

# forestecology package for modeling interspecies competition between trees

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## **Abstract**

Move abstract below here after completed.

*Keywords:* forest ecology, competition, R, Rstats, tidyverse, sf, cross-validation,

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# 1 Abstract (350 words)

1. Set the context for and purpose of the work: The scientific question/problem and the desiderata

- (Eventually) modularly fitting models for interspecific competition and assessing them using spatial crossvalidation
- Leverage ForestGEO protocols providing standardization

2. Indicate the approach and the methods: Use tidyverse, simple features, and tidy-models packages.

- tidyverse: as stated in tidy tools manifesto: standadized data structures, functional programming with pipe, designed for humans
- sf: tidyverse-friendly package that makes wrangling and visualizing spatial data much easier
- tidymodels: given our spatial-crossvalidation, use tidymodels framework is a collection of packages for modeling and machine learning using tidyverse principles
- Dave: hmm, I think here we might need to mention the methods we implement. Something like, the package provides functions to specific a linear, bayesian neighborhood competition model of growth, then fit the model, and compare competing models with spatial cross validation. Or somethign like that.

3. Outline the main results: We replicate from scratch the figure in PLOSONe paper using Big Woods data, conduct similar analysis for SCBI data.

- Code would've been way more complicated in base.
- We don't have to worry about how the component functions work, only that sequence/converyor belt is correct and output is correct.
- Scientist is abstracted away from ugly programming details.

4. Identify the conclusions and wider implications:

- New scientific conclusions from SCBI data
- Modularly switch out our bayesian `lm()` functions to anything you want.
- this can serve as blue print for other modeling situations.

## 2 Introduction

Repeat-censused forest plots offer excellent data to test neighborhood models of tree competition Allen & Kim (2020) Canham et al. (2006) Uriarte et al. (2004). Here we describe an R package, `forestecology`, to do that. This package implements the methods in Allen & Kim (2020). It provides: a convenient way to specify and fit models of tree growth based on neighborhood competition; a spatial cross validation method to test and compare model fits Roberts et al. (2017); and an ANOVA-like method to assess whether the competitor identity matters in these models. The model is written to work with ForestGEO plot data Anderson-Teixeira et al. (2015), but we envision that it could easily be modified to work with data from other forest plots, e.g. the US Forest Service Forest Inventory and Analysis plots Smith (2002).

## 3 Example

We demonstrate the `forestecology` package’s features on two data sets, both based on inventory censuses of two sites from the Smithsonian Institution’s ForestGEO international network of 72 long-term forest dynamics research sites Anderson-Teixeira et al. (2015). First, the Michigan Big Woods Forest Dynamics Plot located at the Edwin S. George Reserve in Pinckney, MI, USA. The 23 ha plot is situated in mature oak-hickory forest. The canopy is dominated by white oak (*Quercus alba*), northern red oak (*Q. rubra*), black oak (*Q. velutina*), shagbark hickory (*Carya ovata*) and pignut hickory (*C. glabra*) Allen et al. (2020). In the example below, we will preface any data frames from this plot in with `bw_`.

Second, the Smithsonian Conservation Biology Institute (SCBI) large forest dynamics plot, located at the Smithsonian’s National Zoo and Conservation Biology Institute in Front Royal, VA, USA. The 25.6 ha (640 x 400 m) plot is located at the intersection of three of the major physiographic provinces of the eastern US: the Blue Ridge, Ridge and Valley, and Piedmont provinces and is adjacent to the northern end of Shenandoah National Park. The forest type is typical mature secondary eastern mixed deciduous forest, with a canopy dominated by tulip poplar (*Liriodendron tulipifera*), oaks (*Quercus* spp.), and

hickories (*Carya* spp.), and an understory composed mainly of spicebush (*Lindera benzoin*), paw-paw (*Asimina triloba*), American hornbeam (*Carpinus caroliniana*), and witch hazel (*Hamamelis virginiana*) Bourg et al. (2013). In the example below, we will preface any data frames from this plot in with `scbi_`.

The code that generates Figures are included in the supplementary materials.

We load all the necessary packages.

```
library(forestecology)

# Load tidyverse packages:
library(tidyverse)
library(lubridate)

# Load spatial packages:
library(blockCV)
library(sf)
library(sfheaders)

# Load other packages:
library(snakecase)
library(yardstick)
```

### 3.1 Preprocess census data

We start by preprocessing the census data for both sites. While ForestGEO data protocols ensure a high degree of standardization between site, minor variations still exist Anderson-Teixeira et al. (2015). While the Big Woods data comes pre-loaded in the `forestecology` package, we load the SCBI data as they are saved in .csv files in the SCBI-ForestGEO-Data repository on GitHub Gonzalez-Akre et al. (2020). In both cases, we load the census data as R as “tibble” data frames thereby ensuring a standardized input/output format that can be used across all `tidyverse` packages Wickham et al. (2019).

Furthermore, we ensure that the different variables have the correct names, types (`dbl`, `data`, `factor`).

### 3.1.1 Big Woods

We load census data from 2008 and 2014 saved in the package, then merge species data (genus, species, linnean classification, family, etc).

```
data(bw_census_2008, bw_census_2014, bw_species)

# Append additional species data
bw_census_2008 <- bw_census_2008 %>%
  left_join(bw_species, by = "sp") %>%
  select(-c(genus, species, latin))
```

### 3.1.2 SCBI

We load census data from 2008 and 2014 from `.csv` files saved from GitHub on November 20, 2020. Furthermore, we perform two additional pre-processing steps. First, in order to speed up computation for purposes of this example, we only consider a 9 ha subsection of the 25.6 ha of the SCBI site: `gx` from 0–300 instead of 0–400 and `gy` from 300–600 instead of 0–640. Second, in order to standardize comparisons between Big Woods and SCBI, we convert the units of `dbh` from mm to cm.<sup>1</sup>

```
scbi_2013 <- read_csv("scbi.stem2.csv") %>%
  select(treeID, stemID, sp, ExactDate, gx, gy, dbh, codes, status) %>%
  mutate(
    date = ExactDate,
    dbh = as.numeric(dbh),
    date = mdy(date)
```

---

<sup>1</sup>A rule of thumb to ascertain if `dbh` is in mm or cm is to verify if the smallest non-zero and non-missing measurement is 1 or 10. If the former, then cm. If the later, then mm. This is because ForestGEO protocols state that only trees with `dbh` greater or equal to 1cm should be included in censuses.

```

) %>%
filter(gx < 300, between(gy, 300, 600)) %>%
mutate(dbh = dbh / 10)

scbi_2018 <- read_csv("scbi.stem3.csv") %>%
select(treeID, stemID, sp, ExactDate, gx, gy, dbh, codes, status) %>%
mutate(
  date = ExactDate,
  dbh = as.numeric(dbh),
  date = mdy(date)
) %>%
filter(gx < 300, between(gy, 300, 600)) %>%
mutate(dbh = dbh / 10)

```

## 3.2 Compute annual growth

For each plot we then compute average annual growth between the two censuses using the `compute_growth()` function. This function takes the two census data frames as well as a character indicating which variable in both data frames uniquely identifies each stem. This function returns a single data frame that includes a numerical variable `growth` reflecting the average annual dbh growth (in cm) of all trees alive at both time points. Furthermore, variables that (in theory) remain unchanged between censuses appear only once, such as location variables `gx` and `gy`; as well as species-related variables. Variables that should change between censuses are suffixed with 1 and 2 indicating the earlier and later censuses, such as `dbh1/dbh2` and `codes1/codes2`. Here the resulting data frames are named with some variation of `growth_df`.

