

Jedidiah Carlson, Ph.D.

POPULATION GENETICS | BIOINFORMATICS | METARESEARCH

Minneapolis, Minnesota, USA

✉ jed [dot] e [dot] carlson [at] gmail [dot] com

🏠 jedidiahcarlson.com | 📄 carjed | 🌐 carjed | 🐦 jedmsp | ☎ 0000-0002-1363-872X

📁 Professional Experience

Research Associate

THE UNIVERSITY OF TEXAS AT AUSTIN — DEPARTMENT OF INTEGRATIVE BIOLOGY

11/2022 - present

Bioinformatics Scientist I

TWINSTRAND BIOSCIENCES

01/2022 - 10/2022

Senior Research Scientist

HELIX

02/2021 - 10/2021

Postdoctoral Fellow

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

M.S., BIOSTATISTICS

2013-2015

- Certificate in Public Health Genetics

Bethel University

St. Paul, MN

B.A., MATHEMATICS

2008-2011

📄 Publications

- K Liao, **J Carlson**, S Zöllner. The effect of mutation subtypes on the allele frequency spectrum and population genetics inference. *G3 Genes|Genomes|Genetics*. (2023). [doi:10.1093/g3journal/jkad035].
- **J Carlson**, BM Henn, DR Al-Hindi, S Ramachandran. Counter the weaponization of genetics research by extremists. *Nature*. (2022). [doi:10.1038/d41586-022-03252-z].
- LA Bergeron, S Besenbacher, T Turner, CJ Versoza, RJ Wang, AL Price, et al. The mutationathon highlights the importance of reaching standardization in estimates of pedigree-based germline mutation rates. *eLife*. (2022). [doi:10.7554/elife.73577].
- **J Carlson**, K Harris. The apportionment of citations: A scientometric analysis of Lewontin 1972. *Philosophical Transactions of the Royal Society B: Biological Sciences*. (2022). [doi:10.1098/rstb.2020.0409].
- 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].
- 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

Society for the Study of Evolution President's Symposium

[INVITED TALK][VIRTUAL]

Albuquerque, NM

6/2023

Stanford University School of Medicine

[INVITED TALK]

Stanford, CA

12/2022

King's College London Social, Genetic, and Developmental Psychiatry Centre

[INVITED TALK][VIRTUAL]

London, UK

12/2022

Brown University Data Science Initiative

[INVITED TALK]

Providence, RI

11/2022

Johns Hopkins University, Project Bridge SciComm

[INVITED TALK][VIRTUAL]

Baltimore, MD

10/2022

University of Bristol Inclusive Research Collective

[INVITED TALK][VIRTUAL]

Bristol, UK

6/2022

Stanford University EvolGenome Seminar

[INVITED TALK][VIRTUAL]

Stanford, CA

11/2021

NIH Bibliometrics & Research Assessment Symposium

[CONTRIBUTED TALK][VIRTUAL]

Bethesda, MD

10/2020

Germline Mutation Rate Workshop

[CONTRIBUTED TALK][VIRTUAL]

Copenhagen, DK

06/2020

University College London ReproducibiliTea Journal Club

[INVITED TALK][VIRTUAL]

London, UK

06/2020

Probabilistic Modeling in Genomics

[POSTER]

Aussois, FR

10/2019

Biology of Genomes Meeting

[POSTER]

Cold Spring Harbor, NY

05/2019

University of Washington Department of Genome Sciences

[INVITED TALK]

Seattle, WA

02/2018

Brown University Center for Computational Molecular Biology

[INVITED TALK]

Providence, RI

02/2018

DNA Repair and Genome Instability Satellite Meeting, 67th Annual Meeting of The American Society of Human Genetics

[INVITED TALK]

Orlando, FL

10/2017

67th Annual Meeting of The American Society of Human Genetics

[POSTER]

Orlando, FL

10/2017

Fourth Midwest Population Genetics Conference

[POSTER]

East Lansing, MI

07/2017

DNA Repair and Genome Instability Satellite Meeting, 66th Annual Meeting of The American Society of Human Genetics

[INVITED TALK]

Vancouver, BC

10/2016

66th Annual Meeting of The American Society of Human Genetics

[POSTER]

Vancouver, BC

10/2016

Third Midwest Population Genetics Conference

[CONTRIBUTED TALK]

Chicago, IL

07/2016

Keystone Symposia: Understanding the Function of Human Genome Variation

[POSTER]

Uppsala, SE

06/2016

NHGRI Research Training and Career Development Annual Meeting

[POSTER]

Bethesda, MD

05/2016

Second Midwest Population Genetics Conference

[CONTRIBUTED TALK]

Ann Arbor, MI

07/2015

Biology of Genomes Meeting

[POSTER]

Cold Spring Harbor, NY

05/2015

First Midwest Population Genetics Conference

[POSTER]

Chicago, IL

07/2014

Teaching Experience

Big Data Summer Institute

INSTRUCTOR

University of Michigan

2016, 2017, 2018

Department of Mathematics and Computer Science

TEACHING ASSISTANT AND GROUP TUTOR

Bethel University

2009-2011

Department of Physics

TEACHING ASSISTANT

Bethel University

2011

Honors and Awards

Paper selected as 'Editor's Top Pick'

PLOS BIOLOGY

05/2021

Paper featured in Nature Research Highlights

NATURE

09/2020

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, Nature Machine Intelligence, PLOS Biology, PLOS Computational Biology, The Quarterly Review of Biology, Science

Coordinator

UNIVERSITY OF MICHIGAN INTERDISCIPLINARY GROUP SEMINAR

2016-2017

Organizing committee

2ND MIDWEST POPULATION GENETICS CONFERENCE

2015

Media

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[AUTHOR]

Science for the People

09/2022

The Twisted 'Science' of Great Replacement Theory

[INTERVIEW]

Darts and Letters

06/2022

It's Not Just Great Replacement Theory That Influenced the Buffalo Shooter

[SOURCE]

Gizmodo

05/2022

Twitter's Science Stars Fight Misinformation

[SOURCE]

The Scientist

01/2022

Scientific Studies are Distorted on Social Media

KNKX Public Radio

[INTERVIEW]

09/2020

The Misinformation Virus

BBC Radio 4

[INTERVIEW]

12/2019

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

Science

[INTERVIEW]

05/2018

The Ancient Origins of Both Light and Dark Skin

The Atlantic

[SOURCE]

10/2017

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

The Atlantic

[SOURCE]

12/2016

Skills

Analytical

STATISTICAL MACHINE LEARNING — TOPIC MODELING — REGRESSION — ANOVA — ANOMALY DETECTION — DIMENSIONALITY
REDUCTION — BIG DATA

Programming

R — PYTHON — MONGODB — PERL — JULIA

Tools

GIT — DOCKER — JUPYTER — RSTUDIO — APACHE SPARK — AWS — IGV