Tyler Grimes

October 28, 2023

Email: tylerlukegrimes@gmail.com

Website: t-grimes.github.io

Education

Ph.D. Biostatistics   2016 – 2020
University of Florida, Gainesville FL
Dissertation Advisor: Somnath Datta
Thesis: "Some contributions to the differential network analysis of –omics data"

M.S. Mathematics, concentration in Statistics   2014 – 2016
University of North Florida, Jacksonville FL
Thesis: "A saddlepoint approximation to hypothesis test of variance for non-normal
populations" (Thesis Advisor: Ping Sa)

B.S. Mathematics, minor in Computer Science   2010 – 2014
University of Central Florida, Orlando FL

Employment

Senior Bioinformatics Analyst   2021 – present
The Emmes Company
-   Provide statistical guidance for developing clinical study protocols with -omics
    endpoints, ensuring the design and methods are scientifically valid and feasible.
-   Author statistical analysis plans (SAPs) to outline analysis strategies and
    algorithms for -omics data analysis.
-   Develop workflows for the processing, analysis, and management of -omics data.
-   Author study reports and manuscripts for research utilizing -omics endpoints.

Assistant Professor of Statistics   2020 – 2023
University of North Florida, Department of Mathematics and Statistics
-   Conducted collaborative and independent research focused on applying
    probabilistic graphical models to high-dimensional genomics data.
-   Taught graduate and undergraduate courses on statistics methods, design of
    experiments, quality control, and probability.
-   Directed graduate and undergraduate student projects. Titles included:
    "Probabilistic graphical models and their applications", "Survival prediction using
    autoencoders and AFT models", and "Unsupervised learning: principal
    component analysis."

Statistician – VA IPA   2018 – 2020
U.S. Department of Veterans Affairs, Brain Rehabilitation Research Center
- Assisted in the design and analysis of experiments; coded simulations for sample size calculations; wrote the statistical analysis plan for grant applications; analyzed experimental data; reported and discussed results with collaborators.

Graduate Research Assistant   2016 – 2020
University of Florida, Department of Biostatistics
- Worked on various research projects involving high-dimensional data analysis, dimension reduction, high-throughput RNA-sequencing, metabolomics data, predictive modeling, data visualization, and differential network analysis.

Graduate Teaching Assistant   2014 – 2016
University of North Florida, Department of Mathematics and Statistics

Teaching Experience

Assistant Professor, University of North Florida   2020 – present
- Courses taught include:
  - Sampling (Graduate – STA 6226 and Undergraduate – STA 4664)
  - Statistical Quality Control (Graduate/Undergraduate – STA 6666/4664)
  - Probability and Statistics (Undergraduate – STA 4321)
  - Statistical Methods I & II (Undergraduate – STA 3163/4, Graduate – STA 6166)
  - Elementary Statistics for Health and Social Sciences (STA 2014)
- Directed student projects through Capstone and Independent Study. Titles include:
  - "Probabilistic graphical models and their applications"
  - "Survival prediction using autoencoders and AFT models"
  - "Unsupervised learning: principal component analysis"

Temporary Instructor – Large Sample Theory, University of Florida   Spring 2019, 2020
- Lectured topics included probability, modes of convergence, U-statistics, and MLE.

Instructor, University of North Florida   Spring 2016
- Courses include: MAC 2233 (Calculus for Business).

Teaching Assistant, University of North Florida   2014 – 2016
- Assisted in elementary statistics courses by leading discussions in weekly breakout sessions, managing computer lab sessions, and holding weekly office hours.

