

Libraries used

```

library(nlme)
library(lme4)

## Loading required package: Matrix

## 
## Attaching package: 'lme4'

## The following object is masked from 'package:nlme':
## 
##     lmList

library(asreml)

## Loading required package: lattice

## Licensed to: Uni of Edinburgh
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library(asremlPlus)
library(ape)
library(MCMCglmm)

## Loading required package: coda

data<-read.table("~/Dropbox/SoilExp2/SoilExp2_new_analyses/soil_clean.csv",h=T)

#cOD indicates data set not corrected for different soil storage conditions, corOD indicates corrected growth values.

```

Variance component models with and without Block effects (corrected data)

```

#Genotype
var1<-lmer(corOD~1+(1|Isolate)+(1|Haplo2)+(1|genus2),data=data)
summary(var1)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ 1 + (1 | Isolate) + (1 | Haplo2) + (1 | genus2)
##   Data: data
##
## REML criterion at convergence: -23254.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -10.2182 -0.3511  0.0386  0.4404  8.5128
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Isolate (Intercept) 0.002556 0.05055
##   Haplo2   (Intercept) 0.009831 0.09915
##   genus2  (Intercept) 0.004609 0.06789
##   Residual            0.007200 0.08485
## Number of obs: 11264, groups: Isolate, 64; Haplo2, 43; genus2, 5
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.21571   0.03874  5.568

```

```

var1b<-lmer(corOD~1+(1|Isolate)+(1|Haplo2)+(1|genus2)+(1|Block),data=data)
summary(var1b)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ 1 + (1 | Isolate) + (1 | Haplo2) + (1 | genus2) + (1 |
##   Block)
##   Data: data
##
## REML criterion at convergence: -23256.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -10.2052 -0.3551  0.0392  0.4407  8.5283
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Isolate (Intercept) 2.556e-03 0.050555
##   Haplo2   (Intercept) 9.831e-03 0.099150
##   genus2  (Intercept) 4.609e-03 0.067891
##   Block    (Intercept) 3.792e-06 0.001947
##   Residual            7.198e-03 0.084839
## Number of obs: 11264, groups:
## Isolate, 64; Haplo2, 43; genus2, 5; Block, 2
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.21568   0.03876  5.564

```

```
#Environment
var2<-lmer(corOD~1+(1|site)+(1|loc),data=data)
summary(var2)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ 1 + (1 | site) + (1 | loc)
##   Data: data
##
## REML criterion at convergence: -11087.8
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -1.6500 -0.5828 -0.1504  0.3934  7.1067
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   site      (Intercept) 0.0000000 0.00000
##   loc       (Intercept) 0.0002781 0.01668
##   Residual            0.0218506 0.14782
## Number of obs: 11264, groups: site, 4; loc, 2
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.23219   0.01187 19.55
```

```
var2b<-lmer(corOD~1+(1|site)+(1|loc)+(1|Block),data=data)
summary(var2b)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ 1 + (1 | site) + (1 | loc) + (1 | Block)
##   Data: data
##
## REML criterion at convergence: -11088.3
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -1.6587 -0.5819 -0.1509  0.3949  7.1161
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   site      (Intercept) 0.000e+00 0.000000
##   loc       (Intercept) 2.809e-04 0.016759
##   Block     (Intercept) 5.283e-06 0.002299
##   Residual            2.185e-02 0.147811
## Number of obs: 11264, groups: site, 4; loc, 2; Block, 2
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.23216   0.01204 19.28
```

