

RHONDA BACHER

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EDUCATION

University of Wisconsin-Madison 2012 - 2017

Ph.D. in Statistics

Emphasis in Biostatistics

Thesis Advisor: Christina Kendzioriski, Ph.D.

University of Florida 2008 - 2012

B.S in Statistics (Magna Cum Laude), B.S in Mathematics (Cum Laude)

College of Agriculture and Life Sciences Honors Scholar

Honors Thesis: "RNA-seq data: normal models and missing data"

Thesis Advisor: Lauren McIntyre, Ph.D.

PROFESSIONAL EXPERIENCE

Assistant Professor January 2018 - present

Department of Biostatistics, University of Florida

Postdoctoral Research Fellow July 2017 - December 2017

Center for Predictive Computational Phenotyping, University of Wisconsin-Madison

An NIH Center of Excellence for Big Data Computing established by the Big Data to Knowledge Initiative

Bio-Data Science Trainee (NIH; T32) 2016 - 2017

Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison

- Training in bioinformatics.

Research Assistant 2015 - 2016

Center for Predictive Computational Phenotyping, University of Wisconsin-Madison

- Consulted with Biology/Genetics faculty investigators.

Biostatistics Trainee (NIGMS; T32) 2012 - 2015

Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison

- Consulted across a broad range of topics in genetics and genomics.
- Ethics training.
- Presented scientific talks in department seminars.

HONORS AND AWARDS

Featured in Amstat News cover story on influential women in Statistics and Data Science 2019

<https://magazine.amstat.org/blog/2019/03/01/rhonda-bacher/>

Selected for the NIH Data Science Innovation Lab (NIH BD2K) 2018

Only 30 total applicants were selected by committee.

Outstanding poster award, Symposium on Advances in Genomics, Epidemiology and Statistics	2017
Travel award, Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine Conference	2015
Travel award, 8th International Purdue Symposium on Statistics	2012
Travel award, Department of Statistics, University of Florida - To attend the 53rd Drosophila Research Conference	2012
Outstanding poster award, University of Florida Annual Microbiology and Cell Science Undergraduate Research Symposium	2012
Mu Sigma Rho Honor Society, University of Florida	2012
Phi Beta Kappa Honor Society, University of Florida	2012
Anderson Scholar with Distinction, University of Florida	2010
Florida Academic Scholars Award, Florida Bright Futures Scholarship Program	2008 - 2012

PUBLICATIONS

Key: * indicates co-first authors; † indicates corresponding authors; trainees are underlined.

Pre-prints

Knight, P., Gauthier, M.-P.L., Pardo, C.E., Darst, R.P., Riva, A., Kladde, M.P., **Bacher, R**†. methylscaper: an R/Shiny app for joint visualization of DNA methylation and nucleosome occupancy in single-molecule and single-cell data. bioRxiv. (2020); <https://doi.org/10.1101/2020.11.13.382465>

Bacher R., Chu L.-F., Argus C., Bolin J.M., Knight P., Thomson J.A., Stewart, R., Kendziorski, C. Enhancing biological signals and detection rates in single-cell RNA-seq experiments with cDNA library equalization. bioRxiv. (2020); <https://doi.org/10.1101/2020.10.05.326553>

Brown, J., Ni, Z., Mohanty, C., **Bacher, R.**, Kendziorski, C. Normalization by distributional resampling of high throughput single-cell RNA-sequencing data. bioRxiv. (2020); <https://doi.org/10.1101/2020.10.28.359901>

Ogut, F., Newman, J.R.B., **Bacher, R.**, Concannon P.J., Verhoeven K.J.F., and McIntyre, L.M. Experimental design for large scale omic studies. bioRxiv. 532580, (2019).

