1 Supplementary resources

1.1 Software and Dunnett procedure description

Throughout this study we used the software R Studio under R version 4.1.2 (R Core Team, 2021). The datasets simulation will be done using the parameters of control presented bellow. We will present the *Dunnett* control group PCP. Additionally, a practical session in R will be presented. We then considered fictive data.

Illustrative data: For this practical we consider the following data on maize production (yield). We deal with 05 repeated measures treated with 03 different fertilizers, say $(G1, G2, G3)$, repeated five (05) times within six (06) different blocks (B1, B2, B3, B4, B5 and B6). The first 10 lines of database are presented bellow:

```
load('data.rda')
head(d2, 10)
```

```
##    block group yield
## 1     B1    G1  6.01
## 2     B1    G1  5.10
## 3     B1    G1  7.77
## 4     B1    G2  5.37
## 5     B1    G2  6.84
## 6     B1    G2  5.52
## 7     B1    G3  5.80
## 8     B1    G3  5.75
## 9     B1    G3  4.72
## 10    B2    G1  7.72
```

We first performed the LMEM using the function **lme()** from the package **nlme** (Pinheiro *et al.*, 2021). The fitted model is stored in the object **model** what we will use next for the PCPs running.

```
require(nlme)
model <- lme(yield ~ group, random = ~1|block , data = d2)
summary(model)
```

```
## Linear mixed-effects model fit by REML
##   Data: d2
##        AIC      BIC    logLik
##   149.7223 159.3814 -69.86113
##
## Random effects:
```

```
##  Formula: ~1 | block
##         (Intercept) Residual
## StdDev:   0.2764528 0.846088
##
## Fixed effects:  yield ~ group
##                 Value Std.Error DF   t-value p-value
## (Intercept)  6.250000 0.2291462 46 27.275169  0.0000
## groupG2     -0.125000 0.2820293 46 -0.443216  0.6597
## groupG3     -0.845556 0.2820293 46 -2.998112  0.0044
##  Correlation:
##         (Intr) gropG2
## groupG2 -0.615
## groupG3 -0.615  0.500
##
## Standardized Within-Group Residuals:
##         Min          Q1         Med          Q3         Max
## -2.08323965 -0.67585052  0.09802814  0.51102697  2.31346622
##
## Number of Observations: 54
## Number of Groups: 6
```

```
anova(model)
```

```
##             numDF denDF   F-value p-value
## (Intercept)     1    46 1351.1802  <.0001
## group           2    46    5.2375  0.0089
```

Let's consider the following notations:

- X is the random variable which represents the skin pigmentation;
- k the number of groups (families);
- x_{ij} the j^{th} skin pigmentation measured in the i^{th} group;
- n_i the number of observations in the i^{th} group;
- for a group i, the arithmetic mean x_i and sample variance s_i^2 are defined by the following formulas:

$$\bar{x_i} = \frac{1}{n_i}\sum_{j=1}^{n_i} x_{ij} \text{ and } s_i^2 = \frac{1}{n_i - 1}\sum_{j=1}^{n_i}(x_{ij} - \bar{x_i})^2$$

.

To compare two group means $\bar{x_a}$ and $\bar{x_b}$, we define $\alpha = 0.05$, the significance level for the following test in practical session. Let's then define the post-hoc comparison procedures involved in this study. In Appendix, we provide R code lines for running the *Dunnett* procedures based on the illustrative example.

Another Bonferroni procedure modified to control the family-wise error rate is developed by Hommel (1988). Described as more powerful than *Hochberg* procedure, the *Hommel* procedure is performed by first ordering the p-values $\hat{p_1}, \ldots, \hat{p_m}$ obtained from usual pairwise multiple comparison test. Next, we compute

$$j = \max\{i \in \{1, \ldots, n\} : p_{m\hat{-}i+l} \geqslant \frac{l\alpha}{i}, \forall l = 1, \ldots, i\} \tag{1.1}$$

All the m null hypotheses H_i^0 are rejected (significant difference between two means in comparison) if j does not exist else, the null hypotheses H_i^0 s.t. $\hat{p_i}^{Hom} = j * \hat{p_i} \leqslant \alpha$ are rejected.

Dunnett t test

To compare k treatment groups to a control group, the Canadian statistician Charles Dunnett (1955) developed his test for multiple comparison. The Dunnett's two-sides test detects an significant difference between the control group 0 and treatment group i when:

$$|\bar{x}_i - \bar{x}_0| > d_k^{\alpha} \times s \times \sqrt{\left(\frac{1}{n_i} + \frac{1}{n_0}\right)} \tag{1.2}$$

where:

1. $s^2 = \dfrac{\sum_{i=0}^{k} \sum_{j=1}^{n_i} (x_{ij} - \bar{x}_i)^2}{\sum_{i=0}^{k} (n_i - 1)}$
2. d_k^{α} is the upper $\alpha \times 100\%$ point of the distribution of $T = \max_{1 \leqslant i \leqslant k} \{|T_i|\}$ and $T_i = \dfrac{\bar{x}_i - \bar{x}_0}{s\sqrt{\frac{1}{n_i} + \frac{1}{n_0}}}$

1.2 Application Session in R

```
load('data.rda')
head(d2, 20)

##    block group yield
## 1     B1    G1  6.01
## 2     B1    G1  5.10
## 3     B1    G1  7.77
## 4     B1    G2  5.37
## 5     B1    G2  6.84
## 6     B1    G2  5.52
## 7     B1    G3  5.80
## 8     B1    G3  5.75
## 9     B1    G3  4.72
## 10    B2    G1  7.72
## 11    B2    G1  6.03
## 12    B2    G1  6.45
## 13    B2    G2  7.55
## 14    B2    G2  5.73
## 15    B2    G2  6.72
## 16    B2    G3  5.40
## 17    B2    G3  6.15
## 18    B2    G3  5.96
## 19    B3    G1  5.83
## 20    B3    G1  7.43

require(nlme)
model <- lme(yield ~ group, random = ~1|block , data = d2)

summary(model)

anova(model)

require(multcomp)

post <- multcomp::glht(model, linfct = mcp(group = "Dunnett"),
test = adjusted('none'))
summary(post)
```

References

Hommel, G. (1988). A stagewise rejective multiple test procedure based on a modified Bonferroni test. *Biometrika*, *75*(2), 383–386.

Pinheiro, J., Bates, D., DebRoy, S., Sarkar, D., & R Core Team (2021). *nlme: Linear and Nonlinear Mixed Effects Models*. R package version 3.1-153.

R Core Team (2021). *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing.