

Project Portfolio

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Introduction

Seda Radoykova is in the final months of reading *MSci Computational Biology* at University College London (UCL), expecting to graduate with a first-class / distinction degree.



She has pertinent analytical, software, and communication skills, which she developed in a variety of contexts. Being a curious and fast learner, Seda has ended up in different walks of life and science.

Therefore, this portfolio aims to showcase the almost eccentric diversity of competencies she demonstrates.

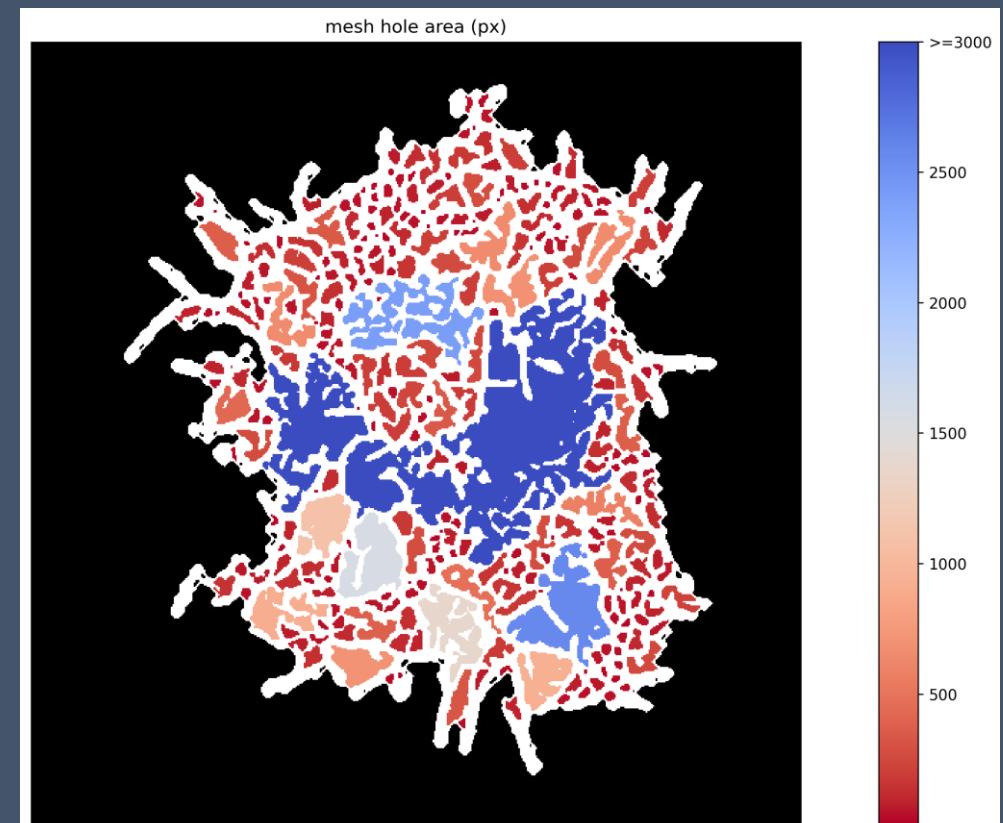
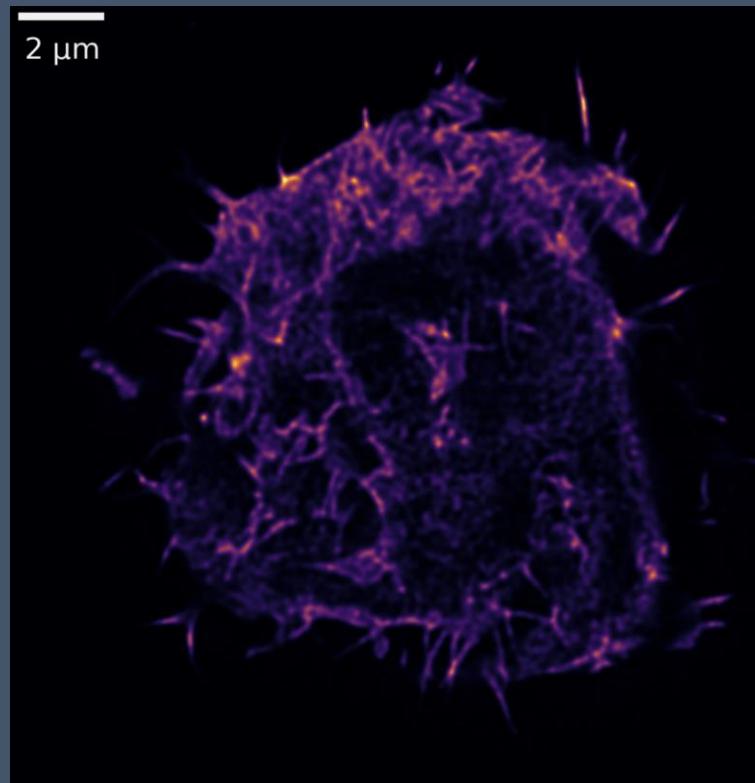
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 - A fully streamlined, expandable, and documented image analysis pipeline in Python.
- Finding fitting lines *[slide 6]*
 - A seemingly trivial but creative problem-solving exercise in image analysis.
- Modelling protometabolism *[slide 7]*
 - A stochastic kinetic model of the chemical reactions at the origin of life.
- Understanding COVID-19 transmissibility *[slide 8]*
 - Data driven and modelling based quantification of COVID-19 transmission dynamics.

