FRE6871 R in Finance

Lecture#5, Spring 2024

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Lists

Lists are a type of vector that contain elements of different *types*.

Lists are recursive object types, meaning each list element can contain other vectors or lists.

The function `list()` creates a list from a list of vectors.

`list()` creates a named list from a list of symbol-value pairs.

The function `is.list()` returns `TRUE` if its argument is a list, and `FALSE` otherwise.

The function `unlist()` collapses a list with atomic elements into a vector (which can cause type coercion).

```
> # Create a list with two elements
> listv <- list(c("a", "b"), 1:4)
> listv
[[1]]
[1] "a" "b"

[[2]]
[1] 1 2 3 4
> c(typeof(listv), mode(listv), class(listv))
[1] "list" "list" "list"
> # Lists are also vectors
> c(is.vector(listv), is.list(listv))
[1] TRUE TRUE
> NROW(listv)
[1] 2
> # Create named list
> listv <- list(first=c("a", "b"), second=1:4)
> listv
$first
[1] "a" "b"

$second
[1] 1 2 3 4
> names(listv)
[1] "first"  "second"
> unlist(listv)
 first1  first2 second1 second2 second3 second4
    "a"     "b"     "1"     "2"     "3"     "4"
```

Subsetting Lists

Lists can be subset (indexed) using:

- the "[" operator (returns sublist),
- the "[[" operator (returns an element),
- the "$" operator (for named listv only),

Partial name matching allows subsetting with partial name, as long as it can be resolved.

```
> listv[2]  # Extract second element as sublist
$second
[1] 1 2 3 4
> listv[[2]]  # Extract second element
[1] 1 2 3 4
> listv[[2]][3]  # Extract third element of second element
[1] 3
> listv[[c(2, 3)]]  # Third element of second element
[1] 3
> listv$second  # Extract second element
[1] 1 2 3 4
> listv$s  # Extract second element - partial name matching
[1] 1 2 3 4
> listv$second[3]  # Third element of second element
[1] 3
> listv <- list()  # Empty list
> listv$a <- 1
> listv[2] <- 2
> listv
$a
[1] 1

[[2]]
[1] 2
> names(listv)
[1] "a" ""
```

Coercing Vectors Into Lists Using `as.list()`

The function `as.list()` coerces vectors and other objects into lists.

`as.list()` returns a list with the same elements as the vector.

`list()` called on a vector returns a single element equal to the vector.

```
> # Convert vector elements to list elements
> as.list(1:3)
[[1]]
[1] 1

[[2]]
[1] 2

[[3]]
[1] 3
> # Convert whole vector to single list element
> list(1:3)
[[1]]
[1] 1 2 3
```

Data Frames

Data frames are 2-D objects (like matrices), but their columns can be of different *types*.

Data frames can be thought of as listv of vectors of the same length.

The function `data.frame()` creates a *data frame* from vectors assigned to column names.

```
> dframe <- data.frame(  # Create a data frame
+                 type=c("rose", "daisy", "tulip"),
+                 color=c("red", "white", "yellow"),
+                 price=c(1.5, 0.5, 1.0)
+               )  # end data.frame
> dframe
   type  color price
1  rose    red   1.5
2 daisy  white   0.5
3 tulip yellow   1.0
> dim(dframe)  # Get dimension attribute
[1] 3 3
> colnames(dframe)  # Get the colnames attribute
[1] "type"  "color" "price"
> rownames(dframe)  # Get the rownames attribute
[1] "1" "2" "3"
> class(dframe)  # Get object class
[1] "data.frame"
> typeof(dframe)  # Data frames are listv
[1] "list"
> is.data.frame(dframe)
[1] TRUE
>
> class(dframe$type)  # Get column class
[1] "character"
> class(dframe$price)  # Get column class
[1] "numeric"
```

Subsetting Data Frames

Data frames can be subset in a similar way to listv and matrices.

Depending on how a data frame is subset, the result can be either a data frame or a vector.

Extracting a single column from a data frame produces a vector.

The data frame class attribute can be preserved by using the parameter `"drop=FALSE"`.

Extracting a single row from a data frame produces a data frame.

The function `unlist()` applied to a single row extracted from a data frame coerces it to a vector.

```
> dframe[, 3]  # Extract third column as vector
[1] 1.5 0.5 1.0
> dframe[[3]]  # Extract third column as vector
[1] 1.5 0.5 1.0
> dframe[3]  # Extract third column as data frame
  price
1   1.5
2   0.5
3   1.0
> dframe[, 3, drop=FALSE]  # Extract third column as data frame
  price
1   1.5
2   0.5
3   1.0
> dframe[[3]][2]  # Second element from third column
[1] 0.5
> dframe$price[2]  # Second element from "price" column
[1] 0.5
> is.data.frame(dframe[[3]]); is.vector(dframe[[3]])
[1] FALSE
[1] TRUE
> dframe[2, ]  # Extract second row
   type color price
2 daisy white   0.5
> dframe[2, ][3]  # Third element from second column
  price
2   0.5
> dframe[2, 3]  # Third element from second column
[1] 0.5
> unlist(dframe[2, ])  # Coerce to vector
   type   color   price
"daisy" "white"   "0.5"
> is.data.frame(dframe[2, ]); is.vector(dframe[2, ])
[1] TRUE
[1] FALSE
```

Data Frames and Factors

By default `data.frame()` does not coerce `character` vectors to `factors`, so no need for the option `stringsAsFactors=FALSE`.

The function `options()` sets global *options*, that determine how `R` computes and displays its results.

If the global `option stringsAsFactors=FALSE` is set, then `character` vectors will not be coerced to `factors` in all subsequent `data frame` operations.

The default is `stringsAsFactors=FALSE` since `R` version `4.0`.

```
> dframe <- data.frame(  # Create a data frame
+                 type=c("rose", "daisy", "tulip"),
+                 color=c("red", "white", "yellow"),
+                 price=c(1.5, 0.5, 1.0),
+                 row.names=c("flower1", "flower2", "flower3")
+               )  # end data.frame
> dframe
         type  color price
flower1  rose    red   1.5
flower2 daisy  white   0.5
flower3 tulip yellow   1.0
> class(dframe$type)  # Get column class
[1] "character"
> class(dframe$price)  # Get column class
[1] "numeric"
> # Set option to not coerce character vectors to factors - that was
> options("stringsAsFactors")
$stringsAsFactors
NULL
> options(stringsAsFactors=FALSE)
> options("stringsAsFactors")
$stringsAsFactors
[1] FALSE
```

Exploring Data Frames

The function `str()` displays the structure of an `R` object.

The functions `head()` and `tail()` display the first and last rows of an `R` object.

```
> str(dframe)  # Display the object structure
'data.frame': 3 obs. of  3 variables:
 $ type : chr  "rose" "daisy" "tulip"
 $ color: chr  "red" "white" "yellow"
 $ price: num  1.5 0.5 1
> dim(cars)  # The cars data frame has 50 rows
[1] 50  2
> head(cars, n=5)  # Get first five rows
  speed dist
1     4    2
2     4   10
3     7    4
4     7   22
5     8   16
> tail(cars, n=5)  # Get last five rows
   speed dist
46    24   70
47    24   92
48    24   93
49    24  120
50    25   85
```

Sorting Vectors

The function `sort()` returns a vector sorted into ascending order.

A permutation is a re-ordering of the elements of a vector.

The permutation index specifies how the elements are re-ordered in a permutation.

The function `order()` calculates the permutation index to sort a given vector into ascending order.

Applying the function `order()` twice: `order(order())`, calculates the permutation index to sort the vector from ascending order into its unsorted (original) order.

So the permutation index produced by: `order(order())` is the reverse of the permutation index produced by: `order()`.

`order()` can take several vectors as input, to break any ties.