After computing the average annual growth for each tree, we ensure to convert all variables denote species from type character to factors; this is to ensure that issues of rare species being accounted for in both training and test sets in our upcoming cross-validation step (see Section REF)

### 3.2.1 Big Woods

In the case of Big Woods data, we first remove all trees that were re-sprouts in the later (2014) census. Additionally, we have included two classification of tree species: `species` and `family`. To illustrate model comparison, we test competition models in which individuals are grouped by species and by family.

```
bw_census_2014 <- bw_census_2014 %>%  
  filter(!str_detect(codes, "R"))  
  
bw_growth_df <-  
  compute_growth(bw_census_2008, bw_census_2014, id = "treeID") %>%  
  # Convert all variables denoting species to factors  
  mutate(  
    sp = sp %>% to_any_case() %>% as.factor(),  
    species = sp,  
    family = as.factor(family),  
    trait_group = as.factor(trait_group)  
  ) %>%  
  # Drop unnecessary variables  
  select(-stemID)
```

### 3.2.2 SCBI

```
scbi_growth_df <-  
  compute_growth(scbi_2013, scbi_2018, "stemID") %>%  
  # Convert all variables denoting species to factors  
  mutate(sp = as.factor(sp))
```

### 3.2.3 Comparison

DAVE: I THINK THIS FIGURE IS UNNEEDED. COULD BE REMOVED FOR SPACE REASONS. Figure 1 displays histograms comparing the distribution of average annual

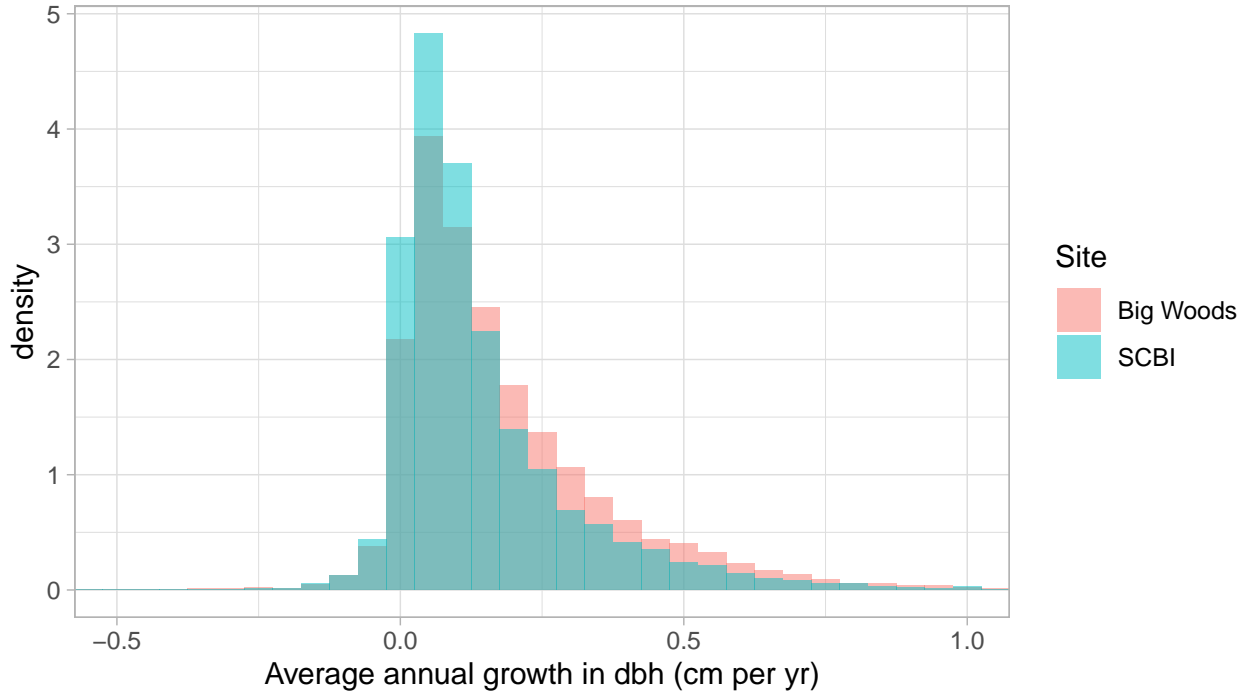


Figure 1: Distribution of average annual growth in DBH for both sites.

107 growth at both sites. Observe that average annual growth appears higher at the Big  
 108 Woods site.

### 109 3.3 Add spatial information

110 We now encode spatial information to the `growth_df` data frames. First, in order to control  
 111 for study region edge effects, we add “buffers” to the periphery of the study region (cite  
 112 Waller?). Our model of interspecific competition relies on a spatial definition of who the  
 113 competitor trees are for focal trees of interest. Since certain explanatory variables such as  
 114 basal area are cumulative, we must ensure that all trees being modeled are not biased to  
 115 have different neighbor structures. This is a particular concern for trees at the boundary  
 116 of study regions, which will not have the same number of neighbors as trees in the internal  
 117 part of the study region.

118 Second, our ultimate method for model assessment will rely on estimates of model error  
 119 as generated by cross-validation. Conventional cross-validation schemes assign observations  
 120 to folds by resampling individual observations at random. However, underlying this scheme



is an assumption that the observations are independent. In the case of forest census data, observations exhibit spatial autocorrelation, and thus this dependence must be incorporated in our resampling scheme in spatial cross-validation Roberts et al. (2017) Pohjankukka et al. (2017) We will therefore associate portions of the study region to spatial folds.

To these two ends, we define two constants, both of which are in the same units as the `gx` and `gy` variables (most often meters).

```
max_dist <- 7.5
cv_fold_size <- 100
```

The first constant is `max_dist` which defines the maximum distance for a tree's competitive neighborhood. Trees within this distance of each other are assumed to compete while those farther than this distance apart do not. Put differently, all trees within `max_dist` of a focal tree will be considered its competitors (see below). Other studies have estimated the value of `max_dist`; we use an average of estimated values Canham et al. (2004), Uriarte et al. (2004), Tatsumi et al. (2013), Canham et al. (2006).

