

# Plots for WV Herp Summit Poster

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## Graphs I would like to use

```
library(ggplot2)
library(dplyr)

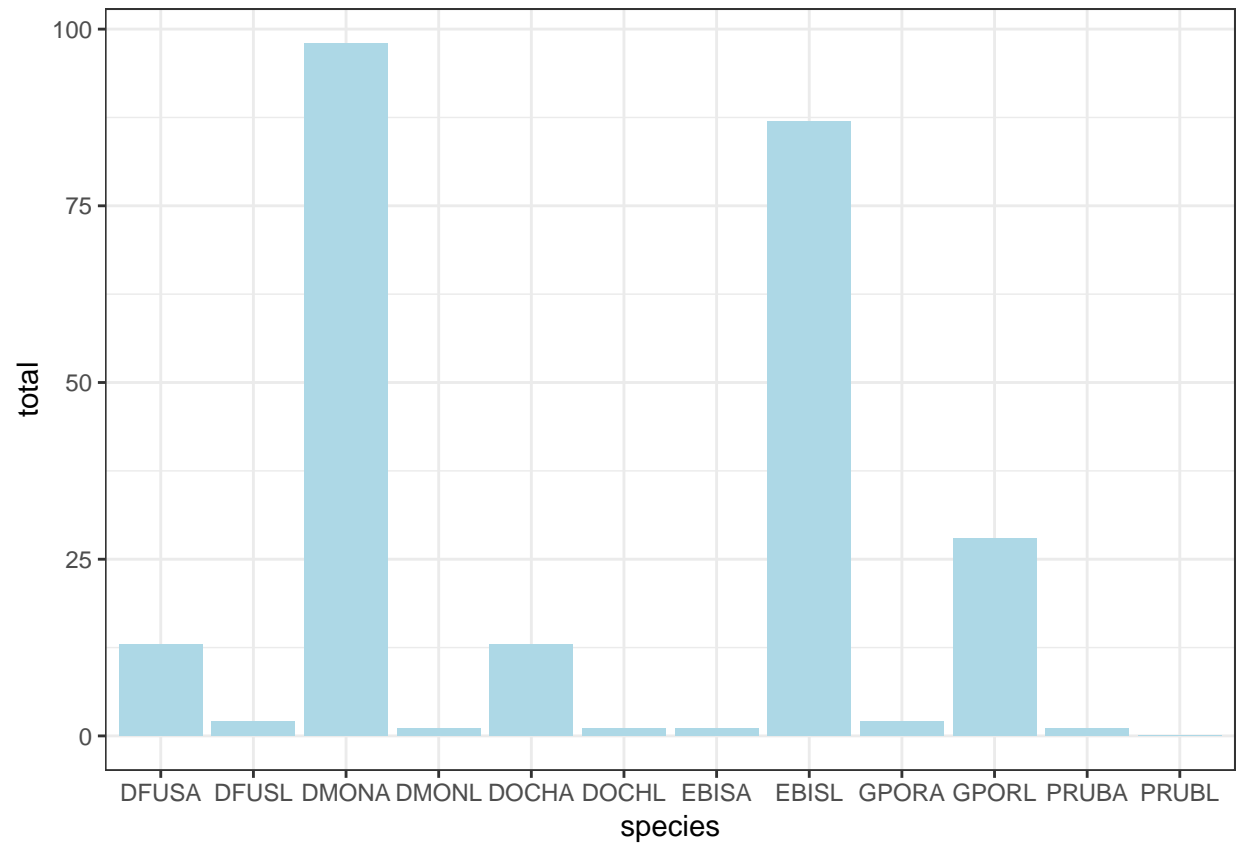
##
## Attaching package: 'dplyr'
##
## The following objects are masked from 'package:stats':
##
##   filter, lag
##
## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

sal <- read.csv("C:/Users/Jacey/Documents/FSU/Research/R_code/MD_Stream_salamanders/Data/Date_Location_1.csv")
counts <- read.csv("C:/Users/Jacey/Documents/FSU/Research/R_code/MD_Stream_salamanders/Data/Just_Count_1.csv")

sal_means <- sal %>%
  group_by(stream, transect, up_down, type) %>%
  dplyr::select(-date, -observers, -visit) %>%
  summarise_all(mean, na.rm = TRUE)

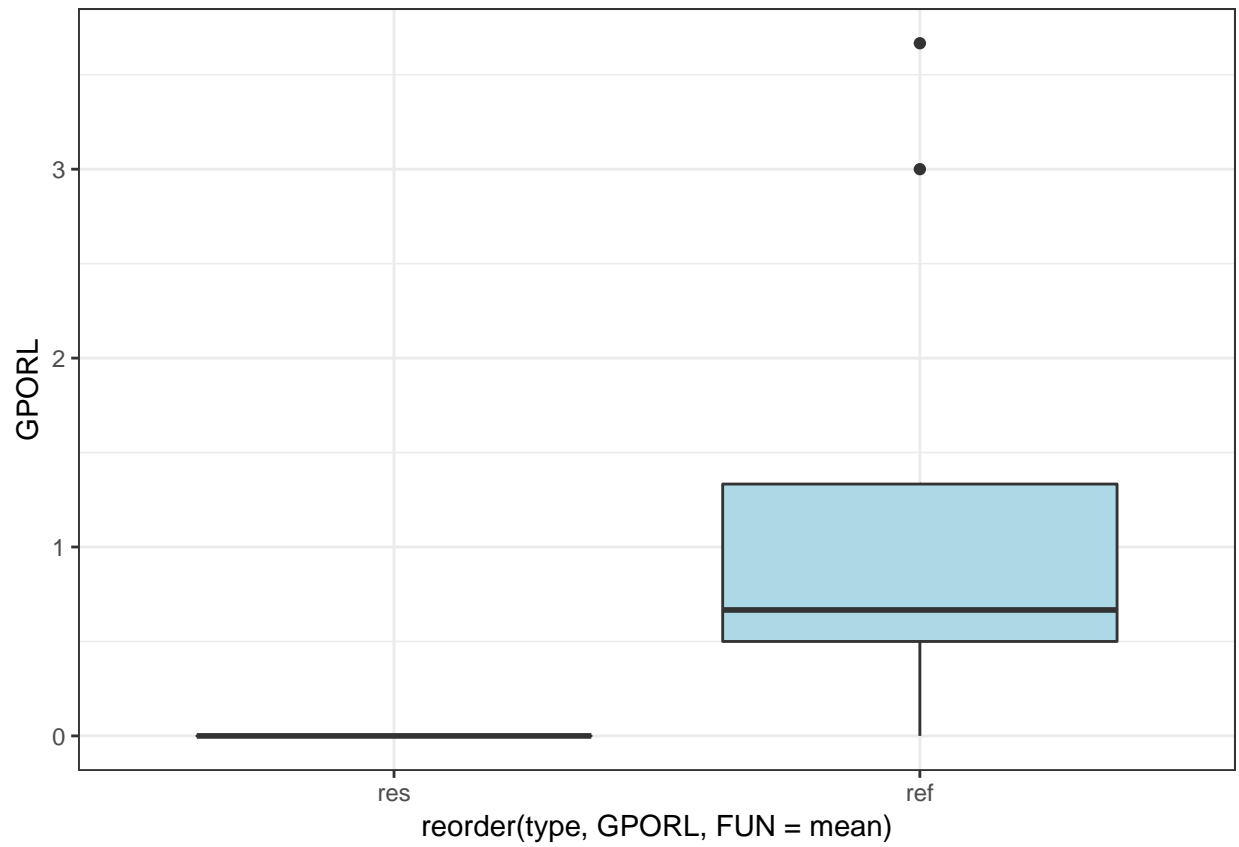
sal_sds <- sal %>%
  group_by(stream, type, transect, up_down) %>%
  dplyr::select(-date, -observers, -visit) %>%
  summarise_all(sd, na.rm = TRUE)

ggplot(data = counts, aes(x=species, y=total)) + geom_bar(data = NULL, stat= "identity", fill = "lightblue")
```