Data frames can be sorted on any column.

```
> # Create a named vector of student scores
> scorev <- sample(round(runif(5, min=1, max=10), digits=2))
> names(scorev) <- c("Angie", "Chris", "Suzie", "Matt", "Liz")
> # Sort the vector into ascending order
> sort(scorev)
Chris Suzie  Matt Angie   Liz
 2.60  6.07  7.92  8.20  9.70
> # Calculate index to sort into ascending order
> order(scorev)
[1] 2 3 4 1 5
> # Sort the vector into ascending order
> scorev[order(scorev)]
Chris Suzie  Matt Angie   Liz
 2.60  6.07  7.92  8.20  9.70
> # Calculate the sorted (ordered) vector
> sortv <- scorev[order(scorev)]
> # Calculate index to sort into unsorted (original) order
> order(order(scorev))
[1] 4 1 2 3 5
> sortv[order(order(scorev))]
Angie Chris Suzie  Matt   Liz
 8.20  2.60  6.07  7.92  9.70
> scorev
Angie Chris Suzie  Matt   Liz
 8.20  2.60  6.07  7.92  9.70
> # Examples for sort() with ties
> order(c(2, 1:4))  # There's a tie
[1] 2 1 3 4 5
> order(c(2, 1:4), 1:5)  # There's a tie
[1] 2 1 3 4 5
```

Sorting Data Frames

Data frames can be sorted on any one of its columns.

```
> # Create a vector of student ranks
> rankv <- c("fifth", "fourth", "third", "second", "first")
> # Reverse sort the student ranks according to students
> rankv[order(order(scorev))]
[1] "second" "fifth"  "fourth" "third"  "first"
> # Create a data frame of students and their ranks
> rosterdf <- data.frame(score=scorev,
+   rank=rankv[order(order(scorev))])
> rosterdf
      score   rank
Angie  8.20 second
Chris  2.60  fifth
Suzie  6.07 fourth
Matt   7.92  third
Liz    9.70  first
> # Permutation index on price column
> order(dframe$price)
[1] 2 3 1
> # Sort dframe on price column
> dframe[order(dframe$price), ]
        type  color price
flower2 daisy  white   0.5
flower3 tulip yellow   1.0
flower1  rose    red   1.5
> # Sort dframe on color column
> dframe[order(dframe$color), ]
        type  color price
flower1  rose    red   1.5
flower2 daisy  white   0.5
flower3 tulip yellow   1.0
```

Coercing Data Frames Into Matrices Using as.matrix()

The function as.matrix() coerces vectors and data frames into matrices.

Coercing a data frame into a matrix causes coercion of numeric values into character.

as.matrix() coerces vectors into single column matrices, as opposed to matrix(), which produces a matrix.

```
> as.matrix(dframe)
        type    color    price
flower1 "rose"  "red"    "1.5"
flower2 "daisy" "white"  "0.5"
flower3 "tulip" "yellow" "1.0"
> vecv <- sample(9)
> matrix(vecv, ncol=3)
     [,1] [,2] [,3]
[1,]    8    3    1
[2,]    9    4    2
[3,]    7    5    6
> as.matrix(vecv, ncol=3)
      [,1]
 [1,]    8
 [2,]    9
 [3,]    7
 [4,]    3
 [5,]    4
 [6,]    5
 [7,]    1
 [8,]    2
 [9,]    6
```

Coercing Matrices Into Data Frames

The generic function `as.data.frame()` coerces matrices and other objects into data frames.

The method `as.data.frame.matrix()` coerces only matrices into data frames.

`as.data.frame.matrix()` is about 50% faster than `as.data.frame()`, because it skips extra `R` code in `as.data.frame()` needed for argument validation, error checking, and method dispatch.

As a general rule, calling generic functions is slower than directly calling individual methods, because generic functions must execute extra `R` code for method dispatch.

The function `data.frame()` can also be used to coerce matrices into data frames, but is much slower than even `as.data.frame()`.

`as.data.frame()` is about three times faster than `data.frame()`, because it doesn't require extra `R` code in `data.frame()` needed for handling different types of vectors, and for method dispatch.

```
> library(microbenchmark)
> # Call method instead of generic function
> as.data.frame.matrix(matv)
> # A few methods for generic function as.data.frame()
> sample(methods(as.data.frame), size=4)
> # Function method is faster than generic function
> summary(microbenchmark(
+   as_dframem=as.data.frame.matrix(matv),
+   as_dframe=as.data.frame(matv),
+   dframe=data.frame(matv),
+   times=10))[, c(1, 4, 5)]  # end microbenchmark summary
```

Coercing Matrices Into Lists

Matrices can be coerced into lists in at least two different ways.

Matrices can be first coerced into a data frame, and then into a list using function `as.list()`.

Matrices can be directly coerced into a list using function `lapply()`.

Using `lapply()` is the faster of the two methods, because `lapply()` is a *compiled* function.

```
> # lapply is faster than coercion function
> summary(microbenchmark(
+   aslist=as.list(as.data.frame.matrix(matv)),
+   lapply=lapply(seq_along(matv[1, ]),
+     function(indeks) matv[, indeks]),
+   times=10))[, c(1, 4, 5)]  # end microbenchmark summary

Error in h(simpleError(msg, call)):  error in evaluating the
argument 'object' in selecting a method for function 'summary':
object 'matv' not found
```

The iris Data Frame

The iris data frame is included in the datasets base package.

iris contains sepal and petal dimensions of 50 flowers from 3 species of iris.

The function unique() extracts unique elements of an object.

sapply() applies a function to a list or a vector of objects and returns a vector.

sapply() performs a loop over the list of objects, and can replace "for" loops in R.

```
> # ?iris  # Get information on iris
> dim(iris)
[1] 150   5
> head(iris, 2)
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
> colnames(iris)
[1] "Sepal.Length" "Sepal.Width"  "Petal.Length" "Petal.Width"  "Spe
> unique(iris$Species)  # List of unique elements of iris
[1] setosa     versicolor virginica
Levels: setosa versicolor virginica
> class(unique(iris$Species))
[1] "factor"
> # Find which columns of iris are numeric
> sapply(iris, is.numeric)
Sepal.Length  Sepal.Width Petal.Length  Petal.Width      Species
        TRUE         TRUE         TRUE         TRUE        FALSE
> # Calculate means of iris columns
> sapply(iris, mean)  # Returns NA for Species
Sepal.Length  Sepal.Width Petal.Length  Petal.Width      Species
        5.84         3.06         3.76         1.20           NA
```

The mtcars Data Frame

The mtcars data frame is included in the datasets base package, and contains design and performance data for 32 automobiles.

```
> # ?mtcars  # mtcars data from 1974 Motor Trend magazine
> # mpg   Miles/(US) gallon
> # qsec   1/4 mile time
> # hp  Gross horsepower
> # wt  Weight (lb/1000)
> # cyl   Number of cylinders
> dim(mtcars)
[1] 32 11
> head(mtcars, 2)
              mpg cyl disp  hp drat   wt qsec vs am gear carb
Mazda RX4      21   6  160 110  3.9 2.62 16.5  0  1    4    4
Mazda RX4 Wag  21   6  160 110  3.9 2.88 17.0  0  1    4    4
> colnames(mtcars)
 [1] "mpg"  "cyl"  "disp" "hp"   "drat" "wt"   "qsec" "vs"   "am"
[11] "carb"
> head(rownames(mtcars), 3)
[1] "Mazda RX4"     "Mazda RX4 Wag" "Datsun 710"
> unique(mtcars$cyl)  # Extract list of car cylinders
[1] 6 4 8
> sapply(mtcars, mean)  # Calculate means of mtcars columns
    mpg     cyl    disp      hp    drat      wt    qsec      vs
 20.091   6.188 230.722 146.688   3.597   3.217  17.849   0.438   0.
   carb
  2.812
```

The Cars93 Data Frame

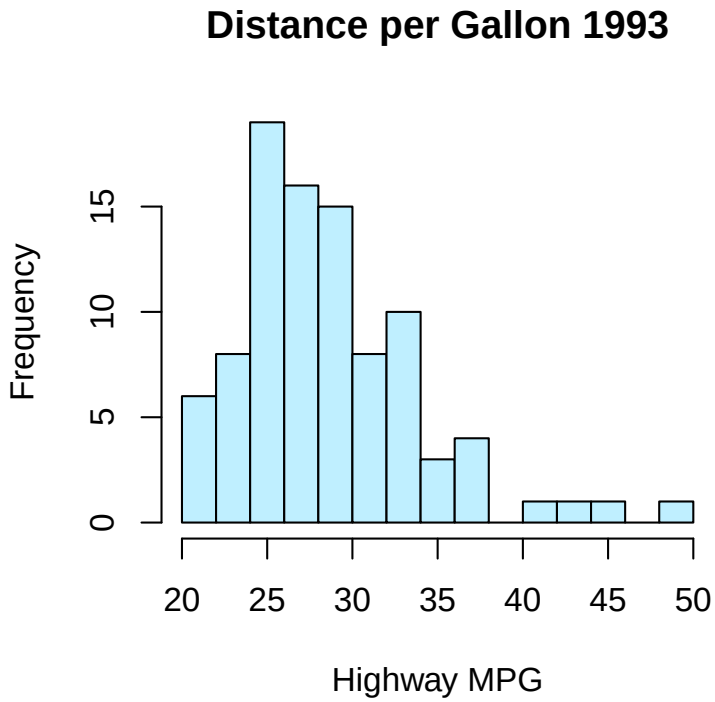
The Cars93 data frame is included in the MASS package, and contains design and performance data for 93 automobiles.

The function hist() calculates and plots a histogram, and returns its data *invisibly*.

