

# TEMPEST: Understory plant community responses to coastal flooding

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## Forests and Rainfall

Heavy rainfall and storm surges are some of the **most common** natural-weather events in the United States. Climate change brings these events *more frequently* and at **greater intensity**. At the *Smithsonian Environmental Research CenterLinks (SERC)*, scientists study how intensified rainfall may affect forests and people.

These scientists have established an experiment called ***TEMPEST (Terrestrial Ecosystem Manipulation to Probe the Effects of Storm Treatments)***. This experiment inundate parts of the forest with *freshwater* and *saltwater* to mimic storms.

This data recorded forest understory communities in three large plots at SERC in Maryland using species cover. *In 2020, prior to inundation*, species cover was estimated within each plot to determine plot differences. This was done to assist interpretation of results following flooding.

Observations in this dataset are the ***estimated percent cover of each plant species or structure that covers the ground*** found within one of 16 5x5 m subplots that were located within three 40 by 50 m plots (C, F, and S). Any additional species are listed as having a percent cover of 0.

```
#Plant data
plantdet= stormbase%>%
  filter(!str_detect(species, c("infrastructure"))) %>%
  filter(!str_detect(species, c("bare"))) %>%
  filter(!str_detect(species, c("basal"))) %>%
  filter(!str_detect(subplot, c('additional')))

plantspec<-as.data.frame(unique(plantdet$species))

#Treatment data
stormtreat<-stormbase %>%
  select(plot, subplot)%>%
  mutate(treatment = ifelse(plot %in% "C", "Control", plot)) %>%
  mutate(treatment=ifelse(plot %in% "S","Saltwater inundation", treatment)) %>%
  mutate(treatment=ifelse(plot %in% "F","Freshwater inundation", treatment))
```

```
#Calculate total plant cover (no non-plants) for each subplot in a new dataframe, removing additional (
```

```
#divide by subplot and cover
subcover<-plantdet %>%
  filter(!str_detect(subplot,c("additonal")))%>%
```

```

group_by(subplot) %>%
summarise(totalcover=sum(cover))%>%
ungroup()

bigdata<-left_join(plantdet,subcover) %>%
group_by(subplot) %>%
mutate(relative_cover=100*(cover/totalcover)) %>%
select(-notes)

```

```
## Joining with 'by = join_by(subplot)'
```

```
#Make 2 new dataframes
```

```
#one with plant species richness by subplot, with mean and st.error of subplot species richness
```

```

sprichness <- bigdata %>%
group_by(subplot) %>%
mutate(splotrichness = n_distinct(species)) %>%
ungroup()

```

```
#The other with plant species richness by plot, including additional species
```

```

plotrichness <- sprichness %>%
group_by(plot) %>%
mutate(plotrichness = n_distinct(species)) %>%
ungroup()

```

```
#Now, we need to make our figures. To make them, we need to find mean and st.error
```

```
std.error <- function(x) sd(x)/sqrt(length(x))
```

```

meanrich <- plotrichness %>% group_by(plot) %>%
mutate(meansprichness = mean(splotrichness)) %>%
mutate(st.errsprichness = std.error(splotrichness))

```

```

plotsprich <- meanrich %>%
group_by(plot) %>%
summarize(plotrichness = n_distinct(species)) %>%
ungroup()

