MATTHIAS E. FUTSCHIK

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PERSONAL PROFILE

- Bioinformatician and systems biologist with 20 years of research experience
- Proven expertise in omics data analysis, integration and modelling
- Developer of various software packages and databases
- Strong interests in collaborative and translational research
- Experienced group and project leader

WORK EXPERIENCE

2021 - **Biostatistician,** Public Health and Clinical Oversight, Test and Trace, UK Health Security Agency, London, UK
- Evaluation of Covid-19 testing devices in in-field trials
- Analysis of contact data and infections

2021 **Senior Bioinformatician,** MRC London Institute of Medical Sciences, Imperial College, London, UK
- Various types of NGS analysis (peak finding, differential expression, functional enrichment) and statistical support for MRC research groups

2020 - 2021 **Health Data Research UK Imperial Lead Bioinformatician**, Faculty of Medicine, Imperial College, London, UK
- Implementation and extension of GWAS & annotation pipelines for UK Biobank data on Imperial´s HPC
- Multi-omics analysis in collaborative projects in cardiovascular research
- Building of local wiki for documentation of software and SOPs

2016 - 2019 **Professor in Bioinformatics**, Faculty of Medicine & Dentistry, University of Plymouth, UK
- Data integration, biomarker discovery and drug repositioning for meningioma
- NGS (WES, RNA-seq) and microarray data analysis in various projects
- Network analysis of neurological diseases and in stem cell biology

2014 - 2016 **Principal investigator in Bioinformatics and Systems Biology**, Centre of Marine Sciences, University of Algarve, Faro, Portugal
- Development of databases for meta-analysis of transcriptome data
- Integration of RNA-seq and ChIP-seq for reconstruction of TF regulons
- Reconstruction of regulatory gene networks for cyanobacteria

2008 - 2014 **Research Group Leader in Computational Biology,** University of Algarve, Faro, Portugal
- Development for integrative databases for network-oriented investigations
- Application of system biology approaches for biomarker and drug target discovery for neurodegenerative diseases and cancer

2004 - 2008 Assistant Professor, Institute for Theoretical Biology, Humboldt-Universität, Berlin, Germany
- o Analysis of protein-protein-interaction networks & construction of database for the human interactome (UniHI).
- o Development of new methods for transcriptome data analysis

2003 - 2004 Research fellow, Humboldt-Universität zu Berlin, Germany
- o Analysis of Affymetrix GeneChip experiments monitoring expression
- o Development of R packages for microarray data processing

2003   Bioinformatics consultant, Pacific Edge Biotechnology Ltd., New Zealand
- o Gene expression profiling for several large-scale cancer projects
- o Statistical analysis for biomarker discovery

2002 - 2003 Senior bioinformatician, Pacific Edge Biotechnology Ltd, New Zealand
- o Design and implementation of a bioinformatics pipeline for analysis of large-scale microarray projects.
- o Construction of a relational database for storage gene expression data
- o Cancer sample classification using artificial neural networks

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EDUCATION

2003   Ph.D. in Information Science, Departments of Information Science & Biochemistry, University of Otago, Dunedin, New Zealand

1998   Master of Science in Physics, Department of Physics, Humboldt-Universität, Berlin, Germany

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RESEARCH INTERESTS

- Genomics & Transcriptomics
- Next generation sequencing
- Single cell data
- Data integration
- Statistics & Data modelling
- Machine Learning & AI
- Molecular networks
- Reverse engineering
- Diseases & biomarkers
- Drug discovery
- Gene regulation
- Translational research

SKILLS & QUALIFICATIONS

General
- Strong analytical and problem-solving as well as organizational and time management skills.
- Excellent communication skills proven in many collaborations across professional fields with scientists, medical specialists and software engineers.
- Demonstrated strong presentation and writing skills
- Track record of successful team leading and collaborative work.
- Holder of Teacher qualification: Fellow of the Higher Education Academy (UK)

