Modelos Lineares Mistos, Teste 31/05/2021

II

1. With the objective of studying the genetic variability of yield (kg/plant) between clones of the olive variety Cobrançosa in the first years of plantation, 125 clones were evaluated regarding this trait in a trial with a randomized complete block experimental design (5 blocks). In each block there is only one observation per clone. Assume that both `block` and `clone` are random effects factors.

a) Describe in detail the adequate model for the study described above.

b) In matrix notation, describe the assumptions of the model defined in a).

c) In R, with the function `lmer` from the package `lme4`, the following commands were executed:

```
> library(lme4)
> library(lmerTest)
> dadoslmer1<-lmer(rend~1+(1|clone)+(1|bloco), data=dados)
> summary(dadoslmer1)
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: rend ~ 1 + (1 | clone) + (1 | bloco)
   Data: dados
REML criterion at convergence: 698.7
Random effects:
 Groups   Name        Variance Std.Dev.
 clone    (Intercept) 0.04020  0.2005
 bloco    (Intercept) 0.01124  0.1060
 Residual             0.14741  0.3839
Number of obs: 625, groups:  clone, 125; bloco, 5
Fixed effects:
            Estimate Std. Error      df t value Pr(>|t|)
(Intercept)  0.55415    0.05296 5.09465   10.46 0.000123 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> logLik(dadoslmer1)
'log Lik.' -349.342
> dadoslmer2<-lmer(rend~1+(1|clone), data=dados)
```

```
> logLik(dadoslmer2)
'log Lik.' -362.997
> dadoslmer3<-lmer(rend~1+(1|bloco), data=dados)
> logLik(dadoslmer3)
'log Lik.' -370.7699
> ranef(dadoslmer1)
$clone
        (Intercept)
CB1011 -0.083164783
CB1013  0.004873856
CB1021 -0.067703213
CB1023 -0.145472601
CB1024  0.239105097
CB1031  0.013412335
...

$bloco
   (Intercept)
B1 -0.15542972
B2  0.06774529
B3  0.10288132
B4  0.01713723
B5 -0.03233413
```

i) Test the variance components associated to the model defined above. Describe in detail only one of the hypothesis tests performed.

ii) According to Akaike's Information Criterion (AIC), what is the best model among the three models fitted?

c) According to the full fitted model, what is the predicted yield for genotype CB1011 in block B1?

2. One researcher argues that, given the small number of levels of the block factor, it would be defensible to admit it as a fixed effects factor. Fitting this model in R, with the lmer function from the lme4 package, the following results were obtained:

```
> dadoslmer4<-lmer(rend~bloco+(1|clone), data=dados)
> summary(dadoslmer4)
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
```

```
Formula: rend ~ bloco + (1 | clone)
   Data: dados
REML criterion at convergence: 703.3
Random effects:
 Groups   Name         Variance Std.Dev.
 clone    (Intercept) 0.0402   0.2005
 Residual             0.1474   0.3839
Number of obs: 625, groups:  clone, 125
Fixed effects:
             Estimate Std. Error        df t value Pr(>|t|)
(Intercept)   0.38241    0.03874 523.79227   9.871  < 2e-16 ***
blocoB2       0.24660    0.04857 496.00000   5.078 5.41e-07 ***
blocoB3       0.28542    0.04857 496.00000   5.877 7.67e-09 ***
blocoB4       0.19068    0.04857 496.00000   3.926 9.85e-05 ***
blocoB5       0.13602    0.04857 496.00000   2.801   0.0053 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

a) Define the covariance between observations made in the same block for the model that admits the `block` as a fixed effects factor and for the model that admits the `block` as a random effects factor. Interpret the results obtained.

b) Knowing that $\bar{y}_{..} = 0.554$ kg/plant and that $\bar{y}_{CB12.} = 0.969$ kg/plant, what is the Empirical Best Linear Unbiased Predictor (EBLUP) of yield of clone CB12? Explain its meaning.

c) Is the yield obtained in block 2 significantly different from the yield obtained in block 1? Justify your answer.