



R has five basic or "atomic" classes of objects:

- Character
- Numeric (real numbers)
- Integer
- Complex
- Logical (True/False)

The most basic object is a **vector**.



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#### **Vectors**



- A vector can only contain objects of the same class.
- BUT: the one exception is a list, which is represented as a vector but can contain objects of different classes
- Empty vectors can be created with the <code>vector()</code> function.

#### > vector(mode = "logical", length = 5)

• You can also create vectors by using  ${\tt c}$  () function, which is short for concatenate (paste together)



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#### **Numbers**



- Numbers in R a generally treated as numeric objects (i.e. double precision real numbers)
- If you explicitly want an integer, you need to specify the  ${ t L}$  suffix
- Ex: Entering 1 gives you a numeric object; entering 1L explicitly gives you an integer.
- There is also a special number Inf which represents infinity; e.g. 1 / 0;
   Inf can be used in ordinary calculations; e.g. 1 / Inf is 0
- The value NaN represents an undefined value ("not a number");
   e.g. 0 / 0; NaN can also be thought of as a missing value (more on that later)

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#### **Attributes**



R objects can have attributes

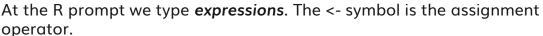
- names, dimnames
- dimensions (e.g. matrices, arrays)
- class
- length
- other user-defined attributes/ metadata

Attributes of an object can be accessed using the attributes () function.

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#### **Entering Input**



```
> x <- 1
> print(x)
[1] 1
> x
[1] 1
> msg <- "hello world"</pre>
```

The grammar of the language determines whether an expression is complete or not.

```
> x <- ## incomplete expression</pre>
```

Note: The # character indicates a comment. Anything to the right of the # (including the # itself) is ignored)

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#### **Evaluation**



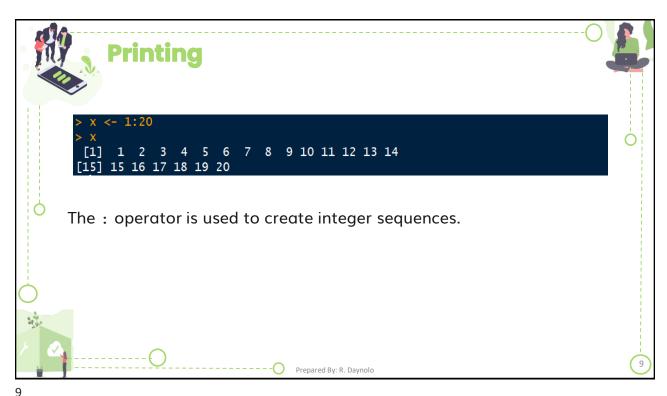
When a complete expression is entered at the prompt, it is evaluated and the result of the evaluated expression is returned. The result may be auto-printed.

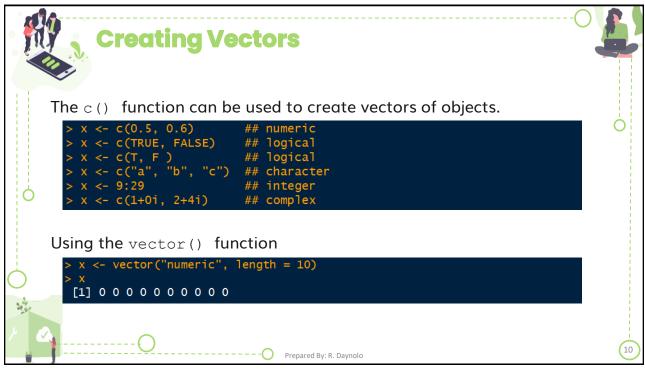
```
> x <- 5 ##nothing printed
> x ##auto-printing occurs
[1] 5
> print(x) ##explicit printing
[1] 5
```

The [1] indicates that x is a vector and 5 is the first element.

