

# CURRICULUM VITAE

Rhonda Bacher, PhD

## CONTACT

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## EDUCATION

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- 2012 - 2017      **Ph.D., Statistics**, University of Wisconsin-Madison, Madison, Wisconsin, USA  
Emphasis in Biostatistics  
*Advisor: Christina Kendzioriski, Ph.D.*  
*Dissertation: Statistical Methods for RNA-Sequencing Data*
- 2008 - 2012      **B.S., Statistics**, University of Florida, Gainesville, FL, USA  
*Magna cum laude, College of Agriculture and Life Sciences Honors Scholar*  
**B.S., Mathematics**, University of Florida, Gainesville, FL, USA  
*Cum laude, Phi Beta Kappa*

## PROFESSIONAL POSITIONS

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### Primary

- 2024 - present      Associate Professor, Department of Biostatistics, College of Public Health and Health Professions and College of Medicine, University of Florida.
- 2018 - 2024      Assistant Professor, Department of Biostatistics, College of Public Health and Health Professions and College of Medicine, University of Florida.

### Other Roles

- 2025 - present      Assistant Director of Data Science, Diabetes Institute, University of Florida.
- 2024 - present      Affiliate Associate Professor, Department of Molecular Genetics and Microbiology, College of Medicine, University of Florida.
- 2022 - present      Preceptor, NIH T32 Training Program in Type 1 Diabetes and Biomedical Engineering, University of Florida.
- 2021 - 2022      Leader, Data Management and Biostatistics Core, University of Florida Sepsis and Critical Illness Research Center.
- 2019 - 2022      Unit Leader for Statistical Genomics, Biostatistics & Computational Biology Shared Resource, University of Florida Health Cancer Center.
- 2019 - present      Faculty Member, Division of Quantitative Sciences, UF Health Cancer Center.
- 2018 - present      Faculty Member, UF Health Cancer Institute.
- 2018 - present      Faculty Member, UF Diabetes Institute.

2018 - present	Faculty Member, UF Genetics Institute.
<b>Previous</b>	
2017 - 2018	Postdoctoral Research Fellow, Center for Predictive Computational Phenotyping, University of Wisconsin-Madison.
2016 - 2017	Bio-Data Science Trainee, NIH T32 NLM, Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison.
2015 - 2016	Research Assistant, Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison.
2012 - 2015	Biostatistics Trainee, NIH T32 NHLBI, Department of Biostatistics and Medical Informatics, University of Wisconsin-Madison.

## HONORS AND AWARDS

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2023	Keynote lecture, Annual Retreat for the Computation and Informatics in Biology and Medicine Training Program, University of Wisconsin-Madison.
2022	Research grant, Maximizing Investigators' Research Award (MIRA), NIH National Institute of General Medical Sciences.
2022	Professional development grant, UF Faculty Enhancement Award.
2018	Travel award, selected to attend the NIH Data Science Innovation Lab (NIH BD2K).
2017	Outstanding poster award, Symposium on Advances in Genomics, Epidemiology and Statistics.
2015	Travel award, Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine Conference.
2012	Travel award, 8th International Purdue Symposium on Statistics.
2012	Travel award, from the Department of Statistics at the 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.
2010	Anderson Scholar with Distinction, University of Florida.
2008-2012	Florida Academic Scholars Award, Florida Bright Futures Scholarship Program.

## PUBLICATIONS

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Key: \* indicates mentored students; † indicates co-first authors; ‡ indicates co-corresponding authors  
 ◆ indicates first or corresponding author manuscripts

### Peer Reviewed Journal Articles

1. Leary JR<sup>\*</sup>, Dong X<sup>\*</sup>, and **Bacher R**<sup>◆</sup>. Interpretable trajectory inference with single-cell Linear Adaptive Negative-binomial Expression (scLANE) testing. *Nucleic Acids Research*, 54(2), p.gkaf1494, (2026). [Google Scholar citations: 2].

2. Sharp RC, **Bacher R**, Brown ME, Peters LD, Jacobsen LM, Brusko TM. Type 1 diabetes SIRPG risk variants increase SIRP $\gamma$  expression and CD47 loss enhances CD8+ T cell cytotoxicity. *npj Autoimmunity*, (2026). In press.
3. Kim C, Zhu Z\*, Tagmount A, Barbazuk WB, **Bacher R**, Stuchal LD, Martyniuk CJ, Vulpe CD. Characterizing common loss-of-function genes and their potential utility in assessing population variability and chemical susceptibility. *NAM Journal*, 2, p.100103, (2025). [Google Scholar citations: 1].
4. Medina-Serpas MA, Brusko M, Golden GJ, Campbell-Thompson M, Rogers T, Reardon S\*, Posgai AL, **Bacher R**, Luning Prak ET, Liu C, Kaestner KH, Naji A, Betts MR, McIntyre LM, Atkinson MA, Brusko TM. Spatial transcriptomics from pancreas and local draining lymph node tissue reveals a lymphotoxin- signature in human type 1 diabetes. *Cell Reports*, 45(4), p.117144, 2026. [Google Scholar citations: 2].
5. Kim C, Zhu Z\*, Tagmount A, Barbazuk WB, **Bacher R**, Vulpe CD. Physiologically relevant 3D CRISPR screening enhances mechanistic insight into chemical toxicity compared to 2D screening. *Toxicology*, 522, p.154422, (2026). [Google Scholar citations: 2].
6. Kim C, Tagmount A, Zhu Z\*, Wilson F, Li D, Ostrov DA, Barbazuk BW, **Bacher R**, Vulpe CD. Identification of functional genetic components modulating toxicity response to PFOS using genome-wide CRISPR screens in HepG2/C3A cells. *Archives of toxicology*, doi: 10.1007/s00204-025-04294-8. Online ahead of print, (2026). [Google Scholar citations: 1].
7. Kim HG, Gauthier MPL, Higgs A, Hernandez DA, Zhou M, Brant JO, **Bacher RL**, Darden DB, Wallet SM, Mathews CE, Moldawer LL, Efron PA, Kladde MP, Maile R. Chromatin remodeling and transcriptional silencing define the dynamic innate immune response of tissue resident macrophages after burn injury. *Shock*, 65(3), pp.538–550, (2026). [Google Scholar citations: 3].
8. Charles AM, Rodhouse CE, Darden DB, Gauthier MPL, Zhou M, Hernandez-Rios M, Wang D, Casadesus G, Bible L, Mohr AM, Xiao F, Cai G, Brant JO, Wallet SM, Mathews CE, Moldawer LL, Chakrabarty P, **Bacher RL**, Efron PA, Maile R, Kladde MP. A Murine Model of Sepsis Induces Age-and Sex-Specific Chromatin Remodeling in Myeloid-Derived Suppressor Cells. *Frontiers in Immunology*, 17, p.1750174, (2026). [Google Scholar citations: 0].
9. Drotar DM, Vazquez Ramos GJA, Williams MD, David ST, Luce C, Smith JA, Posgai AL, **Bacher R**, Campbell-Thompson M, Kusmartseva I, Brusko MA, Atkinson MA, Wasserfall CH. Loss of Insulin-Positive Cell Clusters Precedes the Decrease in Islet Frequency and  $\beta$ -Cell Area in Type 1 Diabetes. *Diabetes*, 74(11), pp.2008-2015, (2025). [Google Scholar citations: 11].
10. Brown ME, Thirawatananond P, Peters LD, Kern EJ, Vijay S, Sachs LK, Posgai AL, Brusko MA, Shapiro MR, Mathews CE, **Bacher R**, Brusko TM. Inhibition of CD226 co-stimulation suppresses diabetes development in the NOD mouse by augmenting regulatory T cells and diminishing effector T cell function. *Diabetologia*, 68(2), pp.397-418, (2025). [Google Scholar citations: 9].
11. Williams MD, Grace CR, Posgai AL, McGrail KM, Brusko MA, Haller MJ, Jacobsen LM, Schatz DA, Brusko TM, Atkinson MA, **Bacher R**<sup>‡</sup>, Wasserfall CH<sup>‡</sup>. Serological markers of exocrine pancreatic function are differentially informative for distinguishing individuals progressing to type 1 diabetes. *BMJ Open Diabetes Research and Care*, 13(1), p.e004655, (2025). [Google Scholar citations: 0].
12. Dong X\*, Leary J\*, Yang C\*, Brusko MA, Brusko TM, **Bacher R**<sup>★</sup>. Data-driven selection of analysis decisions in single-cell RNA-seq trajectory inference. *Briefings in Bioinformatics*, 25(3), p.bbae216, (2024). [Google Scholar citations: 9].
13. Kim C, Zhu Z\*, Barbazuk BW, **Bacher R**, Vulpe CD. Time-course characterization of whole-transcriptome dynamics of HepG2/C3A spheroids and its toxicological implications. *Toxicology Letters*, 401, pp.125-138, (2024). [Google Scholar citations: 64].

