

Analysis Notes for Data Set 2017Jun08_1

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Description:

```
paste0("~/",location,"/",run_name)
## [1] "~/GIT/Analysis/2017Jun08_1"
```

This description & discussion is correct if the data set matches the title: 2017Jun08_1

For the sake of clarity, in this report a “group” refers to set of species: fish, autotrophs, or invertebrates (we clump all other species into the invertebrate category).

We are writing a methods paper describing the effect of including lifehistory in the model.

This compares three different experiments:

1. New lifestages that are linked.
Lifestages are linked with a leslie matrix and grow from one stage to the next once per year. The rest of the year they behave as individual nodes.
2. New lifestages (as in nodes), but they aren’t linked with lifehistory.
There’s no leslie matrix and lifestages behave as individual species.
3. No new lifestages

This means that we have pairs of experiments that we run with the same initial conditions - so when doing our analysis we should take advantage of these links between experiments. Try a repeated measures ANOVA...

Discussion:

Are the results realistic? Does including lifehistory make it seem more realistic?

Can we compare the inclusion of life histories to a real world scenario? For instance, ecosystems with apparently strong life histories versus weak ones (e.g. fish with high adult:offspring body size ratios versus fish with lower ratios. Or fish that dramatically change diet over lifespan versus ones that don’t).

Anna found some interesting results with Lake Constance. If our results are consistent with hers, we can generalize them to other ecosystems. If they aren’t consistent, we can ask why? Is Lake Constance an exception to the norm? Why?

We can also expand this work in other directions:

- Life history evolution:
 - Dietary shifts
 - Increased predation on younger lifestages, less predation on larger
 - Metabolic rate
- Cannibalism - What happens when fish prey on younger lifestages?

Experimental Design

I subsetting the data into further (hopefully temporary) experiments. This just tells you how life histories are created. In this case we will be using:

- lifehis.splitdiet=0
- lifehis.fishpred=0

I’m also only running an analysis on the data once it stabilized.

1 Analysis

Everything in this section should be accurate regardless of the data set. I'm mostly looking at the means of biomass right now, but using the variance of biomass would be just as interesting!

1.0.1 Principle Component Analysis

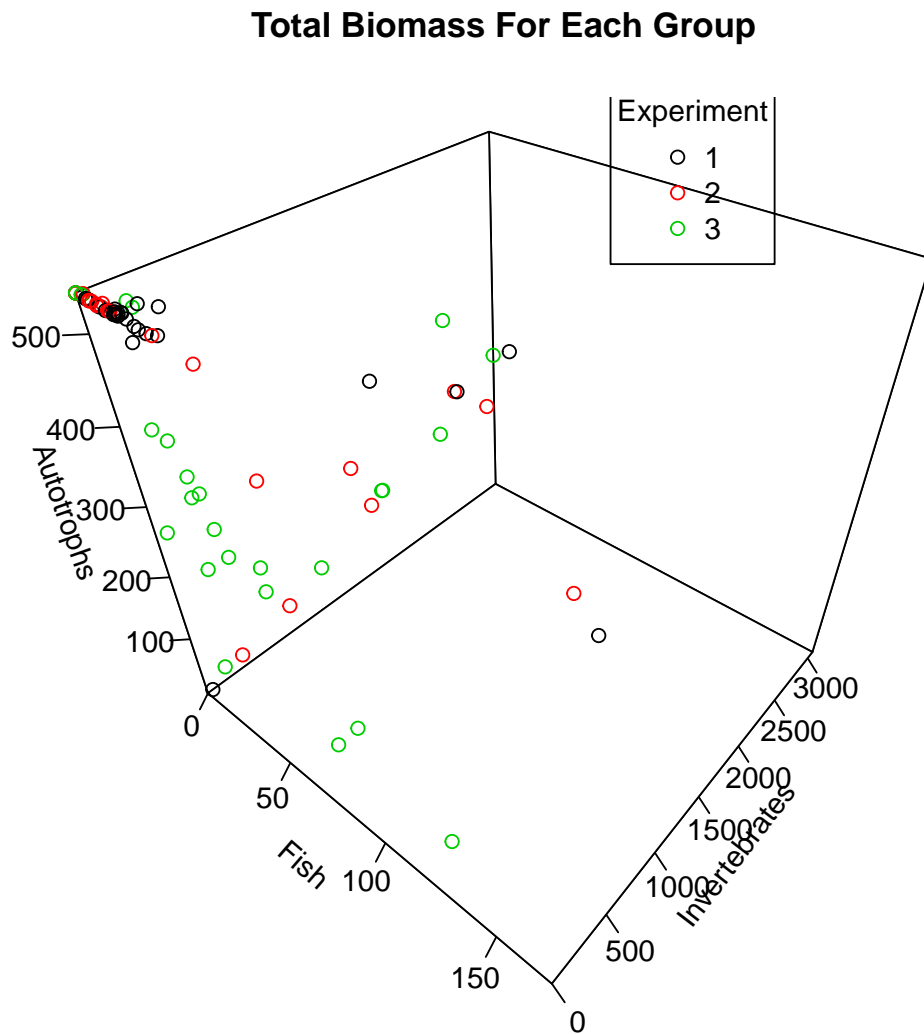
Run a PCA with each experiment as a different colour. This will be interesting, but an LDA seems like a better solution right now. So that didn't work out too well, probably because the data is too extreme. Let's try logging it first

1.1 Linear Discriminant Analysis

What we're really looking for is a way to separate these experimental conditions. It doesn't really matter what the differences are between them (they can be combination of factors), but we do want to find some separation. An LDA would be perfect for this; we can find a distinction between the experimental treatments without forcing it to be a change in a single species. It might also be a good idea to order the nodes so that fish species are always compared against one another rather than ordered by niche value.

