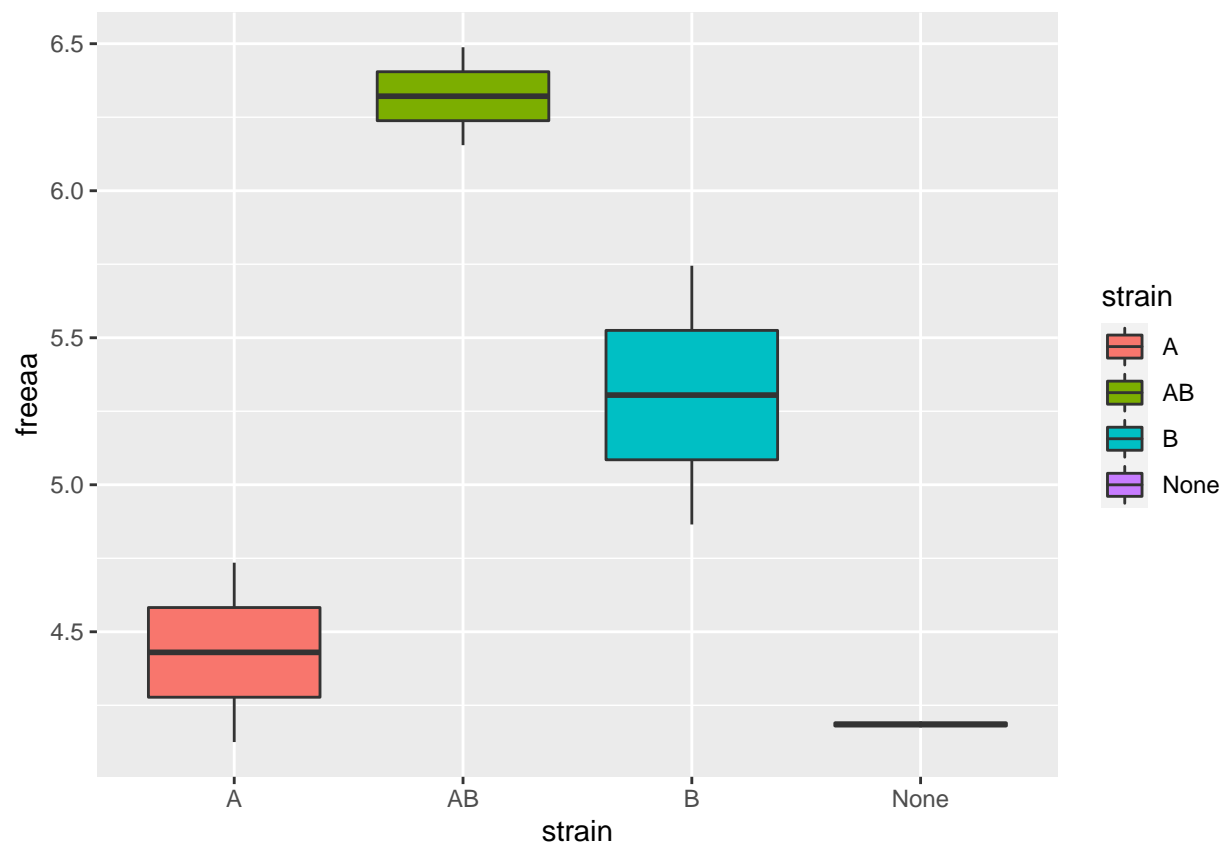


# Multiple Comparisons Tests in R

AGH Practicals

## Cheese

### Boxplot



### Analysis of Variance

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## strain      3  5.628  1.8760   11.93 0.0183 *
## Residuals   4  0.629  0.1572
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Pairwise Comparisons

```
##
##   Posthoc multiple comparisons of means: Scheffe Test
##     95% family-wise confidence level
##
## $strain
##      diff      lwr.ci      upr.ci    pval
## AB-A      1.8915  0.1282748  3.6547252 0.0398 *
## B-A        0.8750 -0.8882252  2.6382252 0.3180
## None-A    -0.2450 -2.0082252  1.5182252 0.9391
## B-AB      -1.0165 -2.7797252  0.7467252 0.2317
## None-AB   -2.1365 -3.8997252 -0.3732748 0.0264 *
## None-B    -1.1200 -2.8832252  0.6432252 0.1841
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
##   Posthoc multiple comparisons of means : Bonferroni
##     95% family-wise confidence level
##
## $strain
##      diff      lwr.ci      upr.ci    pval
## AB-A      1.8915 -0.03199443  3.8149944 0.0530 .
## B-A        0.8750 -1.04849443  2.7984944 0.5518
## None-A    -0.2450 -2.16849443  1.6784944 1.0000
## B-AB      -1.0165 -2.93999443  0.9069944 0.3744
## None-AB   -2.1365 -4.05999443 -0.2130056 0.0344 *
## None-B    -1.1200 -3.04349443  0.8034944 0.2856
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
##   Posthoc multiple comparisons of means : Fisher LSD
##     95% family-wise confidence level
##
## $strain
##      diff      lwr.ci      upr.ci    pval
## AB-A      1.8915  0.7905997  2.99240031 0.0088 **
## B-A        0.8750 -0.2259003  1.97590031 0.0920 .
## None-A    -0.2450 -1.3459003  0.85590031 0.5701
## B-AB      -1.0165 -2.1174003  0.08440031 0.0624 .
## None-AB   -2.1365 -3.2374003 -1.03559969 0.0057 **
## None-B    -1.1200 -2.2209003 -0.01909969 0.0476 *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

##
##   Posthoc multiple comparisons of means : Tukey HSD
##     95% family-wise confidence level
##
## $strain
##      diff      lwr.ci      upr.ci    pval
## AB-A      1.8915  0.2773476  3.5056524 0.0296 *
## B-A       0.8750 -0.7391524  2.4891524 0.2637
## None-A    -0.2450 -1.8591524  1.3691524 0.9212
## B-AB     -1.0165 -2.6306524  0.5976524 0.1871
## None-AB   -2.1365 -3.7506524 -0.5223476 0.0194 *
## None-B   -1.1200 -2.7341524  0.4941524 0.1463
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
##   Posthoc multiple comparisons of means : Duncan's new multiple range test
##     95% family-wise confidence level
##
## $strain
##      diff      lwr.ci      upr.ci    pval
## AB-A      1.8915  0.7664716  3.016528436 0.0097 **
## B-A       0.8750 -0.2259051  1.975905084 0.0920 .
## None-A    -0.2450 -1.3459051  0.855905084 0.5701
## B-AB     -1.0165 -2.1174051  0.084405084 0.0624 .
## None-AB   -2.1365 -3.2672906 -1.005709447 0.0065 **
## None-B   -1.1200 -2.2450284  0.005028436 0.0506 .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
##   Posthoc multiple comparisons of means : Newman-Keuls
##     95% family-wise confidence level
##
## $strain
##      diff      lwr.ci      upr.ci    pval
## AB-A      1.8915  0.4783273  3.30467267 0.0192 *
## B-A       0.8750 -0.2259051  1.97590508 0.0920 .
