

## TAPAN MEHTA

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### EDUCATION

- Currently pursuing **Ph.D. in Biostatistics** at the University of Alabama at Birmingham (GPA 3.88)
- **Master of Science degree (M.S.) in Electrical and Computer Engineering (Dec 2004)**, University of Alabama at Birmingham (GPA 3.78)
- **Bachelor of Engineering (B.E.) in Computer Engineering (Sept 2001)**, Mumbai University, India.

### PEER REVIEW PUBLICATIONS

- Keith SW, Fontaine KR, Pajewski NM, **Mehta T**, Allison DB. Use of self-reported height and weight biases the body mass index-mortality association. *Int J Obes (Lond)*. 2010 Aug 3. [Epub ahead of print] [PMID: 20680015]
- Miller SJ, Jessen WJ, **Mehta T**, Hardiman A, Sites E, Kaiser S, Jegga AG, Li H, Upadhyaya M, Giovannini M, Muir D, Wallace MR, Lopez E, Serra E, Nielsen GP, Lazaro C, Stemmer-Rachamimov A, Page G, Aronow BJ, Ratner N. Integrative genomic analyses of neurofibromatosis tumours identify SOX9 as a biomarker and survival gene. *EMBO Mol Med*. 2009 Jul;1(4):236-48. PubMed PMID: 20049725.
- Feugang JM, Kaya A, Page GP, Chen L, **Mehta T**, Hirani K, Nazareth L, Topper E, Gibbs R, Memili E. Two-stage genome-wide association study identifies integrin beta 5 as having potential role in bull fertility. *BMC Genomics*. 2009 Apr 24;10:176. PubMed PMID: 19393042; PubMed Central PMCID: PMC2684547.
- Guimbellot JS, Erickson SW, **Mehta T**, Wen H, Page GP, Sorscher EJ, Hong JS. Correlation of microRNA levels during hypoxia with predicted target mRNAs through genome-wide microarray analysis. *BMC Med Genomics*. 2009 Mar 25;2:15. PubMed PMID: 19320992; PubMed Central PMCID: PMC2667434.
- Chen L, Page GP, **Mehta T**, Feng R, Cui X. Single nucleotide polymorphisms affect both cis- and trans-eQTLs. *Genomics*. 2009 Jun;93(6):501-8. Epub 2009 Feb 25. PubMed PMID: 19248827.
- Ioannidis JP, Allison DB, Ball CA, Coulibaly I, Cui X, Culhane AC, Falchi M, Furlanello C, Game L, Jurman G, Mangion J, **Mehta T**, Nitzberg M, Page GP, Petretto E, van Noort V. Repeatability of published microarray gene expression analyses. *Nat Genet*. 2009 Feb;41(2):149-55. Epub 2008 Jan 28. PubMed PMID: 19174838.
- Srinivasasainagendra V, Page GP, **Mehta T**, Coulibaly I, Loraine AE. CressExpress: a tool for large-scale mining of expression data from Arabidopsis. *Plant Physiol*. 2008 Jul;147(3):1004-16. Epub 2008 May 8. PubMed PMID: 18467456; PubMed Central PMCID: PMC2442548.
- Falk CT, Finch SJ, Kim W, Mukhopadhyay ND, Gong B, Hinrichs A, Li X, Liu X,

Malhotra A, **Mehta T**, Page G, Rao S, Saccone N, Shete S, Yang Y, Yu R, Zhao JH, Zhou X. Data mining of RNA expression and DNA genotype data: presentation group 5 contributions to Genetic Analysis Workshop 15. *Genet Epidemiol.* 2007;31 Suppl1:S43-50. PubMed PMID: 18046764.

