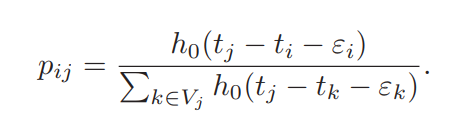
Problem: Solve UA and UE Checklist:

1. **UA (Under Ascertainment): this is the underreported number of people who are considered to be infectious but did not attend to local hospital admission:**
   * 1. Firstly, we will build up a SEIR model to for the first phase of the outbreak (before vaccination stage and under 200 infected cases). In order to do this, we need to estimate the conditional probability of a contact between “an infected” and “a susceptible” that is not observed. If we do not observe who-infects-whom, the conditional probability that j was infected by  
        i ∈ Vj given the observed data is:



* + 1. Then we will use the exposed and death number to compare with the real figure of people participating testing activities in their local clinics (NSW dataset)
    2. We should assume that all people with testing results (either positive or negative) might have interactions with covid infected patients (things would be complicated if we need to filter the types of people going to clinic, in fact, little information of personal diagnostic data can be found online (or at least for free). After that, we will take the probability of exposed population attending healthcare services
    3. Things will be different in the stage of social distancing where regional areas will behave more normally during the outbreak than people in cities like Sydney. However, cross-regional interactions are certain to occur since the travel ban policy was only imposed on inter-state travelling. A new model should be used for this case - SISIR ( (Manfredi, 2017):

In

Sn

R

Ib

Sb

* + 1. From the infected people we can use the rate of E->I (exposed to infected) from the SEIR model above to measure the potential exposed population => we can find the UA’s number (people who are exposed but refuse to have a medical check-up that can be recorded by official data) just like step iii.
    2. To classify regions with b or n, I will put the threshold of classification equalling to the mean of the infected number among postcode areas
    3. Then we came to final stage of covid where vaccination are implemented to preclude the further expansion of the outbreak. There are 3 types of models will be used in this stage:
       1. The model with only vaccination
       2. The model with only self-protective action
       3. Hybrid model incorporating 2 types mentioned above
    4. *Further extension of the work: we can predict the number of reported until the dieout of the outbreak*

1. **UE (Under Estimate): Those who attended healthcare testing practices but receive True Negative results.** 
   * 1. Since surveillance data (diagnostic results sheet) are rare and unreliable, we should only use the official dataset from the gov to estimate the false positive rating of covid testing. Several approaches can be used for UE (which have been used as baseline models) to analyse the specificity and sensitivity of test results.
        1. Generalized Poisson-Mixed
        2. Negative-Binomial
        3. Gaussian Poisson
        4. Beta-Poisson
2. Parameter Estimation – The initial stage of pandemic:
   1. UA: The rate of infection: beta.

+ beta is the rate of S/E becoming I, calculated by multiplying the transmission risk and average number of contacts made by an infected individual (Lelieveld, 2020). We will extract the result of transmission risk from Joe **Lelieveld**’s latest literature (risk rate **∈** [4.5% - 91.5%] with mean = 40% for 5 scenarios of airborne virus transmission).

+ To make comparison and evaluation of these Kendrick ODE’s models, there are at least 7 peer-reviewed approaches in the recent literature, the most efficient one is to consider the problem as NP-hard prob by (Shapiro, 2011). However, I will just use the Branching Process method in my paper as it is also relatively effective. The reason for that is because Simple Branching Process method only focuses on a single-typed population, therefore, I can apply it to the Infected population to see the UA issues. The branching process model provides only an approximation to the initial stages of the spread of an infection in a large population, since no account is taken of the depletion of susceptibles as the outbreak progresses. As the probability of being infected by an individual is distributed by Binomial Distribution (with p= Risk rate, childs = n), we can simulate a new set of infected then compare the result with SEIR models and true counts.