<u>)</u>

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### **Mixing Objects**



What about the following?

```
> y <- c(1.7 , "a")
> y <- c(TRUE, 2)
> y <- c("a", TRUE)
```

When different objects are mixed in a vector, *coercion* occurs so that every element in the vector is of the same class.



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# **Explicit Coercion**



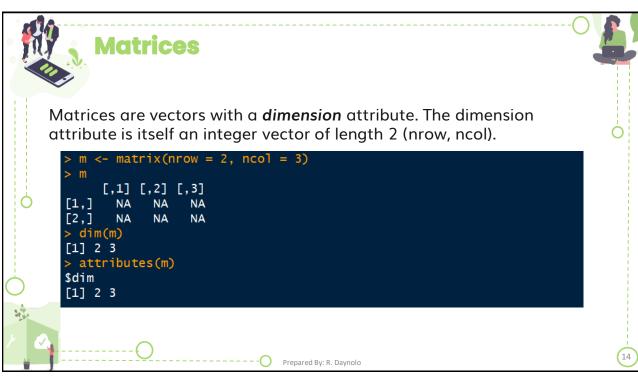
Objects can be *explicitly coerced* from one class to another using the as.\* functions, if available.

```
> x <- 0:6
> class(x)
[1] "integer"
> as.numeric(x)
[1] 0 1 2 3 4 5 6
> as.logical(x)
[1] FALSE TRUE TRUE TRUE TRUE TRUE
> as.character(x)
[1] "0" "1" "2" "3" "4" "5" "6"
```

*>* 

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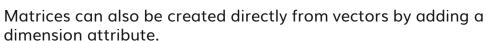
### **Matrices**

Matrices are constructed *column-wise*, so entries can be thought of starting in the "upper-left" corner and running down columns.

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#### **Matrices**



```
> m <- 1:10
> m
[1] 1 2 3 4 5 6 7 8 9 10
> dim(m) <- c(2,5)
> m
     [,1] [,2] [,3] [,4] [,5]
[1,] 1 3 5 7 9
[2,] 2 4 6 8 10
```

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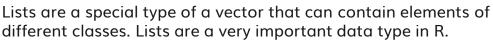
# cbind-ing and rbind-ing

Matrices can be created by *column-binding* or *row-binding* with cbind() and rbind().

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#### Lists



```
> x <- list(1, "a", TRUE, 1+4i)
> x
[[1]]
[1] 1

[[2]]
[1] "a"

[[3]]
[1] TRUE

[[4]]
[1] 1+4i
```

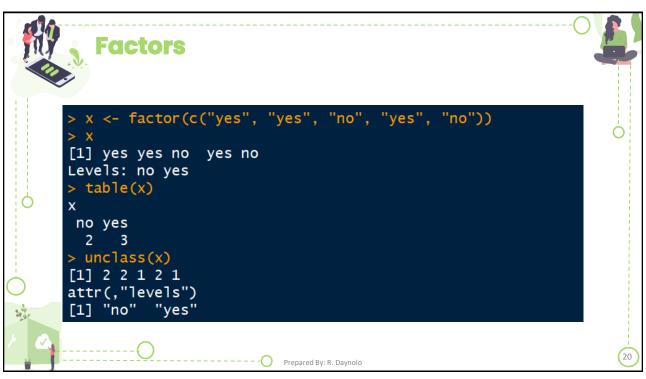


Factors are used to represent categorical data. Factors can be unordered or ordered. One can think of a factor as an integer vector where each integer has a *label*.

- Factors are treated specially by modelling functions like lm() and glm()
- Using factors with labels is *better* than using integers because factors are self-describing; having a variable that has values "Male" and "Female" is better than a variable that has values 1 and 2.