Computer skills

- *Programming languages:* R (proficiency), Perl, JavaScript, SQL, Python (familiarity)
- *Data Visualization:* Cytoscape, R/ggplot2
- *Applications:* Bioconductor packages; NGS tools e.g. bedtools, samtools, aligners, variant callers, peak callers, IGV; GWAS software e.g. BOLT-LMM, GCTA, PLINK, etc.
- *Platforms & Environments:* Linux (bash), HPC (PBS), Conda, Github
- *Pipelines:* Bash, Snakemake, Nextflow, R/drake (familiarity)
- System administration of several Linux, Apache and Tomcat servers

Languages

- German (native), English (fluent), Portuguese (proficient), French, Spanish (basic)

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ACHIEVEMENTS

- Development & maintenance of R/Bioconductor packages (OLIN, OLINGui, Mfuzz, cycle)
- Developer of the CyanoEXpress database (cyanoexpress.sysbiolab.eu) and HeartEXpress database (heartexpress.sysbiolab.eu)
- Lead designer and project manager for the UniHI database (www.unihi.org), StemCellNet web-server (stemcellnet.sysbiolab.eu), StemChecker web-server (stemchecker.sysbiolab.eu), StemMapper database (stemmapper.sysbiolab.eu), HeartMiR database (heartmir.sysbiolab.eu) and HDNetDB database (hdnetdb.sysbiolab.eu)
- Leading PI of research projects funded by the Fundação para a Ciência e a Tecnologia (Portugal), CHDI Foundation (USA), and Deutsche Forschungsgesellschaft (Germany) with a total amount of 1.4 M € of secured external funding
- Building of successful bioinformatic groups in academic and commercial environments with leading of 8 Post-doctoral researchers and 7 research assistants as well as (co-)supervision of 4 PhD theses, 4 MSc & 7 BSc dissertations.
- 62 peer reviewed publications (10 as first and 20 as last author) and 6 book chapters (2 as first and 3 as last author) with total number of citations: 4562 (Google Scholar). My full publication list can be accessed at http://www.sysbiolab.eu/matthias.html
- Erwin-Schrödinger-Prize of the Helmholtz Association for interdisciplinary research (2008)

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FURTHER INFORMATION

- Professional webpages: - https://www.plymouth.ac.uk/staff/matthias-futschik
    - http://www.sysbiolab.eu/matthias.html
- Google scholar profile: https://scholar.google.com/citations?user=zHC1yBQAAAAJ
- Linkedin profile: https://www.linkedin.com/in/matthias-futschik-4775b32a/
- Orchid profile: https://orcid.org/0000-0002-6245-8071

SELECTED PUBLICATIONS

C. Francis*, **M. Futschik***, J. Huang*, W. Bai, M. Sargurupremraj, A. Teumer, M. Breteler, E. Petretto, A. Ho, P. Amouyel, S. Engelter, R. Bülow, U. Völker, H. Völzke, M. Dörr, M-A. Imtiaz, N. A Aziz, V. Lohner, J. Ware, S. Debette, P. Elliott, A. Dehghan, and P. Matthews (2022) Genome-wide associations of aortic distensibility suggest causality for aortic aneurysms and brain white matter hyperintensities. ***Nature Communications***, accepted (* Shared first author)

Jemma Dunn, Vasileios P Lenis, David A Hilton, Rolf Warta, Christel Herold-Mende, C Oliver Hanemann and **Matthias E Futschik** (2020) Integration and Comparison of Transcriptomic and Proteomic Data for Meningioma. ***Cancers,*** 12, 3270.

