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# DCMB BioComputing BootCamp

## Day 3, Session II:

# R Control Structures and Functions

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# Overview

1. Working Directory
2. Reading and Writing Data in R
3. Factors
4. Using Indexes
5. Merging Data Frames
6. Functions
7. Program Control Structures

# Use Directory Structure to Organize Your Work

- Imagine if all of your input data, code, output data, images files were all in the same directory!
- Sounds like a mess!
- There is no perfect/standard directory structure, but here are a few suggestions:
  1. Create a unique directory for each project
  2. Break your code up into parts
  3. Write output (i.e. tables, images) to a separate sub-directory



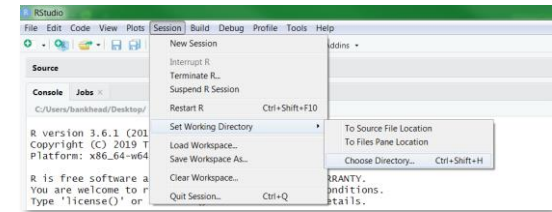
# The R Working Directory

In-Class Exercise:  
Try It Out!

- R executes commands from a 'working directory'
  - scripts, input files, output files
  - absolute and relative directories may be specified
- Use `getwd()` to display current working directory

```
> getwd()
```

```
[1] "C:/Users/bankhead/Documents"
```



- Use Session->Set Working Director->Choose Directory or `setwd()` to change your working directory

```
> setwd("../Desktop/armandsFolder")
```

- Use `dir()` to list files and folders in your working directory

**Exercise: Create a directory/folder outside of R and change R's working directory to that directory**

# Writing Data To Text Files

- First lets create something to write as a text file

```
> m4 = matrix(1:300,nrow=100,ncol=3)
```

```
> colnames(m4) = c('A','B','C')
```

```
> m4 = data.frame(m4,D = c(rep('X',50),rep('Y',50)))
```

- Use `write.table()` to write data to a file

- Many arguments! Use `?write.table` to find out more

```
> write.table(m4, 'myData.txt', quote=F, row.names=F, sep="\t")
```

```
> dir()
```

```
[1] "myData.txt"
```

# Reading Data From Text Files

- Use `read.delim()` to read data from a file

```
> m5 = read.delim('myData.txt')
```

$$> \dim(m5)$$

```
> head(m5)
```

- By default the first row is read in as column names
- Our data appears to be read in correctly but R has converted our text data into something called a factor

> m5\$D

[illegible]

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# Factors in R

- Factors are used to break complex data up into discrete categories
- This comes in handy when we need to group samples for statistical analysis (e.g. fitting linear models)
- Adding new values can generate errors!
- By default R will convert non-numeric data into factors
  - Use `options(stringsAsFactors=FALSE)` in your scripts to over-ride!

```
> options(stringsAsFactors = FALSE)
> m5 = read.delim('myData.txt')
> m5$D
```

```
[1] "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X"
[30] "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "X" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y"
[59] "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y"
[88] "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y" "Y"
```

# Using Indexes

- Indexing is a powerful tool for filtering large data frames or matrices
- There are two commonly used ways to index:

1. Logical vectors:

```
> m5$A < 10
```

```
[1] TRUE TRUE TRUE ....
```

2. Integer vectors:

```
> which(m5$A < 10)
```

```
[1] 1 2 3 4 5 6 7 8 9
```

```
> m5$A < 10
[1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[20] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[39] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[58] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[77] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[96] FALSE FALSE FALSE FALSE FALSE
> which(m5$A < 10)
[1] 1 2 3 4 5 6 7 8 9
```

# Using Indexes

- We can combine multiple conditions use the `&`, `|`, and parens

```
> m5$A < 10 & m5$B > 205
> m5$A < 10 & m5$B > 205 | m5$D == 'Y'
> m5$A < 10 | m5$D == 'Y' & m5$A < 55
```

- Be aware of operator precedence
- Use the `sum` command to count how many positive values survive
- Indexes can be used to index vectors, matrices, or data frames

```
> idx = m5$A < 10 & m5$C > 205
> subMatrix = m5[idx,]
```

