

Tyler Grimes, PhD

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Education

Ph.D. Biostatistics (2020), University of Florida

M.S. Mathematics, concentration in Statistics (2016), University of North Florida

B.S. Mathematics, minor in Computer Science (2014), University of Central Florida

Employment

University of North Florida, Dept. of Mathematics and Statistics – Jacksonville, FL

Assistant Professor of Statistics | Aug. 2026 – Present

Visiting Instructor | Aug. 2025 – May 2026

- Taught graduate and undergraduate statistics courses.
- Supervised undergraduate capstones and graduate exit presentations.

Assistant Professor of Statistics | Aug. 2020 – May 2023

- 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.”

Graduate Teaching Assistant | Aug. 2014 – July 2016

The Emmes Company (CRO) – Remote

Manager, Bioinformatics & Data Science | Apr. 2026 – Present (currently Part-Time)

Senior Bioinformatics Analyst | Dec. 2021 – Apr. 2026

- **Lead analyst** for multiple clinical trials in a client-facing role, responsible for:
 - o Developing the statistical analysis plan for -omics endpoints used to assess immune response in phase I/II vaccine clinical trials and challenge studies.
 - o Authoring FDA-submitted reports and discussing results with PIs and study team.
 - o Statistical methodology involving design of experiments, high-dimensional data analysis, predictive modeling, data visualization, and multi-omics integration.
 - o RNA-seq workflow including pre-processing—alignment, annotation, and quantification—and all downstream analyses run using AWS EC2 and S3 services.
 - o Managing a team of bioinformatics programmers and data scientists.
- **Manager and independent contributor** for various data science projects, including:
 - o Analysis of whole slide tumor images using a VAE for feature extraction and attention-based multiple instance learning (MIL-NN) for interpretable prediction.
 - o Developing an evaluation framework for an LLM tool for report text generation.
 - o Creating tools and workflows in Python and R to automate various aspects of reporting, figure generation, and integrating SAS outputs into Word documents.

- Ad hoc statistical support for various labs within the NHGRI involving the analysis of psychosocial survey data, analysis of social network structures, cluster analyses, regression modeling, and visualizations.
- Technical lead for **business development** proposals involving machine learning (ML).
 - Won several proposals and contract extensions, with projects including development of an ML predictive model for tumor histology images; development of an AI-based meta-analysis workflow; and the analysis of complex longitudinal surveillance data for a childhood-pneumonia study.

U.S. Department of Veterans Affairs, BRRC – Gainesville, FL

Statistician – VA IPA | 2018 – 2020

- 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.

University of Florida, Department of Biostatistics – Gainesville, FL

Graduate Research Assistant | Aug. 2016 – July 2020

- 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.

Teaching Experience

Assistant Professor, University of North Florida

Fall 2026

Courses taught include:

- Statistical Methods I (STA 3136)
- Probability and Statistics for Engineers (STA 3032)
- Directed undergraduate student Capstone projects.
- Directed master's student Thesis.

Visiting Instructor, University of North Florida

Fall 2025 – Spring 2026

- Courses taught include:
 - Sampling (STA 6226)
 - Statistical Quality Control (STA 4664 and STA 6666)
 - Statistical Methods II (STA 6167)
 - Business Statistics (Distance Learning - STA 2023)
- Directed undergraduate student Capstone projects.

Assistant Professor, University of North Florida

Fall 2020 – Spring 2023

- Courses taught include:
 - Sampling (STA 6226 and STA 4664)
 - Statistical Quality Control (STA 4664 and STA 6666)
 - Probability and Statistics (STA 4321)

- Statistical Methods I & II (STA 3163/4 and 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”

Guest 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

13. Derek, J. W., Gautam, S. C., Creech, B., Jimenez, N, Anderson, E. J., Bosinger, S. E., **Grimes, T.** et al. (2025). Transcriptomic Biomarkers Associated with Microbiological Etiology and Disease Severity in Childhood Pneumonia. *The Journal of Infectious Diseases*. 231(2), e277–e289
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
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
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
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
8. **Grimes, T.**, Datta, S. (2021) A novel probabilistic generator for large-scale gene association networks. *PLoS One*. 16(11), e0259193

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

Conference Proceedings:

1. **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.