Peer Reviewed Journal Articles

1. Darden, D.B., **Bacher, R.**, Brusko, M.A., Knight, P., Hawkins, R.B., Cox, M.C., Dirain, M.L., Ungaro, R., Nacionales, D.C., Rincon, J.C., Gauthier, M.-P.L., Kladde, M., Bihorac, A., Brusko, T.M., Moore, F.A., Brakenridge, S.C., Mohr, A.M., Moldawer, L.L., Efron, P.A. Single Cell RNA-SEQ of Human Myeloid Derived Suppressor Cells in Late Sepsis Reveals Multiple Subsets with Unique Transcriptional Responses: A Pilot Study. *Shock*. (2020).
2. Darden, D.B., Stortz, J.A., Hollen, M.K., Cox, M.C., Apple, C.G., Hawkins, R.B., Rincon, J.C., Lopez, M.-C., Wang, Z., Navarro, E., Hagen, J.E., Parvataneni, H.K., Brusko, M.A., Kladde, M., **Bacher, R.**, Brumback, B.A., Brakenridge, S.C., Baker, H.V., Cogle, C.R., Mohr, A.M., Efron, P.A. Identification of Unique mRNA and miRNA Expression Patterns in Bone Marrow Hematopoietic Stem and Progenitor Cells After Trauma in Older Adults. *Frontiers in Immunology*. (2020).
3. Motwani, K., Peters, L.D., Vliegen, W.H., El-sayed, A.G., Seay, H.R., Lopez, M.C., Baker, H.V., Posgai, A.L., Brusko, M.A., Perry, D.J., **Bacher, R.**, Larkin, J., Haller, M.J., Brusko, T.M. Human Regulatory T Cells From Umbilical Cord Blood Display Increased Repertoire Diversity and Lineage Stability Relative to Adult Peripheral Blood. *Frontiers in Immunology*. (2020).

4. Seirup, M., Chu, L.F., Sengupta, S., Leng, N., Browder, H., Kapadia, K., Shafer, C.M., Duffin, B., Elwell, A.L., Bolin, J.M., Swanson, S., Stewart, R., Kendzierski, C., Thomson, J.A., **Bacher, R.**†. Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis. *PLOS ONE*. 15(9): e0239711.(2020).
5. Shapiro, M.R., Wasserfall, C.H., McGrail, S.M., Posgai, A.L., **Bacher, R.**, Muir, A., Haller, M.J., Schatz, D.A., Wesley, J.D., von Herrath, M. and Hagopian, W.A., Speake, C., Atkinson, M.A., Brusko, T.M. Insulin-Like Growth Factor Dysregulation Both Preceding and Following Type 1 Diabetes Diagnosis. *Diabetes*. (2019).
6. Barry, C., Schmitz, M.T., Argus, C., Bolin, J.M., Probasco, M.D., Leng, N., Duffin, B., Steill, J., Swanson, S., McIntosh, B.E., Stewart, R., Kendzierski, C., Thomson, J.A., and **Bacher, R.**†. Automated minute scale RNA-seq of pluripotent stem cell differentiation reveals early divergence of human and mouse gene expression kinetics. *PLOS Computational Biology*. 15.12 (2019).
7. Chu, L.-F., Mamott, D., Ni Z., Thomson, **Bacher, R.**, Liu, C., Swanson, S., Kendzierski, C., Stewart, R.M., and Thomson, J.A. An in vitro human segmentation clock model derived from embryonic stem cells. *Cell Reports*. 28.9 (2019): 2247-2255.
8. **Bacher, R.***†, Leng, N.*, Chu, L.-F., Ni Z., Thomson, J.A., Kendzierski, C., and Stewart, R.M.†. Trendy: Segmented regression approach to reveal expression dynamics in high throughput profiling data with ordered conditions. *BMC Bioinformatics*. 19.1 (2018): 380.
9. Keller, M.P., Simecek, P., Schueler, K.L., Rabaglia, M.E., Stapleton, D.S., Broman, A.T., Gatti, D.M. Vincent, M., Allen, S., **Bacher, R.**, Kendzierski, K., Broman, K.W., Yandell, B.S., Churchill, G.A., Attie, A.D. Genetic drivers of pancreatic islet function. *Genetics*. genetics-300864, (2018).
10. Vermillion, K.L., **Bacher, R.**, Tannenbaum, A.P., Swanson, S., Jiang, P., Chu, L.F., Stewart, R.M., Thomson, J.A., Vereide, D.T. Spatial patterns of gene expression are unveiled in the chick primitive streak by ordering single-cell transcriptomes. *Developmental Biology*. 10.1016/j.ydbio.2018.04.007, (2018).
11. Gasch, A.P., Yu, B., Hose, J., Escalante, L., Place, M., **Bacher, R.**, Kanbar, J., Ciobanu, D., Sandor, L., Grigoriyev, I.V., Kendzierski, C., Quake, S., McClean, M. Single-cell RNA-seq reveals intrinsic and extrinsic regulatory heterogeneity in yeast responding to stress. *PLoS Biology* .15.12: e2004050 (2017).
12. **Bacher, R.***, Chu, L.-F.*†, Leng, N., Thomson, J.A., Gasch, A., Stewart, R.M., Newton, M., and Kendzierski, C. SCnorm: robust normalization of single-cell RNA-seq data. *Nature Methods* 14.6 (2017): 584-586.
 - Recommended by F1000Prime (f1000.com/727515021)
13. Barry, C., Schmitz, M.T., Jiang, P., Schwartz, M.P., Duffin, B.M., Swanson, S., **Bacher, R.**, Bolin, J.M, Elwell, A.L., McIntosh, B.E., Stewart, R., Thomson, J.A. Species-Specific Developmental Timing is Maintained by Pluripotent Stem Cells Ex Utero. *Developmental Biology*. 423, 101-110 (2017).
14. Fischer, B.L., **Bacher, R.**, Bendlin, B.B., Birdsill, A.C., Ly, M., Hoscheidt, S.M., Chappell, R.J., Mahoney, J.E., Gleason, C.E. An Examination of Brain Abnormalities and Mobility in Individuals with Mild Cognitive Impairment and Alzheimer’s Disease. *Frontiers in Aging Neuroscience*. 9, 86 (2017).
15. Ye, S., **Bacher, R.**, Keller, M.P., Attie, A.D., and Kendzierski, C. Statistical Methods for Latent Class Quantitative Trait Loci Mapping. *Genetics*. 206: 1309-1317 (2017).
16. **Bacher, R.** and Kendzierski, C. Design and computational analysis for single-cell RNA-sequencing experiments. *Genome Biology*. 17.1 (2016): 63.