The parameter breaks is the number of cells of the histogram.

"FD" stands for the Freedman-Diaconis rule for calculating histogram breaks,

```
> library(MASS)
> # ?Cars93  # Get information on Cars93
> dim(Cars93)
> head(colnames(Cars93))
> # head(Cars93, 2)
> unique(Cars93$Type)  # Extract list of car types
> # sapply(Cars93, mean)  # Calculate means of Cars93 columns
> # Plot histogram of Highway MPG using the Freedman-Diaconis rule
> hist(Cars93$MPG.highway, col="lightblue1",
+      main="Distance per Gallon 1993", xlab="Highway MPG", breaks="FD")
```



Types of Bad Data

Possible sources of bad data are: imported data, class coercion, numeric overflow.

Types of bad data:

- `NA` (not available) is a logical constant indicating missing data,
- `NaN` means Not a Number data,
- `Inf` means numeric overflow - divide by zero,

When a function produces `NA` or `NaN` values, then it also produces a *warning* condition, but not an *error*.

`NA` or `NaN` values are not *errors*.

The functions `is.na()` and `is.nan()` test for `NA` and `NaN` values.

Many functions have a `na.rm` parameter to remove `NA`s from input data.

```
> as.numeric(c(1:3, "a"))  # NA from coercion
[1]  1  2  3 NA
> 0/0  # NaN from ambiguous math
[1] NaN
> 1/0  # Inf from divide by zero
[1] Inf
> is.na(c(NA, NaN, 0/0, 1/0))  # Test for NA
[1]  TRUE  TRUE  TRUE FALSE
> is.nan(c(NA, NaN, 0/0, 1/0))  # Test for NaN
[1] FALSE  TRUE  TRUE FALSE
> NA*1:4  # Create vector of Nas
[1] NA NA NA NA
> # Create vector with some NA values
> datav <- c(1, 2, NA, 4, NA, 5)
> datav
[1]  1  2 NA  4 NA  5
> mean(datav)  # Returns NA, when NAs are input
[1] NA
> mean(datav, na.rm=TRUE)  # remove NAs from input data
[1] 3
> datav[!is.na(datav)]  # Delete the NA values
[1] 1 2 4 5
> sum(!is.na(datav))  # Count non-NA values
[1] 4
```

Scrubbing Bad Data

The function `complete.cases()` returns `TRUE` if a row has no `NA` values.

```
> # airquality data has some NAs
> head(airquality)
  Ozone Solar.R Wind Temp Month Day
1    41     190  7.4   67     5   1
2    36     118  8.0   72     5   2
3    12     149 12.6   74     5   3
4    18     313 11.5   62     5   4
5    NA      NA 14.3   56     5   5
6    28      NA 14.9   66     5   6
> dim(airquality)
[1] 153   6
> # Number of NA elements
> sum(is.na(airquality))
[1] 44
> # Number of rows with NA elements
> sum(!complete.cases(airquality))
[1] 42
> # Display rows containing NAs
> head(airquality[!complete.cases(airquality), ])
   Ozone Solar.R Wind Temp Month Day
5     NA      NA 14.3   56     5   5
6     28      NA 14.9   66     5   6
10    NA     194  8.6   69     5  10
11     7      NA  6.9   74     5  11
25    NA      66 16.6   57     5  25
26    NA     266 14.9   58     5  26
```

Scrubbing Data Using Carry Forward

Rows containing bad data may be either removed or replaced with an estimated value.

The function `stats::na.omit()` removes individual `NA` values from vectors, and it also removes whole rows of data containing `NA` values from matrices and data frames.

Bad data can also be replaced with the most recent prior values (carry forward good data).

The function `zoo::na.locf()` replaces `NA` values with the most recent non-`NA` values prior to it (*locf* stands for *last observation carry forward*).

Copying the last non-`NA` values forward causes less data loss than removing whole rows of data.

The function `na.locf()` with argument `fromLast=TRUE` replaces `NA` values with non-`NA` values in reverse order, starting from the end.

```
> # Create vector containing NA values
> vecv <- sample(22)
> vecv[sample(NROW(vecv), 4)] <- NA
> # Replace NA values with the most recent non-NA values
> zoo::na.locf(vecv)
 [1]  1 20 17  8 22  9 13 13 16 11 12  4  4 14 18 10  5 15  3 21 21
> # Remove rows containing NAs
> goodair <- airquality[complete.cases(airquality), ]
> dim(goodair)
[1] 111   6
> # NAs removed
> head(goodair)
  Ozone Solar.R Wind Temp Month Day
1    41     190  7.4   67     5   1
2    36     118  8.0   72     5   2
3    12     149 12.6   74     5   3
4    18     313 11.5   62     5   4
7    23     299  8.6   65     5   7
8    19      99 13.8   59     5   8
> # Another way of removing NAs
> freshair <- na.omit(airquality)
> all.equal(freshair, goodair, check.attributes=FALSE)
[1] TRUE
> # Replace NAs
> goodair <- zoo::na.locf(airquality)
> dim(goodair)
[1] 153   6
> # NAs replaced
> head(goodair)
  Ozone Solar.R Wind Temp Month Day
1    41     190  7.4   67     5   1
2    36     118  8.0   72     5   2
3    12     149 12.6   74     5   3
4    18     313 11.5   62     5   4
5    18     313 14.3   56     5   5
6    28     313 14.9   66     5   6
```

Scrubbing Time Series Data

Missing asset prices and returns can be replaced with the most recent prior values (carry forward good data).

But missing asset returns should not be replaced with values from the future. Instead, missing returns should be replaced with zero values.

The function `na.locf.xts()` from package *xts* is faster than `zoo::na.locf()`, but it only operates on time series of class `"xts"`.

```
> # Replace NAs in xts time series
> library(rutils)  # load package rutils
> pricev <- rutils::etfenv$prices[, 1]
> head(pricev, 3)
            VEU
1998-12-22  NA
1998-12-23  NA
1998-12-24  NA
> sum(is.na(pricev))
[1] 2062
> pricez <- zoo::na.locf(pricev, fromLast=TRUE)
> pricex <- xts:::na.locf.xts(pricev, fromLast=TRUE)
> all.equal(pricez, pricex, check.attributes=FALSE)
[1] TRUE
> head(pricex, 3)
             VEU
1998-12-22 32.4
1998-12-23 32.4
1998-12-24 32.4
> library(microbenchmark)
> summary(microbenchmark(
+   zoo=zoo::na.locf(pricev, fromLast=TRUE),
+   xts=xts:::na.locf.xts(pricev, fromLast=TRUE),
+   times=10))[, c(1, 4, 5)]  # end microbenchmark summary
  expr mean median
1  zoo 24.5   21.0
2  xts 23.4   19.2
```

NULL Values

NULL represents a null object, and is a legitimate value, not bad data.

NULL is often returned by functions whose value is undefined.

NULL can also be used to initialize vectors.

NULL is not the same as NA values or zero-length (empty) vectors.

The functions `numeric()` and `character()` return empty (zero-length) vectors of the specified *type*.

The function `is.null()` tests for NULL values.

Very often variables are initialized to NULL before the start of iteration.

A more efficient way to perform iteration is by pre-allocating the vector.

```
> # NULL values have no mode or type
> c(mode(NULL), mode(NA))
[1] "NULL"    "logical"
> c(typeof(NULL), typeof(NA))
[1] "NULL"    "logical"
> c(NROW(NULL), NROW(NA))
[1] 0 1
> # Check for NULL values
> is.null(NULL)
[1] TRUE
> # NULL values are ignored when combined into a vector
> c(1, 2, NULL, 4, 5)
[1] 1 2 4 5
> # But NA value isn't ignored
> c(1, 2, NA, 4, 5)
[1]  1  2 NA  4  5
> # Vectors can be initialized to NULL
> vecv <- NULL
> is.null(vecv)
[1] TRUE
> # Grow the vector in a loop - very bad code!!!
> for (indeks in 1:5)
+   vecv <- c(vecv, indeks)
> # Initialize empty vector
> vecv <- numeric()
> # Grow the vector in a loop - very bad code!!!
> for (indeks in 1:5)
+   vecv <- c(vecv, indeks)
> # Allocate vector
> vecv <- numeric(5)
> # Assign to vector in a loop - good code
> for (indeks in 1:5)
+   vecv[indeks] <- runif(1)
```

Flattening a List of Vectors to a Matrix Using do.call()

A list of vectors can be flattened into a matrix using the functions do.call() and either rbind() or cbind().

If the list contains vectors of different lengths, then R applies the recycling rule.

