Analysis of variance

Variate: Score

Source of variation d.f. (m.v.) s.s. m.s. v.r. F pr.

Rep stratum

Genotype 17 0.1113 0.0065

Residual -15 0.0173

Rep.\*Units\* stratum

Genotype 17 629.9189 37.0541 230.84 <.001

Residual 549 (2) 88.1232 0.1605

Total 568 (2) 717.7118

Information summary

Model term e.f. non-orthogonal terms

Rep stratum

Genotype 0.000

*Message: the following units have large residuals.*

Rep 1 \*units\* 18 1.304 approx. s.e. 0.393

Rep 1 \*units\* 19 1.304 approx. s.e. 0.393

Rep 1 \*units\* 20 2.304 approx. s.e. 0.393

Rep 1 \*units\* 64 -1.512 approx. s.e. 0.393

Rep 1 \*units\* 164 -1.379 approx. s.e. 0.393

Rep 1 \*units\* 165 -1.379 approx. s.e. 0.393

Rep 2 \*units\* 11 1.273 approx. s.e. 0.393

Rep 2 \*units\* 12 2.273 approx. s.e. 0.393

Rep 2 \*units\* 13 1.273 approx. s.e. 0.393

Rep 2 \*units\* 14 1.273 approx. s.e. 0.393

Rep 2 \*units\* 15 2.273 approx. s.e. 0.393

Rep 2 \*units\* 16 1.273 approx. s.e. 0.393

Rep 3 \*units\* 14 1.273 approx. s.e. 0.393

Rep 3 \*units\* 16 1.273 approx. s.e. 0.393

Rep 3 \*units\* 17 1.273 approx. s.e. 0.393

Rep 3 \*units\* 18 1.273 approx. s.e. 0.393

Rep 3 \*units\* 19 1.273 approx. s.e. 0.393

Rep 3 \*units\* 162 -1.411 approx. s.e. 0.393

Tables of means

Variate: Score

Grand mean 0.468

Genotype E. botryoides E. camaldulensis E. citriodora E. dorrigoensis

0.000 0.717 0.000 0.000

rep. 30 60 31 30

Genotype E. goniocalyx E. microcorys E. nicholii E. ovata

0.000 3.533 0.000 -0.001

rep. 30 30 30 30

Genotype E. paniculata E. pilularis E. propinqua E. punctata

0.000 0.000 0.000 0.233

rep. 30 30 30 30

Genotype E. robusta E. saligna E. scoparia E. sideroxylon

0.067 0.100 0.000 3.400

rep. 30 30 30 30

Genotype E. tereticornis E. verminalis

0.133 0.000

rep. 30 30

Standard errors of means

Table Genotype

rep. unequal

d.f. 549

e.s.e. 0.0731 min.rep

0.0517 max.rep

(Not adjusted for missing values)

Standard errors of differences of means

Table Genotype

rep. unequal

d.f. 549

s.e.d. 0.1034 min.rep

0.0896 max-min

0.0731X max.rep

(No comparisons in categories where s.e.d. marked with an X)

(Not adjusted for missing values)

Least significant differences of means (5% level)

Table Genotype

rep. unequal

d.f. 549

l.s.d. 0.2032 min.rep

0.1760 max-min

0.1437X max.rep

(No comparisons in categories where l.s.d. marked with an X)

(Not adjusted for missing values)

Stratum standard errors and coefficients of variation

Variate: Score

Stratum d.f. s.e. cv%

Rep -15 \* \*

Rep.\*Units\* 549 0.4006 85.7

94 APLOT [RMETHOD=simple] fitted,normal,halfnormal,histogram