Progression Timeline

- 15/10/23: Contact established with advisor Graeme Ackland via email
- 18/12/23: High-level general research into compartmental models - Consulted the initial references Graeme had provided in his email (Wikipedia)
- 18/12/23: Report template added and adjusted to fit content of SH Report
- 15/01/24: Initial meeting with Graeme - We discussed the general goals and overview of the project as a whole. I was introduced to different types of models: SIR (Most basic), and SEIR (SIIR - Emphasised the importance of splitting the Infectious period to create a distribution curve instead of an immediate exponential decay in terms of recovery probability - essentially modelling that people will get worse before they get better) and SIRS (discussed endemics/steady-flow systems, Analytical solution is possible and boundary conditions ensuring all quantities stay 0 are necessary).

  Graeme expressed his main interest in finding out why COVID statistics taken by the Office for National Statistics (ONS) show an oscillation in cases affecting roughly 5% of the population at a time with a 2-3 month period, we discussed different strains and how when one comes in it results in the previous one dying out, do they compete? He mentioned there seems to be an alternating trend between strains with mutated "forked spikes", could this be a reason for the consistent waves of infection? Now that fewer tests are being conducted and reported one must be careful when dealing with data to see what the actual effect is on the overall population.

  I expressed interest in dealing with how infection and severity differ amongst demographics and how that is important to model, Graeme provided an example of how sporting events during the lockdowns led to an increase of infections amongst men aged 20-40 which in turn led to a spike in women a few days later, then children and finally the elderly, this propagation through the demographics could be described using a contact matrix.

  Questions left for next time are how can other factors be implemented such as Birth, Death, Underlying health conditions, vaccines, lockdown measures, etc. Also, for general infections (not necessarily COVID) how does the R number fluctuate with the method of transmission?

  Following the meeting basic SIR, SIIR and SIRS models were implemented in Python to visualise and gain a better understanding of how compartmental models work. In addition to this, notes from the meeting were adapted into the basic foundations of the report.
- 17/01/24: Report writing focused on further additions that could be made to the basic SIR model to make it as accurate as possible to real epidemic transmission, detailing several social, biological and geographical factors that are otherwise ignored in the basic version of the model. In addition, the basic structure of the epidemics sections was planned out with notes on COVID-19 and other historical outbreaks.
- 22/01/24: Second meeting with Graeme - We reviewed the progress made last week both during and after our meeting. We noticed that a slight fix in the code is necessary to prevent compartments from rising above 1 in the SIIR model. Another improvement raised was that the time step should be implemented explicitly (s.t. it is less than a day) this will lead to smoother/more continuous curves in the resultant data.

  I expressed interest in ways to enhance and add further complexity to the model where we discussed proximity transmission and differences in demographics, which potentially could

be implemented by having a grid of nodes each of which has its own SIR model where there are pairwise connections between each, the shorter the connection would mean an increased probability of infection between the nodes, this will be extremely interesting to construct however Graeme emphasised the importance of not over complicating the model before discovering the source of the oscillation problem.

In terms of the oscillation problem we consulted the form of a damped SHO held in oscillation by a driving force, F:

$$\frac{\partial^2 y}{\partial x^2} - \gamma \frac{\partial^2 y}{\partial x^2} + Fx = 0 \tag{1}$$

The data gathered by ONS gives us the natural frequency of this oscillation (2-3 months) we can use this to try and solve the problem for γ and F.

Graeme returned to the previous idea raised in the SIIR (SEIR) model where we are trying to create a Gaussian-like probability distribution curve for the infected compartments, where he had noticed a mistake such that more mathematical work is required to gain this intuitive curve, this could perhaps be done by repeatedly convoluting exponential functions.

Finally, we briefly spoke of another type of model - The Lotka-Volterra Model (Predator-Prey)

- 24/01/24: I conducted a brief analysis of several datasets available via the Office for National Statistics and on the UK Government website to back up the idea that cases are in an oscillation. Graphical analysis of two separate sources focuses on dominant COVID genes and variants the data showed that at a time there is only ever one main variant active within the population and as one comes in the old one soon after dies out. These alternations occur on a roughly 3-month cycle and could be plausible to explain the oscillating case numbers over these periods, this could also link back to what Graeme initially mentioned about the forked and unforked spike proteins on the virus.

- 29/01/24: Third meeting with Graeme - We initially discussed the concept of convoluting the negative exponential distributions to create more of a bell-curve shape, I showed him a source showing that it should converge to a Gaussian after roughly 30 convolutions however when I had tried to implement a discontinuous function such as the negative exponential I ran into quite some difficulty. Graeme agreed that this could prove problematic and shifted the idea to a different method of implementing the differing recovery rates.

  The data at each time step should be stored in arrays for each of the compartments such that we can use previous values in later calculations. The model should be initialised with a gamma or log-normal distribution to represent the probability that a person will move from one compartment to the next, this distribution must be truncated and normalised as these do not go to zero.

  We had a look at the datasets I found last week and how I noticed a clear alternating pattern in the genome set between COVID waves that it would be interesting if they aligned well with the actual peaks in cases. Graeme described the key artificial elements that had a role in specific peaks in case data (where the gradient of the case numbers is the R number). However, it is once restrictions were completely lifted and the cases still oscillate that we need to research.

  Graeme showed me a paper he had written during COVID and the code for the model can be found on GitHub.

- 13/02/24: Fourth meeting with Graeme. Previous weeks meeting was cancelled due to illness and other coursework deadlines. This week we returned to the idea of using a gamma distribution

to model the length of time at which anyone will stay in a given compartment, this involves setting parameters for each compartments distribution functions and saving the newly infected for example at every time-step so that we can keep track of how long any person has been there and use the distribution to determine when they transition to the next stage.