ActinMeshure ([github](#))

(1/2)

- **Goal:** implementing an installable package that enables the fully streamlined quantification actin meshes in microscopy images.



ActinMeshure ([github](#))

(2/2)



- **Programming in Python:** object-oriented design of multiple classes.
 - Read-in, manipulate, visualise single images;
 - Process entire directories, summarise, and post-process estimated parameters for easy visualisation and statistical analysis;
 - Raise problems and log unsuccessful analysis cases for interactive analysis and hyperparameter tuning.
- Appropriate version-control, documentation and unit-tests.

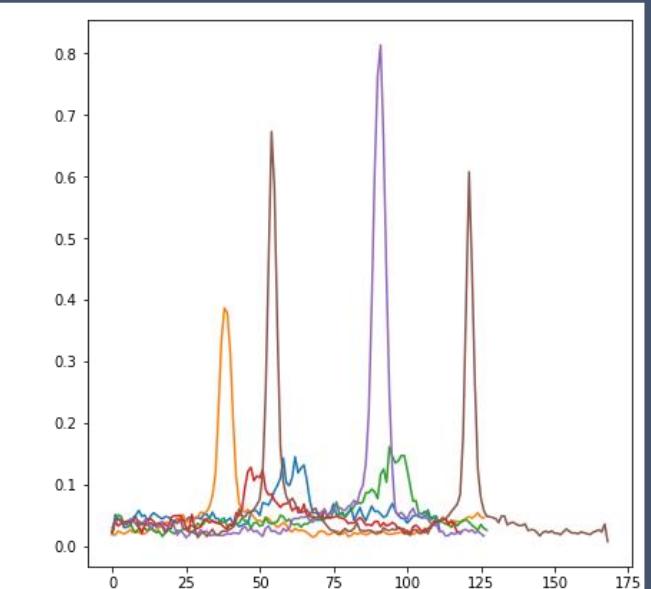
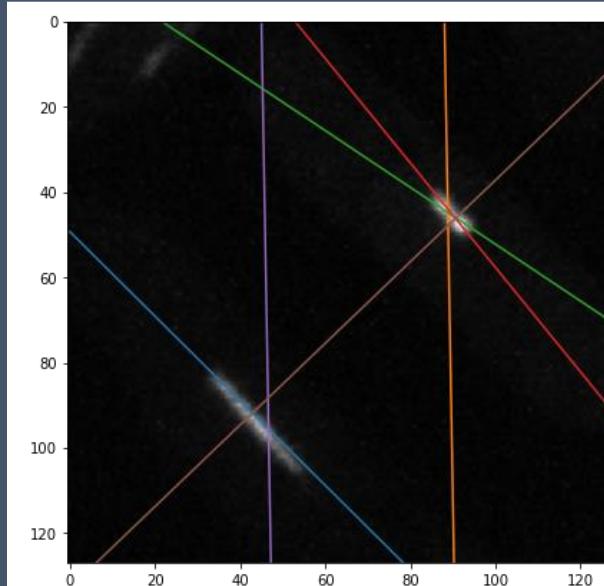
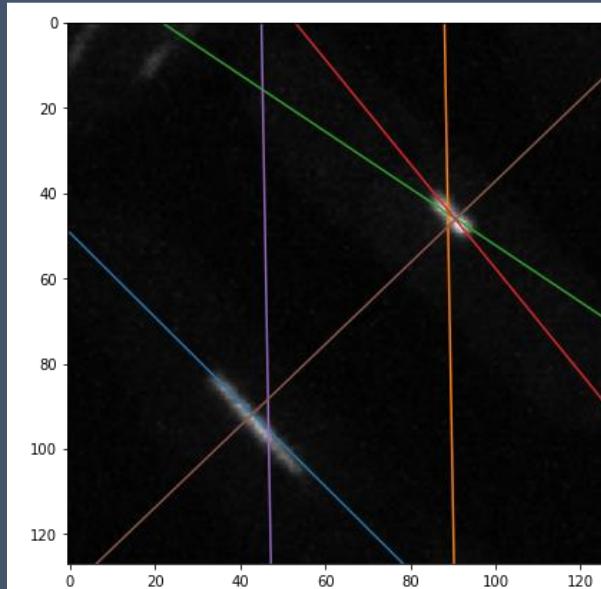
```
>>> sample_data.parametrise_pipeline(*parameters)
>>> sample_data.run_analysis(visualise_as_html=True, return_parameters=False)
files: 100%|██████████| 3/3 [00:31<00:00, 10.40s/it]
files: 100%|██████████| 3/3 [00:29<00:00, 9.71s/it]
cell types: 100%|██████████| 2/2 [01:01<00:00, 30.53s/it]
Analysis completed in 00:01:01.
```

Finding fitting lines ([github](#))

(1/1)



