

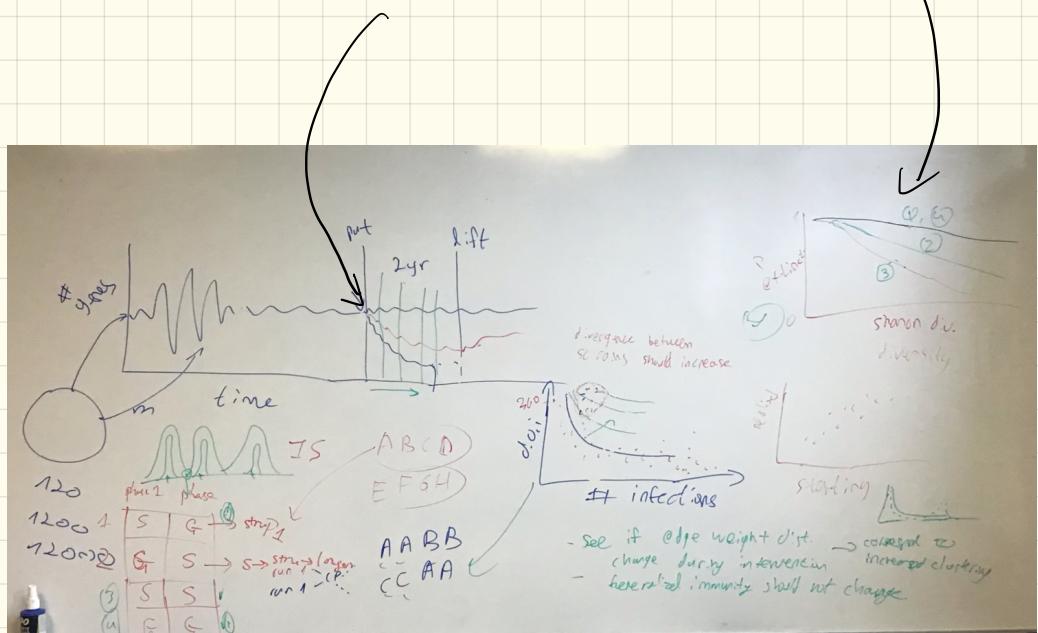
## Malaria Interventions

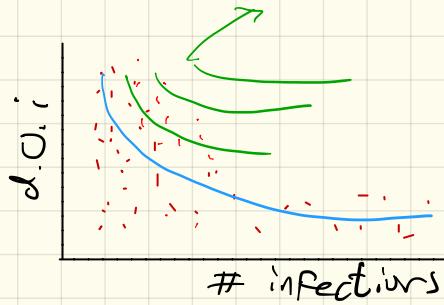
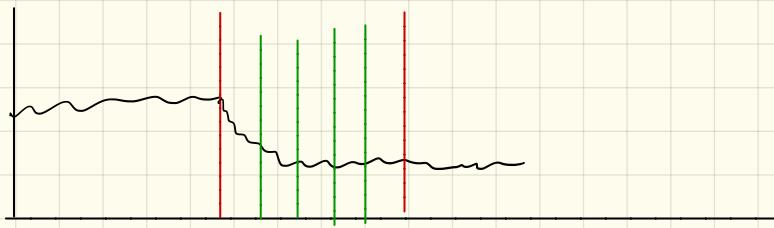
Following discussion  
in lab meeting  
19/10/2012



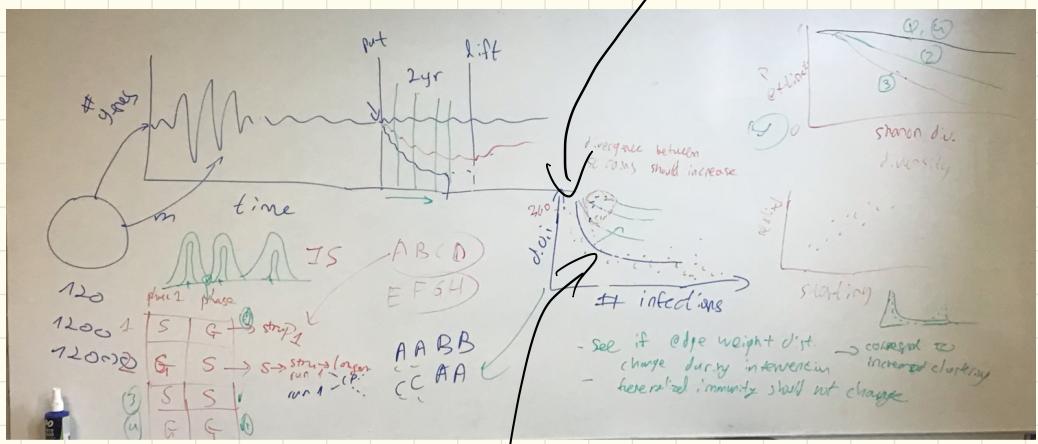
Hypothesis: infections persist because IS  
proteins genomes to be different from each  
other, and this prolongs their infection,  
so there is higher likelihood of at  
least some genomes to be transmitted.

Should plot the Prob. of extinction vs. diversity plot using the gene diversity at the onset of the simulation. And maybe better to use Shannon diversity instead of # genes (still need to think about that).





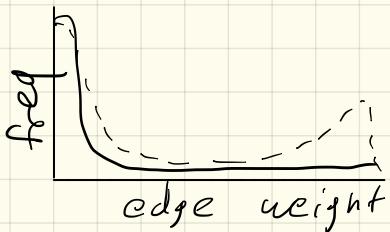
draw the curves  
at different layers  
in the intervention



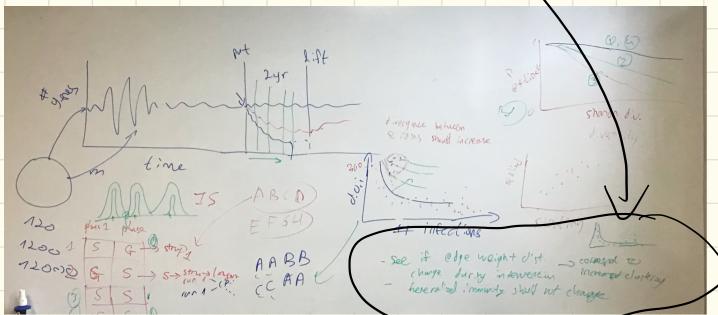
The curve for GZ should not change.

Lack of transmission and reduced competition should create changes in edge weight distributions, in the JS scenario but not in GI.

There should also be other structural changes in the JS scenario but not in GI. But we can only look at properties that are not affected by reduced # of nodes.



bimodality means that there are clusters of very similar genomes, which are very different than other clusters.



# Switching experiment:

To disentangle the evolutionary process and the effect of intervention we can switch between runs at the onset of intervention (checkpoint). We expect that a switch to IS will increase the stability of populations that evolved with GI.

