

CURRICULUM VITAE

Xiaoru Dong, Ph.D

CONTACT

Department of Public Health Sciences
College of Dentistry
Texas A&M University
3302 Gaston Ave
Dallas, TX 75246

Phone: 217-778-5683
Email: xrdong@tamu.edu
Website: xiaorudong.github.io
GitHub: xiaorudong
ORCID: 0000-0003-3039-3004

RESEARCH INTERESTS

My research interests center on the intersection of biology and statistics, focusing on developing statistical and computational tools for genomics and biomedical research. I specialize in analyzing complex datasets, especially human single-cell data from next-generation sequencing technologies using advanced statistical techniques. My aim is to drive novel biological discoveries and enhance our understanding of genomic processes through innovative and data-driven approaches.

EDUCATION

- 08/2019–05/2024 **Ph.D., Biostatistics**
University of Florida, Gainesville, FL, USA
Advisor: Rhonda Bacher, Ph.D.
Dissertation: Improving Analysis and Modeling of Dynamic, High-Dimensional Single-Cell Data
- 08/2014–12/2018 **B.S., Statistics**
University of Illinois Urbana-Champaign, Champaign, IL, USA

PROFESSIONAL POSITIONS

- 07/2025–present Research Assistant Professor
Department of Public Health Sciences, College of Dentistry, Texas A&M University
- 06/2024–06/2025 Postdoctoral Associate
Department of Biostatistics, College of Public Health and Health Professions, University of Florida
- 08/2019–05/2024 Research Assistant
Department of Biostatistics, College of Public Health and Health Professions, University of Florida
- 08/2019–05/2023 Teaching Assistant
Department of Biostatistics, College of Public Health and Health Professions, University of Florida

PUBLICATIONS

Key: [†] indicates co-first authors; * indicates corresponding authors.

Peer-Reviewed Journal Articles

1. **Dong, X.**, Leary, J. R., Yang, C., Brusko, M. A., Brusko, T. M., & Bacher, R.* (2024). Data-driven selection of analysis decisions in single-cell RNA-seq trajectory inference. *Briefings in Bioinformatics*, 25(3), bbae216. <https://doi.org/10.1093/bib/bbae216>

2. Shapiro, M. R.[†], **Dong, X.**[†], Perry, D. J.[†], McNichols, J. M., Thirawatananond, P., Posgai, A. L., Peters, L. D., Motwani, K., Musca, R. S., Muir, A., Concannon, P., Jacobsen, L. M., Mathews, C. E., Wasserfall, C. H., Haller, M. J., Schatz, D. A., Atkinson, M. A., Brusko, M. A., Bacher, R.* & Brusko, T. M.* (2023). Human immune phenotyping reveals accelerated aging in type 1 diabetes. *JCI Insight*. <https://doi.org/10.1172/jci.insight.170767>
3. Jacobsen, L. M.[†], Diggins, K.[†], Blanchfield, L.[†], McNichols, J. A., Perry, D. J., Brant, J., **Dong, X.**, Bacher, R., Gersuk, V. H., Schatz, D. A., Atkinson, M. A., Mathews, C. E., Haller, M. J., Long, S. A.*, Linsley, P. S.*, & Brusko, T. M.* (2023). Responders to low-dose ATG induce CD4 T cell exhaustion in type 1 diabetes. *JCI Insight*. <https://doi.org/10.1172/jci.insight.161812>
4. Darden, D. B., **Dong, X.**, Brusko, M. A., Kelly, L., Fenner, B., Rincon, J. C., Dirain, M. L., Ungaro, R., Nacionales, D. C., Gauthier, M., Kladde, M., Brusko, T. M., Bihorac, A., Moore, F. A., Loftus, T., Bacher, R., Moldawer, L. L., Mohr, A. M., & Efron, P. A.* (2021). A Novel Single Cell RNA-seq Analysis of Non-Myeloid Circulating Cells in Late Sepsis. *Frontiers in Immunology*, 12, 696536. <https://doi.org/10.3389/fimmu.2021.696536>
5. Ross, J. J., Wasserfall, C. H., Bacher, R., Perry, D. J., McGrail, K., Posgai, A. L., **Dong, X.**, Muir, A., Li, X., Campbell-Thompson, M., Brusko, T. M., Schatz, D. A., Haller, M. J., & Atkinson, M. A.* (2021). Exocrine Pancreatic Enzymes Are a Serological Biomarker for Type 1 Diabetes Staging and Pancreas Size. *Diabetes*, 70(4), 944–954. <https://doi.org/10.2337/db20-0995>

Book Chapters

6. **Dong, X.**, & Bacher, R. (2023). Analysis of Single-Cell RNA-seq Data. In B. Fridley & X. Wang (Eds.), *Statistical Genomics* (Vol. 2629, pp. 95–114). Springer US. https://doi.org/10.1007/978-1-0716-2986-4_6

Other Publications

7. **Dong, X.**, & Bacher, R. (2022). Data-driven assessment of dimension reduction quality for single-cell omics data. *Patterns*, 3(3), 100465. <https://doi.org/10.1016/j.patter.2022.100465> [Invited Preview]