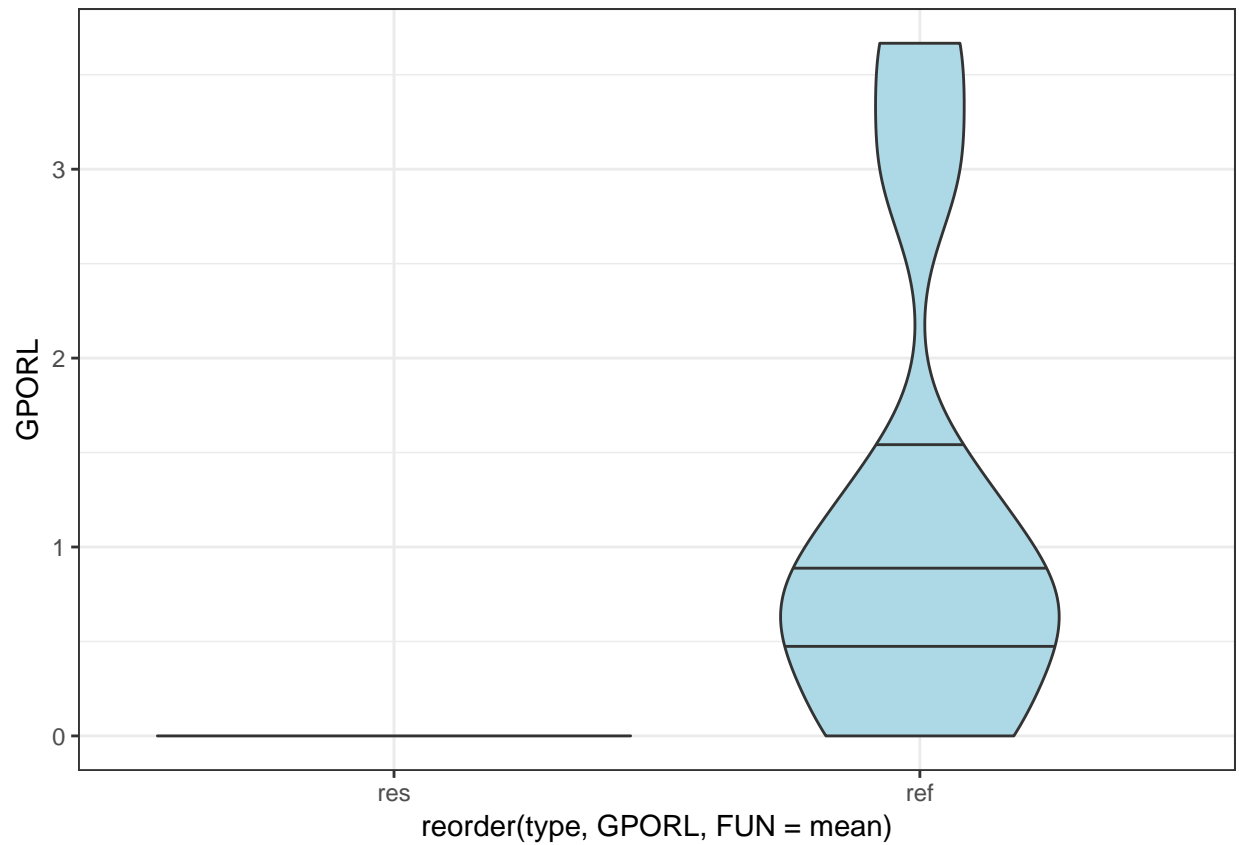


sal\_means box or violin GPORL~type

```
ggplot(sal_means, aes(x = reorder(type, GPORL, FUN = mean), GPORL)) + geom_boxplot(fill = "lightblue") +
```