Operator Precedence in R

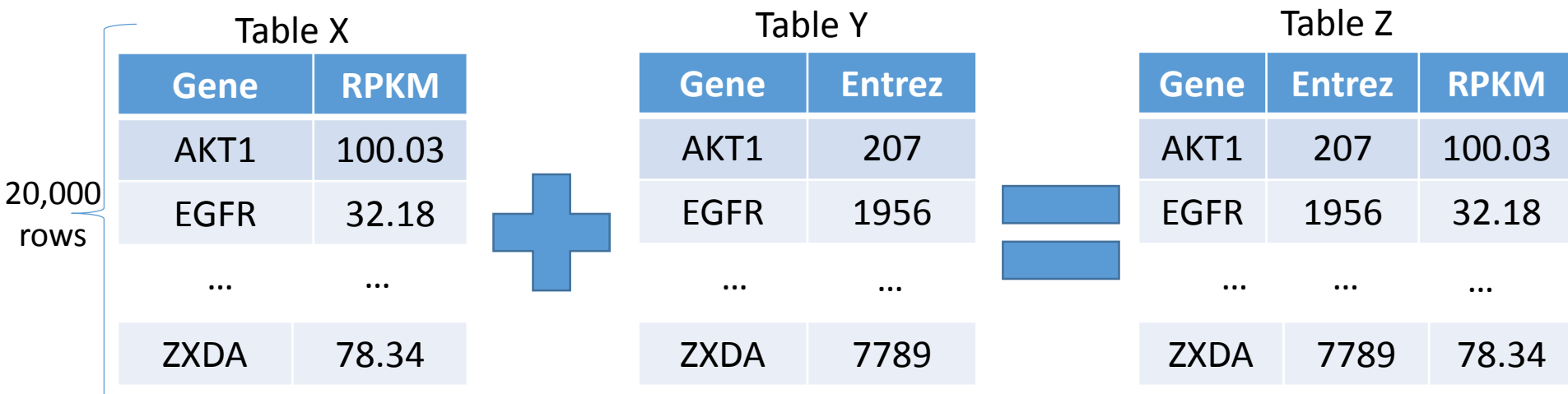
Operator	Description	Associativity
<code>^</code>	Exponent	Right to Left
<code>-X</code> , <code>+X</code>	Unary minus, Unary plus	Left to Right
<code>%%</code>	Modulus	Left to Right
<code>*</code> , <code>/</code>	Multiplication, Division	Left to Right
<code>+</code> , <code>-</code>	Addition, Subtraction	Left to Right
<code>&lt;</code> , <code>&gt;</code> , <code>&lt;=</code> , <code>&gt;=</code> , <code>==</code> , <code>!=</code>	Comparisons	Left to Right
<code>!</code>	Logical NOT	Left to Right
<code>&amp;</code> , <code>&amp;&amp;</code>	Logical AND	Left to Right
<code> </code> , <code>  </code>	Logical OR	Left to Right
<code>-&gt;</code> , <code>-&gt;&gt;</code>	Rightward assignment	Left to Right
<code>&lt;-</code> , <code>&lt;&lt;-</code>	Leftward assignment	Right to Left
<code>=</code>	Leftward assignment	Right to Left

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# Merging Data Frames

- A common programming task in bioinformatics is to “join” two tables:



- Joins are performed in R using the `merge()` function
  - Requires a common column between tables (e.g. gene) be specified using the “by” parameter
  - Multiple types of joins (e.g. inner, outer) are possible, use `?merge` to find out more

# Merging Data Frames

- Use `merge()` to join together data from two different matrices or data frames
- **Important: both matrices must contain unique row identifiers to join on!**

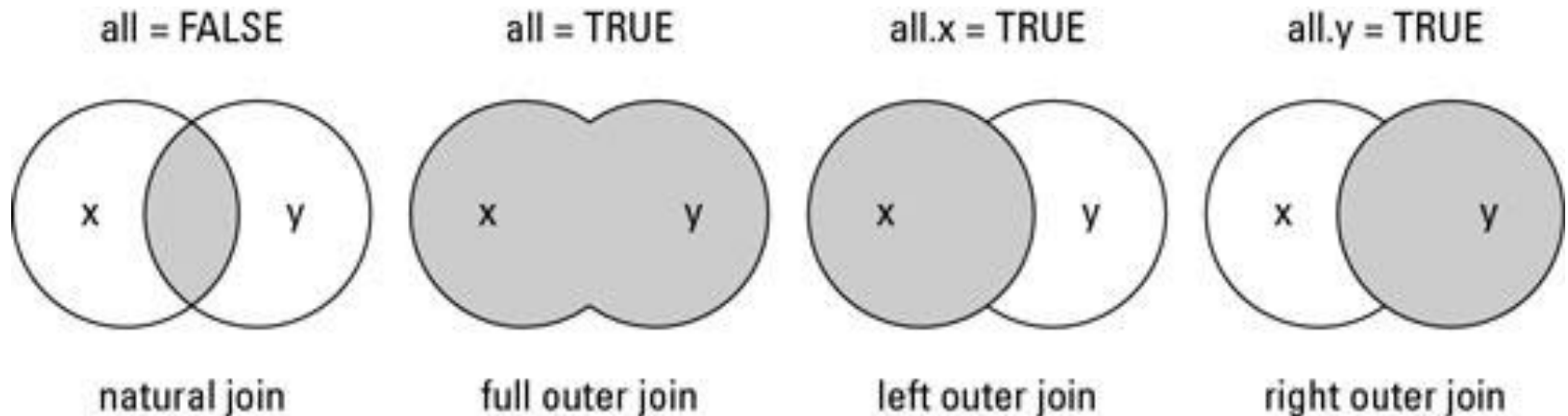
```
> df1 = data.frame(gene = c('AKT1', 'ERBB2', 'EGFR'),  
log2rpkm = c(5, .5, 10))
```

```
> df2 = data.frame(gene = c('AKT1', 'ERBB2', 'EGFR'),  
entrez = c(207, 2064, 1956))
```

```
> combined = merge(df1, df2, by='gene')
```