```

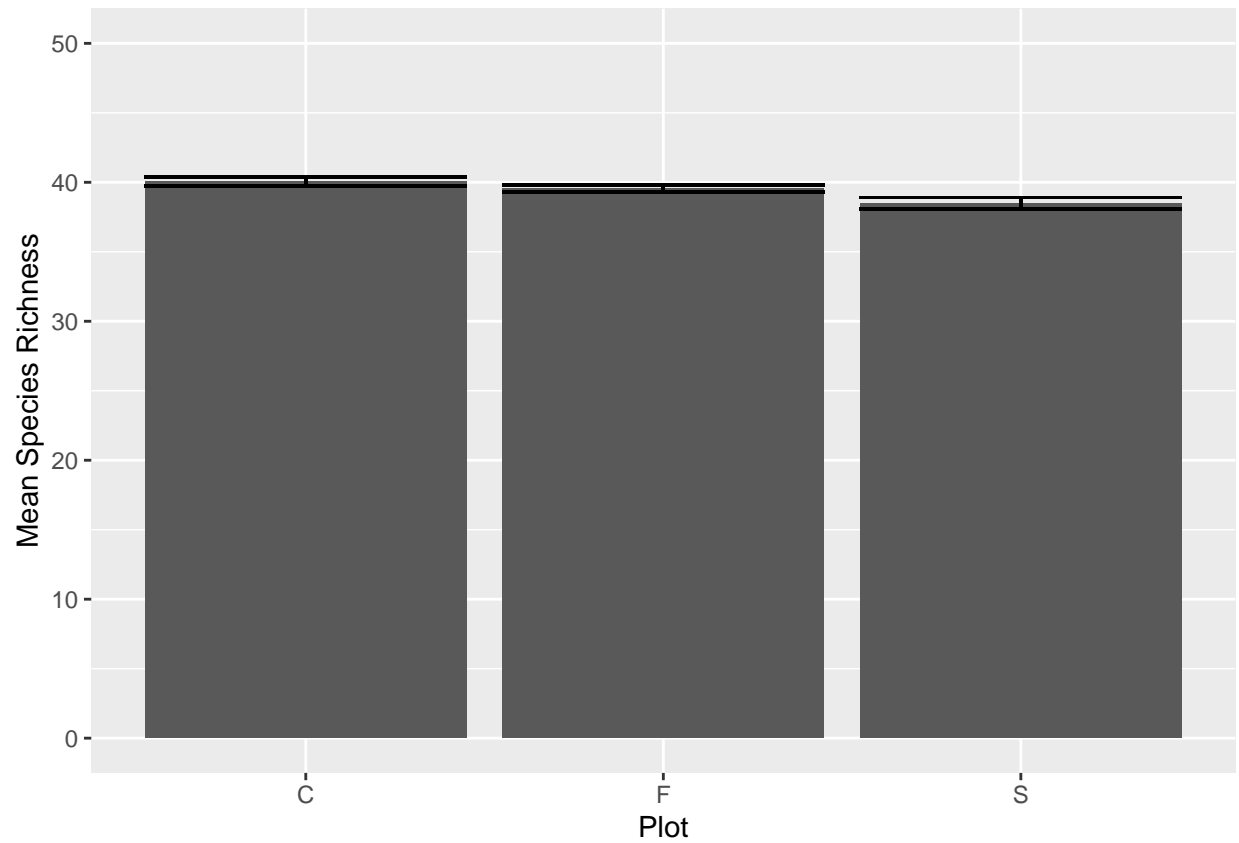
```
#One should be a bar graph showing richness by plot, with mean and st.error by subplot
```

```

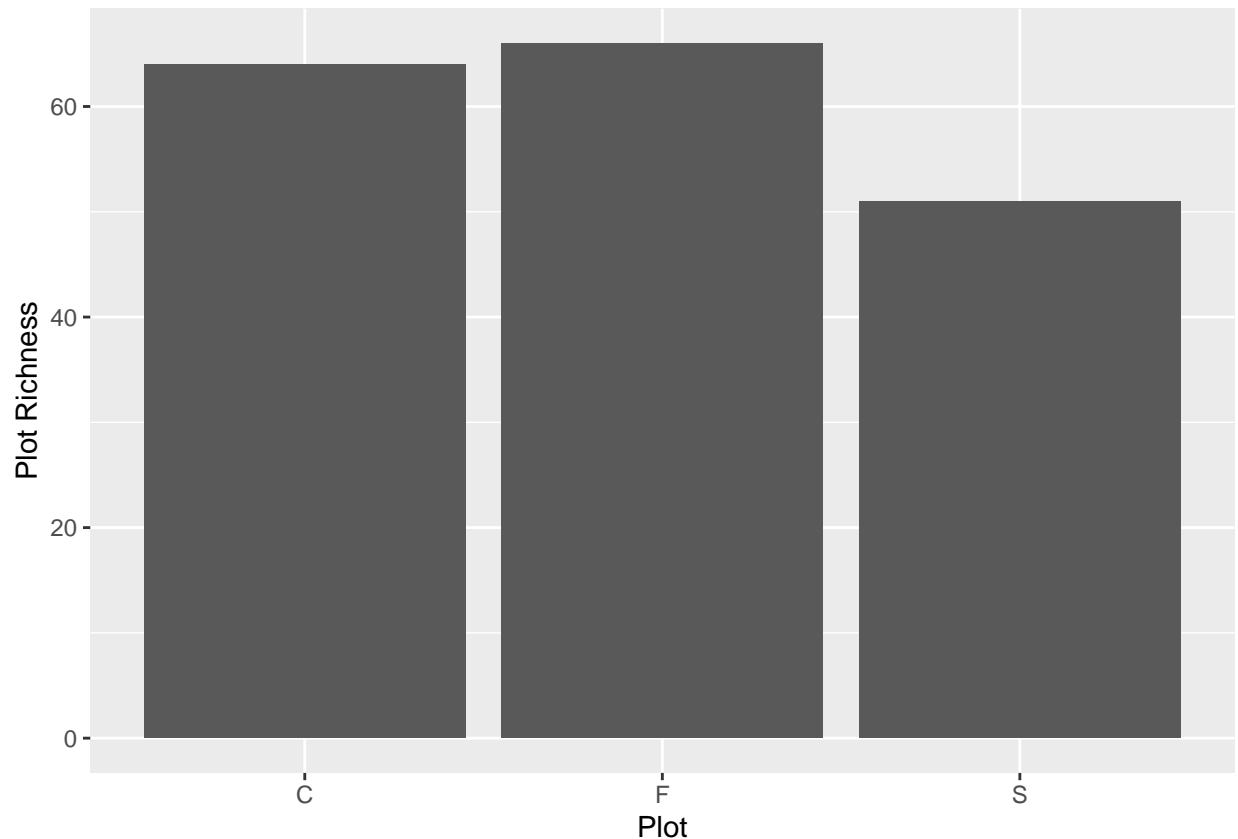
ggplot(meanrich, aes(x=plot, y=meansprichness)) +
geom_bar(stat= "identity") +
geom_errorbar(aes(ymin = meansprichness - st.errsprichness,
ymax = meansprichness + st.errsprichness)) +ylim(0,50) +
xlab("Plot") +
ylab("Mean Species Richness")

