Rajesh Talluri 979-645-0411
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Education

Indian Institute of Technology Guwahati, INDIA
Bachelor of Technology in Electronics and Communication Engineering *Aug. 2001 - May. 2005*

–Thesis: Contour tracking using condensation algorithm

Texas A&M University College Station, TX
Doctor of Philosophy in Statistics *Aug. 2005 - Aug 2011*

–Thesis: Bayesian Gaussian Graphical Models using Sparse Selection Priors and their Mixtures

–Mentors: Prof Bani.K.Mallick, Dr Veerabhadran Baladandayuthapani

Work Experience

The University of Mississippi Medical center October 2016 - Present
Assistant professor

- Collaborate with various clinicians and basic scientists.
- Develop novel statistical methods to identify clinical and genetic factors in epidemiological and genetic studies.

The University of Texas MD Anderson Cancer center October 2011 – October 2016
Post-Doctoral Fellow *Mentor: Prof Sanjay Shete*

- Training fellowship for research on the statistical genetics of addiction.
- Developed an online risk calculator for smoking experimentation risk in Mexican American youth.
- Contributed to rare variant analysis by improving the power of existing methods using information from linkage disequilibrium.
- Collaborated with various researchers from other disciplines and contributed to research in diverse fields.

The University of Texas MD Anderson Cancer center May 2008 - Aug 2008
Internship *Mentor: Dr Veera Baladandayuthapani*

- Developed a model to analyze ACGH data using Bayesian techniques.

Statistics Help Desk Aug 2007 - May 2008
Statistics Consultant *Consulting Guide: Prof Michael T. Longnecker*

- Performed consulting sessions for multiple clients from varied disciplines.
- Coordinated with a group of three consultants to perform the consulting duties.
- Provided efficient solutions for design of experiments for clients.
- Provided reasonable solutions to analyze poorly designed experiments.

Bayesian Bioinformatics Laboratory Aug 2005 - Aug 2011
Research Assistant *Mentor: Prof Bani Mallick*

- Worked on research projects for Bayesian bioinformatics laboratory.
- Participated in seminars and talks given by faculty in Bayesian bioinformatics laboratory.
- Collaborated with multiple faculty members to contribute to the research for the lab.

Department of Statistics Aug 2005 - Aug 2008
Graduate Assistant

- Used SAS, SPSS, MINITAB and JMP in the courses to tutor students.
- Conducted tutoring sessions for students who needed help in statistics courses.

Skills

Proficient in: R, MATLAB, C++

Basic Knowledge in: Julia, SAS, STATA, JMP, WINBUGS, SPSS, MINITAB, HTML, Java, Perl

Miscellaneous: Fast programming and debugging skills

Research Interests

- Statistical Genetics
- Machine Learning
- Survival Analysis
- Bayesian Modeling
- Information Theory
- Survey Data Analysis
- Decision Modeling
- Risk Prediction Models
- Epidemiological Methods

Publications

1. **Talluri R**, Shete S. Using the weighted area under the net benefit curve for decision curve analysis. BMC Medical Informatics and Decision Making 2016;16(1):1-9.

2. **Talluri R**, Shete S. Evaluating Methods for Modeling Epistasis Networks with Application to Head and Neck Cancer. Cancer Informatics. 2015;14(Suppl 2):17-23. doi:10.4137/CIN.S17289.

3. **Talluri R**, Shete S. Gaussian graphical models for phenotypes using pedigree data and exploratory analysis using networks with genetic and nongenetic factors based on Genetic Analysis Workshop18 data. BMC Proceedings. 2014;8(Suppl 1):S99. doi:10.1186/1753-6561-8-S1-S99.

4. **Talluri R**, Wilkinson AV, Spitz MR, Shete S. A Risk Prediction Model for Smoking Experimentation in Mexican American Youth. Cancer epidemiology, biomarkers & prevention: a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology. 2014;23(10):2165-2174. doi:10.1158/1055-9965.EPI-14-0467.

5. **Talluri R**, Wang J, Shete S. Calculation of exact p-values when SNPs are tested using multiple genetic models. BMC Genetics. 2014;15:75. doi:10.1186/1471-2156-15-75.

