Our branching model consists of a tree of nodes where each node represents an individual and all contacts are children of that node. The parameters of the tree and node are explained below:

Tree (Tree.py):

The tree (model) is characterized by three parameters

* **DetectionProb** – the probability that an infected individual will be detected to start contact tracing on (how likely will we detect an individual)
* **InfectionProb** – the probability that a contact of this individual will become infected
* **TracingProb** – the proportion of contacts that can be traced from this individual

Node (Node.py):

* **Traceable and Untraceable** – Two lists called which hold the traceable and untraceable contacts (children) respectively
* **Age** – a number that represents days since first contact with an infected individual
* **Quarantine** – Whether or not the individual is quarantined (and no longer infecting others)
* **Infected** – whether or not the individual carries the COIVD-19 virus
* **DetectionProb\*** – Determined by the Tree parameters above
* **InfectionProb\*** – “ ”
* **TracingProb\*** – “ ”

Model Dynamics:

The branching model operates with discrete time units where one “step” of the simulation represents a single day. What happens during a step is outlined in the pseudocode below

**Step**

For every non-quarantined infected node in the tree:

If the age is greater than 2 and is detected based on detectionProb:

Initiate contact tracing (\*\*) on the individual

If the age is greater than 7, the individual becomes recovered (removed from simulation)

Otherwise, simulate spreading (\*)to other individuals

**Spreading (\*)**

The number of contacts an individual has is determined by a Poisson distribution with lambda=(3-age). Each contact has a chance to be infected based on the infectionProb and is either added to the tracable list or untraceable list based on tracingProb.

**Contact tracing**

Contact tracing consists of two steps. The first is backwards tracing on the detected infected individual. We try to go up the tree following each node’s parent until we hit a missing link. Then, we initiate forward tracing where for each child in the traceable list, we quarantine them and repeat the same process until the links we have are traced.

**Current work/limitations**

The main thing we are working on is determining beta and gamma which represent infection rates and recovery rates respectively. Currently infection is simply a constant probability for each new contact and recovery is automatic after a fixed time period (7 days). This is where we were looking at the SIR model for ideas

The Poisson for number of contacts per node was also arbitrarily set to 3-age to represent decreasing contacts over time because they might be meeting the same people as before after 2 days etc.

Mentioned in our Saturday meeting was implementing a way to have different “risk levels” for individuals aka some who might be more likely to get the virus. This also affects the first point though.