14. Bruggeman BS, Gornisiewicz S, **Bacher R**, McGrail K, Campbell-Thompson M, Wasserfall C, Jacobsen LM, Atkinson M, Haller MJ, Schatz DA. Serum exocrine pancreas enzymes are biomarkers of immunotherapy response in new-onset type 1 diabetes. *Frontiers in Endocrinology*, 15, p.1497373, (2024). [Google Scholar citations: 1].
15. Barrios EL, Leary J<sup>\*</sup>, Darden DB, Rincon JC, Willis M, Polcz VE, Gillies GS, Munley JA, Dirain ML, Ungaro R, Nacionales DC, Gauthier M-PL, Larson SD, Morel L, Loftus TJ, Mohr AM, Maile R, Kladde MP, Mathews CE, Brusko MA, Brusko TM, Moldawer LL, **Bacher R**<sup>‡♦</sup>, Efron PA<sup>‡</sup>. The post-septic peripheral myeloid compartment reveals unexpected diversity in myeloid-derived suppressor cells. *Frontiers in Immunology*, 15, p.1355405, (2024). [Google Scholar citations: 13].
16. Zeidan R, Ohama MK, Evripidou N, Anton SD, Hamed LL, Lin Y, Leeuwenburgh C, Guirguis FW, Efron PA, Flynn S, Smith B, Bacher R, Bakarasan N, Delgado JS, Mankowski RT. Home-based digital exercise training program to improve physical function of older sepsis survivors - Protocol of the HEAL Sepsis Trial. Accepted at *JMIR Research Protocols*, (2024). [Google Scholar citations: 1].
17. Barrios EL, Balzano-Nogueira L, Polcz VE, Rodhouse C, Leary JR, Darden DB, Rincon JC, Dirain ML, Ungaro R, Nacionales DC, Larson SD, Sharma A, Upchurch G, Wallet SM, Brusko TM, Loftus TJ, Mohr AM, Maile R, **Bacher R**, Cai G, Efron PA. Unique lymphocyte transcriptomic profiles in septic patients with chronic critical illness. *Frontiers in Immunology*, 15, p1478471, (2024). [Google Scholar citations: 4]
18. Shapiro MR<sup>†</sup>, Dong Z<sup>†\*</sup>, Perry D<sup>†</sup>, McNichols JM, Thirawatananond P, Posgai AL, Peters L, Motwani K, Musca RS, Muir A, Concannon P, Jacobsen LM, Mathews CE, Wasserfall CH, Haller MJ, Schatz DA, Atkinson MA, Brusko MA, **Bacher R**<sup>‡♦</sup>, and Brusko TM<sup>‡</sup>. Human immune phenotyping reveals accelerated aging in type 1 diabetes. *JCI insight*, 8(17), (2023). [PMCID: PMC10544250. Google Scholar citations: 32].
19. Motwani K, **Bacher R**, Molstad AJ. Binned multinomial logistic regression for integrative cell type annotation. *The Annals of Applied Statistics*, 17(4), pp.3426-3449, (2023). [Google Scholar citations: 4].
20. Jacobsen, LM, Diggins, K, Blanchfield, L, McNichols, J, Perry, DJ, Brant, J, Dong, X<sup>\*</sup>, **Bacher, R**, Gersuk, VH, Schatz, DA, Atkinson, MA, Mathews, CE, Haller, MJ, Long, SA, Linsley, PS, Brusko, TM. Responders to low-dose ATG induce CD4 T cell exhaustion in type 1 diabetes *JCI Insight*, (2022). [PMCID: PMC10543726. Google Scholar citations: 41].
21. Marshall GP, Cserny J, Wang CW, Looney B, Posgai AL, **Bacher R**, Brusko TM. Biomaterials based nanoparticles conjugated to regulatory T cells provide a modular system for localized delivery of pharmacotherapeutic agents. *Journal of Biomedical Materials Research Part A*, 111(2), pp.185-197, (2023). [PMCID: PMC9742177. Google Scholar citations: 15].
22. Barrios EL, Rincon JC, Willis M, Polcz VE, Leary J<sup>\*</sup>, Darden DB, Balch JA, Larson SD, Loftus TJ, Mohr AM, Wallet S, Brusko MA, Balzano-Nogueira L, Cai G, Sharma A, Upchurch GR Jr, Kladde MP, Mathews CE, Maile R, Moldawer LL, **Bacher R**, Efron PA. Transcriptomic Differences in Peripheral Monocyte Populations in Septic Patients Based on Outcome. *Shock*, 62(2), pp.208-216, (2024). [PMID: 38713581. Google Scholar citations: 7].
23. **Bacher R**<sup>‡♦</sup>, Chu LF, Argus C, Bolin JM, Knight P<sup>\*</sup>, Thomson JA, Stewart R, Kendzierski C<sup>‡</sup>. Enhancing biological signals and detection rates in single-cell RNA-seq experiments with cDNA library equalization. *Nucleic Acids Research*, 50(2), e12, (2022). [PMCID: PMC8789062. Google Scholar citations: 9].
24. Brakenridge SC, Chen UI, Loftus T, Ungaro R, Dirain M, Kerr A, Zhong L<sup>\*</sup>, **Bacher R**, Starostik P, Ghita G, Midic U, Darden D, Fenner B, Wacker J, Efron PA, Liesenfeld O, Sweeney TE, Moldawer LL.