If the list contains a NULL element, that element is skipped.

```
> # Create list of vectors
> listv <- lapply(1:3, function(x) sample(6))
> # Bind list elements into matrix - doesn't work
> rbind(listv)
> # Bind list elements into matrix - tedious
> rbind(listv[[1]], listv[[2]], listv[[3]])
> # Bind list elements into matrix - works!
> do.call(rbind, listv)
> # Create numeric list
> listv <- list(1, 2, 3, 4)
> do.call(rbind, listv)  # Returns single column matrix
> do.call(cbind, listv)  # Returns single row matrix
> # Recycling rule applied
> do.call(cbind, list(1:2, 3:5))
> # NULL element is skipped
> do.call(cbind, list(1, NULL, 3, 4))
> # NA element isn't skipped
> do.call(cbind, list(1, NA, 3, 4))
```

Efficient Binding of Lists Into Matrices

A list of vectors can be flattened into a matrix using the functions `do.call()` and either `rbind()` or `cbind()`.

But for large vectors this procedure can be very slow, and often causes an out of memory error.

The function `do_call_rbind()` efficiently combines a list of vectors into a matrix.

`do_call_rbind()` produces the same result as `do.call(rbind, list_var)`, but using recursion.

`do_call_rbind()` calls lapply in a loop, each time binding neighboring list elements and dividing the length of the list by half.

`do_call_rbind()` is the same function as `do.call.rbind()` from package *qmao*:
https://r-forge.r-project.org/R/?group_id=1113

```
> list_vectors <- lapply(1:5, rnorm, n=10)
> matv <- do.call(rbind, list_vectors)
> dim(matv)
> do_call_rbind <- function(listv) {
+   while (NROW(listv) > 1) {
+ # Index of odd list elements
+     odd_index <- seq(from=1, to=NROW(listv), by=2)
+ # Bind odd and even elements, and divide listv by half
+     listv <- lapply(odd_index, function(indeks) {
+ if (indeks==NROW(listv)) return(listv[[indeks]])
+ rbind(listv[[indeks]], listv[[indeks+1]])
+     })  # end lapply
+   }  # end while
+ # listv has only one element - return it
+   listv[[1]]
+ }  # end do_call_rbind
> identical(matv, do_call_rbind(list_vectors))
```

Filtering Data Frames Using subset()

Filtering means extracting rows from a *data frame* that satisfy a logical condition.

Data frames can be filtered using Boolean vectors and brackets "[]" operators.

The function subset() filters *data frames*, by applying logical conditions to its columns, using the column names.

subset() provides a succinct notation and discards NA values, but it's slightly slower than using Boolean vectors and brackets "[]" operators.

```
> airquality[(airquality$Solar.R > 320 &
+         !is.na(airquality$Solar.R)), ]
> subset(x=airquality, subset=(Solar.R > 320))
> summary(microbenchmark(
+     subset=subset(x=airquality, subset=(Solar.R > 320)),
+     brackets=airquality[(airquality$Solar.R > 320 &
+             !is.na(airquality$Solar.R)), ],
+ times=10))[, c(1, 4, 5)]  # end microbenchmark summary
```

Splitting Data Frames Using factor Categorical Variables

The function split() divides an object into a list of objects, according to a factor (categorical variable).

The list's namev attribute is equal to the factor levels.

```
> unique(iris$Species)  # Species has three distinct values
> # Split into separate data frames by hand
> setosa <- iris[iris$Species=="setosa", ]
> versi <- iris[iris$Species=="versicolor", ]
> virgin <- iris[iris$Species=="virginica", ]
> dim(setosa)
> head(setosa, 2)
> # Split iris into list based on Species
> splitiris <- split(iris, iris$Species)
> str(splitiris, max.confl=1)
> names(splitiris)
> dim(splitiris$setosa)
> head(splitiris$setosa, 2)
> all.equal(setosa, splitiris$setosa)
```

The *split-apply-combine* Procedure

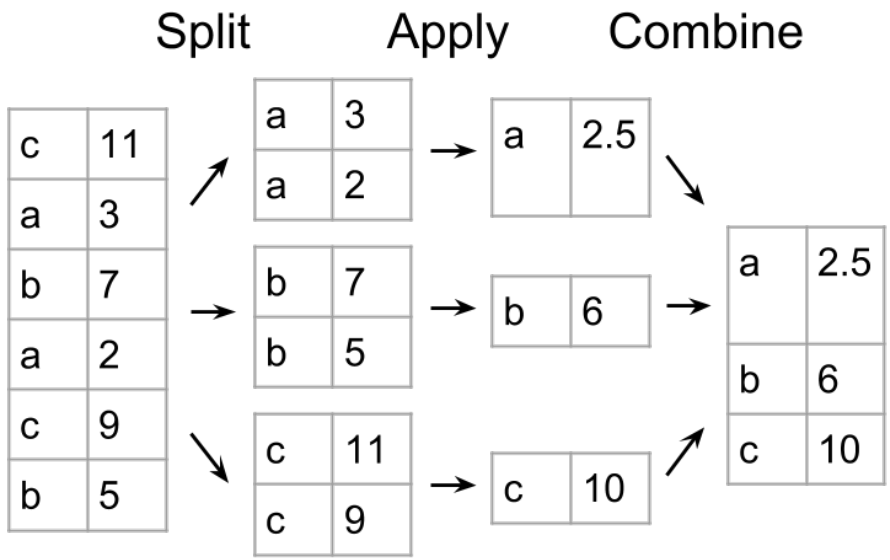
The *split-apply-combine* procedure consists of:

- dividing an object into a list, according to a factor (attribute).
- applying a function to each list element.
- combining the results.

The *split-apply-combine* procedure is also called the *map-reduce* procedure, or simply *data pivoting*, and it's similar to *pivot tables* in *Excel*.

Data pivoting can be performed *data frames*, by aggregating its columns based on categorical data stored in one of its columns.

You can read more about the *split-apply-combine* procedure in Hadley Wickham's paper:
http://www.jstatsoft.org/v40/i01/paper



Data Pivoting Example

Data pivoting can be performed through successive applications of functions `split()`, `apply()`, and `unlist()`.

A *data frame* can be *pivoted* either by first splitting it into a list of *data frames* and then aggregating, or by splitting just a single column and aggregating it.

The function `split()` divides an object into a list of objects, according to a `factor` (categorical variable).

The list's `namev` attribute is equal to the `factor` levels.

The functional `aggregate()` *pivots* the columns of a *data frame*.

`aggregate()` can accept a `"formula"` argument with the column names, or it can accept `"x"` and `"by"` arguments with the columns.

`aggregate()` returns a *data frame* containing the names of the groups (`factor` confls).

```
> unique(mtcars$cyl)  # cyl has three unique values
> # Split mpg column based on number of cylinders
> split(mtcars$mpg, mtcars$cyl)
> # Split mtcars data frame based on number of cylinders
> split_cars <- split(mtcars, mtcars$cyl)
> str(split_cars, max.confl=1)
> names(split_cars)
> # Aggregate the mean mpg over split mtcars data frame
> sapply(split_cars, function(x) mean(x$mpg))
> # Or: split mpg column and aggregate the mean
> sapply(split(mtcars$mpg, mtcars$cyl), mean)
> # Same but using with()
> with(mtcars, sapply(split(mpg, cyl), mean))
> # Or: aggregate() using formula syntax
> aggregate(x=(mpg ~ cyl), data=mtcars, FUN=mean)
> # Or: aggregate() using data frame syntax
> aggregate(x=mtcars$mpg, by=list(cyl=mtcars$cyl), FUN=mean)
> # Or: using name for mpg
> aggregate(x=list(mpg=mtcars$mpg), by=list(cyl=mtcars$cyl), FUN=mea
> # Aggregate() all columns
> aggregate(x=mtcars, by=list(cyl=mtcars$cyl), FUN=mean)
> # Aggregate multiple columns using formula syntax
> aggregate(x=(cbind(mpg, hp) ~ cyl), data=mtcars, FUN=mean)
```

The tapply() Functional

The functional tapply() is a specialized version of the apply() functional, that applies a function to elements of a *jagged array*.

A *jagged array* is a list consisting of vectors or matrices of different lengths.

tapply() accepts a vector of values "X", a factor "INDEX", and a function "FUN".

tapply() first groups the elements of "X" according to the factor "INDEX", transforming it into a *jagged array*, and then applies "FUN" to each element of the *jagged array*.

tapply() applies a function to sub-vectors aggregated using a factor, and performs *data pivoting* in a single function call.

The by() function is a wrapper for tapply().

