coil behavior and the dimensions of chemically unfolded proteins*. *Proceedings of the National Academy of Sciences* 101(34): 12491-6.
  - **Ruczinski I**, Kooperberg C, LeBlanc M (2003). *Logic regression - methods and software*. *Non-linear Estimation and Classification, Lecture Notes in Statistics* 171: 333-44.
  - **Ruczinski I**, Kooperberg C, LeBlanc M (2003). *Logic regression*. *Journal of Computational and Graphical Statistics* 12(3): 475-511.
  - Bonneau R, Tsai J, **Ruczinski I**, Baker D (2002). *Contact order and ab initio protein structure prediction*. *Protein Science* 11(8): 1937-44.
  - **Ruczinski I**, Kooperberg C, Bonneau R, Baker D (2002). *Distributions of  $\beta$  sheets in proteins with application to structure prediction*. *Proteins: Structure, Function and Genetics* 48: 85-97.
  - Larson S, **Ruczinski I**, Davidson AR, Baker D, Plaxco KW (2002). *Residues participating in the folding nucleus do not exhibit preferential evolutionary conservation*. *Journal of Molecular Biology* 316: 225-33.
  - Kooperberg C, **Ruczinski I**, LeBlanc M, Hsu L (2001). *Sequence analysis using logic regression*. *Genetic Epidemiology* 21(S1): 626-31.
  - Bonneau R, Tsai J, **Ruczinski I**, Chivian D, Rohl C, Strauss C, Baker D (2001). *Rosetta in CASP4: progress in ab initio protein structure prediction*. *Proteins: Structure, Function and*

Genetics 45(S5): 119-26.

- Bonneau R, Tsai J, **Ruczinski I**, Baker D (2001). *Functional inferences from blind ab initio protein structure predictions*. Journal of Structural Biology 134(2-3): 186-90.
- Plaxco KW, Simons KT, **Ruczinski I**, Baker D (2000). *Topology, stability, sequence, and length: defining the determinants of two-state protein folding kinetics*. Biochemistry 39(37): 11177-83.
- Plaxco KW, Larson S, **Ruczinski I**, Riddle DS, Thayer EC, Buchwitz B, Davidson AR, Baker D (2000). *Evolutionary conservation in protein folding kinetics*. Journal of Molecular Biology 298: 303-12.
- Simons KT, Bonneau R, **Ruczinski I**, Baker D (1999). *Ab initio protein structure prediction of CASP3 targets using ROSETTA*. Proteins 37(S3): 171-6.
- Riddle DS, Grantcharova VP, Santiago J, Alm E, **Ruczinski I**, Baker D (1999). *Experiment and theory highlight role of native state topology in SH3 folding*. Nature Structural Biology 6: 1016-24.
- Simons KT, **Ruczinski I**, Kooperberg C, Fox B, Bystroff C, Baker D (1999). *Improved recognition of native-like protein structures using a combination of sequence-dependent and sequence-independent features of proteins*. Proteins 34(1): 82-95.

### Under Review

- Hunninghake GM, Soto-Quiros ME, Avila L, Kim HP, Lasky-Su J, Rafaels N, **Ruczinski I**, Beaty TH, Mathias RA, Barnes KC, Wilk JB, OConnor GT, Gauderman WJ, Baurley JW, Gilliland F, Liang C, Sylvia JS, Klanderma BJ, Sharma SS, Himes BE, Bossley C, Israel E, Raby BA, Bush A, Choi AM, Weiss ST, Celedon JC (2009). *TSLP polymorphisms are associated with asthma in a sex-specific fashion*.
- Murray T, Beaty T, Mathias R, Rafaels N, Faraque M, Watson H, **Ruczinski I**, Dunston G, Barnes KC (2009). *African and non-African admixture components in African Americans and an African Caribbean population*.
- Mathias RA, Kim Y, Sung H, Yanek LR, Herrera-Galeano JE, **Ruczinski I**, Wilson AF, Faraday N, Becker LC, Becker DM (2009). *A combined genome-wide linkage and association approach to find susceptibility loci for platelet function phenotypes in Caucasian and African American families with coronary artery disease*.
- Li Q, Louis TA, Fallin MD, **Ruczinski I** (2009). *Trio logic regression - detection of SNP-SNP interactions in case-parent trios*.
- Li Q, Fallin MD, Louis TA, Lasseter VK, McGrath JA, Avramopoulos D, Wolyniec PS, Valle D, Liang KY, **Ruczinski I**, Pulver AE (2009). *Detection of SNP-SNP interactions in trios of parents with schizophrenic children*.

