Jedidiah Carlson, Ph.D.

POPULATION GENETICS | BIOINFORMATICS | METARESEARCH

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💼 Professional Experience

Bioinformatics Scientist I — *Minneapolis, MN*
TwinStrand Biosciences — *01/2022 - present*

Senior Research Scientist — *Minneapolis, MN*
Helix — *02/2021 - 10/2021*

Postdoctoral Fellow — *Seattle, WA*
University of Washington — Department of Genome Sciences — *11/2018 - 02/2021*

🏛 Education

University of Michigan — *Ann Arbor, MI*
Ph.D., Bioinformatics — *2015-2018*

- Dissertation title: "Mapping the Landscape of Mutation Rate Heterogeneity in the Human Genome: Approaches and Applications"
- Doctoral co-advisers: Sebastian Zöllner & Jun Z. Li

University of Michigan — *Ann Arbor, MI*
M.S., Biostatistics — *2013-2015*

- Certificate in Public Health Genetics

Bethel University — *St. Paul, MN*
B.A., Mathematics — *2008-2011*

📄 Publications

- D Taliun, DN Harris, MD Kessler, **J Carlson**, ZA Szpiech, R Torres, et al. Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature*. (2021). [doi:10.1038/s41586-021-03205-y].
- LA Bergeron, S Besenbacher, TN Turner, CJ Versoza, R Wang, AL Price, et al. Mutationathon: towards standardization in estimates of pedigree-based germline mutation rates. *biorxiv*. (2021). [doi:10.1101/2021.08.30.458162].
- **J Carlson**, K Harris. The apportionment of citations: A scientometric analysis of Lewontin, 1972. *biorxiv*. (2021). [doi:10.1101/2021.09.19.460985].
- JR Adrion, CB Cole, N Dukler, JG Galloway, AL Gladstein, G Gower, et al. A community-maintained standard library of population genetic models. *eLife*. (2020). [doi:10.7554/eLife.54967].
- **J Carlson**, WS DeWitt, K Harris. Inferring evolutionary dynamics of mutation rates through the lens of mutation spectrum variation. *Current Opinion in Genetics and Development*. (2020). [doi:10.1016/j.gde.2020.05.024].
- **J Carlson**, K Harris. Quantifying and contextualizing the impact of bioRxiv preprints through automated social media audience segmentation. *PLoS Biology*. (2020). [doi:10.1371/journal.pbio.3000860].
- **J Carlson**, AE Locke, M Flickinger, M Zawistowski, S Levy, RM Myers, et al. Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. *Nature Communications*. (2018). [doi:10.1038/s41467-018-05936-5].
- **J Carlson**, JZ Li, S Zöllner. Helmsman: Fast and efficient mutation signature analysis for massive sequencing datasets. *BMC Genomics*. (2018). [doi:10.1186/s12864-018-5264-y].

💲 Research Funding

Translational Data Science Postdoctoral Fellowship
Fred Hutchinson Cancer Research Center — *2019-2021*

Genome Sciences Travel Award
University of Washington Department of Genome Sciences — *2019*

Rackham Travel Grant
University of Michigan — *2015, 2016, 2017*

University of Michigan Genome Science Training Program Fellowship (T32 HG00040)
National Human Genome Research Institute — *2013-2016*

🗨 Conferences Presentations and Invited Talks ───────────

EvolGenome Seminar   *Stanford, CA*
[INVITED TALK][VIRTUAL]   *11/2021*

NIH Bibliometrics & Research Assessment Symposium   *Bethesda, MD*
[CONTRIBUTED TALK][VIRTUAL]   *10/2020*

Germline Mutation Rate Workshop   *Copenhagen, DK*
[CONTRIBUTED TALK][VIRTUAL]   *06/2020*

University College London ReproducibiliTea Journal Club   *London, UK*
[INVITED TALK][VIRTUAL]   *06/2020*

Probabilistic Modeling in Genomics   *Aussois, FR*
[POSTER]   *10/2019*

Biology of Genomes Meeting   *Cold Spring Harbor, NY*
[POSTER]   *05/2019*

University of Washington Department of Genome Sciences   *Seattle, WA*
[INVITED TALK]   *02/2018*