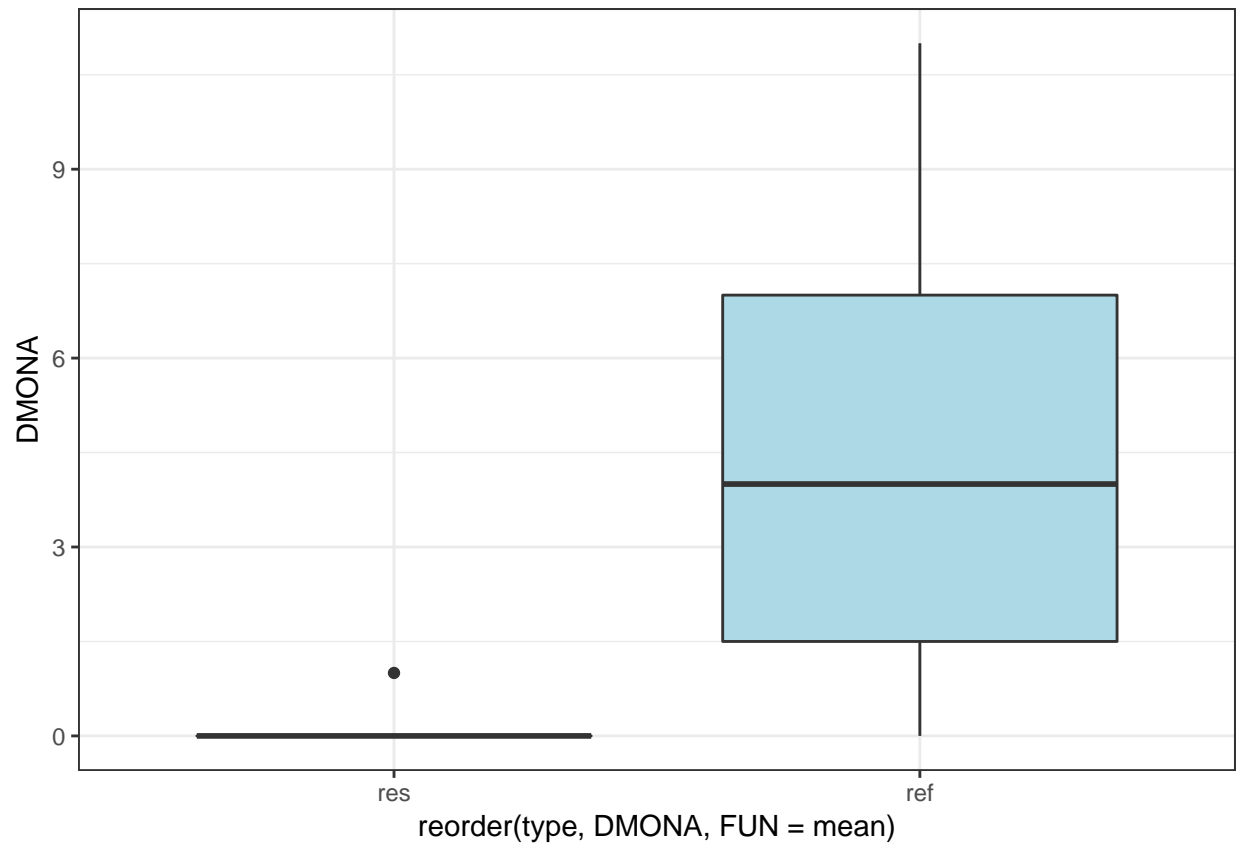


```
ggplot(sal_means, aes(x = reorder(type, GPORL, FUN = mean), GPORL)) + geom_violin(draw_quantiles = c(0.1
```

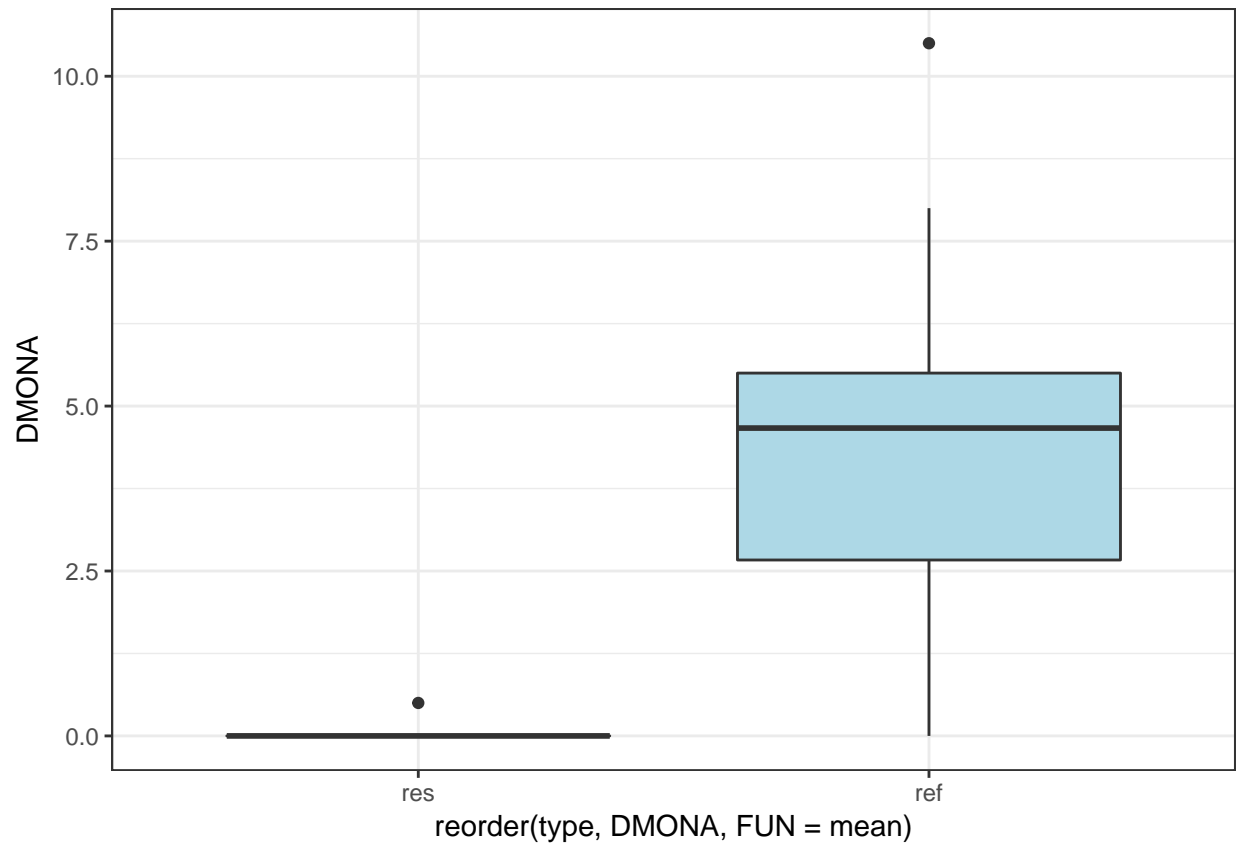


sal or sal\_means box DMONA~type

```
ggplot(sal, aes(x = reorder(type, DMONA, FUN = mean), DMONA)) + geom_boxplot(fill = "lightblue") + theme_minimal()
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).
```

