Curriculum Vitae

BO PENG
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EDUCATION:

2001-	**Rice University**, Houston, TX, GPA: 4.06/4.0
	Pursuing a Ph.D. degree in Statistics, majoring in biostatistics and bioinformatics. Expected completion in May 2006
1999-2001	**University of Houston**, Houston, TX, GPA: 3.95/4.0
	MA in Applied Mathematics. Research topics include numerical analysis, numerical partial differential equation and parallel computation.
1992-1996	**Shanghai Jiao Tong University**, Shanghai, P.R.China, GPA: 3.11/4.0
	BA in Applied Mathematics.

WORK EXPERIENCE:

2001-	**Teaching Assistant and Computing Consultant**, Rice University
	Teaching assistant for *Mathematical Statistics* (STAT310, Fall 2001 and Spring 2002) and *Statistical Methods in Bioinformatics* (STAT655, Spring 2005). Helpdesk consultant of the statistics department from Spring 2002 to Fall 2004.
1999-2001	**Teaching Assistant**, University of Houston
	Teaching assistant for *Calculus I, II, III* and *linear algebra*.
1996-1999	**Lecturer**, Shanghai Jiao Tong University
	Taught courses including *Elements of computer systems, the C++ programming language* and *Mathematical Software* and *the SAS system*.

SKILLS and QUALIFICATIONS:

- Experiences in development, implementation and testing of statistical genetic analysis method, including the implementation, statistical analysis and validation of a new gene mapping method with emphasis on structured population and projects involving microarray and proteomics data analysis.

- Excellent computing skills and expertise in UNIX/Linux systems. Expertise in C/C++, Python, Perl and Fortran, with experiences in Pascal/Delphi, Visual Basic, PHP and Java. Experienced user of R/Splus, Matlab and Mathematica. Some experiences in SAS.

RESEARCH INTERESTS:

- Simulation methods in population genetics and gene mapping

- Study population structure and gene mapping from an evolutionary point of view

AWARDS:

- *Predoctoral W. M. Keck Fellowship*, Jan 1st, 2004 - present
- *R. L. Anderson Student Paper Award* at the Summer Research Conference on Statistics, Southern Regional Council on Statistics (SRCOS) and the American Statistical Association (ASA), June, 2003

PUBLICATIONS and SOFTWARE APPLICATION:

- Lajos Pusztai, Bettsy W. Gregory, Keith A. Baggerly, **Bo Peng**, David Gold, John Koomen, Henry Kuerer6, Franscisco J Esteva1, Gabriel N. Hotobagyi1, Richard R. Drake, Antonia Vlahou. (2004) Pharmacoproteomic analysis of pre- and post-chemotherapy plasma samples from patients receiving neoadjuvant or adjuvant chemotherapy for breast cancer, *Cancer*, 100(9): 1814-1822.
- Olga Gorlova, **Bo Peng**, David Yankelevitz, Claudia Henschke, and Marek Kimmel (2005) Estimating the growth rates of primary lung tumors from samples with missing measurements, *Statistics in Medicine,* 15;24(7):1117-34.
- **Bo Peng** and Marek Kimmel (2005) simuPOP: a forward-time population genetics simulation environment. *bioinformatics.* 21(18): 3686-3687.
- **Bo Peng** and Marek Kimmel (2005) On the allelic structure of human diseases, a simulation study. *submitted.* (manuscript available upon request)
- Author of an open-source forward-time population genetics simulation environment **simuPOP**, available at http://simupop.sourceforge.net.
- **Bo Peng**, François Balloux, Angela J. Frodsham, Adrian V. S. Hill, Emily Lyons, Marek Kimmel and William Amos, A new method to map complex disease genes in structured populations, *in preparation.* (manuscript available upon request)
- **Bo Peng** and Marek Kimmel, Comparison of popular gene mapping methods using simulated virtual populations, *in preparation.* (manuscript available upon request)
- (Early work) Author of software collection *Calculus with Mathematica*, bundled with textbook *Calculus* published by the Shanghai Jiao Tong University Press, 1998; Coeditor of textbook *Mathematical Experiments*, 1999; Co-author of textbook *Mathematical Software*, 1999.

POSTERS and PRESENTATIONS:

- Using spatial coherence to identify artifacts on affymetrix gene chips (poster), Summer Research Conference on Statistics (Poster), Southern Regional Council on Statistics (SRCOS) and the American Statistical Association (ASA), June, 2003
- Bringing population structure into gene mapping (poster), The Ninth Annual Structural Biology Symposium, University Texas Medical Branch at Galveston, April, 2004
- Using population structure to map complex diseases (presentation), Biostatistics seminar (Rice), Apr, 2004; Keck Fellow Meeting, July, 2004
- Are rare variants responsible for susceptibility to complex diseases (presentation), biostatistics seminar (Rice), Sep. 2004
- Using population structure to map complex diseases (poster), Keck Annual Research Conference, Oct. 2004
- A new method to map complex disease genes in structured populations (poster), American Society of Human Genetics annual meeting, Nov. 2004

PROFESSIONAL MEMBERSHIP:

2001-	American Statistical Association
2001-	Institute of Mathematical Statistics
2004-	American Society of Human Genetics