NATALIE STANLEY

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EDUCATION

- **Stanford University** *2018-2020*
  Postdoctoral Fellow in Computational Immunology
  Postdoc Mentor: Professor Nima Aghaeepour
- **The University of North Carolina at Chapel Hill** *2013-2018*
  PhD in Bioinformatics and Computational Biology
  PhD Advisor: Professor Peter J. Mucha
- **Dickinson College** *2009-2013*
  B.S. in Mathematics

EMPLOYMENT

- **The University of North Carolina at Chapel Hill** *2021-present*
  Assistant Professor of of Computer Science and Computational Medicine

HONORS AND AWARDS

Funding received as faculty.

- **NIH R21 awarded by NIA (1R21AG084251-01A1)**. *Spatial signatures of brain health and vulnerability in aging and Alzheimer's disease* PI: Todd Cohen and Natalie Stanley
- **NIH R21 awarded by NIAID (R21AI171745-01A1)**. *Automating the Discovery of Clinically-Relevant Intracellular Signaling Responses in Immune Cell-Types.* PI: Natalie Stanley
- **NeuroSpark Pilot Award**. *Spatial signatures of brain health and vulnerability in aging and Alzheimer's disease.* PI: Todd Cohen, Co-PI: Natalie Stanley. 2023-2024.
- **Lineberger Pilot Award**. *Epigenetic Regulation of the Tumor Microenvironment.* PI: Justin Milner. Co-PI: Natalie Stanley. 2023-2024.
- **UNC Computational Medicine Medicine Pilot Award**. *A dual screening approach for engineering durable and effective T lymphocyte responses* . PI: Natalie Stanley. Co-PI: Justin Milner. 2023-2024.
- **Bill & Melinda Gates Foundation Award**. *An Integrated Analysis of the Vaginal Microbiome in Zambia.* PI: Joni Price. Investigators: Kristina De Paris, Yuri Sebastiao, Natalie Stanley. 2022-2025.

Funding received as a trainee.

- NIH T32 Postdoctoral Training Grant in Anesthesia. 2019-2020 (Stanford)
- NIH T32 Postdoctoral Training Grant in Immunology. 2018-2019 (Stanford)
- NIH T32 Predoctoral Training Grant in Big Data to Knowledge (BD2K). 2016-2017 (University of North Carolina at Chapel Hill)
- NIH T32 Predoctoral Training Grant in Bioinformatics and Computational Biology. 2014-2015 (University of North Carolina at Chapel Hill).

Other awards.

- **Nova Mentoring Award for Junior Faculty.** 2023. *Awarded by the office of graduate education in the UNC school of medicine.*

- **ACM-BCB 2022 Best Paper Award.** 2022. *Awarded for 'Transparent single-cell set classification with kenel mean embeddings'.*
- **ISAC Travel Award.** 2019. *Travel award to attend the CYTO annual meeting in Vancouver Canada.*
- **SIAM (Society for Industrial Applied Mathematics) Student Paper Prize for 'Clustering Network Layers with the Strata Multilayer Stochastic Block Model'.** 2016. *Prize awarded for an outstanding graduate student lead paper.*
- **SIAM Network Science Student Travel Award.** 2016. *Travel award to attend the annual SIAM Network Science workshop at the SIAM annual meeting in Boston, MA.*

PUBLICATIONS

Google Scholar: `https://scholar.google.com/citations?user=ak3dqLoAAAAJ&hl=en&authuser=1`

- Given the interdisciplinary nature of my research, publications include both peer-reviewed journal articles and peer-reviewed conference proceedings. In computer science, conference papers are full-length, peer-reviewed papers and are the standard of publishing.

40. Dominant CD4+ T cell receptors remain stable throughout antiretroviral therapy-mediated immune restoration in people with HIV. A Sponaugle, AMK Weidman, JS Ranek. G. Atassi, J. Kuruc, AA Adimora, NM Archin, C. Gay, DR Kuritzkes, DM Margolis, BG Vincent, **N. Stanley**, MG Hudgens, JJ Eron, N. Goonetilleke. **Cell Reports Medicine.** 2023.

39. scLKME: A Landmark-based Approach for Generating Multi-cellular Sample Embeddings from Single-cell Data. H. Yi, **N. Stanley**. **Under Review.** 2023.

