Isin Altinkaya

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EDUCATION

PhD — University of Copenhagen, Denmark
Faculty of Health and Medical Sciences, Globe Institute, Section for GeoGenetics — 2022/1 - 2025/4
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

Postdoctoral researcher — University of Cologne, Germany
Collaborative Research Centre for Predictability in Evolution — 2025/6 -

Visiting Researcher at the Moltke Lab — University of Copenhagen, Denmark
Faculty of Science, Department of Biology, Section for Computational and RNA Biology — 2024/9 - 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 - 2025/4
- 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, read trimming and quality assessment, detecting contamination, 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 HMMPloidy 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

[7] **Isin Altinkaya**, Lei Zhao, Rasmus Nielsen, Thorfinn S. Korneliussen. ngsAMOVA: A probabilistic framework for Analysis of Molecular Variance, d_{XY} and Neighbor-Joining trees with low depth sequencing data. *bioRxiv* (2025) (under review by *Molecular Ecology and Resources*)

[6] **Isin Altinkaya**, Thorfinn S. Korneliussen, Rasmus Nielsen. vcfgl: A flexible genotype likelihood simulator for VCF/BCF files. *Bioinformatics* (2025)

[5] Fulya E. Yediay [et al, including **Isin Altinkaya**]. Ancient genomics support deep divergence between Eastern and Western Mediterranean Indo-European languages. *bioRxiv* (2024) (under review by *Nature*)

[4] Hugh McColl [et al, including **Isin Altinkaya**]. Steppe Ancestry in western Eurasia and the spread of the Germanic Languages. *bioRxiv* (2024) (under review by *Nature*)

[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

[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**, **JavaScript**, **HTML&CSS**, **AWK**, and **Bash scripting** to perform data analysis and customized program development.
  - Delivered customized solutions for clients, developing strong problem-solving and programming skills.

Skills

Programming languages:
C [Expert], R [Expert], Python [Advanced], C++ [Advanced], Rust [Intermediate], Perl [Intermediate], Java [Beginner]

Scripting and typesetting: LaTeX, Markdown, HTML&CSS, JavaScript, Angular, Google Apps Script, sed, AWK, Bash

Operating systems: GNU/Linux (including server administration and HPC environments)

Other tools and frameworks: Git, Conda/Bioconda, Snakemake, Nextflow, Docker, RShiny, Dash, Django, Make

Relevant Courses

Computational Statistics, Department of Mathematical Sciences, University of Copenhagen, (2022)
Advanced Topics in Data Analysis, Faculty of Health and Medical Sciences, University of Copenhagen, (2021)
Fundamentals in Computational Analysis of Large-Scale Datasets, Faculty of Health and Medical Sciences, University of Copenhagen, (2021)
RevBayes Workshop, Topics: Tree inference from molecular data, evaluating MCMC performance, assessing model adequacy and macroevolutionary analyses, (2020)
Fundamentals of Bioinformatics, Department of Computer Science, Hacettepe University, Lect.: Tunca Doğan, (2019)
Population Genetics, Graduate course, Department of Molecular Biology and Genetics, Middle East Technical University, Lect.: Mehmet Somel, (2018)
Population Genetics Simulations with R, Middle East Technical University, (2018)
Introduction to Game Theory, Anadolu University, (2017)
Evolutionary Genomics Winter School, Hacettepe University, (2017)

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

- gptchatteR: An **R** package for interacting with **OpenAI's language models** in the R console, enabling AI-driven data analysis, visualization, and learning. (2022 - 2023).

- ngsAMOVA: A **C/C++** toolkit for AMOVA, d_{xy}, Neighbor-Joining, and IBD segment detection from NGS data using probabilistic frameworks (see Publications/Manuscripts in Preparation). (2022 - present).

- google-slides_scripts: Custom **Google Apps Script** functions to enhance Google Slides' features. (2022).

- vcfgl: A **C/C++** tool for fast and efficient simulation of genotype likelihoods (see Publications/5). (2022 - present).

- ANGSD: Contributed to the development and maintenance of ANGSD, a **C/C++** toolkit for analyzing next-generation sequencing data. (2021 - 2024).

- bash-functions: A collection of custom **Bash** functions for various tasks, including 'runda' for safe **conda** environments and 'treemd' for generating **Markdown**-formatted Git repository structures. (2021 - present).

- decluster: A **C++** tool for identifying and stratifying duplicate reads in high-throughput sequencing data, including functionality for detecting cluster duplicates, PCR duplicates, and calculating sequence complexity and GC content. (2021 - 2022).

- PopulasyonBuyumesi: An **RShiny** app for teaching population ecology through population growth simulations and interactive plots (in Turkish). Available at popbsim.isinaltinkaya.com. (2020).

- cheatsheets: Custom **Markdown** tutorials with tips and examples for tools like **Bash**, **Git**, **Jupyter**, **Make**, **Conda**, and **R**. (2020 - present).

- HMMploidy: A **Python** tool to calculate ploidy levels from genotype likelihoods and coverage using Hidden Markov Models. (see Publications/2), (2019).

- i3gcalendar: Google Calendar integration with i3blocks, written in **Python**, for the 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-5, L-5, W-5)
- **German:** Elementary proficiency (ILR level R-1, S-1, L-0, W-0+)
- **Danish:** Elementary proficiency (ILR level R-1, S-1, L-0+, W-1)

References

- **Rasmus Nielsen** ⓘ • rasmus_nielsen@berkeley.edu
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University of Copenhagen, Faculty of Health and Medical Sciences, Globe Institute, Section for GeoGenetics
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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