- Scharpf RB, **Ruczinski I**, Carvalho B, Doan B, Chakravarti A, Irizarry RA (2009). *A multilevel model to address batch effects in copy number estimation using SNP arrays*.
- Lam TK, **Ruczinski I**, Helzlsouer K, Shugart YY, Li KE, Clipp S, Caulfield LE, Alberg AJ (2009). *Dietary isothiocyanates and lung cancer risk: a nested case-control study*.
- **Ruczinski I**, Li Q, Carvalho B, Fallin MD, Irizarry RA, Louis TA (2009). *Association tests that accommodate genotyping errors*.

### Refereed Letters, Book Chapters, and Extended Conference Proceedings

- Scharpf RB, **Ruczinski I** (2009). *R classes and methods for SNP array data*. Bioinformatics in Clinical OMICs Research, Humana Press.
- **Ruczinski I**, Kooperberg C (2009). *Logic regression*. Encyclopedia of Medical Decision Making.
- Alberg AJ, Chen J, **Ruczinski I**, Jorgensen TJ, Alani R, Liegeois NJ (2009). *Response: Re: Nonmelanoma skin cancer and risk for subsequent malignancy*. Journal of the National Cancer Institute 101(3): 210-1.
- **Ruczinski I** (2007). *Hidden Markov models for the assessment of chromosomal alterations using high-throughput SNP arrays*. INSERM Workshop #179 Proceedings, LaLonde les Maures, France.

### Software

- *Logic regression*:  
Logic regression is a regression methodology primarily for the detection of gene-gene and gene-environment interactions in SNP association studies. The Logic Regression methodology and software was developed in collaboration with Charles Kooperberg and Michael LeBlanc at the Fred Hutchinson Cancer Research Center. Logic Regression is available as Free Software under the terms of the Free Software Foundation's GNU General Public License in source code form.
- *$\Phi$  estimation*:  
Methods and software for the analysis of kinetic data derived from denaturing experiments were developed in collaboration with Kevin Plaxco at the University of California Santa Barbara, and Tobin Sosnick at the University of Chicago. The software was implemented as a web tool, using Perl, HTML, and the statistical software environment R.
- *SNPchip*:  
The R package SNPchip contains S4 classes and methods useful storing, visualizing, and analyzing high density SNP data. SNPchip was developed in collaboration with Robert Scharpf at the Johns Hopkins Bloomberg School of Public Health, and Jonathan Pevsner and Jason Ting in the Kennedy Krieger Institute. The R package SNPchip is freely available from the Bioconductor webpage as free software in source code form under the terms of the GNU General Public License of the Free Software Foundation.

- *VanillaICE*:

The R package ICE contains the software for fitting hidden Markov models on genomic array data to infer chromosomal alterations, including deletions, amplifications, and regions with loss of heterozygosity. In addition, measures of uncertainty for the genotype and copy number estimates can be incorporated, which can be crucial for the detection of micro-deletions and micro-amplifications. ICE was developed in collaboration with Robert Scharpf and Giovanni Parmigiani at the Johns Hopkins Bloomberg School of Public Health. The R package is available from the Bioconductor webpage as free software in source code form under the terms of the GNU General Public License of the Free Software Foundation.

- *Rosetta ab initio*:

Rosetta is a software suite relevant for the prediction and design of protein structures, protein folding mechanisms, and protein-protein interactions. Rosetta ab initio is a tool for de novo prediction of protein structures, and was developed in collaboration with members in the laboratory of David Baker at the University of Washington. The license for the Rosetta code is available through the Baker laboratory.

# CURRICULUM VITAE

Ingo Ruczinski

## Part II

### TEACHING

#### Advisees

- Long, Ezhou. Master of Science, Biostatistics (2005).
- Scharpf, Robert. Doctor of Philosophy, Biostatistics (2007).
- Paithankar, Sameer. Master of Science, Bioinformatics (2008).
- Li, Qing. Doctor of Philosophy, Biostatistics (2009).
- Liu, Yun. Master of Health Sciences, Biostatistics (2009).

#### Academic Advisees

- Wang, Jian. Master of Science, Biostatistics (2001-2002).
- Shum, Kenny. Doctor of Philosophy, Biostatistics (2002-2004).
- Ho, Yen-Yi. Doctor of Philosophy, Biostatistics (2003-2005).
- Chang, Howard. Doctor of Philosophy, Biostatistics (2004-2006).
- Murakami, Peter. Doctor of Philosophy, Biostatistics (2006-2007).
- Jaffe, Andrew. Master of Science, Bioinformatics (2009-present).
- Wei, Yingying. Doctor of Philosophy, Biostatistics (2009-present).
- Gellar, Jonathan. Master of Science, Biostatistics (2009-present).
- Zhou, Xian Chong. Master of Science, Biostatistics (2009-present).
- Seth, Sahil. Master of Science, Bioinformatics (2009-present).