38. Feature selection for preserving biological trajectories in single-cell data. JS Ranek, W. Stallert, J. Milner, **N. Stanley**. **In Revision.** Preprint: `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10197710/`. 2023.

37. The interplay between sketching and graph generation algorithms in identifying biologically cohesive cell-populations in single-cell data. E. Crawford, A. Plotkin, J.S. Ranek, **N. Stanley**. **Under Review.** Preprint: `https://www.biorxiv.org/content/10.1101/2023.09.15.557825v1.abstract`. 2023.

36. Benchmarking differential abundance methods for finding condition-specific prototypical cells in multi-sample single-cell datasets. H. Yi, A. Plotkin, **N. Stanley**. **Accepted to Genome Biology.** Preprint: `https://www.biorxiv.org/content/10.1101/2023.02.24.529894v1.abstract`. 2023.

35. Cellograph: A semi-supervised approach to analyzing multi-condition single-cell RNA sequencing data using graph neural networks. JA Shahir, **N. Stanley**, JE Purvis. **Under Review.** Preprint: https://www.biorxiv.org/content/10.1101/2023.02.24.528672v1.abstract. 2023.

34. Early prediction and longitudinal modeling of preeclampsia from multiomics. I. Maric, K. Contrepois, MN Moufarrej, IA Stelzer, D. Feyarts, X. Han, A. Tang, **N. Stanley**, RJ Wong, GM Traber, M. Ellenberger, AL Chang, R. Fallahzadeh, H. Nassar, M. Becker, M. Xenochristou, C. Espinosa, D. De Francesco, MS Ghaemi, EK Costello, A. Culos, XB Ling, KG Sylverster, GL Darmstadt, VD Winn, GM Shaw, DA Relman, SR Quake, MS Angst, MP Snyder, DK Stevenson, B Gaudilliere, N Aghaeepour. **Patterns**. 2023.

33. A Graph Coarsening Algorithm for Compressing Representations of Single-Cell Data with Clinical or Experimental Attributes. CJ. Chen, E. Crawford, **N. Stanley. Pacific Symposium on Biocomputing 2023 (PSB)**. 2023.

32. Integrating temporal single-cell gene expression modalities for trajectory inference and disease prediction. J. Ranek, **N. Stanley***, JE Purvis*. **Genome Biology.** 2022. (* denotes co-senior author)

31. Transparent single-cell set classification with kernel mean embeddings. S. Shan, VA Baskaran, H. Yi, **N. Stanley**, JB Oliva. **Proceedings of the 13th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)**. 2022. *Received the 2022 ACM-BCB Best Paper Award!*

30. CytoEMD: detecting and visualizing between-sample variation in relation to phenotype with earth mover's distance. H. Yi and **N. Stanley**. **Proceedings of the 13th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB).** 2022.

29. Distribution-Based Sketching of Single-Cell Samples. VA Baskaran, J. Ranek, S. Shan, **N. Stanley**, JB Oliva. **Proceedings of the 13th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)**. 2022.

28. Integrated Single-cell and Plasma Proteomic Modeling to Predict Surgical Site Complications: A Prospective Cohort Study. KK Rumer, J. Hedou, J. Einhaus, F. Verdonk, **N. Stanley**, B. Choisy, E. Ganio, A. Bonham, D. Jacobsen, B. Warrington, X. Gao, M. Tingle, TN McAllister, R. Fallahzadeh, D. Fayerts, I. Stelzer, D. Gaudilliere, K. Ando, A. Shelton, A. Morris, E. Kebebew, N. Aghaeepour, C. Kin, MS Angst, B. Gaudilliere. **Annals of Surgery**. 2022.

27. An Updated Guide for the Perplexed: Cytometry in the High-Dimensional Era. T. Liecheti, LM Weber, TM Ashurt, **N. Stanley**, M. Prlic, S. Van Gassen, F. Mair. **Nature Immunology** . 2021.

26. CytoSet: Predicting clinical outcomes via set-modeling of cytometry data. H. Yi and **N. Stanley**. **Proceedings of the 12th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)**. 2021.

