

BIOGRAPHICAL SKETCH

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NAME Yandell, Brian	POSITION TITLE Professor		
eRA COMMONS USER NAME (credential, e.g., agency login)			
EDUCATION/TRAINING <i>(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)</i>			
INSTITUTION AND LOCATION	DEGREE <i>(if applicable)</i>	MM/YY	FIELD OF STUDY
California Institute of Technology	B.A. honors	1974	Mathematics
University of California, Berkeley, CA	M.Sc.	1978	Statistics
University of California, Berkeley, CA	Ph.D.	1981	Biostatistics

A. Personal Statement:

I am a Professor in the Departments of Statistics and Horticulture. My statistical research is in the area of statistical genomics. I collaborate extensively with investigators conducting biomedical research, in particular in the area of obesity and diabetes research; these collaborations often motivate research projects for predoctoral trainees. My primary contributions have been in the area of systems genetics.

B. Positions and Honors.

1996—present	Professor, Departments of Statistics and Horticulture, University of Wisconsin, Madison, WI
1988-1996	Associate Professor, Departments of Statistics and Horticulture, University of Wisconsin, Madison, WI
1982-1988	Assistant Professor, Departments of Statistics and Horticulture, University of Wisconsin, Madison, WI
2006—present	Professor, Department of Biostatistics & Medical Informatics,
2006—present	Comprehensive Cancer Center
1996—present	Plant Breeding and Plant Genetics Program,
1984—present	Institute of Environmental Studies
1982—present	Biometry Program
1999-2005	Instructor, NC State U Summer Institute in Statistical Genetics
2006—present	Instructor, U WA Seattle Summer Institute in Statistical Genetics
2001—present	Instructor, Mathematical Approaches to the Analysis of Complex Phenotypes, The Jackson Laboratory

Honors and awards

2001	David P. Byar Young Investigator Award to student Fei Zou, ASA Biometrics Section
1990	Anna M. Jackson Award to student Penelope Reynolds, Amer. Soc. Mammalogists
1982	Evelyn Fix Memorial Medal, UC-Berkeley
1976-81	NIH Traineeship, UC-Berkeley
1977-78, 75-76	UC Regents Fellow, UC-Berkeley
1976	Organization for Tropical Studies Program, U Costa Rica
1974-75	Thomas J. Watson, Jr., Fellow, Caltech

Professional societies (throughout past ten years)

American Statistical Association (ASA): Chair, Consulting Section 2000; Gnome Club, Caltech; International Biometrics Society; Institute of Mathematical Statistics: Committee on Electronic Issues 2002-06; Biometrika Association; Royal Statistical Society.

Editorial boards and Professional Activities

Editor, Amstat Online (www.amstat.org), ASA, 1999-2002.
Associate Editor, BMC Genetics, 2009--.

Trainer, UW-Madison: Computation and Informatics in Biology and Medicine Program (NLM) 2002-12; Genomic Sciences Training Program (NHGRI) 2003-08; Interdisciplinary Biostatistics (NIGMS) 2005-10; Interdisciplinary Biostatistics (NHLBI) 2007-12.
 Grant Study Sections: Bioinformatics, U.S. Dept. of Agriculture, 2001; Metabolism, National Institutes of Health, 2003; NIH/NIAAA, 2005-6

C. Selected peer-reviewed publications (in chronological order). (Total: 96 refereed journal articles; 1 in review; 1 book; 11 book chapters)

