

Jamie Scheper

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Languages: Dutch (native) and English (fluent)
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Portfolio: jscscherper.github.io

Profile

Bioinformatics graduate who ships software. Experienced with RNA-seq and multi-omics in clinical research at UMCG (sepsis transcriptomics, biomarker discovery, multi-omics integration). Furthermore, I build reproducible pipelines (Snakemake, Nextflow/nf-core, Docker) and full-stack tools (Flask + React, REST APIs, SQL) that make analysis workflows usable for non-coders. I'm motivated by removing friction: solid backends, clean data models, and intuitive interfaces. Seeking bioinformatics and/or software engineering roles!

Technical Skills

- Data analysis: RNA-seq differential expression, enrichment analysis, multi-omics integration, biomarker discovery
- Programming: Python, R, Java, JavaScript, SQL, Bash/Linux
- Bioinformatics tooling: DESeq2, edgeR, Seurat, GSEA, STAR, BWA, samtools, mixOmics (DIABLO)
- Pipelines & reproducibility: Snakemake, Nextflow, nf-core, Docker, Singularity, Conda/Mamba
- Web & backend: Flask, React, REST APIs, SQLAlchemy, TailwindCSS
- Cloud & dev tooling: Git/GitHub, CI/CD, AWS (S3, EC2, Lambda)

Education

Bachelor of Bioinformatics

Hanze University of Applied Sciences — 2020 – 2025

- Minor: Advanced Data Mining & High-Performance Computing

Research Experience

Bioinformatics intern – Clinical hibernation research

University Medical Center Groningen, Dep. Clinical Pharmacy & Pharmacology — May 2024 – Jan. 2025

- Integrated 3 omics layers (~15,000 features across transcriptomics, proteomics, and metabolomics) using DIABLO and multiGSEA to discover a 47-feature molecular hibernation signature.
- Identified *Dync1li2* as a novel regulator of metabolic suppression, linking decreased microtubule transport to torpor survival.
- Mapped new pathways in energy metabolism and oxidative stress; findings currently under review for publication (Scherper et al., 2025).

Bioinformatics intern – Mitochondrial dysfunction in early sepsis

University Medical Center Groningen, AcuteLines Research Group — Sep. 2023 – Mar. 2024

- Discovered two novel mitochondrial-driven sepsis endotypes by analyzing RNA-seq data from a 348-patient ER/ICU cohort.

- Engineered an 11-gene LASSO model predicting patient endotypes with 96% (ER) and 93% (ICU) accuracy.

- Identified transcriptomic biomarkers for early-stage organ failure to enable rapid patient stratification in acute care settings.

Portfolio

DEApp – Full-stack RNA-seq differential expression platform — View on GitHub

- Developed a Dockerized Flask/React platform to run DESeq2, edgeR, and GSEA pipelines via a web UI, reducing the need for command-line analysis.

- Designed interactive visualizations (volcano plots, heatmaps) for publication-ready exploration.

CDSnake – 16S amplicon processing pipeline — View on GitHub

- Rebuilt the CD-HIT-OTU workflow as a reproducible Snakemake pipeline with YAML configuration, automated QC, clustering, and reporting for microbiome analysis.

Pedigree tracker — View on GitHub

- Built a Java/Thymeleaf web application for constructing family pedigrees with automated Mendelian disease risk calculations.

- Implemented user authentication, MySQL databases, and an interactive pedigree visualization interface.

Neural network library — View on GitHub

- Implemented MLPs from scratch in Python with modular layers, multiple activation functions, and loss functions.

- Applied to MNIST classification with visualization of decision boundaries and training curves.

Additional Experience

Freelance web developer — 2018 – 2021

- Designed and developed responsive websites for local businesses.

- Focused on UX optimization and mobile responsiveness.

Store clerk / customer support — 2017 – 2022

Makro Groningen

- Student job

Publications

Scheper, J.S.C., et al. “Multi-omics integration identifies intracellular adaptations in hibernating golden hamster livers.” *Journal of Comparative Physiology B* (Under review, 2025). Manuscript available upon request.