

R Programming Course Notes

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Overview and History of R

- **R** = dialect of the **S** language
 - S was developed by John Chambers @ Bell Labs
 - initiated in 1976 as internal tool, originally FORTRAN libraries
 - 1988 rewritten in C (version 3 of language)
 - 1998 version 4 (what we use today)
- **History of S**
 - Bell labs → insightful → Lucent → Alcatel-Lucent
 - in 1998, S won the Association for computing machinery's software system award
- **History of R**
 - 1991 created in New Zealand by Ross Ihaka & Robert Gentleman
 - 1993 first announcement of R to public
 - 1995 Martin Machler convinces founders to use GNU General Public license to make R free
 - 1996 public mailing list created R-help and R-devel
 - 1997 R Core Group formed
 - 2000 R v1.0.0 released
- **R Features**
 - Syntax similar to S, semantics similar to S, runs on any platforms, frequent releases
 - lean software, functionalities in modular packages, sophisticated graphics capabilities
 - useful for interactive work, powerful programming language
 - active user community and **FREE** (4 freedoms)
 - * freedom to run the program
 - * freedom to study how the program works and adapt it
 - * freedom to redistribute copies
 - * freedom to improve the program
- **R Drawbacks**
 - 40 year-old technology
 - little built-in support for dynamic/3D graphics
 - functionality based on consumer demand
 - objects generally stored in physical memory (limited by hardware)
- **Design of the R system**
 - 2 conceptual parts: base R from CRAN vs. everything else
 - functionality divided into different packages
 - * **base R** contains core functionality and fundamental functions
 - * other utility packages included in the base install: `util`, `stats`, `datasets`, ...
 - * Recommended packages: `bootclass`, `KernSmooth`, etc
 - 5000+ packages available

Coding Standards

- Always use text files/editor
- Indent code (4 space minimum)
- limit the width of code (80 columns)
- limit the length of individual functions

Workspace and Files

- `getwd()` = return current working directory
- `setwd()` = set current working directory
- `?function` = brings up help for that function
- `dir.create("path/foldername", recursive = TRUE)` = create directories/subdirectories
- `unlink(directory, recursive = TRUE)` = delete directory and subdirectories
- `ls()` = list all objects in the local workspace
- `list.files(recursive = TRUE)` = list all, including subdirectories
- `args(function)` = returns arguments for the function
- `file.create("name")` = create file
 - `.exists("name")` = return true/false exists in working directory
 - `.info("name")` = return file info
 - `.info("name")$property` = returns value for the specific attribute
 - `.rename("name1", "name2")` = rename file
 - `.copy("name1", "name2")` = copy file
 - `.path("name1")` = return path of file

R Console and Evaluation

- `<-` = assignment operator
- `#` = comment
- expression is evaluated after hitting **enter** and result is returned
- autoprining occurs when you call a variable
 - `print(x)` = explicitly printing
- `[1]` at the beginning of the output = which element of the vector is being shown

R Objects and Data Structures

- 5 basic/**atomic** classes of objects:
 1. character
 2. numeric
 3. integer
 4. complex
 5. logical
- **Numbers**
 - numbers generally treated as **numeric** objects (double precision real numbers - decimals)
 - Integer objects can be created by adding **L** to the end of a number(ex. `1L`)
 - **Inf** = infinity, can be used in calculations
 - **NaN** = not a number/undefined
 - `sqrt(value)` = square root of value
- **Variables**
 - `variable <- value` = assignment of a value to a variable name

Vectors and Lists

- **atomic vector** = contains one data type, most basic object
 - `vector <- c(value1, value2, ...)` = creates a vector with specified values
 - `vector1*vector2` = element by element multiplication (rather than matrix multiplication)
 - * if the vectors are of different lengths, shorter vector will be recycled until the longer runs out
 - * computation on vectors/between vectors (`+`, `-`, `==`, `/`, etc.) are done element by element by default
 - * `%*%` = force matrix multiplication between vectors/matrices
 - `vector("class", n)` = creates empty vector of length n and specified class
 - * `vector("numeric", 3)` = creates 0 0 0
- `c()` = concatenate
 - **T**, **F** = shorthand for **TRUE** and **FALSE**
 - `1+0i` = complex numbers
- **explicit coercion**
 - `as.numeric(x)`, `as.logical(x)`, `as.character(x)`, `as.complex(x)` = convert object from one class to another
 - nonsensible coercion will result in **NA** (ex. `as.numeric(c("a", "b"))`)
 - `as.list(data.frame)` = converts a **data.frame** object into a **list** object
 - `as.character(list)` = converts list into a character vector
- **implicit coercion**
 - matrix/vector can only contain one data type, so when attempting to create matrix/vector with different classes, forced coercion occurs to make every element to same class
 - * *least common denominator* is the approach used (basically everything is converted to a class that all values can take, numbers → characters) and *no errors generated*
 - * coercion occurs to make every element to same class (implicit)
 - * `x <- c(NA, 2, "D")` will create a vector of character class
- `list()` = special vector with different classes of elements

