Xenofon **Giannoulis**

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Work Experience

Statistical Geneticist
Pheiron Gmbh,DE

Genetics & Platform Development *July 2025 - now*

- Developing large-scale genomic evidence systems supporting target validation for drug discovery.
- Leading cross-functional efforts to integrate multi-layered biological data into decision-grade systems.
- Engineering ETL pipelines to harmonize, integrate, and analyze large-scale genetic data into unified resources.
- Designing unified interfaces for fast gene-, variant-, and phenotype-level genetic association queries.
- Collaborating with product teams, scientific partners, and clients to deliver decision-ready genetic insights.

Postdoctoral Researcher
Helmholtz Munich,DE

Institute of Computational Neurobiology *January 2025 - June 2025*

- Applied knowledge-graph and network medicine approaches to identify potential therapeutic targets in Alzheimer's disease.
- Directed multi-omics integration efforts using AI, machine learning, and graph-based models to decode disease pathways.
- Built interactive exploration tools using R Shiny and Neo4j to support network-based hypothesis generation (www.adatlas.org).
- Developed scalable pipelines to harmonize and analyze high-dimensional omics datasets from NIH-funded consortia.

Doctoral Researcher
Helmholtz Pioneer Campus,DE

Institute of Translational Genetics *June 2020 - December 2024*

- Designed the first comprehensive catalog of mtDNA variation effects on gene expression regulation across 48 human tissues.
- Applied advanced machine learning models to uncover key mechanisms into mitochondria-nuclear communication.
- Built an ensemble model integrating RNAseq and eQTL data, to identify central genes in regulatory networks.
- Validated findings in large-scale neuropsychiatric cohorts to uncover disease-relevant mitonuclear interactions.
- Integrated multiple databases and tools to cross-reference, annotate and confirm analytical results.
- Organized two Munich School of Data Science retreats, managing speaker engagement and scientific programming.
- Presented research at international conferences and contributed to interdisciplinary collaborations.

Research Fellow
LMU, Munich,DE

Data Science for Social Good | Munich Center for Machine Learning *August 2023 - September 2023*

- Developed geospatial and machine learning tools to optimize emergency response infrastructure in Bavaria.
- Built a full-stack web application enabling real-time routing and resource planning for fire brigades.
- Integrated statistical mapping and geolocation data to produce an intuitive, high-utility UX interface.
- Deployed the platform on AWS using a containerized architecture for scalable field use.
- Presented the solution and project findings to the German federal parliament.

Higher Education Instructor
TUM Munich,DE

Faculty of Medicine (ME1660) *October 2022 - March 2023*

- Served as a tutor and provided hands-on support to students in computational genomics coursework.
- Enhanced learning materials and workshop structure for practical data analysis in Jupyter Lab.
- Covered UNIX, quality control, association testing, meta-analysis and polygenic risk score methodology.

Quantitative Analytics Intern
Helmholtz Munich,DE

Institute of Translational Genomics *October 2019 - April 2020*

- Analyzed genome-wide association data from multi-center joint replacement cohorts to identify genetic risk factors.
- Processed and harmonized data generated from multiple Illumina exome arrays across different sequencing centers.
- Developed quality control workflows to detect batch effects, biases and inconsistencies in pre-processed data.
- Performed genotype imputation using the Haplotype Reference Consortium via the Michigan Imputation Server.

Education

Technical University of Munich (TUM) - Experimental Medicine *Munich, DE*

Ph.D. / Dr.rer.nat. in School of Medicine (MGC) *Dec 2024*

Thessaly University - Computer Science and Biomedical Informatics *Lamia, GR*

MSc. in Informatics and Computational Biomedicine *April 2020*

Piraeus University - Department of Statistics and Insurance Science *Athens, GR*

Ptychion (4-year BSc.) in Statistics and Actuarial Science *February 2018*

Technical Experience

Engineering	Proficient in Python, R, Bash, and Linux for large-scale data processing and workflow automation Experience designing reproducible genomic workflows using Nextflow, containerization, and cloud compute. Web and API development with RShiny, Flask, and REST interfaces. Knowledge graph and semantic web technologies: Neo4j, Protégé, RDF, SPARQL Certified Oracle MySQL Developer (1z0-882) Version control with GitHub, documentation with LaTeX and RMarkdown Fluent in AI-assisted development with Cursor, Copilot, and LLM-based tooling.
Genetics	GWAS, PheWAS, eQTL/ct-eQTL mapping, WGS, RNA-seq, variant calling and Illumina array processing. Tools: Regenie, PLINK, LDAK, Bioconductor, MendelianRandomization, Coloc. Expertise in PRS construction, burden testing, fine-mapping, conditional analysis and annotation integration. Multi-omics integration (genomic, transcriptomic, proteomic, regulatory). Experience with biobanks: GTEx, PsychEncode, UK Biobank, All of Us.
Data Science	Statistical rigor & hypothesis testing, permutations, corrections, model evaluation Univariate and multivariate analysis, multicollinearity checks, outlier detection, feature selection Feature engineering, dimensionality reduction (PCA), ensemble learning for gene prioritization
Cloud	Experienced with cloud-based genomic workflows (DNAnexus, AWS/S3, Docker containers)

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.