Jemma Dunn, Sara Ferluga, Vikram Sharma, **Matthias Futschik**, David A. Hilton, Claire L. Adams, Edwin Lasonder and C. Oliver Hanemann (2019) Proteomic analysis discovers the differential expression of novel proteins and phosphoproteins in meningioma including NEK9, HK2 and SET and deregulation of RNA metabolism, **EBioMedicine,** 40, 77 – 91

José Pinto, Rui Machado, Ramiro Magno, Daniel Oliveira, Susana Machado, Raquel Andrade, José Bragança, Isabel Duarte & **Matthias Futschik** (2018) StemMapper: A Curated Gene Expression Database for Stem Cell Lineage Analysis, ***Nucleic Acids Research,*** 46(D1): D788–D793

Davood Sabour, Rui S.R. Machado, José P. Pinto, Susan Rohani, Raja G.A. Sahito, Jürgen Hescheler, **Matthias E. Futschik** and Agapios Sachinidis (2018) Parallel Genome-wide Profiling of Coding and Non-coding RNAs to Identify Novel Regulatory Elements in Embryonic and Maturated Heart, ***Molecular Therapy - Nucleic Acids***, 12, 158-173

R. Kalathur, J.P. Pinto, B. Sahoo, G. Chaurasia and **M. E. Futschik** (2017) HDNetDB: A Molecular Interaction Database for Network-Oriented Investigations into Huntington's Disease, ***Scientific Reports*** 7: 5216

M. Strödicke, Y. Bounab, N. Strempel, K. Klockmeier, S. Yigit, RP Friedrich, G. Chaurasia, S. Li, F. Hesse, SP Riechers, J. Russ, C. Nicoletti, A. Boeddrich, T. Wiglenda, C. Haenig, S. Schnoegl, D. Fournier, RK Graham, MR Hayden, S. Sigrist, GP Bates, J. Priller, M Andrade-Navarro, **M.E. Futschik** and EE Wanker (2015) Systematic interaction network filtering identifies CRMP1 as a novel suppressor of huntingtin misfolding and neurotoxicity. ***Genome Research*** 25: 701-713

R. Hill, RK. Kalathur, L. Colaço, R. Brandão, S. Ugurel, **M. Futschik** and W. Link (2015) TRIB2 as a biomarker for diagnosis and progression of melanoma. ***Carcinogenesis.*** 36(4):469-77.

José P. Pinto, Ravi K. Kalathur, Daniel V. Oliveira, Tânia Barata, Rui S. R. Machado, Susana Machado, Ivette Pacheco-Leyva, Isabel Duarte and **Matthias E. Futschik** (2015) StemChecker: a web-based tool to discover and explore stemness signatures in gene sets, ***Nucleic Acids Research***, 43 (W1): W72-W77

Ravi K. Kalathur, José P. Pinto, Miguel Hernandez-Prieto, Rui Machado, Dulce Almeida, Gautam Chaurasia and **Matthias Futschik**. (2014) UniHI 7: an enhanced database for retrieval and interactive analysis of human molecular interaction networks, ***Nucleic Acids Research***, Database issue, 42 (D1): D408-D414.

T.Wallach, K. Schellenberg, B. Maier, R. Kalathur, P. Porras, EE. Wanker, **M. E. Futschik** and A. Kramer (2013) Dynamic Circadian Protein-Protein Interaction Networks Predict Temporal Organization of Cellular Functions, ***PloS Genetics***, 9(3): e1003398.

Jörg Gsponer, **Matthias E. Futschik**, Sarah A. Teichmann and M. Madan Babu (2008) Tight regulation of intrinsically unstructured proteins: from transcript synthesis to protein degradation, ***Science***, 322, 1365-1368

D. Lindell, J. Jaffe, M. Coleman, **M. Futschik**, I. Axmann, T. Rector, G. Kettler, M. Sullivan, R. Steen, W. Hess, G. Church and S. Chisholm (2007) Genome-Wide Expression Dynamics of a Marine Virus and its Host Reveal Features of Co-evolution, ***Nature***, 449, 83 – 86

L. Kumar and **M.E. Futschik** (2007) Mfuzz: a software package for soft clustering of microarray data, ***Bioinformation***, 2(1) 5-7

M. Futschik and T. Crompton (2004) Model selection and efficiency testing for normalization of cDNA microarray, ***Genome Biology***, 5(8):R60