y <- c (8.3, 8.6, 10.7, 10.8, 11, 11, 11.1, 11.2, 11.3, 11.4)

> #3.3 Extraction and missing values section

> y[1]

[1] 8.3

> y[1:3]

[1] 8.3 8.6 10.7

> #extracting values greater than average

> y > mean(y)

[1] FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE

[10] TRUE

> y[y>mean(y)]

[1] 10.7 10.8 11.0 11.0 11.1 11.2 11.3 11.4

> #testing which elements are missing

> a <- c(5, 3, 6, NA)

> a

[1] 5 3 6 NA

> is.na(a)

[1] FALSE FALSE FALSE TRUE

> !is.na(a)

[1] TRUE TRUE TRUE FALSE

#testing which elements are missing

> a <- c(5, 3, 6, NA)

> a

[1] 5 3 6 NA

> is.na(a)

[1] FALSE FALSE FALSE TRUE

> !is.na(a)

[1] TRUE TRUE TRUE FALSE

> a[!is.na(a)]

[1] 5 3 6

> attr(, "na.action")

Error in attr(, "na.action") : argument 1 is empty

> attr(,"na.action")

Error in attr(, "na.action") : argument 1 is empty

> attr(,"class")

Error in attr(, "class") : argument 1 is empty

> mean(a)

[1] NA

> mean(a, na.rm=TRUE)

[1] 4.666667

> d <-na.exclude(a)

> mean(d)

[1] 4.666667

|  |
| --- |
| #3.4 Matrices  > matrix(letters[1:4], ncol = 2)  [,1] [,2]  [1,] "a" "c"  [2,] "b" "d"  > M <- matrix(1:2, nrow =2)  > M  [,1]  [1,] 1  [2,] 2  > M <- matrix(1:4, nrow = 2)  > M  [,1] [,2]  [1,] 1 3  [2,] 2 4  > #filling out matrix by rows  > M2 <- matrix(1:4, nrow = 2, byrow = TRUE)  > M2  [,1] [,2]  [1,] 1 2  [2,] 3 4  > #making a matrix with 1s on the diagonal  > I <- diag(1, nrow = 2)  > I  [,1] [,2]  [1,] 1 0  [2,] 0 1  > #is the number of rows always equal number of columns if using nrow or ncol function?  > #solving for inverse of matrix  > Minv <- solve (M)  > M % % Minv  Error: could not find function "% %"  > M %\*% Minv  [,1] [,2]  [1,] 1 0  [2,] 0 1 |
|  |
| |  | | --- | | > #Extraction in matrices  > M[1, 2]  [1] 3  > M[1, 1:2]  [1] 1 3  > M[, 2]  [1] 3 4  > M[, ]  [,1] [,2]  [1,] 1 3  [2,] 2 4 | |
| # 3.5 Data frames  > #making columns ofa data frame  > dat <- data.frame(species = c("S.altissima", "S.rugosa", "E.graminifolia", "A.pilosus"), treatment = factor(c("control", "water", "control", "water")), height = c(1.1, 0.8, 0.9, 1), width =c (1, 1.7, 0.6, 0.2))  > dat  species treatment height width  1 S.altissima control 1.1 1.0  2 S.rugosa water 0.8 1.7  3 E.graminifolia control 0.9 0.6  4 A.pilosus water 1.0 0.2  > #extracting data from data frames with dat [column, row]  > dat[2, ]  species treatment height width  2 S.rugosa water 0.8 1.7  > dat[3, 4]  [1] 0.6  > #testing elements in data frames by using extracted data, use same > < or == tests  > dat[, 2] == "Water"  [1] FALSE FALSE FALSE FALSE  > dat[dat[, 2 == "water",]]  Error in `[.default`(dat, dat[, 2 == "water", ]) :  invalid subscript type 'list'  > dat[dat[, 2] == "water", ]  species treatment height width  2 S.rugosa water 0.8 1.7  4 A.pilosus water 1.0 0.2  > #extracting data of the first two rows in the treatment of water  > #can also use a subset function for the same above  > subset(dat, treatment == "Water")  [1] species treatment height width  <0 rows> (or 0-length row.names)  > subset(dat, treatment == "water")  species treatment height width  2 S.rugosa water 0.8 1.7  4 A.pilosus water 1.0 0.2 |
|  |
| |  | | --- | | > | |