

Mykhaylo M Malakhov

mykmal.xyz | malak039@umn.edu | (530) 840-6245

EDUCATION

UNIVERSITY OF MINNESOTA

PHD IN BIOSTATISTICS

Expected 2025 | Minneapolis, MN

Advised by Wei Pan

Funded by an NIH T32 grant

ANDREWS UNIVERSITY

BS IN MATHEMATICS

May 2020 | Berrien Springs, MI

Minor in Computing

J. N. Andrews Honors Scholar

BUDAPEST SEMESTERS IN MATHEMATICS

STUDY ABROAD

Fall 2019 | Budapest, Hungary

LINKS

Twitter: twitter.com/MykMal

LinkedIn: [linkedin.com/in/mykmal](https://www.linkedin.com/in/mykmal)

GitHub: github.com/MykMal

ORCID: [0000-0002-6856-3913](https://orcid.org/0000-0002-6856-3913)

Google Scholar: [e5Q7sMQAAAAAJ&hl](https://scholar.google.com/citations?user=e5Q7sMQAAAAAJ&hl)

GRADUATE COURSES

THEORY

- Honors Real Analysis I & II
- Theory of Statistics I & II
- Biostatistics: Regression
- Advanced Regression and Design
- Linear Models
- Probability Models for Biostatistics
- Advanced Statistical Inference
- Bayesian Decision Theory and Data Analysis
- Survival Analysis

ELECTIVES

- Statistics for Human Genetics and Molecular Biology
- Advanced Statistical Genetics and Genomics
- GIS and Spatial Analysis for Public Health
- Statistical Learning and Data Mining
- Seminar: Transethnic Association Studies
- Seminar: Imaging Genetics
- Seminar: Bioinformatics Methods

OTHER

- Research Skills in Biostatistics
- Foundations of Public Health
- Biomedical Ethics

CURRENT POSITIONS

DENALI THERAPEUTICS | HUMAN GENETICS INTERN

Summer 2023 | South San Francisco, CA

- Leveraging public GWAS data to better understand the molecular mechanisms of genetic variants associated with neurodegenerative disease
- Developing computational infrastructure to internalize, store, and readily access public GWAS data

UNIVERSITY OF MINNESOTA | PREDOCTORAL TRAINEE

2020 - present | Minneapolis, MN

- Proposed and implemented DRAB (Differential Regulation Analysis by Bootstrapping), a statistical framework for identifying genes with context-specific patterns of local genetic regulation
- Currently working on ensemble learning methods for more accurate transcriptome imputation
- Currently working on boosting GWAS power by integrating proteomics data

PUBLICATIONS

1. **M. M. Malakhov**, B. Dai, X. T. Shen, W. Pan, A bootstrap model comparison test for identifying genes with context-specific patterns of genetic regulation. *bioRxiv*, (<https://doi.org/10.1101/2023.03.06.531446>) (Mar. 2023).
2. Z. Lin, H. Xue, **M. M. Malakhov**, K. A. Knutson, W. Pan, Accounting for nonlinear effects of gene expression identifies additional associated genes in transcriptome-wide association studies. *Human Molecular Genetics* **31**, 2462–2470, (<https://doi.org/10.1093/hmg/ddac015>) (Jan. 2022).
3. J. C. Blackwood, **M. M. Malakhov**, J. Duan, J. J. Pellett, I. S. Phadke, S. Lenhart, C. Sims, K. Shea, Governance structure affects transboundary disease management under alternative objectives. *BMC Public Health* **21**, (<https://doi.org/10.1186/s12889-021-11797-3>) (Oct. 2021).
4. J. Duan, **M. M. Malakhov**, J. J. Pellett, I. S. Phadke, J. Barber, J. C. Blackwood, Management efficacy in a metapopulation model of white-nose syndrome. *Natural Resource Modeling* **34**, e12304, (<https://doi.org/10.1111/nrm.12304>) (Apr. 2021).

SELECTED AWARDS

National

2018 Barry M. Goldwater Scholarship

University of Minnesota

2022 1st place, People's Choice Award at the SPH Research Day conference

2022 2nd place, Best Poster Award at the SPH Research Day conference

2022 3rd place in the Interdisciplinary Health Data Competition

2020 Dean's PhD Scholars Award

2020 Jean Roberts Biostatistics Fellowship

Andrews University

2018 Harold T. Jones Scholarship for highest mathematical excellence

2018 Louis Ulloth Scholarship for most significant leadership

2016 Full tuition ACT/SAT Scholarship