# Işın Altınkaya

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## Language

| Turkish *(Native)* | English *(Fluent)* | German *(Beginner)* | Danish *(Beginner)* |
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## Education

- **PhD** — University of Copenhagen, Denmark
  Faculty of Health and Medical Sciences — 2022/1 - expected in 2025/1
    **Title:** Statistical methods for population genetic inference based on low-depth sequencing data
    **Advisors:** Thorfinn S. Korneliussen and Rasmus Nielsen

- **BSc in Biology** — Hacettepe University, Ankara, Turkey
  Faculty of Science, Department of Biology — 2020/7

## Research Experience

- **Globe Institute, Section for GeoGenetics** — University of Copenhagen, Denmark
  Research assistant, Advisors: Thorfinn S. Korneliussen and Rasmus Nielsen — 2020/10 - 2021/12

  Contributed to a number of independent projects which resulted in 2 publications and 3 manuscripts in preparation. Worked on the development and evaluation of the Lundbeck center bioinformatics pipeline processing thousands of ancient genomes.

- **Fumagalli Lab** — Imperial College London, United Kingdom
  Intern, Advisor: Matteo Fumagalli — 2019/7 - 2019/9

  Contributed to the HMMPloidy project by implementing various methods, including the genotype likelihood estimation for any N-ploidy, which resulted in a publication. Funded by Erasmus+ Traineeship Grant.

- **Biogeography Research Laboratory** — Hacettepe University, Turkey
  Intern, Advisor: Barış Özüdoğru — 2019/2 - 2020/7

  Developed a snakemake-based bioinformatic pipeline for the processing and phylogenomic analyses of RADSeq data, which resulted in a manuscript in preparation.

- **Laboratory of Comparative and Evolutionary Biology** — Middle East Technical University, Turkey
  Intern, Advisor: Mehmet Somel — 2018/8 - 2019/6

  Carried out analyses to evaluate the effects of the properties of probe sequences in the 1240K SNP capture method.

- **Laboratory of Evolutionary and Quantitative Genetics** — Hacettepe University, Turkey
  Intern, Advisor: Ergi Deniz Özsoy — 2015/10 - 2018/12

  Contributed to the statistical analyses of quantitative genetics projects based on Drosophila Genetic Reference Panel 2 (DGRP2) data, which resulted in a poster presentation and acknowledgments in two MSc and one PhD thesis.

## Publications

[2]   Alex Mas-Sandoval, Nathaniel S. Pope, Knud Nor Nielsen, **Isin Altinkaya**, Matteo Fumagalli, and Thorfinn Sand Korneliussen. Fast and accurate estimation of multidimensional site frequency spectra from low-coverage high-throughput sequencing data. *GigaScience* (2022).

[1]   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).

### Preprints

•   Morten E. Allentoft [et al, including **Isin Altinkaya**.] Population Genomics of Stone Age Eurasia, *bioRxiv*, (2022).

### Manuscripts in preparation

•   **Isin Altinkaya**, Emrullah Yılmaz, Ismail Kudret Saglam, Barış Özüdoğru. Understanding the phylogenetic relationships within the Noccaea species complex from RADseq data using the multi-species coalescent.

- **Isin Altinkaya**, Lei Zhao, Rasmus Nielsen, Thorfinn S. Korneliussen. A Genotype Likelihood Framework for Analysis of Molecular Variance (AMOVA) with Low Depth Sequencing Data.

- Hugh McColl, José Victor Moreno Mayar, **Isin Altinkaya**, Thorfinn Sand Korneliussen, Accurate and precise library complexity estimations for ancient DNA libraries using patterned flowcell technology.

- Fulya E. Yediay [et al, including **Isin Altinkaya**.] Population genomics of Bronze Age Mediterranean.

- Hugh McColl [et al, including **Isin Altinkaya**.] Population genomics of Iron Age.

## Skills

**Programming languages**: C/C++, R, Python, Java, Perl, Rust
**Scripting and typesetting**: LaTeX, Markdown, HTML&CSS, JavaScript, Google Apps Script, sed, awk, Bash
**Operating systems**: GNU/Linux
**Other tools and frameworks**: Git, Conda, Snakemake, RShiny, Dash, Django, Make

## Conferences, Workshops, and Talks

[**5**]  A Genotype Likelihood Framework for the Analysis of Molecular Variance (AMOVA), *Evolution and Population Genetics in Denmark (EPIC) Conference*, Denmark, (2022).

[**4**]  Evolutionary Biology and Preventing the Species Extinction, *7th National Environment and Ecology Student Congress*, Turkey, (2016).

[**3**]  Biological Evolution, *Science and Future Magazine Science for Youth Seminar*, Turkey, (2018).

[**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

[**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*, 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, Hacettepe University, **Teaching Assistant**, (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 the organization of 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, (June 2017 - May 2018).
- Popular Science Magazine, Turkey branch, **Popular science news editor and translator**, (February - May 2016).
- Tree of Evolution, **Writer and editor**; Subject: Evolutionary biology, (November 2015 - 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)

- Science and Utopia Magazine, Issue: 283, Examining the thin line between living and non-living matter, co-authored with Martin Hanczyc.

- Science and Utopia Magazine, Issue: 278, Education and perceptions: Evolution in Turkey.

- Atheist Magazine, Issue: 16, The evolving brain.

- Atheist Magazine, Issue: 14, Evolutionary biology and LGBTI+ in nature.

- Atheist Magazine, Issue: 13, Understanding evolution through the human body.

## Open Source Contributions

**[10]**    gptchatteR : An experimental R package for interacting with OpenAI GPT models in R. It provides a framework for using AI language models to help learning and conducting data analysis, plotting and data wrangling from R console. (2023).

**[9]**    gs_scripts : Custom scripts providing various additional functionalities to Google Slides (2022).

**[8]**    vcfgl : A tool for fast and efficient simulation of genotype likelihoods from VCF GT tags (2022).

**[7]**    ANGSD : Actively contributing to the development and maintenance of the ANGSD software. (2021 - ongoing).

**[6]**    bash-functions : Custom functions designed for bashrc to perform various tasks, including runda (environment-safe wrapper for conda), treemd (format and print the tree structure of a git repository for markdown), lns (easy and safe wrapper for creating symbolic links) (2021).

**[5]**    i3pomodoror : i3blocks wrapper for the R package pomodoror (2020).

**[4]**    PopulasyonBuyumesi : An RShiny application for teaching population ecology, including population growth simulations and interactive plots. The RShiny app is available at isinaltinkaya.shinyapps.io/PopulasyonBuyumesiSimulasyonlari/ (in Turkish), (2020).

**[3]**    cheatsheets : Custom Markdown tutorials containing custom functions, examples, tips and tricks for using various tools and programming languages effectively, such as bash, git, jupyter, Make, conda and R (2020).

**[2]**    HMMploidy : A tool to calculate ploidy levels from genotype likelihoods and coverage using Hidden Markov Models. Contributed to the development of the open source software as a part of an academic project (see Publications/1), (2020).

**[1]**    i3gcalendar : Google Calendar i3blocks integration for i3wm (2018).

## Scholarships & Awards

**[5]**    Erasmus+ Traineeship Grant, Imperial College London, (2019).
**[4]**    Hacktoberfest Award, for contributing to open source projects, (2019).
**[3]**    Hacktoberfest Award, for contributing to open source projects, (2018).
**[2]**    Atheist Alliance International Foundation Scholarship for Students in Underdeveloped Countries, (2017).
**[1]**    Atheist Alliance International Foundation Scholarship for Students in Underdeveloped Countries, (2016).

## 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*