Last week

- How to implement linear mixed models in R
  - Different packages
  - How to specify the models and random effects structure (syntax)

- Hypothesis testing in the mixed model framework

This week

- Today: brief intro to the lazy way of using mixed models to analyze repeatedly-measured and spatially heterogeneous data
  - Also including an example for nesting random effects
- Time for Q/A about final projects

- Thursday: Guest lecture by Dr. Cristy Portales Reyes about time series analysis

- No homework this week! Use time to get to know your final project datasets

A road map for the next ~10 weeks
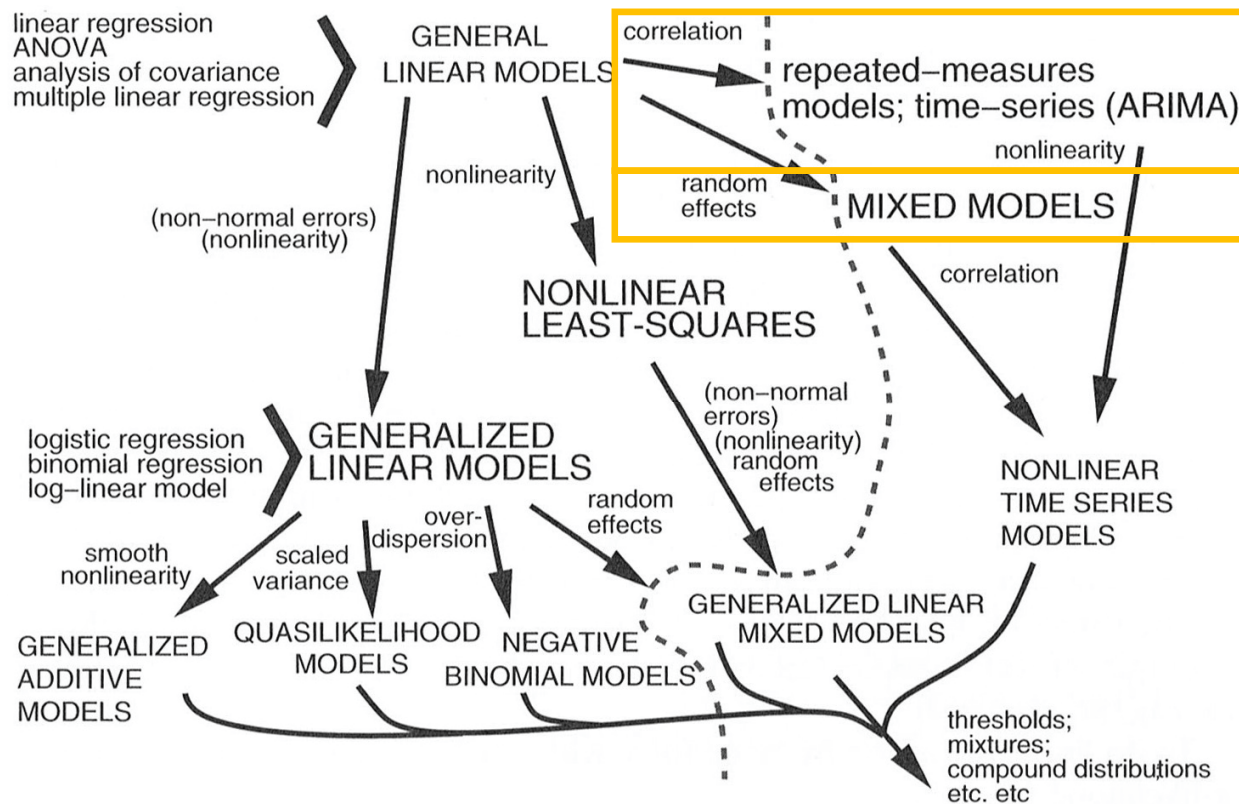
We'll use one data set to demonstrate

