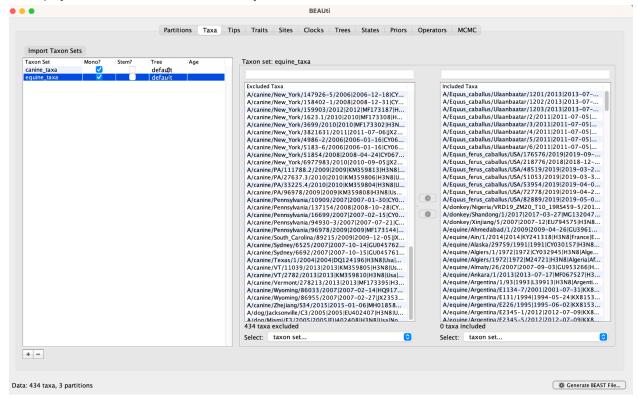
Analysis 2: Adding in a local clock

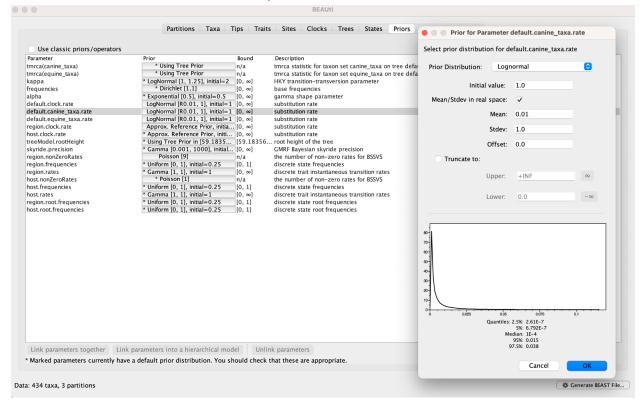
In this analysis, we will be exploring different clock rates, and adding in a fixed local clock to the analysis. When viruses jump to new host species, they often require adaptation to that new host. The HA gene encodes the influenza receptor binding protein, which is a common target for host-specific selection. It is a reasonable hypothesis that transmission from horses to dogs could impose selection on the HA gene, resulting in faster evolution and accumulation of amino acid changes. In this analysis, we will test that hypothesis by adding in a fixed local clock. This model allows the clock rate to vary among monophyletic groups in the tree. In our case, we will define two different host partitions in the data, canine and equine, and use a fixed local clock model to estimate the TMRCA for each host and the clock rate within each host species. We can then compare the estimates to determine whether there is evidence of increased adaptation in dogs following transmission from horses.

Part 1: Setting up the analysis

1. We will be using most of the same parameters for this analysis that we did in Analysis 1. So, starting with the Beauti input from Analysis 1, now go back to the 2nd tab, labeled "Taxa". In order to assign different hosts different clock rates, we need to specify taxon groups, which we will do in this tab. In the bottom on this panel, click on the plus sign, which should add a new taxon group. Label the first one "equine_taxa" and select the equine sequences to include by selecting them in the left box and clicking on the right arrow to include them in the equine taxon set. Do the same for canine. For both, select "mono". This enforces these groups to be monophyletic, which we know that they are. The results should look like below:



- 2. Now navigate to the "clocks" panel. For the default clock rate, select "fixed local clock" instead of strict clock.
- 3. Now, navigate to the "priors" panel. You should now see a new set of priors for the clock rates. We should change the default for the "canine_taxa" and "equine_taxa" clock rates, which are specified as "default.canine_taxa.rate" and "default.equine_taxa.rate". Because our a priori assumption of the clock rates is that they should not deviate too far beyond the overall influenza clock rate, we can use the same prior we used for the strict clock in Analysis 1, a Lognormal with a mean of 0.01, with mean in real space.



4. Save the xml as before, and launch!