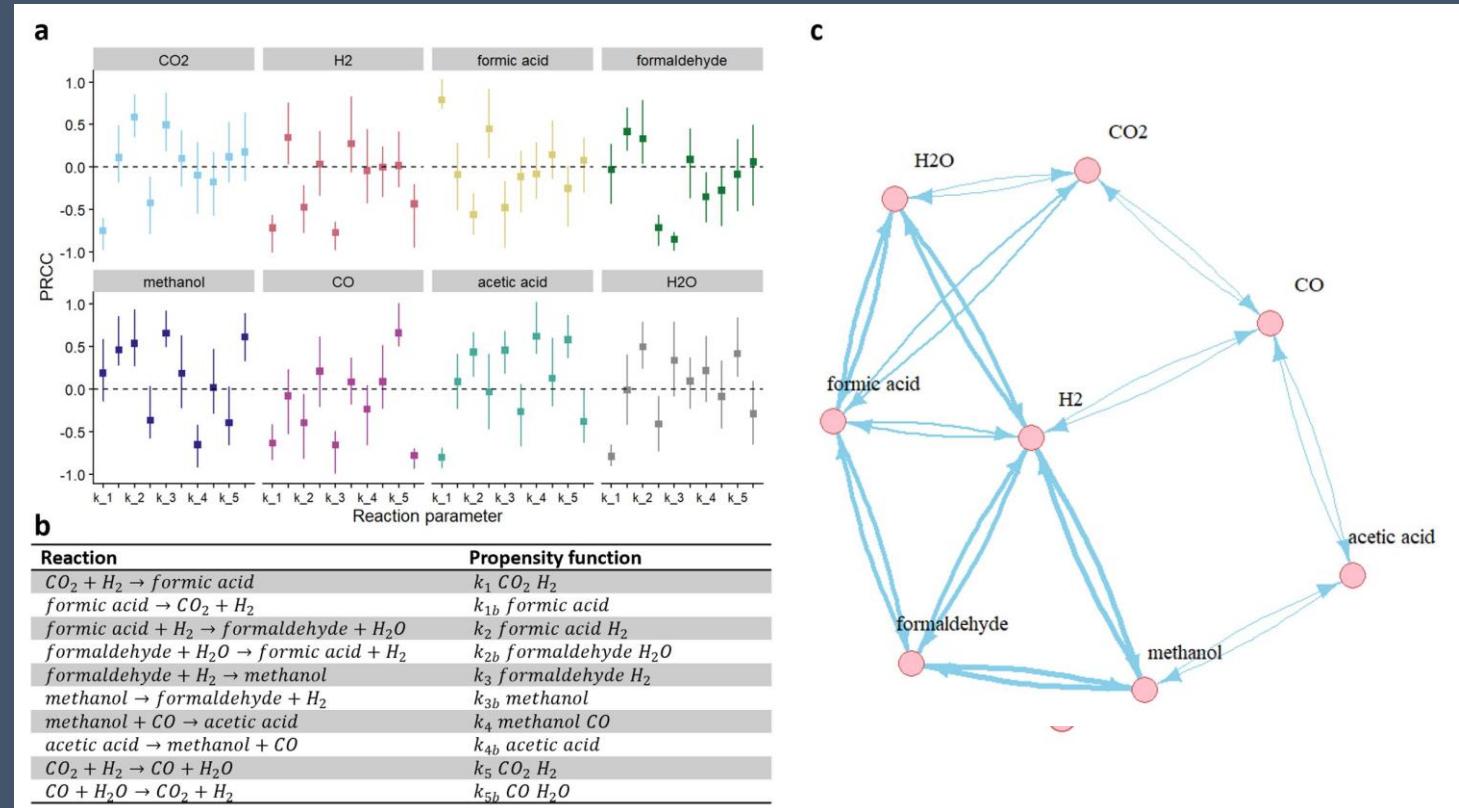
- **Goal:** identify, parametrise, and quantify biologically relevant lines from image data.
- **Skills developed:** problem solving exercise was approached from multiple perspectives, creatively using mathematics and deep learning.
- **Programming in Python:** Hough transform, Gaussian, nonlinear fitting, convolutional neural networks (CNN).



Modelling protometabolism ([github](#)) (1/1)