100% Blue grama   50/50   100% Black grama
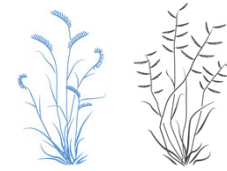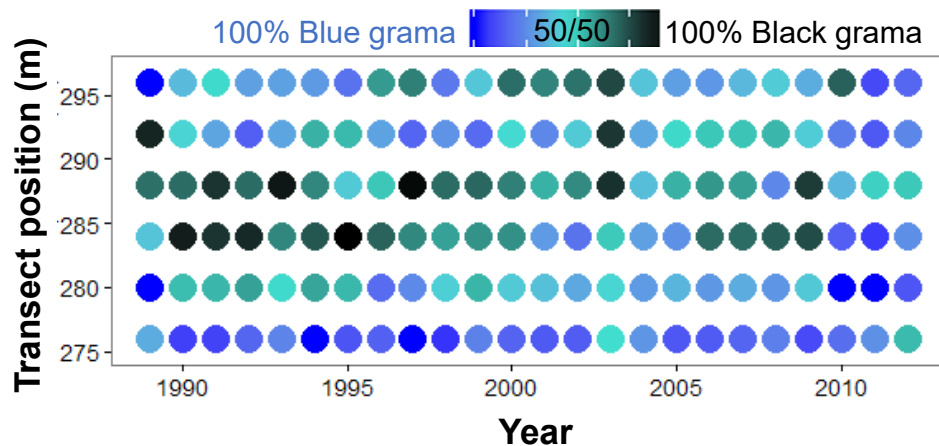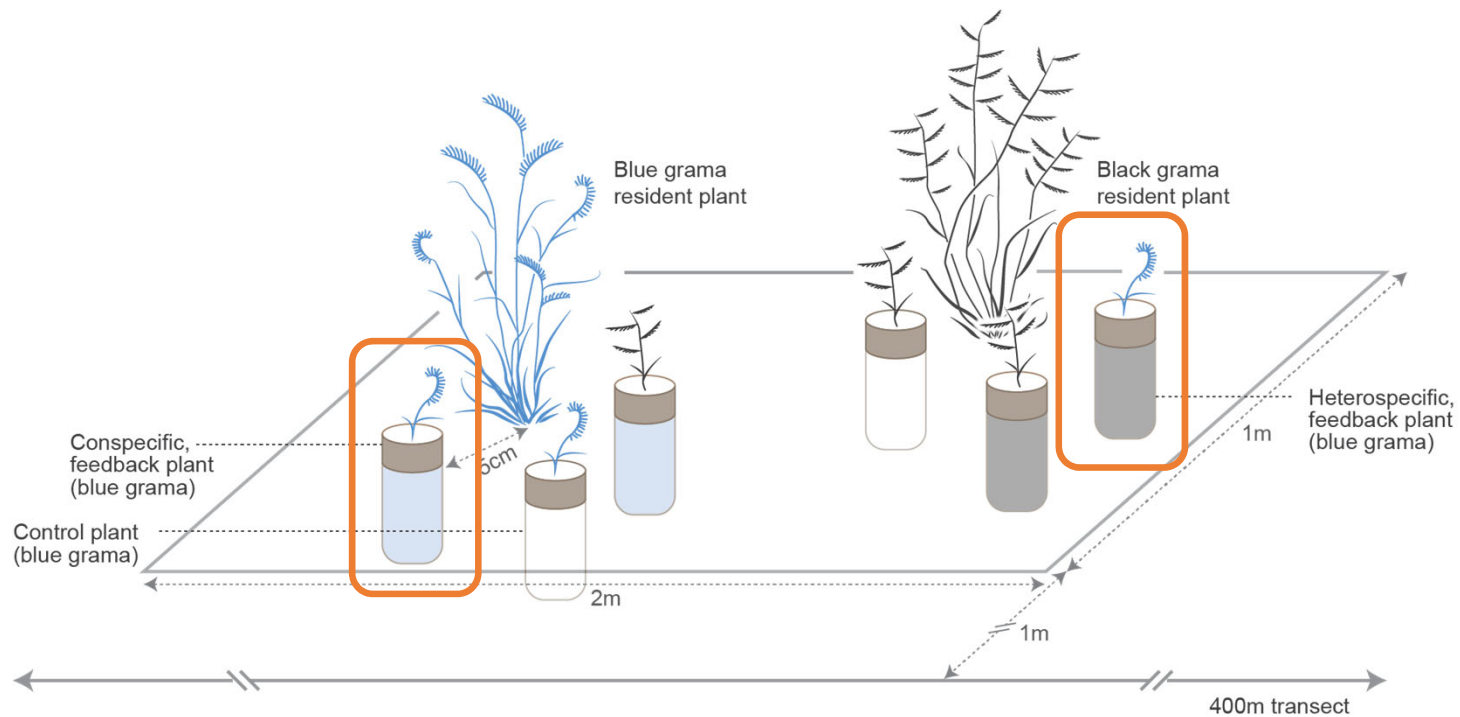
Patterns are not driven by abiotic differences