Variance component models (uncorrected data) with and without Block effects

```
#Genotype
var3<-lmer(cOD~1+(1|Isolate)+(1|Haplo2)+(1|genus2),data=data)
summary(var3)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: cOD ~ 1 + (1 | Isolate) + (1 | Haplo2) + (1 | genus2)
##   Data: data
##
## REML criterion at convergence: -22825.5
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -10.1966 -0.3484  0.0434  0.4262  8.1811
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Isolate (Intercept) 0.002556 0.05056
##   Haplo2   (Intercept) 0.009829 0.09914
##   genus2  (Intercept) 0.004605 0.06786
##   Residual           0.007481 0.08649
## Number of obs: 11264, groups: Isolate, 64; Haplo2, 43; genus2, 5
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.23053   0.03873  5.953
```

```
var3b<-lmer(cOD~1+(1|Isolate)+(1|Haplo2)+(1|genus2)+(1|Block),data=data)
summary(var3b)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: cOD ~ 1 + (1 | Isolate) + (1 | Haplo2) + (1 | genus2) + (1 |
##   Block)
##   Data: data
##
## REML criterion at convergence: -22825.5
##
## Scaled residuals:
##   Min     1Q Median     3Q    Max
## -10.1966 -0.3484  0.0434  0.4262  8.1811
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Isolate (Intercept) 2.556e-03 5.056e-02
##   Haplo2   (Intercept) 9.829e-03 9.914e-02
##   genus2  (Intercept) 4.605e-03 6.786e-02
##   Block    (Intercept) 8.701e-27 9.328e-14
##   Residual           7.481e-03 8.649e-02
## Number of obs: 11264, groups:
##   Isolate, 64; Haplo2, 43; genus2, 5; Block, 2
##
## Fixed effects:
##   Estimate Std. Error t value
## (Intercept)  0.23053   0.03873   5.953

```

```

#Environment
var4<-lmer(cOD~1+(1|site)+(1|loc),data=data)
summary(var4)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: cOD ~ 1 + (1 | site) + (1 | loc)
##   Data: data
##
## REML criterion at convergence: -10939.8
##
## Scaled residuals:
##   Min     1Q Median     3Q    Max
## -1.7351 -0.5802 -0.1502  0.3891  6.9565
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   site     (Intercept) 0.0000000 0.00000
##   loc      (Intercept) 0.0002517 0.01587
##   Residual           0.0221399 0.14879
## Number of obs: 11264, groups: site, 4; loc, 2
##
## Fixed effects:
##   Estimate Std. Error t value
## (Intercept)  0.24704   0.01131   21.85

```

```
var4b<-lmer(cOD~1+(1|site)+(1|loc)+(1|Block),data=data)
summary(var4b)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: cOD ~ 1 + (1 | site) + (1 | loc) + (1 | Block)
##   Data: data
##
## REML criterion at convergence: -10939.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.7351 -0.5802 -0.1502  0.3891  6.9565
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   site     (Intercept) 0.0000000 0.00000
##   loc      (Intercept) 0.0002517 0.01587
##   Block    (Intercept) 0.0000000 0.00000
##   Residual           0.0221399 0.14879
## Number of obs: 11264, groups: site, 4; loc, 2; Block, 2
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.24704   0.01131  21.85
```

Variance components of basic model components with and without Block effects (corrected data)

```
var5<-lmer(corOD~1+(1|Haplo2)+(1|locmo)+(1|Haplo2:locmo),data=data)
summary(var5)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ 1 + (1 | Haplo2) + (1 | locmo) + (1 | Haplo2:locmo)
##   Data: data
##
## REML criterion at convergence: -23424.8
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -8.7358 -0.4340 -0.0327  0.4303  9.7183
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   Haplo2:locmo (Intercept) 0.0001948 0.01396
##   Haplo2        (Intercept) 0.0176995 0.13304
##   locmo        (Intercept) 0.0008642 0.02940
##   Residual                 0.0069012 0.08307
## Number of obs: 11264, groups: Haplo2:locmo, 1376; Haplo2, 43; locmo, 32
##
## Fixed effects:
##           Estimate Std. Error t value
## (Intercept) 0.22473   0.02097 10.72