Brown Unviersity Center for Computational Molecular Biology   *Providence, RI*
[INVITED TALK]   *02/2018*

DNA Repair and Genome Instability Satellite Meeting, 67th Annual Meeting of The American Society of Human Genetics   *Orlando, FL*
[INVITED TALK]   *10/2017*

67th Annual Meeting of The American Society of Human Genetics   *Orlando, FL*
[POSTER]   *10/2017*

Fourth Midwest Population Genetics Conference   *East Lansing, MI*
[POSTER]   *07/2017*

DNA Repair and Genome Instability Satellite Meeting, 66th Annual Meeting of The American Society of Human Genetics   *Vancouver, BC*
[INVITED TALK]   *10/2016*

66th Annual Meeting of The American Society of Human Genetics   *Vancouver, BC*
[POSTER]   *10/2016*

Third Midwest Population Genetics Conference   *Chicago, IL*
[CONTRIBUTED TALK]   *07/2016*

Keystone Symposia: Understanding the Function of Human Genome Variation   *Uppsala, SE*
[POSTER]   *06/2016*

NHGRI Research Training and Career Development Annual Meeting   *Bethesda, MD*
[POSTER]   *05/2016*

Second Midwest Population Genetics Conference   *Ann Arbor, MI*
[CONTRIBUTED TALK]   *07/2015*

Biology of Genomes Meeting   *Cold Spring Harbor, NY*
[POSTER]   *05/2015*

First Midwest Population Genetics Conference   *Chicago, IL*
[POSTER]   *07/2014*

🖥 Teaching Experience ────────────────────────

Big Data Summer Institute   *University of Michigan*
INSTRUCTOR   *2016, 2017, 2018*

Department of Mathematics and Computer Science   *Bethel University*
TEACHING ASSISTANT AND GROUP TUTOR   *2009-2011*

Department of Physics   *Bethel University*
TEACHING ASSISTANT   *2011*

🏅 Honors and Awards ──────────────────────────

Paper selected as 'Editor's Top Pick'

PLOS Biology   *05/2021*

Invited moderator for 'Natural Selection and Human Phenotypes' session

67th Annual Meeting of The American Society of Human Genetics   *10/2017*

Awarded 'Best Graduate Student Talk'

Fourth Midwest Population Genetics Conference   *07/2017*

Sigma Zeta Honor Society

Bethel University   *2009-2012*

President's Scholarship

Bethel University   *2008-2012*

Edgar G. Johnson Physics Scholarship

Bethel University   *2008-2012*

National Merit Scholar

Bethel University   *2008-2012*

⊕ Service

***Ad hoc* reviewer**

Bioinformatics, Biology Direct, BMC Biology, eLife, Genome Research, Nature Communications, PLOS Biology, PLOS Computational Biology, Science

Coordinator

University of Michigan Interdisciplinary Group Seminar   *2016-2017*

Organizing committee

2nd Midwest Population Genetics Conference   *2015*

▦ Media

Twitter's Science Stars Fight Misinformation   *The Scientist*

                                                                                                       01/2022

Scientific Studies are Distorted on Social Media   *KNKX Public Radio*

                                                                                                       09/2020

The Misinformation Virus   *BBC Radio 4*

                                                                                                       12/2019

'It's a toxic place.' How the online world of white nationalists distorts population genetics   *Science*

                                                                                                       05/2018

The Ancient Origins of Both Light and Dark Skin   *The Atlantic*

                                                                                                       10/2017

Will the Alt-Right Promote a New Kind of Racist Genetics?   *The Atlantic*

                                                                                                       12/2016

🧠 Skills

Analytical

Statistical Machine Learning — Topic Modeling — Regression — ANOVA — Anomaly Detection — Dimensionality Reduction — Big Data

Programming

R — Python — SQL — mongoDB — Perl — Julia

Tools

Git — Docker — Jupyter — RStudio — Apache Spark — AWS