

Aaron Pfennig, Ph.D.

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EDUCATION

Georgia Institute of Technology, Atlanta, GA

Aug 2020 - Jul 2024

Ph.D. in Quantitative Biosciences

Thesis: "Theoretical and empirical population genetics of admixture and introgression"

Advisor: Joseph Lachance

Georgia Institute of Technology, Atlanta, GA

Aug 2019 - Jul 2020

Master of Science in Bioinformatics

Project: "MgCod: Gene Prediction in Phage Genomes with Multiple Genetic Codes"

Advisor: Mark Borodovsky

Reutlingen University, Germany

Mar 2015 - Feb 2019

Bachelor of Science in Biomedical Sciences

Thesis: "A Peak Detection Method for Breath Gas Analysis using Deep Learning"

Advisors: Carl-Martin Bell and Jan Baumbach

RESEARCH EXPERIENCE

Akey Lab, Princeton University, Princeton, NJ

Sep 2024 - Present

Postdoctoral Fellow

- Developing novel statistical methods for comprehensively analyzing structural variants, enabling their integration into standard population genetic analyses
- Developed an innovative variant phasing method (LongHap) that resolves sequences into paternal and maternal chromosomes, leveraging methylation information in long-read sequencing technology. LongHap significantly improves phasing accuracy and contiguity compared to existing methods.
- Performed evolutionary and population genetics analyses of a high-frequency insertion that contributes to unique skin and hair phenotypes in Oceania, showing that it was likely introgressed from Denisovans and underwent recent selection
- Jointly genotyped 4,124 individuals from the 1000 Genomes Project and Human Genome Diversity Project relative to the new telomere-to-telomere human reference genome to more comprehensively study human genetic variation

Lachance Lab, Georgia Institute of Technology, Atlanta, GA

Mar 2021 - Jul 2024

Graduate Research Assistant

- Studied human evolutionary history through the lens of admixture across timescales
- Developed a population genetics model showing that the genetic background in hybrids alters the dynamics of introgressed alleles
- Analyzed 30,780 admixed genomes in *All of Us*, showing that the remaining Neanderthal introgressed sequences in modern human genomes do not significantly contribute to fitness
- Conducted sensitivity analyses of models for estimating magnitudes of sex-biased admixture from genetic data, revealing that these models are confounded by violations of standard assumptions, such as random mating and non-continuous gene flow, but interpretability can be improved by approximating confidence intervals through bootstrapping
- Contributed evolutionary analyses to studies elucidating the genetic basis of prostate cancer and male pattern baldness in men of African descent

Regeneron Genetics Center LLC, Tarrytown, NY

Jun 2023 - Aug 2023

Intern in the Therapeutic Area Genetics department reporting to Jing He, Mgr. Integrative Translational Genetics

- Developed an analytical pipeline for calling heterozygous variants from single-cell data to quantify allelic heterogeneity. The pipeline allows for the identification of alleles overrepresented in disease-relevant cell types

Torres Lab, Georgia Institute of Technology, Atlanta, GA

Jan 2021 - Mar 2021

Graduate Research Assistant

- Studied the impact of post-translational modifications (PTMs)
- Developed a computational pipeline to harmonize large proteomic datasets from a public database and analyze detected PTMs with regard to whether their dynamics are indicative of a biological function

Borodovsky Lab, Georgia Institute of Technology, Atlanta, GA**Aug 2019 - Jul 2020**

Graduate Research Assistant

- Developed a computational tool (MgCod) combining the recognition of genetic code, segmentation, and annotation of protein-coding regions in phage genomes with multiple genetic codes, that is, *crAss*-like phages
- Used MgCod to analyze the genome structure of *crAss*-like phages with multiple genetic codes to propose a new mechanism for how these phages may infect a host with a different genetic code and switch between the genetic codes in their genome

Noyes Lab, University of Minnesota, Saint Paul, MN**Apr 2019 – Jul 2019**

Research Intern

- Performed taxonomic profiling of a cow's udder microbiome
- Analyzed metagenomic shotgun sequences derived from cow udders and identified differences in the taxonomic compositions between different sampling locations

Rahmann Lab, University of Essen, Germany**Mar 2019 – Jul 2019**

Research Intern

- Identified potential drug targets for chronic lymphocytic leukemia (CLL)
- Analyzed a mass spectrometric protein dataset using machine learning to identify potential biomarkers for CLL and validated the findings using pathway and gene set enrichment analyses

Baumbach Lab, University of Southern Denmark, Odense**Aug 2017 – Feb 2018 & Aug 2018 - Feb 2019**

