**ROADMAP**

**Community level approach:**

1. Work at the community level, not at the species level
2. We first focus on extinction debt
3. Identify species present in 2001 (2000, 2001 and 2002), and characterize each partition to include only those species which were present in all three years (so we are sure the species were present in the partition)
4. **GOAL:** Ask how biodiversity has changed over time (decline or stabilize) according to land use change.
5. To do so, we can estimate biodiversity metrics from the community for every studied period, and repeat the estimations separating long and short-lived species (using percentiles, to avoid sampling unbalance).
6. **First decision:** What level of analyses, partition or cluster?
   1. We can start by asking whether we can conduct the analyses at the partition level, including ecoregion as random effect to deal with geographic and climatic differences.
      1. Advantages: Habitats more homogenous, same sampling effort, higher sensitivity to land use change
      2. Disadvantages: Greater effect of stochasticity, which can make it difficult to properly define communities (e.g. species from different partitions of a same).
      3. We therefore need to characterize communities, i.e. ascertain whether the species representative of the community are all detected.
         1. Examine beta diversity (turn-over and nestedness) to ask whether partitions within an ecoregion have similar species composition.
         2. Use rarefaction curves
   2. If partitions from a same ecoregion differ in species composition, we can try to cluster them according to habitat similarity, and ask whether now species composition within partitions are more similar.
   3. If we still find differences, we should aggregate species from partitions of a same cluster, and estimate biodiversity metrics at the cluster level
      1. Disadvantages: A habitat decline in one partition can be obscured with the lack of change in the rest.
   4. An alternative is to classify communities with cluster analyses, pooling together partitions with similar species composition.
      1. This could make more sense to look at the rougher geographical scale (ecosystem/habitat cluster) because extinctions are more important when looking at a larger area
7. Check the comments of the reviewers of Nat Ecol Evol to assess other potential biases.
8. Estimate alpha biodiversity metrics at the appropriate level of analysis.
9. How to estimate land use change?
   1. Quantitatively or categorically (cluster analyses of the %habitat loss)?
10. Build database with raw data: cluster, ecoregion, partition as rows, alpha diversity metrics, land use,

**Species level approach:**

Species level modelling:

1. We focus on extinction debts first.
2. Identify species present in all three first years (2000-2001-2002) at a segment, so we can make sure the species are really present and to reduce stochasticity.
   1. We average the abundance across the three years for a species at a segment.
   2. We summarize the abundances according to the animal\_jetz species name for multiple entries of a species at a segment for a year.
   3. Decision:
      1. Do we focus on terrestrial species only? Yes, we focus on the terrestrial and diurnal species as classified in the Bird et al., 2020 Cons Biol paper
3. **General Goal**: Investigate the extinction debts for a species and explore the causes.
   1. Do species in a shared habitat differ in their time to extinction?
      1. If so
         1. Is it due to differences in life history?
         2. Or difference in tolerance to land use change?
         3. Or is it a bias associated with the detectability?
         4. Or is it due to stochasticity?
         5. Is it due to the initial abundance of the species?
4. The first question is: How do we characterize the time to extinction?
   1. Decision: We focus on the habitat cluster level.
   2. We estimate the abundance of each species over time in a cluster as the sum of all individuals recorded per year.
   3. Then we follow the script provided in the course on demographic population models to estimate the time to extinction.
5. Does the abundance in initial years explain the time to extinction of a species? With this question we want to check the sensitivity of species to random local extinctions, and the effect of the initial abundance.
   1. First, we investigate the time point of local extinctions of species.
      1. Decisions:
         1. How do we deal with species, whose abundance at a segment was not recorded for the whole timespan? Have minimum recording period for a bird + segment combination. I used 10 years.
         2. How do we deal with segment + bird combinations that are not present in the initial three years? Omit.
         3. How do we deal with species that disappear from a segment for more than three years and then return? For example: species is present in 2005 and then again in 2013.
         4. How do we deal with species that were observed at a segment in the first three years (2000-2002) and then do not reappear from 2003 onwards?
   2. Then we use the abundance of the previous years and model the local extinction and try and find which abundance explains the local extinctions.
   3. In the single species approach we don’t need to include species or segment as random factor but Ecoregion.
6. Given that we find a species is sensitive to initial abundance and local extinctions, we then want to investigate what makes a species sensitive to local extinctions. We want to investigate two variables, namely life history and land use change, and their interaction.
   1. Life history: We use generation time to characterize the life history strategies along the slow to fast lived species. We hypothesize that the species with faster generation times and therefore faster life history strategies won’t experience strong legacy effects.
      1. How do we interpret the results? *we expect shorter generation times to be better predictor of sensitivity to local extinctions?*
   2. Land use change: We use the difference in land use from one year to the next as the land use change variable.
      1. How do we interpret the results? *If the land use change that occurred a long time ago explains the sensitivity to local extinctions, then we can expect legacy effects due to land use change?*
      2. First decision: Do we summarize the change across all land use types for a segment or do we investigate each land use type and the change in each land use separately?
      3. Second decision: How do we build the variable? There are three ways we discussed to incorporate land use change as a variable.
         1. Binary (0 no change, 1 change)
         2. Bins (0-2 % minor, 2-5% moderate, 5-10% big)
         3. Continuous variable as percentage of land use change
   3. Interaction: Then we also want to know if land use change and life history strategy interact to influence the sensitivity to local extinction. Therefore, we build a model with an interaction term of these two variables.