25. Objective Activity Parameters Track Patient-Specific Recovery Trajectories After Surgery and Link With Individual Preoperative Immune States. R. Fallahzadeh, F. Verdonk, E. Ganio, A. Culos, **N. Stanley**, I. Maric, AL Chang, M. Becker, T. Phongpreecha, M. Xenochristou, D. De Francesco, C. Espinosa, X. Gao, A. Tsai, P. Sultan, M. Tingle, DF Amanatullah, JI Huddleston, SB Goodman, B. Gaudilliere, MS Angst, N. Aghaeepour. **Annals of Surgery.** 2021.

24. MultImp: Multiomics Generative Models for Data Imputation. J. Park, W. Mu, Y. Jiao, MI Love, M. Niethammer, **N. Stanley**. **Proceedings of the 2021 ICML Workshop on Computational Biology.** 2021.

23. CytoSet: A Deep Learning Model for Predicting Clinical Outcomes from Cytometry Data. H. Yi and **N. Stanley**. **Proceedings of the AI For Public Health Workshop at ICLR.** 2021.

22. Integrated trajectories of the maternal metabolome, proteome, and immunome predict labor onset. I. Stelzer [et al. including **N. Stanley**]. **Science Translational Medicine.** 2021.

21. Proteomic signatures predict preeclampsia in individual cohorts but not across cohorts- implications for clinical biomarker studies. Gahemi [et al. including **N. Stanley**]. **The Journal of Maternal-Fetal and Neonatal Medicine.** 2021.

20. Multiomics Characterization of Preterm Birth in Low-and Middle-Income Countries. [et al. including **N. Stanley**]. **JAMA Network Open**. 2020

19. Single-cell peripheral immunoprofiling of Alzheimer's and Parkinson's diseases. T. Phongpreecha, R. Fernandez, D. Mrdjen, A. Culos, C.R Gajera, A.M Wawro, **N. Stanley**, B. Gaudilliere, K.L Poston, N. Aghaeepour, T.J Montine. **Science Advances.** 2020.

18. Integration of Mechanistic Immunological Knowledge into a Machine Learning Pipeline Increases Clinical Predictive Power. T. Culos [et al. including **N. Stanley**]. **Nature Machine Intelligence.** 2020.

17. VoPo Leverages Cellular Heterogeneity for Predictive Modeling of Single-Cell Data. **N. Stanley**, I. Stelzer, *et al.* **Nature Communications** 2020.

16. Glucocorticoid administration in patients with acute surgical trauma preferentially inhibits adaptive immune cell dynamics: A deep immune profiling clinical study. E. Ganio*, **N. Stanley***, V. Lindberg-Larsen*, *et al.* (*=co-first author). **Nature Communications**. 2020

15. Stochastic Block Models with Multiple Continuous Attributes. **N. Stanley**, T. Bonacci. R. Kwitt, M. Niethammer, PJ Mucha. **Applied Network Science**. 2019.

14. Guidelines for the Use of Flow Cytometry and Cell Sorting in Immunological Studies. A. Cossarizza [et al. including **N. Stanley**]. **European Journal of Immunology.** 2019.

13. Systemic Immunologic Consequences of Chronic Periodontitis. DK Gaudilliere, A. Culos, K. Djebali, AS Tsai, EA Ganio, WM Choi, X. Han, A. Maghaireh, B. Choisy, Q. Baca, JF Einhaus, JJ Hedou, B. Bertrand, K. Ando, R. Fallahzadeh, MS Ghaemi, R. Okada, **N. Stanley**, A. Tanada, M. Tingle, T. Alpagot, JA Helms, MS Angst, N. Aghaeepour, B. Gaudilliere. **Journal of Dental Research.** 2019.

12. Differential dynamics of the maternal immune system in healthy pregnancy and preeclampsia. X. Han, MS Ghaemi, Kazuo Ando, L. Peterson, EA Ganio, AS Tsai, DK Gaudilliere, J. Einhaus, B. Bertrand, **N. Stanley**, A. Culos, A. Taneda, ES Tsai, R. Fallahzadeh, RJ Wong, AE Judy, VD Winn, DL Maurice, YJ Blumenfeld, MA Hlatky, CC Quaintance, RS Gibbs, B. Carvalho, GM Shaw, DK Stevenson, MS Angst, N. Aghaeepour, B. Gaudilliere. **Frontiers in Immunology.** 2019.