- `list` = vector of objects of different classes
- elements of `list` use `[[]]`, elements of other vectors use `[]`
- **logical vectors** = contain values `TRUE`, `FALSE`, and `NA`, values are generated as result of logical conditions comparing two objects/values
- `paste(characterVector, collapse = " ")` = join together elements of the vector and separating with the `collapse` parameter
- `paste(vec1, vec2, sep = " ")` = join together different vectors and separating with the `sep` parameter
 - ***Note:** vector recycling applies here too*
 - `LETTERS`, `letters` = predefined vectors for all 26 upper and lower letters
- `unique(values)` = returns vector with all duplicates removed

Matrices and Data Frames

- `matrix` can contain **only 1** type of data
- `data.frame` can contain **multiple**
- `matrix(values, nrow = n, ncol = m)` = creates a `n` by `m` matrix
 - constructed **COLUMN WISE** → the elements are placed into the matrix from top to bottom for each column, and by column from left to right
 - matrices can also be created by adding the dimension attribute to vector
 - * `dim(m) <- c(2, 5)`
 - matrices can also be created by binding columns and rows
 - * `rbind(x, y)`, `cbind(x, y)` = combine rows/columns; can be used on vectors or matrices
 - * and / = element by element computation between two matrices
 - * `%*%` = matrix multiplication
- `dim(obj)` = dimensions of an object (returns `NULL` if a vector)
 - `dim(obj) <- c(4, 5)` = assign `dim` attribute to an object
 - * if object is a vector, R converts the vector to a `n` by `m` matrix (i.e. 4 rows by 5 column from the example command)
 - ***Note:** if `n` by `m` is larger than length of vector, then an error is returned*
 - * ***example***

```
# initiate a vector
x <-c(NA, 1, "cx", NA, 2, "dsa")
class(x)
```

```
## [1] "character"
```

```
x
```

```
## [1] NA      "1"      "cx"     NA       "2"      "dsa"
```

```
# convert to matrix
dim(x) <- c(3, 2)
class(x)
```

```
## [1] "matrix"
```

```
##      [,1] [,2]
## [1,] NA   NA
## [2,] "1"  "2"
## [3,] "cx" "dsa"
```

- `data.frame(var = 1:4, var2 = c(...))` = creates a data frame
 - `nrow()`, `ncol()` = returns row and column numbers
 - `data.frame(vector, matrix)` = takes any number of arguments and returns a single object of class “data.frame” composed of original objects
 - `as.data.frame(obj)` = converts object to data frame
 - data frames store tabular data
 - special type of list where every list has the same length (can be of different type)
 - data frames are usually created through `read.table()` and `read.csv()`
 - `data.matrix()` = converts a matrix to data frame
- `colMeans(matrix)` or `rowMeans(matrix)` = returns means of the columns/rows of a matrix/dataframe in a vector
- `as.numeric(rownames(df))` = returns row indices for rows of a data frame with unnamed rows
- **attributes**
 - objects can have attributes: `names`, `dimnames`, `row.names`, `dim` (matrices, arrays), `class`, `length`, or any user-defined ones
 - `attributes(obj)`, `class(obj)` = return attributes/class for an R object
 - `attr(object, "attribute") <- "value"` = creates/assigns a value to a new/existing attribute for the object
 - `names` attribute
 - * all objects can have names
 - * `names(x)` = returns names (NULL if no name exists)
 - `names(x) <- c("a", ...)` = can be used to assign names to vectors
 - * `list(a = 1, b = 2, ...)` = `a`, `b` are names
 - * `dimnames(matrix) <- list(c("a", "b"), c("c" , "d"))` = assign names to matrices
 - use list of two vectors: row, column in that order
 - `colnames(data.frame)` = return column names (can be used to set column names as well, similar to `dim()`)
 - `row.names` = names of rows in the data frame (attribute)

Arrays

- multi-dimensional collection of data with k dimensions
 - matrix = 2 dimensional array
- `array(data, dim, dimnames)`
 - `data` = data to be stored in array
 - `dim` = dimensions of the array
 - * `dim = c(2, 2, 5)` = 3 dimensional array → creates 5 2x2 array
 - `dimnames` = add names to the dimensions
 - * input must be a `list`

- * every element of the `list` must correspond in length to the dimensions of the array
- * `dimnames(x) <- list(c("a", "b"), c("c", "d"), c("e", "f", "g", "h", "i"))` =
 set the names for row, column, and third dimension respectively (2 x 2 x 5 in this case)
- `dim()` function can be used to create arrays from vectors or matrices
 - `x <- rnorm(20); dim(x) <- c(2, 2, 5)` = converts a 20 element vector to a 2x2x5 array

Factors

- factors are used to represent *categorical data* (integer vector where each value has a label)
- 2 types: **unordered** vs **ordered**
- treated specially by `lm()`, `glm()`
- Factors easier to understand because they self describe (vs. 1 and 2)
- `factor(c("a", "b"), levels = c("1", "2"))` = creates factor
 - `levels()` argument can be used to specify baseline levels vs other levels
 - * ***Note:**without explicit specification, R uses alphabetical order*
 - `table(factorVar)` = how many of each are in the factor

