

#COPY AND PASTE INTO R

```
require(RCurl)
```

```
require(sciplot)
```

#This pulls the data from Google Docs and places in the form called fede_hali

```
myCsv <-
```

```
getURL("https://docs.google.com/spreadsheet/pub?key=0AkJuO1gYG12tdHNPN2NRVHJWSH  
JxRURxejNJTDFrMmc&single=true&gid=0&output=csv")
```

```
fede_hali <- read.csv(textConnection(myCsv))
```

#Next, Plot All treatments

```
bargraph.CI( fede_hali$Treatment,           #X-axis factor  
              fede_hali$Nematocytes,        #Y-axis value  
              fede_hali$Light,               #Grouping Factor  
              legend=T)
```

####BELOW HERE NOT USED

```
require(ggplot2)
```

#Next, create datasets based on each experiment

```
proline<-subset(fede_hali, fede_hali$Treatment=='proline')
```

```
noPtx<-subset(fede_hali,fede_hali$Ptx==0)
```

```
Ptx<-subset(fede_hali,fede_hali$Ptx>0)
```

```
boxplot(Nematocytes ~ Light, data = noPtx,  
xlab = "Light", ylab = "Nematocytes Captured",  
main = "Haliplanella (Box and whisker)"  
)
```

```
plot(Ptx$Ptx, Ptx$Nematocytes)
```

```
library(sciplot)
```

```
library(sciplot)
```

```
bargraph.CI( noPtx$NANA,           #X-axis factor
```

noPtx\$Nematocytes,	#Y-axis value
noPtx\$Light,	#Grouping Factor
legend=T)	

bargraph.CI(fede_hali\$Ptx,	#X-axis factor
fede_hali\$Nematocytes,	#Y-axis value
fede_hali\$Light,	#Grouping Factor
legend=T)	