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## A. Grant Schissler

### EDUCATION

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**PhD Statistics** 2012-2017  
*University of Arizona, Tucson, AZ, [Statistics Graduate Interdisciplinary Program \(GIDP\)](#)*  
Advisors: Walter W. Piegorsch (Statistics) & Yves A. Lussier (Informatics)

**MS Applied Statistics** 2009-2011  
*Kennesaw State University, Kennesaw, GA*  
Honors Graduate (4.0 GPA)

**BS Applied Mathematics** 2002-2005  
*Georgia Institute of Technology, Atlanta, GA*  
Dean's List, Social/Personality Psychology Certificate

### RESEARCH AREAS

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*Bayesian models/computation/prediction, empirical Bayesian methods, multilevel/hierarchical models, variance reduction, survival analysis, high-dimensional data analysis/computation/simulation, large-scale hypothesis testing, information theory, causal inference, single-subject inference/n-of-1 experiments, multivariate statistics, statistical machine learning, clustering, big data, data visualization, high-throughput data, time series analysis, zero-inflated models*

### WORK EXPERIENCE

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**Assistant Professor of Statistics** 2017-current  
*[The University of Nevada, Reno](#), [Department of Mathematics & Statistics](#), [University of Nevada, Reno](#)*

- Created/leading an interdisciplinary research team in statistics and applications.
- Served as Principal Investigator for a sponsored project.
- Developed project management strategies combining Kanban/Agile/Action Method/GTD philosophies.
- Mentored and supervised master's and doctoral statistics & data science students.
- Provided statistical expertise and guidance for over 15 graduate student theses and dissertations.
- Authored and published over 10 peer-reviewed journal articles and book chapters in 4.5 years.
- Gave over 30 conference presentations, talks, and seminars in 4.5 years.
- Created and co-authored 2 software packages in R, Python, and Julia.
- Taught over 10 undergraduate & graduate courses in statistical theory, computation, and applications.
- Developed and taught the first Bayesian statistics course in the Nevada Higher System of Education.
- Affiliated faculty with the Renown Institute of Cancer.

**Research Assistant** 2014-2017  
*[Lussier Group](#), [Center for Biomedical Informatics & Biostatistics](#), [University of Arizona](#)*

- Developed statistical informatics methodology for precision medicine.
- Applied statistical machine learning to cancer survival.
- Developed innovative n-of-1 experimental design frameworks.
- Authored and published 7 peer-reviewed journal articles 3.5 years.
- Gave over 10 conference presentations, talks, and seminars in 3.5 years.
- Mentored undergraduate & secondary school researchers.
- Created and authored 1 software packages in R.

- Communicated our work to the public. E.g., See this [link](#) (@1:30 minutes) filmed by Tucson ABC-affiliate KGUN9.

### **Biostatistician & Statistical Consultant**

2013-2014

#### *HTG Molecular*

- Developed market-competitive high-throughput gene expression analytics.
- Began as an intern and was retained as a consultant.
- Worked in an team of biostatisticians, cancer biologists, geneticists, engineers, and computer scientists.
- Conducted data analyses/visualization, biotechnology data quality control, and software engineering.
- Developed and communicated recommendations for business leaders.
- Developed dynamic reporting pipelines for customers.

### **Instructor/Teaching Assistant**

2012-2014

#### *University of Arizona*

- Developed curriculum and served as an instructor of Preparation for University-Level Mathematics.
- Taught Statistical Foundations in the Information Age including R programming.

### **Mathematics Instructor/Athletic Coach**

2006-2012

#### *Tri-Cities High School, East Point, GA*

- Taught nearly every secondary mathematics course offered in the State of Georgia.
- Specialized in AP Statistics.
- Implemented effective classroom management and motivational systems.
- Designed and delivered professional development for teachers.
- Led the Boys Tennis Team to first-ever State Playoff appearance.