Publications

1. **Grimes, T.**, Walker, A., Datta, S., Datta, S., (2018) Predicting survival times for neuroblastoma patients using RNA-Seq expression profiles. *Biology Direct*. 13(1), 11

2. Walker, A., **Grimes, T.**, Datta, S., Datta, S., (2018) Unraveling bacterial fingerprints of city subways from microbiome 16S gene profiles. *Biology Direct*. 13(1), 10

3. **Grimes, T.**, Potter, S., Datta, S., (2019) Integrating gene regulatory pathways into differential network analysis of gene expression data. *Scientific Reports.* 9(1), 5479

4. Boissoneault, C., **Grimes, T.**, Rose, D., Waters, M.F., Khanna, A., Datta, S. and Daly, J.J., (2020) Innovative long-dose neurorehabilitation for balance and mobility in chronic stroke: a preliminary case series. *Brain Sciences*. 10(8), 555

5. **Grimes, T.**, Datta, S., (2021) SeqNet: an R package for generating gene-gene networks and simulating RNA-seq data. *Journal of Statistical Software.* 98(12), 10.18637/jss.v098.i12

6. Boissoneault, C., Rose, D. K., **Grimes, T**., Waters, M. F., Khanna, A., Datta, S., & Daly, J. J. (2021). Trajectories of stroke recovery of impairment, function, and quality of life in response to 12-month mobility and fitness intervention. *NeuroRehabilitation*. 49(4), 573-584

7. Ahn, S., **Grimes, T.**, Datta, S. (2021) The analysis of gene expression data incorporating tumor purity information. *Frontiers in Genetics.* 12(1), 642759

8. **Grimes, T.**, Datta, S. (2021) A novel probabilistic generator for large-scale gene association networks. *PLoS One*. 16(11), e0259193

9. Ahn, S., **Grimes, T.**, & Datta, S. (2023). A pseudo-value regression approach for differential network analysis of co-expression data. *BMC Bioinformatics*. 24(1), 8

10. Goll, J. B., Bosinger, S. E., Jensen, T. L., Walum, H., **Grimes, T.**, Tharp, G. K., ... & Hoft, D. F. (2023). The Vacc-SeqQC project: Benchmarking RNA-Seq for clinical vaccine studies. *Frontiers in Immunology*. 13(1), 1093242

11. Waid-Ebbs, J. K., Wen, P. S., **Grimes, T.**, Datta, S., Perlstein, W. M., Hammond, C. S., & Daly, J. J. (2023). Executive function improvement in response to meta-cognitive training in chronic mTBI/PTSD. *Frontiers in Rehabilitation Sciences*. 4(1), 1189292

12. DeZern, A. E., Goll, J. B., Lindsley, R. C., Bejar, R., Wilson, S. H., Hebert, D., ..., **Grimes, T.**, … & Walter, M. J. (2023). Utility of targeted gene sequencing to

differentiate myeloid malignancies from other cytopenic conditions. *Blood Advances*. 7(14), 3749-3759

Conference Proceedings:

13. **Grimes, T.**, Datta, S., (2019) A random graph generation model for transcription networks and nonparametric simulator for RNA-seq expression data. *Computer Data Analysis and Modeling*. Proceedings of the XII International Conference, Minsk. September 18-22, 2019, Eds: P. Filzmoser and Y. Kharin, pp. 37-42. ISBN 978-985-566-811-5.

In Progress:

14. **Grimes, T.**, Datta, S., dnapath: an R package for pathway-based differential network analysis.

15. **Grimes, T.**, Datta, S., (tentative) Inferring dynamic networks from scRNA-seq data

16. **Grimes, T.**, Datta, S., (tentative) Identifying cancer driver genes from differential co-expression networks.

17. **Grimes, T.**, Ping, S., A saddlepoint approximation to hypothesis tests of variance for non-normal populations.