#### Rotation Students

- Aripirala, Srinivas. Doctor of Philosophy, IMMBI (2007).

#### Post-Doctoral Fellows

- Scharpf, Robert (2007-present).
- Schwender, Holger (2009-present).
- Taub, Margaret (2009-present).

#### Advisory Committees

- Tsai, Yuhjung (2008-present).

#### Visitors

- Cristian Pattaro, EURAC, Bolzano, Italy (2008).

- Florentina Bunea, Florida State University, Tallahassee, FL (2008).

### **Exam Committees / Thesis Reader**

- Tarr, Deirdre Ellen. Doctor of Philosophy, Molecular Microbiology and Immunology (2004).
- Liu, Youngmei. Doctor of Philosophy, Epidemiology (2004).
- Sefcovic, Natasha. Doctor of Philosophy, Biology NIH/Johns Hopkins (2006).
- Wang, Wenyi. Doctor of Philosophy, Biostatistics (2007).
- Nicodemus, Kristin. Doctor of Philosophy, Epidemiology (2007).
- Gamston, Courtney. Master of Science, Molecular Microbiology and Immunology (2007).
- Lam, Tram Kim. Doctor of Philosophy, Epidemiology (2007).
- Wang, Ming Hsi. Doctor of Philosophy, Epidemiology (2008).
- Cheng, Yu-Ching. Doctor of Philosophy, Epidemiology (2008).
- Murakami, Peter. Master of Science, Biostatistics (2008).
- Carvalho, Benilton. Doctor of Philosophy, Biostatistics (2008).
- Venkatesan, Meera. Doctor of Philosophy, Molecular Microbiology and Immunology (2008).
- Chang, Yi-Ting. Master of Science, Biostatistics (2009).
- Roberson, Eli. Doctor of Philosophy, Human Genetics, JHMI (2009).
- McCall, Matthew. Doctor of Philosophy, Biostatistics (2009, expected).
- Chu, Audrey. Doctor of Philosophy, Epidemiology (2009, expected).
- Bowers, Katherine. Doctor of Philosophy, Epidemiology (2009, expected).
- Boca, Simina. Doctor of Philosophy, Biostatistics (2010, expected).
- Dluzniewski, Paul. Doctor of Philosophy, Epidemiology (2010, expected).
- Shaw, Patrick. Doctor of Philosophy, Biochemistry and Molecular Biology (2010, expected).
- Koskimaki, Jacob. Doctor of Philosophy, Biomedical Engineering (2011, expected).
- Pichard, Luis. Doctor of Philosophy, Environmental Health Sciences (2011, expected).
- Provost, Katie. Doctor of Philosophy, Molecular Microbiology and Immunology (2011, expected).
- Garvin, Heather. Doctor of Philosophy, School of Medicine (2011, expected).
- Wu, Tao. Doctor of Philosophy, Epidemiology (2011, expected).
- Edmonds, Susan. Doctor of Philosophy, Biomedical Engineering (2011, expected).

### **Preliminary Oral Participation** \* committee chair

- Ziegler, Kathryn. Doctor of Philosophy, Biostatistics (2003).
- Kittleson, Michelle. Doctor of Philosophy, Clinical Investigation (2004).
- Scharpf, Robert. Doctor of Philosophy, Biostatistics (2004).
- Lam, Tram Kim. Doctor of Philosophy, Epidemiology (2005).
- Naj, Adam. Doctor of Philosophy, Epidemiology (2005).
- Wang, Ming Hsi. Doctor of Philosophy, Epidemiology (2005).
- Cheng, Yu-Ching. Doctor of Philosophy, Epidemiology (2006).
- Li, Qing. Doctor of Philosophy, Biostatistics (2006).