Phylogenetic based analysis where the response will be time to extinction per species within a cluster. Because we have the same species in several clusters, we include species as a random effect. And similarly, because we have several species within one cluster, we have to use cluster as a random effect. This is to avoid pseudo-replications and ensure that observations are independent. We introduce the phylogeny because species that are closely related share traits due to common ancestors. Therefore, we have to include the phylogeny as a random factor. (Search for phylogeny brms to look at examples)

1. Then we want to look at the species per cluster: analyze all species in a cluster simultaneously to see if we can find patterns across bird groups due to similar ecological traits
   1. We expect differences in sensitivity to land use change across bird groups.
      1. In fast vs slow lived species
      2. In specialist versus generalist species: Specialist species are stronger affected by land use change since they are dependent on the initial habitat.
      3. Depending on the initial habitat (for example: forest vs urban): This might be correlated with other characteristics. For example: in urban environment there might be more generalist species.
      4. Across feeding strategies:
      5. In better vs worse dispersers: Better dispersers are not able to move away and find suitable habitat/conditions and are therefore dependent on the local conditions.
   2. In this approach we need to add as random factors:
      1. The species
      2. The phylogeny
      3. The location (for example segment nested in cluster or in ecoregion)

Meeting notes 28.07.2023:

Avoid using “legacy effect”, we focus on extinction debts. We focus on species that decline. We need to identify the species that are declining: population viability analysis. Analyse the temporal series of abundances, work at the cluster level 🡪 sum up the invididual species abundance across segments in a cluster, lambda = population growth rate (neg = decline, 0 = stable, pos = increase), log(lambda) = intrinsic rate of increase, mean(lambda of all years) = tells you what , var(lambda) = ?, put these metrics in a demographic model that estimates the abundances and run simulations, estimate the time to extinction, and then model the time to extinction with detectability/initial abundance/life history traits,

Unclear...: To estimate the initial population size: Use only species present at a segment in years 2000-2002, but then sum up for each year the species count per cluster,

Assumption of these demographic models: no density dependence, no age specific parameters, you know the initial population size, arbitrary quasi-extinction threshold (differs between species)

Good for us because: mechanistic approach, easy to use,

Take one cluster and one species that is well sampled (?) and run the demographic model to see if it can characterize the time to extinction,

Ideal data set in the end:

Species | cluster | lambda | log(lambda) | var(lambda) | time\_to\_extinction

Then use time\_to\_extinction in the same way I described the models in the species\_level approach above.

**Look at the literature if someone has already used demographic models to characterize the extinction debts.**