RAdvanced
Lists

PhD Toolbox - R introductory course - stream II
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object class: list

A list is a group of any type of objects (vector, matrix, data.frame)

- function is **list**(), each object in the list can be identified by a name

```
> vector <- rep(c("A", "B"), 2, each=2)

> matrix <- rbind(c(1,2),c(1,2),c(1,2))

> df<-data.frame(  "colname_1"=rep(c("A", "B"), 2, each=2),
                   "colname_2"=sample(seq(1,30), 8),
                   "colname_3"=seq(8,11.5, by=0.5))


> my_list<-list("vector"=vector, "matrix"=matrix, "dataframe"=df)

> str(my_list)
List of 3
 $ vector   : chr [1:8] "A" "A" "B" "B" ...
 $ matrix   : num [1:3, 1:2] 1 1 1 2 2 2
 $ dataframe:'data.frame':8 obs. of  3 variables:
  ..$ colname_1: chr [1:8] "A" "A" "B" "B" ...
  ..$ colname_2: int [1:8] 7 24 20 23 22 25 1 10
  ..$ colname_3: num [1:8] 8 8.5 9 9.5 10 10.5 11 11.5
```

rows/columns/object indexing in lists

select element in list

```
> my_list[[1]]  # positional selection (select the first element)
```

```
[1] "A" "A" "B" "B" "A" "A" "B" "B"
```

```
> my_list[["df"]] # selection by name
```

```
  colname_1 colname_2 colname_3
1         A        13       8.0
2         A         5       8.5
3         B        20       9.0
4         B        21       9.5
5         A         9      10.0
6         A        28      10.5
7         B         8      11.0
8         B        12      11.5
```

rows/columns/object indexing (lists)

select column in a dataframe included in a list

```
> my_list[["df"]]$colname_1
[1] "A" "A" "B" "B" "A" "A" "B" "B"
```

select rows (or columns) in element included in a list

```
> my_list[["df"]][1:5,]
  colname_1 colname_2 colname_3
1         A        13       8.0
2         A         5       8.5
3         B        20       9.0
4         B        21       9.5
5         A         9      10.0
```

Why to work with lists in R

Few....but worth reasons!

- reduce lines of code
- Enhance reproducibility in your data analysis

  functions are applied simultaneously to all list elements (less prone to human errors)

- speed-up complex data analysis (also with multi-core functions)
- The only way to go when dealing with hundreds separate datasets

functions to work with lists

Main functions are:

- **list()**
- lapply()
- sapply
- unlist()
- do.call() / rbindlist

lapply() list-apply

We first need to introduce the **apply**() function

What it does?

Takes a matrix or data.frame in input and applies functions to it **column-wise** or **row-wise**

```
> m1 <- matrix(1:10,nrow=5, ncol=6)
> m1
     [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    1    6    1    6    1    6
[2,]    2    7    2    7    2    7
[3,]    3    8    3    8    3    8
[4,]    4    9    4    9    4    9
[5,]    5   10    5   10    5   10
```

apply()

We first need to introduce the **apply**() function. Not really....

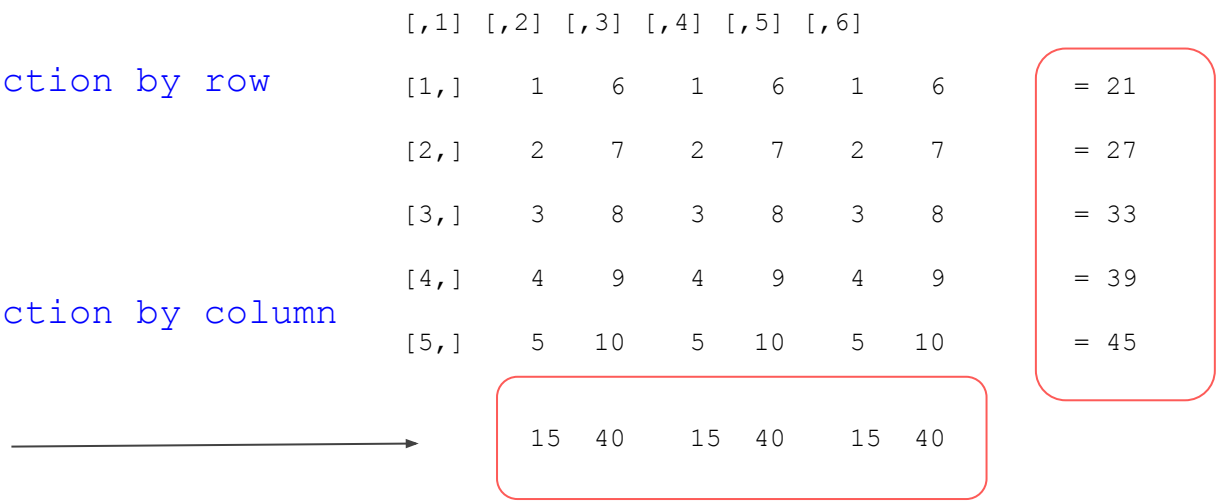
apply(object, margin, function)

```
# margin=1 applies function by row

> apply(m1, 1, sum)
[1] 21 27 33 39 45

# margin=2 applies function by column

> apply(m1, 2, sum)
[1] 15 40 15 40 15 40
```