```

```

var5b<-lmer(corOD~1+(1|Haplo2)+(1|locmo)+(1|Haplo2:locmo)+(1|Block),data=data)
summary(var5b)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ 1 + (1 | Haplo2) + (1 | locmo) + (1 | Haplo2:locmo) +
##           (1 | Block)
##   Data: data
##
## REML criterion at convergence: -23441.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -8.6825 -0.4378 -0.0352  0.4300  9.7562
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   Haplo2:locmo (Intercept) 1.958e-04 0.013993
##   Haplo2        (Intercept) 1.770e-02 0.133039
##   locmo        (Intercept) 8.794e-04 0.029655
##   Block         (Intercept) 2.745e-05 0.005239
##   Residual                 6.888e-03 0.082993
## Number of obs: 11264, groups:
##   Haplo2:locmo, 1376; Haplo2, 43; locmo, 32; Block, 2
##
## Fixed effects:
##           Estimate Std. Error t value
## (Intercept) 0.2246    0.0213 10.55

```

Variance components of basic model components (uncorrected data) with and without Block effect

```
var7<-lmer(cOD~1+(1|Haplo2)+(1|locmo)+(1|Haplo2:locmo),data=data)
summary(var7)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: cOD ~ 1 + (1 | Haplo2) + (1 | locmo) + (1 | Haplo2:locmo)
##   Data: data
##
## REML criterion at convergence: -23330.5
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -8.6996 -0.4314 -0.0318  0.4296  9.6736
##
## Random effects:
##   Groups      Name        Variance Std.Dev.
##   Haplo2:locmo (Intercept) 0.000197 0.01404
##   Haplo2       (Intercept) 0.017696 0.13303
##   locmo       (Intercept) 0.001099 0.03315
##   Residual            0.006954 0.08339
## Number of obs: 11264, groups: Haplo2:locmo, 1376; Haplo2, 43; locmo, 32
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.23925   0.02114   11.32
```

```
var7b<-lmer(cOD~1+(1|Haplo2)+(1|locmo)+(1|Haplo2:locmo)+(1|Block),data=data)
summary(var7b)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ 1 + (1 | Haplo2) + (1 | locmo) + (1 | Haplo2:locmo) + (1 |
##   Block)
##   Data: data
##
## REML criterion at convergence: -23347.3
##
## Scaled residuals:
##   Min     1Q Median     3Q    Max
## -8.6458 -0.4350 -0.0342  0.4300  9.7120
##
## Random effects:
##   Groups      Name        Variance Std.Dev.
##   Haplo2:locmo (Intercept) 1.981e-04 0.014074
##   Haplo2          (Intercept) 1.770e-02 0.133027
##   locmo          (Intercept) 1.127e-03 0.033565
##   Block          (Intercept) 2.806e-05 0.005298
##   Residual                   6.941e-03 0.083311
## Number of obs: 11264, groups:
## Haplo2:locmo, 1376; Haplo2, 43; locmo, 32; Block, 2
##
## Fixed effects:
##   Estimate Std. Error t value
## (Intercept)  0.23916   0.02149   11.13

```

Main models with and without Block effects (corrected data)

```

m1<-gls(corOD~Haplo2*locmo,data=data)
anova(m1)

```

```

## Denom. DF: 9888
##           numDF  F-value p-value
## (Intercept)      1 87518.94 <.0001
## Haplo2          42  539.61 <.0001
## locmo          31   47.81 <.0001
## Haplo2:locmo  1302    1.15  4e-04

```

```

m1b<-lmer(corOD~Haplo2*locmo+(1|Block),data=data)
anova(m1b)

```

```

## Analysis of Variance Table
##           Df  Sum Sq Mean Sq  F value
## Haplo2       42 157.985  3.7616 540.6995
## locmo        31 10.443   0.3369  48.4249
## Haplo2:locmo 1302 10.422   0.0080   1.1506

