Data structures in R
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This is from the first chapter of learn.r-journalism.com.

Vectors

A vector is a sequence of data elements of the same basic type. The parts that consist of a vector are called components or elements.

```
vec1 <- c(1,4,6,8,10)
vec1
## [1] 1 4 6 8 10
```

A vector vec is explicitly constructed by the concatenation function c().

```
vec1[5]
## [1] 10
```

Elements in vectors can be addressed by standard [i] indexing

```
vec1[3] <- 12
vec1
## [1] 1 4 12 8 10
```

One of the elements in the array is replaced with a new number.

```
vec2 <- seq(from=0, to=1, by=0.25)
vec2
## [1] 0.00 0.25 0.50 0.75 1.00
```

This shows another useful way of creating a vector: the seq() or sequence function.

```
sum(vec1)
## [1] 35
```

Data frames

If you’re used to working with spreadsheets, then data frames will make the most sense to you in R.

This is how to create a data frame from arrays. You don’t have to fully understand this at this point– the data you’ll be working with will come pre-structured if you’re importing spreadsheets.
patientID <- c(111, 208, 113, 408)
age <- c(25, 34, 28, 52)
sex <- c(1, 2, 1, 1)
diabetes <- c("Type1", "Type2", "Type1", "Type1")
status <- c(1, 2, 3, 1)

patientdata <- data.frame(patientID, age, sex, diabetes, status)

patientdata

## patientID age sex diabetes status
## 1 111 25 1 Type1 1
## 2 208 34 2 Type2 2
## 3 113 28 1 Type1 3
## 4 408 52 1 Type1 1

But this is what’s happening. A set of arrays are being created and a function called data.frame() joins them together into a data frame structure.

How to pull elements from a data frame:

# a : means "through"

patientdata[1:2]

## patientID age
## 1 111 25
## 2 208 34
## 3 113 28
## 4 408 52

# So 1:2 means 1 through 2

patientdata[c("diabetes", "status")]

## diabetes status
## 1 Type1 1
## 2 Type2 2
## 3 Type1 3
## 4 Type1 1

patientdata$age

## [1] 25 34 28 52

patientdata[1:2]

## patientID age
## 1 111 25
## 2 208 34
## 3 113 28
## 4 408 52

patientdata[c(1,3), 1:2]

## patientID age
## 1 111 25
## 3 113 28
patientdata[2:3, 1:2]

## patientID age
## 2  208 34
## 3  113 28

mean(patientdata$age)

## [1] 34.75

Instead of using `mean(patientdata[,2])`, you can select the column `age` from the `patientdata` data frame with the `$` sign.

`mean(patientdata[['age']])`

## [1] 34.75

Here's an alternative way to refer to the `age` column of the `patientdata` data frame. But you will rarely use this method.

### Lists

Another basic structure in R is a *list*.

The main advantage of lists is that the “columns” they’re not really ordered in columns any more, but are more of a collection of vectors) don’t have to be of the same length, unlike matrices and data frames.

Kind of like JSON files are structured.

```r
# The line below is creating a matrix that’s 5 rows deep of numbers 1 through(“:”) 10
j <- matrix(1:10, nrow = 5)

k <- c("one", "two", "three")

mylist <- list(title = g, ages = h, j, k)
```

This is how a list would appear in the work space

```r
names(mylist)

## [1] "title"  "ages"  ""  ""
```

How to find out what’s in the list

```r
mylist[[2]]

## [1] 25 26 18 39

mylist[['ages']][[1]]

## [1] 25
```

The code above extracts data from the list

```r
mylist$age + 10

## [1] 35 36 28 49
```

How to refer to and use the numbers in the example list
Functions for working with objects

Let's start with the `sample_df` dataframe below.

```r
# Run the lines of code below
sample_df <- data.frame(id=c(1001,1002,1003,1004), name=c("Steve", "Pam", "Jim", "Dwight"), age=c(26, 65, 15, 7), race=c("White", "Black", "White", "Hispanic"))
sample_df$name <- as.character(sample_df$name)
```

<table>
<thead>
<tr>
<th>id</th>
<th>name</th>
<th>age</th>
<th>race</th>
</tr>
</thead>
<tbody>
<tr>
<td>1001</td>
<td>Steve</td>
<td>26</td>
<td>White</td>
</tr>
<tr>
<td>1002</td>
<td>Pam</td>
<td>65</td>
<td>Black</td>
</tr>
<tr>
<td>1003</td>
<td>Jim</td>
<td>15</td>
<td>White</td>
</tr>
<tr>
<td>1004</td>
<td>Dwight</td>
<td>7</td>
<td>Hispanic</td>
</tr>
</tbody>
</table>

- `length(x)` - Find out how many things there are in an object or array
  ```r
  length(sample_df$name)
  
  ## [1] 4
  
  nchar(x) - If `x` is a string, finds how how many characters there are
  ```
  ```r
  nchar(sample_df$name[1])
  
  ## [1] 5
  
  dim(x) - Gives the dimensions of `x`
  ```
  ```r
  dim(sample_df)
  
  ## [1] 4 4
  ```
  - `ncol(x)` - Counts the number of columns
  ```r
  ncol(sample_df)
  
  ## [1] 4
  ```
  - `nrow(x)` - Returns the number of rows of `x`
  ```r
  nrow(sample_df)
  
  ## [1] 4
  ```
  - `str(x)` - Returns the structure of `x`
  ```r
  str(sample_df)
  
  ## 'data.frame': 4 obs. of 4 variables:
  ## $ id : num 1001 1002 1003 1004
  ## $ name: chr "Steve" "Pam" "Jim" "Dwight"
  ## $ age : num 26 65 15 7
  ## $ race: Factor w/ 3 levels "Black","Hispanic",...
  ```
  - `summary(x)` - Summarizes the object as understood by R
  ```r
  summary(sample_df)
  ```
## id name age race
## Min. :1001 Length:4 Min. : 7.00 Black :1
## 1st Qu.:1002 Class :character 1st Qu.:13.00 Hispanic:1
## Median :1002 Mode :character Median :20.50 White :2
## Mean :1002 Mean :28.25
## 3rd Qu.:1003 3rd Qu.:35.75
## Max. :1004 Max. :65.00

View(x) - A command to open the object to browse in RStudio

View(sample_df)

rm(x) - Removes x

rm(sample_df)
sample_df

## Error in eval(expr, envir, enclos): object 'sample_df' not found

Your turn

Challenge yourself with these exercises so you’ll retain the knowledge of this section.

Instructions on how to run the exercise app are in the intro page to this section.