- Evaluation of a multivalent transcriptomic metric for diagnosing surgical sepsis and estimating mortality among critically ill patients. *JAMA Network Open*, 5(7), e2221520, (2022). [PMCID: PMC9277492. Google Scholar citations: 24].
25. Knight P\*, Gauthier MPL, Pardo CE, Darst RP, Kapadia K\*, Browder H\*, Morton, E\*, Riva A, Kladde MP, **Bacher R**<sup>†</sup>. Methylscaper: an R/Shiny app for joint visualization of DNA methylation and nucleosome occupancy in single-molecule and single-cell data. *Bioinformatics*, 37(24), pp.4857-4859, (2021). [PMCID: PMC8665741. Google Scholar citations: 10].
  26. Japp AS, Meng W, Rosenfeld AM, Perry DJ, Thirawatananond P, **Bacher R**, Liu C, Gardner JS, Atkinson MA, Kaestner KH, Brusko TM, Najj A, Luning Prak ET, Betts MR. TCR+/BCR+ dual-expressing cells and their associated public BCR clonotype are not enriched in type 1 diabetes. *Cell*, 184(3), pp.827-839, (2021). [PMCID: PMC8016147. Google Scholar citations: 28].
  27. Kim MC, Borcharding N, Ahmed KK, Voigt AP, Vishwakarma A, Kolb R, Kluz PN, Pandey G, De U, Drashansky T, Helm EY, Zhang X, Gibson-Corley KN, Klesney-Tait J, Zhu Y, Lu J, Lu, J, Huang X, Xiang H, Cheng J, Wang D, Wang Z, Tang J, Hu J, Wang Z, Liu H, Li M, Zhuang H, Avram D, Zhou D, **Bacher R**, Zheng SG, Wu X, Zakharia Y, Zhang W. CD177 modulates the function and homeostasis of tumor-infiltrating regulatory T cells. *Nature Communications*, 12(1), pp.1-13, (2021). [PMCID: PMC8486774. Google Scholar citations: 98].
  28. Brown J, Ni Z, Mohanty C, **Bacher R**, Kendzioriski C. Normalization by distributional resampling of high throughput single-cell RNA-sequencing data. *Bioinformatics*, 37(22), pp.4123-4128, (2021). [PMCID: PMC9502161. Google Scholar citations: 23].
  29. Simonett SP, Shin S, Herring JA, **Bacher R**, Smith LA, Dong C, Rabaglia ME, Stapleton DS, Schueler KL, Choi J, Bernstein MN, Turkewitz DR, Perez-Cervantes C, Spaeth J, Stein R, Tessem JS, Kendzioriski C, Keles S, Moskowitz IP, Keller MP, Attie AD. Identification of direct transcriptional targets of NFATC2 that promote  $\beta$  cell proliferation. *The Journal of Clinical Investigation*, 131(21), e144833, (2021). [PMCID: PMC8553569. Google Scholar citations: 25].
  30. Darden DB, Dong X\*, Brusko MA, Kelly L, Fenner B, Rincon JC, Dirain ML, Ungaro R, Nacionales DC, Gauthier M, Kladde M, Brusko TM, Bihorac A, Moore FA, Loftus T, **Bacher R**, Moldawer LL, Mohr AM, Efron, PA. A novel single cell RNA-seq analysis of non-myeloid circulating cells in late sepsis. *Frontiers in Immunology*, 12, 696536, (2021). [PMCID: PMC8415415. Google Scholar citations: 63].
  31. Ross JJ, Wasserfall CH, **Bacher R**, Perry DJ, McGrail K, Posgai AL, Dong X\*, Muir A, Li X, Campbell-Thompson M, Brusko TM, Schatz, DA, Haller, MJ, Atkinson, MA. Exocrine pancreatic enzymes are a serological biomarker for type 1 diabetes staging and pancreas size. *Diabetes*, 70(4), pp.944-954, (2021). [PMCID: PMC7980193. Google Scholar citations: 54].
  32. Williams MD, **Bacher R**, Perry DJ, Grace CR, McGrail KM, Posgai AL, Muir A, Chamala S, Haller MJ, Schatz DA, Brusko TM, Atkinson MA, Wasserfall CH. Genetic composition and autoantibody titers model the probability of detecting c-peptide following type 1 diabetes diagnosis. *Diabetes*, 70(4), pp.932-943, (2021). [PMCID: PMC7980194. Google Scholar citations: 28].
  33. Darden DB, **Bacher R**, Brusko MA, Knight P\*, Hawkins RB, Cox MC, Dirain ML, Ungaro R, Nacionales DC, Rincon JC, Gauthier M-PL, Kladde M, Bihorac A, Brusko TM, Moore FA, Brakenridge SC, Mohr AM, Moldawer LL, Efron PA. Single-cell RNA-seq of human myeloid derived suppressor cells in late sepsis reveals multiple subsets with unique transcriptional responses: a pilot study. *Shock*, 55(5), pp.587-595, (2021). [PMCID: PMC8019679. Google Scholar citations: 69].
  34. Darden DB, Ghita GL, Wang Z, Stortz JA, Lopez MC, Cox MC, Hawkins RB, Rincon JC, Kelly LS, Fenner BP, Ozrazgat-Baslanti T, Leeuwenburgh C, Bihorac A, Loftus TJ, Moore FA, Brakenridge SC, Baker HV, **Bacher R**, Mohr AM, Moldawer LL, Efron PA. Chronic critical illness elicits a unique

- circulating leukocyte transcriptome in sepsis survivors. *Journal of Clinical Medicine*, 10(15), 3211, (2021). [PMCID: PMC8348105. Google Scholar citations: 13].
35. Loftus TJ, Ungaro R, Dirain M, Efron PA, Mazer MB, Remy KE, Hotchkiss RS, Zhong L<sup>\*</sup>, **Bacher R**, Starostik P, Moldawer LL, Brakenridge SC. Overlapping but disparate inflammatory and immunosuppressive responses to SARS-CoV-2 and bacterial sepsis: an immunological time course analysis. *Frontiers in Immunology*, 12, 792448, (2021). [PMCID: PMC8696010. Google Scholar citations: 38].
  36. Seirup M<sup>†</sup>, Chu LF, Sengupta S, Leng N, Browder H<sup>\*</sup>, Kapadia K<sup>\*</sup>, Shafer CM, Duffin B, Elwell AL, Bolin JM, Swanson S, Stewart R, Kendzierski C, Thomson JA<sup>‡</sup>, **Bacher R**<sup>‡♦</sup>. Reproducibility across single-cell RNA-seq protocols for spatial ordering analysis. *PLOS ONE*, 15(9), e0239711, (2020). [PMCID: PMC7521718. Google Scholar citations: 9].
  37. Motwani K<sup>†</sup>, Peters LD<sup>†</sup>, Vliegen WH, El-sayed AG, Seay HR, Lopez MC, Baker HV, Posgai AL, Brusko MA, Perry DJ, **Bacher R**, Larkin J, Haller MJ, Brusko TM. Human regulatory T cells from umbilical cord blood display increased repertoire diversity and lineage stability relative to adult peripheral blood. *Frontiers in Immunology*, 11, 611, (2020). [PMCID: PMC7174770. Google Scholar citations: 56].
  38. Shapiro MR, Wasserfall CH, McGrail SM, Posgai AL, **Bacher R**, Muir A, Haller MJ, Schatz DA, Wesley JD, von Herrath M, Hagopian WA, Speake C, Atkinson MA, Brusko TM. Insulin-like growth factor dysregulation both preceding and following type 1 diabetes diagnosis. *Diabetes*, 69(3), pp.413-423, (2020). [PMCID: PMC7034187. Google Scholar citations: 55].
  39. Darden DB, Stortz JA, Hollen MK, Cox MC, Apple CG, Hawkins RB, Rincon JC, Lopez MC, Wang Z, Navarro E, Hagen JE, Parvataneni HK, Brusko MA, Kladde M, **Bacher R**, Brumback BA, Brakenridge SC, Baker HV, Cogle CR, Mohr AM, Efron PA. Identification of Unique mRNA and miRNA Expression Patterns in Bone Marrow Hematopoietic Stem and Progenitor Cells After Trauma in Older Adults. *Frontiers in Immunology*, 11, 1289, (2020). [PMCID: PMC7326804. Google Scholar citations: 13].
  40. Barry C<sup>‡</sup>, Schmitz MT, Argus C, Bolin JM, Probasco MD, Leng N, Duffin B, Steill J, Swanson S, McIntosh BE, Stewart R, Kendzierski C, Thomson JA, **Bacher R**<sup>‡♦</sup>. 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), e1007543, (2019). [PMCID: PMC6922475. Google Scholar citations: 14].
  41. Chu LF, Mamott D, Ni Z, **Bacher R**, Liu C, Swanson S, Kendzierski C, Stewart RM, Thomson JA. An in vitro human segmentation clock model derived from embryonic stem cells. *Cell Reports*, 28(9), pp.2247-2255, (2019). [PMCID: PMC6814198. Google Scholar citations: 76].
  42. **Bacher R**<sup>‡♦</sup>, Leng N<sup>†</sup>, Chu LF, Ni Z, Thomson JA, Kendzierski C, Stewart RM<sup>†</sup>. Trendy: segmented regression analysis of expression dynamics in high throughput ordered profiling experiments. *BMC Bioinformatics*, 119(1), 380, (2018). [PMCID: PMC6192113. Google Scholar citations: 41].
  43. Keller MP, Gatti DM, Schueler KL, Rabaglia ME, Stapleton DS, Simecek P, Vincent M, Allen S, Broman AT, **Bacher R**, Kendzierski C, Broman KW, Yandell BS, Churchill GA, Attie AD. Genetic drivers of pancreatic islet function. *Genetics*, 209(1), pp.335-356, (2018). [PMCID: PMC5937189. Google Scholar citations: 86].
  44. Vermillion KL, **Bacher R**, Tannenbaum AP, Swanson S, Jiang P, Chu LF, Stewart RM, Thomson JA, Vereide DT. Spatial patterns of gene expression are unveiled in the chick primitive streak by ordering single-cell transcriptomes. *Developmental Biology*, 439(1), pp.30-41, (2018). [PMID: 29678445. Google Scholar citations: 13].
  45. **Bacher R**<sup>‡♦</sup>, Chu LF<sup>†</sup>, Leng N, Thomson JA, Gasch A, Stewart RM, Newton M, Kendzierski C. SCnorm: robust normalization of single-cell RNA-seq data. *Nature Methods*, 14(6), pp.584-586, (2017).

