

EDUCATION

- **PhD** University of Copenhagen, Denmark
Faculty of Health and Medical Sciences, Globe Institute, Section for GeoGenetics 2022/1 - 2025/3 (expected)
Title: Statistical Methods for Population Genetic Inference Based on Low-Depth Sequencing Data
Advisors: Thorfinn Sand Korneliussen and Rasmus Nielsen
- **BSc in Biology** Hacettepe University, Turkey
Faculty of Science, Department of Biology 2015/8 - 2020/7

RESEARCH EXPERIENCE

- **Visiting Researcher at the Moltke Lab** University of Copenhagen, Denmark
Faculty of Science, Department of Biology, Section for Computational and RNA Biology 2024/09 - 2024/12
- Collaborated with Ida Moltke on a research project on IBD segment identification with low-depth sequencing data.
- **PhD Fellow** University of Copenhagen, Denmark
Faculty of Health and Medical Sciences, Globe Institute, Section for GeoGenetics 2022/1 - Present (expected 2025/3)
- Supervised by Thorfinn Sand Korneliussen and Rasmus Nielsen.
- Developed statistical methods and frameworks for population genetic inference, with a focus on low-depth NGS data.
- Implemented computational tools for genomic analysis emphasizing efficiency and accuracy.
- Authored three first-author papers: one under review and two manuscripts in preparation.
- Presented research findings at three conferences and one poster session.
- Contributed to collaborative projects outside of the primary PhD projects, resulting in one paper published in *Nature*, and two papers submitted to *Nature* (under review).
- Delivered training on workload management using Slurm in the *Introduction to Slurm* workshop for the section.
- Gained and actively applied expertise in C, C++, Python, and R programming, Git, Conda/Bioconda, Snakemake, Make, \LaTeX , sed, AWK, and Bash, as well as utilizing Slurm and HPC environments for efficient execution of large-scale research and computational tasks.
- **Research Assistant** University of Copenhagen, Denmark
Faculty of Health and Medical Sciences, Globe Institute, Section for GeoGenetics 2020/10 - 2021/12
- Contributed to developing and evaluating the Lundbeck Center's ancient DNA bioinformatics pipeline, facilitating the processing of hundreds of ancient genomes, resulting in one preprint.
- Contributed to the development and maintenance of the [ANGSD](#) toolkit.
- Contributed to a collaborative research project, resulting in a publication.
- Managed the Geogenetics servers used by many research groups as a server administrator, supporting large-scale computational research and bioinformatics workflows.
- Utilized skills in diverse research and computational tasks, including sequence alignment, performing analyses such as PCA and admixture inference, and developing scalable pipelines for high-throughput genomic data processing.
- **Research Intern at the Fumagalli Lab** Imperial College London, United Kingdom
Department of Life Sciences 2019/7 - 2019/9
- Supervised by Matteo Fumagalli.
- Contributed to the HMMPloddy project by implementing methods such as genotype likelihood estimation for arbitrary N-ploidies, resulting in a publication.
- Supported by the Erasmus+ Traineeship Grant.
- Enhanced proficiency in Python programming, Bash/Shell scripting, and Git.
- **Research Intern at the Biogeography Research Lab** Hacettepe University, Turkey
Faculty of Science, Department of Biology 2019/2 - 2020/7
- Supervised by Barış Özüdoğru.
- Developed and optimized a Snakemake pipeline for phylogenomic analyses using RADSeq data, resulting in a manuscript in preparation.

- Delivered presentations on Linux/Bash and phylogenetic methods during internal lab meetings and taught the practical session in the *Introduction to Bioinformatics and Computational Biology* workshop, refining teaching and presentation skills.
- Enhanced proficiency in Python, Snakemake, R, Bash/Shell scripting, Git, and gained experience in executing large analyses on HPC clusters with Slurm.

