* Consider pulling generation times from IUCN Red List DB
  + Seems to have pretty good record for Generation Length (Years) per species
  + Might even use this as an alternative for the gen times estimated for birds
    - [Link](https://www.iucnredlist.org/species/22732795/208237218)
  + This [paper](https://natureconservation.pensoft.net/article/1343/list/5/) has some good data on generation times
  + Consider using the same generation length for species in the same genus/family/order if information is lacking
  + On bird data
    - See how clustered generation lengths are to the groups:
      * Order
      * Family
      * Genus
* Maybe sort DBA by X’s. There might be an unintentional violation of space time from tslearn
* Learn how to use Erik/Cade’s CCGP workflow
  + Consider adding more marine life samples
  + Consider clustering multiple samples of the same species/genus to see if they show patterns of shared ancestry in their MSMC curves
  + How do we differentiate between coevolutio/homoplasyn and results of shared ancestry?
  + Learn how to estimate species divergence

Running pipeline

* Figure out if PE sequencing was used in 200 Mammals Project
  + Option for pairs of fastqs in CCGP pipeline

Running MSMC

* Fits demographic model to data
* Requires

Phylogenetic Signal: When Mammals make their own cluster, distinct from what Avians have

There can be many things that the clusters mean

* Geographical spacing
* Same selective pressures
* Suffering same effects
* Same separation histories