6. **Talluri R**, Baladandayuthapani V, Mallick BK. Bayesian sparse graphical models and their mixtures. Stat. 2014;3(1):109-125. doi:10.1002/sta4.49.

7. Baladandayuthapani V*,**Talluri R***, Ji Y, et al. Bayesian sparse graphical models for classification with application to protein expression data. The Annals of Applied Statistics. 2014;8(3):1443-1468. doi:10.1214/14-AOAS722. (* Joint First Author)

8. **Talluri R**, Shete S. A Linkage Disequilibrium Based Approach to Selecting Disease-Associated Rare Variants. Yu Z, ed. PLoS ONE. 2013;8(7):e69226. doi:10.1371/journal.pone.0069226.

9. Richardson, S, Bottolo, L, Rosenthal, JS, Mallick, B, Dhavala, SS, Liang, F, **Talluri R** & Wu, M 2012, 'Bayesian Models for Sparse Regression Analysis of High Dimensional Data'. In Bayesian Statistics 9. Oxford University Press., 10.1093/acprof:oso/9780199694587.003.0018

10. Baladandayuthapani V, Ji Y,**Talluri R**, Nieto-Barajas LE, Morris JS. Bayesian Random Segmentation Models to Identify Shared Copy Number Aberrations for Array CGH Data. Journal of the American Statistical Association. 2010;105(492):1358-1375. doi:10.1198/jasa.2010.ap09250.

Publications (Submitted/In preparation)

1. **Talluri R**, Shete S. Mediation Analysis of Bi-directional Associations with Application to Diabetes and Obesity , Annals of Human Genetics (Submitted)

2. Gritz ER, **Talluri R**, Tami-Maury I, Shete S. Smoking behaviors in survivors of smoking-related and non-smoking-related cancers. Journal of Clinical Oncology (Submitted)

3. **Talluri R**, Shete S. Using censored regression in threshold models for improving clinical decision making , BMC Medical Informatics and Decision Making (In preparation)

4. **Talluri R**, Shete S. Identifying risk factors for the progression of smoking in different stages using state transition disease models , Cancer epidemiology, biomarkers & prevention (In preparation)

Conference Presentations

- **Topic contributed Presentation**, Bayesian sparse graphical models for classification with application to protein expression data, JSM 2014.
- **Invited Talk**, A linkage disequilibrium based approach to selecting disease associated rare variants. NIDA Consortium Meeting, Rockville, MD, Jan 2013.
- **Platform Presentation**, A linkage disequilibrium based approach to selecting disease associated rare variants. Stevenson, WA, October 2012.
- **Platform Presentation**, Group presentation for GAW 18 for joint association analysis of multiple phenotypes. Genetic Analysis Workshop, Stevenson, WA, October 2012.
- **Platform Presentation**, Gaussian graphical models using Covariance Selection, JSM 2009.
- **Poster**, A novel risk prediction algorithm with application to smoking experimentation. International Genetic Epidemiology Society, Vienna, Austria August 2014
- **Poster**, Exact p-values for SNPs accounting for testing of multiple genetic models. International Genetic Epidemiology Society, Chicago, IL, September 2013
- **Poster**, Classification and Clustering using Gaussian Graphical Models, JSM 2010
- **Poster**, Finding relations between genes using covariance information, Alliance for Bioinformatics, Computational Biology, and Systems Biology (ABCS) Workshop, 2008.

Seminar Presentations

- Survey regression using the NHIS survey Data, Statistical Modeling Workshop, September 2014.(2 lectures)
- Reconsidering association testing methods using single-variant test statistics as alternatives to pooling tests for sequence data with rare variants, Statistical Genetics Journal Club 2014.
- Rare and common variants: twenty arguments by Greg Gibson, Statistical genetics Journal Club 2014.
- Population demographic history can cause the appearance of recombination hotspots by Henry R. Johnston and David J. Cutler, Statistical Genetics Journal Club 2013.
- Accurate genome-scale percentage DNA methylation estimates from microarray data. Statistical Modeling Workshop Jan 2012.
- Increased methylation variation in epigenetic domains across cancer types, Statistical Modeling Workshop Feb 2012.(4 lectures)

Professional Membership/Activities

- American Statistical Association Member, 2009-present
- International Genetic Epidemiology Society, Member 2012-present
- Journal reviewer, Genetic Epidemiology 2011-Present