Missing Values

- NaN or NA = missing values
 - NaN = undefined mathematical operations
 - NA = any value not available or missing in the statistical sense
 - * any operations with NA results in NA
 - * NA can have different classes potentially (integer, character, etc)
 - **Note:** *NaN is an NA value, but NA is not NaN*
- `is.na()`, `is.nan()` = use to test if each element of the vector is NA and NaN
 - **Note:** *cannot compare NA (with `==`) as it is not a value but a **placeholder** for a quantity that is not available*
- `sum(my_na)` = sum of a logical vector (`TRUE` = 1 and `FALSE` = 0) is effectively the number of `TRUE`s
- **Removing NA Values**
 - `is.na()` = creates logical vector where T is where value exists, F is NA
 - * subsetting with the above result can return only the non NA elements
 - `complete.cases(obj1, obj2)` = creates logical vector where `TRUE` is where both values exist, and `FALSE` is where any is NA
 - * can be used on data frames as well
 - * `complete.cases(data.frame)` = creates logical vectors indicating which observation/row is good
 - * `data.frame[logicalVector,]` = returns all observations with complete data
- **Imputing Missing Values** = replacing missing values with estimates (can be averages from all other data with the similar conditions)

Sequence of Numbers

- `1:20` = creates a sequence of numbers from first number to second number
 - works in descending order as well
 - increment = 1
- `?':'` = enclose help for operators
- `seq(1, 20, by=0.5)` = sequence 1 to 20 by increment of .5
 - `length=30` argument can be used to specify number of values generated
- `length(variable)` = length of vector/sequence
- `seq_along(vector)` or `seq(along.with = vector)` = create vector that is same length as another vector
- `rep(0, times = 40)` = creates a vector with 40 zeroes
 - `rep(c(1, 2), times = 10)` = repeats combination of numbers 10 times
 - `rep(c(1, 2), each = 10)` = repeats first value 10 times followed by second value 10 times

Subsetting

- R uses **one based index** → starts counting at 1
 - `x[0]` returns `numeric(0)`, not error
 - `x[3000]` returns `NA` (not out of bounds/error)
- `[]` = always returns object of same class, can select more than one element of an object (ex. `[1:2]`)
- `[[]]` = can extract one element from list or data frame, returned object not necessarily list/dataframe
- `$` = can extract elements from list/dataframe that have names associated with it, not necessarily same class

Vectors

- `x[1:10]` = first 10 elements of vector `x`
- `x[is.na(x)]` = returns all NA elements
- `x[!is.na(x)]` = returns all non NA elements
 - `x > 0` = would return logical vector comparing all elements to 0 (`TRUE/FALSE` for all values except for NA and NA for NA elements (NA a placeholder))
- `x[x>"a"]` = selects all elements bigger than a (lexicographical order in place)
- `x[logicalIndex]` = select all elements where logical index = `TRUE`
- `x[-c(2, 10)]` = returns everything **but** the second and tenth element
- `vect <- c(a = 1, b = 2, c = 3)` = names values of a vector with corresponding names
- `names(vect)` = returns element names for object
 - `names(vet) <- c("a", "b", "c")` = assign/change names of vector
- `identical(obj1, obj2)` = returns `TRUE` if two objects are exactly equal
- `all.equal(obj1, obj2)` = returns `TRUE` if two objects are near equal

Lists

- `x <- list(foo = 1:4, bar = 0.6)`
- `x[1]` or `x["foo"]` = returns the list object `foo`
- `x[[2]]` or `x[["bar"]]` or `x$bar` = returns the content of the second element from the list (in this case vector without name attribute)
 - **Note:** `$` can't extract multiple elements
- `x[c(1, 3)]` = extract multiple elements of list
- `x[[name]]` = extract using variable, where as `$` must match name of element
- `x[[c(1, 3)]]` or `x[[1]][[3]]` = extracted nested elements of list third element of the first object extracted from the list

Matrices

- `x[1, 2]` = extract the (row, column) element
 - `x[,2]` or `x[1,]` = extract the entire column/row
- `x[, 11:17]` = subset the `x data.frame` with all rows, but only 11 to 17 columns
- when an element from the matrix is retrieved, a vector is returned
 - behavior can be turned off (force return a matrix) by adding `drop = FALSE`
 - * `x[1, 2, drop = F]`

Partial Matching

- works with `[[]]` and `$`
- `$` automatically partial matches the name (`x$a`)
- `[[]]` can partial match by adding `exact = FALSE`
 - `x[["a", exact = false]]`

Logic

- `<`, `>=` = less than, greater or equal to
- `==` = exact equality
- `!=` = inequality
- `A | B` = union
- `A & B` = intersection
- `!` = negation
- `&` or `|` evaluates every instance/element in vector
- `&&` or `||` evaluate only first element
 - ***Note:** All AND operators are evaluated before OR operators*
- `isTRUE(condition)` = returns TRUE or FALSE of the condition
- `xor(arg1, arg2)` = exclusive OR, one argument must equal TRUE one must equal FALSE
- `which(condition)` = find the indices of elements that satisfy the condition (TRUE)
- `any(condition)` = TRUE if one or more of the elements in logical vector is TRUE
- `all(condition)` = TRUE if all of the elements in logical vector is TRUE

