# Introduction to Bioinformatics

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# Special Values I

## NA (not available)

A placeholder for a missing value

```
> x <- c(1,NA,10,100)
> x
[1]   1  NA  10 100
> mean(x)
[1] NA
> mean(x,na.rm=T)
[1] 37
```

# Special Values II

## NULL

NULL represents the absence of a value, as opposed to the NA representing the lack of an existing value

```
> x <- c(1,NULL,10,100)
> x
[1]   1  NULL  10 100
> mean(x)
[1] 37
```

# which()

```
> x = 10:20
> x
 [1] 10 11 12 13 14 15 16 17 18 19 20
> x%%2==1
```

# which()

```
> x = 10:20
> x
 [1] 10 11 12 13 14 15 16 17 18 19 20
> x%%2==1
 [1] FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE
    TRUE FALSE
> which(x%%2==1)
[1]  2  4  6  8 10
```

# which()

```
> x = 10:20
> x
 [1] 10 11 12 13 14 15 16 17 18 19 20
> x%%2==1
 [1] FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE  TRUE FALSE
    TRUE FALSE
> which(x%%2==1)
[1]  2  4  6  8 10
> x[which(x%%2==1)]
[1] 11 13 15 17 19
```

# subset()

```
> x = 10:20
> x
 [1] 10 11 12 13 14 15 16 17 18 19 20
> subset(x,x > 13)
 [1] 14 15 16 17 18 19 20
```

# length()

```
> x <- c(1,2,3)
> length(x)
[1] 3
> x=NULL
> length(x)
[1] 0
> x=NA
> length(x)
[1] 1
```

# dim()

```
> a <- array(1:6,dim=c(3,2))
> a
     [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
> dim(a)
[1] 3 2
> length(a)
[1] 6
> attributes(a)
$dim
[1] 3 2
```

# colnames()/rownames

```
> a <- array(1:6,dim=c(3,2))
> a
     [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
> colnames(a)
NULL
> rownames(a)=c("a","b","c")
> colnames(a)=c("A","B")
> a
  A B
a 1 4
b 2 5
c 3 6
```

# rbind()

```
> a=1:5
> a
 [1]  1  2  3  4  5
> b=6:10
> b
 [1]  6  7  8  9  10
> rbind(a,b)
  [,1] [,2] [,3] [,4] [,5]
a    1    2    3    4    5
b    6    7    8    9   10
```

# cbind()

```
> a=1:5
> a
 [1]  1  2  3  4  5
> b=6:10
> b
 [1]  6  7  8  9  10
> cbind(a,b)
     a  b
[1,] 1  6
[2,] 2  7
[3,] 3  8
[4,] 4  9
[5,] 5 10
```

# table()

```
> a=c(1,0,1,0,1,0,2,3,4,"hello")
> table(a)
a
    0     1     2     3     4 hello
    3     3     1     1     1     1
```

# Set comparison

```
> A=10:19
> B=5:15
> A%in%B
 [1]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE FALSE FALSE FALSE
    FALSE
> A[A%in%B]
[1] 10 11 12 13 14 15
> A[!A%in%B]
[1] 16 17 18 19
```

# Logical operations

| Operator | Description |
|---|---|
| $x \&\& y$ | Logical AND (evaluates left to right ) |
| $x \& y$ | Logical AND (vectorized - returns vector) |
| $x \| \| y$ | Logical OR (evaluates left to right ) |
| $x \| y$ | Logical OR (vectorized - returns vector) |
| $!x$ | Logical NOT |

```
> x=c(T,F,F)
> y=c(T,T,T)
> x
[1]  TRUE FALSE FALSE
> x&y
[1]  TRUE FALSE FALSE
> x[1]&&y[2]
[1] TRUE
```

# if/else

```
> a=10
> if (a>5)
+ a=11
> a
[1] 11
> if (a<5)
+ {
+ b=1
+ } else {
+ b=2
+ }
> b
[1] 2
```

# loops

```
> for (i in 1:5)
+ print(i)
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
> for (i in c(2,4))
+ print(i^3)
[1] 8
[1] 64
```

# apply() I

```
> a <- array(1:6,dim=c(3,2))
> a
     [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
>for (i in 1:dim(a)[1])
+ print(mean(a[i,]))
[1] 2.5
[1] 3.5
[1] 4.5
> apply(a,1,mean)
[1] 2.5 3.5 4.5
```

# apply() II

```
> a
     [,1] [,2]
[1,]    1    4
[2,]    2    5
[3,]    3    6
> for (i in 1:dim(a)[2])
+ print(mean(a[,i]))
[1] 2
[1] 5
> apply(a,2,mean)
[1] 2 5
```

# apply() III

`apply(m,dimcode,f,fargs)`

- *m* is an array
- *dimcode* is the dimension of interest
  - 1 indicates rows
  - 2 indicates columns
- *f* is the function to be applied
- *fargs* optional arguments to function f

# lapply()

```
> mylist=list(1:3,6:7)
> mylist
[[1]]
[1] 1 2 3

[[2]]
[1] 6 7

> lapply(mylist,median)
[[1]]
[1] 2
[[2]]
[1] 6.5
```

