**Variant calling and file generation**

* Call variants without indels. Generate consensus fastas from these.

*Fastas*

* + Estimate sliding window trees, etc.
  + Read into MVFtools and do D statistic stuff

*VCFs*

* + Pixy

*Bams*

* + Pull mapped sequences in genic regions and generate *de novo* (?) sequences for these genes from the bams. Then realign on a gene-by-gene basis. This helps identify actual indels and generates gene sequence files. (samtools consensus? – simple basecalling -- <https://github.com/samtools/bcftools/issues/1459>)

**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