Hypothesis: *Negative plant-soil feedbacks* could promote *stable coexistence* in static patches

Field experimental design

10 Dynamic (D) plots
10 Static (S) plots
Dynamic and Static plots paired in 10 spatial blocks
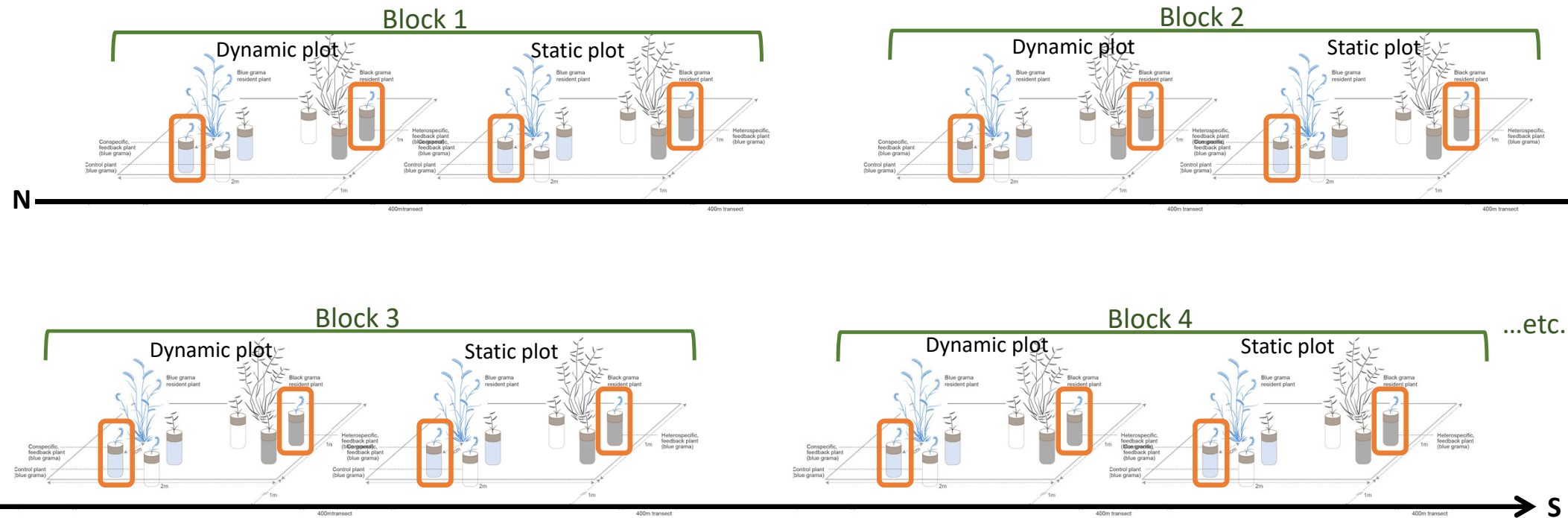
Field experimental design