"apply is simpler only if your data are already simpler than reality."

apply()

We first need to introduce the **apply**() function

apply(object, margin, function)

```
# with custom functions
> apply(m1, 2, function(x) x+1)
     [,1] [,2] [,3] [,4] [,5] [,6]
[1,]    2    7    2    7    2    7
[2,]    3    8    3    8    3    8
[3,]    4    9    4    9    4    9
[4,]    5   10    5   10    5   10
[5,]    6   11    6   11    6   11
```

Note: apply() returns a vector or a matrix/dataframe depending on the input and the function applied.

lapply()

the workhorse of iteration in R

What it does?

Applies a function to list/vector of elements. Functions are applied to each element individually.

lapply(object, function)

```
# a simple example on a vector

> vector<-c(1,2,3,4)

> lapply_output<-lapply(vector, function(x) x+100)

> str(lapply_output)

List of 4
 $ : num 101
 $ : num 102
 $ : num 103
 $ : num 104


> unlist(lapply output)
[1] 101 102 103 104
```

lapply() list-apply

What it does?

Applies a function to list/vector of elements. Functions are applied to each element individually.

lapply(object, function)

```
# a simple example on list

# generate a list from two simple vectors
> fruits=c("banana", "apple", "apricot", "peach")
> colors=c("yellow", "red", "orange", "pink")

> items<-list(fruits=fruits,colors=colors)

> items
$fruits
[1] "banana"  "apple"   "apricot" "peach"

$colors
[1] "yellow" "red"    "orange" "pink"
```

lapply() list-apply

What it does?

Applies a function to list/vector of elements. Functions are applied to each element individually.

lapply(object, function)

```
# a simple example on list

> lapply(items, length)
$fruits
[1] 4

$colors
[1] 4
```

lapply() list-apply

What it does?

Applies a function to list/vector of elements. Functions are applied to each element individually.

lapply(object, function)

```
# a simple example on list using custom functions

> lapply(items, function(x) str_length(x))
$fruits
[1] 6 5 7 5

$colors
[1] 6 3 6 4
```

lapply()

lapply() is useful mostly when you have list of data.frames!

If you want to recursively work on data.frames in a list, they must contain the same columns

```
# create a list of two dataframes
> list_df<-list(df_1=df_1, df_2=df_1)

> list_df
$df_1
   fruits colors
1  banana yellow
2   apple    red
3 apricot orange
4   peach   pink

$df_2
   fruits colors
1  banana yellow
2   apple    red
3 apricot orange
4   peach   pink
```

df_1<-data.frame(
fruits=fruits, colors=colors)

lapply()

lapply() is useful mostly when you have list of data.frames!

```
# list class of each elements in the list
> lapply(list_df, class)
$df_1
[1] "data.frame"

$df_2
[1] "data.frame"

# count words length in the first column of each element
> lapply(list_df, function(x) str_length(x[,1]))
$df_1
[1] 6 5 7 5

$df_2
[1] 6 5 7 5
```

lapply()

lapply() is useful mostly when you have list of data.frames!

```
# select columns in a list of data.frames

> lapply(list_df, "[", c(2))
$df_1
  colors
1 yellow
2    red
3 orange
4   pink

$df_2
  colors
1 yellow
2    red
3 orange
4   pink
```

```
# by column name
> lapply(list_df, "[", "fruits")

# using tidyverse grammar
>lapply(list_df, function(x) x %>%
select(fruits))
```

sapply() simplified apply

What it does?