Furthermore, `max_dist` will define the size of all buffers considered, which will be encoded as a binary variable `buffer` as computed by the `add_buffer_variable()` function. This function takes as input the main `growth_df` data frame, the `size` of the buffer which we set as `max_dist`, and the boundary of the study region encoded as a simple features polygon Pebesma (2018). DESCRIBE SF PACKAGE. In the Big Woods example below we will use a pre-loaded simple features polygon while for the SCBI example we present example code on how to manually construct one.

The second constant is `cv_fold_size` which defines the length and width of the spatial folds (note that for now the spatial folds are restricted be squares). We will then use this constant to associate each observed tree to one of  $k$  folds in the respective study region. In the Big Woods example below we will use the `blockCV` R package that has implemented spatial cross-validation while for the SCBI we will do this manually Valavi et al. (2019)

### 3.3.1 Big Woods

First, we indicate which trees are part of the buffer. This necessitates information about the study region boundary. In this case, we use a `sf_polygon` object `bw_study_region`

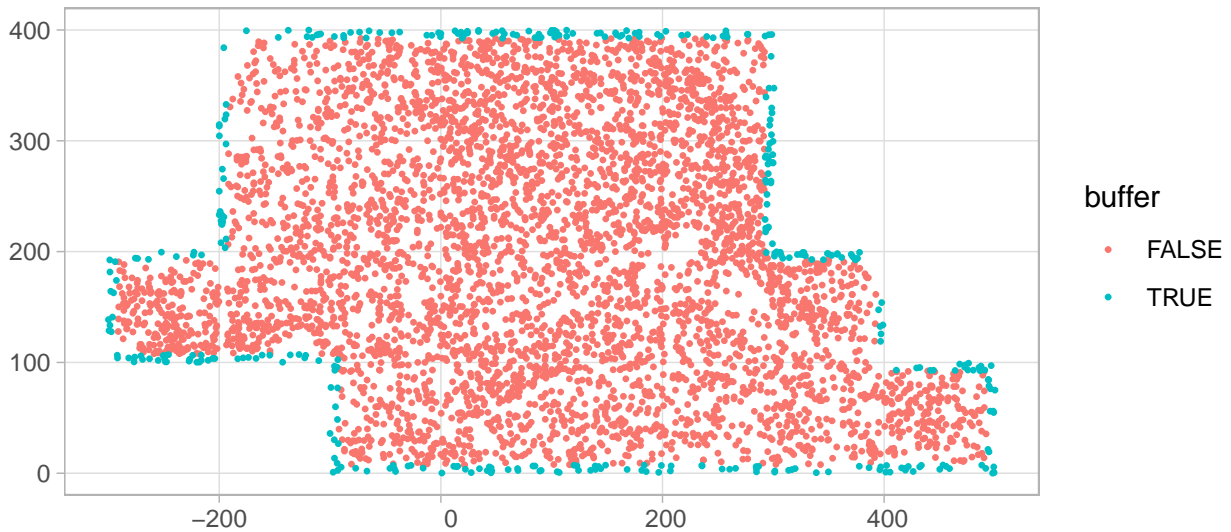


Figure 2: Buffer region for Big Woods study region.

148 which comes pre-loaded in the `forestecology` packages. After loading `bw_study_region`,  
 149 we illustrate the results of the `add_buffer_variable()` function in Figure 2. Trees on the  
 150 periphery denote with lighter colors are part of the buffer and will not be considered as  
 151 “focal” trees of interest going forward; they will only be considered as competitor trees.

```
data(bw_study_region)

bw_growth_df <- bw_growth_df %>%
  add_buffer_variable(direction = "in", size = max_dist,
                     region = bw_study_region)

ggplot() +
  geom_sf(data = bw_growth_df %>% sample_frac(0.2),
         aes(col = buffer), size = 0.5)
```

152 Second, we associate each tree to spatial cross validation folds. In this case, we use the  
 153 `spatialBlock()` function from the `blockCV` package to define the spatial grid which

154 THIS IS A MESS. We use the Valavi et al. (2019), whose elements will act as the folds  
 155 in our leave-one-out (by “one” we mean “one grid block”) cross-validation scheme. The  
 156 upshot here is we add `foldID` to `growth_df` which identifies which fold each individual is

157 in, and the creation of a `cv_grid_sf` object which gives the geometry of the cross validation  
158 grid.

```
set.seed(76)
bw_spatialBlock <- spatialBlock(
  speciesData = bw_growth_df, theRange = cv_fold_size, k = 28, xOffset = 0.5,
  yOffset = 0, verbose = FALSE, showBlocks = FALSE
)
```

## 159 4 Add foldID to each tree

```
bw_growth_df <- bw_growth_df %>%
  mutate(foldID = bw_spatialBlock$foldID)
```

```
# Visualize grid. Why does fold 19 repeat?
ggplot() +
  geom_sf(data = bw_spatialBlock$blocks %>% st_as_sf()) +
  geom_sf(data = bw_growth_df %>% sample_frac(0.2),
    aes(col = factor(foldID)), size = 0.1, show.legend = FALSE) +
  geom_sf_text(data = bw_spatialBlock$blocks %>% st_as_sf(),
    aes(label = folds))
```

## 160 5 Remove empty folds

```
bw_growth_df <- bw_growth_df %>%
  filter(!foldID %in% c(19, 23, 21, 17, 8, 19)) %>%
  mutate(foldID = as.character(foldID))
```