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The order of the levels can be set using the levels argument to factor(). This can be important in linear modelling because the first level is used as the baseline level.

```
> x <- factor(c("yes", "yes", "no", "yes", "no"),
  levels = c("yes", "no"))
> x
[1] yes yes no yes no
Levels: yes no
```

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## **Missing Values**



Missing values are denoted by  $\mathtt{NA}$  or  $\mathtt{NaN}$  for undefined mathematical operations.

- is.na() is used to test objects if they are NA
- is.nan() is used to test for NaN
- NA values have a class also, so there are integer NA, character NA, etc.
- A NaN value is also NA but the converse is not true



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# **Missing Values**

```
> x <- c(1, 2, NA, 10, 3)
> is.na(x)
[1] FALSE FALSE TRUE FALSE FALSE
> is.nan(x)
[1] FALSE FALSE FALSE FALSE FALSE
> x <- c(1, 2, NaN, NA, 4)
> is.na(x)
[1] FALSE FALSE TRUE TRUE FALSE
> is.nan(x)
[1] FALSE FALSE TRUE FALSE FALSE
```

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#### **Data Frames**



Data frames are used to store tabular data.

- They are represented as a special type of list where every element of the list has to have the same length
- Each element of the list can be thought of as a column and the length of each element of the list is the number of rows
- Unlike matrices, data frames can store different classes of objects in each column (just like lists); matrices must have every element be the same class
- Data frames also have a special attribute called row.names
- Data frames are usually created by calling read.table() or read.csv()
- Can be converted to a matrix by calling data.matrix()