Research Intern

- Established a pipeline for the analysis of breath gas data (MCC/IMS), incl. data preprocessing and peak detection
- Analyzed breath gas datasets to predict disease states of patients with suspected lung diseases (e.g., sarcoidosis)

PUBLICATIONS**Preprints:**

1. **Aaron Pfennig** and Joseph Lachance, The evolutionary fate of Neanderthal DNA in 30,780 admixed genomes with recent African-like ancestry, *bioRxiv*, 2024, <https://doi.org/10.1101/2024.07.25.605203>

Published and accepted journal articles:** indicates joint first-authorship*

1. Rohini Janivara, Ujani Hazra, **Aaron Pfennig** (author 3 out of 22), ..., and Joseph Lachance, Uncovering the genetic architecture and evolutionary roots of androgenetic alopecia in African men, *Human Genetics and Genomics Advances*, 2025, Volume 6, Issue 3, 100428, <https://doi.org/10.1016/j.xhgg.2025.100428>
2. **Aaron Pfennig**, Alexandre Lomsadze, and Mark Borodovsky, MgCod: Gene Prediction in Phage Genomes with Multiple Genetic Codes, *Journal of Molecular Biology*, 2023, Volume 435, Issue 14, 168159, <https://doi.org/10.1016/j.jmb.2023.168159>.
3. **Aaron Pfennig**, Lindsay N Petersen, Paidamoyo Kachambwa, Joseph Lachance, Evolutionary genetics and admixture in African populations, *Genome Biology and Evolution*, 2023, Volume 15, Issue 4, evad054, <https://doi.org/10.1093/gbe/evad054>
4. **Aaron Pfennig** and Joseph Lachance, Challenges of accurately estimating sex-biased admixture from X chromosomal and autosomal ancestry proportions, *The American Journal of Human Genetics*, Volume 110, Issue 2, 359–367, 2023, <https://doi.org/10.1016/J.AJHG.2022.12.012>
5. Carl J Dyson*, **Aaron Pfennig***, Daniel Ariano-Sánchez, Joseph Lachance, Joseph R Mendelson III, Michael A D Goodisman, Genome of the endangered Guatemalan Beaded Lizard, *Heloderma charlesbogerti*, reveals evolutionary relationships of squamates and declines in effective population sizes, *G3 Genes|Genomes|Genetics*, 2022, Volume 12, Issue 12, jkac276, <https://doi.org/10.1093/g3journal/jkac276>
6. **Aaron Pfennig** and Joseph Lachance, Hybrid fitness effects modify fixation probabilities of introgressed alleles, *G3 Genes|Genomes|Genetics*, 2022, Volume 12, Issue 7, jkac113, <https://doi.org/10.1093/g3journal/jkac113>

7. Burcu F. Darst, Raymond Hughley, **Aaron Pfennig** (author 3 out of 101), ..., and Christopher A. Haiman, A Rare Germline HOXB13 Variant Contributes to Risk of Prostate Cancer in Men of African Ancestry, *European Urology*, 2022, Volume 81, Issue 5, pp. 458-462, <https://doi.org/10.1016/j.eururo.2021.12.023>
8. Nirojah Subramaniam, ..., **Aaron Pfennig** (author 9 out of 20), ..., and Daniel Robert Engel, Proteomic and bioinformatic profiling of neutrophils in CLL reveals functional defects that predispose to bacterial infections, *Blood Advances*, 2021, Volume 5, Issue 5, pp. 1259–1272, <https://doi.org/10.1182/bloodadvances.2020002949>
9. Christopher J Dean, Ilya B Slizovskiy, Kathryn K Crone, **Aaron Pfennig**, Bradley J Heins, Luciano S Caixeta, and Noelle R Noyes, Investigating the Cow Skin and Teat Canal Microbiomes of the Bovine Udder Using Different Sampling and Sequencing Approaches, *Journal of Dairy Science*, 2021, Volume 104, Issue 1, pp. 644–661, <https://doi.org/10.3168/jds.2020-18277>

INVITED PRESENTATIONS

1. Revealing the hidden parts of the genome. *Invited Seminar* (Max-Planck Institute of Evolutionary Anthropology, Leipzig, Germany - July 2025)

CONFERENCE PRESENTATIONS

Oral presentations:

1. The evolutionary fate of Neanderthal DNA in 30,780 admixed genomes with recent African-like ancestry. *SMBE 2024* (Puerto Vallarta, Mexico - 2024)
2. Hybrid fitness effects modify fixation probabilities of introgressed alleles. *Population Genetics Group Meeting 56* (London, UK - 2023)
3. Hybrid fitness effects modify fixation probabilities of introgressed alleles. *Population, Evolutionary, and Quantitative Genetics Conference* (Pacific Grove, CA - 2022)