- Research Intern at the Comparative and Evolutionary Biology Lab** Middle East Technical University, Turkey
 Department of Biological Sciences: Molecular Biology and Genetics 2018/8 - 2019/6
 - Supervised by Mehmet Somel.
 - Performed analyses to evaluate the effects of the properties of probe sequences in the 1240K SNP capture method.
 - Applied and further developed skills in data analysis using R.
- Research Intern at the Evolutionary and Quantitative Genetics Lab** Hacettepe University, Turkey
 Faculty of Science, Department of Biology 2015/10 - 2018/12
 - Supervised by Ergi Deniz Özsoy.
 - Conducted statistical analyses for quantitative genetics projects using Drosophila Genetic Reference Panel 2 data, which resulted in a poster presentation and acknowledgments in two MSc and one PhD thesis.
 - Gained and applied skills in data analysis using R.

PUBLICATIONS

- [6] Fulya E. Yediay [et al, including **Isin Altinkaya**]. Ancient genomics support deep divergence between Eastern and Western Mediterranean Indo-European languages. (under review by *Nature*). *bioRxiv* (2024).
- [5] **Isin Altinkaya**, Thorfinn S. Korneliussen, Rasmus Nielsen. vcfgl: A flexible genotype likelihood simulator for VCF/BCF files. (under review by *Bioinformatics*). *bioRxiv* (2024).
- [4] Hugh McColl [et al, including **Isin Altinkaya**]. Steppe Ancestry in western Eurasia and the spread of the Germanic Languages. (under review by *Nature*). *bioRxiv* (2024).
- [3] Morten E. Allentoft [et al, including **Isin Altinkaya**]. Population genomics of post-glacial western Eurasia. *Nature* (2024).
- [2] Samuele Soraggi, Johanna Rhodes, **Isin Altinkaya**, Oliver Tarrant, François Balloux, Matthew C. Fisher, Matteo Fumagalli. HMMploidy: inference of ploidy levels from short-read sequencing data. *Peer Community Journal* (2022).
- [1] Alex Mas-Sandoval, Nathaniel S. Pope, Knud Nor Nielsen, **Isin Altinkaya**, Matteo Fumagalli, and Thorfinn S. Korneliussen. Fast and accurate estimation of multidimensional site frequency spectra from low-coverage high-throughput sequencing data. *GigaScience* (2022).

Manuscripts in Preparation

- [3] **Isin Altinkaya**, Lei Zhao, Rasmus Nielsen, Thorfinn S. Korneliussen. ngsAMOVA: A genotype likelihood framework for analysis of molecular variance (AMOVA) with low-depth sequencing data.
- [2] **Isin Altinkaya**, Ida Moltke, Rasmus Nielsen, Thorfinn S. Korneliussen. IBDGL: A method for the accurate detection of IBD segments in low- and medium-depth genomic data without phasing.
- [1] **Isin Altinkaya**, Emrullah Yılmaz, İsmail K. Sağlam, Barış Özüdoğru. Understanding the phylogenetic relationships within the *Noccaea* species complex from RADSeq data using the multi-species coalescent.

PROFESSIONAL EXPERIENCE

- Freelance Programmer** Remote
 Self-Employed 2019/1 - 2020/10
 - Applied various **AI** and **ML** techniques such as **Random Forest** and **K-Means Clustering** to solve complex problems.
 - Utilized programming languages and tools such as **Python**, **R**, **AWK**, and **Bash scripting** to perform data analysis.
 - Delivered customized solutions for clients, developing strong problem-solving and programming skills.