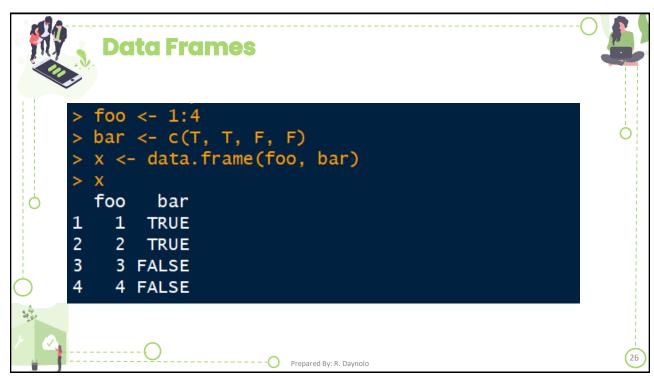
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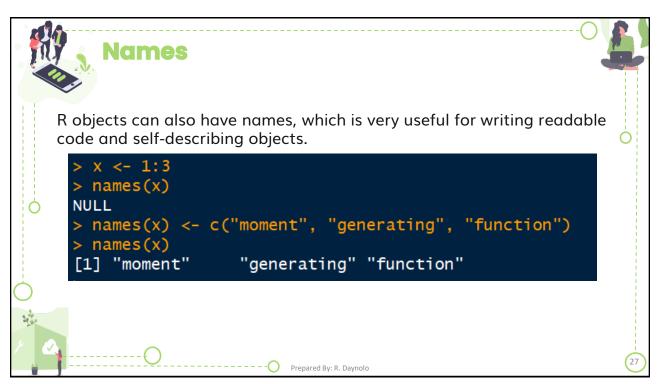
```
Data Frames

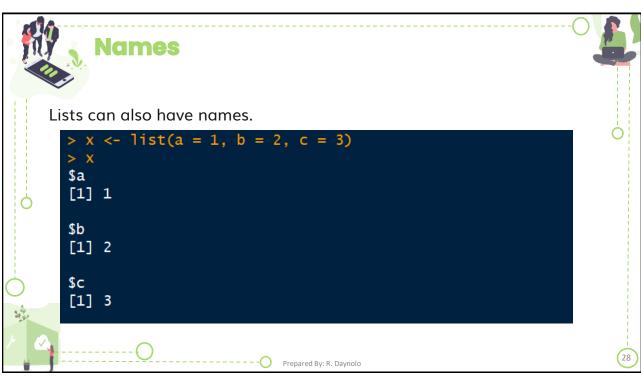
> x <- data.frame(foo = 1:4, bar = c(T, T, F, F))
> x
foo bar
1 1 TRUE
2 2 TRUE
3 3 FALSE
4 4 FALSE
> nrow(x)
[1] 4
> ncol(x)
[1] 2

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```













# **Reading Data**



There are a few principal functions reading data into R.

- read.table(), read.csv(), for reading tabular data
- readLines(), for reading lines of a text file
- source(), for reading in R code files (inverse of dump())
- dget(), for reading in R code files (inverse of dput())
- load(), for reading in saved workspaces
- unserialize(), for reading single R objects in binary form



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# **Writing Data**



There are analogous functions for writing data to files

- write.table()
- writeLines()
- dump()
- dput()
- save()
- serialize()



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# **Reading Data Files with read.table**



The read.table() function is one of the most commonly used functions for reading data. It has a few important arguments:

- file, the name of a file, or a connection
- header, logical indicating if the file has a header line
- sep, a string indicating how the columns are separated
- colClasses, a character vector indicating the class of each column in the dataset
- nrows, the number of rows in the dataset



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# Reading Data Files with read.table



The read.table function is one of the most commonly used functions for reading data. It has a few important arguments:

- comment.char, a character string indicating the comment character
- skip, the number of lines to skip from the beginning
- stringsAsFactors, should character variables be coded as factors?



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#### read.table



For small to moderately sized datasets, you can usually call read.table() without specifying any other arguments

#### > data <- read.table("foo.txt")</pre>

R will automatically

- skip lines that begin with a #
- figure out how many rows there are (and how much memory needs to be allocated)
- figure what type of variable is in each column of the table telling R all these things directly makes R run faster and more efficiently.
- read.csv() is identical to read.table() except that the default separator is a comma.



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# Reading in Larger Datasets with read.table



With much larger datasets, doing the following things will make your life easier and will prevent R from choking.

- Read the help page for read.table(), which contains many hints
- Make a rough calculation of the memory required to store your dataset. If the dataset is larger than the amount of RAM on your computer, you can probably stop right here.
- Set comment.char = "" if there are no commented lines in your file.





# Reading in Larger Datasets with read.table



Use the colClasses argument. Specifying this option instead of using the default can make 'read.table' run MUCH faster, often twice as fast. In order to use this option, you have to know the class of each column in your data frame. If all of the columns are "numeric", for example, then you can just set colClasses = "numeric". A quick an dirty way to figure out the classes of each column is the following:

```
> initial <- read.table("datatable.txt", nrows=100)
> classes <- sapply(initial,class)
> tabAll <- read.table("datatable.txt", colClasses = classes)</pre>
```

Set nrows. This doesn't make R run faster but it helps with memory usage.

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# **Know Thy System**



In general, when using R with larger datasets, it's useful to know a few things about your system.

- How much memory is available?
- What other applications are in use?
- Are there other users logged into the same system?
- · What operating system?
- Is the OS 32 or 64 bit?



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# **Calculating Memory Requirements**



I have a data frame with 1,500,000 rows and 120 columns, all of which are numeric data. Roughly, how much memory is required to store this data frame?



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#### **Text Formats**



- dumping and dputing are useful because the resulting textual format is edit-able, and in the case of corruption, potentially recoverable.
- Unlike writing out a table or csv file, <code>dump()</code> and <code>dput()</code> preserve the metadata (sacrificing some readability), so that another user doesn't have to specify it all over again.
- Textual formats can work much better with version control programs like subversion or git which can track changes meaningfully in text files
- Textual formats can be longer-lived; if there is corruption somewhere in the file, it can be easier to fix the problem



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### dput-ing R Objects

Another way to pass data around is by deparsing the R object with dput and reading it back in (parsing it) using dget ().