- Nicodemus, Kristin. Doctor of Philosophy, Epidemiology (2006).
- Bowers, Katherine\*. Doctor of Philosophy, Epidemiology (2007).
- McCall, Matthew. Doctor of Philosophy, Biostatistics (2007).
- Chu, Audrey\*. Doctor of Philosophy, Epidemiology, (2008).
- Boca, Simina. Doctor of Philosophy, Biostatistics (2008).
- Pichard, Luis\*. Doctor of Philosophy, Environmental Health Sciences (2009).
- Koskimaki, Jacob. Doctor of Philosophy, Biomedical Engineering (2009).
- Wu, Tao. Doctor of Philosophy, Epidemiology (2009).
- Edmonds, Susan. Doctor of Philosophy, Biomedical Engineering (2009).
- Garvin, Heather\*. Doctor of Philosophy, School of Medicine (2009).

### **Final Oral Participation** \* committee chair

- Liu, Youngmei. Doctor of Philosophy, Epidemiology (2004).
- Tarr, Deirdre Ellen. Doctor of Philosophy, Molecular Microbiology and Immunology (2004).
- Peila, Rita. Doctor of Philosophy, Epidemiology (2005).
- Sefcovic, Natasha. Doctor of Philosophy, Biology, NIH/Johns Hopkins (2006).
- Scharpf, Robert. Doctor of Philosophy, Biostatistics (2007).
- Nicodemus, Kristin. Doctor of Philosophy, Epidemiology (2007).
- Lam, Tram Kim. Doctor of Philosophy, Epidemiology (2007).
- Wang, Ming Hsi. Doctor of Philosophy, Epidemiology (2008).
- Cheng, Yu-Ching\*. Doctor of Philosophy, Epidemiology (2008).
- Venkatesan, Meera\*. Doctor of Philosophy, Molecular Microbiology and Immunology (2008).
- Li, Qing. Doctor of Philosophy, Biostatistics (2009).

### **Classroom Instruction - Principal Instructor**

- 140.615 Statistics for Laboratory Scientists I (2007,2008,2009).
- 140.616 Statistics for Laboratory Scientists II (2002,2007,2008,2009).
- 140.751 Advanced Methods in Biostatistics I (2002,2003,2004,2005).
- 140.752 Advanced Methods in Biostatistics II (2002,2003,2004,2005).

### **Classroom Instruction - Co-Instructor**

- 140.668 Statistical Topics in Genetics and Genomics (2004).
- 140.776 Statistical Computing (2003,2004).
- 260.655 Protein Bioinformatics (2004,2005,2006,2008).

### **Classroom Instruction - Invited Guest Lecturer**

- 140.636 Perl for Bioinformatics (2003,2004).
- 140.638 Analysis of Biological Sequences (2005,2006,2007,2008).
- 140.649 Statistical Learning: Algorithmic and Nonparametric Approaches (2007).

- 140.668 Statistical Topics in Genetics and Genomics (2008).
- 140.754 Advanced Methods in Biostatistics IV (2002,2004,2005,2006,2007).
- 140.756 Advanced Methods in Biostatistics VI (2008).
- 140.776 Statistical Computing (2009).
- 140.778 Advanced Statistical Computing (2002).
- 260.602 Introduction to Bioinformatics (2006,2007).
- 260.655 Protein Bioinformatics (2007).
- 340.611 Methodologic Issues in Cancer Epidemiology (2005).
- 340.631 Methods for Association Analysis in Genetic Epidemiology (2007,2008,2009).
- 550.865 Public Health Perspectives on Research (2005).

## RESEARCH GRANT PARTICIPATION

### Ongoing Research Support

- *Preprocessing and Analysis Tools for Contemporary Microarray Applications (NIH)*.  
Dates: September 2007 - November 2012. Principal Investigator: Rafael Irizarry, PhD.  
Responsibility: Co-Principal Investigator (10%).
- *Institute for Clinical and Translational Research (NIH/NCRR)*.  
Dates: September 2007 - May 2012. Principal Investigator: Daniel Ford, MD.  
Responsibility: Co-Investigator (15%).
- *Novel Statistical Methods for Gene-Environment Interactions in Complex Diseases (NHLBI)*.  
Dates: September 2007 - July 2010. Principal Investigator: Kung-Yee Liang, PhD.  
Responsibility: Co-Principal Investigator (20%).
- *Hierarchical Models in Health Services Research (NIDDK)*.  
Dates: September 2007 - July 2010. Principal Investigator: Tom Louis, PhD.  
Responsibility: Co-Investigator (10%).
- *Genome-Wide Association Studies of Asthma In Populations Of African Descent (NIH)*.  
Dates: October 2006 - September 2009. Principal Investigator: Kathleen Barnes, PhD.  
Responsibility: Co-Investigator (10%).
- *DNA Repair, Skin Cancer and Overall Cancer Risk (NIH)*.  
Dates: July 2005 - June 2009. Principal Investigator: Anthony Alberg, PhD.  
Responsibility: Co-Investigator (15%).
- *Genotypic Determinants of Aspirin Response in High Risk Families (NIH)*.  
Dates: January 2008 - May 2009. Principal Investigator: Lewis Becker, MD.  
Responsibility: Co-Investigator (5%).