10 Dynamic (D) plots
10 Static (S) plots
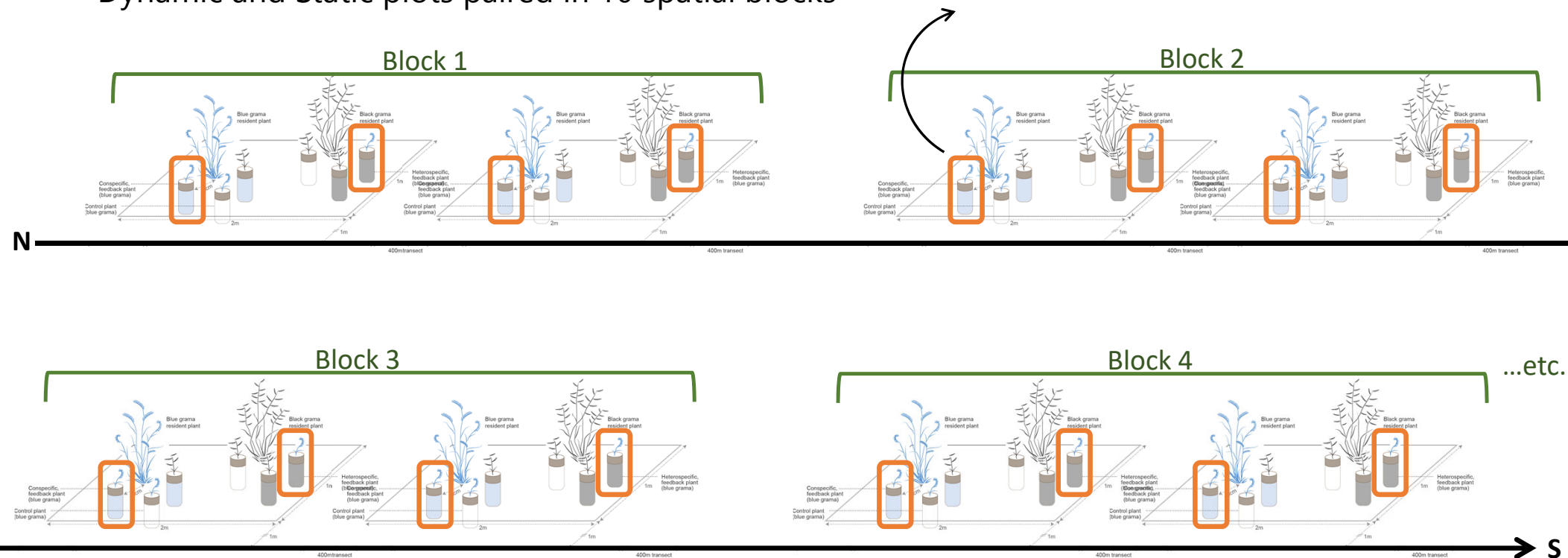Dynamic and Static plots paired in 10 spatial blocks

Field experimental design

10 Dynamic (D) plots
10 Static (S) plots
Dynamic and Static plots paired in 10 spatial blocks

Every single experimental plant has a unique ID (1-120)
Each plant (if alive) measured for size over 15 censuses during 2014-2016

...etc.

Data structure

Historical pattern at that location (dynamic or static)

Type of soil microbe community

Census 1-15

ID	State	PSF	Census	Height	Tiller	logMass.harv	Block
1	D	Away	1	10.6	3	-0.30246	1
5	D	Home	1	10.7	3	-0.30083	1
...	...	...	...	...	...	...	...
113	D	Home	1	4.9	1	-0.57818	10
119	S	Home	1	7.8	1	-0.53099	10
...	...	...	...	...	...	...	...
71	S	Home	15	21.4	4	0.222757	6
83	S	Home	15	5	8	-0.12289	7
95	S	Home	15	9.5	4	-0.88984	8

Question: Do plant-soil feedback effects on plant growth (logMass.harv) differ between locations with dynamic or static historical stability patterns?