Book Chapters

17. **Bacher, R.** Normalization for single-cell RNA-seq data analysis. In *Computational methods for single-cell data analysis*, Guo-Cheng Yuan (Ed.). Methods in Molecular Biology. DOI 10.1007/978-1-4939-9057-3, 2019.

SOFTWARE AND OPEN SCIENCE PACKAGES

Bioconductor software packages

1. SCnorm: An R/Bioconductor package to normalize single-cell RNA-seq data. 2,982 Unique IP downloads since August 2017.
Available at: <https://bioconductor.org/packages/devel/bioc/html/SCnorm.html>
2. Trendy: An R/Bioconductor package that implements breakpoint analysis on RNA-seq expression data with ordered conditions. The package also contains an R/Shiny application to interactively explore results from the Trendy package and extract gene patterns of interest. 923 Unique IP downloads since February 2018.
Available at: <https://bioconductor.org/packages/devel/bioc/html/Trendy.html>
3. methylscaper: an R/Shiny app for joint visualization of DNA methylation and nucleosome occupancy in single-molecule and single-cell data.
Available at: <https://github.com/rhondabacher/methylscaper>

Reproducible and open science repositories

4. LiverSpatialCompare: A Github repository containing scripts to reproduce the analysis comparing MARS-seq and Smart-seq protocols for reconstructing the zonation axis using cells from the liver lobule. The repository contains an R/Shiny application that interactively performs and presents visualization of KEGG pathway enrichments on the processed data.
Available at: <https://github.com/rhondabacher/LiverSpatialCompare>
5. RobotNeuralDiffPaper: A Github repository containing scripts to reproduce the analysis from the paper "Automated minute scale RNA-seq of pluripotent stem cell differentiation reveals early divergence of human and mouse gene expression kinetics." The repository contains all processed RData objects that can be uploaded to the Trendy Shiny application.
Available at: <https://github.com/rhondabacher/RobotNeuralDiffPaper>