### Completed

- *Protecting Childrens & Womens Health through Global Control (Gates Foundation)*.  
Dates: March 2009 - June 2009. Principal Investigator: Keith West, PhD.  
Responsibility: Co-Investigator (10%).
- *Genetic Influences on Age-Related Decline In Strength (NIH)*.  
Dates: February 2005 - December 2007. Principal Investigator: Brock Beamer, MD.  
Responsibility: Co-Investigator (5%).
- *Novel Approaches to Studying the In Situ Bioremediation Potential of Complex Mixtures (NIEHS)*.  
Dates: September 2006 - December 2007. Principal Investigator: Rolf Halden, PhD.  
Responsibility: Co-Investigator (3%).
- *Johns Hopkins Center in Urban Environmental Health (NIEHS)*.  
Dates: April 2003 - September 2007. Principal Investigator: Scott Zeger, PhD.  
Responsibility: Co-Investigator (10%).
- *Adaptive Function Estimation for Genomic Data (NIH)*.  
Dates: September 2003 - August 2007. Principal Investigator: Ingo Ruczinski, PhD.  
Responsibility: Principal Investigator (15%).
- *Gene-Gene Interaction Involved In Nasopharyngeal Carcinoma (NCI)*.  
Dates: September 2005 - August 2006. Principal Investigator: Yin Yao Shugart, PhD.  
Responsibility: Co-Investigator (5%).
- *Analysis of SNP Data using Logic Regression (MDHMM)*.  
Dates: July 2002 - June 2004. Principal Investigator: Ingo Ruczinski, PhD.  
Responsibility: Principal Investigator (40%).
- *Gene-Environment Interactions: The Odyssey Cohort (NCI)*.  
Dates: September 1999 - June 2004. Principal Investigator: Kathy Helzlsouer, MD.  
Responsibility: Co-Investigator (20%).
- *Modeling of Mass Spectrometry MALDI Data (DARPA)*.  
Dates: July 2003 - December 2003. Principal Investigator: Fernando Pineda, PhD.  
Responsibility: Co-Investigator (5%).
- *Using All-Atom Potentials to Improve Protein Structure Prediction (JHU Faculty Innovation)*.  
Dates: July 2002 - June 2003. Principal Investigator: Ingo Ruczinski, PhD.  
Responsibility: Principal Investigator (20%).

## **ACADEMIC SERVICE**

### **Department of Biostatistics**

- Member, Committee for Biostatistics Information Technology (2001-present).
- Member, Second Year Oral Examination Committee (2003-2005).
- Chair, Honors and Awards Committee (2003-present).

- Seminar Coordinator (2004-2005).
- Faculty Senate Representative (2004-2006).
- Member, Intellectual Environment Committee (2005-present).
- Member, Faculty Recruitment Committee (2009).

### **Bloomberg School of Public Health**

- Member, Steering Committee, Malaria Research Institute (2002-present).
- Member, Curriculum Committee MHS in Bioinformatics (2003-present).
- Member, Bioinformatics and Biostatistics Core, Center in Urban Env. Health (2003-present).
- Affiliate, Cancer Epidemiology Prevention & Control Training Fellowship Program (2005-present).
- Co-Director, MHS in Bioinformatics Program (2007-present).
- Committee on Information Technology (2007-present).
- Co-Chair, CTSA Innovative Working Group on Genome-wide Association Studies (2008-present).

## **PRESENTATIONS**

### **Scientific Meetings**

- *Inference for SNPchip Data in the Presence of Genotype and Copy Number Uncertainty.*  
BioC2009 Conference, Seattle, WA (2009).
- *Some New Methods to Detect Signal in Association Studies.*  
NHLBI PROGENI Analysis Workshop, Baltimore, MD (2009).
- *On Protein Folding Kinetics and Structure Prediction.*  
International Biometric Society WNAR Meeting, Portland, OR (2009).
- *On Genotype Uncertainty in Association Studies.*  
SFB 475, Reduction of Complexity in Multivariate Data Structures, Dortmund, Germany (2009).
- *New Statistical Methods to Assess Interactions in Complex Disease.*  
The Genes, Environment, and Health Initiative Investigators Meeting, Bethesda, MD (2009).
- *On Missing Data and Genotyping Errors in Association Studies.*  
GEI Analyze This! Workshop, National Institutes of Health, Bethesda, MD (2008).
- *On Missing Data and Genotyping Errors in Association Studies.*  
Emerging Challenges in Genome and Translational Research, Banff, Canada (2008).
- *Novel Statistical Methods for Gene-Environment Interactions in Complex Diseases.*  
GEI Investigators Meeting, National Institutes of Health, Bethesda, MD (2008).
- *On Genotyping Errors and Missing Data in Genome-Wide Association Studies.*  
GENEVA Investigator Meeting, National Institutes of Health, Bethesda, MD (2008).