```

```
m2<-gls(cod~Haplo2*loc*as.factor(month),data=data)
anova(m2)
```

```
## Denom. DF: 9888
##                               numDF  F-value p-value
## (Intercept)                  1 87518.94 <.0001
## Haplo2                      42   539.61 <.0001
## loc                          1   227.38 <.0001
## as.factor(month)              15    47.19 <.0001
## Haplo2:loc                   42     1.33  0.0757
## Haplo2:as.factor(month)       630     1.26 <.0001
## loc:as.factor(month)          15    36.47 <.0001
## Haplo2:loc:as.factor(month)   630     1.02  0.3383
```

```
m2b<-lmer(cod~Haplo2*loc*as.factor(month)+(1|Block),data=data)
anova(m2b)
```

```
## Analysis of Variance Table
##                               Df  Sum Sq Mean Sq F value
## Haplo2                      42 157.985 3.7616 540.6995
## loc                          1   1.607  1.6074 231.0485
## as.factor(month)              15   4.927  0.3285 47.2184
## Haplo2:loc                   42   0.389  0.0093  1.3316
## Haplo2:as.factor(month)       630   5.538  0.0088  1.2635
## loc:as.factor(month)          15   3.909  0.2606 37.4565
## Haplo2:loc:as.factor(month)   630   4.495  0.0071  1.0255
```

Main models (uncorrected data) with and without Block effects

```
m3<-gls(cod~Haplo2*locmo,data=data)
anova(m3)
```

```
## Denom. DF: 9888
##                               numDF  F-value p-value
## (Intercept)                  1 98253.99 <.0001
## Haplo2                      42   535.27 <.0001
## locmo                       31    59.07 <.0001
## Haplo2:locmo                1302     1.15  4e-04
```

```
m3b<-lmer(cod~Haplo2*locmo+(1|Block),data=data)
anova(m3b)
```

```
## Analysis of Variance Table
##                               Df  Sum Sq Mean Sq F value
## Haplo2                  42 157.940 3.7605 536.3725
## locmo                   31 13.008 0.4196 59.8493
## Haplo2:locmo            1302 10.504 0.0081 1.1508
```

```
m4<-gls(cOD~Haplo2*loc*as.factor(month),data=data)
anova(m4)
```

```
## Denom. DF: 9888
##                                         numDF  F-value p-value
## (Intercept)                           1 98253.99 <.0001
## Haplo2                                42   535.27 <.0001
## loc                                    1   204.54 <.0001
## as.factor(month)                      15    71.38 <.0001
## Haplo2:loc                            42     1.34  0.0677
## Haplo2:as.factor(month)                630     1.26 <.0001
## loc:as.factor(month)                  15    37.06 <.0001
## Haplo2:loc:as.factor(month)           630     1.02  0.3374
```

```
m4b<-lmer(cOD~Haplo2*loc*as.factor(month)+(1|Block),data=data)
anova(m4b)
```

```
## Analysis of Variance Table
##                               Df  Sum Sq Mean Sq F value
## Haplo2                  42 157.940 3.7605 536.3725
## loc                     1   1.439  1.4392 205.2844
## as.factor(month)          15   7.564  0.5043 71.9235
## Haplo2:loc                42   0.397  0.0094  1.3471
## Haplo2:as.factor(month)    630   5.577  0.0089  1.2627
## loc:as.factor(month)      15   4.005  0.2670 38.0794
## Haplo2:loc:as.factor(month) 630   4.530  0.0072  1.0257
```

Variance components of main model with and without Block effect (corrected data)

```
var6<-lmer(corOD~1+(1|Haplo2)+(1|loc)+(1|month)+(1|loc:month)+(1|loc:Haplo2)+(1|month:Ha
plo2),data=data)
summary(var6)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## corOD ~ 1 + (1 | Haplo2) + (1 | loc) + (1 | month) + (1 | loc:month) +
##      (1 | loc:Haplo2) + (1 | month:Haplo2)
## Data: data
##
## REML criterion at convergence: -23418
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -8.8733 -0.4389 -0.0323  0.4325  9.7638
##
## Random effects:
## Groups       Name        Variance Std.Dev.
## month:Haplo2 (Intercept) 1.263e-04 0.011238
## loc:Haplo2   (Intercept) 1.708e-05 0.004133
## Haplo2       (Intercept) 1.767e-02 0.132931
## loc:month    (Intercept) 7.259e-04 0.026943
## month        (Intercept) 6.763e-05 0.008224
## loc          (Intercept) 1.593e-04 0.012620
## Residual            6.964e-03 0.083448
## Number of obs: 11264, groups:
## month:Haplo2, 688; loc:Haplo2, 86; Haplo2, 43; loc:month, 32; month, 16; loc, 2
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.22472   0.02277  9.867

