MALWINA PRATER

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SUMMARY

Computational biologist with >6 years of experience in collaborative research and NGS data analysis. Providing bioinformatics support to Patrick Chinnery's group at MRC MBU, University of Cambridge. 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
- 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

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

- Collaborative research with multiple scientific projects, consulting on experimental design, data analysis, helped in preparing manuscripts for publications
- Involved in grant applications, supervising a PhD student 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 courses: RNA-seq analysis on Placental Biology Course (July 2017 and July 2019), Introduction to RNA-seq and Functional Interpretation course (Experimental Design) at EMBL-EBI (Jan 2020), Festival of Genomics 2017 in London (title: Misleading Bioinformatics).
- 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).
- Trained others in basic RNA-seq analysis and coding in R (2019).
- Successfully applied for High Performance Computing Grant for 450k core hours (~£5k) (2019).
- Data Champion at the University of Cambridge – as a member of research data community to promote good research data management.
- For multiple projects, mined data, performed thorough QC (clustering, anomaly detection, classification, dependencies, patterns, dimensional reduction, etc.) and statistical analysis.
- Developed quality control tool for assessment of mitochondrial and ribosomal RNA in samples, and together with other team members developing a quality control tool for broad NGS applications

(cuPCAke).

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

- Computer operating systems: Unix, Linux, Windows
- Programming languages: bash, R, python, basic SQL
- Running NGS pipelines (clusterflow and nextflow)
- Routinely using GitHub for data versioning
- NGS Tools: samtools, bcftools, bedtools, aligners (Hisat2, STAR, Tophat2) and pseudoaligners (Kallisto), htseq, MultiQC, fastqc, trim_galore, cutadapt, bismark, Picard, preseq, qualimap, dupRadar
- Other softwares/tools: Markdown, mdwiki, Slurm, IGV2, SeqMonk, RStudio, Meme, SCENIC, singularity, Bermuda, mgatk

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

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*

Preprint: 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.