

Malwina Prater, PhD

SENIOR DATA SCIENTIST

EXPERIENCE

Senior Data Scientist

Jan 2025–Present

Altos Labs, Cambridge UK

- Built spatial transcriptomics (Xenium) QC infrastructure in the nf-xenium-processing pipeline: an SNR and focus-quality module from scratch (GMM blur detection with Laplacian fallback, YAML-driven gates), redesigned image and molecule QC reports, and multi-stain tissue-extent segmentation masks
- Ran metric drift analysis and cross-cohort calibration across a growing multi-tissue cohort so QC reliably gates high-quality slides into downstream machine-learning analysis
- Developed CRISPR screen infrastructure: migrated the CRISPRlibQC pipeline from a command-line tool to a Seqera pipeline with speed and memory optimisation to scale to whole-genome guide design, and built interactive dashboards for visualisation, filtering and reporting
- Delivered guide design and selection across CRISPRa / CRISPRi / knockout modalities, plus screen-design tooling for FACS, colony-forming-efficiency (CFE) and viability screens
- Key point of contact for CRISPR screens across teams — advising on experimental design, controls and analysis strategy, and troubleshooting screens (non-targeting-control selection, CRISPResso2 analysis, and diagnosing unsuccessful ORF screens)
- Contributed Xenium spatial analysis to a manuscript revision, establishing transcription-factor expression at transcript level and cross-species validation despite low-quality human tissue
- Engineering and infrastructure: Nextflow / Seqera pipeline development and Seqera compute-environment tuning, containerisation with Docker and image management via AWS ECR, HPC and AWS, and infrastructure-as-code in Terraform (GitHub Actions OIDC CI roles and least-privilege, read-only ECR access)

Senior Bioinformatician

2023–2025

Functional Genomics Centre, Cancer Research Horizons

- Led a single-cell project portfolio (Perturb-seq) in a dynamic environment, coordinating task distribution across the team and ensuring quality work and timely delivery
- Line-managed the bioinformatics team and led recruitment of new staff
- Managed multiple CRISPR projects, working closely with wet lab scientists and stakeholders, consulting on experimental design, running pipelines and custom projects, and delivering results and reports to timelines
- Contributed to development and deployment of bioinformatic solutions on AWS
- Established new CRISPR screen capabilities
- Performed lethality, isogenic, epigenetic, gene-tiling and in-vivo CRISPR screen analyses
- Collaborated with other bioinformaticians and researchers on technology development and portfolio projects

Bioinformatician

2021–2023

MRC Mitochondrial Biology Unit, University of Cambridge, UK

- Collaborative research across multiple scientific projects: consulting on experimental design, performing data analysis, and helping prepare manuscripts for publication
- Involved in grant applications; line-managed a PhD student and supervised and coached others
- Analysis of complex multi-omic datasets (e.g. scRNA-seq + ATAC-seq + CROP-seq), allele-specific single-cell RNA-seq, dataset integration and

CONTACT

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ABOUT ME

Bioinformatician with 9 years of experience, now at Altos Labs working on spatial transcriptomics (Xenium) QC, CRISPR screen design and analysis, and the pipelines and infrastructure that scale them.

Uniquely positioned to integrate and consult across both wet lab and dry lab research. My passion is seeing scientific advances benefiting the world.

SKILLS

Spatial transcriptomics (Xenium) · CRISPR screen design & analysis · Single-cell multiomics · NGS processing pipelines & analysis

Nextflow · Seqera · AWS (incl. ECR) · Docker · Terraform · HPC · Slurm · GitHub

R · Python · SQL · Bash

EDUCATION

PhD in Oncology

Cancer Research UK CI, University of Cambridge

Prize for Best Presentation, Methyl Donors and Human Health Symposium

BSc Biotechnology (1st class)

University of Edinburgh

James Rennie Bequest Travel Award; Darwin Trust of Edinburgh Scholarship (twice)

STRENGTHS

- Strong infrastructure and pipeline engineering: scalable, production-grade tooling and infrastructure-as-code (Nextflow/Seqera, containers, AWS, Terraform)
- Broad knowledge base in molecular biology, oncology and epigenetics
- Rapidly adjusts priorities and adapts to shifting needs while staying focused on the main objective
- Focus on data transparency and reproducibility
- Project and people management

variant calling

Bioinformatician

2016–2021

Centre for Trophoblast Research, University of Cambridge, UK

- Collaborative research with 10+ research groups and 25+ projects: consulting on experimental design and data analysis, and helping prepare manuscripts for publication
- Drove own research and first-author publications
- Co-supervised and co-trained summer students and visiting scientists
- Analysis of microarray, RNA-seq, single-cell RNA-seq, DNA methylation and ChIP-seq experiments, and transcription-factor motif search
- Taught bioinformatics courses on RNA-seq analysis (Placental Biology Course, 2017 & 2019) and experimental design (EMBL-EBI, 2020)
- Supervised a summer student project (2017) and a Part II student project (2020–2021)
- Awarded a High Performance Computing grant for 450k core hours (~£5k, 2019)
- Data Champion at the University of Cambridge, promoting good research data management

R&D Scientist

2014–2016

Cambridge Epigenetix, Cambridge, UK

- Applied knowledge of epigenetics and biochemistry in an emerging start-up
- Supported development of a novel epigenetic kit ahead of commercialisation

SELECTED PUBLICATIONS

Burr, S.P., Auckland, K., Glynos, A., ... Prater, M., ... van den Amelee, J. (2026) MitoPerturb-Seq identifies gene-specific single-cell responses to mitochondrial DNA depletion and heteroplasmy. *Nature Structural & Molecular Biology* 33, 711–723.

Burr, S., Klimm, F., Glynos, A., Prater, M., ... Chinnery, P. (2023) Cell lineage-specific mitochondrial resilience during mammalian organogenesis. *Cell* 186(6):1212–1229.

Prater, M., Hamilton, R.S., Yung, H.W., Sharkey, A.M., Robson, P., Jauniaux, E., Charnock-Jones, S., Burton, G.J., Cindrova-Davies, T. (2021) RNA-Seq reveals changes in human placental metabolism, transport and endocrinology function in the first–second trimester transition. *Biology Open* 10(6).

Prater, M. & Hamilton, R.S. (2018) Epigenetics: Analysis of cytosine modifications at single base resolution. *Encyclopedia of Bioinformatics and Computational Biology*, 3, 341–353.

Turco, M.Y., Gardner, L., Kay, R., Hamilton, R.S., Prater, M., ... Moffett, A. (2018) Trophoblast organoids as a model for maternal-fetal interactions during human placentation. *Nature* 564, 263–267.

Stojic, L., Niemczyk, M., Orjalo, A., ... Gergely, F., Murrell, A. (2016) Transcriptional silencing of long noncoding RNA GNG12-AS1 uncouples its transcriptional and product-related functions. *Nature Communications* 7 (10406).

Niemczyk, M., Ito, Y., Huddleston, J., Git, A., Abu-Amero, S., Caldas, C., Moore, G.E., Stojic, L., Murrell, A. (2013) Imprinted chromatin around DIRAS3 regulates alternative splicing of GNG12-AS1, a long noncoding RNA. *American Journal of Human Genetics*.

Shah, P., Ding, Y., Niemczyk, M., Kudla, G., Plotkin, J.B. (2013) Rate-limiting steps in yeast protein translation. *Cell* 153(7):1589–1601.