[PMCID: PMC5473255. Google Scholar citations: 353].

- Recommended on [F1000Prime](#) (now Faculty Opinions)

- Barry C, Schmitz MT, Jiang P, Schwartz MP, Duffin BM, Swanson S, **Bacher R**, Bolin JM, Elwell AL, McIntosh BE, Stewart R, Thomson JA. Species-specific developmental timing is maintained by pluripotent stem cells ex utero. *Developmental Biology*, 423(2), pp.101-110, (2017). [PMCID: PMC5384572. Google Scholar citations: 68].
- Gasch AP<sup>†</sup>, Yu FB<sup>†</sup>, Hose J, Escalante LE, Place M, **Bacher R**, Kanbar J, Ciobanu D, Sandor L, Grigoriyev IV, Kendzierski C, Quake SR, McClean MN. Single-cell RNA-seq reveals intrinsic and extrinsic regulatory heterogeneity in yeast responding to stress. *PLoS Biology*, 15(12), e2004050, (2017). [PMCID: PMC5746276. Google Scholar citations: 179].
- Fischer BL, **Bacher R**, Bendlin BB, Birdsill AC, Ly M, Hoscheidt SM, Chappell RJ, Mahoney JE, Gleason CE. An examination of brain abnormalities and mobility in individuals with mild cognitive impairment and Alzheimer's disease. *Frontiers in Aging Neuroscience*, 9, 86, (2017). [PMCID: PMC5380746. Google Scholar citations: 7].
- Ye S, **Bacher R**, Keller MP, Attie AD, Kendzierski C. Statistical Methods for Latent Class Quantitative Trait Loci Mapping. *Genetics*, 206(3), pp. 1309-1317, (2017). [PMCID: PMC5500132. Google Scholar citations: 0].
- Bacher R**<sup>★</sup> and Kendzierski C. Design and computational analysis of single-cell RNA-sequencing experiments. *Genome Biology*, 17(1), pp.1-14, (2016). [PMCID: PMC4823857. Google Scholar citations: 575].

## Book Chapters

- Dong X<sup>\*</sup> and **Bacher R**<sup>★</sup>. Analysis of single-cell RNA-seq data. In: Fridley B, Wang X (eds) Statistical Genomics. *Methods in Molecular Biology*, vol 2629, pp. 95-114. Humana, New York, NY, (2023). [PMID: 36929075. Google Scholar citations: 2].
- Bacher R**<sup>★</sup>. Normalization for single-cell RNA-seq data analysis. In: Yuan GC (ed) Computational Methods for Single-Cell Data Analysis. *Methods in Molecular Biology*, vol 1935, pp.11-23. Humana Press, New York, NY, (2019). [PMID: 30758817. Google Scholar citations: 8].

## Other Publications

- Zhong L<sup>\*</sup> and **Bacher R**<sup>★</sup>. Leveraging remeasured samples in highly confounded biomedical studies. *Nature Computational Science*, 3(3), 100465, (2023). (Invited Preview). [PMID: 38177325. Google Scholar citations: 0]
- Dong X<sup>\*</sup> and **Bacher R**<sup>★</sup>. Data-driven assessment of dimension reduction quality for single-cell omics data. *Patterns*, 3(3), 100465, (2022). (Invited Preview). [PMCID: PMC9058902. Google Scholar citations: 4].

## Pre-prints

- Zhong L<sup>\*</sup>, Ensberg K, Tibbetts S, Molstad AJ, **Bacher R**<sup>★</sup>. scDEcrypter: Uncertainty-aware differential expression analysis for viral infection in scRNA-seq. *bioRxiv*, (2026). doi: <https://doi.org/10.64898/2026.03.09.710583> [Google Scholar citations: 0].
- Wang D, Qin F, Bao W, **Bacher R**, Chung D, Lu Q, Efron PA, Cai G, Xiao F. CN-RNN: a deep learning framework for copy number variation detection with exome sequencing data. *bioRxiv*, (2026). doi: <https://doi.org/10.64898/2026.05.13.724920> [Google Scholar citations: 0].

