Malwina Prater, PhD

SENIOR BIOINFORMATICIAN

EXPERIENCE

SENIOR BIOINFORMATICIAN 2023-Present

Functional Genomics Centre, Cancer Research Horizons

- Leading single-cell project portfolio (Perturb-seq) in dynamic environment, coordinating task distribution between team members, and ensuring quality work and timely project delivery
- Line-managing and leading recruitment of new staff for bioinformatic team
- Managing multiple other CRIPSR projects, working closely with wet lab scientists and project stakeholders, consulting on experimental design, running pipelines and custom projects, and delivering results and reports within timelines
- Contributing to development and deployment of bioinformatic solutions on AWS
- Established new CRISPR screen capabilities
- Performing lethality, isogenic, epigenetic, gene tiling and in-vivo CRISPR screen analyses
- Collaboratively working with other bioinformaticians and researchers on technology development and portfolio projects
- Writing a manuscript for publication

BIOINFORMATICIAN 2021-2023

MRC Mitochondrial Biology Unit, University of Cambridge, UK

- Collaborative research with multiple scientific projects, consulting on experimental design, performing data analysis, helped in preparing manuscripts for publications
- Involved in grant applications, line-managed a PhD student, supervised and coached others
- Analysis of complex multi-omic datasets (e.g. scRNA-seq + ATAC-seq + CROP-seq), (allelic specific) single-cell RNA-seq, integrating multiple datasets, variant calling

BIOINFORMATICIAN 2016-2021

Centre for Trophoblast Research, University of Cambridge, UK

- Collaborative research with 10+ research groups, 25+ projects, consulting on experimental design, data analysis, and helped in preparing manuscripts for publications.
- Driving own research and first author publications.

CONTACT

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🔗 https://nmalwinka.github.io/about/

ABOUT ME

Bioinformatician with 7.5 years of experience in bioinformatics. Providing bioinformatics expertise, leading projects and people at the Functional Genomics Centre, Cancer Research Horizons. Deep expertise and experience in scientific research &bioinformatics. Uniquely positioned to integrate and consult on both areas of wet lab and dry lab research. My passion is seeing scientific advances benefiting the world.

SKILLS

AWS Cloud Computing, HPC,

Bioinformatics, Jenkins,

Slurm, Nextflow, GitHub,

NGS processing pipelines and analysis,

single cell multiomics,

R, Python, SQL, Bash.

- 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, Transcription Factor motif search.
- Taught bioinformatic courses on RNA-seq analysis (Placental Biology Course in 2017 & 2019) and experimental design (EMBL-EBI, 2020).
- Supervised summer student project (2017) and Part II Student project (2020-2021).
- Successfully applied for 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.

- Utilised my knowledge of epigenetics and biochemistry in an emerging start-up company.
- Supported development of novel epigenetic kit ahead of commercialization.

SELECTED PUBLICATIONS

Shah, P., Ding, Y., **Niemczyk, M.**, Kudla, G., Plotkin, JB. (2013). Rate-Limiting Steps in Yeast Protein Translation. *Cell* 153(7):1589-601.

Niemczyk, M., Ito, Y., Huddleston, J., Git, A., Abu-Amero, S., Caldas, C., Moore, GE., Stojic, L., Murrell, A. (2013). Imprinted Chromatin around DIRAS3 Regulates Alternative Splicing of GNG12-AS1, a Long Noncoding RNA. *American Journal of Human Genetics* pii: S0002-9297(13)00279-6.

Stojic, L., **Niemczyk, M.**, Orjalo, A., Ito, Y., Ruiter, AEM., Uribe-Lewis, S., Joseph, N., Weston, S., Menon, S., Odom, DT., Rinn, J., Gergely, F., Murrell, A. (2016). Transcriptional silencing of long noncoding RNA *GNG12-AS1* uncouples its transcriptional and product-related functions. *Nature Communications* 7 (Article number: 10406).

Turco, M.Y., Gardner, L., Kay, R., Hamilton, R.S., **Prater, M.**, Hollinshead, M., McWhinnie, A., Esposito, L., Fernando, R., Skelton, H., Reimann, F., Gribble, F., Sharkey, A., Marsh, S.G.E., O'Rahilly, S., Hemberger, M., Burton, G.J. and Moffett. A. (2018) Trophoblast organoids as a model for maternal-fetal interactions during human placentation. *Nature*, **564**, 263–267

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

Prater, M., Hamilton, RS., Yung, HW., Sharkey, AM., Robson, P., Jauniaux, E., Charnock-Jones, S., Burton, GJ., 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).

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

EDUCATION

PhD in Oncology
Cancer Research UK CI
UNIVERSITY OF CAMBRIDGE

Awarded Prize for the Best Presentation at the Methyl Donors and Human Health Symposium

BSc Biotechnology (1st class)
UNIVERSITY OF EDINBURGH

Awarded James Rennie bequest Travel Award
Awarded Darwin Trust of Edinburgh Scholarships twice

STRENGTHS

Broad knowledge base in molecular biology, oncology, epigenetics

Can rapidly adjust priorities and adapt to shifting needs while staying focused on the main objective

Focus on data transparency and reproducibility

Project and people management

PASSION

Seeing scientific advances benefiting the world