Andrew Beck

PhD Candidate, Department of Biostatistics
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EDUCATION

Ph.D., Biostatistics, University of Michigan 2018 - 2025 (expected)
Thesis: *Investigations into Mutation Rates and Statistical Phasing Errors*

Master of Science, Biostatistics, University of Michigan 2014 - 2016

Master of Science, Applied Statistics, Loyola University Chicago 2013 - 2014

Bachelor of Science, Mathematics, Loyola University Chicago 2009 - 2013

RESEARCH EXPERIENCE

Graduate Student, University of Michigan (PI: Sebastian Zöllner, PhD) 2018 -

- Analyzed germline mutation rates by developing a novel statistical model, integrating singleton mutations and control sampling to quantify the influence of neighboring nucleotides.
- Analyzed and benchmarked three statistical phasing methods with human sequencing data, detailing the causes and locations of phasing errors.
- Developed statistical models to predict the locations of statistical phasing errors.

Trainee, Genome Science Training Program, University of Michigan 2014 - 2016

- Analyzed mRNA sequencing data to identify genes differentially expressed in skeletal muscle biopsy tissues samples between Type 2 diabetics and controls.

TEACHING AND MENTORSHIP EXPERIENCE

Lecturer, Big Data Summer Institute, University of Michigan June 2023, 2024

- Lead a seminar on applied linear regression analysis using R

Teaching Assistant, Big Data Summer Institute, University of Michigan June - July 2022

- Assisted in the design of summer research projects in Genomics.
- Mentored students using R, python, bash, and other tools to organize and analyze large datasets from genetic sequencing and methylation studies.

PROFESSIONAL EXPERIENCE

Software Developer, Epic Systems, Verona, WI 2016 - 2018

- Implemented social determinants of health documentation and visualizations in the patent record for Epic's Healthy Planet population health management module.

PUBLICATIONS

1. Hainline, A., Alvarez, C., Luedtke, A., Greco, B., Beck, A., & Tintle, N. L. (2014). Evaluation of the power and type I error of recently proposed family-based tests of association for rare variants. BMC Proceedings, 8(Suppl 1). PMCID: PMC4143711
2. Greco, B., Luedtke, A., Hainline, A., Alvarez, C., Beck, A., & Tintle, N. L. (2014). Application of family-based tests of association for rare variants to pathways. BMC Proceedings, 8(Suppl 1). PMCID: PMC4143675
3. Rogers, A., Beck, A., & Tintle, N. L. (2014). Evaluating the concordance between sequencing, imputation and microarray genotype calls in the GAW18 data. BMC Proceedings, 8(Suppl 1). PMCID: PMC4143748

4. Scott, L. J., Erdos, M. R., Huyghe, J. R., Welch, R. P., Beck, A. T., Wolford, B. N., . . . Parker, S. C. (2016). The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 7(1). PMCID: PMC4931250
5. Beck, A., Luedtke, A., Liu, K., & Tintle, N. (2016). A Powerful Method For Including Genotype Uncertainty In Tests Of Hardy-Weinberg Equilibrium. Pac Symp Biocomput. 2017. PMCID: PMC5149397
6. M. E. K. Niemi, J. Karjalainen, R. G. Liao, B. M. Neale, et al., (2021) Mapping the human genetic architecture of COVID-19. Nature 600: 472–477. PMCID: PMC8674144

Preprints

1. Beck, A., Zöllner, S., Kang, H. (2025+) A Benchmark of Modern Statistical Phasing Methods. bioRxiv: 2025.06.24.660794

Presentations

1. B. Wolford, S. C. Hanks, L. Taylor, A. U. Jackson, A. Varshney, N. Manickam, A. Ramirez, **A. T. Beck**, H. M. Stringham, P. Orchard, N. Narisu, L. Bonnycastle, M. Erdos, M. Sweeney, J. Tuomilehto, M. Melbye, T. Lakka, M. Laakso, H. Koistinen, F. Collins, M. Boehnke, S. C. J. Parker, L. J. Scott. “Differential gene expression and regulation at single nucleus resolution in muscle of statin users” ASHG Annual Meeting. Washington, DC. November 2023
2. **Beck, A, T.**, Si, Y., Kang, H.M., Zoellner, S. “Evaluating the impact of parallel mutations on the accuracy of statistical phasing” ASHG Annual Meeting. Los Angeles, CA. November 2022
3. **Beck, A. T.**, Zoellner, S., Li, J. Z., “Exploring the role of local sequence context on patterns of germline mutation” ASHG Annual Meeting. Virtual. November 2021
4. **Beck, A. T.**, Zoellner, S., Li, J.Z., “The Impact of Local Sequence Context on Patterns of Germline Mutation” iBRIGHT. Houston, TX. November 2019
5. Scott, L. J., Erdos, M. R., Huyghe, J. R., Welch, R. P., **Beck, A. T.**, Wolford, B. N., . . . Parker, S. C. “Differential expression and gene ontology enrichment analysis of 271 diabetic and non-diabetic Finnish individuals” NHGRI Research Training and Career Development Annual Meeting. Bethesda, MD. April 2016

6. C. Fu, M. O'Connell, A. Benitez, J. Arbet, K. Grinde, K. Liu, A. Luedtke, **A. Beck**, N. Tintle. “Powerful methods for including genotype uncertainty in tests of HardyWeinberg Equilibrium”. ASHG Annual Meeting. Boston, MA. November 2013
7. **Beck, A.T.**, Alvarez, C., Hainline, A., Greco, B., Tintle, N. "Testing Hardy-Weinberg equilibrium in the presence of genotype uncertainty" 1000 Genomes Project Community Meeting. Ann Arbor, MI. July 2012

Honors and Awards

iBRIGHT Conference Travel Award, 2019

University Service

Student Representative, Biostatistics Faculty Meetings, 2021 - 2022

Student Member, Biostatistics Search Committee, 2019 - 2020