

# Arin Wongprommoon

[arin.wongprommoon@ed.ac.uk](mailto:arin.wongprommoon@ed.ac.uk) (academic), [arin.wongprommoon@gmail.com](mailto:arin.wongprommoon@gmail.com) (general),  
[arin.wongprommoon](https://www.linkedin.com/in/arinwongprommoon) (Skype) • [www.linkedin.com/in/arinwongprommoon](https://www.linkedin.com/in/arinwongprommoon)

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 – expected 2023

Thesis: *Single-cell time-series analysis of flavin-based yeast metabolic rhythms*

University of Cambridge (Homerton College)

CAMBRIDGE, UNITED KINGDOM

**BA Hons Natural Sciences**

2016 – 2019

3rd year – 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)pmid 30583665, 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, CI/CD, 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 – present

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  
 Formedium 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.