161 Separately, we save the spatial cross-validation grid as an `sf_polygon` object `bw_cv_grid`

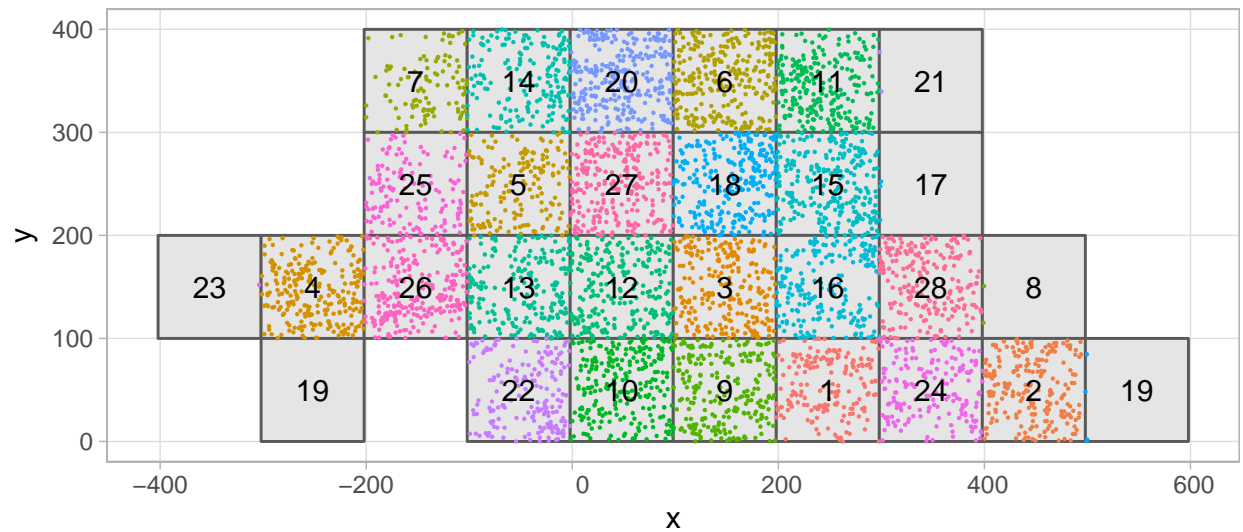


Figure 3: Inspect blocks closely.

```
bw_cv_grid <- bw_spatialBlock$blocks %>%
  st_as_sf()
```

### 5.0.1 SCBI

First, we indicate which trees are part of the buffer. In this case however we manually define the study region boundary based on the subregion we defined in Section 3.1.2 and create an `sf_polygon` object using the `sf_polygon()` function from the `sfheaders` package. Figure 4 displays the resulting buffer trees.

```
scbi_study_region <- tibble(
  x = c(0, 300, 300, 0, 0),
  y = c(300, 300, 600, 600, 300)
) %>%
  sf_polygon()

scbi_growth_df <- scbi_growth_df %>%
  add_buffer_variable(direction = "in", size = max_dist,
    region = scbi_study_region)
```

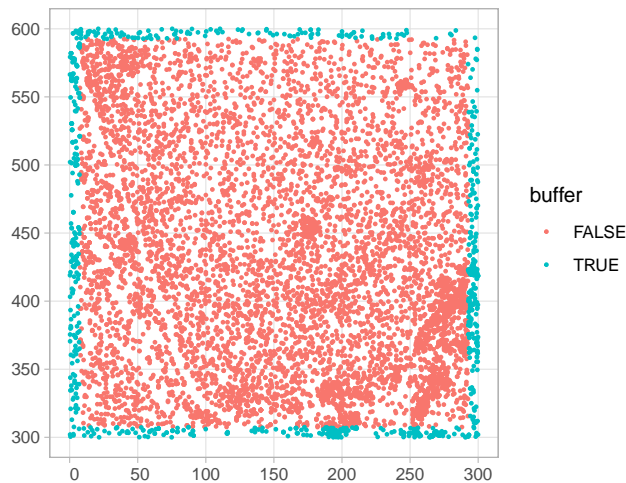


Figure 4: Buffer region for SCBI study region.

```
ggplot() +  
  geom_sf(data = scbi_growth_df, aes(col = buffer), size = 0.5)
```

167      Second, we associate each tree to spatial cross validation folds. In this case we manually  
168      define a spatial crossvalidation grid. Figure 5 displays the resulting cross-validation folds  
169      along with the buffer from Figure 4.

170      Here we manually define the spatial cross-validation grid as an `sf_polygon` object

171      `scbi_cv_grid`

```
fold1 <- rbind(c(0, 300), c(150, 300), c(150, 600), c(0, 600)) %>%  
  sf_polygon() %>%  
  mutate(folds = 1)  
fold2 <- rbind(c(150, 300), c(300, 300), c(300, 600), c(150, 600)) %>%  
  sf_polygon() %>%  
  mutate(folds = 2)  
scbi_cv_grid <- bind_rows(fold1, fold2)
```

```
scbi_spatialBlock <- spatialBlock(  
  speciesData = scbi_growth_df, k = 2, verbose = FALSE, showBlocks = FALSE,  
  # Note new arguments:
```

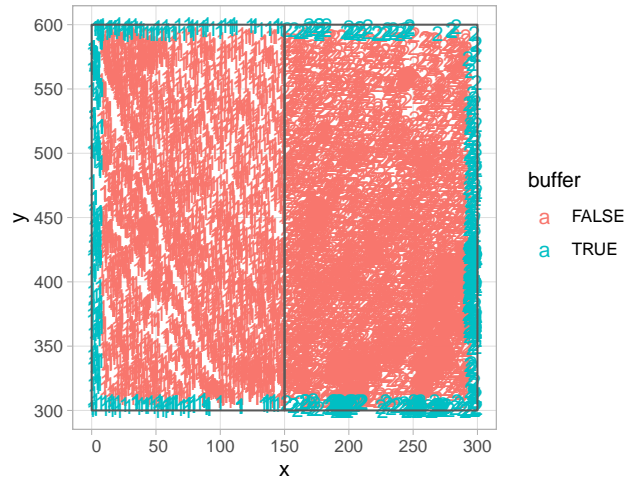


Figure 5: Buffer region for SCBI study region.

```

selection = "systematic", blocks = scbi_cv_grid
)

# Add foldID to each tree
scbi_growth_df <- scbi_growth_df %>%
  mutate(foldID = scbi_spatialBlock$foldID)

ggplot() +
  geom_sf_text(data = scbi_growth_df,
              aes(label = foldID, col = buffer)) +
  geom_sf(data = scbi_cv_grid, fill = "transparent")

```

## 5.1 Define focal versus competitor trees

Next we define `focal_vs_comp` data frames which connects each focal tree in the `growth_df` data frames to the trees in its competitive neighborhood range as defined by the `max_dist` constant. So for example, if `growth_df` consisted of two focal trees with two and three neighbors with `max_dist` respectively, `focal_vs_comp` would be a data frame of 5 rows connecting each focal tree to its competitors. The `create_focal_vs_comp()` function makes this connection taking as inputs the `growth_df` data frame; the `max_dist` constant defining

179 competitive range; `cv_grid_sf`, giving the cross validation grid; and the `id` variable.