3. Brant JO, Gauthier MP, Rodhouse CE, Wu R, Hernandez-Rios M, Zeumer-Spataro L, Dirain ML, Ungaro RF, Rocha IL, Wiggins WB, Charles AM, Xiao F, Bible LE, Mohr AM, Larson SD, Rincon JC, Wallet SM, Brusko MA, Loftus TJ, Moldawer LL, Mathews CE, **Bacher R**, Cai G, Maile R, Efron PA, Kladde MP. Divergent chromatin remodeling trajectories in CD66b<sup>+</sup> MDSCs distinguishes recovery from chronic critical illness after sepsis. *bioRxiv*, (2026). doi: <https://doi.org/10.64898/2026.01.21.700934> [Google Scholar citations: 0].
4. Dong X\*, Goyal A\*, Liang M, Brusko MA, Brusko TM, **Bacher R**<sup>★</sup>. Penalized Linear Models for Highly Correlated High-Dimensional Immunophenotyping Data. *arXiv preprint*, (2025). doi: <https://doi.org/10.48550/arXiv.2504.07771> [Google Scholar citations: 0].
5. Kim C, Tagmount A, Zhu Z\*, Barbazuk WB, **Bacher R**, Vulpe CD. Genome-wide CRISPR screens identified C18orf32 as a novel regulator of lipid metabolism that mediates PFOA-induced toxicity. *bioRxiv*, (2025). doi: <https://doi.org/10.64898/2025.12.23.696201> [Google Scholar citations: 0].
6. Peters LD, Brusko MA, Seay HR, Posgai AL, Wasserfall CH, Atkinson MA, **Bacher R**, Brusko TM. Aberrant immune regulation and enrichment of stem-like CD8+ T cells in the pancreatic lymph node during type 1 diabetes development. *bioRxiv*, (2025). doi: <https://doi.org/10.1101/2025.05.23.655848> [Google Scholar citations: 0].
7. Newman JR, Zhou M, Pires JC, **Bacher R**, Kladde M, Concannon P. Multi-omics profiling reveals ethylene signalling as a key pathway underlying both genetic and epigenetic responses to low-dose ionizing radiation in Arabidopsis. *bioRxiv*, (2023). doi: <https://doi.org/10.1101/2023.10.14.562363> [Google Scholar citations: 1].
8. Zhou M, Nabils NH, Wang A, Gauthier MPL, Murray KO, Azari H, Owens WS, Newman JRB, Pardo-Palacios FJ, Conesa A, Riva A, Clanton TL, Reynolds BA, Concannon P, Brant JO, **Bacher R**, Kladde MP. Flap-enabled next-generation capture (FENGCC): precision targeted single-molecule profiling of epigenetic heterogeneity, chromatin dynamics, and genetic variation. *bioRxiv*, (2022). doi: <https://doi.org/10.1101/2022.11.08.515732> [Google Scholar citations: 4].
9. Ogut F, Newman JRB, **Bacher R**, Concannon PJ, Verhoeven KJF, and McIntyre LM. Experimental design for large scale omic studies. *bioRxiv*, (2019). doi: <https://doi.org/10.1101/532580> [Google Scholar citations: 2].

## Interviews

1. Women in STEM - Math. WSKG PBS. 2021 Mar 6. [link](#).
2. Generating success in regenerative biology. Tecan Journal. 2020 Sep 28. [link](#).
3. Celebrating Women in Statistics and Data Science. American Statistical Association Amstat News. 2019 Mar 1. [link](#).

## Media Coverage

1. Rhonda Bacher elected president of American Statistical Association's Florida chapter. UF College of Public Health and Health Professions. 2023 Apr 4. [link](#).
2. Rhonda Bacher receives NIH Maximizing Investigators' Research Award for Early Stage Investigators. UF College of Public Health and Health Professions. 2022 Oct 5. [link](#).
3. UF biostatistics team develops tool to help scientists understand disease at the cellular level. UF College of Public Health and Health Professions. 2026 Mar 12. [link](#).

## SOFTWARE

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## Bioconductor software packages

1. scLANE: Builds flexible, interpretable models of single cell gene expression over pseudotime or latent time. The modeling architectures currently supported are Negative-binomial GLMs, GEEs, & GLMMs. Downstream analysis functionalities include model comparison, dynamic gene clustering, smoothed counts generation, gene set enrichment testing, & visualization. Published in [Leary et al., \(2026\)](#). [594 unique IP downloads. Available at: [Bioconductor](#)].
2. Methyscaper: Methodology and an R/Bioconductor package that implements a weighted PCA approach for visualizing data from experiments that jointly profile methylation and chromatin accessibility (MAPit, NOME-seq, scNMT-seq, nanoNOME, etc.). Published in [Knight et al., \(2021\)](#). [4,443 unique IP downloads. Available at: [Bioconductor](#)].
3. Trendy: Methodology and an R/Bioconductor package that implements Trendy. This method fits breakpoint models on time-course RNA-seq expression data. An R/Shiny application is included to explore model results and extract gene patterns of interest. Published in [Bacher et al., \(2018\)](#). [7,229 unique IP downloads. Available at: [Bioconductor](#)].
4. SCnorm: Methodology and an R/Bioconductor package that implements SCnorm. This method estimates group specific scaling factors for normalizing single-cell RNA-seq data, where groups of genes contain similar count-depth relationships. Published in [Bacher et al. \(2018\)](#). [13,275 unique IP downloads. Available at: [Bioconductor](#)].

## GitHub software packages

5. scDEcrypter: Models infection status and other cell-level variables as latent variables with partial observability via a regularized two-way mixture model, where mixture weights estimate cells' probabilistic membership to combinations of cell states (e.g., infection status and cell type). The resulting weights are used to estimate cell-state-specific mean expression profiles and to account for cell-state uncertainty in differential expression testing. [Available at: [GitHub](#)].
6. berm: Bootstrap-Enhanced Regularization Method is a statistical approach to enhance the robustness and accuracy of variable selection and coefficient estimation in immunophenotyping datasets. These datasets are typically characterized by high multicollinearity and dependence, alongside substantially skewed distributions. [Available at: [GitHub](#)].
7. Escort: a framework for evaluating a single-cell RNA-seq dataset's suitability for trajectory inference and for quantifying trajectory properties influenced by analysis decisions. [Available at: [GitHub](#) and [Website](#)].
8. Scaffold: Methodology and an R package implementing scaffold. This method simulates single-cell RNA-seq data by mathematically modeling the data-generation process. Published in [Bacher et al., \(2022\)](#). [Available at: [GitHub](#)].

## Open science applications and repositories

9. UFDI Spatial Data Portal: Houses visualizations of the 10x Visium spatial transcriptomics data and analysis on human donor pancreas and associated pancreatic lymph node sections from non-diabetic controls, non-diabetic islet auto-antibody positive donors at high risk, and T1D donors. Pre-print at [bioRxiv](#). [Available at: <https://ufdi.rc.ufl.edu/>].
10. ImmScape: Interactive data visualization portal of flow cytometric immune profiling data and our immune-age predictive model. Published in [Shapiro et al., \(2023\)](#). [Available at: <https://ufdiabetes.shinyapps.io/ImmScape/>].
11. scEqualization-Paper: A Github repository containing scripts to reproduce our analysis in [Bacher et al., \(2022\)](#) evaluating cDNA equalization in single-cell RNA-seq data. [Available at: [GitHub](#)].

12. LiverSpatialCompare: A Github repository containing scripts to reproduce our analysis in [Seirup et al., \(2020\)](#) comparing MARS-seq and Smart-seq protocols for spatially reconstructing the zonation axis using cells from the liver lobule. A Shiny application is included to performs KEGG pathway enrichments on the processed data. [Available at: [GitHub](#)].
13. RobotNeuralDiffPaper: A Github repository containing scripts to reproduce our analysis in [Barry et al., \(2019\)](#) comparing human and mouse gene expression kinetics. The repository contains all processed RData objects that can be explored in our Trendy package. [Available at: [GitHub](#)].

