

# Sebastian Zöllner

# Curriculum Vitae

ASSISTANT PROFESSOR  
DEPARTMENT OF BIostatISTICS  
DEPARTMENT OF PSYCHIATRY  
UNIVERSITY OF MICHIGAN  
1420 WASHINGTON HEIGHTS  
ANN ARBOR, MICHIGAN, 48109

## Education and Employment History

- 1990 - 1997 Diploma degree (M. Sc.) in Mathematics with minor degree in genetics  
University of Munich, Germany  
Title of Diploma Thesis: “Determining the existence of fixed points of the Poincaré – Operator and approximating solutions of simple differential equations”.
- 1997 - 1991 Ph. D. Biological Sciences advised by Arndt von Haeseler  
Zoological Institute of the University of Munich/Max-Planck Institute for Evolutionary Anthropology, Leipzig.  
Title of Ph D Thesis: “Population-based gene mapping using Linkage Disequilibrium”
- 2001 Post Doctoral Fellow, Department of Genetics Max-Planck Institute for Evolutionary Anthropology with Arndt von Haeseler
- 2001 - 2005 Post Doctoral Fellow at Department of Human Genetics, University of Chicago with Jonathan Pritchard
- 2005 – Assistant Professor, Departments of Psychiatry and Biostatistics, University of Michigan

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## Professional Affiliations

Center for Statistical Genetics, University of Michigan  
Center for Computational Medicine and Biology, University of Michigan  
Depression Center, University of Michigan  
American Society of Human Genetics

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## Referee Work

American Journal of Human Genetics, Human Heredity, Theoretical Population Biology, Biometrics, Bioinformatics, Genome Research, European Journal of Human Genetics, PLoS One, Genetic Epidemiology, PLoS Genetics, Annals of Human Genetics, American Journal of Medical Genetics, Statistical Applications in Genetics and Molecular Biology.

## Honors

2002 Katz Postdoctoral Fellowship (University of Chicago)  
2006 Rachel Upjohn Clinical Scholar Award

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## GRANT SUPPORT

### Ongoing Research Support

1 R01 HL90564-01 (Zöllner) 09/01/07 – 08/31/10 1.8 academic  
NIH \$250,000 0.6 summer

Computational Statistic Approaches to Gene-Environment Interaction

The goal of this proposal is to develop statistical methods to estimate gene-environment interaction both from family data and from samples of unrelated individuals in a genome-wide association (GWA) study.

U01 HL084729-02 (Abecasis) 04/01/06 – 03/31/09 1.4 academic  
NIH \$199,993 0.4 summer

Integrated Parametric and Non-parametric Mapping for Genome-Wide Association Data

The goal of this grant is to develop and evaluate parametric and non-parametric methods for whole genome association mapping.

31069 (Zöllner) 03/01/06 – 02/28/11 1.4 academic  
University of Chicago/NIH - subcontract \$15,233 0.4 summer

Genome Wide Association Mapping in Arabidopsis Thaliana

The goal of this grant is to analyze the generated data using Bayesian statistics and Monte Carlo methods. To develop methods to estimate the ancestry of the sample and the true underlying genotypes based on the patterns of matches and mismatches in the sample by using the data at linked tiles.

1-R01-MH070775-03 (McInnis) 11/01/04 - 10/31/09 2.4 academic  
NIMH \$400,000 0.6 summer

Finemapping in 8q24

The goal of this project is to assess the NIMH sample for evidence of association between bipolar disorder and a locus under the linkage peak on 8q24. The Illumina genotype data is used to infer CNV segregating in this chromosomal region.

(Ringold) 05/01/08 – 01/31/13 1.2 cal  
NIMH \$321,184.00

Antipsychotic and Folate Pharmacogenetics

The goal is to advance schizophrenia treatment as more is learned about genetic, dietary and lifestyle factors that relate to AAP associated metabolic complications. Dr. Zoellner will be responsible for overseeing the statistical analysis of this proposal.

