

# dplyr - working with data

`filter()` - pick observations by their values

`select()` - pick columns by name

`arrange()` - reorder rows

`mutate()` - create new variables from existing variables

`summarise()` - collapse values to a summary statistic

`group_by()` - all the above split by group

`%>%` pipe to combine

Base R: `subset()`, `order()`, `sort()`, `table()`, `aggregate()`, `|>`

**Tibbles** – data frames with different display behavior

# tibbles

Printing more of tibbles

```
?print.tbl > options
```

We want to inspect all the data by default:

```
options(tibble.width=Inf)
```

```
options(tibble.print_max=Inf)
```

```
options(max.print=1500)
```

You probably spent a lot of time collecting data.

Wouldn't you want to spend a few minutes to inspect each row?

# dplyr vs base

How many trees with known status and mortality are missing a diameter in 2013?

```
tree_dat %>%  
  filter(status13==1) %>%  
  filter(!is.na(mortality)) %>%  
  mutate(diam_missing=is.na(diam13)) %>%  
  summarize(sum(diam_missing))
```

```
sum(is.na(subset(tree_dat, status13==1 &  
  !is.na(mortality))$diam13))
```

# Independent project

- Complete analysis (EDA through inference & conclusions)
- ggplot, dplyr
- Preferably hierarchical model:
  - rstanarm: stan\_glmer or stan\_lmer
- Submit .md from .R or .Rmd
- Due end of semester

