**Measuring discordance among gene trees**

**NOTE – that incongruence statistics can be done for a specific triplet topology. This can still be confusing when there are aberrant individuals, but nonetheless…**

1. -t ASTRAL branch annotations. And/or gCFS annotations in IQtree.
2. Quartet sampling (pease et al. 2018)
3. Robinson-Foulds distance, can be done in ete3
4. Gene-wise log likelihoods for alternate topologies (how strongly does gene support topology of interest?) -> Shen et al. 2021