**The story so far:**

1. *Consistent species tree topology* regardless of method used. All methods used to construct trees produced the same general topology, which is consistent with the topology recovered from RADseq data (Stone & Wolfe 2021).
2. *Evidence of both historical and contemporary gene flow.* Excess allele sharing is common at both contemporary and historical time scales. Plots of excess allele sharing indicate the presence of both what is likely recent introgression into specific lineages (*P. cardwellii;* Mt. St. Helens, *P. rupicola*; Cle Elum and Mt. Shasta; *P. davidsonii*; Crater Lake) and what is likely historical introgression into entire species groups (*P. newberryi* x *P. davidsonii*).
3. **Summary of Dinvestigate – forthcoming? How does one summarize this?**

**Dinvestigate**

1. **(MOVING FORWARD, DO A GENE DENSITY VS. f\_DM plot)**
2. **MOVING FORWARD, JUST COMPARE AVERAGE f\_DM BETWEEN DAVIDSONII?**

**Davidsonii x newberryi --- davidsonii (Crater Lake) x rupicola**

* F\_dM generally hovers around 0, which is expected for ancestral introgression for newberryi comp. But at Crater lake, avg. f\_dm is much higher, it looks like.
* Outliers dav x new introgression are on, just eyeballing:
  + Low genic areas for
    - 1086, 1087
  + High genic areas for
    - 2687, 1087, 2533, 2686
  + Mixed for
    - 2532, 2685, 1086, 2687
  + None for
    - 2684

**Moving forward:**

* Relationship with metrics and gene density: how is gene density related to:

1. Gene tree discordance
   1. RF distance
   2. gCF (targeted triplets)
2. Genetic distance (targeted triplets)
3. Introgression
4. Genetic diversity

**In progress/planned**

* 10kb sliding windows
  + Discordance metrics & targeted discordance summaries
    - RF distance
    - gCF and sCF
    - gene-wise log-likelihoods (Shen et al. 2021)
    - Quartet sampling (Pease et al. 2018)
* Scaffold/scaffold analysis
  + Pixy

**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