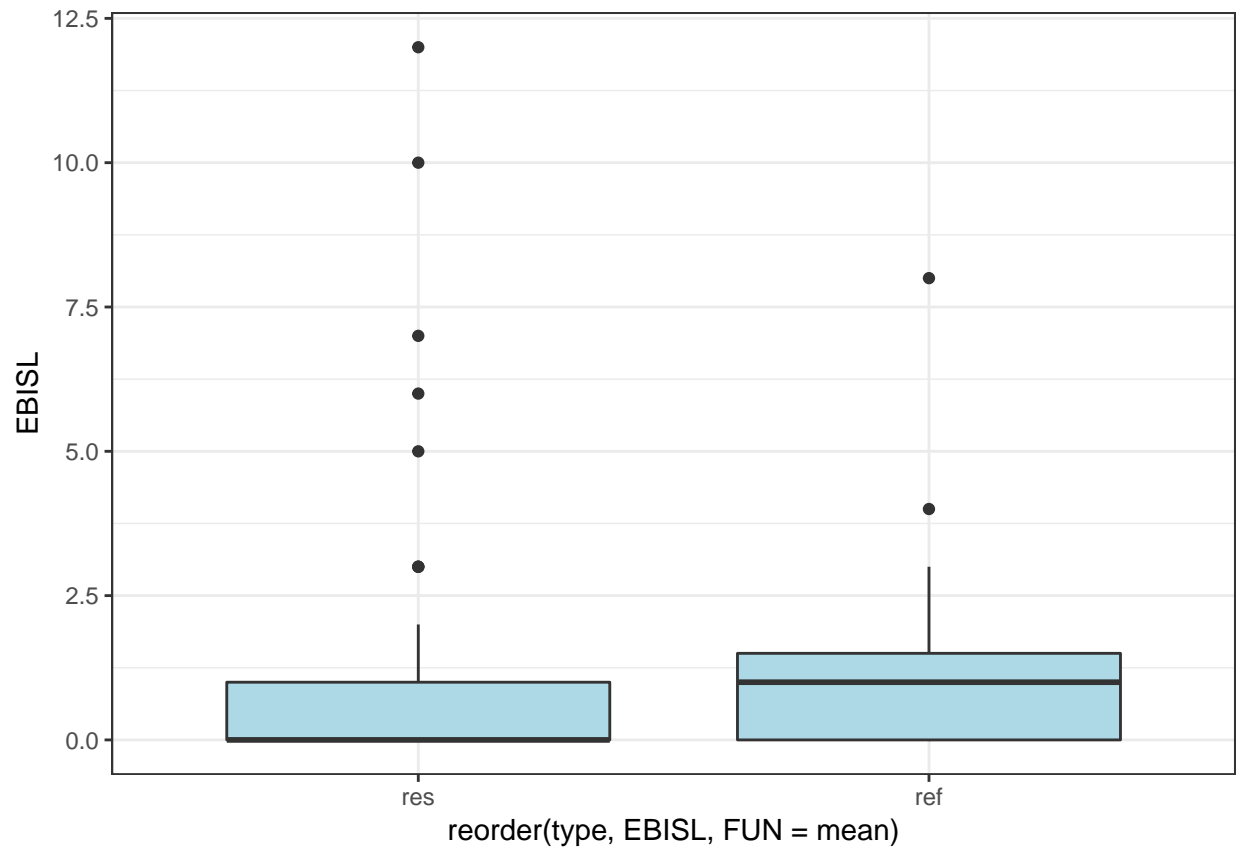


```
ggplot(sal_means, aes(x = reorder(type, DMONA, FUN = mean), DMONA)) + geom_boxplot(fill = "lightblue")
```