SKILLS

Programming languages: ^{Expert} C , ^{Expert} R , ^{Advanced} Python , ^{Advanced} C++ , ^{Intermediate} Rust , ^{Intermediate} Perl , ^{Beginner} Java
Scripting and typesetting: L^AT_EX, Markdown, HTML&CSS, JavaScript, Google Apps Script, sed, AWK, Bash
Operating systems: GNU/Linux (including server administration and HPC environments)
Other tools and frameworks: Git, Conda/Bioconda, Snakemake, RShiny, Dash, Django, Make

CONFERENCES, WORKSHOPS, AND TALKS

Oral Presentations

- [6] A Genotype Likelihood Framework for Identifying Identity-by-Descent (IBD) Segments Based on Low-Depth Sequencing Data, *Evolution and Population Genetics in Denmark (EPIC) Conference*, Denmark, (2023).
- [5] A Genotype Likelihood Framework for the Analysis of Molecular Variance (AMOVA), *Evolution and Population Genetics in Denmark (EPIC) Conference*, Denmark, (2022).
- [4] Biological Evolution, *Science and Future Magazine Science for Youth Seminar*, Turkey, (2018).
- [3] Evolutionary Biology and Preventing the Species Extinction, *7th National Environment and Ecology Student Congress*, Turkey, (2016).
- [2] Evolutionary Biology and Environmental Problems, *Turkey Meets Evolution: Bilkent University*, Turkey, (2016).
- [1] Evolutionary Biology and Preventing the Species Extinction, *7th National Environment and Ecology Student Congress*, Turkey, (2016).

Poster Presentations

- [2] **Isin Altinkaya**, Lei Zhao, Rasmus Nielsen, Thorfinn S. Korneliussen. A Genotype Likelihood Framework for Analysis of Molecular Variance, d_{xy} , and Neighbor-Joining Trees with Low-Depth Sequencing Data. *Society for Molecular Biology and Evolution (SMBE)*, Italy, (2023).
- [1] Damla Aygün, **Isin Altinkaya**, Murat Yılmaz, Ergi Deniz Özsoy, Efe Sezgin. Host Genetics of Microbiota Diversity in *Drosophila melanogaster*. *Ecology and Evolutionary Biology Symposium (EEBST)*, Turkey, (2018).

TEACHING EXPERIENCE

- Advanced Bioinformatics for NGS, Graduate Course, **Teaching Assistant**, University of Copenhagen, (2021).
- Introduction to Computational Biology and Bioinformatics, **Teaching Assistant**, Hacettepe University, (2020).
- Biometry, 4th Year Elective Course, **Teaching Assistant**, Hacettepe University, (2019).
- Introductory Evolutionary Biology, Science and Utopia Magazine Evolution Courses, **Lecturer**, (2017).
- Introduction to Evolution, Hacettepe University Evolution Workshops, **Lecturer**, (2016).

SCIENTIFIC OUTREACH, PUBLIC ENGAGEMENT, AND ACTIVITIES

Contributed to organizing various free symposiums, workshops, and events focusing on teaching evolution and scientific thinking to the public, with a special focus on underdeveloped regions.

- 12th Aykut Kence Evolution Conference, **Organizer**, (2018).
 - Science and Utopia Magazine, **Popular science writer**, Subject: Evolutionary biology, (2017/6 - 2018/5).
 - Popular Science Magazine, Turkey branch, **Popular science news editor and translator**, (2016/2 - 2016/5).
 - **Tree of Evolution**, **Writer and editor**; Subject: Evolutionary biology, (2015/9 - present).
- Authored multiple popular science articles, which can be found at evrimagaci.org/isinaltinkaya.
- Turkey Meets Evolution: Izmir, **Organizer**, (2012).
 - Tree of Evolution Bornova Anatolian High School Evolution Conference, **Organizer**, (2012).

Popular Science Publications in Magazines (in Turkish):

- [5] **Isin Altinkaya** and Dr. Martin Hanczyc. Examining the thin line between living and non-living matter. *Science and Utopia Magazine*, Issue: 283 (2018).
- [4] **Isin Altinkaya**. Education and perceptions: Evolution in Turkey. *Science and Utopia Magazine*, Issue: 278 (2017).
- [3] **Isin Altinkaya**. The evolving brain. *Atheist Magazine*, Issue: 16 (2016).
- [2] **Isin Altinkaya**. Evolutionary biology and LGBTI+ in nature. *Atheist Magazine*, Issue: 14 (2016).
- [1] **Isin Altinkaya**. Understanding evolution through the human body. *Atheist Magazine*, Issue: 13 (2016).