Presentations

Talks:

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| 5. University of Maryland, statistics colloquium invited talk, virtual seminar
“Predictive modeling with differential co-expression of RNA-seq data” | 2022 |
| 4. UNF Biomedical Sciences Research in Progress seminar, Jacksonville, FL.
“Identifying cancer driver genes from differential co-expression networks” | 2021 |
| 3. CMStatistics International Conference, virtual conference
“Identifying cancer driver genes from differential co-expression networks” | 2020 |

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

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

Posters:

9. JSM, Denver, CO. 2019
“Integrating gene regulatory pathways into differential network analysis of gene expression data”

8. UF College of PHHP Research Day, Gainesville, FL. 2019
“A pathway-based approach to differential network analysis of gene expression data”

7. 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”

5. UF College of Medicine Celebration of Research, Gainesville, FL. 2018
“Differential network analysis based on next-generation sequencing data”

4. UF Graduate Student Research Day, Gainesville, FL. 2018
“Predicting Survival Times for Neuroblastoma Patients Using RNA-Seq Expression Profiles”

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

2. JSM, Baltimore, MD. 2017
“Differential network analysis based on next-generation sequencing”

1. 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

Software

My research methodology is implemented in open-source R packages:

- [CpmERCCutoff](#), implements an empirical method to derive log₂ counts per million (LCPM) cutoff to filter out lowly expressed genes using External RNA Controls Consortium (ERCC) spike-ins.
- [SeqNet](#), tools for generating realistic gene-association network graphs and simulating RNA-sequencing data with the association structure of a given graph.
- [dnapath](#), performs differential network analysis based on known pathway information; includes tools 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
GigaScience
Scientific Reports

Honors and Awards

Best Application of Data Science Award Emmes Scientific Symposium <i>A cloud-based framework for clinical predictive modeling using unannotated whole-slide pathology images, leveraging segmentation, feature extraction via transfer learning, clustering, and attention-based multiple instance learning.</i>	2025
Outstanding Dissertation Award Department of Biostatistics, University of Florida	2020
Student Travel Award (multiple awards) Department of Biostatistics, University of Florida and by College of Public Health and Health Professionals, University of Florida	2017, 2019
Travel Fellowship 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	2017, 2018
Outstanding Graduate Student in Statistics University of North Florida	2016
UCF Scholars Award (scholarship and summer grant) University of Central Florida	2012 – 2013
Florida Academic Scholars Award (four-year scholarship)	2010 – 2014

Clinical Research Currently Supporting

Clinical Research in Infectious Disease (CRID), NIH/NIAID

In support of the NIH NIAID's Division of Microbiology and Infectious Diseases (DMID) clinical research projects, Emmes serves as the Statistical and Data Coordinating Center providing statistical design and analysis; computerized systems for data collection, management, and quality control; an electronic specimen tracking system;

preparation of study-related materials; website development; study communication, collaboration, and reporting; clinical site training, assessment, and technical assistance; and data storage for complete DMID-sponsored clinical studies. Under this contract, Emmes supports a broad range of clinical research, including single-site and multi-center, domestic and international, Phase 1-4 clinical trials of bacterial, viral, and parasitic vaccines, therapeutics, and other biologics and drugs as preventive and therapeutic measures against infectious diseases in people of all ages and risk categories.

Role: Sr. Bioinformatics Analyst

Project duration: 2021-2028

National NeuroHIV Tissue Consortium – Statistical and Data Coordinating Center – NIH/NIMH

The National NeuroHIV Tissue Consortium (NNTC) is a unique, NIH-supported multi-site repository that collects and distributes well-characterized antemortem and postmortem tissue specimens with clinical and serological data from HIV-infected individuals, thereby facilitating NeuroHIV research, NNTC supports extensive data management services for the growing NNTC cohort, as well as tissue request coordination. Since 2003, Emmes has served as the NNTC Data Coordinating Center (DCC), providing biostatistics, bioinformatics, project management, data management, and website development/maintenance services.