## PRESENTATIONS

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### Invited Seminars

1. *Interpretable models for uncovering dynamic biological signals in single-cell RNA-seq data*. BME Seminar Series, J. Crayton Pruitt Family Department of Biomedical Engineering. University of Florida, Gainesville, FL, USA. Jan 2024.
2. *An examination of the evolving views on normalization for single-cell RNA-seq data*. PANORAMICS - A Vision (pan-Canadian collaborative group). Toronto, ON, Canada (Virtual). Jun 2023.
3. *Developing Interactive Platforms and Interpretable Models for Uncovering Complex Biological Signals in Single-Cell Genomics Data*. **Keynote presentation** at the Computation and Informatics in Biology and Medicine Annual Retreat. Madison, WI, USA. Jun 2023.
4. *Design and Analysis of single-cell RNA-seq experiments*. Animal Molecular and Cellular Biology Seminar. University of Florida, Gainesville, FL, USA (Virtual). Sep 2020.
5. *Segmented regression analysis of gene expression dynamics using Trendy*. Biomath Seminar Series, Department of Mathematics. University of Florida, Gainesville, FL, USA. Feb 2020.
6. *Using single-cell RNA-seq data to infer spatial and temporal gene expression patterns*. Animal Genetics and Genomics Seminar. University of Florida, Gainesville, FL, USA. Feb 2020.
7. *On Methods for Normalizing Single-Cell RNA-Seq Data*. Biostatistics Department Seminar Series. Johns Hopkins University. Baltimore, MD, USA. Oct 2019.
8. *Exploring gene expression dynamics in time-course RNA-seq experiments using the Trendy R package*. Human Genetics and Genomics Program Seminar Series. University of Colorado Denver, Denver, CO, USA. Mar 2019.
9. *Single-cell RNA-seq data analysis: Design to Discovery*. Diabetes Institute Seminar Series. University of Florida, Gainesville, FL, USA. Feb 2019.
10. *Analyzing expression dynamics for high-throughput ordered profiling experiments*. Department of Physiology and Functional Genomics Seminar Series. University of Florida, Gainesville, FL, USA. Aug 2018.
11. *Single-cell RNA-seq technologies, quality control, and normalization*. Genentech Invited Seminar. San Francisco, CA, USA. Aug 2018.
12. *Statistical Methods for Single Cell RNA Sequencing Data*. Department of Statistics Seminar Series. University of Florida, Gainesville, FL, USA. Apr 2018.

### Invited Conference Presentations

13. *scDEcrypter: Uncertainty-aware differential expression analysis for viral infection in scRNA-seq*. STATGEN 2026: Conference on Statistics in Genomics and Genetics. Atlanta, GA, USA. May 2026.
14. *scDEcrypter: Uncertainty-aware differential expression analysis for viral infection in scRNA-seq*. MCBIOS 2026. Tampa, FL, USA. March 2026.
15. *Accessible Tools and Interpretable Models for Uncovering Complex Biological Signals in Single-Cell Genomics Data*. Joint Statistical Meetings. Nashville, TN, USA. August 2025.
16. *Streamlining complex genetic disease research with efficient methods for single-cell transcriptomics*. STATGEN 2025: Conference on Statistics in Genomics and Genetics. Minneapolis, MN, USA. May 2025.
17. *Interpretable model for uncovering dynamic biological signals in single-cell RNA-seq data*. STATGEN 2024: Conference on Statistics in Genomics and Genetics. Pittsburgh, PA, USA. May 2024.
18. *Interpretable models for uncovering dynamic biological signals in single-cell RNA-seq data*. MidSouth Computational Biology and Bioinformatics Society 2024 Conference. Atlanta, GA, USA. March 2024.

19. *scLANE: single-cell linear adaptive negative-binomial expression testing*. Annual Florida ASA Chapter Meeting. Tallahassee, FL, USA. March 2024.
20. *scLANE: single-cell linear adaptive negative-binomial expression testing*. 16th International Conference of the ERCIM WG on Computational and Methodological Statistics. Berlin, Germany. Dec 2023. (Virtual)
21. Invited session on *Thinking deeply about sequencing and omics data*. Women in Statistics and Data Science Conference. Bellevue, WA, USA. Oct 2023.
22. *Scaffold - data generation based simulation framework for single-cell RNA-seq data*. International Chinese Statistical Association Applied Statistics Symposium. Gainesville, FL, USA. Jun 2022.
23. *Segmented regression models for exploring expression dynamics in high-throughput ordered profiling experiments*. Florida Chapter of the American Statistical Association Annual Meeting. (Online format). Feb 2022.
24. *Recent Advances and Opportunities in Large-Scale and Multi-Omic Single-Cell Data Analysis (Discussant)*. International Biometric Society Eastern North American Region Annual Meeting (Online format). Mar 2020.
25. *Single-cell RNA-seq data analysis: Design to Discovery*. Southeastern Association of Shared Resources Annual Meeting. Atlanta, GA, USA. Jun 2019.
26. *SCnorm: A quantile-regression based approach for normalization of single-cell RNA-seq data*. International Chinese Statistical Association Applied Statistics Symposium. Raleigh, NC, USA. Jun 2019.
27. *Characterizing Technical Artifacts in Single-Cell RNA-Seq Data Using A Data Generation Simulation Framework*. International Biometric Society Eastern North American Region Annual Meeting. Philadelphia, PA, USA. Mar 2019.
28. *SCnorm: A quantile-regression based approach for normalization of single-cell RNA-seq data*. International Conference on Advances in Interdisciplinary Statistics and Combinatorics. Greensboro, NC, USA. Oct 2018.
29. *Trendy: Segmented regression analysis of expression dynamics in high-throughput ordered profiling experiments*. Southern Regional Council on Statistics Conference. Virginia Beach, VA, USA. Jun 2018.
30. *SCnorm: A quantile-regression based approach for normalization of single-cell RNA-seq data*. International Indian Statistical Association Conference. Gainesville, FL, USA. May 2018.
31. *SCnorm: A quantile-regression based approach for robust normalization of single-cell RNA-seq data*. International Chinese Statistical Association - Symposium on Single Cell Sequencing. Chicago, IL, USA. Jun 2017.

### Invited Workshops

32. *Michigan State University Workshop on: Spatial and Time-Resolved Single-Cell Transcriptomics Analysis*  
Two-day workshop organized and hosted by Michigan State University to advance research in omics and genetics analysis. East Lansing, MI, USA. Nov 2023.
33. *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. New York City, NY, USA. Nov 2019.
34. *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. Bend, OR, USA. Jun 2018.

### Contributed Presentations

35. *scLANE: Single-cell Linear Adaptive Negative-binomial Expression Testing*. Joint Statistical Meetings. Invited to contribute. Toronto ON, Canada. Aug 2023.
36. *Scaffold - Data generation based simulation framework for single-cell RNA-seq data*. Joint Statistical Meetings. Invited to contribute. Washington DC, USA. Aug 2022.
37. *Assumptions and methods for normalizing single-cell RNA-seq data*. Joint Statistical Meetings. Invited to contribute. Denver, CO, USA. Aug 2019.
38. *Data generation based simulation framework for single-cell RNA-Seq data*. Joint Statistical Meetings. Invited to contribute. Vancouver, BC, Canada. Aug 2018.
39. *Trendy: Segmented regression analysis of expression dynamics for high-throughput ordered profiling experiments*. International Biometric Society Eastern North American Region Annual Meeting. Atlanta, GA, USA. Mar 2018.
40. *SCnorm: robust normalization of single-cell RNA-seq data* Symposium on Advances in Genomics, Epidemiology, and Statistics Annual Meeting. Contributed poster. Philadelphia, PA, USA. Jun 2017.
41. *Normalization of single cell RNA-sequencing data* International Biometric Society Eastern North American Region Annual Meeting. Contributed poster. Austin, TX, USA. Mar 2016.
42. *Normalization of single cell RNA-sequencing data* Program in Quantitative Genomics Conference. Contributed poster. Boston, MA, USA. Nov 2015.
43. *Normalization of single cell RNA-sequencing data* Integrative Biostatistics Research for Imaging, Genomics, & High-throughput Technologies in Precision Medicine Conference. Contributed poster. Houston, TX, USA. Oct 2015.
44. *Challenges in single cell RNA-seq experiments* International Biometric Society Eastern North American Region Annual Meeting. Contributed poster. Miami, FL, USA. Mar 2015.