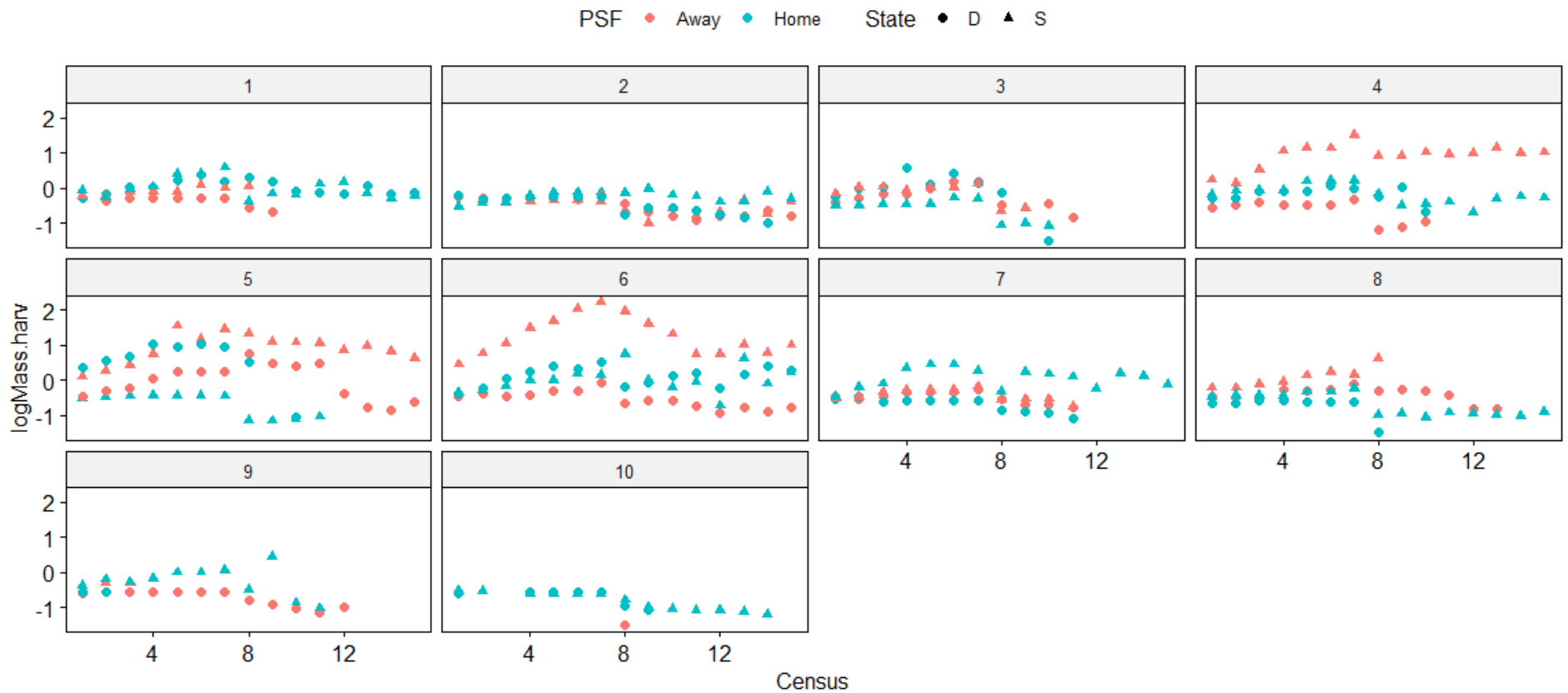| ID	State	PSF	Census	Height	Tiller	logMass.harv	Block
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Visualize random effect of ID (repeated measures)
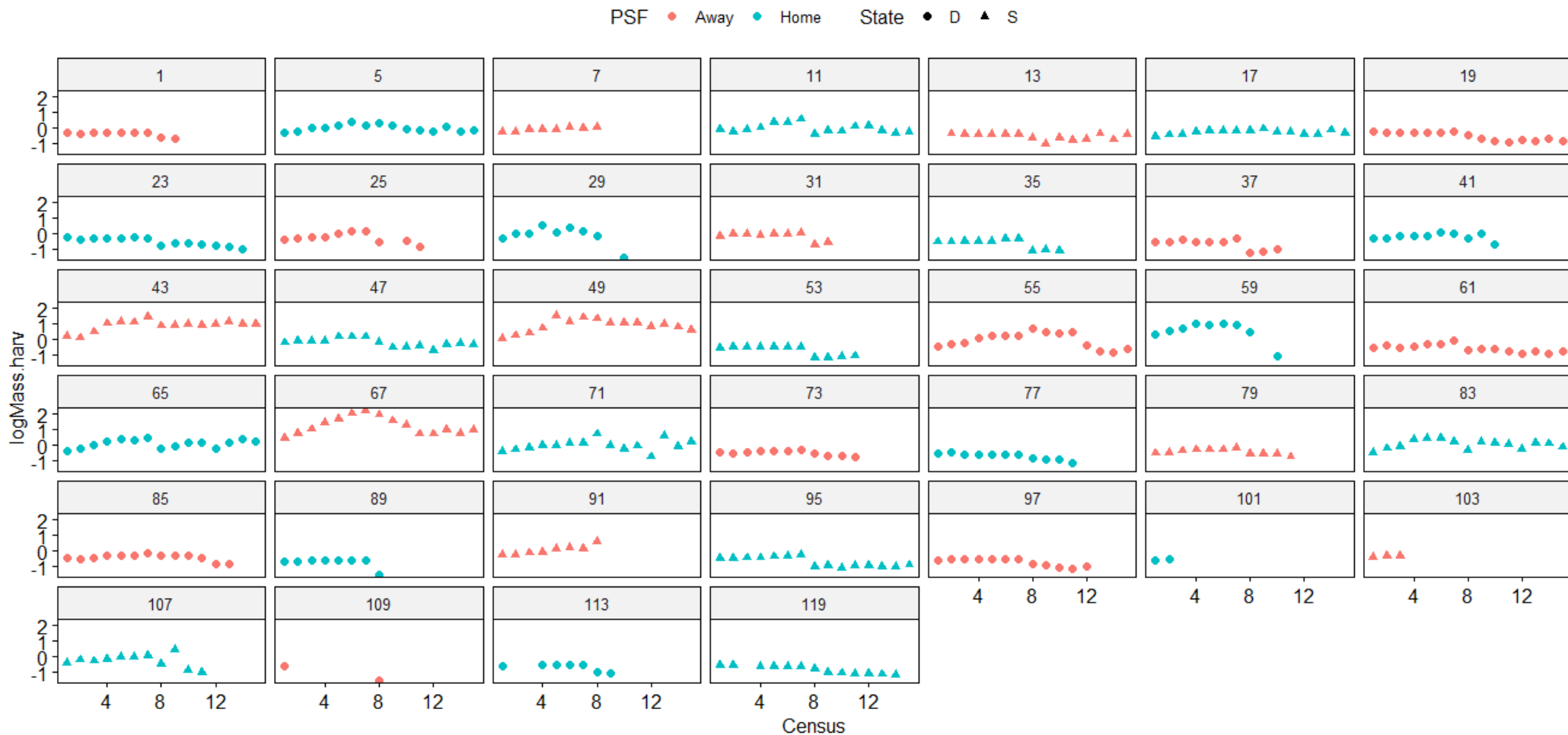
Visualize random effect of Block (spatial heterogeneity)