The with() function evaluates an expression in an environment constructed from the data.

```
> # Mean mpg for each cylinder group
> tapply(X=mtcars$mpg, INDEX=mtcars$cyl, FUN=mean)
> # using with() environment
> with(mtcars, tapply(X=mpg, INDEX=cyl, FUN=mean))
> # Function sapply() instead of tapply()
> with(mtcars, sapply(sort(unique(cyl)), function(x) {
+  structure(mean(mpg[x==cyl]), names=x)
+      }))  # end with
> # Function by() instead of tapply()
> with(mtcars, by(data=mpg, INDICES=cyl, FUN=mean))
```

Data Pivoting Returning a Matrix

Sometimes *data pivoting* returns a list of vectors.

A list of vectors can be flattened into a matrix using the functions `do.call()` and either `rbind()` or `cbind()`.

The function `do.call()` executes a function call using a function name and a list of arguments.

`do.call()` passes the list elements individually, instead of passing the whole list as one argument: `do.call(fun, list)= fun(list[[1]], list[[2]], ...)`

```
> # Get several mpg stats for each cylinder group
> cardata <- sapply(split_cars, function(x) {
+   c(mean=mean(x$mpg), max=max(x$mpg), min=min(x$mpg))
+ }  # end anonymous function
+ )  # end sapply
> cardata  # sapply() produces a matrix
> # Now same using lapply
> cardata <- lapply(split_cars, function(x) {
+   c(mean=mean(x$mpg), max=max(x$mpg), min=min(x$mpg))
+ }  # end anonymous function
+ )  # end sapply
> is.list(cardata)  # lapply produces a list
> # do.call flattens list into a matrix
> do.call(cbind, cardata)
```

Data Pivoting of Panel Data

The *data frame* `panel_data` contains fundamental financial data for *S&P500* stocks.

The `Industry` column has 22 unique elements, while the `Sector` column has 10 unique elements.

Each `Industry` belongs to a single `Sector`, but each `Sector` may have several `Industries` that belong to it.

The functional `aggregate()` allows aggregating over the `Industry` column, by performing *data pivoting*.

```
> # Download CRSPpanel.txt from the NYU share drive
> # Read the file using read.table() with header and sep arguments
> paneld <- read.table(file="/Users/jerzy/Develop/lecture_slides/dat
+                      header=TRUE, sep="\t")
> paneld[1:5, 1:5]
> attach(paneld)
> # Split paneld based on Industry column
> panelds <- split(paneld, paneld$Industry)
> # Number of companies in each Industry
> sapply(panelds, NROW)
> # Number of Sectors that each Industry belongs to
> sapply(panelds, function(x) {
+   NROW(unique(x$Sector))
+ })  # end sapply
> # Or
> aggregate(x=(Sector ~ Industry),
+   data=paneld, FUN=function(x) NROW(unique(x)))
> # Industries and the Sector to which they belong
> aggregate(x=(Sector ~ Industry), data=paneld, FUN=unique)
> # Or
> aggregate(x=Sector, by=list(Industry), FUN=unique)
> # Or
> sapply(unique(Industry), function(x) {
+   Sector[match(x, Industry)]
+ })  # end sapply
```

Data Pivoting Returning a *Jagged Array*

A *jagged array* is a list consisting of vectors or matrices of different lengths.

The functional `aggregate()` returns a *data frame*, so it's output must be coerced if the *data pivoting* attempts to return a *jagged array*.

The functional `tapply()` returns an array, so it's output must be coerced if the *data pivoting* attempts to return a *jagged array*.

`tapply()` accepts a vector of values `"X"`, a factor `"INDEX"`, and a function `"FUN"`.

`tapply()` first groups the elements of `"X"` according to the factor `"INDEX"`, transforming it into a *jagged array*, and then applies `"FUN"` to each element of the *jagged array*.

`tapply()` applies a function to sub-vectors aggregated using a factor, and performs *data pivoting* in a single function call.

```
> # Split paneld based on Sector column
> panelds <- split(paneld, paneld$Sector)
> # Number of companies in each Sector
> sapply(panelds, NROW)
> # Industries belonging to each Sector (jagged array)
> secind <- sapply(panelds, function(x) unique(x$Industry))
> # Or use aggregate() (returns a data frame)
> secind2 <- aggregate(x=(Industry ~ Sector),
+   data=paneld, FUN=function(x) unique(x))
> # Or use aggregate() with "by" argument
> secind2 <- aggregate(x=Industry, by=list(Sector),
+     FUN=function(x) as.vector(unique(x)))
> # Coerce secind2 into a jagged array
> namev <- secind2[, 1]
> secind2 <- secind2[, 2]
> names(secind2) <- namev
> all.equal(secind2, secind)
> # Or use tapply() (returns an array)
> secind2 <- tapply(X=Industry, INDEX=Sector, FUN=unique)
> # Coerce secind2 into a jagged array
> secind2 <- drop(as.matrix(secind2))
> all.equal(secind2, secind)
```

Data Pivoting Over Multiple Columns

Data pivoting over multiple columns can be performed by splitting the *data frame* and then performing an sapply() loop using an anonymous function.

Splitting the *data frame* allows aggregations over multiple columns.

An anonymous function allows applying different aggregations on the same column.

```
> # Average ROE in each Industry
> sapply(split(ROE, Industry), mean)
> # Average, min, and max ROE in each Industry
> t(sapply(split(ROE, Industry), FUN=function(x)
+   c(mean=mean(x), max=max(x), min=min(x))))
> # Split paneld based on Industry column
> panelds <- split(paneld, paneld$Industry)
> # Average ROE and EPS in each Industry
> t(sapply(panelds, FUN=function(x)
+   c(mean_roe=mean(x$ROE),
+     mean_eps=mean(x$EPS.EXCLUDE.EI))))
> # Or: split paneld based on Industry column
> panelds <- split(paneld[, c("ROE", "EPS.EXCLUDE.EI")],
+   paneld$Industry)
> # Average ROE and EPS in each Industry
> t(sapply(panelds, FUN=function(x) sapply(x, mean)))
> # Average ROE and EPS using aggregate()
> aggregate(x=paneld[, c("ROE", "EPS.EXCLUDE.EI")],
+   by=list(paneld$Industry), FUN=mean)
```

Exception Conditions: Errors and Warnings

Exception conditions are `R` objects containing information about *errors* or *warnings* produced while evaluating expressions.

The function `warning()` produces a *warning* condition, but doesn't halt function execution, and returns its message to the warning handler.

The function `stop()` produces an *error* condition, halts function execution, and returns its message to the error handler.

The handling of *warning* conditions depends on the value of `options("warn")`:

- *negative* then warnings are ignored,
- *zero* then warnings are stored and printed after the top-confl function has completed,
- *one* - warnings are printed as they occur,
- *two* or larger - warnings are turned into errors,

The function `suppressWarnings()` evaluates its expressions and ignores all warnings.

```
> # ?options  # Get info on global options
> getOption("warn")  # Global option for "warn"
> options("warn")  # Global option for "warn"
> getOption("error")  # Global option for "error"
> calc_sqrt <- function(inputv) {
+ # Returns its argument
+   if (inputv < 0) {
+     warning("calc_sqrt: input is negative")
+     NULL  # Return NULL for negative argument
+   } else {
+     sqrt(inputv)
+   }  # end if
+ }  # end calc_sqrt
> calc_sqrt(5)
> calc_sqrt(-1)
> options(warn=-1)
> calc_sqrt(-1)
> options(warn=0)
> calc_sqrt()
> options(warn=1)
> calc_sqrt()
> options(warn=3)
> calc_sqrt()
```

Validating Function Arguments

Argument validation consists of first determining if any arguments are *missing*, and then determining if the arguments are of the correct *type*.

An argument is *missing* when the formal argument is not bound to an actual value in the function call.

The function `missing()` returns `TRUE` if an argument is missing, and `FALSE` otherwise.

Missing arguments can be detected by:
- assigning a `NULL` default value to formal arguments and then calling `is.null()` on them,
- calling the function `missing()` on the arguments.

The argument *type* can be validated using functions such as `is.numeric()`, `is.character()`, etc.

The function `return()` returns its argument and terminates futher function execution.

```
> # Function valido validates its arguments
> valido <- function(inputv=NULL) {
+ # Check if argument is valid and return double
+   if (is.null(inputv)) {
+     return("valido: input is missing")
+   } else if (is.numeric(inputv)) {
+     2*inputv
+   } else cat("valido: input not numeric")
+ }  # end valido
> valido(3)
> valido("a")
> valido()
> # valido validates arguments using missing()
> valido <- function(inputv) {
+ # Check if argument is valid and return double
+   if (missing(inputv)) {
+     return("valido: input is missing")
+   } else if (is.numeric(inputv)) {
+     2*inputv
+   } else cat("valido: input is not numeric")
+ }  # end valido
> valido(3)
> valido("a")
> valido()
```

Validating Assertions Inside Functions

If assertions about variables inside a function are `FALSE`, then `stop()` can be called to halt its execution.