Applies a function to list/vector of elements

sapply(object, function)

```
# sapply
# same as lapply but returns a vector
> sapply(list, function(x) str_length(x))
     fruits colors
[1,]      6      6
[2,]      5      3
[3,]      7      6
[4,]      5      4
```

Map()

What it does? It applies a function to the corresponding (aligned) elements of given vectors (or lists).

Map(function, **item_1**, **item_2**)

```
# Map object name to a column

> Map( cbind, list_df, new_col=names(list_df) )
```

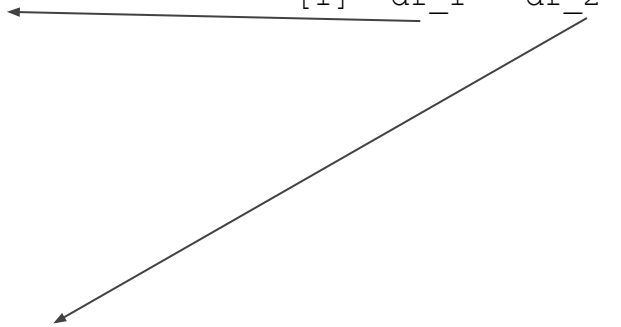
item_1

```
$df_1
   fruits colors
1  banana yellow
2   apple    red
3 apricot orange
4   peach   pink

$df_2
   fruits colors
1  banana yellow
2   apple    red
3 apricot orange
4   peach   pink
```

item_2

```
> names(list df)
[1] "df_1" "df_2"
```



Output

```
$df_1
   fruits colors new_col
1  banana yellow    df_1
2   apple    red    df_1
3 apricot orange    df_1
4   peach   pink    df_1

$df_2
   fruits colors new_col
1  banana yellow    df_2
2   apple    red    df_2
3 apricot orange    df_2
4   peach   pink    df_2
```

Map()

Map applies a function to the corresponding (aligned) elements of given vectors (or lists).

Map(function, item_1, item_2)

```
# Map object name to a column

> Map(cbind, list_df, new_col=names(list_df))
$df_1
   fruits colors new_col
1  banana yellow    df_1
2   apple    red    df_1
3 apricot orange    df_1
4   peach   pink    df_1

$df_2
   fruits colors new_col
1  banana yellow    df_2
2   apple    red    df_2
3 apricot orange    df_2
4   peach   pink    df_2
```

```
> lapply(   list_df, function(x) cbind(x,
                new_col=names(list_df)) )
$df 1
   fruits colors new col
1  banana yellow    df 1
2   apple    red    df 2
3 apricot orange    df 1
4   peach   pink    df_2

$df 2
   fruits colors new col
1  banana yellow    df 1
2   apple    red    df 2
3 apricot orange    df 1
4   peach   pink    df_2
```

unwanted behavior!

multi-core versions

`library(parallel)` implements parallelized version of many functions

mclapply(..., mc.cores=n)

mcMap(..., mc.cores=n)

...

When are they useful?

- your dataset is really big and your standard function takes too long to run
- when using functions which query a remote database (you can forward multiple queries at once)

do.call()

What it does?

Calls a function on a list of arguments.

do.call(function, list)

lapply(): function is applied to each element of a list

do.call(): function is applied only one time with the arguments provided (list)

```
> do.call(sum, list(1,1))

[1] 2

> do.call(sum, list(c(1,1), c(1,1)))

[1] 4
```

```
> lapply(list(c(1,1), c(1,1)), sum)
[[1]]
[1] 2

[[2]]
[1] 2
```

do.call() - Collapse lists

An example use case on lists:

You have done your analysis or summarized your data and you need to collapse your list

do.call()

```
> list_df
$df_1
   fruits colors
1  banana yellow
2   apple    red
3 apricot orange
4   peach   pink

$df_2
   fruits colors
1  banana yellow
2   apple    red
3 apricot orange
4   peach   pink
```

```
> do.call(rbind, list_df)

      fruits colors
df_1.1  banana yellow
df_1.2   apple    red
df_1.3 apricot orange
df_1.4   peach   pink
df_2.1  banana yellow
df_2.2   apple    red
df_2.3 apricot orange
df_2.4   peach   pink
```

rbindlist() - Collapse lists

You have done your analysis or summarized your data and you need to collapse your list

