* Plan Overview:
  + Main manuscript covering evaluation of reintroduction
    - similar to USACE report (Demography + Modeling)
    - target journal: TAFS
    - Start drafting now, Nick has time around mid-March for revision
  + “readaptation to the wild”
    - Send to Mike Ford for perspective first, then plan how to move forward
    - Potentially publish at Evo Apps special edition
* Questions from Nick:
  + What is the age of NOR immigrants and how does it differ from NORs assigned to HOR parents? Are there scales taken?
  + How does the finding that BOTH male and female NORs are more fit than their HOR counterparts match with previous results? In previous work isn’t the origin fitness difference mediated mostly through males?
  + Is there a way to look at lambda for each group (HOR, F1, NOR immigrants)
  + Can the age structure of offspring explain TLF or CRR for parents?
  + Can we spend more effort parsing Nb, Ne, Nc for different groups (HORs, F1s, NOR immigrants)? (consider Ryman-Laikre effects)
  + Does the variance in TLF differ between NORs and HORs (it looks like it from the figures)?
* Suggestions from Nick:
  + How to address the mate pair fitness question
    - Look into the Araki 2005 RRS randomization approach (also the type II error rate framing will be useful when thinking about the NOR immigrant confidence)
    - Build my own null distributions of fitness based on empirical dataset sizes, (e.g. empirical number of NOR and HOR males and females, empirical number of offspring)
      * Consider both a simple model where a mate pair produces a single offspring, and a complex model where reproductive success follows the empirical distribution (large variance, neg bin distribution)
    - Look into the approach in the Whitcomb et al 2014 paper
  + It may be necessary to confirm any differences in diversity between groups with an independent set of loci (assignment probability may be related to diversity -see pronghorn Waples paper)
  + Table A2: change to He and Fis, years are rows, columns are loci
  + Mate pair figure could be improved by plotting like Fis: (1-observed )/ expected
* the mate pairs analysis is probably worth separating out from the rest, but is a lower priority, given the statistical challenges
* RS vs TLF
  + Nick will have time in summer and will take the lead.
  + Assignment approach is currently confounded (RS is Solomon, TLF is colony + cervus consensus)
  + David will send pedigrees (need to make sure Nick can match sample names), scripts for assignment, as well genotypes if the goal is to unify assignment approach.
* Other Notes
  + Consider the readaptation piece a debate starter about “what is a wild fish?” and try to incorporate a perspective about genetic architecture and plasticity
  + Reframing the readaptation paper so that NOR immigrants are not so critical to interpreting the results will make it easier to digest. The central finding is that F1s are more fit than HORs. The additional finding that F1s are not less fit than NOR immigrants provides *additional context* to the central result.