

Arin Wongprommoon

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Work address: C.H. Waddington Building, Max Born Crescent, King's Buildings, Edinburgh EH9 3BF, 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

Publications

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>

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), Linux (Arch and Ubuntu distributions)

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

Characterised and classified time series of metabolic cycles and cell division cycles in *Saccharomyces cerevisiae* in response to gene deletions and nutrient conditions. Part of a team to develop [an image analysis software pipeline](#). Full funding by Edinburgh Global and the School of Biological Sciences.

Computational techniques: time series analysis, supervised/unsupervised classification, image segmentation

Laboratory techniques: CRISPR-Cas9, single-cell microfluidics, yeast cell culture

Alan Turing Institute Data Study Group

LONDON, UNITED KINGDOM

Participant

Dec 2022

Five-day collaborative hackathon: worked with a team of 12 researchers and data scientists to engineer a machine learning model to predict sound annoyance of 2,980 urban sound recordings; my focus was on development infrastructure and final presentation. Found that a pre-trained audio neural network trained on high-resolution spectrograms had best prediction ability.

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.

Prof Steve Oliver's group,
 Cambridge Systems Biology Centre, University of Cambridge CAMBRIDGE, UNITED KINGDOM
Internship, under the supervision of Dr Jorge Júlvez Jun 2018 – Aug 2018, Jul 2019 – Sep 2019
 Extended a kinetic model for *E. coli* metabolism to investigate reaction fluxes and used this information to enrich a stoichiometric model. Used a genetic algorithm to optimise parameters.
Computational techniques: deterministic metabolic simulations, flux balance analysis

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 \(2018\)](#). This evolved into a funded (£3,000) project under the Cambridge-JIC Biomaker Challenge 2019. In this framework, teams verified the auxotrophy of ecological strains from the Ackermann Lab (Eawag, Switzerland).
Elected one of two project managers for 2018-19 May 2018 – May 2019
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.