The modern way:

```
> dplyr::bind_rows(list_df, .id="df") )
```

```
> data.table::rbindlist(list_df, idcol = "df")
```

```
     df  fruits colors
1: df_1  banana yellow
2: df_1   apple    red
3: df_1 apricot orange
4: df_1   peach   pink
5: df_2  banana yellow
6: df_2   apple    red
7: df_2 apricot orange
8: df_2   peach   pink
```

A real use case example

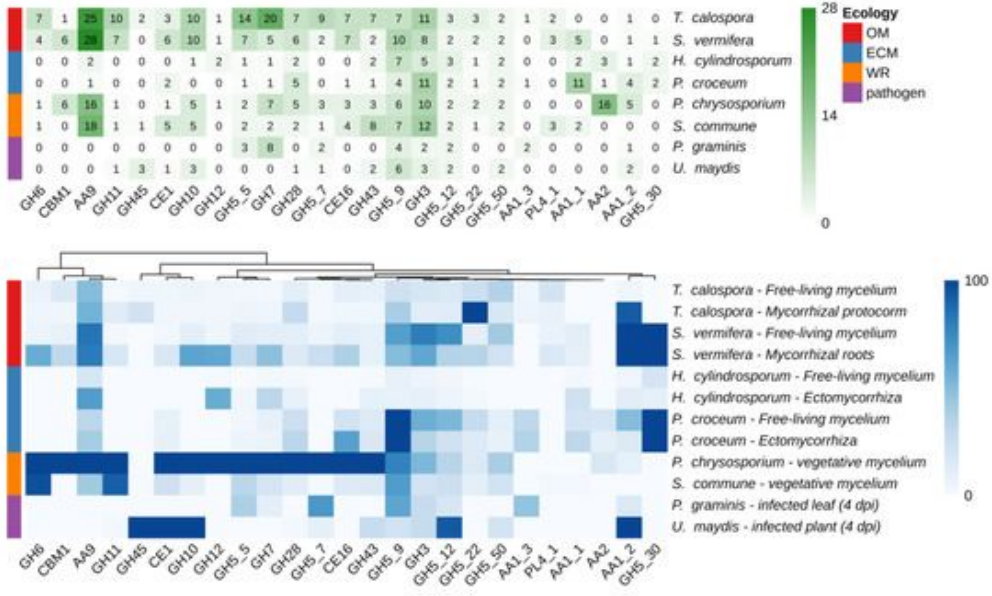
The dataset contains CAZymes genes predictions (enzymes involved in the assembly, modification or deconstruction of carbohydrates) in the transcriptomes of 8 fungal species.

Adamo, Chialva et al., 2020.

- The software who generated predictions outputs 1 file for each species.

List all the files in your folder

```
>files<-list.files(pattern =
".txt")
```



A real use case example

Import all the files listed in the object files into a list

- for each elements in the field vector do the read.delim() function
- be careful since text files has an header

A real use case example

Import all the files listed in the object files into a list

- for each elements in the field vector do the read.delim() function
- be careful since text files has an header

```
# import multiple predictions in a list at once
> pred <- lapply(files, function(x) read.delim(x, header = T))
```

A real use case example

Assign the species names to each elements in the list

Suggestion 1: the species name is contained in the names of each file in “file” object.

Suggestion 2: remove “.txt” file extension using str_replace()

A real use case example

Assign the species names to each elements in the list

Suggestion 1: the species name is contained in the names of each file in “file” object.

Suggestion 2: remove “.txt” file extension using str_replace()

```
# assign names to list elements
> names(pred)<-str_replace(files, ".txt", "")
```

A real use case example

Filter each data.frame in the list by `X.ofTools` column >=2

- use **filter**()

A real use case example

Add a column in each data.frame indicating the name of the Species

- use **Map**()

A real use case example

operations on columns

split the Gene.ID column

- use **separate**() to split fields in Gene.ID column
- field separator “|” is a special character: use “\\|” to escape

A real use case example

####### Collapse the list into a data.frame

- use **rbindlist**() or **do.call**()

####### export each element of the list into a .tsv file

- use write.table
- tab separator is “\t”