**Exercise: Execute the code above. Using the `dim()` function, what are the number of rows and columns of the 'combined' data frame?**

# Merging Data Frames: Types of Joins



- natural join: intersection of common rows
- full outer join: union of rows
- left outer join: all x rows represented
- right outer join: all y rows represented

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# Functions

- Functions allow us to break our R scripts up into modular pieces
- Modular program design has already been discussed in unix (day1) and python (day2)
- Benefits to our code include:
  - Program design
  - Readability
  - Re-use
  - Trouble-shooting

- Functions are specified using the 'function' key word

```
myFunction = function(arg1, arg2, ...) {  
  statements  
}
```

- When multiple arguments are specified R will match first by name, prefix matching arguments, then by position

# Function Example #1

```
sql = function(x) return(x * x)
```

```
randomValues1 = rnorm(30)
```

```
randomValues2 = sql(randomValues1)
```

Exercise: Create an R script that contains the code above. How do randomValues1 differ from randomValeus2?

# Function Example #2

```
sql = function(x) return(x * x)
```

```
randomValues1 = rnorm(30)
```

```
randomValues2 = sql(randomValues1)
```

```
myAnalysis = function(values1, values2) {  
  vector1 = values1  
  vector2 = values2  
  result = cor(vector1, vector2)  
}
```

```
result = myAnalysis(randomValues1, randomValues2)  
print(result)
```

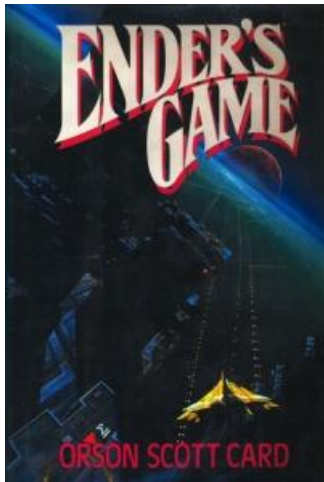
**Exercise: Create an R script that contains the code above.  
What correlation value is generated?**

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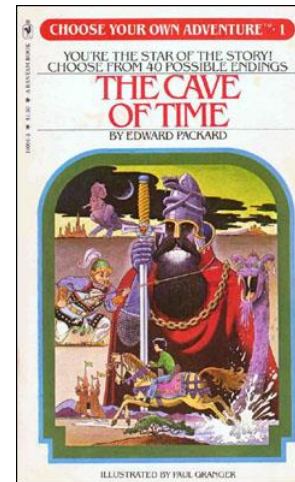
# What is a Control Structure?

- Control structures allow programmers to change the flow of a program
- As programmers we may want code to repeat or be skipped
- Example: if/else statements allow conditional execution of code



One single linear path

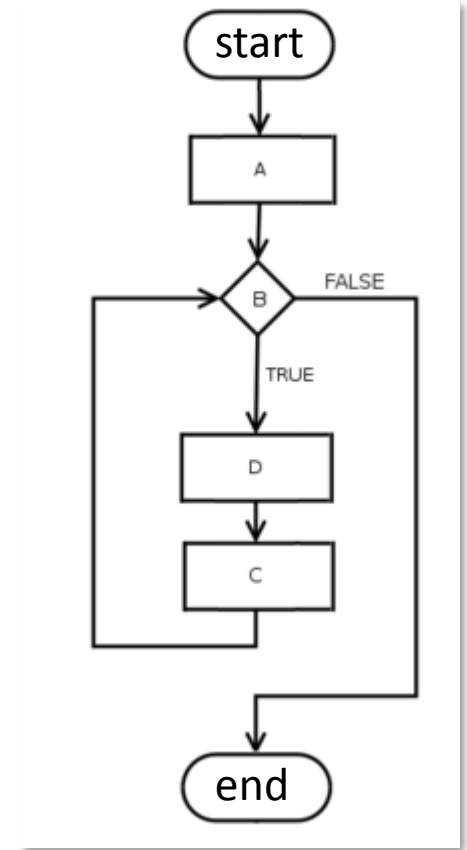
VS.