- *Assessment of Chromosomal Alterations using Copy Number and Genotype Estimates.*  
INSERM Workshop, LaLonde les Maures, France (2007).
- *An Integrated Approach for the Assessment of Chromosomal Abnormalities.*  
BIRS Workshop Statistical Methods for High-Throughput Genetic Data, Banff, Canada (2007).
- *An Integrated Approach for the Assessment of Chromosomal Abnormalities.*  
Statistics for Biomolecular Data Integration and Modeling, Ascona, Switzerland (2007).
- *Detecting Genetic Interactions in Disease.*  
Dementia Consortium Retreat, JHM Alzheimer's Disease Research Center, Baltimore, MD (2007).
- *An Integrated Approach for the Assessment of Chromosomal Abnormalities.*  
Chapter Meeting, International Society of Genetic Epidemiology, Boston, MA (2007).
- *On the Precision of Experimentally Determined Protein Folding Rates and  $\Phi$  Values.*  
Structural Bioinformatics and Computational Biophysics Meeting, Fortaleza, Brazil (2006).
- *Computational and Statistical Tools Relevant for the Exploration of the Protein Folding Process.*  
BIRS Workshop on Computational and Statistical Genomics, Banff, Canada (2006).
- *Visualizing and Analyzing High Density SNP Data with SNPscan.*  
International Biometric Society Spring Meeting, Tampa, FL (2006).
- *On Missing Data and Interactions in SNP Association Studies.*  
Statistical Methods in Molecular Epidemiology, Ruhr University, Bochum, Germany (2005).
- *Logic Regression and its Applications in SNP Association Studies.*  
Annual Conference of the International Society for Clinical Biostatistics, Szeged, Hungary (2005).
- *Logic Regression in SNP Association Studies.*  
BIRS Workshop on Statistical Science for Genome Biology, Banff, Canada (2004).
- *Protein Folding and Structure Prediction.*  
North American New Researchers Conference, York University, Toronto, Canada (2004).
- *Improvements for Logic Regression.*  
Meeting of the International Federation of Classification Societies IFCS, Chicago, IL (2004).
- *Statistical and Computational Issues in Protein Folding and Structure Prediction.*  
Interface 2004: Computational Biology and Bioinformatics, Baltimore, MD (2004).
- *Protein Structure Prediction using Rosetta.*  
IPAM Workshop on Structural Proteomics at UCLA, Los Angeles, CA (2004).
- *Finding Interactions and Assessing Variable Importance in SNP Association Studies.*  
DIMACS Workshop, Data Mining and Epidemiology, Rutgers Univ. , New Brunswick, NJ (2004).
- *Finding Simple Classification Rules in Risk Analysis.*  
Joint Statistical Meetings, San Francisco, CA (2003).

- *Exploring Interactions in Genomic Data.*  
International Biometric Society Meeting, Tampa, FL (2003).
- *Statistical and Computational Issues in Ab Initio Protein Structure Prediction.*  
Joint Statistical Meetings, New York, NY (2002).
- *Classification using Boolean Functions.*  
Conference of the International Federation of Classification Societies, Cracow, Poland (2002).
- *Logic Regression.*  
Annual Meeting, Classification Society of North America, Madison, WI (2002).
- *Computational and Statistical Issues in Ab Initio Protein Structure Prediction.*  
American Statistical Association Chapter Meeting, Albany, NY (2002).
- *Logic Regression.*  
International Biometric Society ENAR Spring Meeting, Arlington, VA (2002).
- *A New Regression Methodology using Boolean Logic.*  
Joint Statistical Meetings, Atlanta, GA (2001).
- *Logic Regression.*  
MSRI Workshop on Nonlinear Estimation and Classification, Berkeley, CA (2001).