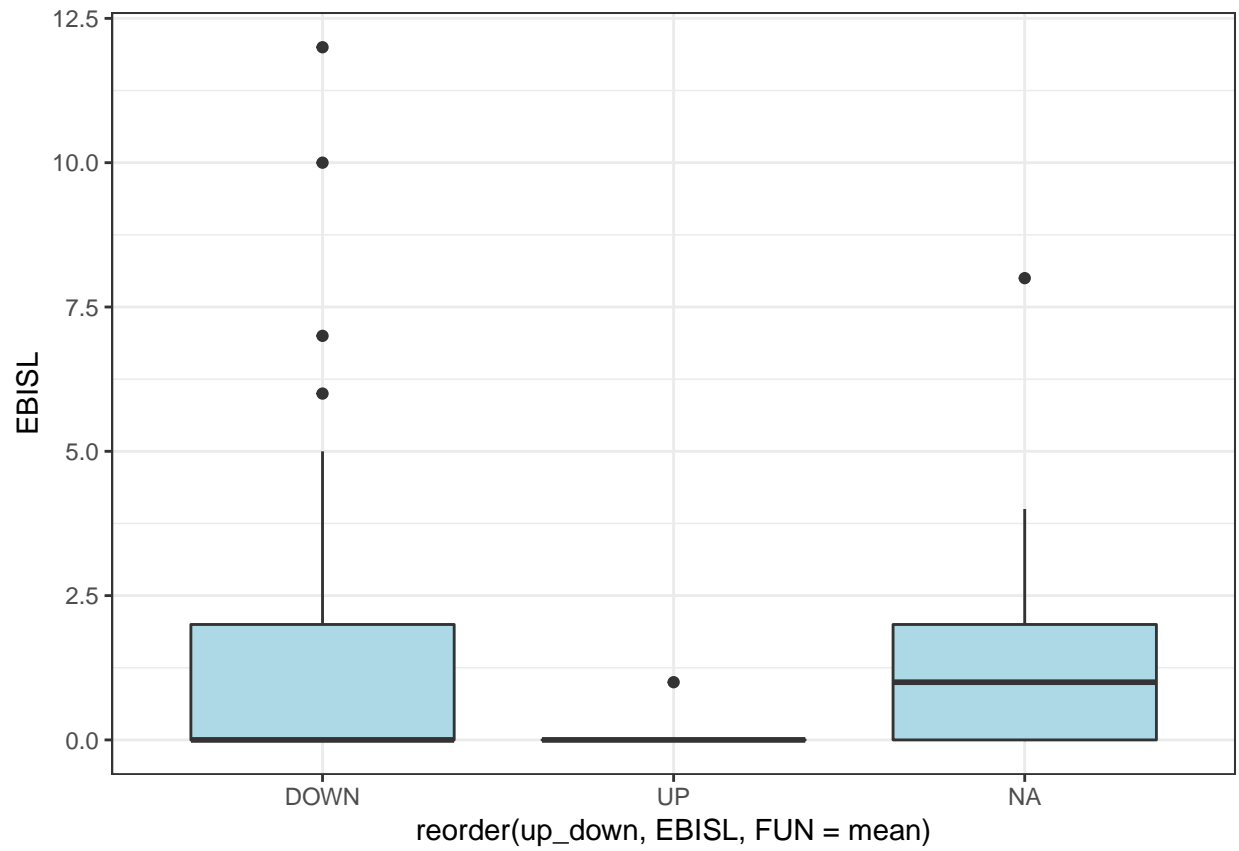
sal box EBISL~type

```
ggplot(sal, aes(x = reorder(type, EBISL, FUN = mean), EBISL)) + geom_boxplot(fill = "lightblue") + theme_minimal()
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).
```



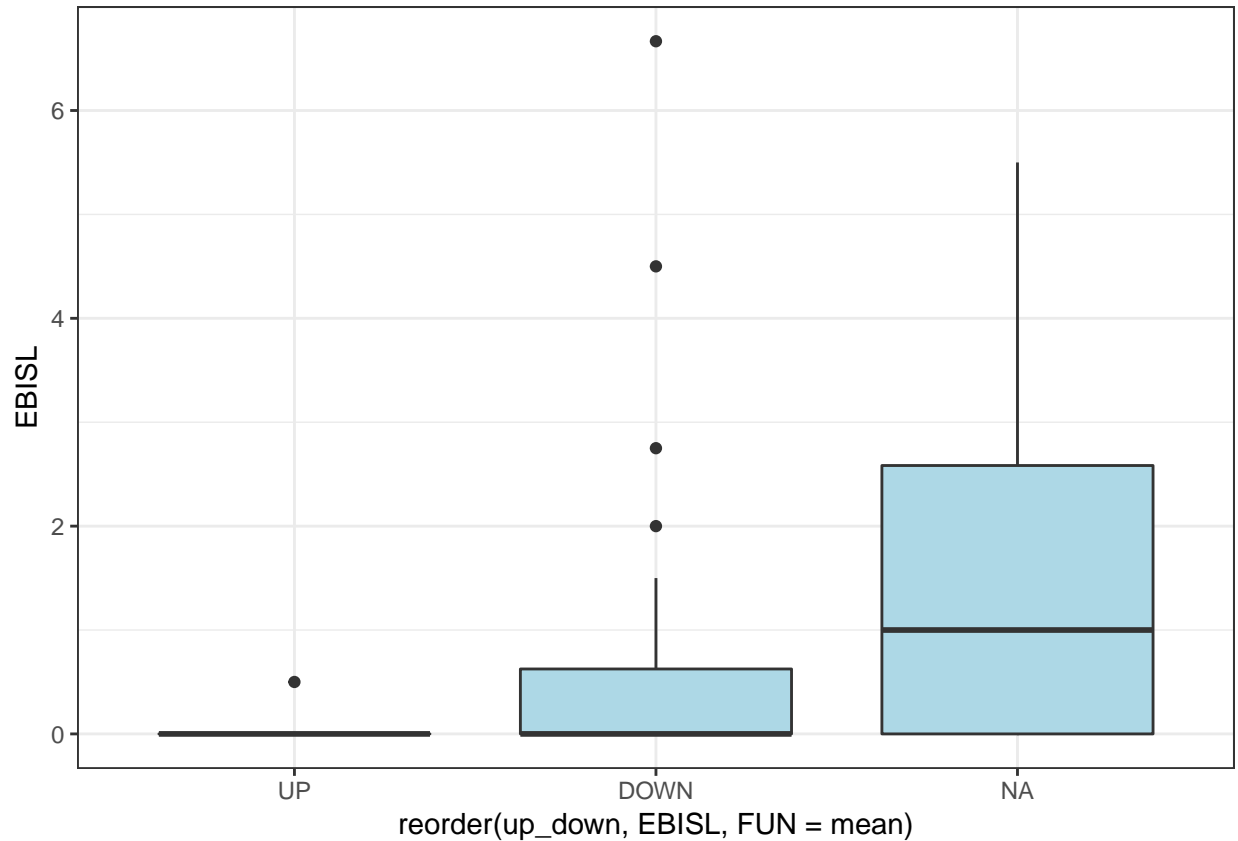
sal or sal\_means box EBISL~up\_down

```
ggplot(sal, aes(x = reorder(up_down, EBISL, FUN = mean), EBISL)) + geom_boxplot(fill = "lightblue") + theme_minimal()
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).
```



```
ggplot(sal_means, aes(x = reorder(up_down, EBISL, FUN = mean), EBISL)) + geom_boxplot(fill = "lightblue")
```