Understanding Data

- use `class()`, `dim()`, `nrow()`, `ncol()`, `names()` to understand dataset
 - `object.size(data.frame)` = returns how much space the dataset is occupying in memory
- `head(data.frame, 10)`, `tail(data.frame, 10)` = returns first/last 10 rows of data; default = 6
- `summary()` = provides different output for each variable, depending on class,
 - for numerical variables, displays min max, mean median, etc.
 - for categorical (factor) variables, displays number of times each value occurs
- `table(data.frame$variable)` = table of all values of the variable, and how many observations there are for each
 - ***Note:** mean for variables that only have values 1 and 0 = proportion of success*
- `str(data.frame)` = structure of data, provides data class, num of observations vs variables, and name of class of each variable and preview of its contents
 - compactly display the internal structure of an R object
 - “What’s in this object”
 - well-suited to compactly display the contents of lists
- `view(data.frame)` = opens and view the content of the data frame

Split-Apply-Combine Functions

- loop functions = convenient ways of implementing the Split-Apply-Combine strategy for data analysis

split()

- takes a vector/objects and splits it into groups by a factor or list of factors
- `split(x, f, drop = FALSE)`
 - `x` = vector/list/data frame
 - `f` = factor/list of factors
 - `drop` = whether empty factor levels should be dropped
- `interactions(gl(2, 5), gl(5, 2)) = 1.1, 1.2, ... 2.5`
 - `gl(n, m)` = group level function
 - * `n` = number of levels
 - * `m` = number of repetitions
 - `split` function can do this by passing in `list(f1, f2)` in argument
 - * `split(data, list(gl(2, 5), gl(5, 2)))` = splits the data into 1.1, 1.2, ... 2.5 levels

apply()

- evaluate a function (often anonymous) over the margins of an array
- often used to apply a function to the row/columns of a matrix
- can be used to average array of matrices (general arrays)
- `apply(x, margin = 2, FUN, ...)`
 - `x` = array
 - `MARGIN` = 2 (column), 1 (row)
 - `FUN` = function
 - ... = other arguments that need to be passed to other functions
- *examples*
 - `apply(x, 1, sum)` or `apply(x, 1, mean)` = find row sums/means
 - `apply(x, 2, sum)` or `apply(x, 2, mean)` = find column sums/means
 - `apply(x, 1, quantile, probs = c(0.25, 0.75))` = find 25% 75% percentile of each row
 - `a <- array(rnorm(2*2*10), c(2, 2, 10))` = create 10 2x2 matrix
 - `apply(a, c(1, 2), mean)` = returns the means of 10

lapply()

- loops over a **list** and evaluate a function on each element and always returns a **list**
 - ***Note:** since input must be a list, it is possible that conversion may be needed*
- `lapply(x, FUN, ...)` = takes list/vector as input, applies a function to each element of the list, returns a list of the same length
 - `x` = list (if not list, will be coerced into list through “as.list”, if not possible —> error)
 - * **data.frame** are treated as collections of lists and can be used here
 - `FUN` = function (without parentheses)
 - * anonymous functions are acceptable here as well - (i.e `function(x) x[,1]`)

- ... = other/additional arguments to be passed for FUN (i.e. `min`, `max` for `runif()`)

- *example*

- `lapply(data.frame, class)` = the `data.frame` is a list of vectors, the `class` value for each vector is returned in a list (name of function, `class`, is without parentheses)
- `lapply(values, function(elem), elem[2])` = example of an anonymous function

`sapply()`

- performs same function as `lapply()` except it simplifies the result
 - if result is of length 1 in every element, `sapply` returns vector
 - if result is vectors of the same length (>1) for each element, `sapply` returns matrix
 - if not possible to simplify, `sapply` returns a `list` (same as `lapply()`)

`vapply()`

- safer version of `sapply` in that it allows to you specify the format for the result
 - `vapply(flags, class, character(1))` = returns the `class` of values in the `flags` variable in the form of character of length 1 (1 value)

`tapply()`

- split data into groups, and apply the function to data within each subgroup
- `tapply(data, INDEX, FUN, ..., simplify = FALSE)` = apply a function over subsets of a vector
 - `data` = vector
 - `INDEX` = factor/list of factors
 - `FUN` = function
 - ... = arguments to be passed to function
 - `simplify` = whether to simplify the result
- *example*
 - `x <- c(rnorm(10), runif(10), rnorm(10, 1))`
 - `f <- gl(3, 10); tapply(x, f, mean)` = returns the mean of each group (f level) of x data

`mapply()`

- multivariate apply, applies a function in parallel over a set of arguments
- `mapply(FUN, ..., MoreArgs = NULL, SIMPLIFY = TRUE)`
 - `FUN` = function
 - ... = arguments to apply over
 - `MoreArgs` = list of other arguments to `FUN`
 - `SIMPLIFY` = whether the result should be simplified
- *example*

```
mapply(rep, 1:4, 4:1)
```

```
## [[1]]
## [1] 1 1 1 1
##
## [[2]]
## [1] 2 2 2
##
## [[3]]
## [1] 3 3
##
## [[4]]
## [1] 4
```