Calling `stop()` is preferable to calling `return()`, or inserting `cat()` statements into the code.

Using `stop()` inside a function allows calling the function `traceback()`, if an error was produced.

The function `traceback()` prints the call stack, showing the function that produced the *error* condition.

`cat()` statements inside the function body provide information about the state of its variables.

```
> # valido() validates its arguments and assertions
> valido <- function(inputv) {
+ # Check if argument is valid and return double
+   if (missing(inputv)) {
+     stop("valido: input is missing")
+   } else if (!is.numeric(inputv)) {
+     cat("input =", inputv, "\n")
+     stop("valido: input is not numeric")
+   } else 2*inputv
+ }  # end valido
> valido(3)
> valido("a")
> valido()
> # Print the call stack
> traceback()
```

Validating Assertions Using stopifnot()

R provides robust validation and debugging tools through *type* validation functions, and functions missing(), stop(), and stopifnot().

If the argument to function stopifnot() is FALSE, then it produces an *error* condition, and halts function execution.

stopifnot() is a convenience wrapper for stop(), and eliminates the need to use if () statements.

stopifnot() is often used to check the validity of function arguments.

stopifnot() can be inserted anywhere in the function body in order to check assertions about its variables.

```
> valido <- function(inputv) {
+ # Check argument using long form '&&' operator
+   stopifnot(!missing(inputv) && is.numeric(inputv))
+   2*inputv
+ }  # end valido
> valido(3)
> valido()
> valido("a")
> valido <- function(inputv) {
+ # Check argument using logical '&' operator
+   stopifnot(!missing(inputv) & is.numeric(inputv))
+   2*inputv
+ }  # end valido
> valido()
> valido("a")
```

Validating Function Arguments and Assertions

The functions `stop()` and `stopifnot()` halt function execution and produce *error* conditions if certain assertions are `FALSE`.

The *type* validation functions, such as `is.numeric()`, `is.na()`, etc., and `missing()`, allow for validation of arguments and variables inside functions.

`cat()` statements can provide information about the state of variables inside a function.

`cat()` statements don't return values, so they provide information even when a function produces an `error`.

```
> # sumtwo() returns the sum of its two arguments
> sumtwo <- function(input1, input2) {  # Even more robust
+ # Check if at least one argument is not missing
+   stopifnot(!missing(input1) && !missing(input2))
+ # Check if arguments are valid and return sum
+   if (is.numeric(input1) && is.numeric(input2)) {
+     input1 + input2  # Both valid
+   } else if (is.numeric(input1)) {
+     cat("input2 is not numeric\n")
+     input1  # input1 is valid
+   } else if (is.numeric(input2)) {
+     cat("input1 is not numeric\n")
+     input2  # input2 is valid
+   } else {
+     stop("none of the arguments are numeric")
+   }
+ }  # end sumtwo
> sumtwo(1, 2)
> sumtwo(5, 'a')
> sumtwo('a', 5)
> sumtwo('a', 'b')
> sumtwo()
```

The R Debugger Facility

The function `debug()` flags a function for future debugging, but doesn't invoke the debugger.

After a function is flagged for debugging with the call `"debug(myfun)"`, then the function call `"myfun()"` automatically invokes the debugger (browser).

When the debugger is first invoked, it prints the function code to the console, and produces a *browser* prompt: `"Browse[2]>"`.

Once inside the debugger, the user can execute the function code one command at a time by pressing the *Enter* key.

The user can examine the function arguments and variables with standard R commands, and can also change the values of objects or create new ones.

The command `"c"` executes the remainder of the function code without pausing.

The command `"Q"` exits the debugger (browser).

The call `"undebug(myfun)"` at the R prompt unflags the function for debugging.

```
> # Flag "valido" for debugging
> debug(valido)
> # Calling "valido" starts debugger
> valido(3)
> # unflag "valido" for debugging
> undebug(valido)
```

Debugging Using browser()

As an alternative to flagging a function for debugging, the user can insert the function `browser()` into the function body.

`browser()` pauses the execution of a function and invokes the debugger (browser) at the point where `browser()` was called.

Once inside the debugger, the user can execute all the same browser commands as when using `debug()`.

`browser()` is usually inserted just before the command that is suspected of producing an *error* condition.

Another alternative to flagging a function for debugging, or inserting `browser()` calls, is setting the `"error"` option equal to `"recover"`.

Setting the `"error"` option equal to `"recover"` automatically invokes the debugger when an *error* condition is produced.

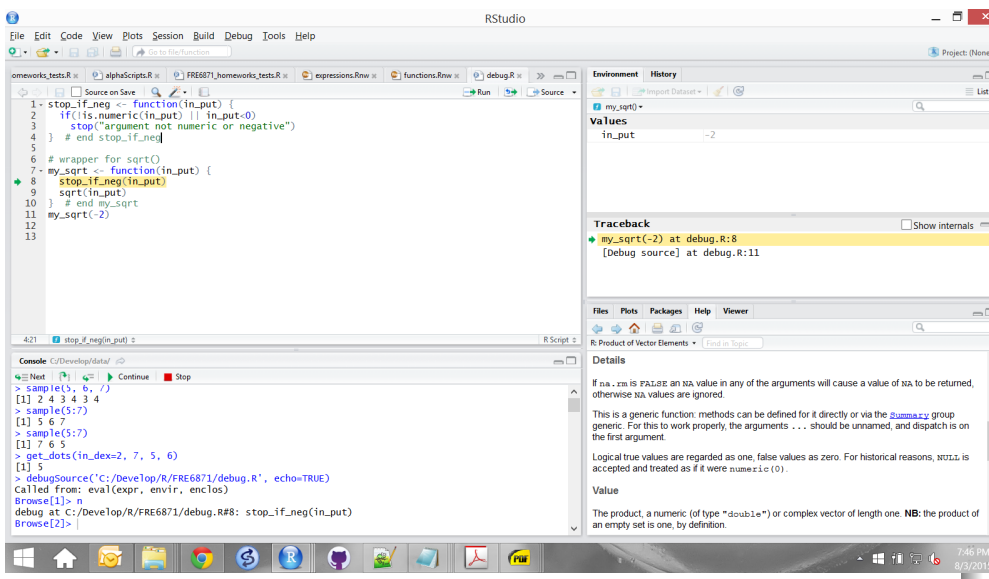
```
> valido <- function(inputv) {
+   browser()  # Pause and invoke debugger
+ # Check argument using long form '&&' operator
+   stopifnot(!missing(inputv) && is.numeric(inputv))
+   2*inputv
+ }  # end valido
> valido()  # Invokes debugger
> options("error")  # Show default NULL "error" option
> options(error=recover)  # Set "error" option to "recover"
> options(error=NULL)  # Set back to default "error" option
```

Using the Debugger in *RStudio*

RStudio has several built-in debugging facilities that complement those already installed in `R`:

- toggling breakpoints, instead of inserting `browser()` commands,
- stepping into functions,
- environment pane with environment stack, instead of calling `ls()`,
- traceback pane, instead of calling `traceback()`,

RStudio provides an online debugging tutorial:
https://support.rstudio.com/hc/en-us/articles/205612627-Debugging-with-RStudio



Handling Exception Conditions

The function `tryCatch()` executes functions and expressions, and handles any *exception conditions* produced when they are evaluated.

`tryCatch()` first evaluates its `"expression"` argument.

If no error or warning `condition` is produced then `tryCatch()` just returns the value of the expression.

If an `exception condition` is produced then `tryCatch()` invokes error and warning *handlers* and executes other expressions to provide information about the `exception condition`.

If a *handler* is provided to `tryCatch()` then the error is captured by the *handler*, instead of being broadcast to the console.

At the end, `tryCatch()` evaluates the expression provided to the `finally` argument.

```
> str(tryCatch)  # Get arguments of tryCatch()
> tryCatch(  # Without error handler
+   {  # Evaluate expressions
+     numv <- 101  # Assign
+     stop("my error")  # Produce error
+   },
+   finally=print(paste0("numv = ", numv))
+ )  # end tryCatch
>
> tryCatch(  # With error handler
+   {  # Evaluate expressions
+     numv <- 101  # Assign
+     stop("my error")  # Produce error
+   },
+   # Error handler captures error condition
+   error=function(msg) {
+     print(paste0("Error handler: ", msg))
+   },  # end error handler
+   # Warning handler captures warning condition
+   warning=function(msg) {
+     print(paste0("Warning handler: ", msg))
+   },  # end warning handler
+   finally=print(paste0("numv = ", numv))
+ )  # end tryCatch
```

Error Conditions in Loops

If an *error* occurs in an `apply()` loop, then the loop exits without returning any result.

`apply()` collects the values returned by the function supplied to its `FUN` argument, and returns them only after the loop is finished.

