

# Tyler Grimes

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## Education

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**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 Advisor: Ping Sa

Thesis: “A saddlepoint approximation to hypothesis test of variance for non-normal populations”

**B.S. Mathematics**, minor in Computer Science 2010 – 2014

University of Central Florida, Orlando FL

## Employment

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**Assistant Professor of Statistics** 2020 – present

University of North Florida, Department of Mathematics and Statistics

**Graduate Research Assistant** 2016 – 2020

University of Florida, Department of Biostatistics

**Graduate Teaching Assistant** 2014 – 2016

University of North Florida, Department of Mathematics and Statistics

## Teaching Experience

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Assistant Professor, University of North Florida 2020 – present

- Courses include: STA 6226 (Sampling) and STA 3163 (Statistical Methods I)

Temporary Instructor – Large Sample Theory, University of Florida Spring 2019, 2020

- Gave lectures on probability, modes of convergence, U-statistics, and maximum likelihood estimation in the absence of Professor Somnath Datta.

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**

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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. **Grimes, T.**, Datta, S., (in press) SeqNet: an R package for generating gene-gene networks and simulating RNA-seq data. *Journal of statistical software*.
5. 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.

### *Under Review:*

6. **Grimes, T.**, Datta, S., A probabilistic generator for large-scale gene association networks. *Bioinformatics*.

### *Conference Proceedings:*

7. **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:*

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

9. Seungjun, A. **Grimes, T.**, Datta, S., Effect of tumor purity on the analysis of gene expression data
10. **Grimes, T.**, Datta, S., (tentative) Inferring dynamic networks from scRNA-seq data
11. **Grimes, T.**, Datta, S., (tentative) Identifying cancer driver genes from differential co-expression networks.
12. **Grimes, T.**, Ping, S., A saddlepoint approximation to hypothesis tests of variance for non-normal populations.

## **Presentations**

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### *Talks:*

1. ISMB/CAMDA International Conference, Chicago, IL 2018  
“An exploratory approach for identifying novel biomarkers in high-risk cancer patients from RNA-seq data”
2. ISMB/ECCB International Conference, Prague, Czech Republic 2017  
“Predicting survival times for neuroblastoma patients using RNA-Seq expression profiles”

### *Posters:*

3. JSM, Denver, CO. 2019  
“Integrating gene regulatory pathways into differential network analysis of gene expression data”
4. UF College of PHHP Research Day, Gainesville, FL. 2019  
“A pathway-based approach to differential network analysis of gene expression data”
5. IISA International Conference on Statistics, Gainesville, FL. 2018  
“Predicting Survival Times for Neuroblastoma Patients Using RNA-Seq Expression Profiles”
6. UF College of PHHP Research Day, Gainesville, FL. 2018  
“Predicting Survival Times for Neuroblastoma Patients Using RNA-Seq Expression Profiles”

7. UF College of Medicine Celebration of Research, Gainesville, FL. 2018  
“Differential network analysis based on next-generation sequencing data”
8. UF Graduate Student Research Day, Gainesville, FL. 2018  
“Predicting Survival Times for Neuroblastoma Patients Using RNA-Seq Expression Profiles”
9. UF Dept. of Statistics Winter Workshop, Gainesville, FL. 2018  
“Differential network analysis based on next-generation sequencing”
10. JSM, Baltimore, MD. 2017  
“Differential network analysis based on next-generation sequencing”
11. FaceBase Scientific Meeting, Boston, MA. 2017  
“A differential network analysis of palatal development”

## Service

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**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

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My [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**

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American Statistical Association (ASA)

International Society for Computational Biology (ISCB)

## **Journal Referee**

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Bioinformatics (1)

BMC Bioinformatics (3)

Communications in Statistics - Simulation and Computation (2)

## **Honors and Awards**

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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**

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**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