PRESENTATIONS

Invited Presentations

1. "Design and Analysis of single-cell RNA-seq experiments." Animal Molecular and Cellular Biology. September 2020. University of Florida, Gainesville, FL, USA.
2. "Exploring gene expression dynamics in time-course RNA-seq experiments using the Trendy R package." Human Genetics and Genomics Program Seminar Series. March 2019. University of Colorado Denver, Denver, CO, USA.
3. "Single-cell RNA-seq data analysis: Design to Discovery." Diabetes Institute Seminar Series. February 2019. University of Florida, Gainesville, FL, USA.
4. "Analyzing expression dynamics for high-throughput ordered profiling experiments." Department of Physiology and Functional Genomics Seminar Series. August 2018. University of Florida, Gainesville, FL, USA.
5. "Single-cell RNA-seq technologies, quality control, and normalization." Genentech Invited Seminar. August 2018. San Francisco, CA, USA.
6. "Statistical Methods for Single Cell RNA Sequencing Data." Department of Statistics Seminar Series. April 2018. University of Florida, Gainesville, FL, USA.

Invited Conference Presentations

7. "Single-cell RNA-seq data analysis: Design to Discovery" Southeastern Association of Shared Resources Annual Meeting. June 2019. Atlanta, GA, USA.

8. *"SCnorm: A quantile-regression based approach for normalization of single-cell RNA-seq data"* International Chinese Statistical Association Applied Statistics Symposium. June 2019. Raleigh, NC, USA.
9. *"Characterizing Technical Artifacts in Single-Cell RNA-Seq Data Using A Data Generation Simulation Framework"* International Biometric Society Eastern North American Region (ENAR) Annual Meeting. March 2019. Philadelphia, PA, USA.
10. *"SCnorm: A quantile-regression based approach for normalization of single-cell RNA-seq data"* International Conference on Advances in Interdisciplinary Statistics and Combinatorics. October 2018. Greensboro, NC, USA.
11. *"Trendy: Segmented regression analysis of expression dynamics in high-throughput ordered profiling experiments"* Southern Regional Council on Statistics Conference. June 2018. Virginia Beach, VA, USA.
12. *"SCnorm: A quantile-regression based approach for normalization of single-cell RNA-seq data"* International Indian Statistical Association Conference. May 2018. Gainesville, FL, USA.
13. *"SCnorm: A quantile-regression based approach for robust normalization of single-cell RNA-seq data"* International Chinese Statistical Association - Symposium on Single Cell Sequencing. June 2017. Chicago, IL, USA.

Other Invited Meetings

14. *normjam: A normalization workshop and jamboree for scRNA-seq data*
Two-day workshop organized and hosted by the New York Genome Center and the Chan Zuckerberg Initiative to discuss challenges and solutions to normalize scRNA-seq data. November 2019. New York City, NY, USA.
15. *Data Science Innovation Lab: Mathematical Challenges of Single Cell Dynamics*
Five-day workshop organized by the NIH BD2K Training Coordinating Center to facilitate collaboration between early-career biomedical and quantitative investigators to tackle the technology and mathematical challenges of single cell data. June 2018. Bend, OR, USA.

