

Analysis and Modelling of the Nosocomial Transmission of Covid-19 within a Group of UK Hospitals

Dylan Adlard

During the height of the Covid-19 pandemic, UK hospitals, as elsewhere, experienced varying levels of patient-patient, patient-staff, and staff-staff nosocomial transmission of Covid-19. This undoubtedly increased the frequency of illness in patients and staff, and unfortunately a number of them tragically died as result of Covid-19 related complications.

Throughout the months of July and August I was fortunate to be given the opportunity by Dr David Eyre of the Nuffield Department of Population Health, Oxford, to study the patient-patient transmission of Covid-19 within a group of UK hospitals. The project had three primary aims: to quantify the extent of Covid-19 nosocomial transmission, to identify any patterns in the outcomes of Covid-19 infected patients, and to model and trace patient-patient transmission through the wards of each hospital.

The core patient data sets provided included ward entrance and exit dates and times, the dates patients tested positive either before or during hospitalisation, severity of infection on testing, dates of death, as well as data such as patient age, gender and ethnicity. The models used to study transmission were based on the SIR (susceptible, infectious, recovered) model of disease transmission.

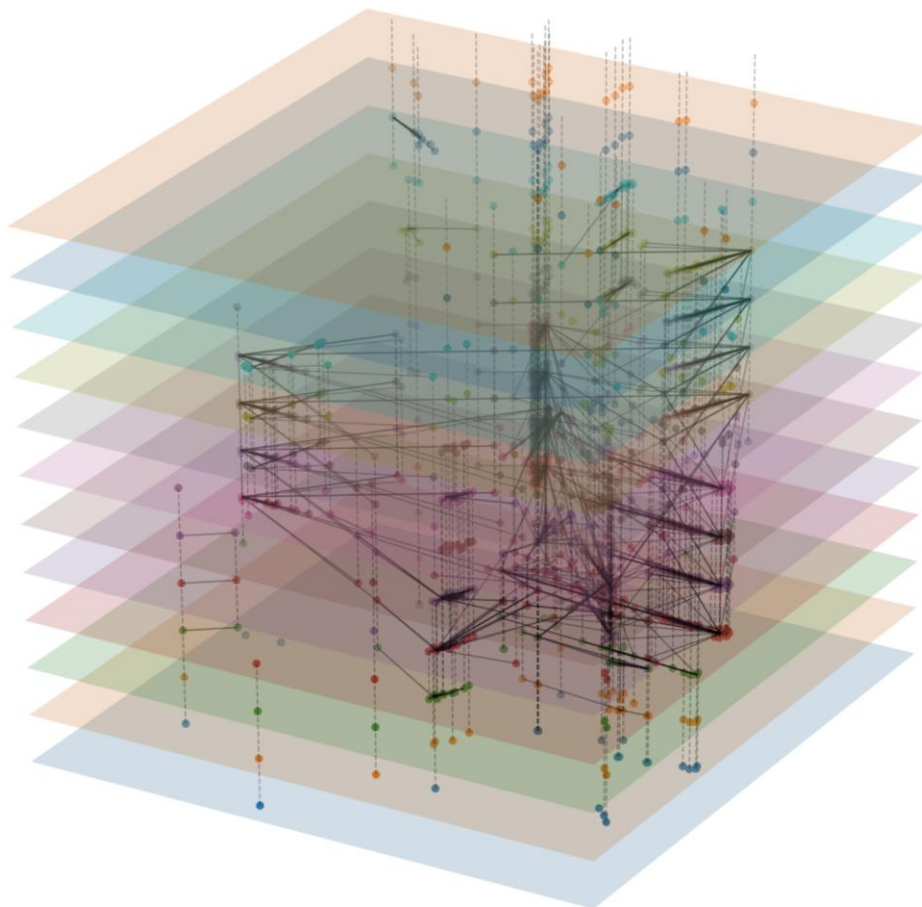
The computational methods employed revolved around data analysis using Python. The numerical analysis was primarily carried out using Pandas, which is a powerful software library built on top of Python that provides data structures and data analysis tools for manipulating numerical data frames and series. Graphical figures were generated using Matplotlib which is a plotting library for Python, as well as Seaborn which is a data visualisation library based on Matplotlib.

Nosocomial transmission was visually traced through the wards of each hospital by generating 2-dimensional transmission networks, and was subsequently represented as a function of time by generating 3-dimensional networks with consecutive weeks represented on the z-axis. Finally, a dynamical 2-dimensional network was created, which enabled visualisation of pseudo real-time patient to patient transmission within and between each ward. These graphs were programmed using NetworkX, which is a Python package developed for the study, manipulation and visualisation of complex networks.

The aims of the project were all met, and provide a framework to facilitate analysis of the factors that contributed to the observed nosocomial transmission rates, such as ward occupancy levels, bed spacing, frequency of patient testing, adequate and appropriate PPE for staff, ward and hospital ventilation, etc.

The project was also of significant personal benefit because it provided an opportunity to learn to programme in Python, to use its powerful data handling libraries, and to develop my skills in scientific data analysis. I am hoping to pursue a DPhil/PhD position relating to computational biochemistry and biomedical informatics, so the importance of these outcomes cannot be understated.

I am indebted to Dr David Eyre for his mentorship and guidance, as well as having been given the opportunity to work on a current and very relevant project. I am also most appreciative to Merton College for a generous stipend to carry out this project as a beneficiary of Merton's Summer Projects Scheme.



An example of a generated 3D transmission network