

Ratchanon “RP” Pornmongkolsuk

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SUMMARY

Ph.D. candidate in population genetics with a natural curiosity about human adaptations, a strong foundation in statistical and computational approaches, and a deep passion for engaging non-scientific audiences through writing and content creation.

EDUCATION

Duke University <i>Genetics and Genomics - PhD Candidate</i>	2021 - Present GPA - 3.944
Brown University <i>Biology - Bachelor of Arts</i>	2017 - 2021 GPA - 3.83

TECHNICAL SKILLS

General: Adobe Illustrator, Procreate, Adobe Photoshop, MS Office Suite, project planning and database organization using Notion, Adobe Premier Pro.

Languages: Proficient in R, Python, & Bash/Shell. Some experience in Golang & Java.

Software: Plink, Bcftools, GLIMPSE, ADMIXTURE, Minimac, Beagle, Snakemake, Admixtools, SLiM, Msprime, GATK & Haplostrips.

Methods: Principal Component Analysis (PCA), population structure analyses, generalized linear model, linear mixed effect model, analyses of temporal-geographical data, coalescence-based simulation, Patterson’s D Statistics.

Computing: High-performance clusters (Duke Computing Cluster; SLURM workload manager), version control (Git), package manager (Conda/Mamba), data transfer (Globus).

RELEVANT RESEARCH EXPERIENCE

Dissertation Project | Duke University

Alejandro Ochoa Lab

Durham, NC
May 2022 – Present

- Project: *Leveraging ancient DNA in studying human adaptation to vivax malaria in Africa in admixture context.*
- Developing a novel, regression-based single-nucleotide imputation approach that improves imputation accuracy on ancient African DNA which are challenging due to (1) low coverage of ancient DNA sequences and (2) low linkage disequilibrium among African populations.
- Benchmarked performance of the low-coverage imputation tool GLIMPSE2 in the imputation of ancient African genomes using simulations (SLiM, Msprime, Tskit).
- Built and performed pipelines for nucleotide imputation of the Duffy antigen receptor locus with custom African reference panel using Minimac4 and Beagle5.4 on ancient African genomes. Performance evaluation of above imputations was done via leave-one-out cross-validation.
- Characterized population structures in ancient and modern African human sequencing data using Principal Component Analyses (PCA), F_{ST} , F-statistics, ADMIXTURE software and the popkin R package.

Selected Research Rotations | Duke University

Amy Goldberg Lab

Durham, NC
March – April 2022

- Developed a pipeline for joint analyses of archaeological (radiocarbon dating) and genetic data (whole genome sequences) in studying the Neolithic Revolution—a wide-scale transition into agricultural society promoting population growth—in East Asian populations.

Craig Lowe Lab

January – February 2022

- Designed and programmed a genome simulation algorithm as part of the novel genomic toolkit (Gonomics) using Golang.
- The program simulates genetic sequences from populations under the Wright-Fisher model with adjustable (1) population size, (2) number of generations, (3) mutation rate & (4) selection coefficient. The simulation extends beyond the Wright-Fisher model’s infinite-site assumption, allowing back mutation and multiallelic polymorphism in the simulated sequences.

Jenny Tung Lab

November – December 2021

- Built a linear mixed-effect regression model for studying the effects of energy expenditure (3-dimensional motion measured by accelerometers) on gene expression (bulk RNAseq data) in Kalahari meerkats. The model included random effects from kinship coefficients from known pedigrees.

Mohamed Noor Lab

September – October 2021

- Implemented the GATK best practice pipeline to prepare and analyze sequencing data generated from *Drosophila melanogaster*.

Undergraduate Research | Brown University

Providence, RI

Emilia Huerta-Sanchez Lab

June 2020 – May 2021

- Detected signals of adaptive introgression in *MUC19*, a gene encoding a gel-forming mucin protein, from Denisovans in admixed American populations.
- Assisted in the identification of Native American and European ancestries in the American populations from the 1000 Genomes Project.
- Calculated genetic distances between haplotypes from Native American ancestries in comparison to the Denisovan haplotype using the program Haplostrips.
- Constructed and analyzed the Principal Components (PCA) of genetic distances among the admixed American populations.
- Designed, built, and maintained the Huerta-Sanchez laboratory website on Weebly platform, created illustrations of the research topics page on the lab website.

TEACHING & LEADERSHIP EXPERIENCE

BIOL202L: Genetics and Evolution: Graduate Teaching Assistant

Fall 2025

- Independently supervise and teach weekly lab sections.
- Assist students in understanding genetics and evolutionary concepts during office hours and exam reviews.
- Engage in and lead Canvas discussions on genetics and evolution in the news.
- Grade weekly lab assignments.

