

Project Portfolio

by Seda Radoykova

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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.

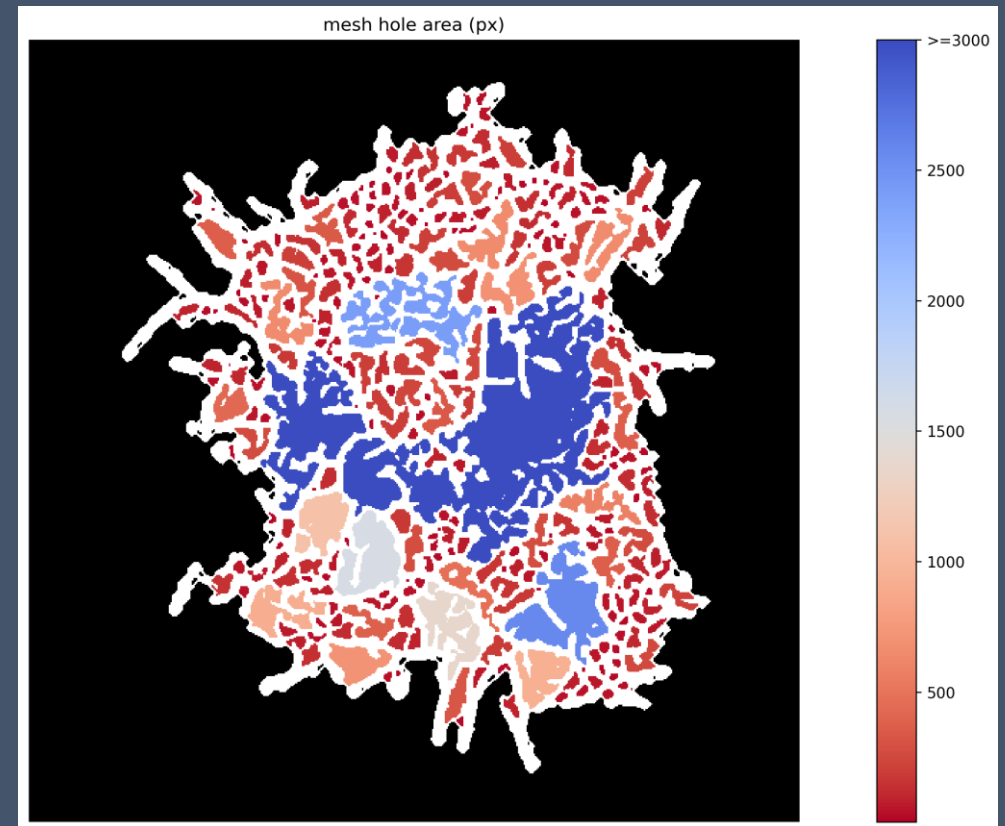
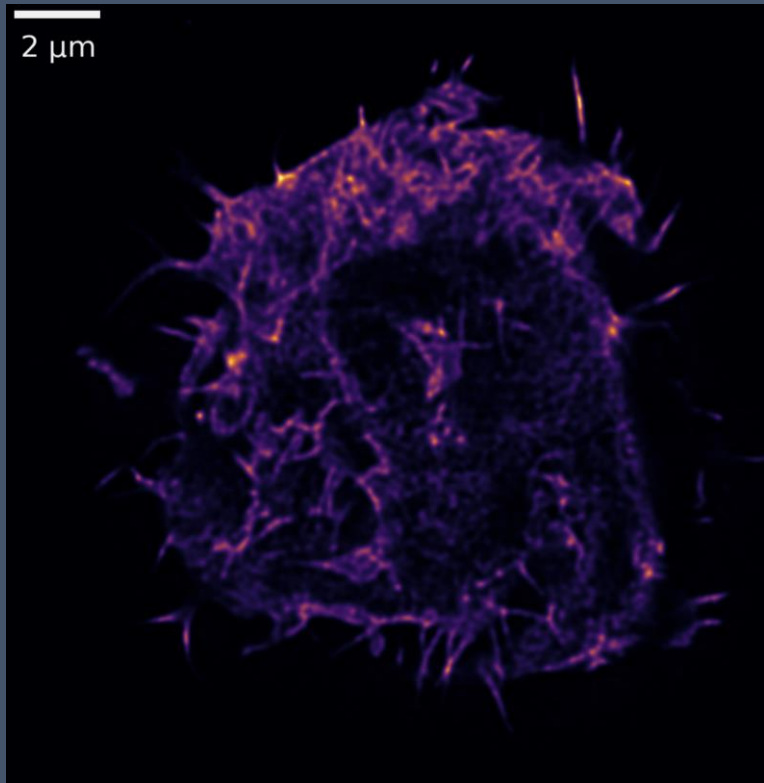
Table of contents

- **ActinMeshure** *[slide 4]*
 - 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.

