MALWINA PRATER

nmalwinka@gmail.com, 07895250510 (Mobile)
ORCID record: 0000-0002-8202-5345

SUMMARY

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 and 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.

EDUCATION

2010-2014 University of Cambridge (Cancer Research UK Cambridge Institute): PhD in Oncology
- Gained broad knowledge in fields of molecular biology, epigenetics and cancer. Focused on alternative splicing of a long non-coding RNA.
- Awarded Prize for the Best Presentation at the Methyl Donors and Human Health Symposium

2006-2010 University of Edinburgh: BSc Biological Sciences (Hons Biotechnology) (1st Class Honours)
• Awarded James Rennie bequest Travel Award and Darwin Trust of Edinburgh Scholarships.

EMPLOYMENT HISTORY

2023-Present   Functional Genomics Centre, Cancer Research Horizons, Senior Bioinformatician

- 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 recruiting new staff for bioinformatic team
- Managing multiple other CRIPSR projects, working closely with wet lab scientists and project stakeholders, consulting on experimental design, managing people resources to projects, 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

2021-2023   Chinnery's group, MRC Mitochondrial Biology Unit, University of Cambridge: Bioinformatician

- 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

2016-2021   **Centre for Trophoblast Research, University of Cambridge, UK: Bioinformatician**

- Analysis of microarray, RNA-seq, single-cell RNA-seq, DNA methylation and ChIP-seq experiments, Transcription Factor motif search.
- 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.
- Co-supervised and co-trained summer students and visiting scientists.
- Taught bioinformatic courses on RNA-seq analysis (Placental Biology Course in 2017 & 2019) and experimental design (EMBL-EBI, 2020).
- Supervised summer student project focused on identifying genes with intron retention unique to placenta (2017) and Part II Student project to identify estrogen and progesterone regulated gene networks in kisspeptin neurons (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.

2014-2016   **R&D Scientist at 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.

TECHNICAL SKILLS

- Programming languages: R, bash, python, basic SQL
- Working on High Performance Computing and AWS Cloud computing
- Running NGS pipelines (clusterflow, nextflow, Jenkins)
- Routinely using GitHub for data versioning
- NGS Tools: CellRanger, samtools, bcftools, bedtools, aligners (Hisat2, STAR, Tophat2) and pseudoaligners (Kallisto), htseq, MultiQC, fastqc, trim_galore, cutadapt, bismark, Picard, preseq, qualimap, dupRadar, SNPsplit, Mageck, AceR
- Other softwares/tools: Markdown, mdwiki, Slurm, IGV2, SeqMonk, RStudio, Meme, SCENIC, singularity, Bermuda, mgatk, nextflow

STRENGHTS

- Broad knowledge base in molecular biology, epigenetics and cancer.
- Can rapidly adjust priorities and adapt to shifting needs while staying focused on the main objective.
- Passion for learning and continuous improvement, such as learning new programming languages and new constantly evolving softwares.
- Focus on data transparency and reproducibility: using version control tools such as GitHub, sharing scripts and depositing data in public repositories

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.

Menelaou, K., **Prater, M.**, Tuster, S.J., Blake, G.E.T, Geary-Joo, C., Cross, J.C., Hamilton, R.S. and Watson, E.D. (2019) Blastocyst transfer in mice alters the placental transcriptome and growth. *Reproduction*, **159:2**, 115–132

Carnicer-Lombarte, A. Barone, D.G., Dimov, I.B., Hamilton, R.S., **Prater, M.,** Rutz, R.L., Malliaras, G.G., Lacour, S.P., Bryant, C.E., Fawcett, J.W. & Franze, K. (2019) Mechanical mismatch as a driver of foreign body reaction to implanted materials. *bioRxiv* 82:9648. 10.1101/829648.

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).

Barone, D., Carnicer-Lombarte, A., Tourlomousis, P., Hamilton, R, **Prater, M**., …. , Franze, K, Fawcett, J. and Bryant, C. (2022) Prevention of the foreign body response to implantable medical devices by inflammasome inhibition. *PNAS*

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

Senner, C., .., **Prater, M.**, Watson, E. (2023) One-carbon metabolism is required for epigenetic stability in the mouse placenta. *Frontiers in Cell and Developmental Biology*. Vol **11**

Manchishi, S., **Prater, M.**, Colledge, W. (2023) Transcriptional profiling of Kiss1 neurons from arcuate and rostral periventricular hypothalamic regions in female mice. *Reproduction* **167** e230342.