**Methods**

*Forest inventory data*

Adapt from subalpine fir paper, describe filtering for ABLA/PIEN plots and distribution. Build map figure with plots and ecoregions, etc

*Population trajectories*

Adapt population estimation sections from subalpine fir paper, population estimates as well as disturbance and mortality estimates.

*Community trajectories*

Start with section describing single-species trajectory bins (i.e., decline, turnover, densification, development) > then >

Describe conceptual framework for comparing population trajectories of multiple coexisting species based on basal area and stem density trends, e.g., persistence, structural change, compositional change, replacement – grounded in Seidl & Turner paper. Perhaps here is where conceptual diagram figure is referenced.

*Demographic models*

Mortality model

Filtered tree data to get remeasured subalpine fir and Engelmann spruce from co-occurring stands that were alive at T1. Used tree status (i.e., live or dead) at time two as a response variable – that is, individual survival over a 10-year period. Model incorporates predictors at three levels of organization: tree, plot, and landscape. Tree-level predictors included tree size at T1, crown ratio at T1, and the presence/absence of insect or disease damage at T1. Plot-level predictors include climate normal and climate anomalies, stand density. Landscape-level predictors include the proportion of ecoregion subsection impacted by fire and biological disturbances. We built a binomial GLMM in a Bayesian framework using these predictors for each species.

Where the survival *S* of individual *i* in plot *p* nested in ecoregion *r* at time *t2* is modeled as a linear function of a fixed intercept b0 modified by a random term g1 varying between ecoregions *r*, and predictors varying between individuals *i*, plots *p,* and ecoregions *r*. Individual-level predictors include the diameter of tree *i* at time *t1*, crown ratio of tree *I* at time *t1*, and the damage status of tree *i* at time *t1*. Damage status was coded as 0 if the tree was undamaged, and 1 if any fire, insect, or disease damage was recorded. Plot-level predictors included climate normals *CN* between 1980 and 2010 (the time period corresponding to plot establishment), recent climate anomalies *CA* observed between time *t1* and time *t2,* and interactions between normal and anomalies. The index *j* indicates the climate normal variable (mean annual temperature or mean annual precipitation), whereas the index *k* indicates the climate anomaly variable (mean annual temperature, mean annual precipitation, or climatic moisture deficit). Ecoregion-level predictors include the proportion of spruce-fir forest in each ecoregion impacted by fire mortality *AF* or biological disturbance agent mortality *AB* between time *t1* and time *t2*. The model also included selected cross-scale interactions, namely between tree size *DIA,* climate anomalies *CA*, and disturbed area *AF* and *AB*.

Regeneration model

Modeled regeneration as the probability of seedling presence (from SEED table) at the plot level during the most recent inventory period, as a function of plot and landscape-level predictors. Plot-level predictors include climate normal and recent anomalies, estimated fire severity, BDA severity, slope, aspect, elevation. Landscape-level predictors are the proportion of ecoregion impacted by fire or BDA. We again built a binomial GLMM in a Bayesian framework for each species. (build out equation).

Community trajectory categorization

Potentially another part here saying we took model-predicted mortality and regen, aggregated them to the ecoregion subsection level, and compared them across community trajectory categories to get a sense of what combinations of demographic rates area associated with coexistence.

*Future Projections*