## None-A    -0.2450 -1.3459051  0.85590508 0.5701
## B-AB     -1.0165 -2.1174051  0.08440508 0.0624 .
## None-AB   -2.1365 -3.7506524 -0.52234758 0.0194 *
## None-B   -1.1200 -2.5331727  0.29317267 0.0987 .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
##
##   Dunnett's test for comparing several treatments with a control :
##     95% family-wise confidence level
##
## $None
##      diff      lwr.ci   upr.ci   pval
## A-None  0.2450 -1.1966114 1.686611 0.8693
## AB-None 2.1365  0.6948886 3.578111 0.0129 *
## B-None  1.1200 -0.3216114 2.561611 0.1038
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## $statistics
##      MSerror Df      Mean      CV
##  0.1572236  4 5.060375 7.835671
##
## $parameters
##   test name.t ntr alpha
##  REGW strain   4  0.05
##
## $regw
##      Table CriticalRange
## 2 4.923441      1.380425
## 3 5.040241      1.413173
## 4 5.757058      1.614152
##
## $means
##      freeaa      std r   Min   Max    Q25    Q50    Q75
## A      4.4300 0.43133514 2 4.125 4.735 4.27750 4.4300 4.58250
## AB     6.3215 0.23546656 2 6.155 6.488 6.23825 6.3215 6.40475
## B      5.3050 0.62225397 2 4.865 5.745 5.08500 5.3050 5.52500
## None  4.1850 0.01414214 2 4.175 4.195 4.18000 4.1850 4.19000
##
## $comparison
## NULL
##
## $groups
##      freeaa groups
## AB      6.3215    a
## B       5.3050   ab
## A       4.4300    b
## None  4.1850    b
##
## attr(,"class")
## [1] "group"
```

```
DunnettTest.formula <- function (formula, data, subset, na.action, ...) {
  if (missing(formula) || (length(formula) != 3L) || (length(attr(terms(formula)[-2L])),
```

```

    stop("'formula' missing or incorrect")
    m <- match.call(expand.dots = FALSE)
    if (is.matrix(eval(m$data, parent.frame())))
      m$data <- as.data.frame(data)
    m[[1L]] <- quote(stats::model.frame)
    m$... <- NULL
    mf <- eval(m, parent.frame())
    if (length(mf) > 2L)
      stop("'formula' should be of the form response ~ group")
    DNAME <- paste(names(mf), collapse = " by ")
    names(mf) <- NULL
    response <- attr(attr(mf, "terms"), "response")
    y <- DoCall("DunnettTest", c(as.list(mf), list(...)))
    y$data.name <- DNAME
  }
}

DunnettTest.default <- function (x, g, control = NULL
                                , conf.level = 0.95, ...) {

  if (is.list(x)) {
    if (length(x) < 2L)
      stop("'x' must be a list with at least 2 elements")
    DNAME <- deparse(substitute(x))
    x <- lapply(x, function(u) u <- u[complete.cases(u)])
    k <- length(x)
    l <- sapply(x, "length")
    if (any(l == 0))
      stop("all groups must contain data")
    g <- factor(rep(1:k, l))
    x <- unlist(x)
  } else {
    if (length(x) != length(g))
      stop("'x' and 'g' must have the same length")
    DNAME <- paste(deparse(substitute(x)), "and", deparse(substitute(g)))
    OK <- complete.cases(x, g)
    x <- x[OK]
    g <- g[OK]
    if (!all(is.finite(g)))
      stop("all group levels must be finite")
    g <- factor(g)
    k <- nlevels(g)
    if (k < 2)
      stop("all observations are in the same group")
  }
  N <- length(x)
  if (N < 2)
    stop("not enough observations")

  # just organisational stuff so far, got a fine x and g now

  if (is.null(control)) control <- levels(g)[1]