Reminder: LDAs work by looking for the (combination of) dimensions which maximizes the difference between treatments while minimizing the variance within treatments. In this case our dimensions will be species biomass.

We can also take advantage of the paired treatments with a paired LDA.



```

pca_logGroups=tapply(alldata$Biomass,list(alldata$Simnum,alldata$Nodes_df,alldata$Exper),mean)
pca_logGroups=pca_logGroups[,c("Fish_tot_df","inverts_tot_df","basal_tot_df"),]
pca_logGroups=log10(pca_logGroups)
# pca_groups=pca_groups[1:27,,]
# pca_logGroups=pca_logGroups[1:27,,]
# scatter3D(pca_groups[,1,],pca_groups[,2,],pca_logGroups[,3,])
scatter3D(pca_logGroups[,1,],pca_logGroups[,2,],pca_logGroups[,3,], xlab="Fish",ylab="
  Invertebrates",zlab="Autotrophs",main="Total_Logged_Biomass_For_Each_Group",colkey=F,
  ticktype = "detailed",colvar=rep(1:N_Exper,each=dim(pca_logGroups)[1]),col=1:3)

## Error in persp.default(plist$xlim, plist$ylim, z = matrix(nrow = 2, ncol = 2, : invalid 'x'
limits
  legend(-0.4,.45,1:N_Exper,col=1:N_Exper,pch=1,title="Experiment")

```

Figure 2: A plot where the dimensions represent the total logged biomass of different groups (fish, invertebrates, autotrophs). This is still a bit buggy - see attached picture for this instead (The code itself is fine, it just doesn't show up in this report for some reason⁴).

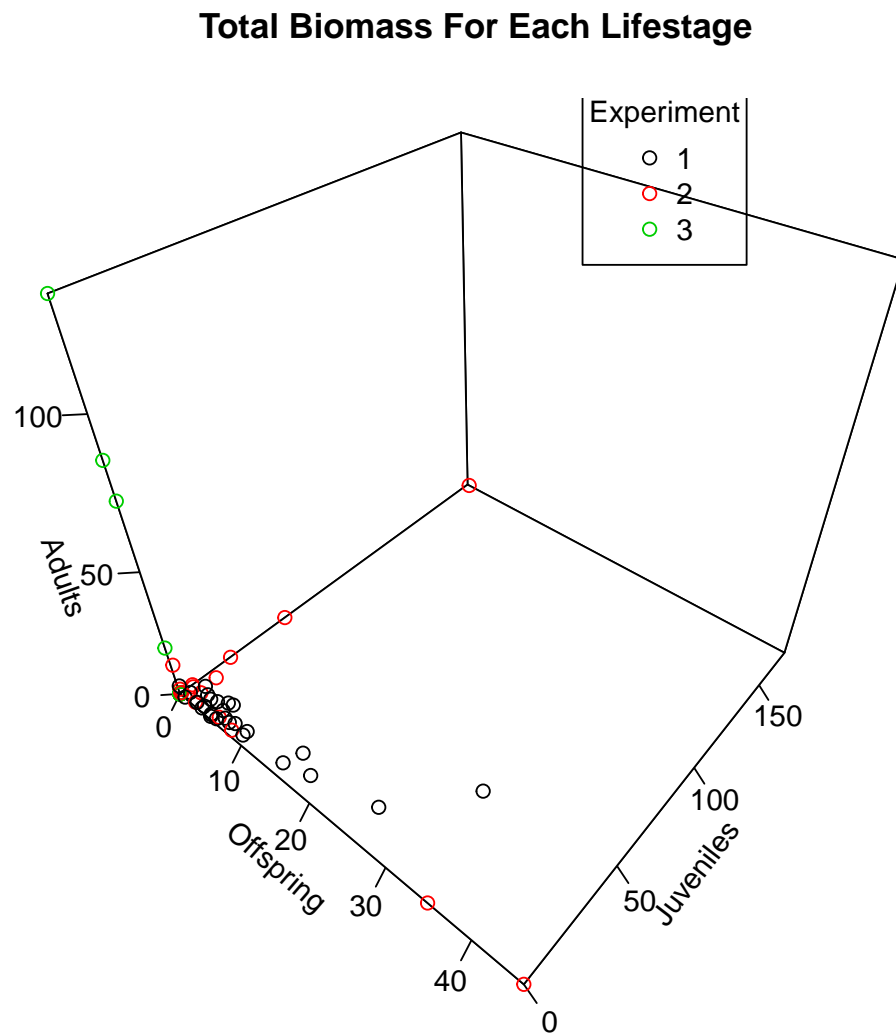


Figure 3: A plot where the dimensions represent different fish lifestages. Of course, since we can't make a 4D plot, we're only using lifestages 1,2, and 4.