

### Operators

=	Assigns a value to an object
<-	
x > y	x greater than y
x < y	x is less than y
x >= y	x greater than or equal to y
x <= y	x is less than or equal to y
!= x	not equal to x
!x	not x
x   y	x OR y
x & y	x AND y

### Basic R Functions

Access a function's help file

```
help( function name)
```

Load a csv file

```
read.csv( " snails.csv", header = TRUE, row.names = NULL)
```

Install a library

```
install.packages( " library name")
```

Load an installed library

```
library( library name)
```

Resize images in Jupyter and Google Collab

```
options( repr.plot.width = x, repr.plot.height = y)
```

Return the amount of values in x

```
length(x)
```

Return the number of rows in a dataframe

```
nrow(df)
```

Return the absolute value(s) in x

```
abs(x)
```



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### Basic R Functions (cont)

Return the sum of all the values in x

```
sum(x)
```

Return the square-root of the value(s) in x

```
sqrt(x)
```

Return the mean of the values in x with optional arguments for trimming and removing NAs

```
mean(x, tr = 0, na.rm = FALSE)
```

Return the median of the values in x with optional arguments removing NAs

```
median(x, na.rm = FALSE)
```

Return the sample standard deviation of values in x with optional argument for removing NAs

```
sd(x, na.rm = FALSE)
```

Return the sample variance of values in x with optional argument for removing NAs

```
var(x, na.rm = FALSE)
```

Return the quartiles for x with optional argument for removing NAs

```
quantile(x, na.rm = FALSE)
```

Sort the values of x into ascending order

```
sort(x)
```

Compute the median absolute deviation of x with optional argument to remove NAs

```
mad(x, na.rm = FALSE)
```

Find NA values in x (returns TRUE/FALSE)

```
is.na(x)
```

Paste things together into a single string

```
paste(x, y, z, sep = " ")
```

Create a table of counts

Examples:

```
table(x)
```

```
table(x, y)
```



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### Data Frames

Create a new data frame

```
Column_1 = c("A ", " B", " C")
Column_2 = c(21, 22, NA)
new_df = data.frame(Column_1, Column_2)
```

Add a column

```
new_df$column_3 = c(51, 52, 53)
```

Select a specific value (e.g., 52 = row 2, column 3)

```
new_df[2, 3]
```

Select a series of values (e.g., all of row 2)

```
new_df[2, c(1,2,3)]
or
new_df[2, ]
```

Select an entire column (e.g., column 2)

```
new_df$column_2
or
new_df[, 2]
```

Isolate column values that are not NAs

```
new_df$column_2[!is.na(new_df$column_2)]
```

### Subset Function

Used to select specific observations from a dataframe according to a rule you specify.

```
subset(dataframe, subset rule, select = ("columns to keep"))
```

Example:

```
outliers = subset(HeightData, Father < 60.1 | Father > 75.3, select = c("Father"))
```

### Library Functions

#### library(car)

Levene's Test

```
leveneTest(dataframe$response, dataframe$predictor, center = median)
```

Bootstrapping a Regression Model

```
x = Boot(model, R = 2000)
hist(x)
confint(x)
summary(x)
```

Type III Sum of Squares ANOVA

```
Anova(model, type = "III")
```



### Library Functions (cont)

#### library(effsize)

Cohen's d and Hedges g

```
cohen.d (y~x, data, hedges.co r r e ction = FALSE)
```

#### library(plyr)

Aggregate data frames

```
new_df = ddply( da t a frame, c("P red ictor1, Predic tor 2"), summarise,
  n = length (S c o r e _C o lumn),
  Means = mean(S cor e_C olumn) )
```

#### library(polycor)

Biserial Correlation

```
polyse rial(y, x)
```

#### library(pwr)

Sample Size for a Two-Sample T-test

```
pwr.t.t est(d, sig.level, power, type = c("t wo.s ample, " pai red "))
```

Sample Size for a One-Way ANOVA

```
pwr.an ova.te st(k, f, sig.level, power)
```

#### library(rcompanion)

Calculates lambda for Tukey's ladder of powers

```
trans for mT u k ey(x, plotit = FALSE, return Lambda = TRUE)
```

#### library(WRS2)

Winsorized variance of x

```
winvar(x, tr = .2)
```

Yuen's two sample t-test for trimmed independent means

```
yuen(y ~ x, tr = .2)
```

One-Way Robust Independent ANOVA with bootstrapping: F-tests

```
tlwayb t(R esponse ~ Predictor, data = data, tr = 0.2, nboot = 2000)
```

One-Way Robust Independent ANOVA with bootstrapping: Post Hoc

```
mcppb2 0(R esp onse~ Predictor, data = data, tr = 0.2, nboot = 2000)
```