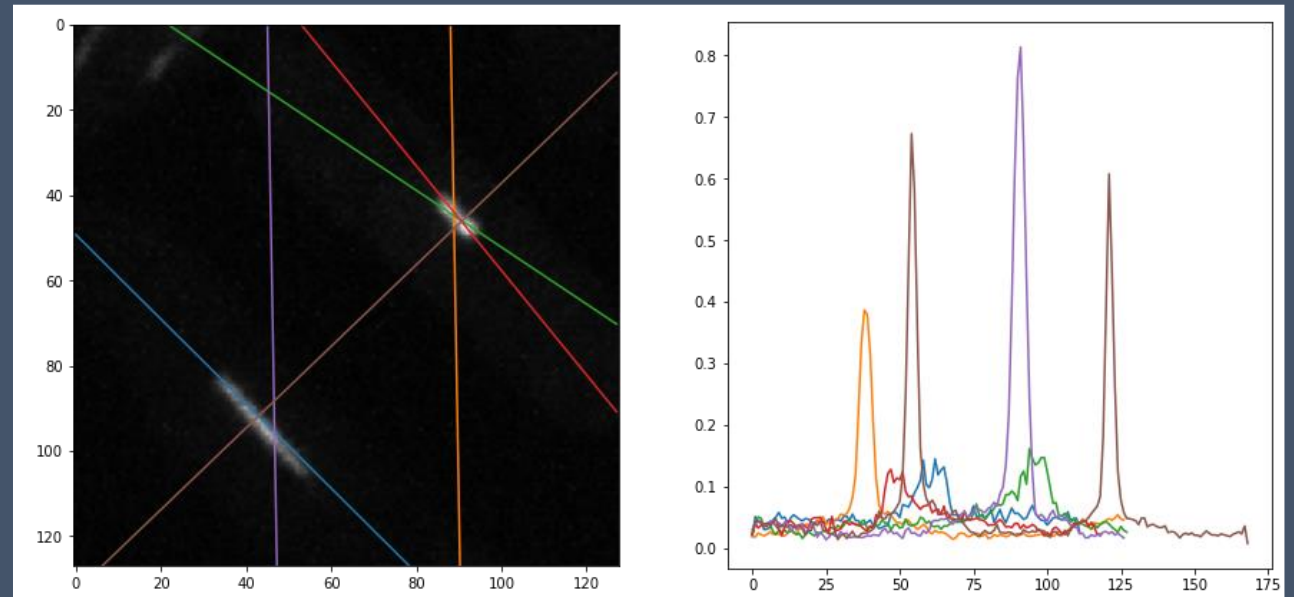
```
>>> sample_data.parametrise_pipeline(*parameters)
>>> sample_data.run_analysis(visualise_as_html=True, return_parameters=False)
files: 100%|██████████████████████████████████████████████████████████████████████████| 3/3 [00:31<00:00, 10.40s/it]
files: 100%|██████████████████████████████████████████████████████████████████████████| 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)



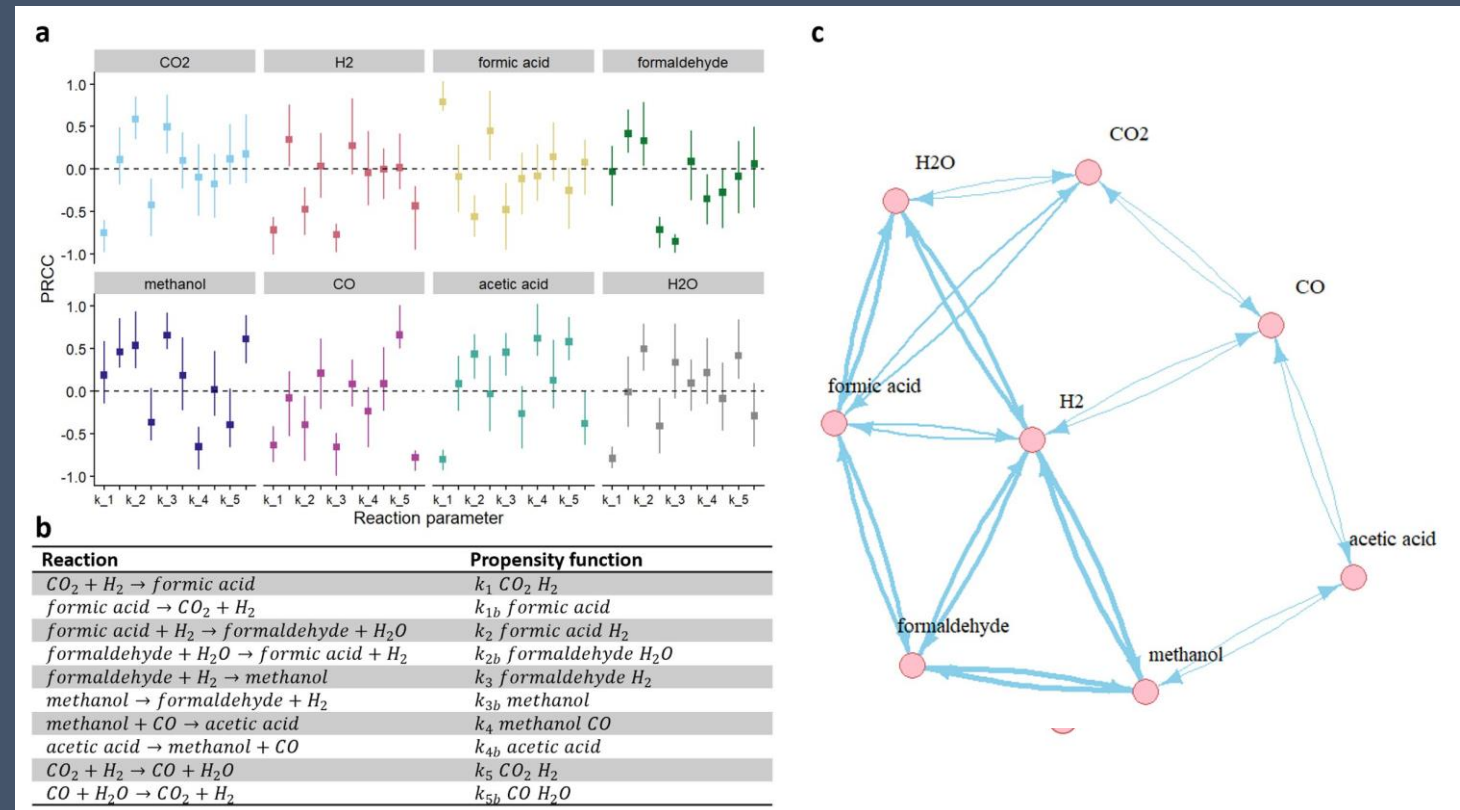
- **Goal:** identify, parametrise, and quantify biologically relevant lines from image data.