Pre-prints

8. **Dong, X.**, Goyal, A., Liang, M., Brusko, M. A., Brusko, T. M., & Bacher, R.* (2025). Penalized Linear Models for Highly Correlated High-Dimensional Immunophenotyping Data. *arXiv*. <https://arxiv.org/abs/2504.07771>
9. Leary, J. R., **Dong, X.**, & Bacher, R.* (2025). Interpretable Trajectory Inference with Single Cell Linear Adaptive Negative-binomial Expression (scLANE) Testing. *bioRxiv*. <https://doi.org/10.1101/2023.12.19.572477>

SOFTWARE

GitHub Software Packages

1. simCRISPR: An R package for simulating pooled CRISPR screening data under various experimental designs to support method development and benchmarking in CRISPR analysis. Available at: GitHub.
2. Escort: Methodology and an R package implementing Escort. This method evaluates a single-cell RNA-seq dataset's suitability for trajectory inference and for quantifying trajectory properties influenced by analysis decisions. Available at: GitHub.
3. berm: Bootstrap-Enhanced Regularization Method. This package implements the Bootstrap-Enhanced Regularization Method (BERM), a statistical approach aiming to enhance the robustness and accuracy of variable selection and coefficient estimation in immunophenotyping datasets. Available at: GitHub.

Interactive Tools and Applications

4. shinyEscort: An interactive Shiny application for guiding trajectory construction in single-cell RNA-seq data. Available at: shinyEscort website.

PRESENTATIONS

National Talks

1. "Realistic Simulation for Benchmarking and Designing CRISPR-Pooled Screen." American Statistical Association (ASA) Section on Statistics in Genomics and Genetics (SSGG). Contributed talk. Minneapolis, "MN", USA. May 2025.
2. "Data-driven Selection of Trajectory in Single-cell RNA-seq Data." International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Contributed talk. Baltimore, MD, USA. March 2024.

Local Talks

3. "Penalized Linear Models for Highly Correlated Immunophenotyping Data." 2025 Annual Meeting of the Florida Chapter of the American Statistical Association (ASA). Contributed presentation. University of Central Florida, Orlando, FL, USA. February 2025.
4. "Enhancing Feature Selection and Estimation in Immunophenotype Data Analysis." Brusko Lab, University of Florida Diabetes Institute, Gainesville, FL, USA. March 2024.
5. "Data-driven Trajectory Construction in Single-Cell RNA-seq Data." Mark C. K. Yang Award Ceremony. Contributed talk. University of Florida, Gainesville, FL, USA. October 2023.
6. "Trajectory Goodness of Fit in Single-Cell RNA-seq Data." Brusko Lab, University of Florida Diabetes Institute, Gainesville, FL, USA. December 2021.

National Posters

7. "Data-driven Selection of Trajectory in Single-cell RNA-seq Data." American Statistical Association (ASA) Section on Statistics in Genomics and Genetics (SSGG). Contributed poster. Pittsburgh, PA, USA. May 2024.
8. "Data-driven Evaluation of Trajectories in Single-Cell RNA-seq Data." International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Contributed poster. Nashville, TN, USA. March 2023.

Local Posters

9. "Data-driven Evaluation of Trajectories in Single-Cell RNA-Seq Data." 2023 Annual Meeting of the Florida Chapter of the American Statistical Association (ASA). Contributed poster. University of Florida, Gainesville, FL, USA. March 2023.
10. "Immune Phenotypic Profiling across the Human Lifespan Demonstrates Accelerated Immune Aging in Subjects with Type 1 Diabetes." 2022 College of Medicine Research Day. Contributed poster. University of Florida, Gainesville, FL, USA. April 2022.
11. "Analyzing Inclusion Criteria of 7000 Cochrane Systematic Reviews." Undergraduate Research Symposium. Contributed poster. University of Illinois at Urbana-Champaign, Champaign, IL, USA. April 2018.
12. "Distortions in Scientific Literature - A Replication Analysis of Greenberg's Citation Network of 302 Alzheimer's Science Research Papers." Undergraduate Research Symposium. Contributed poster. University of Illinois at Urbana-Champaign, Champaign, IL, USA. April 2018.

TEACHING

Teaching Assistant

Spring 2023	PHC6088 - Statistical Analysis of Genetic Data, University of Florida.
Fall 2022	PHC6059 - Introduction to Applied Survival Analysis, University of Florida.
Spring 2022	PHC6088 - Statistical Analysis of Genetic Data, University of Florida.
Fall 2021	PHC4094 - Introduction to Biostatistics for Health Science and Public Health, University of Florida.
Spring 2021	PHC6088 - Statistical Analysis of Genetic Data, University of Florida.
Fall 2020	PHC6052 - Introduction to Biostatistical Methods, University of Florida.
Spring 2020	PHC6089 - Public Health Computing, University of Florida.
Fall 2019	PHC6052 - Introduction to Biostatistical Methods, University of Florida.

ACADEMIC SERVICE

Journal Reviewer

- Bioinformatics
- Bioinformatics Advances
- BMC Bioinformatics
- Communications Biology
- Scientific Reports

Service in Statistics

11/2024	Poster judge. 2024 Florida Genetics Symposium.
03/2023	Session moderator. Annual Meeting of the Florida Chapter of the American Statistical Association (ASA).
06/2022	Session moderator. Annual Applied Statistics Symposium of the International Chinese Statistical Association (ICSA).

HONORS & AWARDS

10/2023	Mark C. K. Yang Student Presentation Award
03/2023	Student Competition Award, American Statistical Association Florida Chapter

PROFESSIONAL SOCIETY MEMBERSHIPS

- International Biometric Society (ENAR)
- American Statistical Association (ASA)