## TEACHING

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### Classroom Instruction, University of Florida

- PHC 7090 Advanced Biostatistical Methods I. Instructor, 2025.
- PHC 6088 Statistical Analysis of Genetic Data. Instructor, 2020, 2022-2025.
- PHC 6937 Genetic Data Analysis. Instructor, 2019.
- PHC 6937 Genetic Data Analysis. Instructor, 2018.

### Independent Studies

- HSC 4913 Supervised Research. Saesha Wani, undergraduate. *Normalizing methylation sequencing data*, Summer 2025.
- HSC 4913 Supervised Research. Parker Knight, undergraduate. *Visualization of methylation sequencing data*, Spring 2020.

### Short Courses

- Co-Instructor, [Recent Advances in Statistical Methods and Computational Algorithms for Single-Cell Omics Analysis](#). International Society for Computational Biology Conference - the largest and most high profile annual meeting of scientists working in computational biology. Basel, Switzerland. Jul 2019.
- Co-Instructor, [Statistical methods for single-cell RNA-seq analysis](#). Joint Statistical Meetings - the largest gathering of statisticians held in North America. Vancouver, BC, Canada. Aug 2018.

### Guest Lectures

- Guest Lecture, *Normalization of single-cell RNA-seq data*. BIOS 785 - Statistical Methods for Gene Expression Analysis. Department of Biostatistics, University of North Carolina, Raleigh, NC, USA. 2019, 2020.
- Guest Instructor (week-long instruction), *Analysis of scRNA-seq data*. PHC 6937 Frontiers in Biostatistics. Department of Biostatistics, University of Florida. 2019, 2022.

### Teaching Assistant

- STAT 877 Statistical Methods for Molecular Biology. University of Wisconsin-Madison. 2017.

## ADVISING

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### Postdoctoral Research Fellows

1. Xiaoru (Ruby) Dong, 2024-2025, Research Assistant Professor at Texas A&M University.

### Primary Advisor of Doctoral Students in Biostatistics

1. Apoorva Goyal, 2024-present.
2. John (Jack) Leary, 2022-present.
3. Zhaohan Zhu, 2022-present.

#### *Previous*

4. Luer Zhong, 2025.
5. Xiaoru (Ruby) Dong, 2024.

### Doctoral Committees in Biostatistics

#### *Current*

1. Dayuan Wang

#### *Previous*

2. Owen Visser, 2026.
3. Ian Murphy, 2025.
4. Haocheng Ding, 2024.
5. Meilin Jiang, 2023.
6. Dorothy Ellis, 2023.

### Other UF Doctoral Committees (\*Committee chair)

#### *Current*

1. Reed Berkowitz, PhD in Biomedical Sciences - Immunology and Microbiology, 2025-present.
2. Jennifer Yu, PhD in Biomedical Sciences - Immunology and Microbiology, 2025-present.
3. Adriana Del Pino Herrera, PhD in Biomedical Engineering, 2024-present.
4. Karl Ensberg, PhD in Biomedical Sciences, 2024-present.
5. Natalia E. Padillo-Anthemides, PhD in Genetics & Genomics, 2023-present.
6. Christian Maugee, PhD in Genetics and Genomics, 2022-present.

#### *Previous*

7. Yisen Jin, PhD in Statistics, 2025.
8. Zeyu Yuwen, PhD in Statistics, 2025.
9. Dain Chun, PhD in Pharmaceuticals, 2024.

10. Kartik Motwani, PhD in Medical Sciences - Immunology and Microbiology (MD/PhD), 2023.
11. Leena Peters, PhD in Medical Sciences - Immunology and Microbiology, 2023.
12. Puchong Thirawatananond, PhD in Medical Sciences - Immunology and Microbiology (MD/PhD), 2023.
13. Adalena Nanni<sup>\*</sup>, PhD in Genetics and Genomics, 2022.
14. Rodrigo Rampazo Amadeu, Horticultural Sciences, 2021.

### **Master's Committees**

#### *Current*

1. Lazarus Mramba, MS in Biostatistics, University of Florida.

#### *Previous*

2. Chuanhao Yang, MS in Biostatistics, University of Florida, 2026.
3. Geoffrey Anyuga, MS in Biostatistics, University of Florida, 2024.
4. Matthew Corcoran, MS in Biostatistics, University of Florida, 2023.
5. Yu Chen, MS in Biostatistics, University of Florida, 2023.
6. William Golden, MS in Biostatistics, University of Florida, 2021.
7. Vladislav Bravman, MS in Biostatistics, University of Florida, 2020.
8. Lee Panter, MS in Statistics, University of Colorado, 2020.
9. Dain Chun, MS in Biostatistics, University of Florida, 2020.
10. Shuzheng Li, MPH - Biostatistics, University of Florida, 2019.
11. Mengmeng Li, MS in Biostatistics, University of Florida, 2018.

### **Biostatistical Mentor**

#### *Previous*

1. K08 DK128628 (Jacobsen), 7/15/2021- 4/30/2026, NIH/NIDDK  
Development of a Predictive Response Signature to Anti-Thymocyte Globulin in Type 1 Diabetes.
2. F30 DK128945 (Puchong Thirawatananond), 5/16/2021- 5/15/2026, NIH/NIDDK  
Generation of Islet Specific T Follicular Regulatory Like Cells for Autologous Cell Therapy of T1D.
3. F31 DK129004 (Leena Peters), 5/16/2021- 5/15/2025, NIH/NIDDK  
Multi-modal single cell analysis for investigation of T1D pathogenesis.

### **Bachelor's Honors Committees**

1. Kevin Kapadia, BS in Psychology, University of Florida, 2022.

### **Undergraduate Research Assistants and Mentees**

1. Aseel Ismail, BS in Data Science, expected 2028.
2. Saesha Wani, BS in Statistics, expected 2028.
3. Samantha Pattey, BS in Mathematics, expected 2026.
4. Chuanhao Yang, BS in Statistics and BS in Mathematics, 2023.
5. Kevin Kapadia, BS in Psychology, 2022.
6. Eliza Morton, BS in Psychology, 2022.
7. Hadley Browder, BS in Statistics, 2022.
8. Parker Knight, BS in Mathematics, 2020.

## UNIVERSITY SERVICE

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### Committees

- Chair, Biostatistics Qualifying Exam Committee (2025-present).
- Chair, Biostatistics Department Space Committee (2024-present).
- Member, Biostatistics Graduate Admissions Committee (2023-present).
- Member, Biostatistics Department Space Committee (2022-2024).
- Member, PPHP Research Committee (2022 - 2024).
- Member, Search committee for Vice Chair for Research in the Department of Pathology, Immunology and Laboratory Medicine (2023).
- Chair, Biostatistics Department Social Wellness Committee (2021-2022).
- Member, UFHCC Scientific Review and Monitoring Committee (2018-2022).
- Chair, Biostatistics Seminar Committee (May 2018 - 2020).

### Activities

- Reviewer, 2026 Pew Biomedical Scholars (2025).
- Speaker, Faculty Talks at Preview (2023). Discussion and Q&A session with incoming freshman on positive academic behaviors and expectations.
- Reviewer, PPHP Research Opportunity Seed Grant (2022).
- Reviewer, UFHCC Pilot Project Program (2021).