`aggregate()`

- `aggregate` computes summary statistics of data subsets (similar to multiple `tapply` at the same time)
- `aggregate(list(name = dataToCompute), list(name = factorVar1, name = factorVar2), function, na.rm = TRUE)`
 - `dataToCompute` = this is what the function will be applied on
 - `factorVar1`, `factorVar2` = factor variables to split the data by
 - **Note:** *order matters here in terms of how to break down the data*
 - `function` = what is applied to the subsets of data, can be sum/mean/median/etc
 - `na.rm = TRUE` → removes NA values

Simulation

- `sample(values, n, replace = FALSE)` = generate random samples
 - `values` = values to sample from
 - `n` = number of values generated
 - `replace` = with or without replacement
 - `sample(1:6, 4, replace = TRUE, prob=c(.2, .2...))` = choose four values from the range specified with replacing (same numbers can show up twice), with probabilities specified
 - `sample(vector)` = can be used to permute/rearrange elements of a vector
 - `sample(c(y, z), 100)` = select 100 random elements from combination of values y and z
 - `sample(10)` = select positive integer sample of size 10 without repeat
- Each probability distribution functions usually have 4 functions associated with them:
 - `r***` function (for “random”) → random number generation (ex. `rnorm`)
 - `d***` function (for “density”) → calculate density (ex. `dunif`)
 - `p***` function (for “probability”) → cumulative distribution (ex. `ppois`)
 - `q***` function (for “quantile”) → quantile function (ex. `qbinom`)
- If Φ is the cumulative distribution function for a standard Normal distribution, then `pnorm(q) = $\Phi(q)$` and `qnorm(p) = $\Phi^{-1}(q)$` .
- `set.seed()` = sets seed for random number generator to ensure that the same data/analysis can be reproduced

Simulation Examples

- `rbinom(1, size = 100, prob = 0.7)` = returns a binomial random variable that represents the number of successes in a give number of independent trials
 - `1` = corresponds number of observations
 - `size = 100` = corresponds with the number of independent trials that culminate to each resultant observation
 - `prob = 0.7` = probability of success
- `rnorm(n, mean = m, sd = s)` = generate n random samples from the standard normal distribution (mean = 0, std deviation = 1 by default)
 - `rnorm(1000)` = 1000 draws from the standard normal distribution
 - `n` = number of observation generated
 - `mean = m` = specified mean of distribution
 - `sd = s` = specified standard deviation of distribution
- `dnorm(x, mean = 0, sd = 1, log = FALSE)`
 - `log` = evaluate on log scale
- `pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)`
 - `lower.tail` = left side, `FALSE` = right
- `qnorm(p, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)`
 - `lower.tail` = left side, `FALSE` = right
- `rpois(n, lambda)` = generate random samples from the poisson distribution
 - `n` = number of observations generated
 - `lambda` = λ parameter for the poisson distribution or rate

- `rpois(n, r)` = generating Poisson Data
 - `n` = number of values
 - `r` = rate
- `ppois(n, r)` = cumulative distribution
 - `ppois(2, 2) = Pr(x <= 2)`
- `replicate(n, rpois())` = repeat operation n times

Generate Numbers for a Linear Model

- Linear model

$$y = \beta_0 + \beta_1 x + \epsilon \text{ where } \epsilon \sim N(0, 2^2), x \sim N(0, 1^2), \beta_0 = 0.5, \beta_1 = 2$$

```
set.seed(20)
x <- rnorm(100)           # normal
x <- rbinom(100, 1, 0.5)  # binomial
e <- rnorm(100, 0, 2)
y <- 0.5 + 2* x + e
```

- Poisson model

$$Y \text{ Poisson}(\mu) \log(\mu) = \beta_0 + \beta_1 x \text{ where } \beta_0 = 0.5, \beta_1 = 2$$

```
x <- rnorm(100)
log.mu <- 0.5 + 0.3* x
y <- rpois(100, exp(log.mu))
```

Dates and Times

- `Date` = date class, stored as number of days since 1970-01-01
- `POSIXct` = time class, stored as number of seconds since 1970-01-01
- `POSIXlt` = time class, stored as list of sec min hours
- `Sys.Date()` = today's date
- `unclass(obj)` = returns what obj looks like internally
- `Sys.time()` = current time in `POSIXct` class
- `t2 <- as.POSIXlt(Sys.time())` = time in `POSIXlt` class
 - `t2$min` = return min of time (only works for `POSIXlt` class)
- `weekdays(date)`, `months(date)`, `quarters(date)` = returns weekdays, months, and quarters of time/date inputed
- `strptime(string, "%B %d, %Y %H:%M")` = convert string into time format using the format specified
- `difftime(time1, time2, units = 'days')` = difference in times by the specified unit

