

# Demonstration

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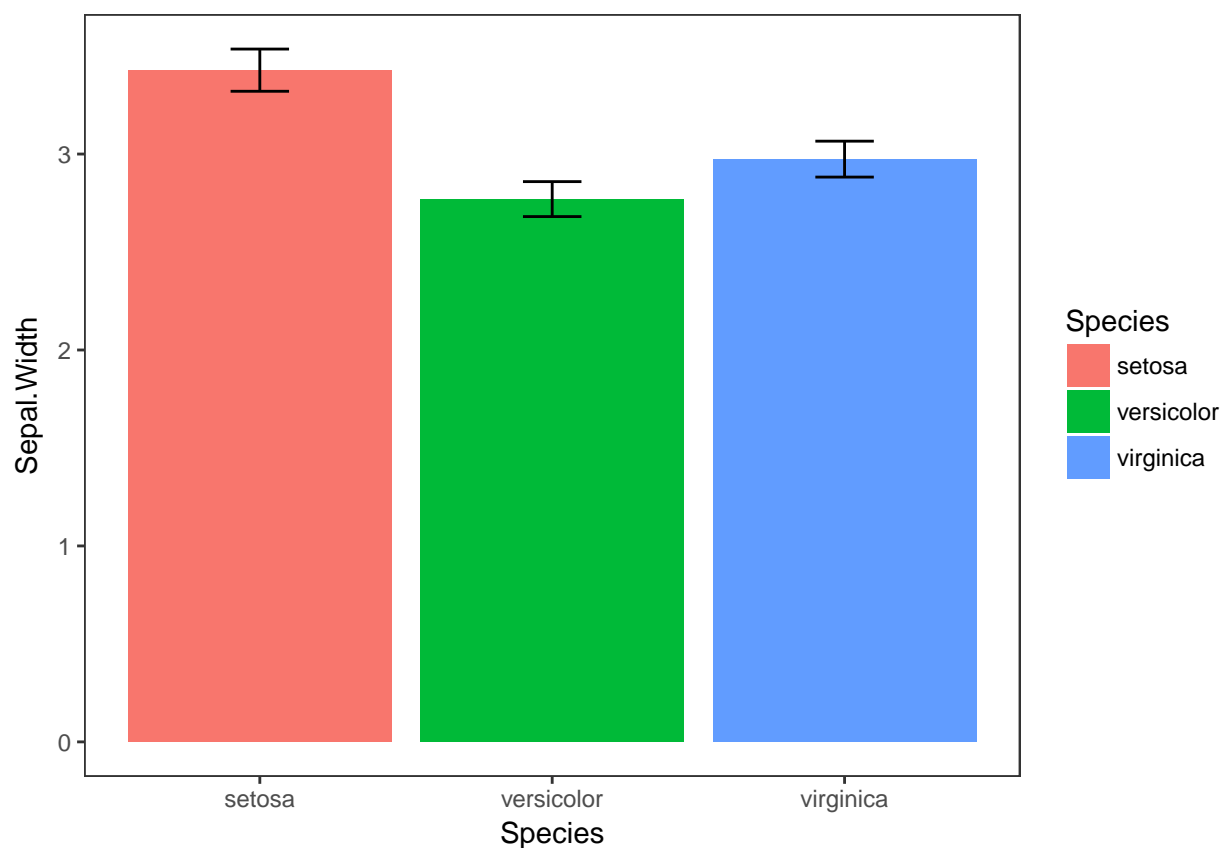
```
# baromax<- function(data, x, y, fill, error_width=.2){  
#   ggplot(data) +  
#     aes_string(x, y, fill = fill) +  
#     stat_summary(fun.y=mean, geom = "bar") +  
#     stat_summary(fun.data = mean_cl_normal,  
#                   geom="errorbar",  
#                   width=error_width,  
#                   position=position_dodge(width=.9)) +  
#     theme_bw() +  
#     theme(panel.grid.major = element_blank(),  
#           panel.grid.minor = element_blank())  
# }  
}
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.3.3
```

```
library(graphomax)
```

```
baromax(data = iris, x = "Species", y = "Sepal.Width", fill = "Species")
```



```
# histomax <- function(data, colorz="gray85"){
#   names<-names(data)
#   NCOL<-ncol(data)
#   for (i in 1:NCOL){
#     if (is.numeric(i)==FALSE)
#       next
#     hist(data[,names[i]],
#          main = paste(colnames(data)[i]),
#          xlab = "",
#          col=colorz)
#   }
# }
```

```
iris$Species<-NULL
histomax(iris)
```