```

```

var6b<-lmer(corOD~1+(1|Haplo2)+(1|loc)+(1|month)+(1|loc:month)+(1|loc:Haplo2)+(1|month:Haplo2)+(1|Block),data=data)
summary(var6b)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## corOD ~ 1 + (1 | Haplo2) + (1 | loc) + (1 | month) + (1 | loc:month) +
##          (1 | loc:Haplo2) + (1 | month:Haplo2) + (1 | Block)
## Data: data
##
## REML criterion at convergence: -23434.3
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -8.8216 -0.4378 -0.0319  0.4338  9.8018
##
## Random effects:
## Groups      Name        Variance Std.Dev.
## month:Haplo2 (Intercept) 1.268e-04 0.011262
## loc:Haplo2   (Intercept) 1.718e-05 0.004144
## Haplo2       (Intercept) 1.767e-02 0.132930
## loc:month    (Intercept) 7.470e-04 0.027331
## month        (Intercept) 5.928e-05 0.007699
## Block        (Intercept) 2.744e-05 0.005238
## loc          (Intercept) 1.635e-04 0.012786
## Residual           6.951e-03 0.083370
## Number of obs: 11264, groups:
## month:Haplo2, 688; loc:Haplo2, 86; Haplo2, 43; loc:month, 32; month, 16; Block, 2; loc, 2
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.22463   0.02312   9.715

```

Variance components of main model (uncorrected data) with and without Block effects

```

var8<-lmer(cOD~1+(1|Haplo2)+(1|loc)+(1|month)+(1|loc:month)+(1|loc:Haplo2)+(1|month:Haplo2),data=data)
summary(var8)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula:
## COD ~ 1 + (1 | Haplo2) + (1 | loc) + (1 | month) + (1 | loc:month) +
##       (1 | loc:Haplo2) + (1 | month:Haplo2)
## Data: data
##
## REML criterion at convergence: -23324.1
##
## Scaled residuals:
##   Min     1Q Median     3Q    Max
## -8.8386 -0.4362 -0.0326  0.4328  9.7204
##
## Random effects:
## Groups      Name        Variance Std.Dev.
## month:Haplo2 (Intercept) 1.270e-04 0.01127
## loc:Haplo2   (Intercept) 1.823e-05 0.00427
## Haplo2       (Intercept) 1.767e-02 0.13291
## loc:month    (Intercept) 7.431e-04 0.02726
## month        (Intercept) 2.922e-04 0.01709
## loc          (Intercept) 1.611e-04 0.01269
## Residual            7.018e-03 0.08377
## Number of obs: 11264, groups:
## month:Haplo2, 688; loc:Haplo2, 86; Haplo2, 43; loc:month, 32; month, 16; loc, 2
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  0.23923   0.02311 10.35

```

```

var8b<-lmer(COD~1+(1|Haplo2)+(1|loc)+(1|month)+(1|loc:month)+(1|loc:Haplo2)+(1|month:Haplo2)+(1|Block),data=data)
summary(var8b)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula:
##   COD ~ 1 + (1 | Haplo2) + (1 | loc) + (1 | month) + (1 | loc:month) +
##     (1 | loc:Haplo2) + (1 | month:Haplo2) + (1 | Block)
## Data: data
##
## REML criterion at convergence: -23340.7
##
## Scaled residuals:
##   Min      1Q  Median      3Q     Max
## -8.7865 -0.4351 -0.0312  0.4337  9.7588
##
## Random effects:
##   Groups      Name        Variance Std.Dev.
##   month:Haplo2 (Intercept) 1.275e-04 0.011293
##   loc:Haplo2   (Intercept) 1.833e-05 0.004282
##   Haplo2       (Intercept) 1.767e-02 0.132914
##   loc:month    (Intercept) 7.649e-04 0.027658
##   month        (Intercept) 2.958e-04 0.017199
##   Block        (Intercept) 2.802e-05 0.005293
##   loc          (Intercept) 1.653e-04 0.012858
##   Residual           7.004e-03 0.083693
## Number of obs: 11264, groups:
##   month:Haplo2, 688; loc:Haplo2, 86; Haplo2, 43; loc:month, 32; month, 16; Block, 2; loc, 2
##
## Fixed effects:
##   Estimate Std. Error t value
## (Intercept)  0.23914   0.02348   10.19