- **Skills developed:** problem solving exercise was approached from multiple perspectives, creatively using mathematics and deep learning.
- **Programming in Python:** Hough transform, Gaussian, nonlinear fitting,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



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

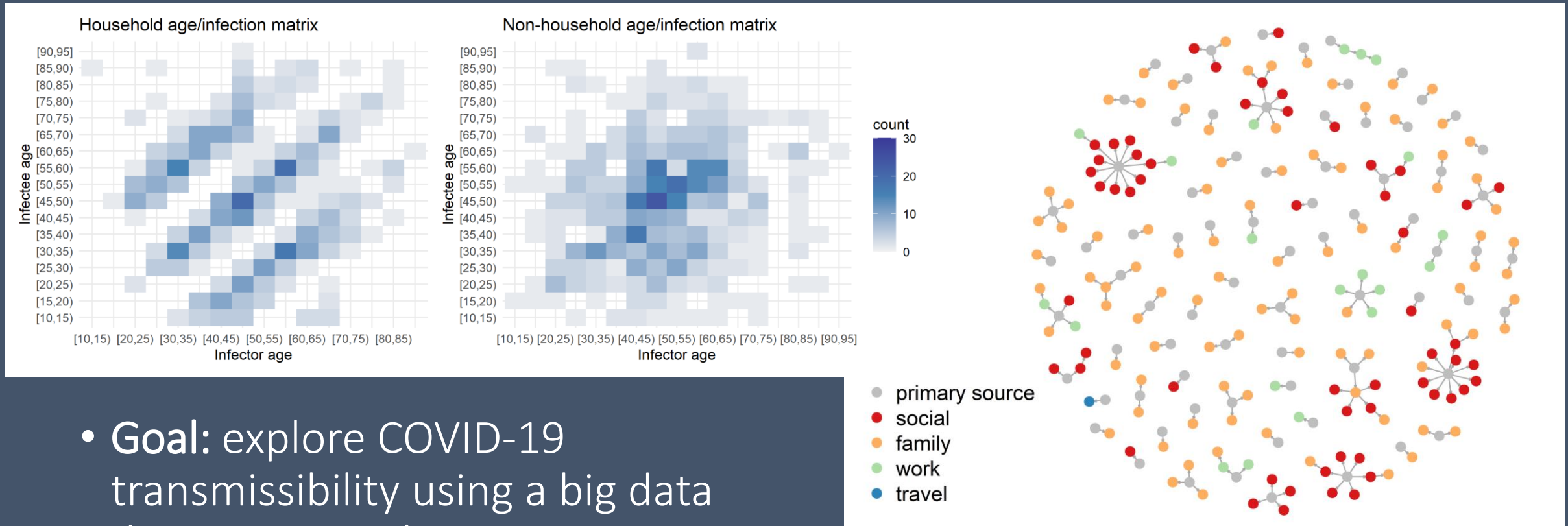


- **Goal:** elucidate the kinetic requirements to drive chemical reactions through the foundations of protometabolism at the origin of life.