1. Chaibub Neto E, Keller MP, Attie AD, Yandell BS (2010) Causal Graphical Models in Systems Genetics: a unified framework for joint inference of causal network and genetic architecture for correlated phenotypes. *Ann Appl Statist* 3: 000-000. (in press)
2. Manichaikul A, Moon JY, Sen S, Yandell BS, Broman KW (2009) A model selection approach for the identification of quantitative trait loci in experimental crosses. *Genetics* 181: 1077-1086.
3. Banerjee S, Yandell BS, Yi N (2008) Bayesian QTL mapping for multiple traits. *Genetics* 179: 2275-2289.
4. Chaibub Neto E, Ferrara C, Attie AD, Yandell BS (2008) Inferring causal phenotype networks from segregating populations. *Genetics* 179: 1089-1100.
5. Ferrara CT, Wang P, Chaibub Neto E, Stevens RD, Bain JR, Wenner BR, Ilkayeva OR, Keller MP, Blasiole DA, Kendzierski C, Yandell BS, Newgard CB, Attie AD (2008) Genetic networks of liver metabolism revealed by integration of metabolic and transcriptomic profiling. *PLoS Genet* 4: e1000034.
6. Keller MP, Choi YJ, Wang P, Davis DB, Rabaglia ME, Oler AT, Stapleton DS, Argmann C, Schueler KL, Edwards S, Steinberg HA, Neto EC, Kleinhanz R, Turner S, Hellerstein MK, Schadt EE, Yandell BS, Kendzierski CM, Attie AD (2008) A gene expression network model of type 2 diabetes establishes a relationship between cell cycle regulation in islets and diabetes susceptibility. *Genome Res* 18: 706-716.
7. Jin C, Fine J, Yandell B (2007) A unified semiparametric framework for QTL analyses, with application to spike phenotypes. *J Amer Statist Assoc* 102: 56-67.
8. Weber A, Clark R, Vaughn L, Sanchez-Gonzalez JdeJ, Yu J, Yandell BS, Bradbury P, Liu K, Doebley J (2007) Association genetics in Balsas teosinte (*Zea mays* ssp. *parviglumis*). *Genetics* 177: 2349-2359.
9. Yandell BS, Mehta T, Banerjee S, Shriner D, Venkataraman R, Moon JY, Neely WW, Wu H, von Smith R, Yi N (2007) R/qtlbim: QTL with Bayesian interval mapping in experimental crosses. *Bioinformatics* 23: 641-643.
10. Yi N, Banerjee S, Shriner D, Pomp D, Yandell BS (2007) Bayesian mapping of genome-wide interacting QTL for ordinal traits. *Genetics* 176: 1855-1864.
11. Yi N, Shriner D, Banerjee S, Mehta T, Pomp D, Yandell BS (2007) Efficient strategies for Bayesian mapping of genome-wide interacting QTL. *Genetics* 176: 1865-1877.
12. Clee SM, Yandell BS, Schueler KM, Rabaglia ME, Richards OC, Raines SM, Kabara EA, Klass DM, Mui ETK, Stapleton DS, Gray-Keller MP, Young MB, Stoehr JP, Lan H, Boronenkov I, Raess PW, Flowers MT, Attie AD (2006) Positional cloning of Sorcs1, a type 2 diabetes quantitative trait locus. *Nat Genet* 38: 688-693.
13. Guan Q, Zheng W, Tang S, Liu X, Zinkel R, Tsui KW, Yandell BS, Culbertson MR (2006) Predicting global changes in transcript stability in upf1- strains of budding yeast. *PLoS Genetics* 2: e203.
14. Lan H, Chen M, Byers JE, Yandell BS, Stapleton DS, Mata CM, Mui ETK, Flowers MT, Schueler KL, Manly KF, Williams RW, Kendzierski C, Attie AD (2006) Combined expression trait correlations and expression quantitative trait locus mapping. *PLoS Genetics* 2: e6.
15. Yi N, Yandell BS, Churchill GA, Allison DB, Eisen EJ, Pomp D (2005) Bayesian model selection for genome-wide epistatic QTL analysis. *Genetics* 170: 1333-1344.

D. Research Support.

ACTIVE

5 R01 DK058037-07 (Attie) NIH/NIDDK The Genetics of Obesity and Diabetes.	06/01/06-5/31/11 \$1,326,388	2.4 calendar
5 R01 GM074244-03 (Broman) NIH/NIGMS	06/01/05-05/31/10 \$176,956	0.6 calendar

Statistical Methods and Software for QTL Mapping

This project aims to develop improved model selection methods of multiple QTL mapping in experimental crosses, develop improved methods for the analysis of recombinant inbred lines and related strains, and develop and disseminate the R/qtl software for QTL mapping.

R01 GM069430-01 (N Yi, U Alabama Birmingham) NIH/NIGMS Bayesian Methods for Mapping Complex Epistatic Genes. This project is to develop Bayesian model selection methods and computer software for mapping epistatic genes in experimental crosses.	06/01/05-5/31/10 \$185,596	2.4 calendar
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R01 (Nickells) NIH/National Eye Institute (NEI) Characterization of RGC death susceptibility alleles.	02/01/09-01/31/14 ~\$1,250,000	.6 calendar
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PENDING

R01 (Attie) NIH/NIDDK Gene & gene networks associated with obesity & diabetes. [Impact/Priority 17; 7.0%]	11/01/09-10/31/14 \$2,480,298	1.2 calendar
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R01 (Yi) NIH/NIGMS Bayesian Methods for Genome Wide Interacting QTL mapping.	07/01/10-06/30/15 \$434,000 subcontract	1.2 calendar
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R01 (Hoeschele) NIH/NIGMS Highly multivariate methods for QTL mapping in systems genetics.	07/01/10-06/30/12 \$6,000 consulting fee	consultant
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(Brunet) NSF/IOS The influence of environmental factors on floral traits and associated changes in gene expression.	01/01/10-12/31/12 ~\$400,000	0.6 calendar
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(Splitter) NIH/AI-09-101 Brucella spp. immunomodulatory factors for protection.	05/01/10-04/30/15 \$3.25M (\$2.5M direct)	0.5 calendar
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(Broman) NIH/NIGMS Statistical methods and software for QTL mapping.	06/01/10-05/31/15 \$1.6M	0.6 calendar
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OVERLAP

NONE