If one of the function calls produces an error, then the loop is interrupted and `apply()` exits without returning any result.

The function `tryCatch()` captures errors, allowing loops to continue after the error `condition`.

```
> # Apply loop without tryCatch
> apply(matrix(1:5), 1, function(numv) {  # Anonymous function
+     stopifnot(!(numv = 3))  # Check for error
+     # Broadcast message to console
+     cat("(cat) numv = ", numv, "\n")
+     # Return a value
+     paste0("(return) numv = ", numv)
+   }  # end anonymous function
+ )  # end apply
```

Exception Handling in Loops

If the body of the function supplied to the `FUN` argument is wrapped in `tryCatch()`, then the loop can finish without interruption and return its results.

The messages produced by *errors* and *warnings* can be caught by *handlers* (functions) that are supplied to `tryCatch()`.

The *error* and *warning* messages are bound (passed) to the formal arguments of the *handler* functions that are supplied to `tryCatch()`.

`tryCatch()` always evaluates the expression provided to the `finally` argument, even after an *error* occurs.

```
> # Apply loop with tryCatch
> apply(as.matrix(1:5), 1, function(numv) {  # Anonymous function
+     tryCatch(  # With error handler
+ {  # Body
+   stopifnot(numv != 3)  # Check for error
+   # Broadcast message to console
+   cat("(cat) numv = ", numv, "\t")
+   # Return a value
+   paste0("(return) numv = ", numv)
+ },
+ # Error handler captures error condition
+ error=function(msg)
+   paste0("handler: ", msg),
+ finally=print(paste0("(finally) numv = ", numv))
+     )  # end tryCatch
+   }  # end anonymous function
+ )  # end apply
```

Date Objects

R has a Date class for date objects (but without time).

The function as.Date() parses character strings and coerces numeric objects into Date objects.

R stores Date objects as the number of days since the *epoch* (January 1, 1970).

The function difftime() calculates the difference between Date objects, and returns a time interval object of class difftime.

The "+" and "-" arithmetic operators and the "<" and ">" logical comparison operators are overloaded to allow these operations directly on Date objects.

numeric *year-fraction* dates can be coerced to Date objects using the functions attributes() and structure().

```
> Sys.Date()  # Get today's date
> as.Date(1e3)  # Coerce numeric into date object
> datetime <- as.Date("2014-07-14")  # "%Y-%m-%d" or "%Y/%m/%d"
> datetime
> class(datetime)  # Date object
> as.Date("07-14-2014", "%m-%d-%Y")  # Specify format
> datetime + 20  # Add 20 days
> # Extract internal representation to integer
> as.numeric(datetime)
> datep <- as.Date("07/14/2013", "%m/%d/%Y")
> datep
> # Difference between dates
> difftime(datetime, datep, units="weeks")
> weekdays(datetime)  # Get day of the week
> # Coerce numeric into date-times
> datetime <- 0
> attributes(datetime) <- list(class="Date")
> datetime  # "Date" object
> structure(0, class="Date")  # "Date" object
> structure(10000.25, class="Date")
```

POSIXct Date-time Objects

The POSIXct class in R represents *date-time* objects, that can store both the date and time.

The *clock time* is the time (number of hours, minutes and seconds) in the local *time zone*.

The *moment of time* is the *clock time* in the UTC *time zone*.

POSIXct objects are stored as the number of seconds that have elapsed since the *epoch* (January 1, 1970) in the UTC *time zone*.

POSIXct objects are stored as the *moment of time*, but are printed out as the *clock time* in the local *time zone*.

A *clock time* together with a *time zone* uniquely specifies a *moment of time*.

The function as.POSIXct() can parse a character string (representing the *clock time*) and a *time zone* into a POSIXct object.

POSIX is an acronym for "Portable Operating System Interface".

```
> datetime <- Sys.time()  # Get today's date and time
> datetime
> class(datetime)  # POSIXct object
> # POSIXct stored as integer moment of time
> as.numeric(datetime)
> # Parse character string "%Y-%m-%d %H:%M:%S" to POSIXct object
> datetime <- as.POSIXct("2014-07-14 13:30:10")
> # Different time zones can have same clock time
> as.POSIXct("2014-07-14 13:30:10", tz="America/New_York")
> as.POSIXct("2014-07-14 13:30:10", tz="UTC")
> # Format argument allows parsing different date-time string format
> as.POSIXct("07/14/2014 13:30:10", format="%m/%d/%Y %H:%M:%S",
+      tz="America/New_York")
```

Operations on POSIXct Objects

The "+" and "-" arithmetic operators are overloaded to allow addition and subtraction operations on POSIXct objects.

The "<" and ">" logical comparison operators are also overloaded to allow direct comparisons between POSIXct objects.

Operations on POSIXct objects are equivalent to the same operations on the internal integer representation of POSIXct (number of seconds since the *epoch*).

Subtracting POSIXct objects creates a time interval object of class difftime.

The method seq.POSIXt creates a vector of POSIXct *date-times*.

```
> # Same moment of time corresponds to different clock times
> timeny <- as.POSIXct("2014-07-14 13:30:10", tz="America/New_York")
> timeldn <- as.POSIXct("2014-07-14 13:30:10", tz="UTC")
> # Add five hours to POSIXct
> timeny + 5*60*60
> # Subtract POSIXct
> timeny - timeldn
> class(timeny - timeldn)
> # Compare POSIXct
> timeny > timeldn
> # Create vector of POSIXct times during trading hours
> timev <- seq(
+   from=as.POSIXct("2014-07-14 09:30:00", tz="America/New_York"),
+   to=as.POSIXct("2014-07-14 16:00:00", tz="America/New_York"),
+   by="10 min")
> head(timev, 3)
> tail(timev, 3)
```

Moment of Time and Clock Time

`as.POSIXct()` can also coerce `integer` objects into `POSIXct`, given an `origin` in time.

The same *moment of time* corresponds to different *clock times* in different *time zones*.

The same *clock times* in different *time zones* correspond to different *moments of time*.

```
> # POSIXct is stored as integer moment of time
> datetimen <- as.numeric(datetime)
> # Same moment of time corresponds to different clock times
> as.POSIXct(datetimen, origin="1970-01-01", tz="America/New_York")
> as.POSIXct(datetimen, origin="1970-01-01", tz="UTC")
> # Same clock time corresponds to different moments of time
> as.POSIXct("2014-07-14 13:30:10", tz="America/New_York") -
+   as.POSIXct("2014-07-14 13:30:10", tz="UTC")
> # Add 20 seconds to POSIXct
> datetime + 20
```

Methods for Manipulating POSIXct Objects

The generic function `format()` formats R objects for printing and display.

The method `format.POSIXct()` parses `POSIXct` objects into a `character` string representing the *clock time* in a given *time zone*.

The method `as.POSIXct.Date()` parses `Date` objects into `POSIXct`, and assigns to them the *moment of time* corresponding to midnight `UTC`.

`POSIX` is an acronym for "Portable Operating System Interface".

```
> datetime  # POSIXct date and time
> # Parse POSIXct to string representing the clock time
> format(datetime)
> class(format(datetime))  # Character string
> # Get clock times in different time zones
> format(datetime, tz="America/New_York")
> format(datetime, tz="UTC")
> # Format with custom format strings
> format(datetime, "%m/%Y")
> format(datetime, "%m-%d-%Y %H hours")
> # Trunc to hour
> format(datetime, "%m-%d-%Y %H:00:00")
> # Date converted to midnight UTC moment of time
> as.POSIXct(Sys.Date())
> as.POSIXct(as.numeric(as.POSIXct(Sys.Date())),
+       origin="1970-01-01",
+       tz="UTC")
```

POSIXlt Date-time Objects

The POSIXlt class in R represents *date-time* objects, that are stored internally as a list.

The function as.POSIXlt() can parse a character string (representing the *clock time*) and a *time zone* into a POSIXlt object.

The method format.POSIXlt() parses POSIXlt objects into a character string representing the *clock time* in a given *time zone*.

The function as.POSIXlt() can also parse a POSIXct object into a POSIXlt object, and as.POSIXct() can perform the reverse.

Adding a number to POSIXlt causes implicit coercion to POSIXct.

POSIXct and POSIXlt are two derived classes from the POSIXt class.

The methods round.POSIXt() and trunc.POSIXt() round and truncate POSIXt objects, and return POSIXlt objects.

```
> # Parse character string "%Y-%m-%d %H:%M:%S" to POSIXlt object
> datetime <- as.POSIXlt("2014-07-14 18:30:10")
> datetime
> class(datetime)  # POSIXlt object
> as.POSIXct(datetime)  # Coerce to POSIXct object
> # Extract internal list representation to vector
> unlist(datetime)
> datetime + 20  # Add 20 seconds
> class(datetime + 20)  # Implicit coercion to POSIXct
> trunc(datetime, units="hours")  # Truncate to closest hour
> trunc(datetime, units="days")  # Truncate to closest day
> methods(trunc)  # Trunc methods
> trunc.POSIXt
```

Time Zones and Date-time Conversion

date-time objects require a *time zone* to be uniquely specified.