```
> y <- data.frame(a = 1, b = "a")
> dput(y)
structure(list(a = 1, b = structure(1L, .Label = "a", class = "factor")),
    class = "data.frame", row.names = c(NA,
-1L))
> dput(y, file = "y.R")
> new.y <- dget("y.R")
> new.y
    a b
1 1 a
```

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### **Dumping R Objects**



```
> x <- "foo"
> y <- data.frame(a = 1, b = "a" )
> dump(c("x", "y"), file = "data.R")
> rm(x, y)
> source("data.R")
> y
    a b
1 1 a
> x
[1] "foo"
```

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#### **Interfaces to the Outside World**



Data are read in using *connection* interfaces. Connections can be made to files (most common) or to other things.

- file, opens a connection to a file
- url, opens a connection to a webpage
- gzfile, opens a connection to a file compressed with gzip
- bzfile, opens a connection to a file compressed with bzip2



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#### **File Connections**



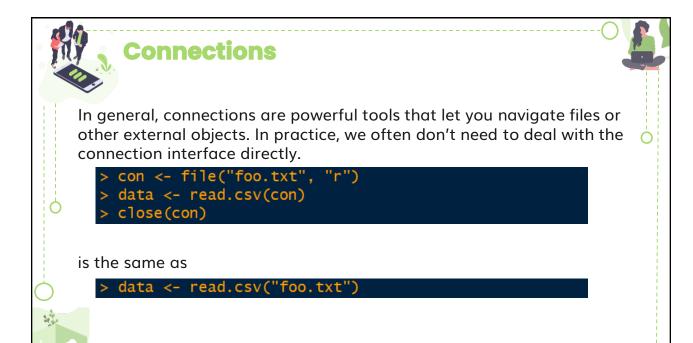
```
∙str(file)
```

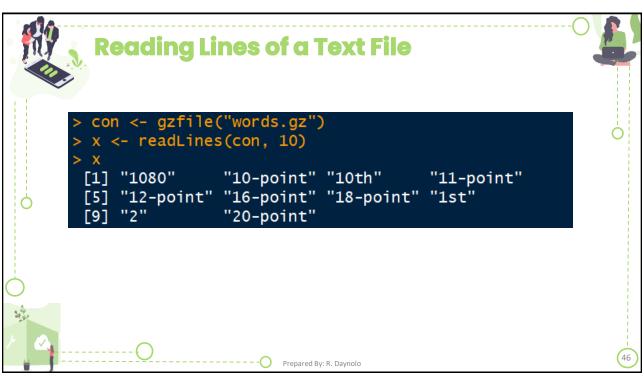
function (description = "", open = "", blocking = TRUE, encoding = getOption("encoding"), raw = FALSE, method = getOption("url.method", "default"))

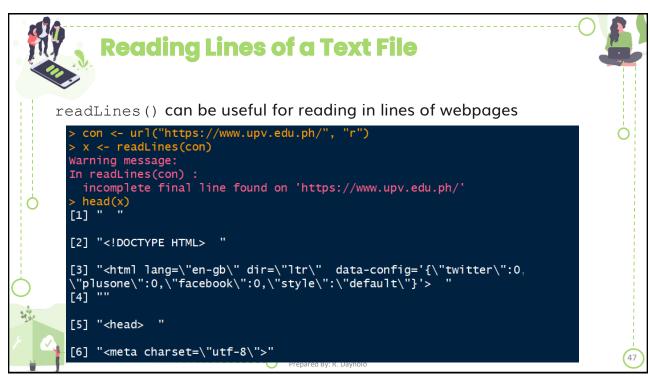
- description is the name of the file
- open is a code indicating
  - "r" read only
  - "w" writing (and initializing a new file)
  - "a" appending
  - "rb", "wb", "ab" reading, writing, or appending in binary mode (Windows)

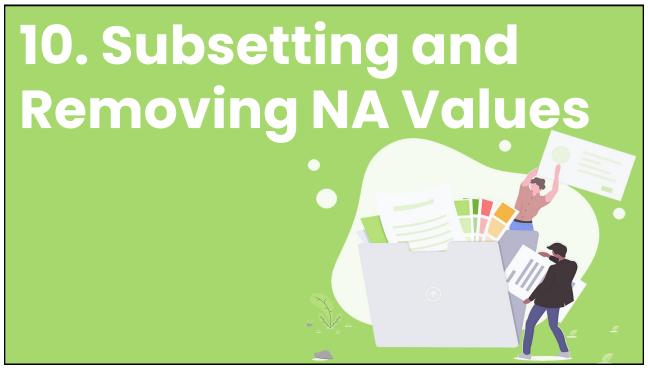


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# Subsetting

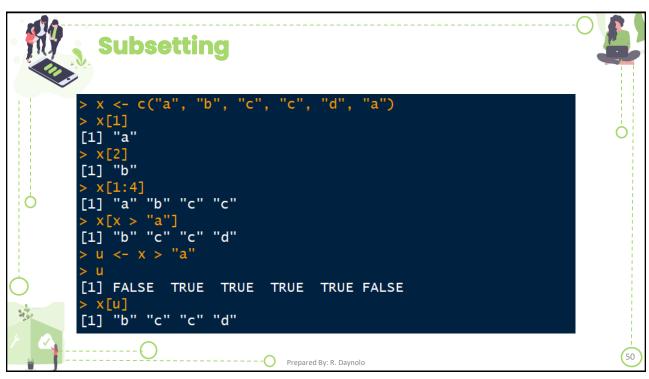


There are a number of operators that can be used to extract subsets of R objects.

- [ always returns an object of the same class as the original; can be used to select more than one element (there is one exception)
- [[ is used to extract elements of a list or a data frame; it can only be used to extract a single element and the class of the returned object will not necessarily be a list or data frame
- \$ is used to extract elements of a list or data frame by name; semantics are similar to that of [[.

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# **Subsetting a Matrix**

Matrices can be subsetted in the usual way with (i,j) type indices.