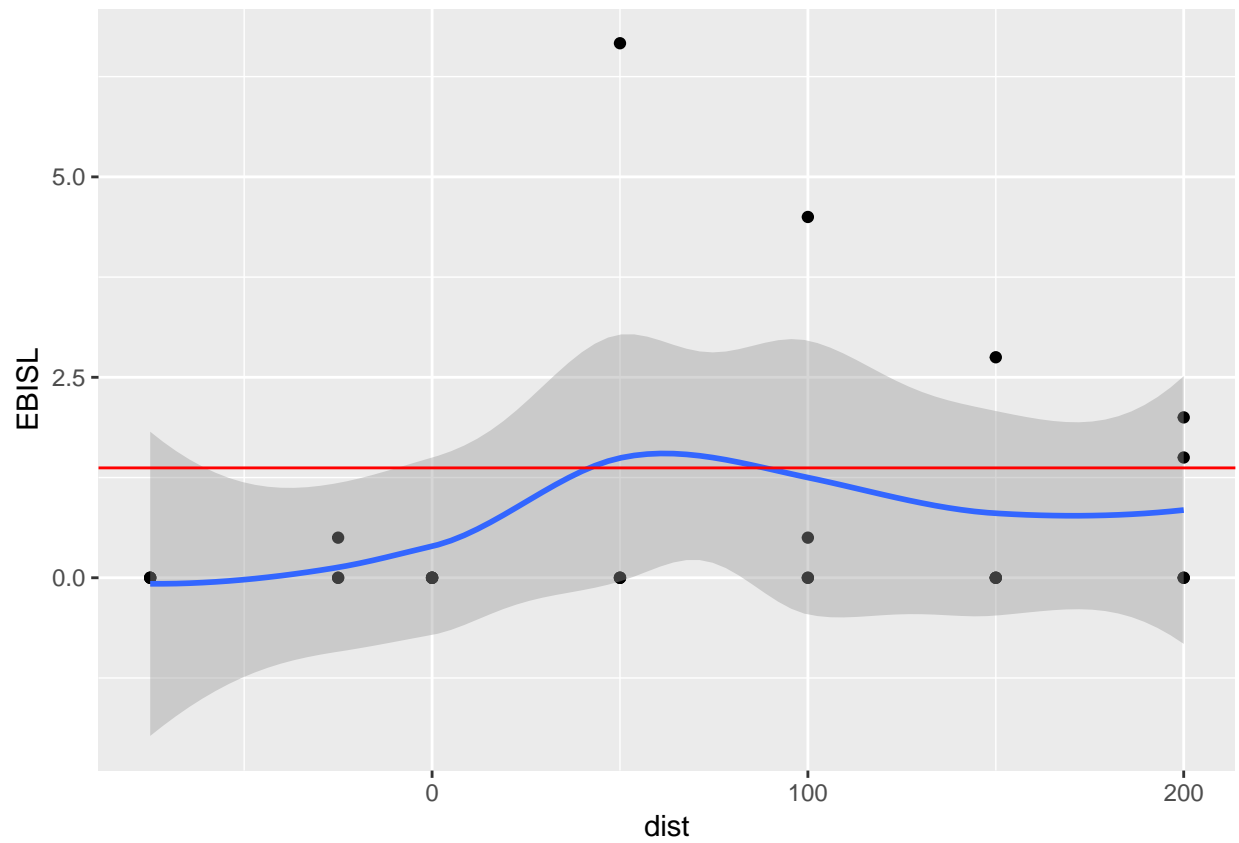


line graphs looking at avg count ~ distance for each species

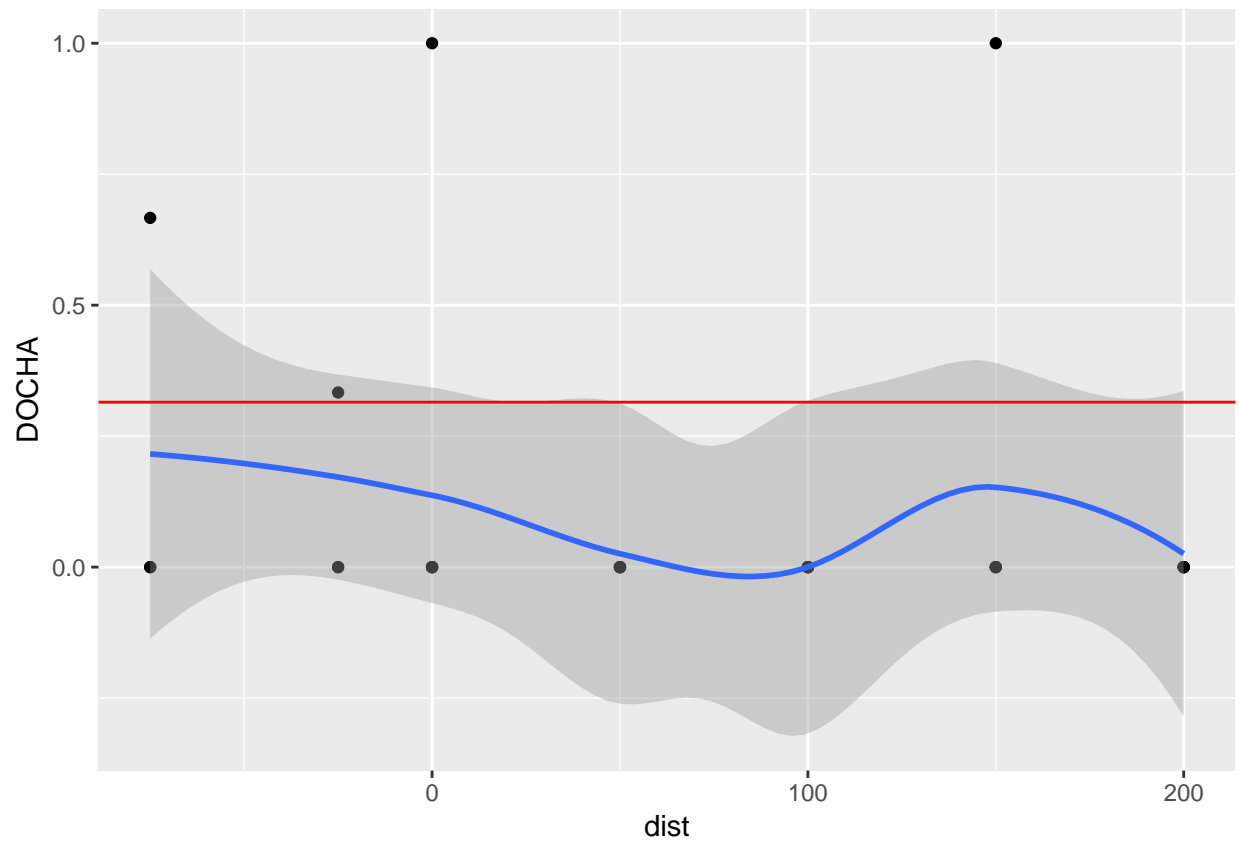
EBISL had a uptick in counts right after the sand dump, while DFUSA and DOCHA had a downtick