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## Previous research support

No number (Zöllner) 11/01/06 – 11/01/07  
Rachel Upjohn \$20,000  
Mapping the Genetic Heterogeneity of Bipolar Disorder using Clinical Traits  
This proposal aims to explore the interaction between genetic and environmental determinants of bipolar disorder to develop a novel and innovative approach to address the problem of genetic heterogeneity.

## Pending research support

(Meeker) 07/01/07 – 06/30/12 0.9 academic  
NIH \$269,606 0.2 summer  
Individual Susceptibility to Pesticide Exposure and Male Reproductive Health  
The goal of Dr. Zöllner is to be involved with data analysis issues and will assist with approaches to present the data with a special emphasis on analyzing and interpreting genetic data.

(Moroi) 12/01/07 – 11/30/11 0.6 cal  
NIH/NEI \$250,000  
Genetic Markers for Glaucoma Treatment Outcomes  
The goal is to identify genetic markers for IOP response variations to topical beta blockers. Dr. Zoellner will do genotyping analysis with particular emphasis on haplotype analysis, design of the high density SNP platform contribution to manuscripts, and presentation at scientific meetings.

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## TEACHING EXPERIENCE

### Thesis Committees

Karen Coneely (Biostatistics) 2006 - 2007  
Riu Xiao (Biostatistics) 2006-  
Jenna van Liere (Bioinformatics) 2007-2008  
Chris van Hout (Human Genetics) 2007 -  
Nicole Scott (Human Genetics) 2007 –

### Supervised Graduate Students

Yi Chen (Biostatistics) 2005-2007  
Peng Zhang (Biostatistics) 2007 –  
Kraig Stevenson (Biostatistics) 2007-  
Mathew Zawistowski (Biostatistics) 2007-  
Dan Maixner (OJOC) 2008-

## Formal Courses

- 1997 – 1998      Teaching assistant for ‘Mathematics for Biologists’
- 2005 –            Various lectures on coalescence theory and evolution.
- 2006 –            Journal Club on Population genetics
- 2006              Developed and taught Biostat 664/Bioinformatics 800 ‘Statistical population genetics’
- 2006              Instructor for ‘Short Course on Coalescence theory in association mapping’, Institute Gulbenkian de Ciena, Portugal
- 2007              Instructor in Biostat 866 “Advanced Topics in statistical Genetics’

## Invited Extramural Presentations

- 2000            •    Tenth conference on mathematical and statistical aspects of molecular biology, Cambridge, UK
- 2001            •    IZKF Summer School, Grossbooten, Germany
- 2002            •    5<sup>th</sup> International Meeting on SNPs and Complex Genome Analysis, Reykjavik, Island
- Department of Genetics, Max-Planck Institute for Evolutionary Anthropology, Leipzig, Germany
- 2003            •    Workshop on Medical Statistics, Oberwolfach, Germany
- Department of Bioinformatics, University of Düsseldorf, Germany
- BSD Retreat, Eagle Ridge, USA
- 2004            •    Workshop on Bioinformatics, Vienna
- Division of Human Cancer Genetics, Ohio State University
- 2005            •    Southwestern University, Dallas
- New York University, New York
- University of Washington, Seattle
- American Society of Human Genetics Annual Meeting, Salt Lake City
- 2006            •    Conference on Psychiatric Genetics, Salt Lake City
- Pennsylvania State University, State College
- Institute Gulbenkian de Ciena, Portugal
- 2007            •    Conference on Psychiatric Genetics, Salt Lake City
- American Society of Human Genetics Annual Meeting, San Diego
- Universität Regensburg, Germany
- Ludwigs-Maximilians Universität München, Germany
- 2008            •    Conference on Psychiatric Genetics, Salt Lake City

## COMMITTEE AND ADMINISTRATIVE SERVICE

2005-2007	Computing Committee, Department of Biostatistics
2006	Reviewer for The Center for Computational Medicine and Biology pilot grant
2007	Review Committee for the Depression Center Innovation Fund
2007-2008	Admissions Committee, Department of Biostatistics
2008	Review Committee for the Center for Genetics in Health and Medicine post doc competition

