

Xenofon Giannoulis

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Work Experience

Statistical Geneticist

PLATFORM & DATA ENGINEERING

Pheiron GmbH, DE

July 2025 – now

- Designed precomputation pipeline supporting three analysis modes (single-variant GWAS, PGS-GWAS, burden tests).
- Engineered streaming ETL for genetics association results at hundreds-of-millions to billions of rows.
- Implemented out-of-core processing with low-memory execution and hour-scale end-to-end runtimes.
- Built post-ETL QC/validation framework with modular checks, resumable runs, and production monitoring.
- Added biological validation against external references to ensure decision-grade result quality.
- Developed external GWAS catalogue: harmonized public biobank summary statistics into a unified resource.
- Designed a query interface for fast gene-, variant-, and phenotype-level association lookups.
- Authored end-to-end documentation (architecture, workflows, benchmarks, troubleshooting) to enable team communication.

Postdoctoral Researcher

INSTITUTE OF COMPUTATIONAL NEUROBIOLOGY

Helmholtz Munich, DE

January 2025 – June 2025

- Used knowledge-graph and network medicine methods to prioritize potential therapeutic targets in Alzheimer's disease.
- Integrated multi-omics data with graph-based and ML models to characterize disease pathways and candidate mechanisms.
- Built interactive exploration tools (R Shiny + Neo4j) for network-based hypothesis generation; AD Atlas.
- Developed reproducible pipelines to harmonize and analyze high-dimensional omics datasets from NIH-funded consortia.

Doctoral Researcher

INSTITUTE OF TRANSLATIONAL GENETICS

Helmholtz Pioneer Campus, DE

June 2020 – December 2024

- Built a multi-tissue atlas of mitonuclear gene regulation in GTEx v8 (684 donors, 48 tissues) using WGS + RNA-seq.
- Mapped 111 independent mtDNA cis-eQTL associations across mtDNA genes, including 86 novel signals.
- Implemented LMM eQTL workflows with rigorous QC, mtDNA haplogroup inference, and tissue-specific covariate control.
- Extended discovery to trans effects and causal follow-ups via colocalization, mediation testing, and Mendelian randomization.
- Identified genome-wide trans mito-nuclear regulatory links, including CNS-enriched cell-type interaction effects.
- Integrated eQTL results into network-based gene prioritization using Speos (GNN/MLP; TAG graph convolution).
- Built an RNA-seq pipeline to quantify mtDNA heteroplasmy and mtRNA modifications (12,577 samples, 49 tissues).
- Built coverage-aware association tests (LM + beta-binomial), finding 109 age and 784 expression associations.
- xCell interaction + mediation analyses found 9 age–heteroplasmy–mtDNA expression links.
- Presented results in interdisciplinary settings and contributed to manuscripts, figures, and reproducible analysis code.

Research Fellow

DATA SCIENCE FOR SOCIAL GOOD | MUNICH CENTER FOR MACHINE LEARNING

LMU, Munich, DE

August 2023 – September 2023

- Built a geospatial planning tool for fire brigades to model hose reachability under real-world obstacles (stairs, rails, buildings).
- Generated reachability polygons from a selected water extraction point for a given hose length.
- Computed reverse-planning polygons for where a water point must lie to cover a selected building/site.
- Developed a full-stack web app for interactive mapping, real-time routing, and resource planning in the field.
- Deployed on AWS using a containerized architecture for reliable, scalable use by partners.
- Delivered to Federal Office for Disaster Control & Munich Fire Brigade; presented to the German federal parliament.

Higher Education Instructor

FACULTY OF MEDICINE (ME1660)

TUM Munich, DE

October 2022 – March 2023

- Tutored and supported students in computational genomics through hands-on labs and office hours.
- Improved course materials and workshop flow for practical analysis in JupyterLab.
- Taught UNIX, QC, association testing, meta-analysis, and polygenic risk score methods.