Base Graphics

- `data(set)` = load data
- `plot(data)` = R plots the data as best as it can
 - `x` = variable, x axis
 - `y` = variable
 - `xlab`, `ylab` = corresponding labels
 - `main`, `sub` = title, subtitle
 - `col` = 2 or `col` = "red" = color
 - `pch` = 2 = different symbols for points
 - `xlim,ylim(v1, v2)` = restrict range of plot
- `boxplot(x ~ y, data = d)` = creates boxplot for x vs y variables using the data.frame provided
- `hist(x, breaks)` = plots histogram of the data
 - `break` = 100 = split data into 100 bins

Reading Tabular Data

- `read.table()`, `read.csv()` = most common, read text files (rows, col) return data frame
- `readLines()` = read lines of text, returns character vector
- `source(file)` = read R code
- `dget()` = read R code files (R objects that have been reparsed)
- `load()`, `unserialize()` = read binary objects
- writing data
 - `write.table()`, `writelnLines()`, `dump()`, `put()`, `save()`, `serialize()`
- `read.table()` arguments:
 - `file` = name of file/connection
 - `header` = indicator if file contains header
 - `sep` = string indicating how columns are separated
 - `colClasses` = character vector indicating what each column is in terms of class
 - `nrows` = number of rows in dataset
 - `comment.char` = char indicating beginning of comment
 - `skip` = number of lines to skip in the beginning
 - `stringsAsFactors` = defaults to TRUE, should characters be coded as Factor
- `read.table` can be used without any other argument to create data.frame
 - telling R what type of variables are in each column is helpful for larger datasets (efficiency)
 - `read.csv()` = `read.table` except default sep is comma (`read.table` default is `sep = " "` and `header = TRUE`)

Larger Tables

- *Note: help page for read.table important*
- need to know how much RAM is required → calculating memory requirements
 - `numRow` x `numCol` x 8 bytes/numeric value = size required in bites
 - double the above results and convert into GB = amount of memory recommended
- set `comment.char = ""` to save time if there are no comments in the file
- specifying `colClasses` can make reading data much faster
- `nrow = n` = number of rows to read in (can help with memory usage)
 - `initial <- read.table("file", rows = 100)` = read first 100 lines
 - `classes <- sapply(initial, class)` = determine what classes the columns are
 - `tabAll <- read.table("file", colClasses = classes)` = load in the entire file with determined classes

Textual Data Formats

- `dump` and `dput` preserve metadata
- text formats are editable, not space efficient, and work better with version control system (they can only track changes in text files)
- `dput(obj, file = "file.R")` = creates R code to store all data and meta data in “file.R” (ex. data, class, names, row.names)
- `dget("file.R")` = loads the file/R code and reconstructs the R object
- `dput` can only be used on one object, where as `dump` can be used on multiple objects
- `dump(c("obj1", "obj2"), file= "file2.R")` = stores two objects
- `source("file2.R")` = loads the objects

Interfaces to the Outside World

- `url()` = function can read from webpages
- `file()` = read uncompressed files
- `gzfile()`, `bzfile()` = read compressed files (gzip, bzip2)
- `file(description = "", open = "")` = file syntax, creates connection
 - `description` = description of file
 - `open` = r - readonly, w - writing, a - appending, rb/wb/ab - reading/writing/appending binary
 - `close()` = closes connection
 - `readLines()` = can be used to read lines after connection has been established
- `download.file(fileURL, destfile = "fileName", method = "curl")`
 - `fileURL` = url of the file that needs to be downloaded
 - `destfile = "fileName"` = specifies where the file is to be saved
 - * `dir/fileName` = directories can be referenced here
 - `method = "curl"` = necessary for downloading files from “<https://>” links on Macs
 - * `method = "auto"` = should work on all other machines

Control Structures

- Common structures are
 - `if, else` = testing a condition
 - `for` = execute a loop a fixed number of times
 - `while` = execute a loop while a condition is true
 - `repeat` = execute an infinite loop
 - `break` = break the execution of a loop
 - `next` = skip an iteration of a loop
 - `return` = exit a function
- ***Note:** Control structures are primarily useful for writing programs; for command-line interactive work, the **apply** functions are more useful*

if - else

```
# basic structure
if(<condition>) {
  ## do something
} else {
  ## do something else
}

# if tree
if(<condition1>) {
  ## do something
} else if(<condition2>) {
  ## do something different
} else {
  ## do something different
}
```

- `y <- if(x>3){10} else {0}` = slightly different implementation than normal, focus on assigning value

for

```
# basic structure
for(i in 1:10) {
  # print(i)
}

# nested for loops
x <- matrix(1:6, 2, 3)
for(i in seq_len(nrow(x))) {
  for(j in seq_len(ncol(x))) {
    # print(x[i, j])
  }
}
```

- `for(letter in x)` = loop through letter in character vector

- `seq_along(vector)` = create a number sequence from 1 to length of the vector
- `seq_len(length)` = create a number sequence that starts at 1 and ends at length specified

while

```
count <- 0
while(count < 10) {
  # print(count)
  count <- count + 1
}
```

- conditions can be combined with logical operators

repeat and break

- `repeat` initiates an infinite loop
- not commonly used in statistical applications but they do have their uses
- The only way to exit a `repeat` loop is to call `break`

```
x0 <- 1
tol <- 1e-8
repeat {
  x1 <- computeEstimate()
  if(abs(x1 - x0) < tol) {
    break
  } else {
    x0 <- x1 # requires algorithm to converge
  }
}
```