### 180 5.1.1 Big Woods

```
focal_vs_comp_bw <- bw_growth_df %>%  
  create_focal_vs_comp(max_dist, cv_grid_sf = bw_cv_grid, id = "treeID")
```

181 TODO: Figure out how to show this data frame's contents.

### 182 5.1.2 SCBI

```
focal_vs_comp_scbi <- scbi_growth_df %>%  
  create_focal_vs_comp(max_dist, cv_grid_sf = scbi_cv_grid, id = "stemID")
```

183 TODO: Figure out how to show this data frame's contents.

## 184 5.2 Fit model and make predictions

185 Next we fit the following linear model to the dbh of each focal tree. Let  $i = 1, \dots, n_j$  index  
186 all  $n_j$  trees of “focal” species group  $j$ ; let  $j = 1, \dots, J$  index all  $J$  focal species groups;  
187 and let  $k = 1, \dots, K$  index all  $K$  “competitor” species groups. We modeled the growth in  
188 diameter per year  $y_{ij}$  (in centimeters per year) of the  $i^{\text{th}}$  tree of focal species group  $j$  as a  
189 linear model  $f$  of the following covariates  $\vec{x}_{ij}$

$$y_{ij} = f(\vec{x}_{ij}) + \epsilon_{ij} = \beta_{0,j} + \beta_{\text{DBH},j} \cdot \text{DBH}_{ij} + \sum_{k=1}^K \lambda_{jk} \cdot \text{BA}_{ijk} + \epsilon_{ij}$$

190 We estimate the model's parameters using Bayesian linear regression implemented in  
191 the `fit_bayesian_model()` function. TODO: define all parameters

192 For this linear model's case, there exists a closed form solution as described here. As  
193 such, the `fit_bayesian_model()` function using matrix algebra to obtain all parameter  
194 estimates, rather than computationally expensive Monte Carlo approximations. The inputs  
195 to this function are a `focal_vs_comp` data frame, `prior_param` a list of priors, and a boolean  
196 flag `run_shuffle` on whether or not to run competitor-species identity permutations which

197 we will demonstrate below on the Michigan Big Woods data. This function returns the  
198 posterior means of all parameters.

199 Using these posterior means, we then use the posterior predictive distribution to obtain  
200 fitted/predicted values  $\hat{y}$  of the dbh for each focal tree using the `predict_bayesian_model()`.  
201 These  $\hat{y}$  can then be compared to the observed  $y$  dbh's to compute the root mean-square  
202 error, a measure of a model's predictive error which has the same units as the observed  
203 data  $y$ .

### 204 5.2.1 Big Woods

205 For the Michigan Big Woods data we present two use cases of the model fitting and pre-  
206 diction scheme. The first use case is the simplest where we assess the fit of the model using  
207 root mean squared error. The second use case then answers the question of whether species  
208 competitor identity matters using permutation test.

209 For the first use case, we fit the linear model specified in Equation XXX to our data  
210 frame of type `focal_vs_comp`. This input/outputs of the `fit_bayesian_model()` function  
211 are lists of the prior/posterior means of parameters of the linear regression specified in  
212 XXX. Generally speaking, there are two classes of regression parameters:  $\beta$  main effects  
213 and  $\lambda$  competitive effects. In the upcoming Section 5.4, we will present code visualizing  
214 this posterior distributions.

```
posterior_param_bw <- focal_vs_comp_bw %>%  
  fit_bayesian_model(prior_param = NULL)
```

215 This output of posterior parameters for the specified competition model are then used  
216 along with the posterior predictive distribution encoded in `predict_bayesian_model()` to  
217 return predicted growths for each individual tree. We join these predicted growths to the  
218 original growth data frame.

```
predictions <- focal_vs_comp_bw %>%  
  predict_bayesian_model(posterior_param = posterior_param_bw) %>%  
  right_join(bw_growth_df, by = c("focal_ID" = "treeID"))
```



219 We then use the `rmse()` function from the `yardstick` package to obtain the root mean  
220 squared error of the observed versus fitted values of growth.

```
predictions %>%  
  yardstick::rmse(truth = growth, estimate = growth_hat) %>%  
  pull(.estimate)  
## [1] 0.148145
```

221 The second use case is near identical to the first, but with a small change in the code  
222 to test whether the identity of the competitor matters. By adding a `run_shuffle = TRUE`  
223 argument to `fit_bayesian_model()`, for each focal tree its competitor trees' species identity  
224 will be “shuffled” randomly much like in a permutation test. By shuffling these species  
225 labels we are effectively fitting the model under a null model that competitor species identity  
226 does not matter. If the “shuffled” RMSE's are consistently lower than the unshuffled RMSE  
227 corresponding to the observed data, then we have evidence to suggest that competitor  
228 identity matters to competitive interactions.

```
posterior_param_bw_shuffle <- focal_vs_comp_bw %>%  
  fit_bayesian_model(prior_param = NULL, run_shuffle = TRUE)
```

```
predictions_shuffle <- focal_vs_comp_bw %>%  
  predict_bayesian_model(posterior_param = posterior_param_bw_shuffle) %>%  
  right_join(bw_growth_df, by = c("focal_ID" = "treeID"))
```

```
predictions_shuffle %>%  
  rmse(truth = growth, estimate = growth_hat) %>%  
  pull(.estimate)  
## [1] 0.1505383
```

229 The RMSE is fact lower for the non-shuffled version, indicative of a better model fit.  
230 This gives support for the idea that competitor identity does matter for competitive inter-  
231 actions. In Allen & Kim (2020) we run this shuffle a large number of times to construct a  
232 full permutation distribution to show that this difference is robust to resampling variation.

### 5.2.2 SCBI

In the case of the SCBI data, we once again perform the same model fitting and computing of fitted growths as with the Big Woods data, but this time we map the residuals of the observed minus fitted values to look for spatial patterns.

```
posterior_param_scbi <- focal_vs_comp_scbi %>%
  fit_bayesian_model(prior_param = NULL, run_shuffle = FALSE)

scbi_growth_df_noCV <- focal_vs_comp_scbi %>%
  predict_bayesian_model(posterior_param = posterior_param_scbi) %>%
  right_join(scbi_growth_df, by = c("focal_ID" = "stemID"))

scbi_growth_df_noCV %>%
  rmse(truth = growth, estimate = growth_hat) %>%
  pull(.estimate)
## [1] 0.1280644
```

In Figures 6 and 7 we present the residuals.

## 5.3 Run spatial cross-validation

The model fits and predictions in Section 5.2 all suffer from a common failing: they use the same data to both fit the model and to assess the model's performance using the RMSE. As argued by Roberts et al. (2017), this can lead to overly optimistic assessments of model quality as the models can be overfit, in particular in situations where spatial-autocorrelation is present. To mitigate the effects of such overfitting, we use a spatially block cross-validation algorithm implemented in the `run_cv()`. This function at its core uses the same model fitting implemented in the `fit_bayesian_model()` function, however trains the model on  $k - 1$  spatial folds of the train and returns fitted values for the test data. Recall that the spatial blocking scheme was encoded in Section 3.3.