- Yi N, Shriner D, Banerjee S, **Mehta T**, Pomp D, Yandell BS. An efficient Bayesian model selection approach for interacting quantitative trait loci models with many effects. *Genetics.* 2007 Jul;176(3):1865-77. Epub 2007 May 4. PubMed PMID: 17483424; PubMed Central PMCID: PMC1931520.
- Yandell BS, **Mehta T**, Banerjee S, Shriner D, Venkataraman R, Moon JY, Neely WW, Wu H, von Smith R, Yi N. R/qtlbim: QTL with Bayesian Interval Mapping in experimental crosses. *Bioinformatics.* 2007 Mar 1;23(5):641-3. Epub 2007 Jan 19. PubMed PMID: 17237038.
- **Mehta TS**, Zakharkin SO, Gadbury GL, Allison DB. Epistemological issues in omics and high-dimensional biology: give the people what they want. *Physiol Genomics.* 2006 Dec 13;28(1):24-32. Epub 2006 Sep 12. PubMed PMID: 16968808.
- Wei H, Persson S, **Mehta T**, Srinivasasainagendra V, Chen L, Page GP, Somerville C, Loraine A. Transcriptional coordination of the metabolic network in Arabidopsis. *Plant Physiol.* 2006 Oct;142(2):762-74. Epub 2006 Aug 18. PubMed PMID: 16920875; PubMed Central PMCID: PMC1586052.
- Zakharkin SO, Kim K, **Mehta T**, Chen L, Barnes S, Scheirer KE, Parrish RS, Allison DB, Page GP. Sources of variation in Affymetrix microarray experiments. *BMC Bioinformatics.* 2005 Aug 29;6:214. PubMed PMID: 16124883; PubMed Central PMCID: PMC1232851.
- Trivedi P, Edwards JW, Wang J, Gadbury GL, Srinivasasainagendra V, Zakharkin SO, Kim K, **Mehta T**, Brand JP, Patki A, Page GP, Allison DB. HDBStat!: a platform-independent software suite for statistical analysis of high dimensional biology data. *BMC Bioinformatics.* 2005 Apr 6;6:86. PubMed PMID: 15813968; PubMed Central PMCID: PMC1087834.
- **Mehta T**, Tanik M, Allison DB. Towards sound epistemological foundations of statistical methods for high-dimensional biology. *Nature Genetics* 2004 Sep;36(9):943-7. PubMed PMID: 15340433.

## POSTERS AND ORAL PRESENTATIONS

- **Mehta T**, Pajweski N, Keith SW, Fontaine K, Allison DB. (2010) Plausible 'Nuisance' Contributor to Decreasing Deleterious Association of Overweight and Obese on Mortality Rate over Calendar Time. Oral Presentation at the Joint Statistical Meeting at Vancouver, BC, Canada.
- Allison DB, **Mehta T**, Keith SW. (2008) Compared to What? Understanding Apparent Secular Changes in the Relation Between Body Mass Index (BMI) and Mortality Rate. (961-P Presentation to 2008 The Obesity Society Annual meeting, in Phoenix AZ, October 3 – 7, 2008. Abstract published in *Obesity*, 16(S1): S328).
- **Mehta T**, Keith SW, Allison DB. (2008) Effect of Change in BMI Distribution on the Association Between BMI and Mortality Rate: A Plausible Partial Explanation for Decrease in Deleterious Effects of Overweight Over Calendar Time? (963-P Presentation to 2008 The Obesity Society Annual meeting, in Phoenix AZ, October 3 – 7, 2008. Abstract published in *Obesity*, 16(S1): S329).
- Keith SW, **Mehta T**, Allison DB. (2008) Estimating Mortality Hazards Associated with BMI: Does using Self-Reported Height and Weight Instead of Measurements Make a Difference? (455-P Presentation to 2008 The Obesity Society Annual Meeting, in Phoenix AZ, October 3 – 7, 2008. Abstract published in *Obesity*, 16(S1): S179).