```
> x <- matrix(1:6, 2, 3)
> x[1,2]
[1] 3
> x[2,1]
[1] 2
```

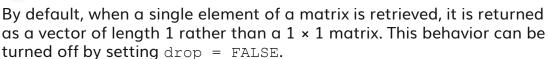
Indices can also be missing.

```
> x[1, ]
[1] 1 3 5
> x[, 2]
[1] 3 4
```

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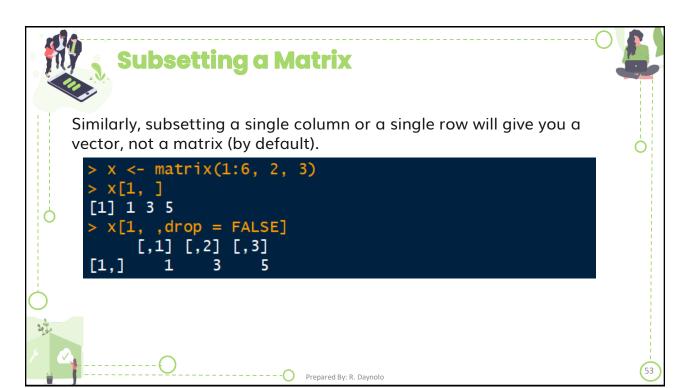


### **Subsetting a Matrix**



```
> x <- matrix(1:6, 2, 3)
> x[1,2]
[1] 3
> x[1,2, drop = FALSE]
       [,1]
[1,] 3
```

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```
Subsetting Lists

> x <- list(foo = 1:4, bar = 0.6)
> x[1]
$foo
[1] 1 2 3 4

> x[1]]
[1] 1 2 3 4

> x$bar
[1] 0.6

> x["bar"]
$bar
[1] 0.6

> x["bar"]
$bar
[1] 0.6
```



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