```

Time shift with and without Block effects (corrected data)

```

ts1<-lmer(corOD~-1+as.factor(tempdis2)+(1|Haplo2)+(1|locmo),data=data)
summary(ts1)

```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ -1 + as.factor(tempdis2) + (1 | Haplo2) + (1 | locmo)
##   Data: data
##
## REML criterion at convergence: -23309.5
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -9.0697 -0.4637 -0.0366  0.4416  9.6891
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Haplo2   (Intercept) 0.017534 0.13242
##   locmo    (Intercept) 0.001300 0.03606
##   Residual           0.006945 0.08334
## Number of obs: 11264, groups: Haplo2, 43; locmo, 32
##
## Fixed effects:
##                     Estimate Std. Error t value
## as.factor(tempdis2)-20  0.14437   0.02519  5.731
## as.factor(tempdis2)-19  0.16812   0.02334  7.204
## as.factor(tempdis2)-18  0.17405   0.02268  7.676
## as.factor(tempdis2)-17  0.17421   0.02237  7.786
## as.factor(tempdis2)-16  0.17449   0.02213  7.883
## as.factor(tempdis2)-15  0.18386   0.02198  8.367
## as.factor(tempdis2)-14  0.18130   0.02185  8.297
## as.factor(tempdis2)-13  0.18109   0.02176  8.322
## as.factor(tempdis2)-12  0.18735   0.02182  8.586
## as.factor(tempdis2)-11  0.19097   0.02191  8.715
## as.factor(tempdis2)-10  0.20692   0.02207  9.376
## as.factor(tempdis2)-9   0.20724   0.02223  9.321
## as.factor(tempdis2)-8   0.20318   0.02259  8.996
## as.factor(tempdis2)-7   0.21764   0.02214  9.831
## as.factor(tempdis2)-6   0.22286   0.02196 10.150
## as.factor(tempdis2)-5   0.23175   0.02197 10.551
## as.factor(tempdis2)-4   0.23354   0.02168 10.770
## as.factor(tempdis2)-3   0.23082   0.02158 10.697
## as.factor(tempdis2)-2   0.22266   0.02151 10.353
## as.factor(tempdis2)-1   0.22857   0.02145 10.656
## as.factor(tempdis2)0    0.23003   0.02141 10.743
## as.factor(tempdis2)1    0.22786   0.02145 10.621
## as.factor(tempdis2)2    0.22735   0.02152 10.567
## as.factor(tempdis2)3    0.22369   0.02161 10.351
## as.factor(tempdis2)4    0.21873   0.02174 10.062
## as.factor(tempdis2)5    0.22720   0.02179 10.425
## as.factor(tempdis2)6    0.23235   0.02205 10.537
## as.factor(tempdis2)7    0.24272   0.02202 11.020
## as.factor(tempdis2)8    0.27058   0.02255 12.001
## as.factor(tempdis2)9    0.27493   0.02225 12.354
## as.factor(tempdis2)10   0.26014   0.02206 11.795
## as.factor(tempdis2)11   0.25093   0.02191 11.454
## as.factor(tempdis2)12   0.25867   0.02184 11.846
## as.factor(tempdis2)13   0.26169   0.02181 11.997

```