## **PEER-REVIEWED JOURNAL PUBLICATIONS [\[Stats\]](#)**

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1. Austin Witt<sup>†</sup>, Taylor Gurnea<sup>†</sup>, Franklin Fuchs<sup>†</sup>, Sahar Sedigh<sup>†</sup>, and A. Grant Schissler, “Estimating the impact of self-directed parallel curriculum on United States Medical Licensing Exam Step 1 performance.”, *American Medical Student Research Journal* , (in press, accepted 15 Aug 2021).
2. Jingyu Liu, Walter W. Piegorsch, A. Grant Schissler, Rachel R. McCaster, and Susan L. Cutter, “Adjusting statistical benchmark risk analysis to account for non-spatial autocorrelation, with application to natural hazard risk assessment”, *Journal of Applied Statistics* , (in press , accepted 12 Mar 2021).
3. Alexander D. Knudson<sup>†</sup>, Tomasz J. Kozubowski, Anna K. Panorska and Alfred G. Schissler, “[A flexible multivariate model for high-dimensional correlated count data analysis and simulation](#)”, *Journal of Statistical Distributions and Applications* **8**, 6 (2021).
4. Tin Nguyen, Adib Shafi, Nguyen Tuan-Minh, A. Grant Schissler, and Sorin Draghici, “[NBIA: a network-based integrative analysis framework - applied to pathway analysis](#)”, *Scientific Reports* **10**, 1 (2020).
5. A. Grant Schissler, Dillon Aberasturi, Colleen Kenost and Yves A. Lussier, “[A single-subject method to detect pathways enriched with alternatively spliced genes](#)”, *Frontiers in Genetics: Current Trends in Translational Bioinformatics* **10**, 414 (2019).
6. Xiang Li<sup>†</sup>, A. Grant Schissler, Rui Wu, Lee Barford, and Frederick C. Harris, Jr., “[A graphical processing unit accelerated NORMAL-To-Anything algorithm for high dimensional multivariate simulation](#)”, *Advances in Intelligent Systems and Computing: Proceedings of ITNG* **46**, 800 (2019).

7. Samir R. Zaim\*, Qike Li\*, [A. Grant Schissler\\*](#), and Yves A. Lussier, “[Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous transcriptomic responses](#)”, *Biocomputing* **2018**, 484-495 (2018).
8. Jingyu Liu, Walter W. Piegorsch, [A. Grant Schissler](#) and Susan L. Cutter, “[Autologistic modeling in quantitative risk analysis, with applications to urban vulnerability assessment of terrorism outcomes](#)”, *Journal of the Royal Statistical Society: Series A* **181**, 3 (2018).
9. [A. Grant Schissler](#), Walter W. Piegorsch and Yves A. Lussier, “[Testing for differentially expressed genetic pathways with single-subject N-of-1 data in the presence of inter-gene correlation](#)”, *Statistical Methods in Medical Research* **27**, 12 (2018).
10. Francesca Vitali, Qike Li, [A. Grant Schissler](#), Joanne Berghout, Colleen Kenost, Yves A. Lussier, “[Developing a ‘personalome’ for precision medicine: emerging methods that compute clinically interpretable effect sizes from single-subject omics](#)”, *Briefings in Bioinformatics* **bbx149**, (2017).
11. V Gardeux\*, J Berghout\*, I Achour\*, [AG Schissler\\*](#), Q Li, C Kenost, J Li, Y Shang, A Bosco, D Saner, MJ Halonen, DJ Jackson, H Li, FD Martinez, and YA Lussier, “[A genome-by-environment interaction classifier for precision medicine: personal transcriptome response to rhinovirus identifies children prone to asthma exacerbations](#)”, *Journal of the American Medical Informatics Association: JAMIA* **ocx069**, (2017).
12. Qike Li\*, [A. Grant Schissler\\*](#), Vincent Gardeux, Ikbel Achour, Colleen Kenost, Joanne Berghout, Haiquan Li, Hao Helen Zhang and Yves A. Lussier, “[N-of-1-pathways MixEnrich: advancing precision medicine via single-subject analysis in discovering dynamic changes of transcriptomes](#)”, *BMC Medical Genomics* **10(Suppl 1)**, 27 (2017).
13. Qike Li\*, [A. Grant Schissler\\*](#), Vincent Gardeux, Joanne Berghout, Ikbel Achour, Colleen Kenost, Haiquan Li, Hao Helen Zhang and Yves A. Lussier, “[kMEn: analyzing noisy and bidirectional transcriptional pathway responses in single subjects](#)”, *Journal of Biomedical Informatics* **66**, (2017).
14. [A. Grant Schissler](#), Qike Li, James Chen, Colleen Kenost, Ikbel Achour, Dean Billheimer, Haiquan Li, Walter W. Piegorsch, and Yves A. Lussier, “[Analysis of aggregated cell-cell statistical distances within pathways unveils therapeutic-resistance mechanisms in circulating tumor cells](#)”, *Bioinformatics* **32**, 12 (2016).
15. [A. Grant Schissler](#), Vincent Gardeux, Qike Li, Ikbel Achour, Haiquan Li, Walter W. Piegorsch and Yves A. Lussier, “[Dynamic changes of RNA-sequencing expression for precision medicine: N-of-1-pathways Mahalanobis distance within pathways of single subjects predicts breast cancer survival](#)”, *Bioinformatics* **31**, 12 (2015).

