**Report of daily progress of my dissertation**

**Day #1 (reported) – 01/04/25**

Today I spent 5 hours trying to adapt what I had of the neutral transmission model to the time averaged variation. I’ve called the former the “Snapshot” model, and the latter the “Time Averaged”. The first hour or so I was trying to figure how to average the generations recorded in the model, and I created a “time averaging factor” and differentiated between total generations or time steps and observed time steps, which are the ones we’re interested in ultimately. To sample which time step out of the factor chosen (in this case it was 10), I simply told the simulation to pick the last one, but I eventually changed it to sample all individuals in the window averaged. It’s not very relevant right now, because I gave it up momentarily to work on sorting the neutrality “snapshot” model.

I spent most of the afternoon/evening battling with the code to detect possible caveats in the current model. I removed and rewrote many chunks of code, until I finally hit the right note. Firstly, I reported 60% of detection of neutrality, but then I modified some bits and went down to 3-6%, which implied an error in the model or conversion of the model to the FIT parameters. I had to go back to Ben Marwick’s repository several times to adequately convert the simulated data into long format, filter variants with less than 3 time points and run the test regardless of NA results. I finally made it, and after some time wrestling with R, I finally got some more realistic results: 43% of neutrality detection.

Next step is to refine the code and modify the parameters to evaluate different outcomes of the test. So far, with an innovation rate of 0.01 after filtering, “fit\_results” has only 54 observations, which means 54 distinct variants that appear at least in 3 time steps. Out of the 100 variants that start off, and after the burn-in stage, we’re left with 54 observed variants. This is likely due to a low innovation rate which leads to a rapid turnover of variants (a phenomenon that we would not be able to record as precisely in the time averaged model). Adjusting the model parameters would likely result in different outcomes:

* With higher *N* or population size, the effect of drift (random fluctuations) would be reduced, meaning that we would expect more observed variants.
* With higher *µ* or innovation rate, we should expect more new variants emerging or reemerging, leading to more observed variants after equilibrium. And if we increase *N,* we should expect an even higher number of variants, as the effect of drift is reduced.

This is all under the assumption of a finite population, however, we should bear in mind that some cultural traits may be better represented within the frame of the infinite allele model (Wright-Fisher Infinite Allele), such as decorative motifs in pottery (Madsen, 2012). In essence, the number of observed variants is defining how diverse or homogeneous was our population in the past 200 generations/time steps.

To conclude, for tomorrow I must **review the current code and look for possible caveats or ways of improving it** (too tired now and might’ve incurred in some mistakes while writing); **modify the parameters of the model** and make predictions; **clean the pipeline to transfer it into the time averaged variation**; make **visualisations of the simulated data** to better understand what’s going on. And, if possible, start off with the time averaged model, which I’ve already started but will need to rewrite.

Another goal for tomorrow is to go forward with the reference writing and summarising for the introductory chapter of the dissertation. So far, I’ve read and summarised the elementary papers on the application of neutrality models, and I’ve been able to raise some questions and get things a little bit clearer. I should carry on with this matter, as it will save me a lot of work later while writing the thesis.

**Day #2 – 02/04/25**

I am currently editing the model’s parameters, and as I predicted, when increasing *N*, we get more variants observed after equilibrium, and the opposite if we indicate a lower number. In fact, with only 10 variants only 4 survive, and three of them record *NA* values after the test, so only one is detected as neutral. I’ll assign 50 number of initial observations, as I think it might relate better with a real-life scenario of, for example, pottery motifs (other traits may vary).

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| --- | --- | --- | --- | --- |
| N | µ | Runs | % | Time |
| 50 | 0.01 | 100 | ~44% | 13” |
| 50 | 0.01 | 1000 | ~44% | 2’ 50” |
| 50 | 0.01 | 10000 | ~44% | 16’ |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| N | µ | Runs | % | Time |
| 50 | 0.02 | 100 | ~84% | 20” |
| 50 | 0.02 | 1000 | ~84% | 3’ 15” |
| 50 | 0.04 | 100 | ~159% (?) | 34” |
| 50 | 0.06 | 100 | ~224% | 40” |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| N | µ | Runs | % | Time |
| 20 | 0.01 | 100 | ~41% | 10” |
| 40 | 0.01 | 100 | ~42% | 18” |
| 60 | 0.01 | 100 | ~45% | 15” |
| 80 | 0.01 | 100 | ~44% | 16” |

As we can see from the tables, innovation rate is biasing the test results. This is likely due to the faster rate of innovation leading to the introduction/invention of new variants to the population, surpassing the initial population of *N*. When computing the average, we divide the sum of neutral detections between the number of runs and *N*, meaning that we are comparing the observed population with the initial one, and this leads to **overrepresentation of variants when innovation is high**. Number of runs and population size does not seem to affect the test results, so perhaps is not worth paying the costs of more time for more runs.

Today, after modifying the parameters of the model and revising the code, I’ve found a possible caveat, which is what I refer to as the **overrepresentation of variants in the test result** due to a high rate of innovation. A task for tomorrow will be **solving the problem of overrepresentation when high µ**. For the rest of the tasks I had for today, the code is almost ready to apply the time averaging factor, tomorrow I’ll be able to go forward in that regard.

I’ve correctly modified one of the plots to show all the observed variants in terms of absolute frequencies, and not relative. Ben Marwick mentions that the FIT requires absolute frequencies, not relative, which is something I had to correct from previous models. So, the division is done between number of unique variants ever recorder and the initial population (N). For this reason, it is more reasonable to represent absolute frequencies, instead of relative frequencies each time step, although it could be more intuitive to plot the latter for actual representations of real data.

For tomorrow, the tasks to complete are as follows: **solve the overrepresentation of variants** in fit\_results, **implement time averaging into the new model**, **plot both models** with different parameters, and **hint at different paths to go** next.