- **Note:** *The above loop is a bit dangerous because there's no guarantee it will stop*
 - Better to set a hard limit on the number of iterations (e.g. using a `for` loop) and then report whether convergence was achieved or not.

next and return

- `next` = (no parentheses) skips an element, to continue to the next iteration
- `return` = signals that a function should exit and return a given value

```
for(i in 1:100) {
  if(i <= 20) {
    ## Skip the first 20 iterations
    next
  }
  ## Do something here
}
```


Functions

- `name <- function(arg1, arg2, ...){ }`
 - inputs can be specified with default values by `arg1 = 10`
 - it is possible to define an argument to `NULL`
 - returns **last expression** of function
 - many functions have `na.rm`, can be set to `TRUE` to remove NA values from calculation


- structure

```
f <- function(<arguments>) {  
  ## Do something interesting  
}
```



- function **are first class object** and can be **treated like other objects** (pass into other functions) 


-  – **functions can be nested**, so that you can define a function inside of another function

- function have named arguments (i.e. `x = mydata`) which can be used to specify **default values**

- `sd(x = mydata)` (matching by name) 






- formal arguments = arguments included in the functional definition

- `formals()` = returns all formal arguments 
 - not all functional call specifies all arguments, some can be missing and may have default values
 - `args()` = return all arguments you can specify
 - multiple arguments inputted in random orders (R performs positional matching) → not recommended 
 - argument matching order: exact → partial → positional
 - * *partial* = instead of typing `data = x`, use `d = x`

- **Lazy Evaluation** 

- R will evaluate as needed, so everything executes until an error occurs
 - * `f <- function (a, b) {a^2}`
 - * if b is not used in the function, calling `f(5)` will not produce an error

- ... argument

- used to extend other functions by representing the rest of the arguments 
 - generic functions use ... to pass extra arguments (i.e. `mean = 1, sd = 2`) 
 - necessary when the number of arguments passed can not be known in advance
 - * functions that use ... = `paste()`, `cat()`  
 - **Note:** arguments coming after ... **must be explicitly matched and cannot be partially matched** 

Scoping

- scoping rules determine how a value is associated with a free variable in a function
- **free variables** = variables not explicitly defined in the function (not arguments, or local variables - variable defined in the function)
- R uses **lexical/static scoping**
 - common alternative = **dynamic scoping**
 - **lexical scoping** = values of free vars are searched in the environment in which the function is defined
 - * environment = collection of symbol/value pairs ($x = 3.14$)
 - each package has its own environment
 - only environment **without** parent environment is the *empty environment*
 - **closure/function closure** = function + associated environment
- search order for free variable
 1. environment where the function is defined
 2. parent environment
 3. ... (repeat if multiple parent environments)
 4. top level environment: global environment (workspace) or namespace package
 5. empty environment → produce error
- when a function/variable is called, R searches through the following list to match the first result
 1. `.GlobalEnv`
 2. `package:stats`
 3. `package:graphics`
 4. `package:grDevices`
 5. `package:utils`
 6. `package:datasets`
 7. `package:methods`
 8. `Autoloads`
 9. `package:base`
- **order matters**
 - `.GlobalEnv` = everything defined in the current workspace
 - any package that gets loaded with `library()` gets put in position 2 of the above search list
 - namespaces are separate for functions and non-functions
 - * possible for object `c` and function `c` to coexist

Scoping Example

```
make.power <- function(n) {  
  pow <- function(x) {  
    x^n  
  }  
  pow  
}  
cube <- make.power(3) # defines a function with only n defined (x^3)  
square <- make.power(2) # defines a function with only n defined (x^2)  
cube(3) # defines x = 3
```



```
## [1] 27
```

```
square(3)           # defines x = 3
```

```
## [1] 9
```

```
# returns the free variables in the function  
ls(environment(cube))
```

```
## [1] "n"    "pow"
```

```
# retrieves the value of n in the cube function  
get("n", environment(cube))
```

```
## [1] 3
```

Lexical vs Dynamic Scoping Example

```
y <- 10  
f <- function(x) {  
  y <- 2  
  y^2 + g(x)  
}  
g <- function(x) {  
  x*y  
}
```

- **Lexical Scoping**

1. $f(3) \rightarrow$ calls $g(x)$
2. y isn't defined locally in $g(x) \rightarrow$ searches in parent environment (working environment/global workspace)
3. finds $y \rightarrow y = 10$

- **Dynamic Scoping**

1. $f(3) \rightarrow$ calls $g(x)$
2. y isn't defined locally in $g(x) \rightarrow$ searches in calling environment (f function)
3. find $y \rightarrow y <- 2$
 - **parent frame** = refers to calling environment in R, environment from which the function was called

- **Note:** when the defining environment and calling environment is the same, lexical and dynamic scoping produces the same result

- **Consequences of Lexical Scoping**

- all objects must be carried in memory
- all functions carry pointer to their defining environment (memory address)