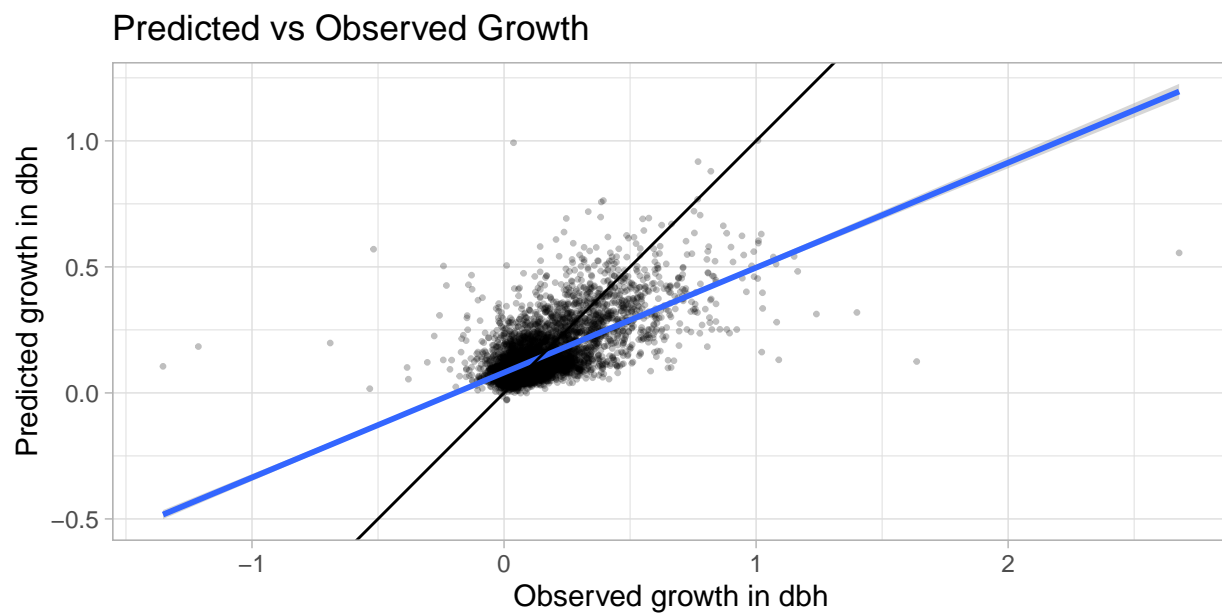


Figure 6: Predicted versus observed growth.

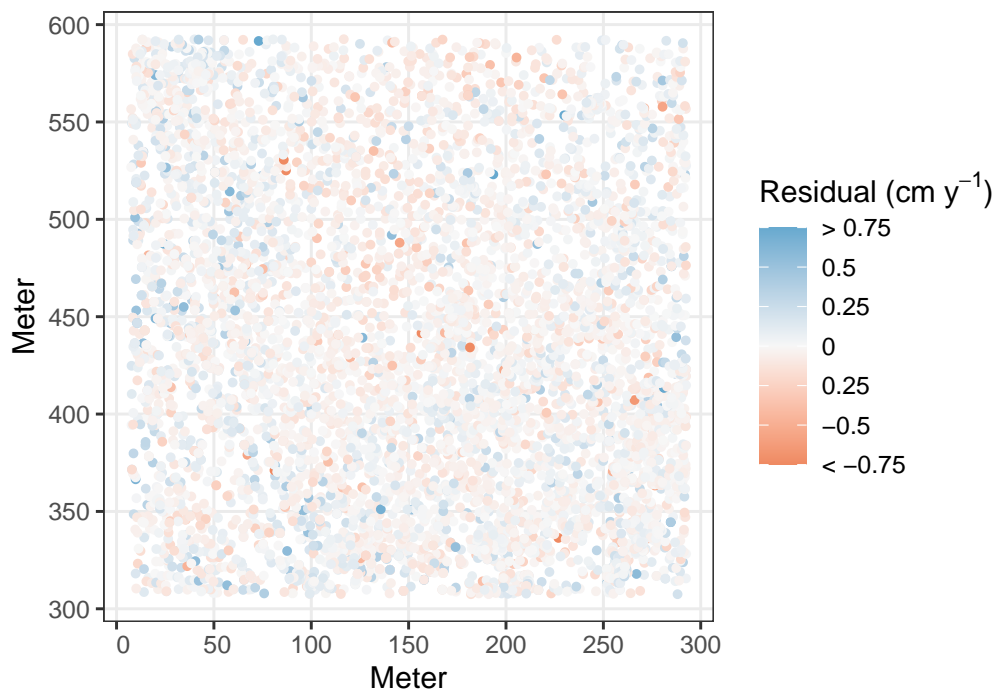


Figure 7: Spatial distribution of residuals for model applied to SCBI data.

### 5.3.1 Big Woods

Applying this spatially cross-validated model fit yields an RMSE is higher than that when the model is fit without cross validation. In other words, our model fits in 5.2 were overly optimistic in the model's fitting power, whereas a cross-validated results yield an estimate that is closer to the truth. See Allen & Kim (2020) for more discussion of this.

```
cv_bw <- focal_vs_comp_bw %>%  
  run_cv(max_dist = max_dist, cv_grid = bw_cv_grid) %>%  
  right_join(bw_growth_df, by = c("focal_ID" = "treeID"))  
  
cv_bw %>%  
  rmse(truth = growth, estimate = growth_hat) %>%  
  pull(.estimate)  
## [1] 0.1533511
```

### 5.3.2 SCBI

Observe once again that this RMSE is much higher than that for the above SCBI model fit without cross-validation.

```
cv_scbi <- focal_vs_comp_scbi %>%  
  run_cv(max_dist = max_dist, cv_grid = scbi_cv_grid) %>%  
  right_join(scbi_growth_df, by = c("focal_ID" = "treeID"))  
  
cv_scbi %>%  
  rmse(truth = growth, estimate = growth_hat) %>%  
  pull(.estimate)  
## [1] 0.1494775
```

## 5.4 Visualize posterior distributions

Lastly, we return to the model fits from Section 5.2 and present tools to visually explore the posterior distributions of all parameters in our model. There are two main groups of parameters to consider. The  $\beta$  coefficients tell us about how fast each species grows and how this depends on DBH while the full matrix of  $\lambda$  values describe the competitive effects between pairs of species. There is a rich literature on this matrix (cite).

DO WE NEED TO DESCRIBE MECHANICS? Because of the structure of the `bw_fit_model` object we cannot simply draw these curves based on the posterior distribution. `bw_fit_model()` gives the parameters *compared* to a baseline. This is not of direct interest. So to display these parameters, as we care about them, we have to sample from the baseline distribution and from the comparison one to get the posterior distribution of interest.