11. A year-long immune profile of the systemic response in acute stroke survivors. AS Tsai, K. Berry, MM Beneyto, D. Gaudilliere, EA Ganio, A. Culos, MS Ghaemi, B. Choisy, K. Djebali, JF Einhaus, B. Bertrand, A. Tanada, **N. Stanley**, R. Fallahzadeh, Q. Baca, LN Quach, E. Osborn, L. Drag, MG. Lansberg, MS Angst, B. Gaudilliere, MS Buckwalter, N. Aghaeepour. **Brain**. 2019.

10. Multi-layer Large-Scale Functional Connectome Reveals Infant Brain Developmental Patterns. H. Zhang, **N. Stanley**, PJ Mucha, W. Yin, W. Lin, D. Shen. **International Conference on Medical Image Computing and Computer-Assisted Intervention. (MICCAI)**. 2018.

9. Multiomics Modeling of the Immunome, Transcriptome, Microbiome, Proteome, and Metabolome Adaptations During Pregnancy. MS Ghaemi, DB DiGiulio, K. Contrepois, B. Callahan, T. Ngo, B. Lee-McMullen, B. Lehallier, A. Robaczewska, D. Mcilwain, Y. Rosenberg-Hasson, R. J Wong, C. Quaintance, A. Culos, **N. Stanley**, A. Tanada, A. Tsai, D. Gaudilliere, E. Ganio, X. Han, K. Ando, L. McNeil, M. Tingle, P. Wise, I. Maric, M. Sirota, T. Wyss-Coray, V.D. Winn, M.L. Druzin, R. Gibbs, G.L. Darmstadt, D.B. Lewis, VP Nia, B. Agard, R. Tibshirani, G. Nolan, MP Snyder, DA Relman, SR Quake, GM Shaw, DK Stevenson, MS Angst, B. Gaudilliere, N. Aghaeepour. **Bioinformatics**. 2018.

8. Cezanne/OTUD7B is a cell cycle-regulated deubiquitinase that antagonizes the degradation of APC/C substrates. T. Bonacci, A. Suzuki, GD Grant, **N. Stanley**, JG Cook, NG Brown, MJ Emmanuele. **EmboJ**. 2018

7. Testing Alignment of Node Attributes with Network Structure Through Label Propagation. **N. Stanley**, M. Niethammer, P.J. Mucha. **Proceedings of the International Workshop on Mining and Learning with Graphs (MLG).** 2018.

6. Compressing Networks with Super Nodes. **N. Stanley**. R. Kwitt, M. Niethammer, P.J. Mucha. **Scientific Reports.** 2018

5. Case Studies in Network Community Detection. S. Shai, **N. Stanley**, C. Granell, D. Taylor, P.J. Mucha. **Book Chapter in Oxford Handbook of Social Networks.** 2017.

4. Identifying Security Critical Properties for the Dynamic Verification of a Processor. R. Zhang, **N. Stanley**, C. Griggs, A. Chi, C. Sturton. **ACM International Conference on Architectural Support For Programming Languages and Operating Systems (ASPLOS).** 2017.

3. Enhanced Detectability of Community Structure in Multilayer Networks Through Layer Aggregation. D. Taylor, S. Shai, **N. Stanley**, P.J. Mucha. **Physical Review Letters**. 2016.

2. Clustering Network Layers with the Strata Multilayer Stochastic Block Model. **N. Stanley**, S. Shai, D. Taylor, P.J. Mucha. **IEEE Transactions on Network Science and Engineering.** 2016.

1. Fenofibrate Unexpectedly Induces Cardiac Hypertrophy in Mice Lacking MuRF1. TL Parry, G. Desai, JC Schisler, L. Li, MT Quintana, **N. Stanley**, P. Lockyer, C. Patterson, MS Willis. **Cardiovascular Pathology.** 2016.

PUBLICATIONS AS PREPRINTS ONLY OR UNDER REVIEW WITHOUT PREPRINT

1. FastPG: Fast Clustering of Millions of Single Cells. M. Bodenheimer, M. Halappanavar, S. Jefferys, R. Gibson, S. Liu , P.J. Mucha, **N. Stanley**, J.S. Parker, S.R. Selitsky. FastPG: Fast Clustering of Millions of Single Cells. Preprint: `https://www.biorxiv.org/content/10.1101/2020.06.19.159749v1`.

