***COBP Analysis Plan***

***Mechanisms of maintaining rare populations and corresponding tests (Dibner, et al. 2019)* :**

1. Negative density dependence
   1. Compare models of lambda w/ and w/out density terms
2. Demographic compensation (different vital rates have opposing responses to environmental variation)
   1. Used correlations between the coefficients for year effects in each vital rate function (from the IPMs)(for vital rates that had significant temporal variation). Negative correlations indicate demographic compensation (Villellas et al. 2015)
   2. Also looked for spatial demographic compensation by comparing coefficients for plot effects for vital rate functions that had significant spatial variation.
   3. Tested the importance of vital rate buffering and temporal demographic compensation (of each vital rate!) for pop. Growth using randomization procedures to simulate 500 stochastic growth trajectories over 100 yrs without one or both of these patterns. Compared these stochastic growth rate estimates (estimated for each transect) with point-estimates of long-term stochastic growth rates that include demographic compensation and vital rate buffering.
3. Vital rate buffering (variability of demographic rates is inversely related to their importance for determining pop. Growth rate)
   1. Compare vital rate variability to their elasticity values (Pfister 1998; Morris and Doak 2004)
      1. Variability: coefficient of variation (CV) for the mean and variance of each vital rate (Morris and Doak, 2004)
      2. Used the ‘standard perturbation approach’ to estimate elasticity values (Caswell 2001, Morris and Doak 2002)
4. Asynchronous responses to environmental variation across subpopulations
   1. Mantel tests; population-level synchrony index (Loreau and de Mazancourt 2008, Thibaut and Connolly 2013); and the mean-variance portfolio effect (Anderson et al. 2013).
5. Fine-scale source-sink dynamics
   1. Can’t directly measure (no seed movement data), but plot-level population growth rates indicate whether or not there are consistent spatial differences in average population performance, a necessary pre-condition for source–sink dynamics.

***Parameters calculated in Dibner, et al. 2019***

* Population growth rates
  + **Plot-level log(*t*)**
  + **Entire population log(*t*)**
  + ﻿(?) To assess synchrony among populations occurring in different patches, we **examined pairwise Pearson correlations in log(*t*) among plots**. We **tested for relationships between different metrics of plot quality**, including mean abundance ( ), mean growth rate, , and the mean correlation coefficient in log(*t*) of a plot with all other plots weighted by each plot’s mean abundance (hereafter ).
  + There are four vital rates that are important to estimate when including the seedbank as a stage in a demographic model, in addition to growth, survival, probability of reproduction, and reproductive output (Paniw et al. 2017):
    - Probability of a seed produced by an adult plant in year *t* will germinate in year *t+1* (i.e. skipping the seedbank) (**Pgerm**)
    - Probability of a seed produced by an adult plant in year *t* will enter the seedbank in year *t+1* (**PgoSB**)
    - Probability that a seed in the seedbank in year *t* will exit the seedbank in year *t+1* (**PSBout**)
    - Probability that a seed in the seedbank in year *t* will stay in the seedbank as a viable seed in year *t+1* (**PSBstay**)
    - \*Vital rates #1 and #2, and #3 and #4 do not need to sum to 1. The remainder of each of these pairs accounts for seed mortality between years.
  + it is possible to incorporate a discrete seedbank stage into an IPM by adding an additional equation to the model (Ellner, Childs, and Rees 2016; Kuss et al. 2008; Paniw et al. 2017). The equation that describes the number and size of individuals in year *t+1* (**n(z’,t+1)**), using data from a pre-reproductive census of a monocarpic perennial, and assuming that probability of flowering and reproductive output is determined by vegetative size in year *t-1*, is as follows:

Where ***z***=the distribution of plant size in year *t*; ***z’***=distribution of plant size in year *t+1*;***pb(z)***=probability of reproduction as a function of size *z*; ***s(z)***=probability of survival as a function of size *z*; **G(z’,z)**=probability of growth to size *z’* as a function of size *z*; ***c0(z’)***=size distribution of new recruits; ***b(z)***=number of offspring produced per individual as a function of size *z*; ***B(t)***=size of seedbank in year *t*; ***U***=upper limit of plant size; ***L***=lower limit of plant size; ***n(z,t)/n(z,t-1)***=number of individuals in year *t* (or *t-1*) as a function of size *z*

