

Keshav Motwani

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PhD Student

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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
- Extension of Haseman-Elston regression for variance component estimation to the multivariate setting
- Application to estimation of covariance matrices of genetic and environmental components of neuroimaging measurements

University of Washington, Seattle, Washington

Independent Study, September 2022 – Present

- Advisor: Daniela Witten
- Empirical comparison of methods for inference using a predicted response variable

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

Methods

1. Ameer Dharamshi, Anna Neufeld, **Keshav Motwani**, Lucy L Gao, Daniela Witten, and Jacob Bien. Generalized data thinning using sufficient statistics. *arXiv*, 2023
2. Aaron J Molstad and **Keshav Motwani**. Multiresolution categorical regression for interpretable cell type annotation. *arXiv, minor revision at Biometrics*, 2022
3. **Keshav Motwani**, Rhonda Bacher, and Aaron J Molstad. Binned multinomial logistic regression for integrative cell type annotation. *arXiv, minor revision 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. *bioRxiv, submitted to Science Immunology*, 2023

Applied

1. 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
2. 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
3. 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
4. **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
5. Emmi-Leena Ihantola, Henna Ilmonen, Anssi Kailaanmaki, Marja Rytönen-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
6. Mohsen Khosravi-Maharlooei, Aleksandar Obradovic, Aditya Misra, **Keshav Motwani**, Markus Holz, 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

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**, Milena Pavlovic, Geir Kjetil Sandve, Victor Greiff, and Todd M Brusko. T-cell receptor repertoires in peripheral blood encode type 1 diabetes status. In *NIH Human Islet Research Network Annual Meeting*, Washington, DC, April 2019
3. **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**. *IBMR: R/C++ package for fitting the integrative binned multinomial regression model*, 2021. <https://github.com/keshav-motwani/IBMR>
2. **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>
3. 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>
4. **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