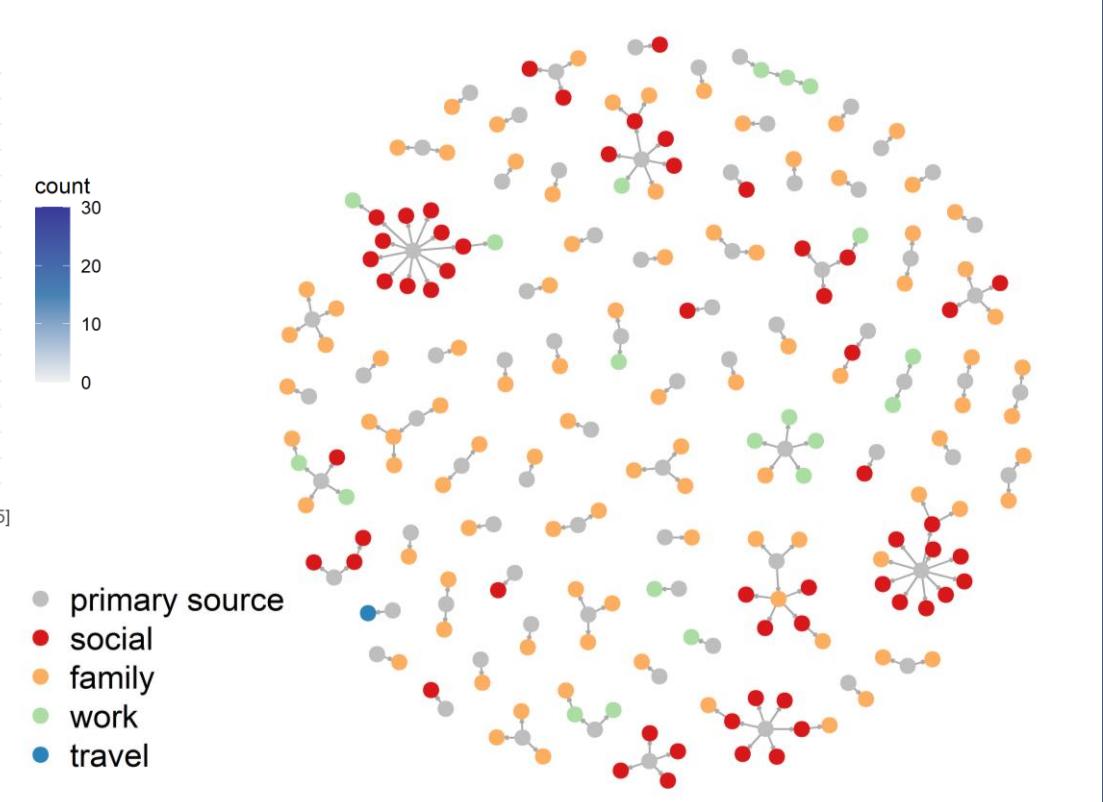
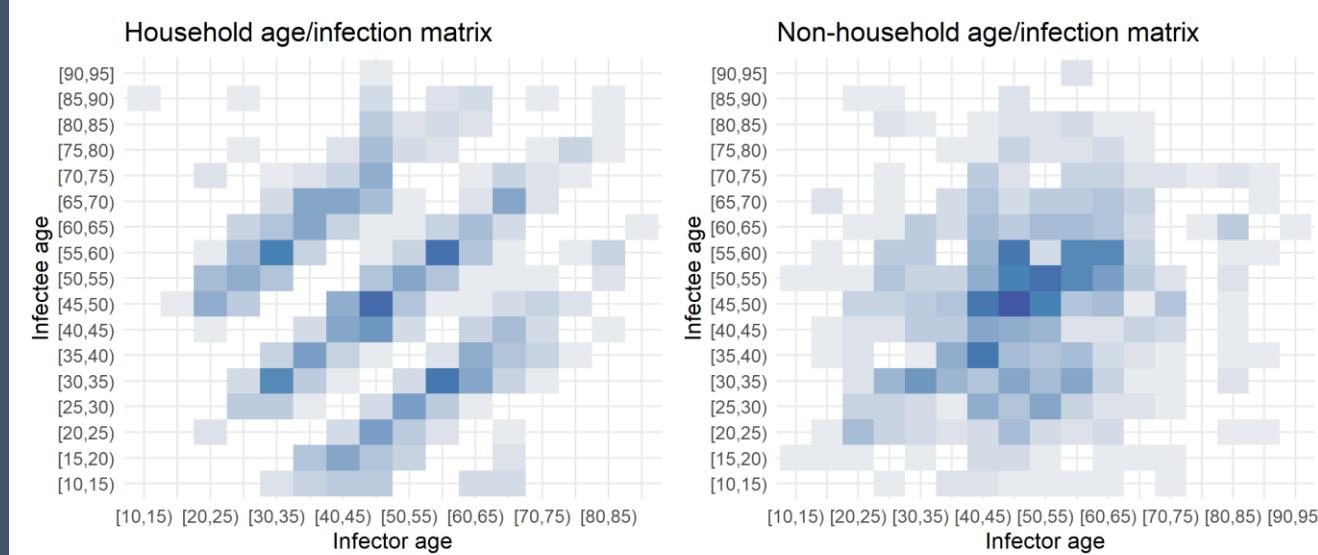


- Goal: elucidate the kinetic requirements to drive chemical reactions through the foundations of protometabolism at the origin of life.
- Programming in R:
 - implemented a stochastic discrete-time model of chemical reactions in R;
 - explored parameter space using brute-force techniques.
- *Harold and Olga Fox prize* for best symposium presentation.



