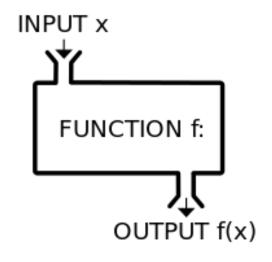
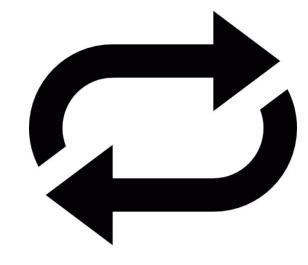
Getting **R** to do your dirty work: automation using functions, apply, and loops

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For code, bigger isn't better

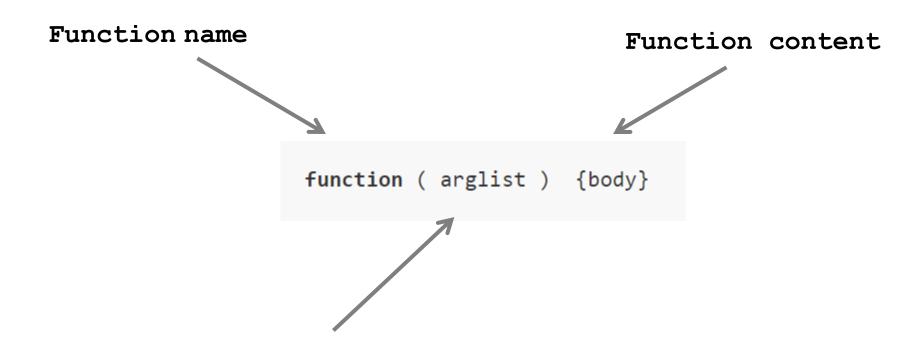
```
## need to code categorical data as ordinal (1/0 for shrub and open)
1188
       micros <- factor (data$Microsite)
1189
       micros <- as.numeric(micros)-1
1190
       consumers <- factor (data$Exclosure)
1191
       consumers <- as.numeric(consumers)-1
1192
       data[, "micros"] <- micros
1193
       data[, "consumer"] <- consumers
1194
1195
       brome.dom <- data$brome/data$abundance ## a measurement of brome dominance
1196
       data[, "brome.dom"] <- brome.dom
1197
1198
1199
       ## specify model. Predictors, responses and latent variables
       mymodel <- '
1200
1201
       # latent variable
1202
       community =~ Biomass + abundance + brome.dom
1203
1204
       # regressions
1205
       community ~ consumer
1206
       community ~ micros
1207
       community ~ SWC.initial
1208
1209
1210
       ## fit model
1211
        fit1 <- sem (mymodel, data = subset (data, Year==2014), estimator = "ML", std.lv=TRUE, se="bootstrap", test="bootstrap")
1212
        fit2 <- sem(mymodel, data = subset(data, Year==2016), estimator = "ML", std.lv=TRUE, se="bootstrap", test="bootstrap")
1213
1214
1215
       ##summarize results
1216
       summary(fit1)
1217
       summary(fit2)
1218
1219
       summary(fit1, standardized=TRUE, rsg=T)
1220
       summary(fit2, standardized=TRUE, rsq=T)
1221
1222
```



General rule

Repetition of tasks between studies = functions

Repetition of tasks within studies = apply family / loops



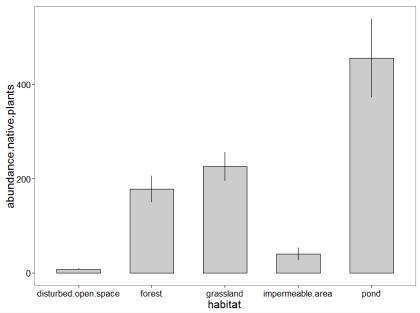
List of arguments, variables, etc

$$\overline{X} = \frac{\sum X}{N}$$

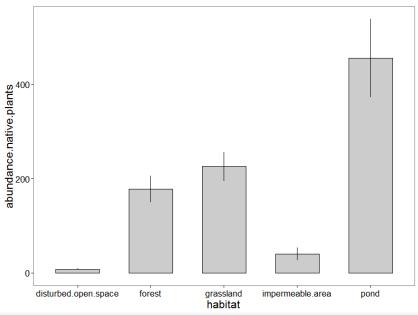
```
mean <- function(x)
{
   sum(x)/length(x)
}</pre>
```

```
RII = \frac{(\text{shrub-open})}{(\text{shrub+open})}
```

```
rii <- function(x, j, var)
{
s1 <- subset(x, Microsite == "shrub", select=var)
o1 <- subset(x, Microsite == "open", select=var)
return1 <- (s1 - o1) / (s1+o1)
x1 <- x[seq(1, nrow(x), by = 2),]
return2 <- cbind(x1[j], return1)
return2[is.na(return2)] <- 0
print(return2)
}</pre>
```



```
bar.plot <- function(data, predictor, response)
{
    ggplot(summary.data, aes(x=summary.data[,predictor], y=summary.data[,response]))
    + geom_bar(stat="identity", fill="grey80", color="black", width=0.6)+ theme_bw()+
        theme(panel.grid.minor=element_blank(),panel.grid.major=element_blank())+geom_er
        rorbar(aes(ymin=y.min,ymax=y.max, width=0))+ xlab(predictor) + ylab(response)+the
        me(text=element_text(size=16))
}</pre>
```



data

predictor – x axis

response – y axis

• •

```
bar.plot <- function(data, predictor, response)
{
    ggplot(summary.data, aes(x=summary.data[,predictor], y=summary.data[,response]))
    + geom_bar(stat="identity", fill="grey80", color="black", width=0.6)+ theme_bw()+
        theme(panel.grid.minor=element_blank(),panel.grid.major=element_blank())+geom_er
        rorbar(aes(ymin=y.min,ymax=y.max, width=0))+ xlab(predictor) + ylab(response)+the
        me(text=element_text(size=16))
}</pre>
```

```
Indices
rii(data, j, var)
LRR (data, treatment, control)
simpsons(data)
SE(x)
Plots
bar.plot(data, predictor, response)
stackedbar.plot(data, predictor1, predictor2, response)
pie.chart(data, predictor, response)
```

source("ecofunctions.r")

Reduces bloated code

Increases efficiency

Reduces mistakes

