Keshav Motwani

PhD Student

Department of Biostatistics
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University of Washington

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EDUCATION

University of Washington, Seattle, Washington
Ph.D. in Biostatistics, September 2022 – June 2027 (expected)

- Coursework: Statistical inference, regression methods, applied biostatistics

University of Florida, Gainesville, Florida
B.S. in Statistics (*summa cum laude*), December 2021
B.S. in Mathematics (*cum laude*), December 2021

RESEARCH
EXPERIENCE

University of Washington, Seattle, Washington
Independent Study, June 2022 – Present

- Advisors: Ali Shojaie and Eardi Lila
- Multivariate restricted Haseman-Elston regression for variance component estimation in mixed effects models
- Application to estimation of covariance matrices of genetic and environmental components of functional MRI data

University of Washington, Seattle, Washington
Independent Study, September 2022 – Present

- Advisor: Daniela Witten
- Valid inference after using a machine learning model to predict the outcome variable
- Generalization of data thinning, an alternative to sample splitting in unsupervised settings, using sufficient statistics

University of Florida, Gainesville, Florida
Research Assistant, March 2020 – June 2022

- Advisors: Aaron J. Molstad and Rhonda Bacher
- High-dimensional multinomial regression with multiresolution/hierarchical categories
- Application to cell type prediction for single-cell gene expression data

University of Oslo, Oslo, Norway
Research Intern, May 2019 – July 2019

- Advisors: Victor Greiff and Geir Kjetil Sandve
- Software development for immune receptor sequencing data analysis and machine learning

University of Florida, Gainesville, Florida
Research Assistant, March 2017 – March 2020

- Advisor: Todd M. Brusko
- Analysis of immune receptor sequencing and single-cell gene expression data in the context of type 1 diabetes immunology

WORK
EXPERIENCE

10x Genomics, Pleasanton, California
Software Product Manager – Bioinformatics, August 2021 – June 2022

- Developed public-facing training materials for statistical analysis of single-cell

RNA-seq data with multi-condition experimental designs
- Defined product requirements and technical implementation details for adding cell-type specific multi-condition differential expression analysis to Loupe Browser
- Conducted user research on quality control and preprocessing using cellranger outputs and defined specific product requirements for future versions of cellranger

PREPRINTS &
SUBMITTED
MANUSCRIPTS

Methods

1. **Keshav Motwani** and Daniela Witten. Valid inference after prediction. *arXiv*, 2023

2. Ameer Dharamshi, Anna Neufeld, **Keshav Motwani**, Lucy L Gao, Daniela Witten, and Jacob Bien. Generalized data thinning using sufficient statistics. *arXiv*, 2023

PUBLICATIONS

Methods

1. Aaron J Molstad and **Keshav Motwani**. Multiresolution categorical regression for interpretable cell type annotation. *In press at Biometrics*, 2022

2. **Keshav Motwani**, Rhonda Bacher, and Aaron J Molstad. Binned multinomial logistic regression for integrative cell type annotation. *In press at Annals of Applied Statistics*, 2021

Applied

1. Melanie R Shapiro, Xiaoru Dong, Daniel Perry, James M McNichols, Puchong Thirawatananond, Amanda L Posgai, Leeana Peters, **Keshav Motwani**, Richard Musca, Andrew Muir, and others. Human immune phenotyping reveals accelerated aging in type 1 diabetes. *JCI Insight*, 2023

2. Chakravarthi Kanduri, Milena Pavlovic, Lonneke Scheffer, **Keshav Motwani**, Maria Chernigovskaya, Victor Greiff, and Geir K Sandve. Profiling the baseline performance and limits of machine learning models for adaptive immune receptor repertoire classification. *GigaScience*, 11, 2022

3. Milena Pavlovic, Lonneke Scheffer, **Keshav Motwani**, Chakravarthi Kanduri, Radmila Kompova, Nikolay Vazov, Knut Waagan, Fabian LM Bernal, Alexandre Almeida Costa, Brian Corrie, and others. immuneML: an ecosystem for machine learning analysis of adaptive immune receptor repertoires. *Nature Machine Intelligence*, 2021