### **Invited Seminars**

- *SNP Association Studies with Case-Parent Trios.*  
Statistics and Genomics Seminar, University of California, Berkeley CA (2009).
- *Detection of SNP-SNP Interactions in Case-Parent Trios.*  
Fakultät Statistik, Technische Universität Dortmund, Dortmund, Germany. (2009).
- *On Missing Data and Genotyping Errors in Association Studies.*  
Seminar für Statistik, Eidgenössische Technische Hochschule Zürich, Switzerland (2008).
- *Hidden Markov Models for the Assessment of Chromosomal Alterations using SNP Arrays.*  
Department of Bioinformatics and Comp. Biology, George Mason Univ, Manassas, VA (2008).
- *Hidden Markov Models for the Assessment of Chromosomal Alterations using SNP Arrays.*  
Section on Stat. Genetics, Department of Biostatistics, U of Alabama, Birmingham AL (2008).
- *Hidden Markov Models for the Assessment of Chromosomal Alterations using SNP Arrays.*  
Statistics and Genomics Seminar, University of California, Berkeley CA (2007).
- *On Missing Data and Interactions in SNP Association Studies.*  
Institute of Genetic Medicine, EURAC, Bolzano, Italy (2007).
- *An Integrated Approach for the Assessment of Chromosomal Abnormalities.*  
Institut für Statistik, Ludwig-Maximilians Universität München, Munich, Germany (2007).

- *On Missing Data in SNP Association Studies, and What to Do About Them.*  
Dept. of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD (2007).
- *Logic Regression as a Statistical Tool to Assess Interactions in SNP Association Studies.*  
Center for Prevention and Clinical Research, Johns Hopkins University, Baltimore, MD (2007).
- *On Missing Data and Interactions in SNP Association Studies.*  
Department of Statistics, University of British Columbia, Canada (2006).
- *On Missing Data and Interactions in SNP Association Studies.*  
Department of Biostatistics and Biomathematics, Georgetown University, Washington, DC (2006).
- *Logic Regression.*  
Department of Statistics, Florida State University, Tallahassee, FL (2006).
- *Logic Regression.*  
Department of Statistics and Applied Probability, U of California, Santa Barbara, CA (2006).
- *Uncertainty about  $\Phi$  Values.*  
Department of Biophysics, Johns Hopkins University, Baltimore, MD (2005).
- *Assessing Interactions in High-Dimensional Genomic Data.*  
Department of Epidemiology and Public Health, Yale School of Medicine, New Haven, CT (2005).
- *Missing Data and Gene Interactions in SNP Association Studies.*  
Centre National de Genotypage, Paris-Evry, France (2005).
- *Protein Folding and Structure Prediction - A Statistician's View.*  
Seminar für Statistik, Eidgenössische Technische Hochschule Zürich, Switzerland (2005).
- *A Statistician's View on Protein Folding.*  
Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA (2005).
- *Protein Folding and Structure Prediction - A Statistician's View.*  
Department of Statistics, Rutgers University, Piscataway, NJ (2005).
- *Protein Folding and Structure Prediction - A Statistician's View.*  
Department of Mathematics and Statistics, McGill University, Montreal, Canada (2005).
- *Functional Inferences from Blind Ab Initio Protein Structure Predictions.*  
Institut für Statistik, Ludwig-Maximilians Universität München, Munich, Germany (2004).
- *Logic Regression.*  
US Census Bureau, Suitland, MD (2004).
- *Logic Regression and Interactions in High Dimensional Genomic Data.*  
Institute of Genetic Medicine, Johns Hopkins University, Baltimore, MD (2003).
- *Logic Regression and Interactions in High Dimensional Genomic Data.*  
Memorial Sloan-Kettering Cancer Center, New York, NY (2003).

- *Logic Regression and its Applications to SNP Association Studies.*  
NCI National Cancer Institute, Rockville, MD (2002).
- *Logic Regression.*  
General Electric, Schenectady, NY (2002).
- *Logic Regression with Application to SNP Data Analysis.*  
Wadsworth Center for Labs and Research, Albany, NY (2002).
- *A New Regression Methodology using Boolean Logic.*  
Department of Biostatistics, Johns Hopkins University, Baltimore, MD. (2001).
- *A New Regression Methodology using Boolean Logic.*  
Department of Statistics, Columbia University, New York, NY (2001).