- **Programming in R:**
 - implemented a stochastic discrete-time model of chemical reactions in R;
 - explored parameter space using brute-force techniques.
-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



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

(1/2)



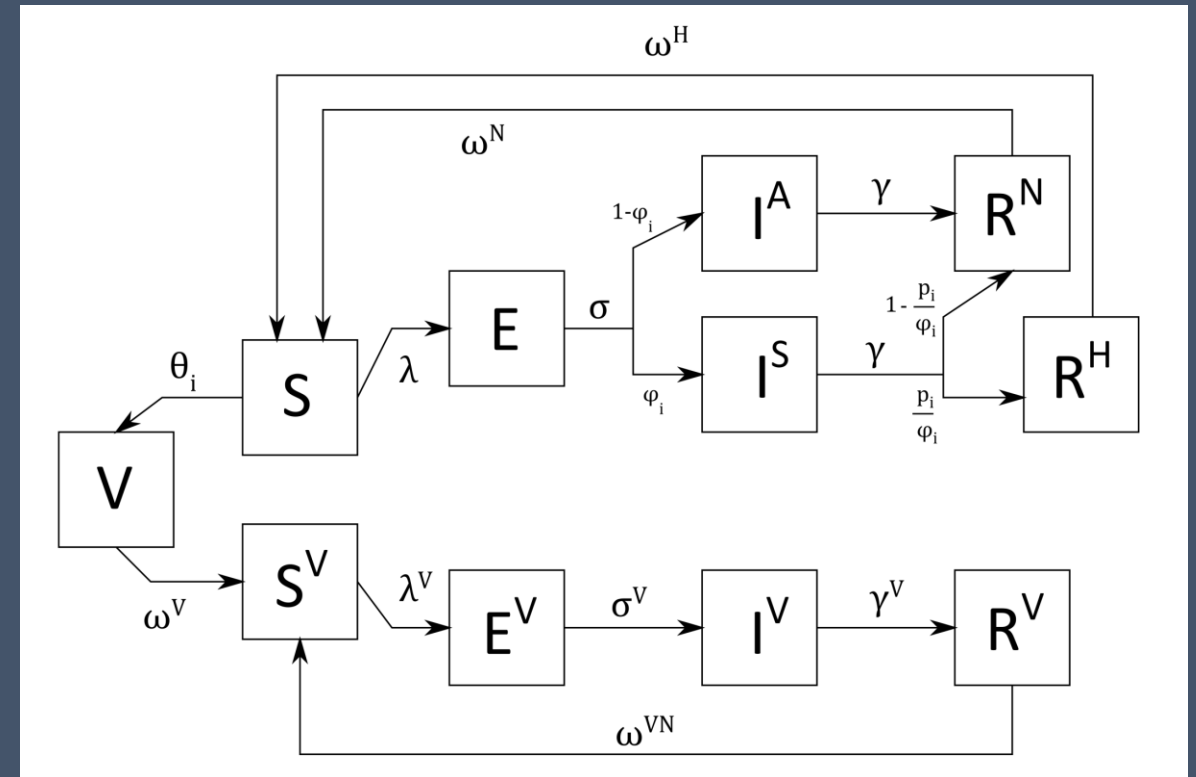
- **Goal:** explore COVID-19 transmissibility using a big data driven approach.
- **Skills:** manipulate and aggregate large data sets from multiple sources.

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

Seda Radoykova

MSci Computational Biology

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Contact details

+44 7732 65004

seda.Radoykova@gmail.com

LinkedIn: [Hale-Seda Radoykova](#)

GitHub: [sedaradoykova](#)