# sapply()

```
> mylist=list(1:3,6:7)
> mylist
[[1]]
[1] 1 2 3

[[2]]
[1] 6 7

> sapply(mylist,median)
[1] 2.0 6.5
```

# Where am I?

- Current location:

```
> getwd()
[1] "/home/alexdem"
```

- Change location:

```
> setwd("/usr")
> getwd()
[1] "/usr"
```

- List directory contents:

```
> list.files()
 [1] "bin" "games" "Gemote" "include"
 [5] "lib" "lib32" "libx32" "local"
 [9] "mips-linux-gnu" "sbin" "share" "src"
```

# Read from a text file I

**read.table()**

Reads a file in table format and creates a data frame from it, with cases corresponding to lines and variables to fields in the file

Indicative parameters:

- *file*: the name of the file which the data are to be read from
- *header*: logical value. Is the first line a header?
- *sep*: the field separator character
- *quote*: the set of quoting characters
- *as.is*: the default behavior of read.table is to convert character variables (which are not converted to logical, numeric or complex) to factors

# Read from a text file II

- *strip.white*: logical. Allows the stripping of leading and trailing white space from unquoted character fields (numeric fields are always stripped)
- . . .

Similar functions: `read.csv()`, `read.csv2()`, `read.delim()`, `read.delim2()`

# Read from a text file III

```
alexdem@pine:$ cat file1.tsv
Name    ID
alex    1234
john    4567
mary    1097

> read.table("file1.tsv")
    V1   V2
1 Name   ID
2 alex 1234
3 john 4567
4 mary 1097
```

# Read from a text file IV

```
> read.table("file1.tsv",header=T)
  Name   ID
1 alex 1234
2 john 4567
3 mary 1097
```

# Attention!

- The path must be inside double quotes
- In Linux & Mac OS the path has the form /tmp
- In Windows the path has the form c:\\tmp
- Spaces in the file header (usually) create reading problems
- The wrong *sep* choice definitely leads to reading errors!

# Writing to a text file I

## write.table()

write.table prints its required argument x (after converting it to a data frame if it is not one nor a matrix) to a file or connection

Similar arguments to `read.table()`

```
> a=array(1:12,dim=c(3,4))
> a
     [,1] [,2] [,3] [,4]
[1,]    1    4    7   10
[2,]    2    5    8   11
[3,]    3    6    9   12
>write.table(a,"/tmp/file2.txt")
```

# Writing to a text file II

```
alexdem@pine:~$ cat /tmp/file2.txt
"V1" "V2" "V3" "V4"
"1" 1 4 7 10
"2" 2 5 8 11
"3" 3 6 9 12
```

# Writing to a text file III

```
write.table(a,"/tmp/file2.txt",quote = F,row.names =
    F,col.names = F)
```

```
alexdem@pine:~$ cat /tmp/file2.txt
1 4 7 10
2 5 8 11
3 6 9 12
```

# Excel files

External packages, such as `readxl` , `XLConnect`, `xlsx`, `gdata`, ... allow reading from Excel files but also **writing** to them. E.g.:

```
library(readxl)
A=read_xlsx("/tmp/file2.xlsx",sheet = 1)
library("xlsx")
write.xlsx(x = A, file = "/tmp/file3.xlsx", sheetName =
   "Status", row.names = FALSE)
```

# External packages/libraries

- Plenty of available packages
- They can be loaded to a session environment using the commands `library()` or `require()`, e.g. `require("readxl")`
- An existing package can easily be downloaded and installed from a repository, e.g.

```
install.packages("MASS")
```

- For bioinformatic applications, the largest repository is bioconductor (`https://www.bioconductor.org/`)

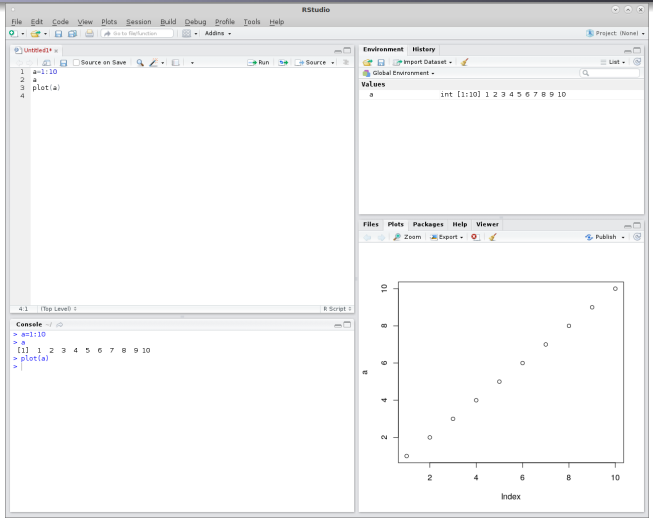
```
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install()
BiocManager::install(c("GenomicFeatures",
   "AnnotationDbi"))
```

# Rstudio IDE I

Rstudio (`https://posit.co/products/open-source/rstudio/`)

- An integrated development environment (IDE) for R
- It includes a console, syntax-highlighting editor that supports direct code execution, as well as tools for plotting, history, debugging and workspace management
- Available in open source and commercial editions
- Runs on the desktop (Windows, Mac, and Linux) or in a browser connected to RStudio Server or RStudio Server Pro (Debian/Ubuntu, RedHat/CentOS, and SUSE Linux)

# Rstudio IDE II



# Questions?