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## BIBLIOGRAPHY

### **Peer-reviewed publications**

1. Terwilliger J, Zöllner S, Laan M, Pääbo S. Mapping genes through the use of Linkage Disequilibrium generated by genetic drift: 'Drift Mapping' in small populations with no demographic expansion. *Hum Hered* 48:138-154, 1998
  2. Zöllner S, von Haeseler A. A Coalescent approach to study Linkage Disequilibrium between Single Nucleotide Polymorphisms *Am J Hum Genet* 66:615-628, 2000.
  3. Kaessmann H\*, Zöllner S\*, Gustafsson AC, Wiebe V, Laan M, Lundeberg J, Uhlén, Pääbo S. Extensive Linkage Disequilibrium in Small Human Populations in Eurasia. *Am J Hum Genet* 70:673-685, 2002; \* denotes equal contribution.
  4. Enard W, Khaitovich P, Klose J, Zöllner S, Heissig F, Giavalisco P, Nieselt-Struwe K, Muchmore E, Varki A, Ravid R, Doxiadis GM, Bontrop RE, Pääbo S. Intra- and Interspecific Variation in Primate Gene Expression Patterns. *Science* 296: 340-343, 2002.
  5. Kaessmann H, Zöllner S, Nekrutenko A, Li HW. Signatures of domain shuffling in the human genome. *Genome Res* 12: 1642-1650, 2002.
  6. Hellmann I, Zöllner S, Enard W, Ebersberger I, Nickel B, Pääbo S. Selection on Human Genes as revealed by comparison to Chimpanzee DNA. *Genome Res* 13: 831-837, 2003.
  7. Zöllner S, Wen X, Hanchard N, Herbert M, Ober C, Pritchard J. Evidence for extensive transmission distortion in the human genome *Am. J. Hum. Genet.* 70:673-685, 2004.
  8. Zöllner S, Pritchard J. Coalescent-based association mapping and fine mapping of complex trait loci. *Genetics* 169: 1071-1092, 2005.
  9. Zöllner S, Wen X, Pritchard JK. Association mapping and fine mapping with TreeLD. *Bioinformatics* 21: 3168-3170, 2005.
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10. Zöllner S, Pritchard JK. Overcoming the winner's curse: Estimating penetrance parameters from case-control data. *Am J Hum Genet* 80: 605-615, 2007
11. Liang L, Zöllner S, Abecasis GR. GENOME: a rapid coalescent-based whole genome simulator. *Bioinformatics* 23:1565-1567, 2007.
12. Zandi PP, Zöllner S, Avramopoulos D, Willour VL, Qin ZS, Burmeister M, Miao K, Gopalakrishnan S, Potash JB, DePaulo JR, McInnis MG. Family – based SNP Association Study on 8q24 in Bipolar Disorder. *Am J Med Genet Part B* *In press*
13. Burmeister M, McInnis MG, Zöllner S. Psychiatric Genetics: Progress among Controversies. *Nat Rev Genet* 9: 527-540, 2008
14. She X, Cheng Z, Zöllner S, Church D, Eichler EE. Extensive Copy Number Variation of Mouse Segmental Duplications. *Nat Genet* 40: 909-914, 2008
15. Zöllner S, Su G, Chen Y, McInnis MG, Burmeister M. EM Algorithm for scoring polymorphic deletions from SNP data and application to a common CNV on 8q24. *In revision*
16. Henrichsen CN\*, Vinckenbosch N\*, Zöllner S\*, Chaignat E, Pradervand S, Ruedi M, Kaessmann H, Reymond A. Catalog of mouse Copy Number Variations and gene expression reveals long distance effects of CNVs on expression levels. *Submitted* \* denotes equal contribution

## Other Articles

1. Zöllner S, von Haeseler A. History and Linkage Disequilibrium. *Encyclopedia of Life Sciences*, Nature Publishing Group (2002)
  2. Zöllner S. Population History and Linkage Disequilibrium. *Encyclopedia of Life Sciences*, John Wiley & Sons, Ltd, (2008)
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