`UTC` stands for "Universal Time Coordinated", and is synonymous with `GMT`, but doesn't change with Daylight Saving Time.

`EST` stands for "Eastern Standard Time", and is `UTC - 5` hours.

`EDT` stands for "Eastern Daylight Time", and is `UTC - 4` hours.

The function `Sys.setenv()` can be used to set the default *time zone*, but the environment variable `"TZ"` must be capitalized.

```
> # Set time-zone to UTC
> Sys.setenv(TZ="UTC")
> Sys.timezone()  # Get time-zone
> Sys.time()  # Today's date and time
> # Set time-zone back to New York
> Sys.setenv(TZ="America/New_York")
> Sys.time()  # Today's date and time
> # Standard Time in effect
> as.POSIXct("2013-03-09 11:00:00", tz="America/New_York")
> # Daylight Savings Time in effect
> as.POSIXct("2013-03-10 11:00:00", tz="America/New_York")
> datetime <- Sys.time()  # Today's date and time
> # Convert to character in different TZ
> format(datetime, tz="America/New_York")
> format(datetime, tz="UTC")
> # Parse back to POSIXct
> as.POSIXct(format(datetime, tz="America/New_York"))
> # Difference between New_York time and UTC
> as.POSIXct(format(Sys.time(), tz="UTC")) -
+   as.POSIXct(format(Sys.time(), tz="America/New_York"))
```

Manipulating Date-time Objects Using *lubridate*

The package *lubridate* contains functions for manipulating `POSIXct` date-time objects.

The `ymd()`, `dmy()`, etc. functions parse `character` and `numeric` *year-fraction* dates into `POSIXct` objects.

The `mday()`, `month()`, `year()`, etc. accessor functions extract date-time components.

The function `decimal_date()` converts `POSIXct` objects into `numeric` *year-fraction* dates.

The function `date_decimal()` converts `numeric` *year-fraction* dates into `POSIXct` objects.

```
> library(lubridate)  # Load lubridate
> # Parse strings into date-times
> as.POSIXct("07-14-2014", format="%m-%d-%Y", tz="America/New_York")
> datetime <- lubridate::mdy("07-14-2014", tz="America/New_York")
> datetime
> class(datetime)  # POSIXct object
> lubridate::dmy("14.07.2014", tz="America/New_York")
>
> # Parse numeric into date-times
> as.POSIXct(as.character(14072014), format="%d%m%Y",
+                    tz="America/New_York")
> lubridate::dmy(14072014, tz="America/New_York")
>
> # Parse decimal to date-times
> lubridate::decimal_date(datetime)
> lubridate::date_decimal(2014.25, tz="America/New_York")
> date_decimal(decimal_date(datetime), tz="America/New_York")
```

Time Zones Using *lubridate*

The package *lubridate* simplifies *time zone* calculations.

The package *lubridate* uses the *UTC time zone* as default.

The function `with_tz()` creates a date-time object with the same moment of time in a different *time zone*.

The function `force_tz()` creates a date-time object with the same clock time in a different *time zone*.

```
> datetime <- lubridate::ymd_hms(20140714142010,
+                tz="America/New_York")
> datetime
> # Get same moment of time in "UTC" time zone
> lubridate::with_tz(datetime, "UTC")
> as.POSIXct(format(datetime, tz="UTC"), tz="UTC")
> # Get same clock time in "UTC" time zone
> lubridate::force_tz(datetime, "UTC")
> as.POSIXct(format(datetime, tz="America/New_York"),
+      tz="UTC")
> # Same moment of time
> datetime - with_tz(datetime, "UTC")
> # Different moments of time
> datetime - force_tz(datetime, "UTC")
```

lubridate Time Span Objects

lubridate has two time span classes: `durations` and `periods`.

`durations` specify exact time spans, such as numbers of seconds, hours, days, etc.

The functions `ddays()`, `dyears()`, etc. return `duration` objects.

`periods` specify relative time spans that don't have a fixed length, such as months, years, etc.

`periods` account for variable days in the months, for Daylight Savings Time, and for leap years.

The functions `days()`, `months()`, `years()`, etc. return `period` objects.

```
> # Daylight Savings Time handling periods vs durations
> datetime <- as.POSIXct("2013-03-09 11:00:00", tz="America/New_York")
> datetime
> datetime + lubridate::ddays(1)  # Add duration
> datetime + lubridate::days(1)  # Add period
>
> leap_year(2012)  # Leap year
> datetime <- lubridate::dmy(01012012, tz="America/New_York")
> datetime
> datetime + lubridate::dyears(1)  # Add duration
> datetime + lubridate::years(1)  # Add period
```

Adding Time Spans to Date-time Objects

`periods` allow calculating future dates with the same day of the month, or month of the year.

```
> datetime <- lubridate::ymd_hms(20140714142010, tz="America/New_Yo
> datetime
> # Add periods to a date-time
> c(datetime + lubridate::seconds(1), datetime + lubridate::minutes
+   datetime + lubridate::days(1), datetime + period(months=1))
>
> # Create vectors of dates
> datetime <- lubridate::ymd(20140714, tz="America/New_York")
> datetime + 0:2 * period(months=1)  # Monthly dates
> datetime + period(months=0:2)
> datetime + 0:2 * period(months=2)  # bi-monthly dates
> datetime + seq(0, 5, by=2) * period(months=1)
> seq(datetime, length=3, by="2 months")
```

End-of-month Dates

Adding monthly `periods` can create invalid dates.

The operators `%m+%` and `%m-%` add or subtract monthly `periods` to account for the varible number of days per month.

This allows creating vectors of end-of-month dates.

```
> # Adding monthly periods can create invalid dates
> datetime <- lubridate::ymd(20120131, tz="America/New_York")
> datetime + 0:2 * period(months=1)
> datetime + period(months=1)
> datetime + period(months=2)
>
> # Create vector of end-of-month dates
> datetime %m-% lubridate::months(13:1)
```

Package *RQuantLib* Calendar Functions

The package *RQuantLib* is an interface to the *QuantLib* open source C/C++ library for quantitative finance, mostly designed for pricing fixed-income instruments and options.

The *QuantLib* library also contains calendar functions for determining holidays and business days in many different jurisdictions.

```
> library(RQuantLib)  # Load RQuantLib
>
> # Create daily date series of class "Date"
> dates <- Sys.Date() + -5:2
> dates
>
> # Create Boolean vector of business days
> # Use RQuantLib calendar
> is_busday <- RQuantLib::isBusinessDay(
+   calendar="UnitedStates/GovernmentBond", dates)
>
> # Create daily series of business days
> bus_index <- dates[is_busday]
> bus_index
```

Review of Date-time Classes in R

The `Date` class from the `base` package is suitable for *daily* time series.

The `POSIXct` class from the `base` package is suitable for *intra-day* time series.

The `yearmon` and `yearqtr` classes from the *zoo* package are suitable for *quarterly* and *monthly* time series.

```
> datetime <- Sys.Date()  # Create date series of class "Date"
> dates <- datetime + 0:365  # Daily series over one year
> head(dates, 4)  # Print first few dates
> format(head(dates, 4), "%m/%d/%Y")  # Print first few dates
> # Create daily date-time series of class "POSIXct"
> dates <- seq(Sys.time(), by="days", length.out=365)
> head(dates, 4)  # Print first few dates
> format(head(dates, 4), "%m/%d/%Y %H:%M:%S")  # Print first few dat
> # Create series of monthly dates of class "zoo"
> monthly_index <- yearmon(2010+0:36/12)
> head(monthly_index, 4)  # Print first few dates
> # Create series of quarterly dates of class "zoo"
> qrtly_index <- yearqtr(2010+0:16/4)
> head(qrtly_index, 4)  # Print first few dates
> # Parse quarterly "zoo" dates to POSIXct
> Sys.setenv(TZ="UTC")
> as.POSIXct(head(qrtly_index, 4))
```

Homework Assignment

Required

- Study all the lecture slides in *FRE6871_Lecture_5.pdf*, and run all the code in *FRE6871_Lecture_5.R*

Recommended

- Read about *PCA* in:
  pca-handout.pdf
  pcaTutorial.pdf
- Read about *optimization methods*:
  Bolker Optimization Methods.pdf
  Yollin Optimization.pdf
  Boudt DEoptim Large Portfolio Optimization.pdf