To R

Recap of what we learned from this example

- Using a mixed model to account for repeated measures and spatial heterogeneity
- Hypothesis testing with more complicated mixed models
- Experiment to understand how nested random effects works, and how it is related to the way random effects levels are coded in the data
- Experiment to understand the difference in coding the "time" variable as fixed vs. random in a repeated measures analysis
- Demonstrate fitting random slopes and intercepts
- Demonstrate GLMM

Methods

"To compare plant growth in heterospecific and conspecific soil environments directly, we examined *ln-transformed estimated allometric biomass* for each species separately throughout the experiment in *repeated-measures analysis*. We used a *mixed model* with the *fixed effects* of *feedback environment (heterospecific or conspecific), community stability, their interaction, and census number,* as well as *plant ID and block* as *random effects* (lmer function in package lme4 [Bates et al. 2015]). Within each community stability type, we tested *pairwise differences* between feedback environments using package lsmeans, with *Tukey adjustment* (Lenth 2016)."

Chung et al. *Ecology* 2019

Results

"in dynamic patches, each plant species performed similarly in conspecific and heterospecific soils over the duration of the field experiment (P = 0.23 and 0.76, respectively; Fig. 2E). In static patches, blue grama [...] plants grew 135% larger in heterospecific soils than in conspecific soils (pairwise comparison t = 2.67, df = 26.4, P = 0.01; Fig. 2F)."