```

```
## Warning: Removed 1022 rows containing missing values (geom_bar).
```



```
#The other should be a bar graph showing richness at the plot level  
ggplot(plotsprich, aes(x=plot, y=plotrichness)) +  
  geom_bar(stat= "identity") +  
  xlab("Plot") +  
  ylab("Plot Richness")
```



```
#Make a rank-abundance curve for avg understory plant community composition
```

```
#Calculate relative cover for all species across subplots, in each plot
```

```
relcover <- plantdet %>%
  group_by(plot, species) %>%
  summarize(average_rel_cov = mean(cover)) %>%
  ungroup()
```

```
## 'summarise()' has grouped output by 'plot'. You can override using the
```

```
## '.groups' argument.
```

```
#Calculate relative cover of species across plots
```

```
species_cover <- relcover %>%
  group_by(species) %>%
  summarize(average_rel_cov = mean(average_rel_cov))
```

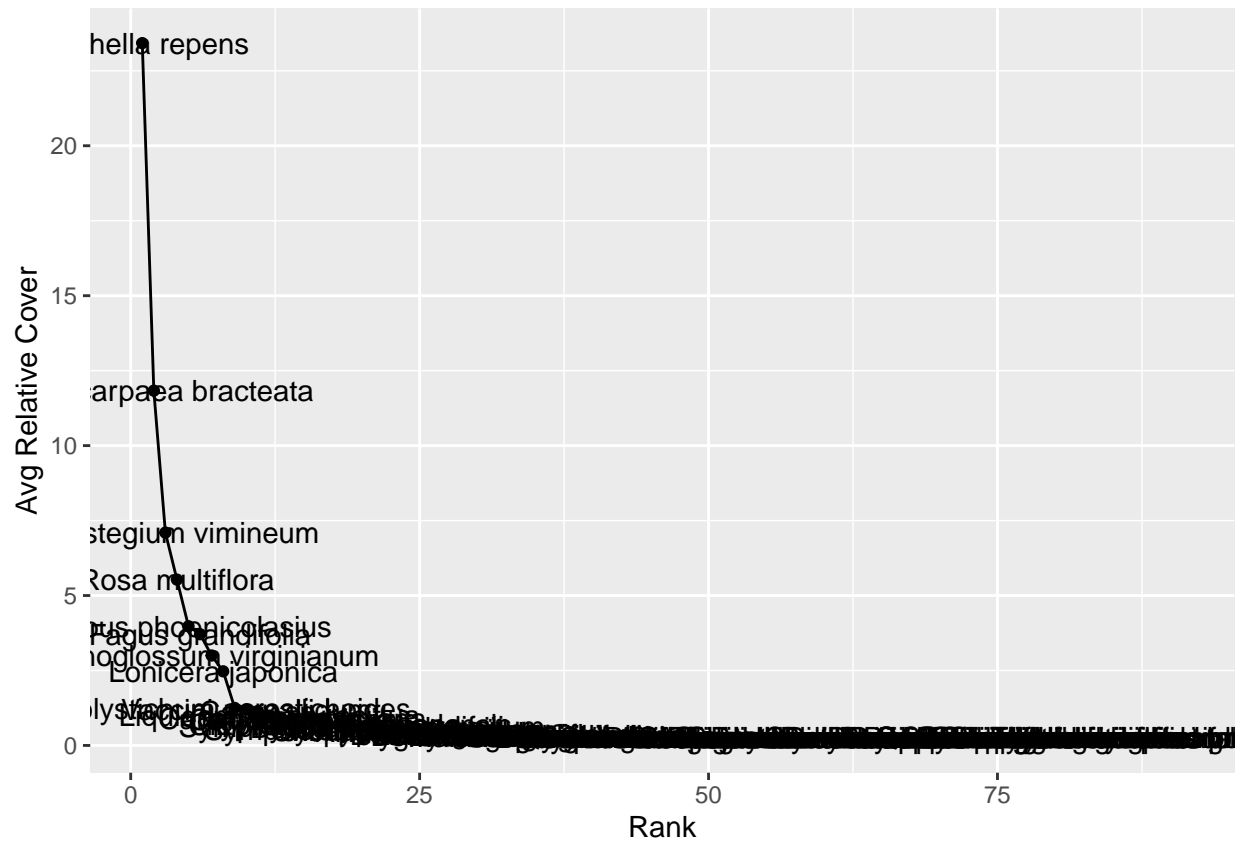
```
#Sort dataframe by highest to lowest cover
```

```
cover_ranked <- species_cover %>%
  arrange(desc(average_rel_cov))
```

```
#Rank species by relative cover
```

```
cover_ranked <- cover_ranked %>%
  mutate(number = 1:91)
```

