Arin Wongprommoon

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Work address: Morgan Building, Wellcome Genome Campus, Hinxton CB10 1SA, UK

Education

University of Edinburgh   EDINBURGH, UNITED KINGDOM
PhD in Quantitative Biology, Biochemistry, and Biotechnology   2019 − 2023
Thesis: *Single-cell time-series analysis of metabolic rhythms in yeast*

University of Cambridge (Homerton College)   CAMBRIDGE, UNITED KINGDOM
BA Hons Natural Sciences   2016 − 2019
2.1: Biochemistry, with research project;
Dissertation: *Sequence Preferences of the Nucleosome and PCR Enzymes*, 5,000 words, marked 80.0/100

Employment

Wellcome Sanger Institute   HINXTON, UNITED KINGDOM
Postdoctoral Fellow   2024 − present
Identifying bacterial pathogen genetic markers, host genetic markers, and host gene expression patterns that predicts disease progression of melioidosis, a neglected tropical disease.

Publications

Wongprommoon, A., Chomkatekaew, C., & Chewapreecha, C. (2024). Monitoring pathogens in wastewater. *Nature Reviews Microbiology*, 1–1. https://doi.org/10.1038/s41579-024-01033-1

Nikolados, E.-M., Wongprommoon, A., Aodha, O. M., Cambray, G., & Oyarzún, D. A. (2022). Accuracy and data efficiency in deep learning models of protein expression. *Nature Communications*, 13(1), 7755. https://doi.org/10.1038/s41467-022-34902-5

Jia, B., & Wongprommoon, A. (2018). Synthetic biology: Engineering order in organisms across scales and species. *BioTechniques*, 65(3), 113–119. https://doi.org/10.2144/btn-2018-0121

Tipgomut, C., Wongprommoon, A., Takeo, E., Ittiudomrak, T., Puthong, S., & Chanchao, C. (2018). Melittin Induced G1 Cell Cycle Arrest and Apoptosis in Chago-K1 Human Bronchogenic Carcinoma Cells and Inhibited the Differentiation of THP-1 Cells into Tumour- Associated Macrophages. *Asian Pacific journal of cancer prevention: APJCP*, 19(12), 3427–3434. https://doi.org/10.31557/APJCP.2018.19.12.3427

Peer Review

Current Microbiology: 1 manuscript since 2024

Computational skills

Programming concepts: machine learning (`tensorflow`, `scikit-learn`), flux balance analysis & genome-scale models (`cobra`, `roadrunner`, `libsbml`), data analysis & visualisation (Python `pandas`, `seaborn`, R `ggplot2`), scientific computing (`scipy`), object-oriented programming, continuous integration, secure research environments

Programming languages: Python, MATLAB, R, C

Software: Git/GitLab (version control & collaborative coding), Docker (virtualisation), LaTeX, Inkscape (graphic design), UNIX-based operating systems (Linux, Arch and Ubuntu distributions; macOS)

Research experience

Biomolecular Control Group (Dr Diego Oyarzún) & Prof Peter Swain's Group,
Centre for Engineering Biology, University of Edinburgh   EDINBURGH, UNITED KINGDOM
PhD project   *Oct 2019 − Oct 2023*
Showed that metabolic cycles in single *Saccharomyces cerevisiae* cells are autonomous from the cell division cycle and are persistent across nutrient conditions and gene deletions, using single-cell microfluidics and time series analysis. Part of a team to maintain an image analysis software pipeline. Predicted that biosynthesis of biomass components in sequence is a time-efficient use of limited enzyme-available proteome resources, using flux balance analysis. *Full funding by Edinburgh Global and the School of Biological Sciences.*

Prof Jussi Taipale's group,
Department of Biochemistry, University of Cambridge   CAMBRIDGE, UNITED KINGDOM
    Final-year undergraduate research project,
    under the supervision of Dr Fangjie Zhu   *Jan 2019 – Mar 2019*
        Used nucleosome EMSA-SELEX to confirm rules for nucleosome positioning and showed that C-methylation aligns phases of dinucleotides with cytosines. Showed that enzyme-introduced biases were most responsible for PCR bias by comparing *k*-mer fold changes of sequencing libraries.

Conferences

Microbiology Society Annual Conference   BELFAST, UNITED KINGDOM
    Poster presentation   *Apr 2022*
        Awarded Society Grant (£360), partly covering registration and travel expenses

British Yeast Group Meeting on the Future of Yeast Research   CAMBRIDGE, UNITED KINGDOM
    Poster presentation   *Dec 2021*
        Best Poster (Graduate Student) Prize (3 recipients out of 43 posters), £150.

Cold Spring Harbor Laboratories Symposium
on Quantitative Biology – Biological Timekeeping   LAUREL HOLLOW, NEW YORK, UNITED STATES
    Poster presentation   *Jun 2021*

Teaching

Practical Systems Biology   EDINBURGH, UNITED KINGDOM
    Demonstrator, Marker   *Jan 2023 – Apr 2023*
        Masters-level course on modelling biological systems using differential equations and stochastic simulations via Python.

Biology 1A: Variation   EDINBURGH, UNITED KINGDOM
    Demonstrator   *Sep 2022 – Dec 2022*
        First-year undergraduate course on genetics and evolution; covered scientific skills, hypothesis testing, and Python.

Genes and Gene Action 2   EDINBURGH, UNITED KINGDOM
    Demonstrator   *Jan 2022 – Mar 2022*
        Second-year undergraduate course on genetics; covered basic bench biology.

Leadership experience

International Genetically Engineered Machine (iGEM) competition   EDINBURGH, UNITED KINGDOM
    Advisor, University of Edinburgh - UHAS Ghana team   *Jun 2022 – Oct 2022*
        Advised a nine-member undergraduate team that constructed and modelled cell-free solutions to mitigate plastic and heavy metal pollution in bodies of water in Ghana. Part of a three-advisor team; my focus was on structural modelling of proteins, documentation, and webpage development with version control. *Team won gold medal and was nominated for best environmental project.*

Graduate School Staff-Student Liaison Committee   EDINBURGH, UNITED KINGDOM
    PhD Student Representative, Institute of Quantitative Biology *Sep 2021 – Sep 2022*
        One of two representatives of 77 PhD students in my institute among a team of 14 across the School of Biological Sciences (333 students). Organised community-building events, e.g. board games.

Cambridge University Synthetic Biology Society   CAMBRIDGE, UNITED KINGDOM
    Project titled *Evolving spatially-defined ecological interactions* *Jan 2019 – Nov 2019*
        Supervised small student teams and encouraged them to work independently to engineer sets of physical and social interactions in *E. coli*. Verified aggregation of adhesion strains described by Glass & Riedel-Kruse (2018). In this framework, teams verified the auxotrophy of ecological strains from the Ackermann Lab (Eawag, Switzerland).
    Project on bacterial edge detection   *Oct 2017 – Mar 2019*
        Engineered a double genetic circuit in *E. coli* that enabled photography and edge detection, reproducing *'A Synthetic Genetic Edge Detection Program'* (Tabor et al., 2009). The project evolved into five weekly workshops on molecular techniques in Oct-Nov 2018. 10-30 participants with biological, chemical, medical, and engineering backgrounds participated in each workshop.