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### Library Functions (cont)

#### Two-Way Robust Independent ANOVA: F-tests

```
t2way( Response ~ Predictor A+ Predictor B + Predictor A : Predictor B, data = depress, tr = 0.2)
```

#### Two-Way Robust Independent ANOVA: Post-Hocs

```
x = mcp2at m(R esponse ~ Predictor A+ Predictor B + Predictor A : Predictor B, data = depress, tr = 0.2)

x$cont rasts
x
```

### Distribution Functions

#### Return the the corresponding *quantile* for a given probability

##### Normal Distribution

```
qnorm (pr ob a b ility, mean, sd)
```

##### T Distribution

```
qt(pr oba bi lity, df, lower.t ail)
```

##### F Distribution

```
qf(pro bab ility, df1, df2, lower.t ail)
```

##### Chi-Square Distribution

```
qchisq (pr oba bility, df, lower.t ail)
```

#### Return the the corresponding *probability* for a given quantile.

##### Normal Distribution

```
pnorm (qu antile, mean, sd)
```

##### T Distribution

```
pt(qua ntile, df, lower.t ail)
```

##### F Distribution

```
pf(qua ntile, df1, df2, lower.t ail)
```

##### Chi-Square Distribution

```
pchisq (qu antile, df, lower.t ail)
```



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### Regression and ANOVA Functions

Factoring a Predictor `data_factor = factor(data_factor_me$Predictor)`

Viewing levels of a factor `levels(data_factor_me$Predictor)`

Linear Model `model = lm(Response ~ Predictor1 + Predictor2, data = data)`

Summary output of a linear model `summary(model)`

Linear Model Confidence Intervals `confint(model)`

F-test Model Comparisons `anova(model1, model2, model3, etc...)`

Anova main effects `summary(aov(model))`

Dummy Coding with 1s and 0s `ifelse(data_factor_me$Predictor == "X", 1, 0)`

Contrasts `cont1 = c(1, 1, -2)`  
`cont2 = c(1, -1, 0)`  
`contrasts(data_factor_me$Predictor) = cbind(cont1, cont2)`

Polynomial Contrasts `contrasts(data_factor_me$Predictor) = contr.poly(1, levels(data_factor_me$Predictor))`

Post Hoc Tests ("bonferroni", "holm", "BH") `pairwise.t.test(data_factor_me$Response, data_factor_me$Predictor, p.adjust.method = c("holm"))`

Tukey HSD `TukeyHSD(aov(model), "Predictor")`

Note: the `lm()` function stores many useful things as attributes:

`model$residuals`  
`model$coefficients`

### Common Statistical Tests and Calculations

T-test `t.test(y~x, alternative = c("two.sided"), mu = 0, var.equal = FALSE, conf.level = 0.95)`

Correlation `cor(x, y)`

Goodness-Of Fit (One Variable) `chisq.test(x = observed, p = expected probabilities)`



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### Common Statistical Tests and Calculations (cont)

#### Pearson's Chi-squared test (Two Variables)

```
chisq.test(table, correct = FALSE)
```

#### Fisher's Exact Test

```
fisher.test(table)
```

### Plotting: library(ggplot2)

#### Histogram

```
ggplot(dataframe, aes(x = Dep_Var)) +
  geom_histogram(colour = "black",
  fill = "white")
```

#### Density Plot

```
ggplot(dataframe, aes(x = Dep_Var)) +
  geom_density(colour = "black", fill = "pink", adjust = 1)
```

#### Boxplots

```
ggplot(dataframe, aes(x = Indep_Var, y = Dep_Var)) +
  geom_boxplot()
```

#### Barplot with errorbars

```
ggplot(plotData, aes(x = Indep_Var, y = Dep_Var, fill = Indep_Var)) +
  geom_bar(stat = "identity", colour = "black") +
  geom_errorbar(aes(ymin = bottom_value, ymax = top_value), width = .25)
```

#### Q-Q Plot For two independent samples

Remove + facet\_wrap() for a single sample

```
ggplot(dataframe, aes(sample = Dep_Var)) +
  stat_qq() +
  stat_qq_line() +
  facet_wrap(~ Indep_Var)
```

#### Line Plot of Means with Two Predictors

```
ggplot(plotData, aes(x = PredictorA, y = Means, group = PredictorB, colour = PredictorB)) +
  geom_line(position = position_dodge(width = 0.4)) +
  geom_point(position = position_dodge(width = 0.4))
```

#### Scatterplot with Regression Line

```
ggplot(dataframe, aes(x = predictor, y = response)) +
  geom_point() +
  geom_abline(intercept = b0, slope = b1)
```