Contributed Presentations

16. *"Assumptions and methods for normalizing single-cell RNA-seq data"* Joint Statistical Meetings. Invited to contribute. August 2019. Denver, CO, USA.
17. *"Data generation based simulation framework for single-cell RNA-Seq data"* Joint Statistical Meetings. Invited to contribute. August 2018. Vancouver, BC, Canada.
18. *"Trendy: Segmented regression analysis of expression dynamics for high-throughput ordered profiling experiments"* International Biometric Society Eastern North American Region (ENAR) Annual Meeting. March 2018. Atlanta, GA, USA.
19. *"SCnorm: robust normalization of single-cell RNA-seq data"* Symposium on Advances in Genomics, Epidemiology, and Statistics Annual Meeting. Contributed poster. June 2017. Philadelphia, PA, USA.
20. *"Normalization of single cell RNA-sequencing data"* International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Contributed poster. March 2016. Austin, TX, USA.
21. *"Normalization of single cell RNA-sequencing data"* Program in Quantitative Genomics (PQG) Conference. Contributed poster. November 2015. Boston, MA, USA.
22. *"Normalization of single cell RNA-sequencing data"* Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine (iBRIGHT) Conference. Contributed poster. October 2015. Houston, TX, USA.
23. *"Challenges in single cell RNA-seq experiments"* International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Contributed poster. March 2015. Miami, FL, USA.

TEACHING

University Courses

1. Instructor, PHC 6937 / PHC 6088 - Statistical Analysis of Genetic Data Spring 2018, 2019, 2020
Department of Biostatistics, University of Florida
2. Guest Instructor, Lectures on Statistical Genomics for PHC 6937 - Frontiers in Biostatistics Spring 2019
Department of Biostatistics, University of Florida
3. Teaching Assistant, STAT 877 - Statistical Methods for Molecular Biology Spring 2017
Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison

Educational Outreach

4. Co-Instructor, Tutorial on *“Recent Advances in Statistical Methods and Computational Algorithms for Single-Cell Omics Analysis.”* July 2019
 - At the International Society for Computational Biology Conference - the largest and most high profile annual meeting of scientists working in computational biology. Basel, Switzerland.
5. Guest Instructor, Lecture on *“Normalization of single-cell RNA-seq data.”* March 2019; September 2020
 - BIOS 785 - Statistical Methods for Gene Expression Analysis. Department of Biostatistics, University of North Carolina, Raleigh, NC, USA.
6. Co-Instructor, Short Course on *“Statistical methods for single-cell RNA-seq analysis.”* August 2018
 - At the Joint Statistical Meetings - the largest gathering of statisticians held in North America. Vancouver, BC, Canada.

ADVISING

Ph.D. Committees

- Ph.D. Committee Member for Angeles Arzalluz Luque 2019-
(Bioinformatics at Centro de Investigación Príncipe Felipe, Valencia, Spain)
- (External) Ph.D. Committee Member for Leeana Peters 2019-
(Immunology and Microbiology at University of Florida)
- Ph.D. Committee Member for Rodrigo Rampazo Amadeu 2019-
(Horticultural Sciences at University of Florida)
- (External) Ph.D. Committee Member for Adalena Nanni 2019-
(Genetics and Genomics at University of Florida)
- (External) Ph.D. Committee Member for Puchong Thirawatananond 2020-
(Immunology and Microbiology at University of Florida)

M.S. Committees

- Supervisor for Mengmeng Li Spring 2018
(Biostatistics at University of Florida)
- Supervisor for Dain Chun 2018-2020
(Biostatistics at University of Florida)

M.P.H. Committees

- Supervisor for Shuzheng Li UF Biostatistics, Spring 2019

Academic Advising

- Natalie DelRocco UF Biostatistics, 2018-2019

SERVICE

UF Service

Member, Scientific Review and Monitoring Committee (SRMC) May 2018 - present
University of Florida Health Cancer Center

Chair, Seminar Committee May 2018 - 2020
Department of Biostatistics

Service in Statistics (Nationally)

Reviewer, NSF December 2020
Ad hoc NSF reviewer for grant proposal in the Methodology, Measurement, and Statistics Program.

Reviewer, NSF December 2019
NSF panel reviewer for grant proposals on statistical methods.

Session Organizer, ENAR Annual Meeting March 2020
"Recent Advances and Opportunities in Large Scale & Multi-Omic Single-Cell Data Analysis" in Nashville, TN.

Session Chair, ENAR Annual Meeting March 2019
For ASA Statistics in Genomics and Genetics Section on "Methods to Robustly Incorporate External Data Into Genetic Tests" in Philadelphia, PA.