* This function is added to describe the size of the discrete seedbank stage in year *t+1* (***B(t+1)***):

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* Density dependence
  + ﻿fit both density-dependent and density-independent models to the census data—for each plot, as well as the entire population.
    - **Model abundance at time *t + 1* as a negative binomial mixed model** (?) (glmm) with an offset for log(Nt), following the general approach of Abbott et al. (2017) and Brown ﻿and Crone (2016).
    - **Compare Ricker models**, which include a fixed effect of abundance at time *t* (Ricker 1954), to density-independent models.
    - For analyses at the plot level, we compared models with random intercepts and/or slopes among years and/or plots with the Akaike information criterion, corrected for sample size (AICc). We fit all models with the lme4. The best supported model was a Ricker model including random variation in the intercept among years and random variation in the intercept and slope among plots.
* Asynchrony among subpopulations
  + We used three analyses to test for asynchrony in population growth among 100-m2 plots and to identify how differences in plot-level responses to environmental drivers could account for any asynchrony in the entire population.
    - To identify if the magnitude of correlations between plots in log(*t*) or log(N) was related to their spatial distance from one another, we used **Mantel tests**. Since the north-south axis most closely corresponds to the slope and hence microhabitat at Sand Draw (higher elevation in the north, lower in the south), we considered Euclidean distance along this axis as well as two-dimensional distance and distance on the east-west axis. ﻿
    - We then quantified the strength of asynchrony among plots and its contribution to population stability with two commonly used empirical metrics: the **population-level synchrony index** (Loreau and de Mazancourt 2008, Thibaut and Connolly 2013), and the **mean-variance portfolio effect** (PE; Anderson et al. 2013). The population-level synchrony index ranges from zero (if all plots are perfectly asynchronous or abundance is constant) to one (if all plots are perfectly synchronous) and a PE greater than one indicates stabilizing effects of among- plot variance on total population size (see Supporting Information for details). ﻿
    - We also tested for climatic drivers of population growth and asynchrony in plot-level responses to climate variation. We summarized the climate data into annual (July–June before census) and spring (April–June before census) precipitation sums and temperature means; these variables are likely important for Yermo performance and correspond with the timing of our demographic surveys in late June to mid-July. We **tested whether each of these climate variables explained variation in log(*t*) among years by comparing negative binomial glmm Ricker models of population growth, as described above, that included one of the four climate variables with AICc**. In particular, we compared Ricker models with random variation in intercepts and slopes among plots, but that substituted fixed effects of climate in each year for randomly varying intercepts in each year. For each climate variable, we fit models that considered linear and quadratic effects of climate and their interactions with plot position along the north-south axis, capturing interactions between climate and the main spatial variation in habitat. Although models with random year effects had the lowest AICc, the best-supported model with climate variables had similar explanatory power. We therefore used the best-supported climate modle, which included linear and quadratic terms for annual precipitation and an interaction between North-South plot position and annual precipitation. While multiple climate factors are likely to drive Yermo dynamics, our data were too temporally limited to fit multifactor models.
* Simulations
  + **Multi-site, count-based PVA** for entire site based on long-term census data (Morris and Doak, 2002)
    - **Simulated population growth in each time step by estimating an expected log(*t*) for each plot based on it’s abundance of plants, climate variable, and the plot-specific coefficients from the best-supported Ricker model**. Then added to this log(*t*) a plot-specific correlated random value estimated from the covariance matrix of the model residuals among plots (following Abbot et al. 2017)—allows for stochasticity
    - Tested the accuracy of these models by starting them at the beginning of the census data, and then comparing modeled to actual data (compare correlation)
    - Then project into the future by using the last year of census data as the starting point and ﻿randomly drawing annual precipitation values from a normal distribution with mean and variance taken from the 99 complete observations of annual precip. From the Riverton NOAA station.
    - Did these simulations 10,000 times over 100-year time window
  + Ran **three additional simulations** to estimate the impact of density dependence and spatial asynchrony
    - Ran simulations based on an alternative model that removed effects of spatial asynchrony in climate responses
    - Ran simulations based on models that removed the stabilizing effects of density dependence while still imposing a density cap on numbers
    - Ran simulations based on models that excluded both of these effects