COVID-19 transmissibility ([github](#))

(1/2)



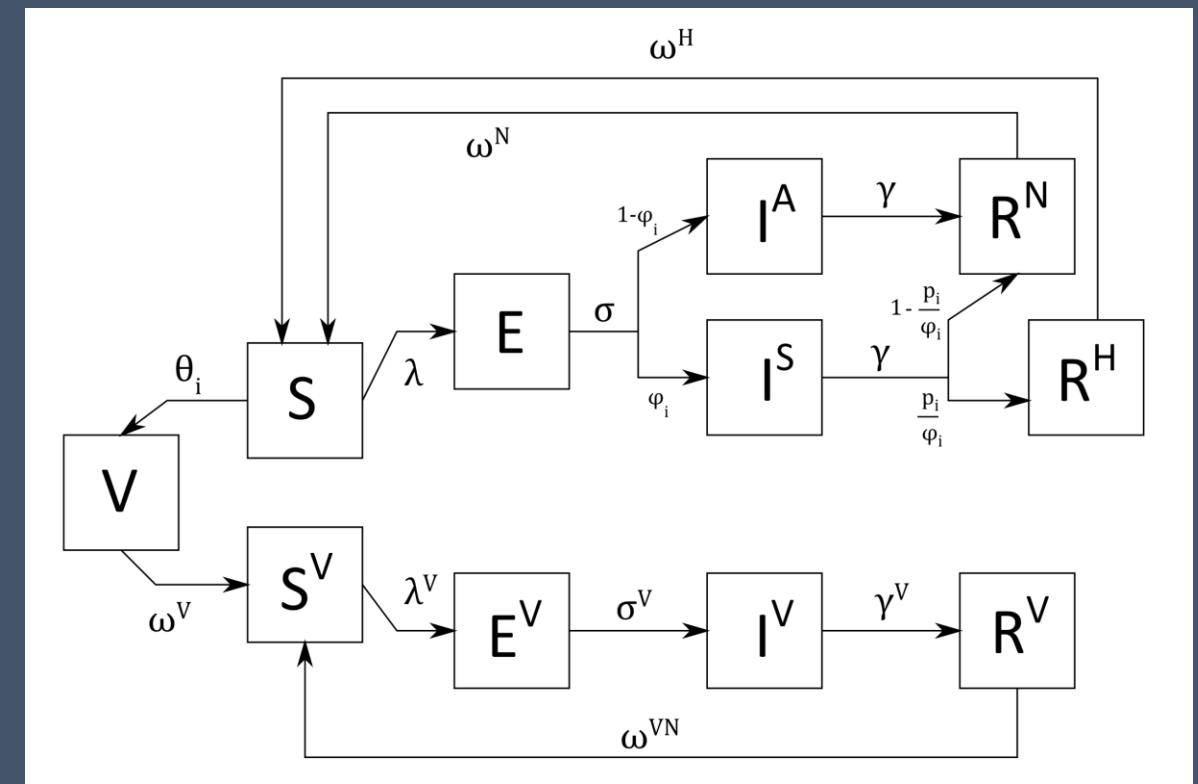
- Goal: explore COVID-19 transmissibility using a big data driven approach.
- Skills: manipulate and aggregate large data sets from multiple sources.

COVID-19 transmissibility ([github](#))

(2/2)



- **Goal:** understand COVID-19 transmissibility through modelling.
- **Programming skills in R:**
 - **Deterministic modelling:** added equations for vaccination compartments to a difference equation COVID-19 transmission-dynamic SEIR model with waning immunity.
 - **Stochastic modelling:** simulated a simple SEIR model in R, using stochastic Partially Observed Markov Processes (POMP) (git).



Staying in touch

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