TEACHING

- **Comp683: Computational Biology (Spring 2024)**
- **Comp790: Computational Biology (Spring 2023)**. 12 students
- **Comp790: Computational Biology (Spring 2022)**. 24 students
- **Comp790: Computational Biology (Spring 2021).**. 26 students.

GRADUATE STUDENTS MENTORED

- **Alec Plotkin.** 2022- Present. *PhD Student in Bioinformatics and Computational Biology @ UNC-Chapel Hill.* Co-mentored with Justin Milner (Microbiology and Immunology).
- **Emma Crawford.** 2021-Present. *PhD Student in Applied Mathematics @ UNC-Chapel Hill.*
- **Chi-Jane Chen.** 2021-Present. *PhD Student in Computer Science @ UNC-Chapel Hill.*
- **Vishal Baskaran**. 2021-2022. *Master's Student in Computer Science @ UNC-Chapel Hill.* Co-mentored with Junier Oliva (CS).
- **Haidong Yi**. 2020-Present. *PhD Student in Computer Science @ UNC-Chapel Hill*
- **Jolene Ranek**. 2020-2023. *PhD Student in Bioinformatics and Computational Biology @ UNC-Chapel Hill.* Co-mentored with Jeremy Purvis (Genetics). **Current Position:** Postdoc at Stanford.

UNDERGRADUATE STUDENTS MENTORED

- **Sneha Jaikumar.** 2021-Present. Undergraduate Student in Computer Science at UNC-Chapel Hill.
- **Ruoting Xia.** 2021-2022. Undergraduate Student in Computer Science and Mathematics at UNC-Chapel Hill.

- **Sean Xiao**. Summer 2015. Undergraduate Student in Computer Science and Mathematics at UNC-Chapel Hill.
- **Nic Larsen**. Summer 2015-2018 Undergraduate Student in Computer Science and Mathematics at UNC-Chapel Hill. Current: Statistics PhD Student at North Carolina State University.

INVITED TALKS

- **Vanderbilt University Quantitative and Systems Biology Seminar Series**. *Featurizing Multi-Sample CyTOF Datasets to Predict Clinical and Experimental Phenotypes.* September, 2023.

STUDENT COMMITTEES

- **Kathryn Kirchoff**. 2022-Present. PhD Student in Computer Science at UNC-Chapel Hill.
- **Siyuan Shan**. 2021-2022. PhD Student in Computer Science at UNC-Chapel Hill.
- **Matthew Regner**. 2021-Present. PhD Student in Bioinformatics and Computational Biology at UNC-Chapel Hill.
- **Lisa Bauer**. 2021-2022. PhD Student in Computer Science at UNC-Chapel Hill.

ACADEMIC SERVICE (COMMITTEES)

- Computer Science Faculty Search Committee (UNC). 2023-2024.
- Faculty Search Committee for the School of Data Science and Society and the Department of Computer Science (UNC). 2023.
- Lineberger Technology Committee (UNC). 2022-Present.
- Faculty Search Committee for the Department of Biostatistics (UNC).2022.
- Faculty Search Committee for the Computational Medicine Program and the Department of Mathematics (UNC). 2021-2022.
- Graduate Admissions Committee for Computational and Systems Biology (UNC Biological and Biomedical Science Program). 2021- Present
- UNC-Computer Science Graduate Admissions Committee. 2021-Present.
- Seminar Speaker Organizer for UNC-Computational Medicine. 2021-2022.

ACADEMIC SERVICE (JOURNAL AND CONFERENCE REVIEWER)

Genome Biology, Nature Communications, Elife, Bioinformatics, Scientific Reports, IEEE Transactions on Network Science and Engineering, Journal of Complex Networks, Physical Review E, Springer Nature, CompleNet 2019 (conference), SIAM Workshop on Network Science 2020 (conference)

RESEARCH SUMMARY

My students and I comprise the CompCy 'computational cytometry' lab at UNC-Chapel Hill. Our primary focus is in developing new computational methods for single-cell bioinformatics and computational immunology. We are specifically interested in designing new algorithms for extracting signals from experimental modalities, such as flow and mass cytometry. We particularly leverage techniques from numerical linear algebra, and graph signal processing to address these problems. We aim to apply the methods that we develop to flow and mass cytometry datasets generated from large clinical cohorts.