

## Aaron Pfennig, Ph.D.

[aaronpfennig@gmail.com](mailto:aaronpfennig@gmail.com) | 404.649.2817 | [Website](#) | [GitHub](#) | [LinkedIn](#) | Philadelphia, PA

### CURRENT POSITION

Postdoctoral Fellow  
Lewis-Sigler Institute for Integrative Genomics  
Princeton University

### 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

**Lachance Lab, Georgia Institute of Technology, Atlanta, GA** **Mar 2021 - Jul 2024**  
Graduate Research Assistant

- Researched various theoretical and empirical population genetics aspects of admixture and introgression

**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

- Quantifying allelic heterogeneity in single-cell data

**Torres Lab, Georgia Institute of Technology, Atlanta, GA** **Jan 2021 - Mar 2021**  
Graduate Research Assistant

- Retrieved proteomic datasets from a public database and analyzed the detected post-translational modifications (PTMs) with regard to whether PTM 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 combining the recognition of genetic code and annotation of protein-coding regions in phage genomes with multiple genetic codes

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

- Performed taxonomic profiling of a cow's udder microbiome

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

- Identified potential drug targets for chronic lymphocytic leukemia (CLL) based on a mass spectrometric protein dataset using machine learning, pathway analysis, and gene set enrichment analysis

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

- Established an automated pipeline for the analysis of breath gas data (MCC/IMS), incl. data preprocessing, peak detection, and sample classification

### PUBLICATIONS

#### Published and accepted journal articles:

\* indicates joint first-authorship

1. **Aaron Pfennig** and Joesph 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>

2. 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, *bioRxiv*, 2024, <https://doi.org/10.1101/2024.01.12.575396>
3. **Aaron Pfennig**, Alexandre Lomsadze, and Mark Borodovsky, MgCod: Gene Prediction in Phage Genomes with Multiple Genetic Codes, *Journal of Molecular Biology*, 2023; 168159, <https://doi.org/10.1016/j.jmb.2023.168159>.
4. **Aaron Pfennig**, Lindsay N Petersen, Paidamoyo Kachambwa, Joseph Lachance, Evolutionary genetics and admixture in African populations, *Genome Biology and Evolution*, 2023; evad054, <https://doi.org/10.1093/gbe/evad054>
5. **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*, 110(2), 359–367, 2023, <https://doi.org/10.1016/J.AJHG.2022.12.012>
6. 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; jkac276, <https://doi.org/10.1093/g3journal/jkac276>
7. **Aaron Pfennig** and Joseph Lachance, Hybrid fitness effects modify fixation probabilities of introgressed alleles, *G3 Genes|Genomes|Genetics*, 2022; jkac113, <https://doi.org/10.1093/g3journal/jkac113>
8. 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. *Eur Urol* 2022; <https://doi.org/10.1016/j.eururo.2021.12.023>
9. 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 Adv* 2021; 5 (5): 1259–1272, <https://doi.org/10.1182/bloodadvances.2020002949>
10. Dean, C J, I B Slizovskiy, K K Crone, **A Pfennig**, B J Heins, L S Caixeta, and N 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, 104 (1): 644–61. <https://doi.org/10.3168/jds.2020-18277>

## **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). Oral presentation.
2. Hybrid fitness effects modify fixation probabilities of introgressed alleles. *Population Genetics Group Meeting 56* (London, UK - 2023). Oral presentation.
3. Hybrid fitness effects modify fixation probabilities of introgressed alleles. *Population, Evolutionary, and Quantitative Genetics Conference* (Pacific Grove, CA - 2022). Oral presentation.

### **Poster presentations:**

1. The evolutionary fate of Neanderthal introgression in recently admixed African American genomes. *ASHG 2023* (Washington, D.C. - 2023). Poster presentation.
2. Challenges of accurately estimating sex-biased admixture from X chromosomal and autosomal ancestry proportions. *SMBE 2023* (Ferrara, Italy - 2023). Poster presentation.

## **AWARDS, SCHOLARSHIPS, FELLOWSHIPS**

- **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
- **Travel Bursary for attending Population Genetics Group Meeting 56 in London, UK**
- **QBioS Student Award 2022 for the best paper in Ecology, Evolution, and Population Biology;** Winning paper: *Hybrid fitness effects modify fixation probabilities of introgressed alleles*
- **QBioS Service Award 2022** for my work as QBioS-SGA Treasurer
- **Interdisciplinary Health & Environment Development Program (IHE-lead) Fellowship (2022 - 23)**
- **Sam Nunn Security Fellowship (2021-22)**

- **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 thesis at Reutlingen University
- **Fulbright FH Summer Institute (2016)**: Entrepreneurship Summer School at UNCG; Greensboro, NC

## **TEACHING EXPERIENCE**

**Georgia Institute of Technology, Atlanta, GA**

**August 2023 - December 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**

**August 2020 - December 2020**

Graduate Teaching Assistant

- Biol 1107L, Introduction to Biological Principles Laboratory

## **MENTORING EXPERIENCE**

- Joey Hasset, B.S. Computer Science, Georgia Institute of Technology, Atlanta

**2022**

## **LEADERSHIP & COMMUNITY SERVICE**

- **Organizing Committee** of the [Urban Air Quality in The Age of Climate Change Symposium 2023](#)
- **Georgia Tech Grandchallenges Facilitator**, Academic Year 2022/23
- **Vice President 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 Fulbright Board at Georgia Tech**, Summer 2020 - Spring 2022

## **REVIEWED PUBLICATIONS**

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