Dynamic patches

Static patches

Chung et al. *Ecology* 2019
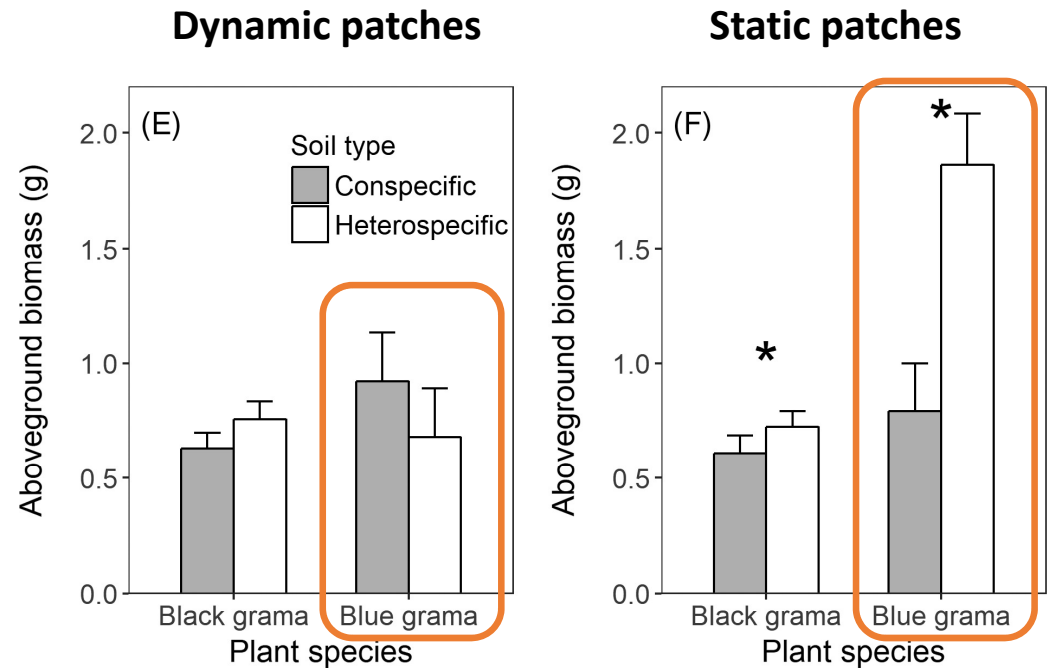
Why is ~(1|ID) the lazy way of doing repeated measures?
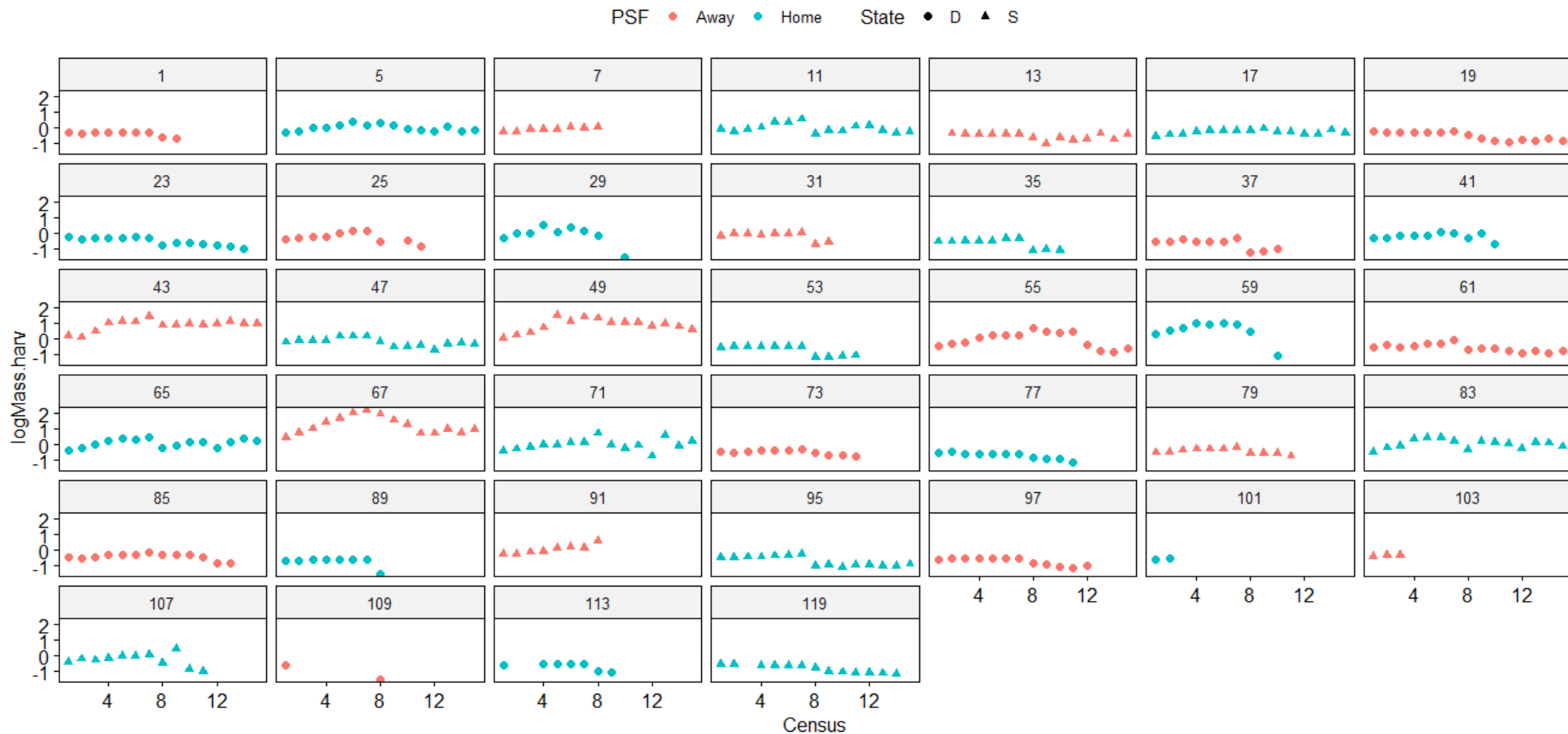
Final project