```

```

ctrls <- control
out <- list()

for(ii in seq_along(ctrls)){

  control <- ctrls[ii]

  ni <- tapply(x, g, length)

  means <- tapply(x, g, mean)
  meandiffs <- means[names(means) != control] - means[control]

  fittedn <- ni[names(ni) != control]
  controln <- ni[control]

  s <- sqrt( sum(tapply(x, g, function(x) sum((x - mean(x))^2) )) /
              (N - k))

  Dj <- meandiffs / (s * sqrt((1/fittedn) + (1/controln)))
  Rij <- sqrt(fittedn/(fittedn + controln))

  R <- outer(Rij, Rij, "*")
  diag(R) <- 1

  set.seed(5) # for getting consistent results every run
  qvt <- mvtnorm::qmvt((1 - (1 - conf.level)/2), df = N - k, sigma = R,
                      tail = "lower.tail")$quantile

  lower <- meandiffs - s * sqrt((1/fittedn) + (1/controln)) * qvt
  upper <- meandiffs + s * sqrt((1/fittedn) + (1/controln)) * qvt

  pval <- c()
  for (i in 1:(k-1)){
    pval[i] <- 1 - mvtnorm::pmvt(-abs(Dj[i]), abs(Dj[i]), corr=R, delta=rep(0, k-1), df=N - k)[1]
  }

  out[[ii]] <- cbind(diff=meandiffs, lower, upper, pval)
  dimnames(out[[ii]]) <- list(paste(names(meandiffs), control, sep="-"),
                              c("diff", "lwr.ci", "upr.ci", "pval"))
}

names(out) <- ctrls

class(out) <- c("PostHocTest")
# attr(out, "orig.call") <- NA
attr(out, "conf.level") <- conf.level
attr(out, "ordered") <- FALSE
attr(out, "method") <- ""
attr(out, "method.str") <- gettextf("\n Dunnett's test for comparing several treatments with a control")

return(out)
}

```