

# Electronic Supplementary Material n°1

## Applications of quantitative genetics and statistical analyses in sugarcane breeding

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SAS code with working data (consisting of cane yield values of 16 sugarcane varieties tested in a complete randomized experiment implying an unbalanced number of replicates per variety) for fitting the two models that allowed the computation of unadjusted means ( $\mu + \text{BLUE}$ ) and shrunk means ( $\mu + \text{BLUP}$ ) of the studied varieties presented in Figure 2.

```
* Data import ;
DATA outdata;
  INPUT Variety$ Cane_Yield;
  DATALINES;
Var1 151.1
Var1 153.3
Var1 162.2
Var2 144.4
Var2 152.2
Var2 162.2
Var3 154.4
Var3 .
Var3 .
Var4 112.2
Var4 153.3
Var4 161.1
Var5 140.0
Var5 146.7
Var5 .
Var6 121.1
Var6 153.3
Var6 .
Var7 138.9
Var7 .
Var7 .
Var8 128.9
Var8 136.7
Var8 136.7
Var9 120.0
Var9 122.2
Var9 144.4
Var10 125.6
Var10 .
Var10 .
```

```

Var11 111.1
Var11 126.7
Var11 .
Var12 113.3
Var12 113.3
Var12 125.6
Var13 103.3
Var13 .
Var13 .
Var14 96.7
Var14 120.0
Var14 .
Var15 93.3
Var15 101.1
Var15 128.9
Var16 82.2
Var16 100.0
Var16 106.7
;
proc print ;
run ;

* Model using Variety effect as fixed effect (BLUE value of varieties) ;
proc mixed data=outdata COVTEST lognote;
class Variety;
model Cane_Yield = Variety / solution outp=resid residual ;
run;

* Model using Variety effect as random effect (BLUP value of varieties) ;
proc mixed data=outdata COVTEST lognote;
class Variety;
model Cane_Yield = / outp=resid residual;
random Variety / solution ;
run;

```