### **Other Meetings and Events**

- *Recent Developments in Genome-Wide Association Studies.*  
Course in Epidemiology, Technische Universität Dortmund, Dortmund, Germany. (2009).
- *On Missing Data and Genotyping Errors in Association Studies.*  
Welch Center, Johns Hopkins University, Baltimore, MD (2008).
- *Novel Statistical Methods for Gene-Environment Interactions in Complex Diseases.*  
National Institutes of Health, Bethesda MD (2008).
- *Bioinformatics - Some Selected Examples and a Bit of an Overview.*  
EnviroHealth Connections Summer Institute, Baltimore MD (2007).
- *Statistical Approaches to assess Gene Copy Number and Loss of Heterozygosity.*  
Expressionists Meeting, Johns Hopkins University, Baltimore, MD (2007).
- *Statistics Schmatistics: On the Folded, the Unfolded, and the Transition State.*  
Johns Hopkins Institute for Multiscale Modeling of Biological Interactions, Baltimore, MD (2006).
- *On Missing Genotype Data.*  
Expressionists Meeting, Johns Hopkins University, Baltimore, MD (2006).
- *Visualizing and Analyzing High Density SNP Data with SNPscan.*  
Department of Biostatistics Retreat, Johns Hopkins University, Baltimore, MD (2006).
- *A Web Based Tool and R Package to Visualize and Analyze Affymetrix SNP Chip Data.*  
SNP Working Group, School of Public Health, Johns Hopkins University, Baltimore, MD (2005).
- *Are You Gellin'?*  
Bayview NHLBI Proteomics Center, Johns Hopkins University, Baltimore, MD (2005).
- *MCMC Methods to Detect Gene-Gene Interactions.*  
SNP Working Group, School of Public Health, Johns Hopkins University, Baltimore, MD (2005).

- *Are You Gellin'?*  
Genome Cafe Opening, Bloomberg School of Public Health, Baltimore, MD (2005).
- *An Add-on R Package for Rosetta.*  
Rosetta Developers Meeting, Leavenworth, WA (2005).
- *The Standard Error of the Lab Scientist.*  
Wall of Wonder, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD (2005).
- *Some SNP Related Stuff I am Working On.*  
Pulver Lab, Department of Psychiatry, Johns Hopkins School of Medicine, Baltimore, MD (2005).
- *How Do Proteins Fold?* Department of Biostatistics Faculty Meeting, Johns Hopkins University, Baltimore, MD (2004).
- *Protein Structure and Folding.*  
Expressionists Meeting, Johns Hopkins University, Baltimore, MD (2004).
- *On  $\beta$  Sheets in Proteins with Application to Structure Prediction.*  
Rosetta Developers Meeting, Leavenworth, WA (2003).
- *A Journey from Gene Expression to Protein Structure.*  
American Statistical Association Chapter Meeting, Albany, NY (2002).

## Posters

- *Detection of SNP-SNP Interactions in Case-Parent Trios.*  
59th Annual ASHG Meeting, Honolulu, HI. (2009).
- *Detection of SNP-SNP Interactions in Case-Parent Trios.*  
18th Annual IGES Meeting, Kahuku, HI (2009).
- *Some Basic Considerations with Regards to Chevron Curves and  $\Phi$ -value Estimation.*  
Gordon Research Conference on Protein Folding Dynamics, Ventura, CA (2008).
- *Inference in Gene Association Studies of Cancer Risks with Partially Missing Family History Data.*  
Annual Meeting of the American Association for Cancer Research, Washington, DC (2006).
- *Uncertainty about  $\Phi$  Values.*  
The 8th Johns Hopkins Folding Meeting, St. Michaels, MD (2005).
- *Statistical Issues in Protein Folding.*  
Johns Hopkins Biostat. Retreat, St. Michaels, MD (2004).
- *Interactions and Variable Importance in Genomic Data.*  
Data Mining, Statistical Learning, & Bioinformatics Workshop, U Florida, Gainesville, FL (2004).
- *Distributions of  $\beta$  Sheets in Proteins with Application to Structure Prediction.*  
Johns Hopkins Biostatistics Retreat, St. Michaels, MD (2003).

- *Exploring Interactions in Genomic Data using Logic Regression Poster.*  
Int. Conference on Research in Computational Molecular Biology, Berlin, Germany (2003).

## **ADDITIONAL INFORMATION**

### **Personal Statement of Research Objectives**

I develop methods and software for the analysis of data arising from complex biological processes, predominantly concerning DNA (gene-gene and gene-environment interactions in SNP association studies; chromosomal alterations such as aneuploidies and loss of heterozygosity) and proteins (protein folding, folding kinetics, and protein structure).

### **Keywords**

Bioinformatics, computational biology, copy number, folding kinetics, genetics, genomics, high throughput, interactions, loss of heterozygosity, statistical learning, protein folding, protein structure, SNP association studies, statistical computing.