Committee of Alumni, Marketing, and PR (cAMP): Co-Chair

Fall 2024 – present

- Lead a committee focusing on building the UPGG alumni network on LinkedIn, creating and maintaining positive public image for the students in the program, and engage the student body with the broader scientific community on social media.

Science Day at Creech Road Elementary: Guest Instructor

March 2025

- Conducted a hands-on lessons on using Monster Maker game and candy DNA exercise for fifth graders at Creech Road Elementary School.

Intro to Data Analysis: Instructor

January 2025

- Instructed an introduction to data analysis using R to the high-school students during their January Term at the North Carolina School of Science and Mathematics (NCSSM). Experience shared on LinkedIn
- Led a poster design session where students designed posters for presenting their January Term research findings.
- Selected testimonies:
 - * “Goated lesson. Very engaging and helpful, like the flexibility, energy, and analogy explanations.”
 - * “Loved the class! Really helped me get a better grasp on programming with R, and since I had a background of Python, the pacing felt slow but it was very clear and easy to understand.”

Distinguished Lecture Series Committee: Co-Chair

Fall 2022 – January 2025

- Organized the Distinguished Lecture Series in which we invite distinguished scientists who have made notable contributions to their fields and are great mentors and communicators.

UPGG Bioinformatics Bootcamp: Instructor

Summers 2022, 2023, & 2024

- Designed and instructed various bioinformatics lessons for the incoming PhD students in the Genetics and Genomics program.
 - * 2024 lesson: Data Exploration and Cleanup in R.
 - * 2023 lessons: Introduction to Programming Using Python & Data Exploration Using Jupyter Notebook.
 - * 2022 lesson: Introduction to Unix and Command Line.
- Adapted and maintained the Bootcamp website via GitHub.

Genetics: Undergraduate Teaching Assistant

Falls 2018 & 2019

- Held office hours for weekly assignments, taught in review sections for exams, graded the weekly assignments.

TALKS, CONFERENCES, AND WORKSHOPS

- Science Talk'25** | Raleigh, NC April 2025
- Participated in three-day conference on various topics on science communications.
- Alan Alda Center for Communicating Science Workshop** | Durham, NC January 2025
- Engaged in two-day hands-on science communication workshop using improvisational techniques based on the Alda Method. Experience shared on [LinkedIn](#).
- ComSciCon-Triangle Workshop** | Chapel Hill, NC January 2025
- Participated in a Write-A-Thon which involved writing a science news article covering interesting recent scientific finding (in-progress).
 - Gave a one-minute, impromptu pop talk about my research (video uploaded on [YouTube](#)).
 - Engaged with a panel of science writing experts on topics including how to write a science article, use effective visual storytelling, and more. Experience shared on [LinkedIn](#).
- American Society of Human Genetics (ASHG) Annual Meeting** | Denver, CO November 2024
- Poster presentation: *Evaluation of imputation methods for ancient African DNA*.
- GradX Talk** | Duke University March 2024
- [A 5-minute talk](#) titled: *How population genetics helps inform us of how we became who we are* to general audience
- American Society of Human Genetics (ASHG) Annual Meeting** | Washington, D.C. November 2023
- Poster presentation: *Single-locus imputation of ancient African DNA using novel regression-based approach*.
- Communicate Your Science through Short Video Workshop** | Duke University August 2023
- Wrote, filmed, and edited a science communication short video ([YouTube](#) or [LinkedIn](#)).
- Society for Molecular Biology & Evolution (SMBE) Annual Meeting** | Remote Attendance July 2023
- AGAR Workshop on Computational Genetics Workshop** | Remote Attendance July 2022
- Hands-on workshop on [Snakemake](#), [Msprime](#), [Admixtools](#) & [Legofit](#) ([workshop details](#)).
- Science at the Intersection of Genetics, Identity, and Health Workshop** | Duke University November 2022
- Discussed the current topics on science of human genetics and how their implications on identity and health.
- Adaptation in Structured Population Workshop** | Remote Attendance June 2023

SCHOLARSHIPS AND HONORS

- Associate Membership** 2025 – present
Sigma Xi - The Scientific Research Honor Society Research Triangle Park, NC
- Royal Thai Government Scholarship** 2016 – 2021
Office of Educational Affairs, Royal Thai Embassy Washington, D.C.
- Silver Medal** 2015
International Biology Olympiad (IBO) Aarhus, Denmark