Flu Surveillance program

1. determining the location and timing of influenza activity
2. defining the types and subtypes of circulating influenza viruses
3. detecting antigenic changes in circulating viruses
4. tracking influenza-like illnesses
5. determining rates of influenza-associated hospitalizations among children
6. tracking influenza-associated mortality

Goal of Meeting:

* to discuss exploratory results on project
* committee : 4th person, a good timeline

Progress

* Added another metric; shannon’s entropy in addition to pairwise distance diversity index
  + measures the evenness of which population is partitioned into different strains
  + sum of the frequency \* log(1/pi)
    - Not maximum
    - 1- all strains are equal quantities
  + try hamming distance
    - try to get values between 0 and 1
* First wanted to explore why max values go down as R0 increases (max.metric.entropy.diversity)
  + Increase mutations (long and short range)
    - Mutations increase exponentially with higher R0s
    - Lag in the peak of metric seems to increase with population size and rnott up to a point (time.scatter.entropy)
  + Does it have to do with the average life span?
    - mutant.life.span.pdf
      * Clearer in the bigger population that with higher R0s the average lifespan of a mutant is shorter
* Can you look at the rate of change of any these metrics
  + **Do they line up with the peak?**
  + *Rate of change in the number of mutations more closely aligns with peak infected for Ro 1-2 range*
    - Mutations.derivative.long
    - Mutations.derivative.short
  + Derivative of entropy and diversity not as clear
    - Entropy-peak of derivative lines up (nosier for smaller R0s)
      * Trajectory.entropy.derivative.long/short

Sampling: Right now implemented post-processing so that if I change proportions/etc, don’t have to rerun the analysis

* Two schemes:
  + Proportional
    - Of the cases in the population, proportion are detected
    - Sample strains according to their frequency
  + Uniform
    - Equal samples per time step, should equal the same number of total samples as the proportional
* Haven’t explored how it works on different R0s and population sizes or proportional sampling (current R0 = 1.5,
  + Which method tracks the true entropy, true number of circulating strains, true diversity better

Lower level of testing it: comparing to what it actually in the population at a time

Higher level of testing: can you recover transmission parameters

\*Rcolgem

Implements a coalescent model

* takes in a genealogy with sample times and reconstructs the dynamics
  + estimates transmission rates
  + estimates pop size through time
* can also simulate trees conditional on a demographic process and sampling model:
  + can compare trees from my simulation, to see if the evo model is working alright
  + lineages through time plot