R tutorial / cheatsheet:

Getting help:

?functionname ??searchterm Functionname

#prints code

Datastructure information:

```
class(), attr(), rownames(),
colnames(), dim(), length(), nrow(),
ncol(), is.vector(), is.numeric(),
is.data.frame()
```

Datastructure manipulation:

```
c(), rbind(), cbind()
as.vector(),as.numeric(),
as.data.frame()
```

Boolean operators:

```
==, !=, &&, ||
exists(), is.na(), is.null(),
is.finite()
```

Filesystem:

```
getwd(), setwd()
dir(), file()
```

Distribution functions:

```
runif(), rnorm(), rgamma(), rbeta()
```

Loading Libraries:

```
require(<lname>)
library(<lname>)
```

Printing loaded objects and functions:

Ic/\

Reading/Writing datasets to disk:

```
data <- read.table(file="out.txt")
write.table(data, file="out.txt")</pre>
```

Handling large datasets:

head(), tail()

Matrices

```
\label{testmatrix} \begin{array}{lll} \text{testmatrix} & <- \text{ matrix}(1:8,8,4) & \# \text{ Empty matrix 8 rows 4 cols} \\ \text{testmatrix}[1,] & \# \text{ First row} \\ \text{testmatrix}[,1] & \# \text{ First column} \\ \text{vector}("list",10) & \# \text{ Empty list with 10 NULL} \\ \text{testdataframe} & <- \text{ as.data.frame}(\text{testmatrix}) \\ \text{testdataframe}\$V1 & \#(\text{First column, auto column on data.frame}) \\ \text{testmatrix}[,-2] & \# \text{ Remove second column} \\ \text{testmatrix}[,-2] & \# \text{ Print without row 1}^{\text{st}},4^{\text{th}} \text{ and 5}^{\text{th}} \text{ column} \\ \end{array}
```

Repeat and iteration:

```
for(var in seq) expr
while(cond) expr
apply(FUN,MARGIN,data)
#USE APPLY not FOR! Margin: cols 1, rows 2, or both c(1,2)
lapply(FUN,data) #Apply over a list
```

Missing data:

```
any(is.na(testmatrix))  # Any to all values in the matrix
testmatrix[2,1] <- NA
testmatrix[5,2] <- NA
any(is.na(testmatrix))  # Any to all values in the matrix
na.omit(testmatrix)</pre>
```

Sorting and matching

```
names1 <- paste("ind",1:10,sep="") #Create names
names2 <- paste("ind",5:15,sep="") #Create names
names1 %in% names2
names2 %in% names1
which(names1 %in% names2)
which(names2 %in% names1)</pre>
```

Text manipulation:

R isn't very good with text; however there are some neat tricks:

Plotting options:

Plotting is powerful the basic call to setup a window for use:

```
plot(x=c(-1,1),y=c(-10,25), xlab="D", ylab="R", main="F", type="n")
image() #for matrices (to make heatmaplike plots)
```

Now add lines/points v calling the functions

hclust() #for matrices (clustering)

```
p <- NULL
p$x <- 25
p$y <- 120
points(p)</pre>
```

However most objects can be plotted directly, or have specialized plotting routines.

Creating your own functions:

Error Handling:

```
stop("Something went terrible wrong")
warning("Some minor thing")
```

Installing packages

Using the Rgui: Packages -> install Packages
Using the commandline: R CMD INSTALL package_name.zip
Using the commandline: R CMD INSTALL package_name.tar.gz

Creating a basic R-script

Create a new file called script.R

```
numbers <- runif(100)
                                                     # Generate 100 random numbers
jpeg(file="graphoutput.jpg")
                                                     # Plot output to he JPEG file
hist(numbers)
                                                     # Make a histogram
dev.off()
                                                     # Close the JPEG
q("no")
                                                     # Quit without saving anything
Execute the script by running:
    R CMD BATCH script.R
A file script.Rout will be created this holds the 'verbose' output of the script (stdout)
Normally the last line in a script file will be something like:
    write.table(results,file="out.txt",sep="\t")
Basic statistics:
 Doing a t-test between two conditions
    cond1 <- rnorm(100)
    cond2 <- runif(100)</pre>
    t.test(cond1,cond2)
 Basic linair model:
    m1 <- as.factor(round(runif(100)))</pre>
    m2 <- as.factor(round(runif(100)))</pre>
    modelm2onm1 <- lm(cond1~m1+m2)</pre>
    modelm1onm2 <- lm(cond1~m2+m1)</pre>
    anova(modelm2onm1)
     anova(modelm1onm2)
```

Data to and from Molgenis

Basic exploration of data: find.data(), add.data(), remove.data()
Retrieving data: find.datamatrix(), add.datamatrix(), remove.datamatrix()

But also for all object types specialized functions are created to map to those objects, like in the case of genetic markers we can use:

And R supports a large number of statistical tests, machine learning algorithms, etc

find.markers(), add.markers(), remove.markers()