### 5.4.1 Big Woods

Here we re-run the model fit to the Big Woods data from Section 5.2, but this time use “family” as the group for comparison which has. This makes the posterior distributions easier to follow. Also, surprisingly, grouping by family performed just as well as grouping by species Allen & Kim (2020). First we re-run `create_focal_vs_comp()` and `fit_bayesian_model()` with no permutation shuffling with the grouping variable as family.

```
focal_vs_comp_bw <- bw_growth_df %>%  
  mutate(sp = family) %>%  
  create_focal_vs_comp(max_dist = max_dist, cv_grid_sf = bw_cv_grid,  
                      id = "treeID")  
  
posterior_param_bw <- focal_vs_comp_bw %>%  
  fit_bayesian_model(prior_param = NULL, run_shuffle = FALSE)
```

Now the posterior parameter outputs of `fit_bayesian_model()` are passed to `plot_bayesian_model_pa` to generate visualizations of the posterior parameters. These visualizations are displayed in Figure 5 of Allen & Kim (2020). For simplicity we only plot a subset of the species families.

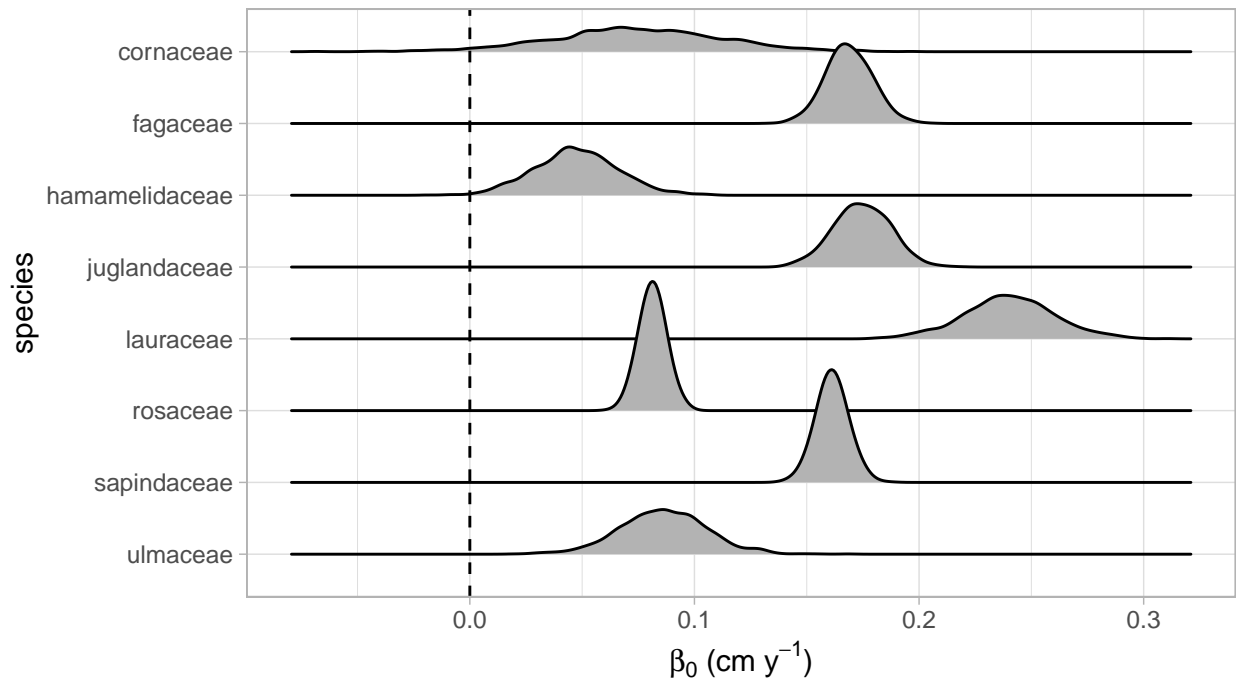


Figure 8: Posterior distribution of beta0.

```
posterior_plots_bw <- plot_bayesian_model_parameters(
  posterior_param = posterior_param_bw,
  sp_to_plot = c("cornaceae", "fagaceae", "hamamelidaceae", "juglandaceae",
    "lauraceae", "rosaceae", "sapindaceae", "ulmaceae")
)
```

277 The output is a list with three plots stored. Figure 8 The element `beta_0` gives the  
 278 baseline growth intercept  $\beta_0$ , i.e., how fast an individual of each group grows independent  
 279 of DBH).

```
posterior_plots_bw[["beta_0"]]
```

280 Figure 9 Next `beta_dbh` gives the slope for DBH slope  $\beta_{dbh,i}$  for each group.

```
posterior_plots_bw[["beta_dbh"]]
```

281 Finally Figure 10 `lambda` gives the competition coefficients  $\lambda$ .

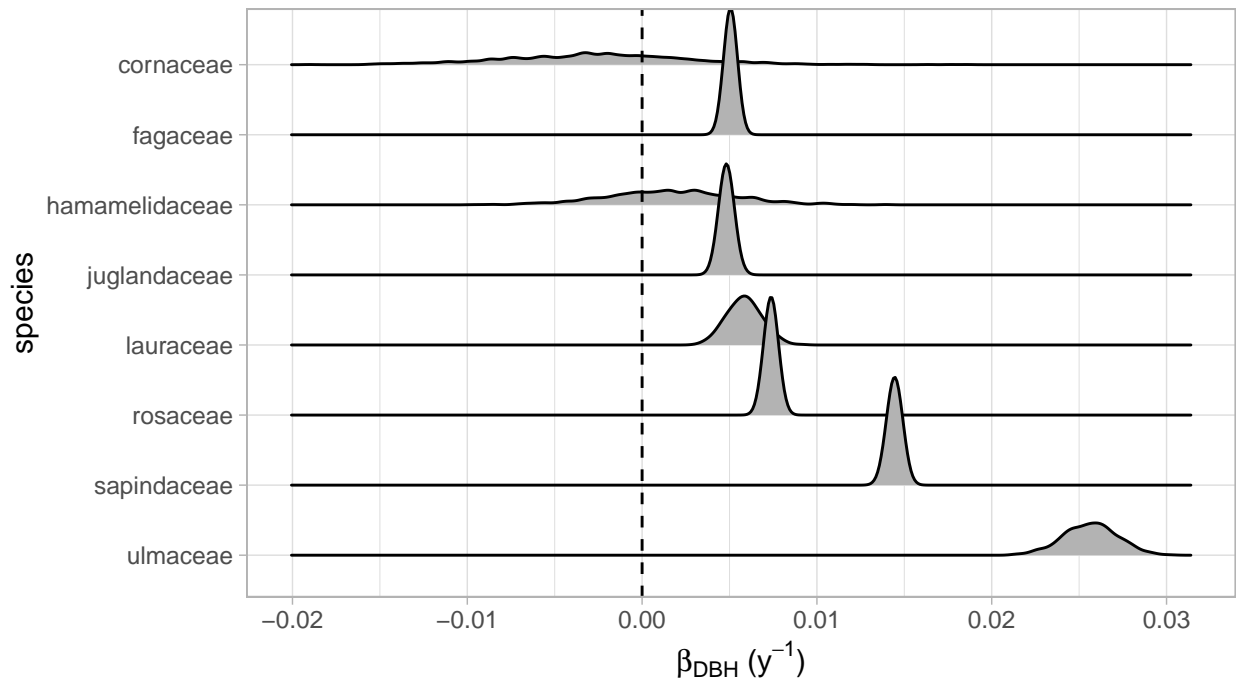


Figure 9: Posterior distribution of betadbh.

```
posterior_plots_bw[["lambda"]]
```

## 5.4.2 SCBI

We revisit the posterior parameters for the SCBI from Section {model-fit-predict}, but this time only focus on the  $\lambda$  competition coefficients.

```
posterior_plots_scbi <- plot_bayesian_model_parameters(
  posterior_param = posterior_param_scbi,
  sp_to_plot = c("quru", "litu", "cagl", "cato")
)
```

```
posterior_plots_scbi[["lambda"]]
```

Add explanation here.