## PROFESSIONAL SERVICE

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### Grant Review

- Reviewer, NIH NIGMS MIRA Special Emphasis Panel (May 2026).
- Reviewer, NIH NIGMS MGG Special Emphasis Panel (Jan 2026).
- Reviewer, NIH NIGMS MIRA Special Emphasis Panel (Jul 2025).
- Ad hoc reviewer, NHLBI Trans-Omics for Precision Medicine (TOPMed) Fellowship (Jan 2025).
- Ad hoc reviewer, Subcommittee for Precision Oncology, VA Precision Oncology (Jul 2024).
- Single proposal reviewer, City of Hope IIDP Data Resource Trainee Scholar Award (Dec 2023).
- Ad hoc member, NSF panel reviewer for applications submitted to a special initiative on statistical methods (Dec 2023).
- Ad hoc member, NIH review of applications submitted to the NIH HEAL Initiative's PRECISION Human Pain Network (Jul 2023).
- Ad hoc member, NIH review of applications submitted to the Human BioMolecular Atlas Program (HuBMAP) Integration, Visualization & Engagement Collaboratory (Mar 2022).
- Single proposal reviewer, NSF expert review of an application submitted to the Methodology, Measurement, and Statistics Program (Dec 2020).
- Ad hoc member, NSF panel reviewer for applications submitted to a special initiative on statistical methods (Dec 2019).

### Editorial Activities

- Member, Statistical Editorial Board, Nature Medicine (2024).

## Participation on Association Boards and Committees

- Communications Officer, Section on Statistics in Genomics and Genetics of the American Statistical Association (2025-2026).
- President, Florida Chapter of the American Statistical Association (2023-2025).
- Secretary/Treasurer, Florida Chapter of the American Statistical Association (2021-2023).
- Information Officer, Florida Chapter of the American Statistical Association (2019-2021).
- Chair, Council for Emerging and New Statisticians within the Eastern North Atlantic Region's Advisory Board (2017-2018).
- Member, Council for Emerging and New Statisticians within the Eastern North Atlantic Region's Advisory Board (2015-2017).
- Member, Department of Statistics Social Committee, University of Wisconsin-Madison (2014-2015).
- Cofounder, University of Florida Statistics Club (2011-2012).

## Organizer

- Meeting Organizer, Annual Meeting for the Florida Chapter of the American Statistical Association ([website](#)) (2023).
- Session Organizer, International Chinese Statistical Association Applied Statistics Symposium (2022). Topic: *Statistical Advances and Applications in Analyzing Large Scale & Multi-Omic Single-Cell Data*.
- Conference Planning Committee, Human Islet Research Enhancement Center (HIRN) Annual Meeting (Jun 2020).
- Local Planning Committee, Florida Chapter of the American Statistical Association sponsored short-course (Sep 2019). Topic: *Tidyverse: An Introduction to R for Data Science*.
- Session Organizer, Eastern North Atlantic Region Meeting (2020). Topic: *Recent Advances and Opportunities in Large Scale & Multi-Omic Single-Cell Data Analysis*.
- Organizer, Department of Statistics Weekly Student Seminar, University of Wisconsin-Madison (2015).
- Organizer, Weekly Statistical Genetics Student Reading Group, University of Wisconsin-Madison (2014).

## Chair

- Session Chair, Eastern North Atlantic Region Meeting (2020). Topic: *Recent Advances in Statistical Methods for Single-Cell Omics Analysis*.
- Session Chair, Eastern North Atlantic Region Meeting (2019). Topic: *Methods to Robustly Incorporate External Data Into Genetic Tests*.
- Session Chair, Joint Statistical Meetings (2018). Topic: *Biometrics Section - Contributed Papers on Categorical Data*.
- Session Chair, Eastern North Atlantic Region Meeting (2018). Topic: *Methods For RNA-Seq Data*.
- Session Chair, Eastern North Atlantic Region Meeting (2016). Topic: *Contributed Papers on Bayesian Causal Inference*.

## PROFESSIONAL SOCIETY MEMBERSHIPS

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International Biometric Society (ENAR), American Statistical Association (ASA), Florida Chapter of the American Statistical Association

## JOURNAL REFEREE

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Annals of Applied Statistics, Bioinformatics, Bioinformatics Advances, Biometrics, BMC Bioinformatics, Briefings in Bioinformatics, F1000, GigaScience, Genome Biology, Genome Research, Journal of the American Statistical Association, Nature Biotechnology, Nature Communications, Nature Computational Science, Nature Genetics, Nature Medicine, Nature Methods, Nucleic Acids Research, Patterns, PLOS Computational Biology, PNAS, Scientific Data, Small Methods, Statistics in Biosciences

## GRANT SUPPORT

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### Current

- R35 GM146895 (PI Bacher), NIH NIGMS, 9/2022 - 6/2027  
*Resolving single-cell analysis challenges via data-driven decision frameworks and novel statistical methods.*  
Role: **Principal Investigator.**
- P01 AI042288 (PI Brusko), NIH NIAID, 12/2022 - 11/2027  
*Immune Function and the Progression to Type 1 Diabetes.*  
Role: Co-Investigator for Core B.
- R01 DK106191 (PI Brusko), NIH NIDDK, 2/2023 - 1/2027  
*The CD226 costimulatory axis in type 1 diabetes.*  
Role: Co-Investigator.
- R01 ES033625 (PI Vulpe), NIH NIEHS, 2/2022 - 11/2026  
*CRISPR screens of population relevant genes governing toxicant resilience.*  
Role: Co-Investigator.
- UH3 DK122638 (PI Stabler), NIH NIDDK, 8/2019 - 7/2024  
*Engineering a Human Microphysiological System for the Characterization of Islet-Immune Interactions.*  
Role: Co-Investigator.

### Previous

- R21 AG075645 (PI Mankowski), NIH NIAID, 3/2022 - 2/2024  
*Home-based digital exercise training program to improve physical function of older sepsis survivors.*  
Role: Co-Investigator.
- P01 AI042288 (PI Atkinson), NIH NIAID, 6/2018 - 5/2023  
*Immune Function and the Progression to Type 1 Diabetes.*  
Role: Co-Investigator for Core B.
- W81XWH2110004 (PI Zhang), DOD, 1/2021 - 12/2023  
*Developing a novel PROTAC-based NR4A1 degrader for breast-cancer therapy.*  
Role: Co-Investigator.
- RM1 GM139690 (PI Moldawer), NIH NIGMS, 4/2021 - 9/2022\*  
*Dysfunctional Myelopoiesis & Myeloid-Derived Suppressor Cells in Sepsis.*  
\*Co-Investigator role terminated early due to NIGMS conflict.
- R35 GM140806 (PI Efron), NIH NIGMS, 4/2021 - 9/2022\*  
*Pathological Myeloid Activation After Sepsis and Trauma.*  
\*Co-Investigator role terminated early due to NIGMS conflict.
- 1-SRA-2019-764-A-N (PI Wasserfall), Juvenile Diabetes Research Foundation, 4/2019 - 3/2020  
*A Composite Serological Risk Score to Predict Type 1 Diabetes Progression and Clinical Diagnosis.*  
Role: Co-Investigator.
- 3-SRA-2019-793-S-B (PI Brusko), Juvenile Diabetes Research Foundation, 6/2019 - 5/2020  
*Single cell sequencing for islet-reactive T cell clonotype and transcript signatures.*  
Role: Co-Investigator.

- Award (PI Bacher, Hendricks, Lopez), The Jayne Koskinas Ted Giovanis Foundation, 8/2018 - 8/2019  
*Uncovering the Life Clock of Red Blood Cells Using Single-Cell Analysis.*  
Role: **Co-Principal Investigator** (multi-PI with Audrey Hendricks and Javier Lopez).