GPORL and DMONA had very little counts and thus no observable relationship other than the fact that counts were lower than the average for ref streams

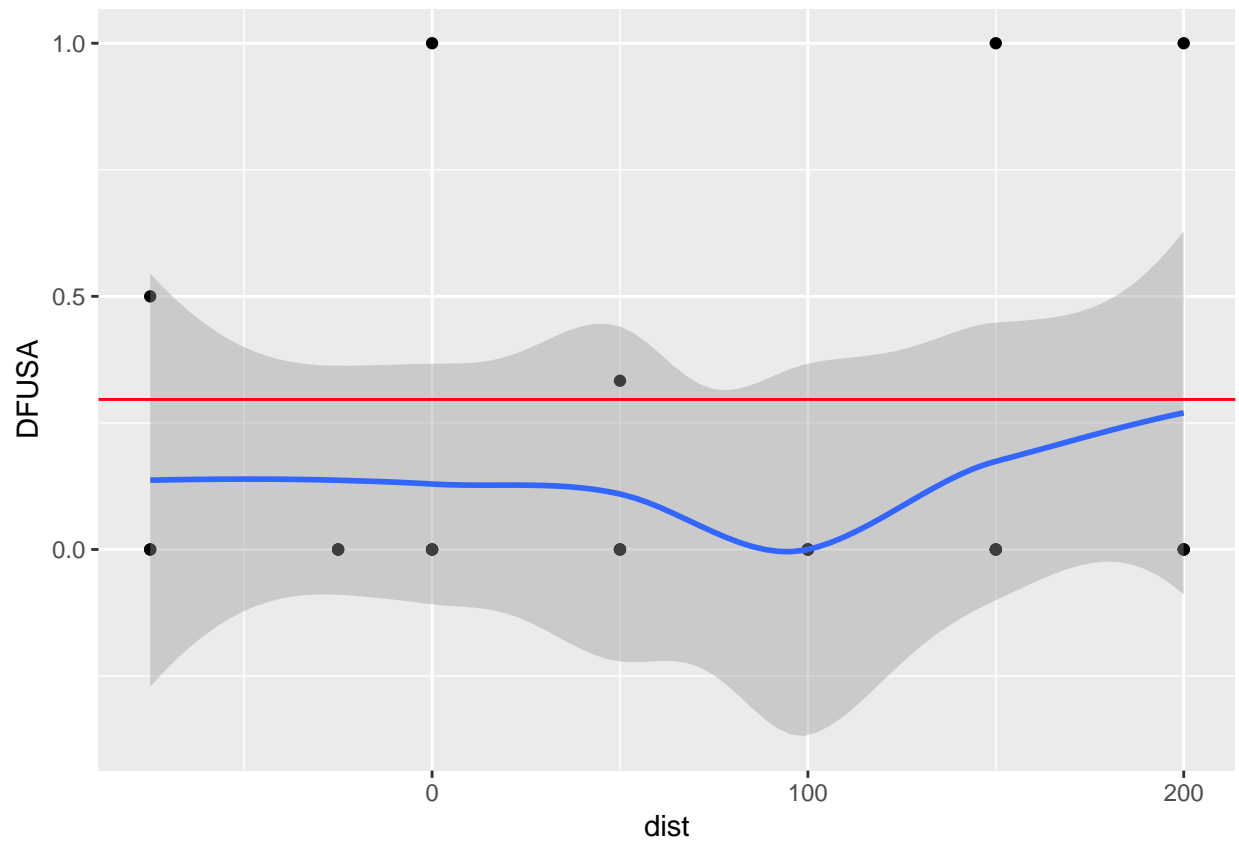
```
ggplot(data = filter(sal_means, type != "ref"), aes(dist, EBISL)) + geom_point() + geom_smooth() + geom_
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



```
ggplot(data = filter(sal_means, type != "ref"), aes(dist, DOCHA)) + geom_point() + geom_smooth() + geom.  
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```