OPEN SOURCE PROJECTS AND CONTRIBUTIONS

- **ngsAMOVA**: A **C/C++** tool designed to perform AMOVA, d_{xy} , Neighbor-Joining, and IBD segment detection from NGS data in a probabilistic framework (see Publications/Manuscripts in Preparation). (2022 - present).
- **gptchatteR**: An **R** package and wrapper for interacting with **OpenAI LLM models** in R console, providing a framework for using AI language models to help learning and conducting data analysis, data visualization and wrangling directly from R console. (2023).
- **google-slides.scripts**: Custom scripts written using **Google Apps Script** providing various additional functionalities to Google Slides. (2022).
- **vcfgl**: A **C/C++** tool for fast and efficient simulation of genotype likelihoods (see Publications/5). (2022-present).
- **ANGSD**: **C/C++** toolkit for analyzing next-generation sequencing data. Actively contributed to the development and maintenance of the ANGSD software (2021-2024).
- **bash-functions**: Custom **Bash** functions for performing various tasks, such as 'runda', an environment-safe wrapper for **conda**, and 'treemd' for printing the tree structure of a **Git** repository in **Markdown** format. (2021-present).
- **i3pomodoror**: i3 window manager wrapper (using **Bash**) for the R library 'pomodoror' (2020).
- **PopulasyonBuyumesi**: An **RShiny** application for teaching population ecology through including population growth simulations and interactive plots. The RShiny app (in Turkish) is available at popbsim.isinaltinkaya.com, (2020).
- **cheatsheets**: Custom **Markdown** tutorials containing custom functions, examples, and tips for using various tools and programming languages effectively, such as **Bash**, **Git**, **Jupyter**, **Make**, **Conda/Bioconda** and **R** (2020-present).
- **HMMploidy**: A **Python** tool to calculate ploidy levels from genotype likelihoods and coverage using Hidden Markov Models. Contributed to the development as a part of an academic project (see Publications/2), (2020).
- **i3gcalendar**: Google Calendar i3blocks integration (written in **Python**) for i3 window manager (2018).

SCHOLARSHIPS & AWARDS

- [5] **Erasmus+ Traineeship Grant**, Imperial College London (2019)
- [3, 4] **Hacktoberfest Open-Source Contribution Award**, DigitalOcean (2018 and 2019)
Awarded for significant contributions to open-source projects.
- [1, 2] **Next-Generation Humanist Leaders Scholarship**, Atheist Alliance International (2016 and 2017)
Granted to support the development of future humanist leaders in underdeveloped or distressed countries.




MEMBERSHIPS & AFFILIATIONS

- Society for Molecular Biology and Evolution, 2023 - present
- Society for the Study of Evolution, 2021 - present
- Free Software Foundation, 2020 - present
- Ecology and Evolutionary Biology Society of Turkey, 2017 - present

LANGUAGES

- **Turkish**: Native
- **English**: Native-like fluency (ILR level R-5, S-4+, L-5, W-5)
- **German**: Elementary proficiency (ILR level R-1, S-0+, L-0, W-0+)
- **Danish**: Elementary proficiency (ILR level R-1, S-0+, L-0+, W-1)

REFERENCES

- **Rasmus Nielsen**  • rasmus_nielsen@berkeley.edu
University of California, Berkeley, Department of Integrative Biology and Department of Statistics
University of Copenhagen, Faculty of Health and Medical Sciences, Globe Institute, Section for GeoGenetics
- **Thorfinn Sand Korneliussen**  • tskorneliussen@sund.ku.dk
University of Copenhagen, Faculty of Health and Medical Sciences, Globe Institute, Section for GeoGenetics
- **Matteo Fumagalli**  • m.fumagalli@qmul.ac.uk
School of Biological and Behavioural Sciences, Queen Mary University of London, United Kingdom