- Timeline:
  - 4/17 Sunday midnight First draft due (10 pts)
  - 4/24 Sunday midnight Peer review due (5 pts)
  - 5/8 Sunday midnight Final draft due (20 pts)
- Key components:
  1. Study design figure and study question/hypotheses
  2. Analysis methods
  3. Results
  4. Short discussion
  5. Supplemental materials: code and data

Rubric

- **Excellent (18-20/20):** All components present. Effective and clear study design diagram. Clearly-articulated research questions or statistical hypotheses. Well-written analysis methods that contain sufficient detail for replication. Statistical results are presented including essential details in text or in tables, and framed in terms of biology and the goal of the study. Effective figures that communicate main results. Discussion interprets the results in the context of the research conducted with nuance.

- **Good (15-17/20):** All components present. Clear study design diagram. Clearly-articulated research questions or statistical hypotheses. Analysis methods contain sufficient detail for replication. Statistical results are presented including essential details in text or in tables, but may need to take a step back to focus on the biology more. Figures communicate main results, but may have a few small areas for improvement. Discussion interprets the results in the context of the research conducted.

- **Acceptable (11-14/20):** Missing one component. Study design diagram may lack some details. Research questions or statistical hypotheses present. Analysis methods missing some documentation. Statistical results are presented including essential details in text or in tables, but may need to take a step back to focus on the biology more. Figures communicate main results, but may have multiple areas for improvement. Discussion interprets the results in the context of the research conducted.

- **Needs further work (0-10/20):** Missing multiple components. Study design diagram may lack some details. Research questions or statistical hypotheses present. Analysis methods missing important documentation or do not actually answer the research questions or test the hypotheses. Statistical results are presented but missing important details such as degrees of freedom. Figures may have multiple areas for improvement. Discussion re-iterates results without further interpretation.