Poster presentations:

1. Harnessing Methylation Information in Long-Read Sequencing Data Improves Variant Phasing. *ASHG 2025* (Boston, MA)
2. The evolutionary fate of Neanderthal introgression in recently admixed African American genomes. *ASHG 2023* (Washington, D.C.)
3. Challenges of accurately estimating sex-biased admixture from X chromosomal and autosomal ancestry proportions. *SMBE 2023* (Ferrara, Italy)

AWARDS, SCHOLARSHIPS, FELLOWSHIPS

- **Future Values Fellowship (2024/25):** Training to design ethically just and inclusive research programs, Princeton University
- **Georgia Tech College of Sciences Graduate Career Connect Travel Grant (2023/24):** Travel grant to attend Population Genetics Group Meeting 57 in St. Andrews, UK
- **Larry S. O'Hara Fellowship (2023):** Outstanding Graduate Student in the College of Sciences, Georgia Institute of Technology
- **Quantitative Biosciences Student Award 2022 for the best paper in Ecology, Evolution, and Population Biology;** Winning paper: *Hybrid fitness effects modify fixation probabilities of introgressed alleles*, Georgia Institute of Technology
- **Quantitative Biosciences Service Award 2022** for my work as Quantitative Biosciences-SGA Treasurer, Georgia Institute of Technology
- **Interdisciplinary Health & Environment Development Program (IHE-lead) Fellowship (2022 - 23):** Training to design interdisciplinary research programs that translate findings into public decision making, Georgia Institute of Technology

- **Summer Institute in Statistical Genetics (2021)** with a focus on Monte Carlo Markov Chain (MCMC) for Genetics and Pathway & Network Analysis for Omics Data at the University of Washington, Seattle, WA
- **J. Leland Jackson Fellowship (2020):** Outstanding Bioinformatics Master's Students based on bioinformatics research and academic studies, Georgia Institute of Technology
- **Computational Biology Faculty Research Award (Summer 2020),** Georgia Institute of Technology
- **Fulbright scholarship (2019-20):** Prestigious scholarship for a study at an American Graduate School
- **Otto-Johannsen-Award (Fall 2018):** Awarded for the most outstanding bachelor's thesis at Reutlingen University

TEACHING EXPERIENCE

Georgia Institute of Technology, Atlanta, GA

Aug 2023 - Dec 2023

Graduate Teaching Assistant

- Biol 3600/6600, Evolutionary Biology

Virtual Quantitative Biosciences Hands-on Modeling Workshop

May 2021

Instructor for Hands-on modeling sessions on epidemic modeling (deterministic & stochastic models)

Georgia Institute of Technology, Atlanta, GA

Aug 2020 - Dec 2020

Graduate Teaching Assistant

- Biol 1107L, Introduction to Biological Principles Laboratory

MENTORING EXPERIENCE

- Mentoring in the Akey Lab, Princeton University, Princeton, NJ **2025**
 - Mentored a B.S. Computer Science undergraduate student developing computational methods for inferring population history in space. Specifically, I supervised the student implementing spatially explicit demographic models in SLiM and training machine learning models on the simulated data before using them to infer aspects of population histories from real data
- Mentoring in the Lachance Lab, Georgia Institute of Technology, Atlanta, GA **2022**
 - Mentored a B.S. Computer Science undergraduate student working to benchmark state-of-the-art methods (e.g., IBDmix, Sstar, hmmix, etc.) for detecting introgressed segments under various demographic scenarios

LEADERSHIP & COMMUNITY SERVICE

- **Organizing Committee** of the [Urban Air Quality in The Age of Climate Change Symposium 2023](#)
- **Georgia Tech Grand Challenges Facilitator**, Academic Year 2022/23
- **VP and Treasurer of the Quantitative Biosciences SGA at Georgia Tech**, Summer of 2021 - Spring 2023
- **Student Chair** of the [Quantitative Biosciences Hands-on Workshop 2021 on epidemic modeling](#)
- **Treasurer of the Fulbright Board at Georgia Tech**, Summer 2020 - Spring 2022

REVIEWED PUBLICATIONS

- *BMC Genomics, Current Biology, Evolution, G3 Genes|Genomes|Genetics, Molecular Biology and Evolution, PCI*

SOCIETY MEMBERSHIPS

- American Society of Human Genetics, Genetics Society of America