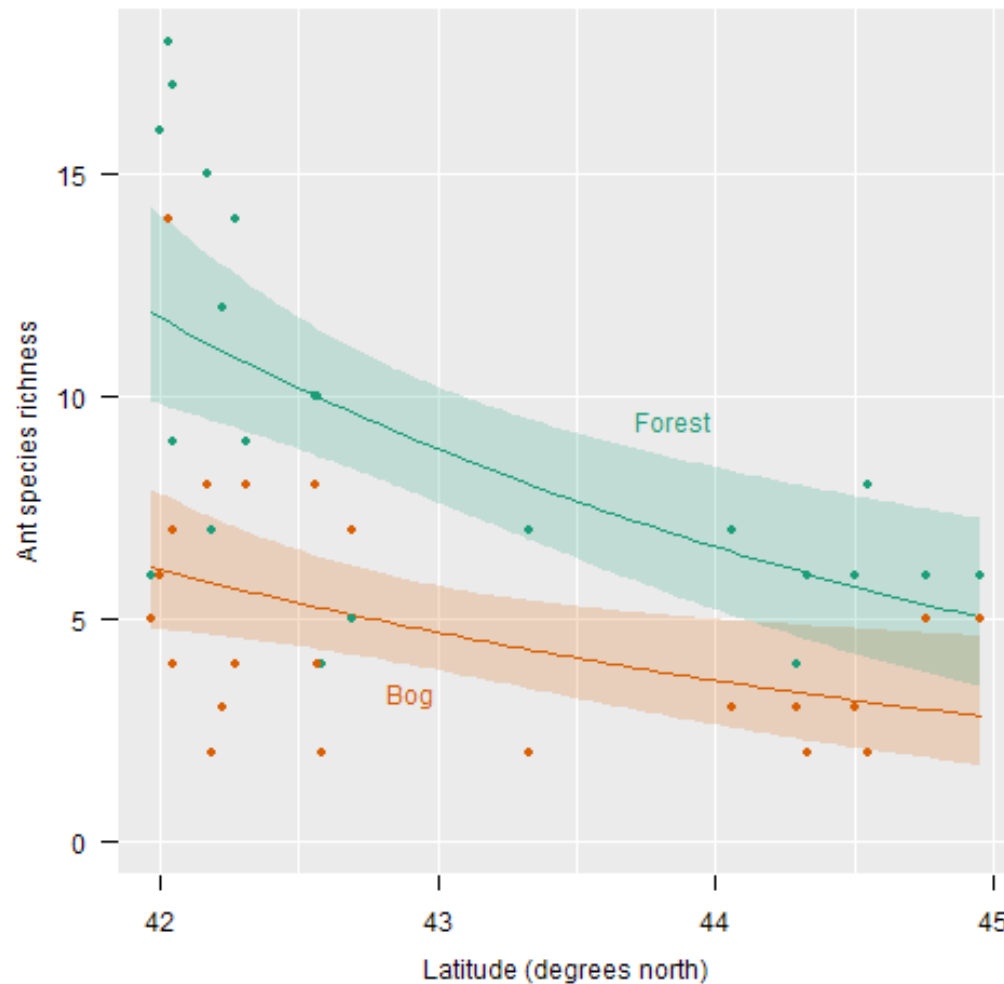
# GLM frequentist

Scientific questions:

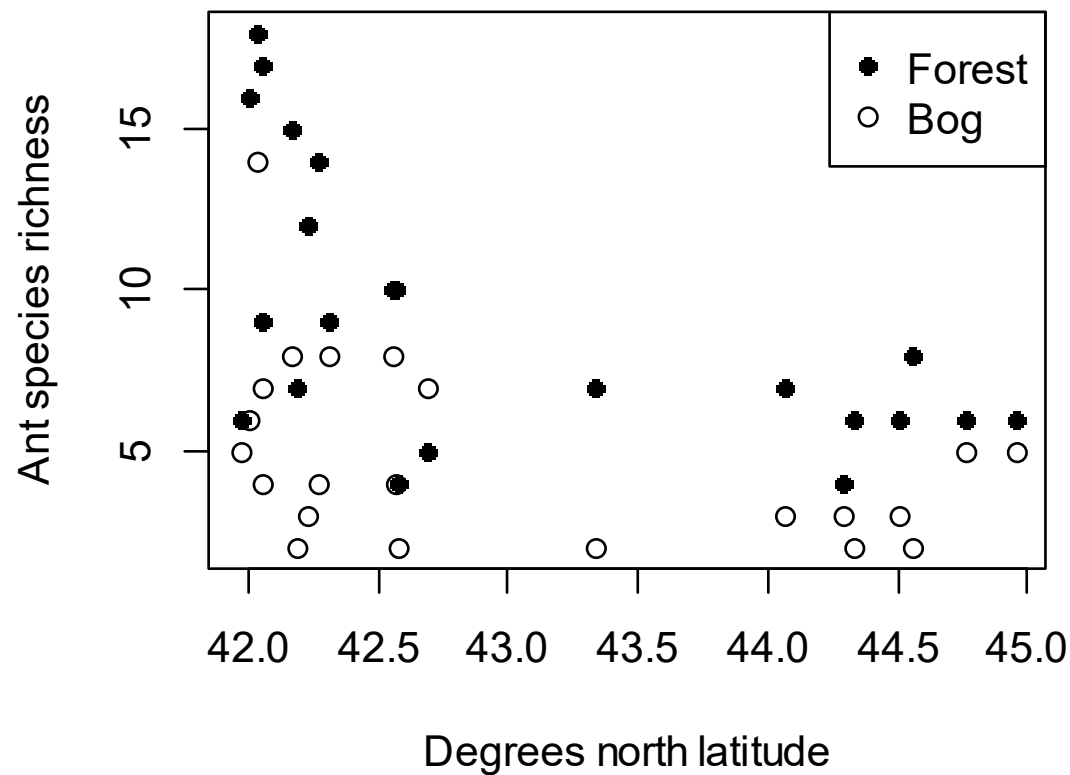
How different is species richness between habitats?

How does species richness vary with latitude?

Is this relationship different between habitats?



# Bayesian model



Could you get inferences?  
Where did you have problems?

# Bayesian model - ants

- We started looking at the code
- Up to and including the summary output
- Next week we'll look at priors and working with the samples