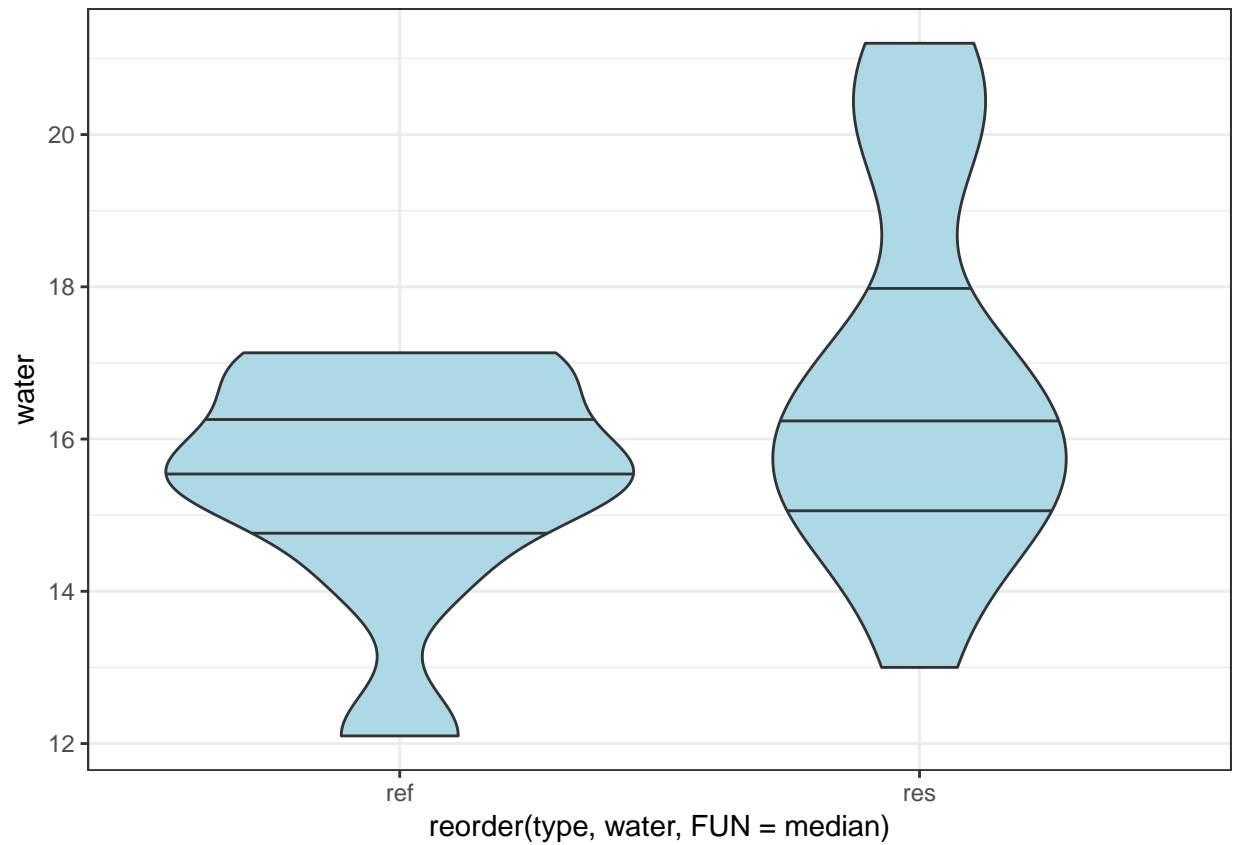


```
ggplot(data = filter(sal_means, type != "ref"), aes(dist, DFUSA)) + geom_point() + geom_smooth() + geom.  
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



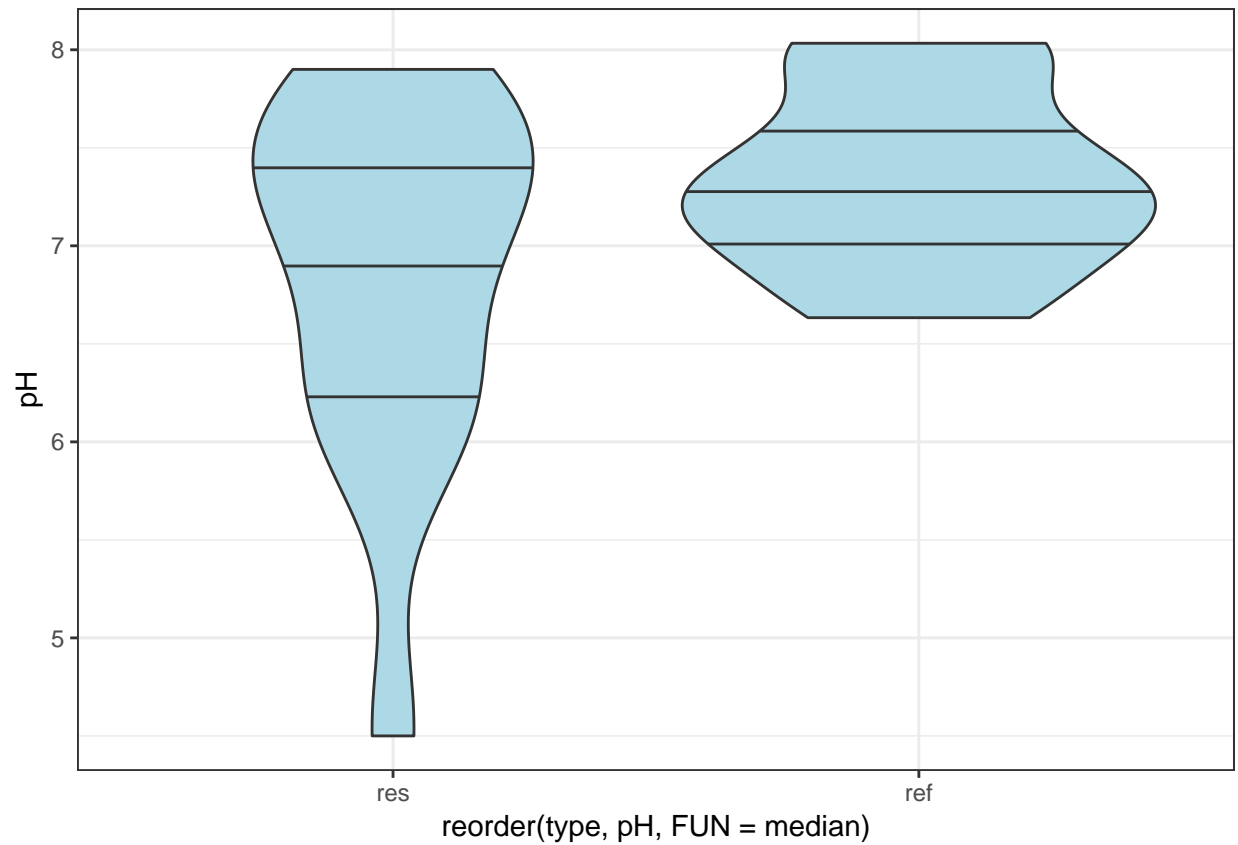
violin sal\_means water temp~ type

```
ggplot(sal_means, aes(x = reorder(type, water, FUN = median), water)) + geom_violin(draw_quantiles = c(
```



violin sal\_means pH~type

```
ggplot(sal_means, aes(x = reorder(type, pH, FUN = median), pH)) + geom_violin(draw_quantiles = c(0.25, 0.5, 0.75))
```



box sal EC~up\_down

```
ggplot(sal, aes(x = reorder(up_down, EC, FUN = median), EC)) + geom_boxplot(fill = "lightblue") + theme_minimal()
## Warning: Removed 22 rows containing non-finite values (stat_boxplot).
```