- Keith SW, **Mehta T**, Fontaine KR, Pajewski NM, Allison DB. Influence of using self-reported height and weight on the BMI-mortality association. Oral abstract accepted for presentation at the 2009 The Obesity Society Annual Meeting in Washington, D.C. October 24-28.
- **Mehta T**, Page G. Determining Stability of Taxonomic Coefficients for Time Series Microarray Data' at Computational Genomics at Computational Genomics conference organized by TIGR in October 2004.
- **Mehta T**, Allison DB, Page G. Applications of Data mining and Machine Learning to Microarrays' at the Data mining and Machine Learning workshop organized by SAMSI in September 2003

## EDITORIAL ACTIVITIES

- Referee for journal of Computational Statistics and Data Analysis in 2007
- Referee for Obesity in 2008-2010
- Referee for Surgery for Obesity and Related Diseases in 2008
- Referee for International Journal of Obesity in 2010
- Referee for Journal of the American Medical Association (JAMA) in 2010

## BOOK CHAPTERS

- Page GP, Zakharkin SO, Kim K, **Mehta T**, Chen L, Zhang K. Microarray analysis. Methods Mol Biol. 2007;404:409-30. Review. PMID: 18450061.
- Zakharkin SO, **Mehta T**, Allison DB. Epistemological Foundations of Statistical Methods for High-Dimensional Biology. DNA MICROARRAYS AND RELATED GENOMICS TECHNIQUES: Design, Analysis, and Interpretation of Experiment. Chapman and Hall/CRC 2006.

## WORK EXPERIENCE

### **Section on Statistical Genetics, UAB**

**Jan 2003– till date**

- To conduct statistical analyses of genetic marker, genomic and epidemiologic data
- Write manuscript, create reports for publications, and assist in grant writing
- Automate and use high performance computing resources to speed up computationally intensive simulations and analyses
- Develop specialized genetic and genomic software to disseminate statistical algorithms
- *Technologies used:* **R, SAS, SPSS, Java, C, Cygwin, Sun Grid Engine, PBSPro, MySQL, Subversion, Confluence, Jira**

### **School of Nursing, UAB**

**2002**

- Developed and maintained relational database that stored details about students, course enrollment, nursing licensing information and the internships. It also included faculty details and hospitals collaborating with School of Nursing for student internships.
- Project profile included requirement gathering, front end designing, designing database schema, developing, and testing. Features include relational design, normalization, workgroup-based security, and automated html reports for queries and summary statistics of queries.
- *Technologies used:* **UML, Visual Basic 6.0, Microsoft Access**

### **School of Engineering, University of Alabama at Birmingham**

**2002**

- Teaching and helping undergraduate students in their C programming assignments.
- String manipulations, file handling, static, and dynamic memory allocation were some of the programming topics frequently handled.
- *Technologies used:* **C**

## TECHNICAL SKILLS

- **Programming Languages:** Java, C
- **Statistical Languages/Packages:** SAS, R, SPSS, JMSL, BioConductor
- **Operating Systems:** Windows, Linux
- **Scripting:** Bash shell, DOS
- **Web Technologies and Web Services:** Servlets, XML
- **Database:** MySQL, Microsoft Access
- **Application/Web Servers:** Tomcat 5.0, Apache 2.0
- **Software Engineering Tools:** Ant, JUnit, Cygwin, Jira, Confluence
- **Other:** Design Patterns, Object Oriented Design, Parallel Programming, Continuous Integration

## SOFTWARE

- **HDBStat:** A desktop application to analyze high dimensional genomic data. Worked on requirement gathering and writing specifications for the statistical algorithms that were used. Implemented statistical classes using JMSL library and generated automated HTML reports using the Velocity library. Unit tested the code using JUnit  
<http://www.ssq.uab.edu/hdbstat/>
- **CressExpress:** A large scale co-expression tool for identifying sets of genes that co-express with each other under different conditions. Designed and developed the co-expression database in MySQL and implemented servlets and statistical algorithms. Developed a sub module for automating the curation of datasets. Developed use case scenarios for different queries to be executed using the coexpression tool.  
<http://cressexpress.org/>
- **R/QtlBim:** An R package for analyzing QTL data for experimental crosses using Bayesian interval mapping techniques. Wrote R routines to connect legacy C code base with R and make the C code available through R API. Duties include refactoring of legacy C code base to make it modular and applying the continuous integration technique for maintaining the project. Also involved in requirement gathering and software engineering of the project. Wrote R routines to preprocess the data and set up the model. Generated summary reports using R routines.  
<http://cran.r-project.org/web/packages/qtlbim/index.html>

## REFERENCES

- Available upon request.