HEY BERT PICK IT UP HERE

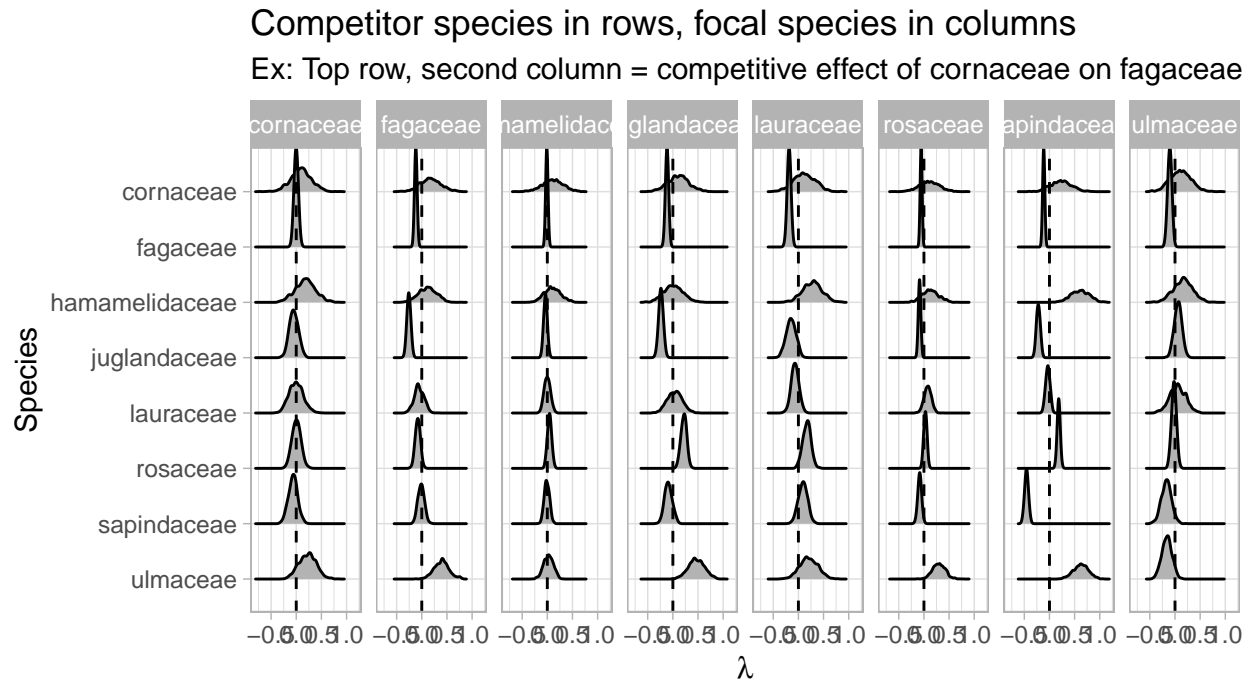


Figure 10: Posterior distribution of lambda's for Big Woods.

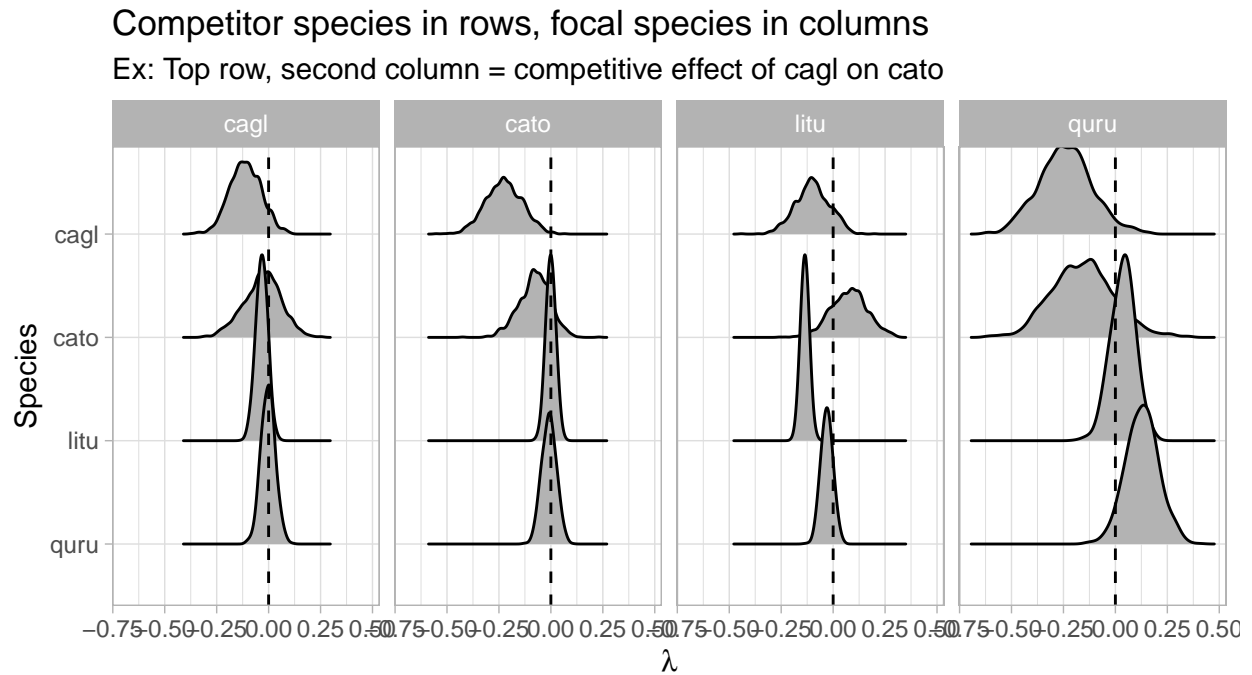


Figure 11: Posterior distribution of lambda's for SCBI.



## 6 Discussion

## 7 Acknowledgments

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