# Mykhaylo M Malakhov

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## EDUCATION

### UNIVERSITY OF MINNESOTA
PHD in Biostatistics
Expected 2025 | Minneapolis, MN
Funded by an NIH T32 grant
Advised by Wei Pan

### 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**
GitHub: **github.com/MykMal**
ORCID: **0000-0002-6856-3913**
Google Scholar: **e5Q7sMQAAAAJ&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

### ELECTIVES
○ Statistics for Human Genetics and Molecular Biology
○ Advanced Statistical Genetics and Genomics
○ GIS and Spatial Analysis for Public Health
○ Seminar: Transethnic Association Studies
○ Seminar: Imaging Genetics
○ Seminar: Bioinformatics Methods

### OTHER
○ Research Skills in Biostatistics
○ Foundations of Public Health
○ Biomedical Ethics

## EXPERIENCE

### UMN SCHOOL OF PUBLIC HEALTH | Predoctoral Trainee
2020 - present | Minneapolis, MN
- Helped develop a nonlinear extension of the transcriptome-wide association study (TWAS) framework and showed that it identifies genes missed by standard TWAS
- Proposed and implemented DRAB (Differential Regulation Analysis by Bootstrapping), a method for identifying genes with context-specific patterns of genetic regulation
- Currently working on leveraging proteomics data to boost the power of genome-wide association studies (GWAS)

### INSTITUTE FOR PURE & APPLIED MATHEMATICS | Researcher
Summer 2019 | Los Angeles, CA
- Proposed novel attractor reconstruction and model calibration methods
- Showcased these methods by inferring reaction rate coefficients for hydrogen-oxygen combustion from a time series of one observable

### WILLIAMS COLLEGE | Research Intern
Summer 2018 | Williamstown, MA
- Project 1: demonstrated how to improve management outcomes for white-nose syndrome in bats by considering metapopulation dynamics
- Project 2: established guidelines for transboundary infectious disease management when multiple administrative jurisdictions set different objectives

## PUBLICATIONS

1. **Malakhov MM**, Dai B, Shen XT, and Pan W. Identifying genes with tissue-specific patterns of genetic regulation. In preparation.

2. Lin Z, Xue H, **Malakhov MM**, Knutson KA, and Pan W. Accounting for nonlinear effects of gene expression identifies additional associated genes in transcriptome-wide association studies. Human Molecular Genetics 2022;31:2462–70.

3. Blackwood JC, **Malakhov MM**, Duan J, Pellett JJ, Phadke IS, Lenhart S, Sims C, and Shea K. Governance structure affects transboundary disease management under alternative objectives. BMC Public Health 2021;21.

4. Duan J, **Malakhov MM**, Pellett JJ, Phadke IS, Barber J, and Blackwood JC. Management efficacy in a metapopulation model of white-nose syndrome. Natural Resource Modeling 2021;34:e12304.

## SELECTED AWARDS

**National**

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| 2018 | Barry M. Goldwater Scholarship |

**University of Minnesota**

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| 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**

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| 2018 | Harold T. Jones Scholarship for highest mathematical excellence |
| 2018 | Louis Ulloth Scholarship for most significant leadership |
| 2016 | Full tuition ACT/SAT Scholarship |