Session Chair, JSM Annual Meeting July 2018
For Biometrics Section - Contributed Papers on "Categorical Data" in Vancouver, BC, Canada.

Session Chair, ENAR Annual Meeting March 2018
For Contributed Papers on "Methods For RNA-Seq Data" in Atlanta, GA.

Chair, Council for Emerging and New Statisticians May 2017 - 2018
Standing committee of twelve members of ENAR's Regional Advisory Board.

Member, Council for Emerging and New Statisticians May 2015 - May 2017
Standing committee of twelve members of ENAR's Regional Advisory Board.

Session Chair, ENAR Annual Meeting March 2016
For Contributed Papers on "Bayesian Causal Inference" in Austin, TX.

Service in Statistics (Locally)

Information Officer, Florida Chapter of the American Statistical Association February 2019 - present

Organizer, Weekly Student Seminar Spring 2015
Department of Statistics, University of Wisconsin-Madison

Member, Statistics Social Committee Fall 2014 - Spring 2015
Department of Statistics, University of Wisconsin-Madison

Organizer, Weekly Statistical Genetics Student Reading Group Fall 2014
Department of Biostatistics, University of Wisconsin-Madison

Cofounder, Statistics Club Fall 2011 - Spring 2012
University of Florida

PROFESSIONAL SOCIETY MEMBERSHIPS

International Biometric Society (ENAR), American Statistical Association (ASA), Genetics Society of America (GSA)

JOURNAL REFEREE

Bioinformatics, Biometrics, Journal of the American Statistical Association, GigaScience, Genome Biology, Genome Research, Molecular Biology and Evolution, Nature Methods, Nature Communications, Nucleic Acids Research, PLOS Computational Biology, Scientific Data

GRANT SUPPORT

Current

NIH UG3DK122638 (Stabler Anderson) 8/1/19- 7/31/24
NIH/NIDDK

Engineering a Human Microphysiological System for the Characterization of Islet-Immune Interactions. Create an integrated three dimensional microphysiological systems platform to more accurately model the complex cellular interactions involved in human type 1 diabetes (T1D) pathogenesis.

Role: Co-Investigator

P01AI042288 (Atkinson) 06/30/2018 - 05/31/23
NIH/NIAID

Immune Function and the Progression to Type 1 Diabetes.

The purpose of this research study is to learn more about the genetics and immune function of blood cells, and viruses in insulin dependent diabetes.

Role: Co-Investigator for Core B

2P30AG028740 (Pahor) 04/01/2018 - 03/31/22
NIH/NIA

Claude D. Pepper Older Americans Independence Center (OAIC)

The mission of the University of Florida Older Americans Independence Center (OAIC) is twofold: 1) to optimize older persons physical performance and mobility through interdisciplinary approaches; and 2) to train new investigators in aging and disability research while developing their leadership qualities. Our goal is to enhance late-life health and independence, with a special focus on mobility.

Role: Co-Investigator

Previous

Award (Bacher, Hendricks, Lopez) 08/15/2018 - 08/14/19

The Jayne Koskinas Ted Giovanis Foundation (\$15,000)

Uncovering the Life Clock of Red Blood Cells Using Single-Cell Analysis.

Role: Principle Investigator (multi-PI with Audrey Hendricks and Javier Lopez)

1-SRA-2019-764-A-N (Wasserfall) 4/1/19 - 3/31/20
JDRF

A Composite Serological Risk Score to Predict Type 1 Diabetes Progression and Clinical Diagnosis.

Develop a combined serological risk score (SRS) that, together with our existing genetic risk score (GRS) model, can aid in the prediction of T1D progression and clinical diagnosis.

Role: Co-Investigator

3-SRA-2019-793-S-B (Brusko) 6/1/19 - 5/31/20
JDRF

Single cell sequencing for islet-reactive T cell clonotype and transcript signatures.

Detect and characterize T cell biomarkers of type 1 diabetes (T1D) from human peripheral blood samples obtained from Stage 4 established T1D patients with biomarker cross-validation from human pancreas, pancreatic draining lymph nodes, and spleen.

Role: Co-Investigator