Presentations

Talks:

1. University of Maryland, statistics colloquium invited talk, virtual seminar   2022
   "Predictive modeling with differential co-expression of RNA-seq data"

2. UNF Biomedical Sciences Research in Progress seminar, Jacksonville, FL.   2021
   "Identifying cancer driver genes from differential co-expression networks"

3. CMStatistics International Conference, virtual conference   2020
   "Identifying cancer driver genes from differential co-expression networks"

4. ISMB/CAMDA International Conference, Chicago, IL   2018
   "An exploratory approach for identifying novel biomarkers in high-risk cancer patients from RNA-seq data"

5. ISMB/ECCB International Conference, Prague, Czech Republic   2017
   "Predicting survival times for neuroblastoma patients using RNA-Seq expression profiles"

Posters:

6. JSM, Denver, CO.   2019
   "Integrating gene regulatory pathways into differential network analysis of gene expression data"

7. UF College of PHHP Research Day, Gainesville, FL.   2019
   *"*A pathway-based approach to differential network analysis of gene expression data"

8. IISA International Conference on Statistics, Gainesville, FL.   2018
   "Predicting Survival Times for Neuroblastoma Patients Using RNA-Seq Expression Profiles"

9. UF College of PHHP Research Day, Gainesville, FL.   2018
   *"*Predicting Survival Times for Neuroblastoma Patients Using RNA-Seq Expression Profiles"

10. UF College of Medicine Celebration of Research, Gainesville, FL.   2018
    *"*Differential network analysis based on next-generation sequencing data"

11. UF Graduate Student Research Day, Gainesville, FL.   2018
    *"Predicting Survival Times for Neuroblastoma Patients Using RNA-Seq Expression
    Profiles"*

12. UF Dept. of Statistics Winter Workshop, Gainesville, FL.   2018
    "Differential network analysis based on next-generation sequencing"

13. JSM, Baltimore, MD.   2017
    "Differential network analysis based on next-generation sequencing"

14. FaceBase Scientific Meeting, Boston, MA.   2017
    "A differential network analysis of palatal development"

Service

Committee Chair – Undergraduate Committee   2021 – 2023
Department of Mathematics and Statistics, University of North Florida

Founding President - Biostatistics Student Organization   2017 – 2019
Department of Biostatistics, University of Florida

Executive Board Member - Doctoral Student Council   2017 – 2019
College of Public Health and Health Professionals, University of Florida

Student Representative - Department of Biostatistics   2019
College of PHHP Development Board Meeting, University of Florida

Student Representative - Department of Biostatistics   2017
College of PHHP Advisory Board Member Meeting, University of Florida

Projects

My old github account hosts various projects including course projects such as
a stochastic approximation algorithm for minimum graph bisection; conference
challenges including the CAMDA 2017 Neuroblastoma challenge; and other personal
projects.

My methodological research is implemented in various R packages. These include SeqNet, an R package for simulating RNA-sequencing data from any underlying association network; and dnapath, an R package that performs differential network analysis based on known pathway information, which includes methods for easily summarizing and visualizing the results.

Professional Memberships

American Statistical Association (ASA)
International Society for Computational Biology (ISCB)

Journal Referee

BioData Mining
Bioinformatics
BMC Bioinformatics
Briefings in Bioinformatics
Communications in Statistics - Simulation and Computation
Scientific Reports
GigaScience

Honors and Awards

Outstanding Dissertation Award   2020
Department of Biostatistics, University of Florida

Student Travel Award (multiple awards)   2017, 2019
Department of Biostatistics, University of Florida
and by College of Public Health and Health Professionals, University of Florida

Travel Fellowship   2017, 2018
Granted by CAMDA committee to present at ISMB/CAMDA 2018, Chicago, Illinois
and at ISMB/ECCB 2017, Prague, Czech Republic
Department of Biostatistics, University of Florida

Outstanding Graduate Student in Statistics   2016
University of North Florida

UCF Scholars Award (scholarship and summer grant)   2012 – 2013

University of Central Florida

Florida Academic Scholars Award (four-year scholarship)   2010 – 2014

Funding

U.S. Department of Veterans Affairs IPA, "Analysis of Traumatic Brain Injury and other Brain Rehabilitation Data", September 2018 – August 2019; VA PIs: Julia Waid-Ebbs and Janis Daly

National Institutes of Health, "Exploratory Statistical Analysis of Differential Network Behaviors based on Gene Expression Atlas of Palate Development", August 2016 - July 2019; PI: Somnath Datta