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Bryan Thornlow

Computational Biologist

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EDUCATION

Ph.D., Biomolecular Engineering, University California, Santa Cruz
Bachelor of Science, Biological Sciences, Cornell University

September 2016 — October 2021
September 2011 — May 2015

PUBLICATIONS

- 2021 Turakhia Y, **Thornlow B**, Hinrichs A, De Maio N, Gozashti L, Lanfear R, Haussler D, and Corbett-Detig R. Ultrafast sample placement on existing trees (USHER) empowers real-time phylogenetics for the SARS-CoV-2 pandemic. *Nature Genetics*.
- 2021 McBroome J*, **Thornlow B***, Hinrichs A, De Maio N, Goldman N, Haussler D, Turakhia Y, and Corbett-Detig R. A daily-updated database and tools for comprehensive SARS-CoV-2 mutation-annotated trees. *Molecular Biology & Evolution*. In Press.
- 2020 Turakhia Y*, De Maio N*, **Thornlow B***, Gozashti L, Lanfear R, Walker C, Hinrichs A, Fernandes J, Borges R, Slodkowitz G, Weilguny L, Haussler D, Goldman N, and Corbett-Detig R. Stability of SARS-CoV-2 phylogenies. *PLOS Genetics*.
- 2020 **Thornlow B**, Armstrong J, Holmes A, Howard J, Corbett-Detig R, and Lowe T. Predicting transfer RNA gene activity from sequence and genome context. *Genome Research*.
- 2018 **Thornlow B**, Hough J, Roger J, Gong H, Lowe T, and Corbett-Detig R. Transfer RNA genes experience exceptionally elevated mutation rates. *Proceedings of the National Academy of Sciences*.
- 2018 Medina P, **Thornlow B**, Nielsen R, and Corbett-Detig R. Estimating the timing of multiple admixture pulses during local ancestry inference. *Genetics*.

PREPRINTS

- 2021 Turakhia Y*, **Thornlow B***, Hinrichs A, McBroome J, Ayala N, Ye C, De Maio N, Haussler D, Lanfear R, and Corbett-Detig R. Pandemic-scale phylogenomics reveals elevated recombination rates in the SARS-CoV-2 Spike region. *Nature*. In Review.
- 2021 **Thornlow B***, Hinrichs A*, Jain M, Dhillon N, La S, ... Akesson, M, Shapiro B, Haussler D, Kilpatrick A, and Corbett-Detig R. A new SARS-CoV-2 lineage that shares mutations with known Variants of Concern is rejected by automated sequence repository quality control. *bioRxiv*.

RESEARCH EXPERIENCE

- 2016-2021 **Graduate Student, Drs. Russell Corbett-Detig and Todd Lowe, University of California, Santa Cruz.** Used comparative genomics and statistical testing to measure mutation rate for highly repetitive family of non-coding elements. Developed machine learning pipeline to infer local transcription rates from DNA alignment data. Analyzed SARS-CoV-2 whole-genome sequences and phylogenies.
- 2015-2016 **Volunteer Researcher, Dr. Daniel Fink, Cornell University Lab of Ornithology.** Analyzed and visualized spatio-temporal migration patterns in various avian species using R.
- 2014-2015 **Undergraduate Researcher, Dr. Christopher Alabi, Cornell University.** Developed a computational model in MATLAB illustrating the effects of cell and antibody characteristics in the context of a drug-delivery system.

TEACHING EXPERIENCE

- 2017-2019 **Research Mentor, BD2K Summer Undergraduate Program.** Mentored undergraduate students for a ten-week summer session, culminating in a poster presentation by the students to the department and local scientific community.
- 2017 **BME Bootcamp Leader.** Organized and led an intensive two-week training program with four other graduate students as part of T32 Training Grant. Guided incoming graduate students to build and test a Drop-Seq machine.
- 2017 **Teaching Assistant, BME 80H: The Human Genome.** Led weekly discussion section to review concepts covered in lectures, held weekly office hours, and graded students' exams and research papers.

WORK EXPERIENCE

- 2015-2016 **Medical Scribe / Quality Assurance Specialist, ScribeAmerica, Ithaca, NY.** Assisted physicians in the emergency department with all documentation related to patient care. Ensured that documentation by all other scribes at location was properly completed.

TECHNICAL SKILLS

- Programming & Visualization with Python, bash, R, C++, SQL, \LaTeX , scipy, seaborn, pandas, scikit-learn, matplotlib, Adobe Illustrator
- Job Management in Docker, SLURM, Google Cloud Platform (GCP) environments

FELLOWSHIPS & AWARDS

2019-2022	NHGRI F31 Predoctoral Fellowship
2019-2020	ARCS Foundation Scholarship
2017-2018	NHGRI T32 Training Grant
2021	NSF RNA 2021 Conference Award
2020	SMBE Young Investigator Award
2020	RNA Society Travel Award
2019	DeLill Nasser Award
2019	American Society of Naturalists Travel Award
2018	NHGRI Annual Meeting Best Poster, 4th Place

ORAL PRESENTATIONS

2020	RNA Society Annual Meeting, Online.
2019	Northern California Computational Biology. Davis, CA.
2019	Evolution. Providence, RI.
2017	Bay Area Population Genomics. Stanford, CA.
2017	UCSC Annual Retreat. Felton, CA.

POSTER PRESENTATIONS

2021	RNA Society Annual Meeting. Online.
2021	NHGRI Annual Meeting. Online.
2020	NHGRI Annual Meeting. Online.
2019	Northern California Computational Biology. Davis, CA.
2019	Probabilistic Modeling in Genomics. Aussois, FR.
2019	RNA Society Annual Meeting. Kraków, PL.
2018	Bay Area RNA Club. San Francisco, CA.
2018	Probabilistic Modeling in Genomics. Cold Spring Harbor, NY.
2018	UCSC Annual Retreat. Felton, CA.
2018	RNA Society Annual Meeting. Berkeley, CA.
2018	Population, Evolutionary and Quantitative Genetics. Madison, WI.
2018	NHGRI Annual Meeting. Los Angeles, CA.
2017	Bay Area RNA Club. San Francisco, CA.
2017	Bay Area Population Genomics. Stanford, CA.
2017	Northern California Computational Biology. Santa Cruz, CA