Transmission Trees in Wave and Particle

a short briefing

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Introduction

Two typical runs of CovidSIMVL were used to generate WAVE and PARTICLE trials. The settings are not equivalent in order to induce the two extreme behaviors. The trials were run with console.logs, which reported on the time and relationship of infector and recipient (susceptible). The transmission trees for 1,000 population in each run were built by hand, and this note captures the most immediate summary of early analysis.

The Trials and Parameters

The data are found in github.com/ecsendmail/MultiverseContagion. Within this repository is a folder called “CovidSIMVL”. There is a subfolder named “PROJECTS”.

Within PROJECTS is a folder called “2021.03.06 WAVE+PARTICLE Transmission Trees”. In this folder there is an Excel file called “2021.03.06 Both Trees and Analyses.xlsx”.

The raw data for console.logs, as well as the reduced infection data and transmission trees, and analyses, can be found in the appropriately named sheets.

To summarize the parameters: SINGLE UNIVERSE

PARTICLE: pop 1000 “Sick or Dx” 9.9 HzR 1.3 mF 7.5

Initial infectives 1 pID 0

WAVE: pop 1000 “Sick or Dx” 13.2 HzR 1.1 mF 0.8

Initial infectives 5 pID 10-14

Overall Results:

PARTICLE: Terminate 1045 gen Day 43 HR 13 Survivor 1 R0 2.41

WAVE: Terminate 4759 gen Day 198 HR 7 Survivor 248 R0 1.73

ANALYSIS OF TRANSMISSION TREES

***PARTICLE:***

The single initial infective created five infections as the first five infections (gen 85, 90, 95, 110, 113), and we analyzed the structure of these subtrees to compare them with the subtrees created in WAVE by the five initial infectives.

This is the summary of the structure of the PARTICLE transmission trees:



At a glance it is obvious that the nodes are markedly asymmetrical within the sub-trees, while the average depths are remarkably similar, with a mean depth of 4.37 and a standard deviation of 0.43.

***WAVE:***

The corresponding table for WAVE is shown below.



Here, the asymmetry of the subtrees is in terms BOTH of number of nodes, as well as average depth, with a mean depth of 8.89 but a large variance of 5.53.

The total number of nodes infected in WAVE was 751 in 4759 generations and for

PARTICLE 999 in 1045 generations

**COMPARING THE TRANSMISSION TREES**

We would like to have metrics for heterogeneity and for the resultant progression of the epidemic which can be used for all transmission trees in Covid.

First, we normalize for size by considering percentages of the total population of infected agents.



By considering each subtree’s size, and its fraction of the whole, compared to the expected if the tree was completely balanced, we get the divergence of each subtree. Taking the absolute values of these, and adding them, we get total divergence. Then, with five subtrees, we have the upper and lower limits of the total divergence for all configurations.

The lower limit is when the divergences are all zero and the sub-trees are totally balanced. The sum must be zero for total divergence.

The upper limit, for five sub-trees, is with the configuration of one sub-tree having ALL the nodes (100%), and the rest having none. This leads to the zero sub-trees of divergences of 0.20 as fractions, and with the single large sub-tree of (100% - 20%) or 0.8 as a fraction. Thus, their sum is 0.8+0.8, which is 1.6.

The Asymmetry Index is then the fraction of the total divergence of the Maximum Divergence. In the case of PARTICLE, it is 0.59. This appears to be quite a large degree of asymmetry.

For WAVE, the corresponding table is shown below.



In comparison to PARTICLE, this value of 0.40 for WAVE shows that the sub-tree asymmetry is less.

**TAKING DEPTH OF SUB-TREES in consideration**

The first tables show that the degree of asymmetry is not the whole picture, because there are marked differences between the PARTICLE and WAVE runs in terms of the depth of the sub-trees. While it is tempting to take the average sub-tree depth for the two prototypes, they exhibit a marked degree of asymmetry in WAVE and not in PARTICLE.

We will adopt the approach of considering each sub-tree, and then normalizing based on the expected fraction of the whole.

For PARTICLE and WAVE, we get the following tables.



Here we have suppressed the two lines leading to the row ABS(divergence) which can be recalled from the previous tables.

With depths of each sub-tree integrated into the DxD index, we see that PARTICLE has a smaller degree of asymmetry than WAVE.

Yet, this is still not the entire picture of the meaning of heterogeneity in comparing PARTICLE and WAVE. After all, PARTICLE (1045) only took about one fourth of the time it took WAVE (4759) to terminate, and WAVE still had 248 survivors.

We want a heterogeneity index which reflects:

Increases with longer time

Increases with more asymmetry

Increases with longer transmission chains (average depths)

We have already taken asymmetry and average depths of sub-trees into consideration with DxD. Now we factor the generations taken for each, and get:

Heterogeneity of PARTICLE 0.44603\*1045 /100 = 4.66

Heterogeneity of WAVE 0.59250\*4759 / 100 = 27.87

There, that produces the index consistent with our expectations of what the configurations of the trials for WAVE and PARTICLE with respect to homogeneity, depth of trees, and speed of the epidemic, would produce.