Optimization

- optimization routines in R (`optim`, `nlm`, `optimize`) require you to pass a function whose argument is a vector of parameters
 - *Note: these functions **minimize**, so use the negative constructs to maximize a normal likelihood*
- **constructor functions** = functions to be fed into the optimization routines
- *example*

```
# write constructor function
make.NegLogLik <- function(data, fixed=c(FALSE,FALSE)) {
  params <- fixed
  function(p) {
    params[!fixed] <- p
    mu <- params[1]
    sigma <- params[2]
    a <- -0.5*length(data)*log(2*pi*sigma^2)
    b <- -0.5*sum((data-mu)^2) / (sigma^2)
    -(a + b)
  }
}
# initialize seed and print function
set.seed(1); normals <- rnorm(100, 1, 2)
nLL <- make.NegLogLik(normals); nLL
```

```
## function(p) {
##     params[!fixed] <- p
##     mu <- params[1]
##     sigma <- params[2]
##     a <- -0.5*length(data)*log(2*pi*sigma^2)
##     b <- -0.5*sum((data-mu)^2) / (sigma^2)
##     -(a + b)
## }
## <environment: 0x7fda426462a8>
```

```
# Estimating Parameters
optim(c(mu = 0, sigma = 1), nLL)$par
```

```
##      mu      sigma
## 1.218239 1.787343
```

```
# Fixing sigma = 2
nLL <- make.NegLogLik(normals, c(FALSE, 2))
optimize(nLL, c(-1, 3))$minimum
```

```
## [1] 1.217775
```

```
# Fixing mu = 1
nLL <- make.NegLogLik(normals, c(1, FALSE))
optimize(nLL, c(1e-6, 10))$minimum
```

```
## [1] 1.800596
```

Debugging

- **message**: generic notification/diagnostic message, execution continues
 - `message()` = generate message
- **warning**: something's wrong but not fatal, execution continues
 - `warning()` = generate warning
- **error**: fatal problem occurred, execution stops
 - `stop()` = generate error
- **condition**: generic concept for indicating something unexpected can occur
- **invisible()** = suppresses auto printing
- **Note**: *random number generator must be controlled to reproduce problems (`set.seed` to pinpoint problem)*
- **traceback**: prints out function call stack after error occurs
 - must be called right after error
- **debug**: flags function for debug mode, allows to step through function one line at a time
 - `debug(function)` = enter debug mode
- **browser**: suspends the execution of function wherever its placed
 - embedded in code and when the code is run, the browser comes up
- **trace**: allows inserting debugging code into a function at specific places
- **recover**: error handler, freezes at point of error
 - `options(error = recover)` = instead of console, brings up menu (similar to **browser**)

R Profiler

- optimizing code cannot be done without performance analysis and profiling

```
# system.time example
system.time({
  n <- 1000
  r <- numeric(n)
  for (i in 1:n) {
    x <- rnorm(n)
    r[i] <- mean(x)
  }
})
```

```
##      user  system elapsed
## 0.148   0.004   0.173
```

- `system.time(expression)`
 - takes R expression, returns amount of time needed to execute (assuming you know where)
 - computes time (in sec) → gives time until error if error occurs
 - can wrap multiple lines of code with `{}`
 - returns object of class `proc_time`
 - * **user time** = time computer experience

- * **elapsed time** = time user experience
- * usually close for standard computation
 - *elapse* > *user* = CPU wait around other processes in the background (read webpage)
 - *elapsed* < *user* = multiple processor/core (use multi-threaded libraries)
- **Note:** *R doesn't multi-thread (performing multiple calculations at the same time) with basic package*
 - * Basic Linear Algebra Standard [BLAS] libraries do, prediction, regression routines, matrix
 - * i.e. `vecLib`/Accelerate, `ATLAS`, `ACML`, `MKL`
- `Rprof()` = useful for complex code only
 - keeps track of functional call stack at regular intervals and tabulates how much time is spent in each function
 - default sampling interval = 0.02 second
 - calling `Rprof()` generates `Rprof.out` file by default
 - * `Rprof("output.out")` = specify the output file
 - **Note:** *should NOT be used with `system.time()`*
- `summaryRprof()` = summarizes `Rprof()` output, 2 methods for normalizing data
 - loads the `Rprof.out` file by default, can specify output file `summaryRprof("output.out")`
 - `by.total` = divide time spent in each function by total run time
 - `by.self` = first subtracts out time spent in functions above in call stack, and calculates ratio to total
 - `$sample.interval` = 0.02 → interval
 - `$sampling.time` = 7.41 → seconds, elapsed time
 - * **Note:** *generally user spends all time at top level function (i.e. `lm()`), but the function simply calls helper functions to do work so it is not useful to know about the top level function times*
 - **Note:** *`by.self` = more useful as it focuses on each individual call/function*
 - **Note:** *`R` must be compiled with profiles support (generally the case)*
- good to break code into functions so profilers can give useful information about where time is spent
- C/FORTRAN code is not profiled

Miscellaneous

- `unlist(rss)` = converts a list object into data frame/vector
- `ls("package:elasticnet")` = list methods in package