† = student under my supervision, \* = joint first authorship

## CREATIVE WORKS UNDER REVIEW

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1. [A. Grant Schissler](#), Alex Knudson†, Richard DL Foote, Tomasz Kozubowski, and Anna Panorska, “Simulating Dependent High-Dimensional Data via the bigsimr R package, with an Application to RNA-sequencing data”, **Journal of Statistical Software**, ().

## BOOK CHAPTERS

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1. [A. Grant Schissler](#), Hung Nguyen, Tin Nguyen, Juli Petereit, Vincent Gardeux, “Statistical Software”, **Wiley StatsRef-Statistics Reference Online**, (2018).
2. [A. Grant Schissler](#) and Alex Knudson†, “Software, Statistical”, **Wiley Handbook of Computational Statistics and Data Science**, (2020).

† = student under my supervision

## PROGRAMMING/COMPUTER SKILLS

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- R
- Bash/command line
- Python
- Julia
- SQL
- PBS/LSF/slurm scheduling
- SPSS
- SAS
- Mac OS, Windows, Linux
- Emacs/lisp
- markdown/rmarkdown/Jupyter notebooks
- MS office / Excel
- Trello / project management
- git

## AWARDS

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- 2019 [Semi-finalist best paper in Trend 3: Pathway-level versus gene-level analyses for Zaim SR, Li Q, Schissler AG, Lussier YA. Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous transcriptomic responses. Pac Symp Biocomput 2018; 23: 484-95.](#), Contributions from the 2018 Literature on Bioinformatics and Translational Informatics: Section Editors for the 2019 IMIA Yearbook Section on Bioinformatics and Translational Informatics.
- 2019 [ITNG 2019 Best Student Paper Award](#), ITNG program committee, Xiang Li.
- 2019 [Westfall Mentor](#), The University of Nevada, Reno, Kyle Murray.
- 2019 [Spring 2019 Herz Gold Medalist](#), The University of Nevada, Reno, Kyle Murray.
- 2019 [Department of Mathematics & Statistics Westfall Scholar](#), The University of Nevada, Reno, Kyle Murray.

## SELECTED PRESENTATIONS

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1. City of Hope Cancer Center<sup>†</sup>, Los Angeles, CA, Jan 2020 (Bespoke computational oncology: How to conduct statistical inference when convention methods fail)
2. CMSTATS 2019<sup>†</sup>, London, GB, Dec 2019 (On Simulating Ultra High-Dimensional Multivariate Data)
3. ISMCO 2019, South Lake Tahoe, NV, Oct 2019 (A single-subject method to detect pathways enriched with alternatively spliced genes)
4. RSS 2019, Belfast, NI, Sep 2019 (On Simulating Ultra High-Dimensional Multivariate Discrete Data)
5. ESCO 2018<sup>†</sup>, Pilsen, Czech Republic, Jun 2018 (A graphical processing unit accelerated NORMal-To-Anything algorithm for high dimensional multivariate simulation)
6. JSM 2016, Chicago IL, August 2016 (Testing for differentially expressed pathways from within-subject matched pairs of RNA-seq data sets)
7. ISMB 2016, Orlando FL, July 2016 (Statistical distances in circulating tumor cells)
8. First workshop on Interdisciplinary Statistics, CIMAT Guanajuato Mexico, June 2016 (Statistical informatics for precision medicine)
9. ISMB/ECCB 2015, Dublin, July 2015 (N-of-1-*pathways* MD)

## ACTIVITIES & INTERESTS

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- Proud parent to rescue dogs and cat / dog training
- Enjoy activity hobbies: tennis, skiing, running, hiking, biking, rowing, camping
- Road tripping and traveling domestically/abroad
- Cooking and eating great food
- Watching TV shows, movies, and live sports
- Video games / eSports (when time allows...)
- Reading: philosophy, self improvement, and leadership/social skills