Role: Sr. Bioinformatics Analyst

Project duration: 2008-2028

NHGRI: Ad Hoc Statistical Support

Emmes' staff has provided the National Human Genome Research Institute (NHGRI) Office of the Clinical Director (OCD) with statistical expertise. Emmes provides consultation with a senior level statistician to assist in the development and execution of clinical research protocols and pre-clinical studies. Issues addressed include power analyses, sample size analyses, group analyses, trends, and stopping rules, as well as more complex topics.

Role: Sr. Bioinformatics Analyst

Project duration: 2003-2025

Data Coordinating Center – The National Myelodysplastic Syndromes (MDS) Natural History Study, NIH/NHLBI

The objective of The National MDS Study is to establish a scientific resource to facilitate the conduct of basic and translational research of the evolution of MDS over time and improve the diagnosis and clinical management of affected individuals. The resource will include a comprehensive, standardized longitudinal clinical dataset linked to consistently processed, well-annotated biospecimens. Potential uses for this resource including: (1) identifying genetic, epigenetic and biological factors associated with initiation and

progression of MDS; (2) uncovering fundamental information on the changes that occur in hematopoietic stem cells and bone marrow stroma during normal aging; (3) revealing clinically useful biomarkers; (4) identifying potential targets for new interventions; and (5) facilitating the understanding of how patients with MDS are managed in practice.

Role: Sr. Bioinformatics Analyst

Project duration: 2014-2025

AIDS Malignancy Consortium Operations and Data Management Center, UCLA

The AIDS Malignancy Consortium (AMC) was founded by the National Cancer Institute (NCI) in 1995 to support innovative clinical trials in the treatment and prevention of AIDS-associated malignancies. Since 2006, Emmes has served as the Operations and Data Management Center, for the AMC, coordinating 5 disease focused Working Groups, 3 AMC biorepositories, and 5 AMC Core Laboratories. Emmes' responsibilities including Consortium communications, vendor/pharma contracting and management, site management, training, regulatory management, data and specimen management, protocol monitoring and medical monitoring. Specific services provided to the AMC include the development and implementation of Advantage eClinical® for data collection, training and certifying sites on use of Advantage eClinical components, data querying, data transfer, and Clinical Data Update System data submission to NCI.

Role: Sr. Bioinformatics Analyst

Project duration: 2006-2025

Clinical Research Previously Supported

U.S. Department of Veterans Affairs IPA, “Analysis of Traumatic Brain Injury and other Brain Rehabilitation Data”

Statistical analysis of stroke and mild traumatic brain injury research. During Dr. Grimes' PhD studies, he served as a statistician consulting with researchers in the Brain Rehabilitation Research Center (BRRC) of the Veterans Affairs (VA). His role was to assist in the design and analysis of experiments; code simulations for sample size and power calculations; write the statistical analysis plan for grant applications; analyze experimental data; and report and discuss results with collaborators.

Role: Statistician

Project duration: 2018-2020

National Institutes of Health, “Exploratory Statistical Analysis of Differential Network Behaviors based on Gene Expression Atlas of Palate Development”

Development of statistical methodology for exploratory analyses of differential network behaviors based on gene expression atlas of palate development. This project funded Dr. Grimes' PhD research, where he undertook a network analysis of next-generation

sequencing data with the goal of understanding the systems biology of palate development. This work resulted in various research projects involving high-dimensional data analysis, non-linear dimension reduction techniques, bulk and single-cell high-throughput RNA-sequencing, clinical predictive modeling, data visualization, and developing a general framework for differential network analysis.

Role: Graduate Research Assistant

Project duration: 2016-2020