4. Peter S Linsley, Fariba Barahmand-pour Whitman, Elisa Balmas, Hannah A DeBerg, Kaitlin J Flynn, Alex K Hu, Mario G Rosasco, Janice Chen, Colin ORourke, Elisavet Serti, Vivian H Gersuk, **Keshav Motwani**, and others. Autoreactive t cell receptors with shared germline-like α chains in type 1 diabetes. *JCI Insight*, 2021

5. **Keshav Motwani**, Leeana D Peters, Willem H Vliegen, Ahmed Gomaa El-Sayed, Howard R Seay, M Cecilia Lopez, Henry V Baker, Amanda L Posgai, Maigan A Brusko, Daniel J Perry, and others. 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

6. Emmi-Leena Ihantola, Henna Ilmonen, Anssi Kailaanmaki, Marja Rytkonen-Nissinen, Aurelien Azam, Bernard Maillere, Cecilia S Lindestam Arlehamn, Alessandro Sette, **Keshav Motwani**, Howard R Seay, and others. Characterization of proinsulin T cell epitopes restricted by type 1 diabetes–associated HLA class II molecules. *The Journal of Immunology*, 204(9):2349–2359, 2020

7. Mohsen Khosravi-Maharlooei, Aleksandar Obradovic, Aditya Misra, **Keshav Motwani**, Markus Holzl, Howard R Seay, Susan DeWolf, Grace Nauman, Nichole Danzl, Haowei Li, and others. Cross-reactive public TCR sequences undergo positive

selection in the human thymic repertoire. *The Journal of Clinical Investigation*, 129(6):2446–2462, 2019

CONTRIBUTED CONFERENCE PRESENTATIONS

1. **Keshav Motwani**, Milena Pavlovic, Geir Kjetil Sandve, Victor Greiff, and Todd M Brusko. T-cell receptor repertoires in peripheral blood encode type 1 diabetes status. In *Adaptive Immune Receptor Repertoire Community Meeting*, Genoa, Italy, May 2019

2. **Keshav Motwani** and Todd M Brusko. The T cell receptor CDR3B contains sequence motifs that predict disease state in nPOD samples. In *Network for Pancreatic Organ Donors with Diabetes (nPOD) Annual Meeting*, Hollywood, FL, February 2018

SOFTWARE

1. **Keshav Motwani**. *mvREHE: R/C++ package for estimating covariance components in multivariate mixed models using restricted Haseman-Elston regression*, 2023. https://github.com/keshav-motwani/mvREHE

2. **Keshav Motwani**. *IBMR: R/C++ package for fitting the integrative binned multinomial regression model*, 2021. https://github.com/keshav-motwani/IBMR

3. **Keshav Motwani**. *MultiLORS: R/C++ package for fitting a multi-dataset version of the LORS model proposed by Yang et al.*, 2021. https://github.com/keshav-motwani/MultiLORS

4. Milena Pavlovic, Lonneke Scheffer, **Keshav Motwani**, Victor Greiff, and Geir Kjetil Sandve. *immuneML: A platform for machine learning analysis of adaptive immune receptor repertoire data*, 2021. https://github.com/uio-bmi/immuneML

5. **Keshav Motwani**. *scanalysis: Multi-sample visualization and immune repertoire analysis utilities for single-cell data*, 2019. https://github.com/keshav-motwani/scanalysis

HONORS AND AWARDS

2022-2027	**NSF Graduate Research Fellowship** ($138000)
2022	Excellence Award ($10000)
	(Department of Biostatistics, University of Washington)
2021	University Scholar ($1750)
	(Center for Undergraduate Research, University of Florida)
2020	**Goldwater Scholar** ($15000)
2019	Summer International Undergraduate Research Program ($5000)
	(Center for Undergraduate Research, University of Florida)
2018	University Scholar ($1750)
	(Center for Undergraduate Research, University of Florida)
2018-2021	Florida Academic Scholar's Award (full tuition)
	(Florida Bright Futures Scholarship Program)

SERVICE

- UF Undergraduate Scholars Research Program Advisory Committee (2018-2020)
- UF American Physician Scientists Association Bioinformatics Director (2018-2020)

SKILLS

Advanced: R, C++, Python, git
Intermediate: Bash, LaTeX
Basic: MATLAB, Java