Quantitative Analytics Intern

INSTITUTE OF TRANSLATIONAL GENOMICS

Helmholtz Munich, DE

October 2019 – April 2020

- Analyzed GWAS data from multi-center joint replacement cohorts to identify genetic risk factors.
- Harmonized Illumina exome-array datasets across multiple centers and processing pipelines.
- Built QC workflows to detect batch effects, technical bias, and cross-center inconsistencies.
- Ran genotype imputation via the Michigan Imputation Server using the HRC reference panel.

Education

Technical University of Munich (TUM) - Experimental Medicine

Ph.D. / DR.RER.NAT. IN SCHOOL OF MEDICINE (MGC)

Munich, DE

Dec 2024

Thessaly University - Computer Science and Biomedical Informatics

MSc. IN INFORMATICS AND COMPUTATIONAL BIOMEDICINE

Lamia, GR

April 2020

Piraeus University - Department of Statistics and Insurance Science

PTYCHION (4-YEAR BSC.) IN STATISTICS AND ACTUARIAL SCIENCE

Athens, GR

February 2018

Technical Experience

Platform/API

Queryable data catalogs and analytical storage: [Apache Iceberg](#), [Parquet](#), partitioning, schema evolution.
Analytical SQL and in-process analytics: [SQL](#), [DuckDB](#).
Interactive apps with [RShiny](#) + [Neo4j](#) for graph exploration and hypothesis generation.
REST query APIs for gene/variant/phenotype lookups and catalog search/querying.
REST services with [Flask](#) for geospatial routing and mapping workflows.
Data validation and monitoring for production pipelines (QC modules, checks, runbooks).

Engineering

[Python](#), [R](#), [Bash](#), [Linux](#) for large-scale data processing and workflow automation.
Reproducible workflows, containerization, and cloud execution.
Knowledge graph / semantic web tooling: [Protégé](#), [RDF](#), [SPARQL](#).
Certified Oracle MySQL Developer (1z0-882).
Version control with [GitHub](#); documentation with [LaTeX](#) and [RMarkdown](#).
AI-assisted development with [Cursor](#), [Copilot](#), and LLM-based tooling.

Genetics

GWAS, PheWAS, eQTL/ct-eQTL mapping, WGS, RNA-seq, variant calling, Illumina array processing.
Tools: [Regenie](#), [PLINK](#), [LDAK](#), [Bioconductor](#), [MendelianRandomization](#), [Coloc](#).
PRS construction, burden testing, fine-mapping, conditional analysis, annotation integration.
Multi-omics integration (genomic, transcriptomic, proteomic, regulatory).
Biobanks: GTEx, PsychEncode, UK Biobank, All of Us, FinnGen, MVP.

Statistics & ML

Linear mixed models (GRM/variance components), GLMs; heteroskedasticity-aware modeling.
Empirical inference: genotype permutations, simulations, likelihood-ratio tests; model evaluation.
Multiple testing control: BH/q-value FDR and Bonferroni at tissue/study-wide levels.
Causal follow-up: Bayesian colocalization, conditional/mediation analysis, Mendelian randomization.
Feature engineering, PCA, ensemble learning for gene prioritization.

Cloud

Cloud-based genomic workflows with [DNAAnexus](#), [AWS/S3](#), and [Docker](#).
Parallel execution, resumable runs, and cost-aware scaling for biobank-scale analyses.

Scientific Publications

Interplay between mitochondrial and nuclear DNA in gene expression regulation. [Biorxiv](#)

Xenofon Giannoulis, SIMON WENGERT, FLORIN RATAJCZAK, MATTHIAS HEINIG, NA CAI.

UNDER REVIEW AT NATURE COMMUNICATIONS.

Tissue-Specific mtDNA Heteroplasmy Linked to Aging and Gene Expression. [Biorxiv](#)

SIMON WENGERT, Xenofon Giannoulis, PETER KREITMAIER, HOLGER PROKISCH, PAOLO CASALE,
MATTHIAS HEINIG, NA CAI.

UNDER REVIEW AT NATURE COMMUNICATIONS.