We spoke about expansions to the expanded model. This model features many different interlinked compartments with each connection having a unique probabilistic chance of transition once an individual has been moved according to the gamma distribution of the previous section. These links could be implemented by using a class based model with each compartment type being its own class with its distinctive fields/features. This could be expanded spatially by creating many instances of each class with probabilities between each.

We then discussed Report 9 which is the main UK based study which lead to the initial lockdowns in 2020. The study was carried out by researchers at Imperial College London, it uses a large compartmental model to predict the outcomes the COVID pandemic could have on the UK and detailed the statistics given varying amounts of lockdown procedures. An interesting finding showed that the most successful outcome (in terms of deaths) came from keeping schools open as this would lead to a fast transmission amongst the younger demographic which was expected to not be severely affected by the disease and such the infection could run its course and not spread to older generations. As convincing as this data is, it is a tough ask and comes at high risk for a government to put children out there and 'want' them to get infected at the same time as expressing how dangerous it is. Realistically, treating all demographics equally is more ethical even if it could (and did) lead to more deaths.

Another point that arose from Report 9 was that the main focus of lockdown measures was to reduce the number of people in critical care as the NHS has a limited capacity on ICU beds over which they could not cope which would cause a huge rise in death toll. Thus, by defining this capacity value we can set a condition on if cases reach a specific % of this value then lockdown measures will be enforces and/or increased, this can be done by reducing the transmission rate when this condition is met.

- 14/02/24 - 16/02/24: Implementation of the gamma distribution was completed for the infected compartment and general code structure for the model was updated. The model was then advanced to SIRS using a Gaussian distribution to determine when people lost their immune resistance and returned to the susceptible compartment however this contained bugs and needs to be fixed. The model reaches endemic too quickly as there are not enough new susceptibles.

- 18/02/24: Added an explanation for the requirement of a Gaussian distribution to the Models section.

- 19/02/24: Re-implemented the SIRS model as a class based program and explored the effects of having a variable infection rate based on a fixed critical capacity

  This new format split the model across multiple files making it easier to expand the model at a later time (e.g to more compartments, or to a spatial model). There is currently 5 files:

  - Control.py - Main file run from the command line, takes in all inputs and initialises class instances of each compartment, it then runs and plots the simulation
  - Compartment.py - Super class from which all subsequent compartment classes are inherited
  - Susceptible.py - Child of Compartment class, contains a function to update an instance at each time step

- Infected.py - Child of Compartment class, contains a function to update an instance at each time step
- Resistant.py - Child of Compartment class, contains a function to update an instance at each time step

4 further class files have been created but not completed, these are: Hospitalised.py, CriticalCare.py, PostCritical.py, Deceased.py. Implementation of these files will complete the expanded model

Added max_capacity to CriticalCare.py allowing an evaluation during each iteration whether lockdown measures were required

- 26/02/24: Fifth meeting with Graeme. We spent time discussing my progress i9n the implementation, and asked a couple of the questions I had been stuck on. We found a peculiar result where the system appears to reach an endemic stage and then the S & I compartments switch at roughly $\frac{T}{2}$, where T is the total time of the simulation.
- 27/02/24: I restructured the report, wrote the abstract and added a contents page. Subsequently, I edited the Models section and added notes for how the uncompleted sections will be filled.
- 29/02/24: I began the introduction, it is currently a bit short but I believe it covers all bases in a concise enough manner. I expanded the Epidemics and Models sections using more research. I updated the title of the report, however, I am open to changing the wording.
- 04/03/24: Sixth Meeting with Graeme: We discussed the 5 page draft report I submitted. In depth feedback is still to come, this was just to go over key aspects such as report structure and content. Overall, Graeme seemed relatively pleased with the progress.

  A couple of key points were made regarding tonality and how the project will be marked. The external marker has no discussion with the main project advisor and will not necessarily be an expert in the area of research. The main takeaway from any paper should be that you have learned something, it should also be an enjoyable read, using anecdotes and metaphors to keep it interesting for the reader (most people never read the full paper - but the markers have to - so be interesting!). The introduction should layout the entire plan for the paper, it should not be set out as a whodunit thus the reader should know why each section is being discussed and not have to wait until the end to be able to piece it all together.

  We also briefly mentioned the poster and had a look through a few examples on the walls of JCMB, Graeme talked me through the posters as though they were a presentation, he said that to benefit the external examiner mine should contain more words to increase comprehension.
- Week beginning 11/03/24: Seventh meeting with Graeme we discussed my implementation of a spatial SIRS model and how waves of oscillations arise throughout the system for certain parameters.

  Majority of week has consisted of report writing focused on the Epidemics, Models and Implementation sections, where I have performed much research and spent time analysing data from WHO and ONS to create informative figures and their captions.
- Week beginning 18/03/24: Eighth meeting with Graeme we discussed the spatial model further and its successful results.

  As before the deadline is rapidly approaching so report writing has taken a key focus

- Week beginning 25/03/24: Ninth and final in-person meeting with Graeme, we discussed my poster design and suggested potential improvements.

  It was decided that due to the huge success of the spatial SIRS models results and my difficulty in implementing a successful expanded model that the expanded model description could be moved to the potential improvements section at the end.

  Majority of the week consisted of rerunning models to produce updated results using more COVID-like parameters

  Received a Masters offer for next year with a 2.1 condition on my project result, so I decided that I would use my learning adjustments to request a weeks extension in order to make the project as good as possible

- Week beginning 01/04/24: Zoom meeting with Graeme to discuss final steps

  The rest of the week consisted of improving the Implementation, Results, and Conclusion sections of the report