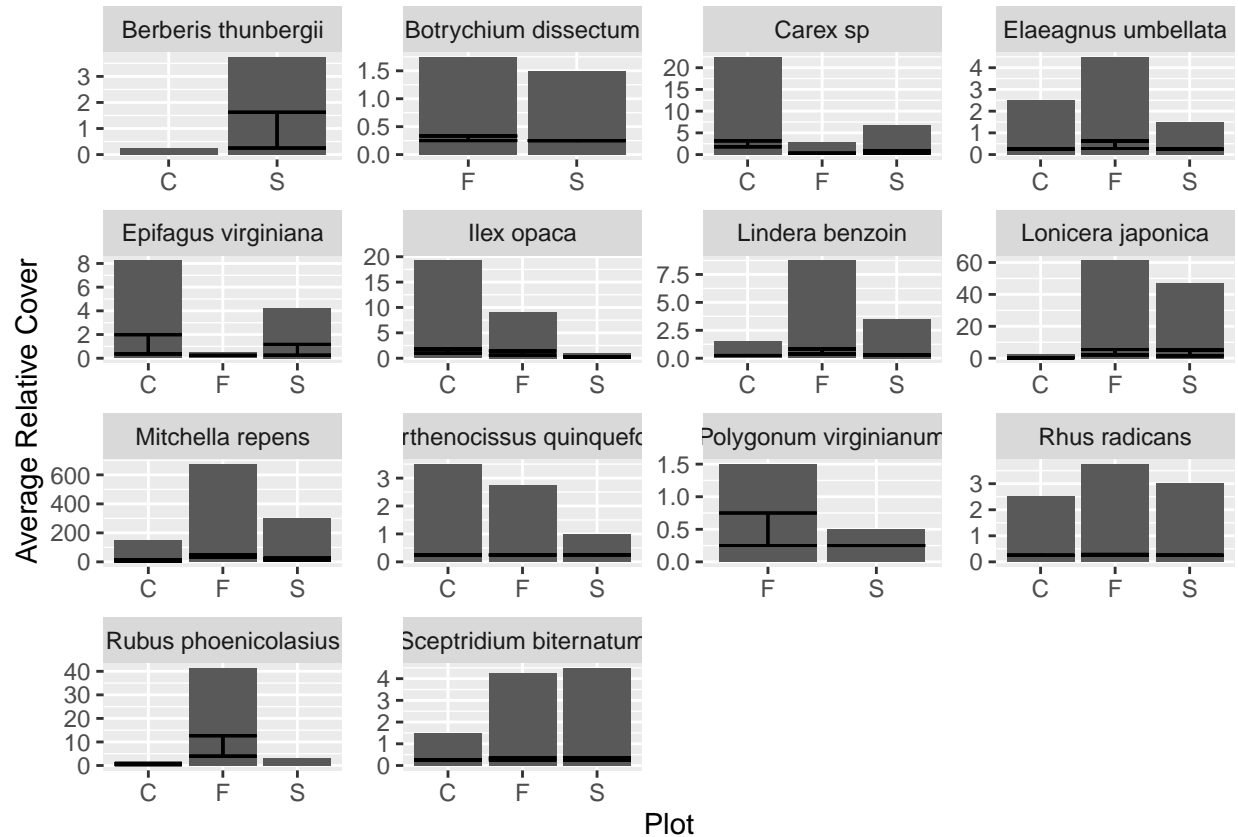
```
ggplot(cover_ranked, aes(x=number, y=average_rel_cov)) +
  geom_point() +
  geom_line() +
  geom_text(aes(label = species)) +
  xlab("Rank") +
  ylab("Avg Relative Cover")
```



```
relcover_mean <- plantdet %>%
  group_by(plot, species) %>%
  mutate(average_rel_cov = mean(cover)) %>%
  mutate(stderror = std.error(cover)) %>%
  select(plot, species, cover, average_rel_cov, stderror) %>%
  ungroup()
```

```
spsubset <- relcover_mean %>%  
  filter(species %in% c("Berberis thunbergii", "Botrychium dissectum", "Carex sp", "Elaeagnus umbellata"  
  
specieslist<-c("Berberis thunbergii", "Botrychium dissectum","Carex sp", "Elaeagnus umbellata", "Epifagy  
  
ggplot(spsubset, aes(x= plot, y=average_rel_cov)) +
```

```
geom_bar(stat="identity") +
geom_errorbar(aes(ymin = average_rel_cov - stderror,
                  ymax = average_rel_cov + stderror)) +
facet_wrap(~species, scales = 'free') +
ylab("Average Relative Cover") +
xlab("Plot")
```



There is relatively little difference between treatment plots or for mean species richness. However, in plot richness, it appears that saltwater inundation lowered richness. *M. repens* appears to make up the most plot cover, with freshwater inundation greatly increasing its relative cover.

*Rubus*, *Lindera*, and *Elaeagnus* seem to respond best to freshwater inundation at the species level, while *Berberis* performed best under saltwater inundation.