

AL DEPOPE, PHD

 ADepope |  Al Depope |  adepope.github.io |  al.depope@ist.ac.at |  0000-0001-8583-0609

Work Eligibility: Croatian EU citizen

PROFILE

As a Postdoctoral Researcher at IST Austria, I specialize in mathematically grounded machine learning and statistical genetics, developing novel Bayesian models and inference procedures to improve biomarker selection and individual risk prediction. I combine probabilistic modeling with high-performance computing (C++, CUDA, distributed systems) and advanced data analysis (Python, R). I am now seeking a computational biology position where I can leverage this and develop tools that drive real-world impact.

Core Competencies: Probabilistic Predictive Modeling · Bayesian Inference · Numerical Optimization · High-Dimensional Inference · High-Performance Computing · Python (Pytorch) · Omics

TECHNICAL SKILLS

Programming	Python (Pandas, PyTorch, Hugging Face, Scikit-learn), C++ (OpenMP, MPI, Eigen), R , CUDA, SQL, Bash
Data Science & ML	High-dimensional Bayesian Inference, Statistics, Probabilistic Predictive Modeling, Numerical Optimization, Survival Analysis
Bioinformatics	Large-scale GWAS, Single-cell Foundation Models, Nextflow, DNAnexus
DevOps & Tools	Git, Docker, SLURM, High-Performance Computing Clusters, Claude Code

PROFESSIONAL EXPERIENCE

Postdoctoral Researcher

INSTITUTE OF SCIENCE AND TECHNOLOGY AUSTRIA (IST AUSTRIA)

Jul 2026 – Present

Klosterneuburg, Austria

Extending my doctoral work by developing [TLgVAMP](#), a transfer-learning framework for improved cross-ancestry polygenic risk scores.

PhD Candidate

INSTITUTE OF SCIENCE AND TECHNOLOGY AUSTRIA (IST AUSTRIA)

Sep 2020 – July 2026

Klosterneuburg, Austria

Engineered high-performance Approximate Message Passing frameworks for Bayesian inference in C++ and Python, achieving **10x speedups** over traditional MCMC methods while maintaining superior variable selection accuracy.

- **Scalable High-Dimensional Genomic Inference:** Developed and open-sourced scalable inference approaches ([gVAMP](#), [gVAMPomi](#)). Processed 17 million single nucleotide polymorphisms (SNPs) to execute the largest joint GWAS to date, achieving a state-of-the-art 46% prediction accuracy for human height.
- **Proteomic Survival Analysis:** Built [vampW](#), a scalable Bayesian framework modeling disease onset times. Applied to the UK Biobank Pharma Proteomics dataset, achieving a 26–33% relative improvement in onset prediction over penalized Cox and baseline deep learning approaches.
- **Cross-Field Collaboration:** Partnered with the Textile Recycling Group at TU Wien to conduct targeted statistical analyses and develop data visualizations supporting its engineering processes.

Relevant coursework: **Pharmacoinformatics, Probabilistic Graphical Models, Deep-learning topics in the field of computer-aided drug design**

Machine Learning & Privacy Intern

UNIVERSITY OF VIENNA

Nov 2024 – Nov 2025

Vienna, Austria

- Developed a modular [Python library](#) for benchmarking Membership Inference Attacks (MIA) on Large Language Models (LLMs).
- Designed and implemented a robust document-level differential privacy auditing framework.

Software Engineer Intern

CERN (EUROPEAN ORGANIZATION FOR NUCLEAR RESEARCH)

Jul 2019 – Aug 2019

Geneva, Switzerland

- Integrated 11 environmental data pipelines into the CERN CMS Online Monitoring System.
- Developed 13 Java-based aggregation layer endpoints and 16 Python-based presentation probes using Plotly.js, optimizing latency and automating detector on-call reporting.

KEY PUBLICATIONS

- **Depope, A.**, Bajzik, J., Mondelli, M., Robinson, M.R. "Joint modelling of whole genome sequence data for human height via approximate message passing." *Cell Genomics*, 2026. [\[DOI\]](#)
- Bajzik J.*, **Depope, A.***, et al. "Joint Variable Selection in Proteomics Survival Models." *ICLR Workshop on ML for Genomics Explorations*, 2026. [\[OpenReview\]](#)
- **Depope, A.**, Mondelli, M., Robinson, M.R. "Inference of Genetic Effects via Approximate Message Passing." *IEEE ICASSP*, 2024. [\[DOI\]](#)

TRANSFERABLE SKILLS

- **Public Speaking:** Delivered 40+ presentations translating complex computational architecture to diverse audiences, winning "Best Student Presentation" at the European Mathematical Genetics Meeting (2024).
- **Mentorship:** Mentored 5 technical interns and served as Teaching Assistant for *Modern Machine Learning* course at IST Austria.
- **End-to-End Delivery:** Directed projects through the entire data lifecycle: from theoretical conception and robust HPC implementation to final publication.

EDUCATION

PhD in Statistical Genetics | IST Austria

Sep 2020 – July 2026

M.Sc. in Mathematical Statistics (GPA: 5.0/5.0) | University of Zagreb

Sep 2018 – Sep 2020

B.Sc. in Mathematics (GPA: 5.0/5.0) | University of Zagreb

Sep 2015 – Sep 2018

LANGUAGES

Croatian (native) · English (fluent) · German (A2)

INTERESTS

In my free time, I enjoy hiking (my most recent peak over 4,000 meters was Mauna Kea in Hawaii) and volunteer by delivering competitive mathematics lectures to gifted high-school students.

REFERENCES

- Prof. [Marco Mondelli](#), IST Austria, marco.mondelli@ist.ac.at
- Prof. [Matthew Robinson](#), IST Austria, matthew.robinson@ist.ac.at