Multiple branching linear paths

# Program Control Structures

- R program flow is not always a linear sequence of operations
- Besides functions, program flow may be modified using control structures
  1. apply
  2. if/else/else if
  3. for
  4. while
- Other important R commands that can alter program flow:
  1. break – exit loop
  2. next – skip to the next iteration



program flowchart

# Program Control Structures: apply

In-Class Exercise:  
Try It Out!

- Use the apply function to iterate through a data.frame, matrix, or arrays
  - Use lapply() to iterate through lists or vectors
- apply function takes at least 3 values
  1. data frame/matrix
  2. 1 or 2 indicating rows or columns respectively
  3. function to 'apply' to each value (standard or custom)

```
> m4 = matrix(1:300,nrow=100,ncol=3)
```

```
> rowMeans = apply(m4,1,mean)
```

```
> columnMeans = apply(m4,2,mean)
```

**Exercise: Run the code above.**

**What data structures are rowMeans and columnMeans?**

**Are rows on average larger or columns?**

# Program Control Structures: if/else/else if

- 'if' statements allow us to condition our program flow
- basic syntax:

```
if(condition) {  
    statement1  
}  
else if(condition) {  
    statement2  
}  
else {  
    statement3  
}
```

- conditions must be TRUE or FALSE
- statements are a series of R commands

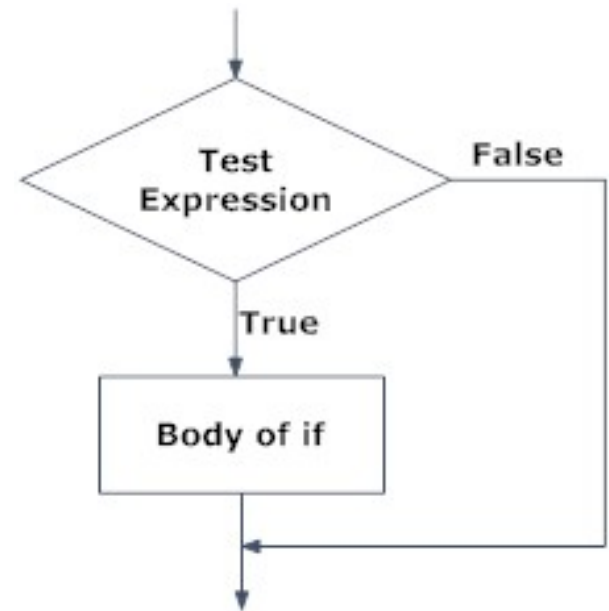


Fig: Operation of if statement



# Program Control Structures: if/else/else if

- Example if statement

```
m5 = read.delim('myData.txt')
if(ncol(m5) == 4 && is.factor(m5$D)) {
  print('factors!')
}
else {
  print('no factors!')
}
```

- Multiple conditions can be combined using:
  - || OR
  - && AND
  - ! NOT
  - () parens

# Program Control Structures: for

- 'for' loops allow us to iterate our code
- Basic syntax:

```
for(counter in vector) {  
    statements  
}
```

- 'vector' can represent a list of numbers (e.g. 1:10) or arbitrary data types (e.g. c('mon','tues','wed',...))

# Program Control Structures: for

- **Example #1:**

```
for(i in 1:5) {  
  print(i)  
}
```

- **Example #2:**

```
m5 = read.delim('myData.txt')  
for(column in 1:ncol(m5)) {  
  print(mean(m5[,column]))  
}
```

- 'break' can be used to exit loop structure
- We could have used apply!

# Program Control Structures:

## while

- while() loops allow iteration until a condition is no longer true
- Basic syntax:

```
while(condition) {  
    statements  
}
```

To exit the loop structure

- 'break' can be used to exit loop structure
- set condition to be false

# Exercises

1. Create a new script called `convertDegrees.R`
2. Write a function that converts Fahrenheit to Celsius
  - input: temperature in Fahrenheit
  - output: temperature in Celsius
3. Write a program that builds a data frame containing degrees in Fahrenheit and Celsius for values of Fahrenheit between -30 to 130

HINT:  $\text{celsius} = (\text{fahrenheit} - 32) \times 5/9$

3. Write the table from #2 to a tab-delimited text file

# References

- Gentleman, Robert. R Programming for Bioinformatics. CRC Press, 2009.
- Slides source in part from Barry Grant and Hui Jiang

# Bonus Exercise (if time!)

- The `unique()` function can be used to get the unique values in a vector
- The CO2 data set contains 84 measurements from an experiment comparing the CO2 uptake of *Echinochloa crus-galli* sourced from Quebec and Mississippi. Plants were measured chilled and nonchilled.
- Using the CO2 data set determine if the average expression of chilled plants from Quebec is higher than plants from Mississippi.