```
## as.factor(tempdis2)14 0.26294 0.02190 12.004
## as.factor(tempdis2)15 0.26521 0.02217 11.961
## as.factor(tempdis2)16 0.25788 0.02221 11.611
## as.factor(tempdis2)17 0.25476 0.02252 11.313
## as.factor(tempdis2)18 0.25828 0.02294 11.257
## as.factor(tempdis2)19 0.25665 0.02394 10.720
## as.factor(tempdis2)20 0.25879 0.02618 9.885
```

```
##
## Correlation matrix not shown by default, as p = 41 > 12.
## Use print(x, correlation=TRUE) or
## vcov(x) if you need it
```

```
ts1b<-lmer(corOD~-1+as.factor(tempdis2)+(1|Haplo2)+(1|locmo)+(1|Block),data=data)
summary(ts1b)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ -1 + as.factor(tempdis2) + (1 | Haplo2) + (1 | locmo) +
##           (1 | Block)
## Data: data
##
## REML criterion at convergence: -23325.8
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -9.0202 -0.4639 -0.0354  0.4414  9.7269
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Haplo2   (Intercept) 1.754e-02 0.13242
##   locmo    (Intercept) 1.329e-03 0.03645
##   Block    (Intercept) 2.725e-05 0.00522
##   Residual            6.932e-03 0.08326
## Number of obs: 11264, groups: Haplo2, 43; locmo, 32; Block, 2
##
## Fixed effects:
##                   Estimate Std. Error t value
## as.factor(tempdis2)-20  0.14418   0.02547  5.660
## as.factor(tempdis2)-19  0.16796   0.02364  7.104
## as.factor(tempdis2)-18  0.17389   0.02299  7.563
## as.factor(tempdis2)-17  0.17407   0.02270  7.669
## as.factor(tempdis2)-16  0.17436   0.02246  7.763
## as.factor(tempdis2)-15  0.18373   0.02230  8.238
## as.factor(tempdis2)-14  0.18119   0.02218  8.168
## as.factor(tempdis2)-13  0.18098   0.02209  8.192
## as.factor(tempdis2)-12  0.18725   0.02215  8.454
## as.factor(tempdis2)-11  0.19087   0.02224  8.582
## as.factor(tempdis2)-10  0.20684   0.02239  9.236
## as.factor(tempdis2)-9   0.20716   0.02256  9.184
## as.factor(tempdis2)-8   0.20311   0.02290  8.868
## as.factor(tempdis2)-7   0.21753   0.02246  9.685
## as.factor(tempdis2)-6   0.22273   0.02228  9.995
## as.factor(tempdis2)-5   0.23162   0.02229 10.390
## as.factor(tempdis2)-4   0.23342   0.02202 10.602
## as.factor(tempdis2)-3   0.23067   0.02191 10.527
## as.factor(tempdis2)-2   0.22255   0.02184 10.189
## as.factor(tempdis2)-1   0.22847   0.02179 10.487
## as.factor(tempdis2)0    0.22994   0.02175 10.573
## as.factor(tempdis2)1    0.22778   0.02179 10.453
## as.factor(tempdis2)2    0.22728   0.02185 10.402
## as.factor(tempdis2)3    0.22363   0.02194 10.191
## as.factor(tempdis2)4    0.21867   0.02207  9.908
## as.factor(tempdis2)5    0.22719   0.02212 10.269
## as.factor(tempdis2)6    0.23230   0.02238 10.381
## as.factor(tempdis2)7    0.24264   0.02235 10.856
## as.factor(tempdis2)8    0.27048   0.02287 11.829
## as.factor(tempdis2)9    0.27483   0.02258 12.173
## as.factor(tempdis2)10   0.25999   0.02238 11.616
## as.factor(tempdis2)11   0.25084   0.02224 11.281

```

```
## as.factor(tempdis2)12 0.25859 0.02217 11.666
## as.factor(tempdis2)13 0.26162 0.02214 11.816
## as.factor(tempdis2)14 0.26288 0.02223 11.824
## as.factor(tempdis2)15 0.26516 0.02250 11.786
## as.factor(tempdis2)16 0.25783 0.02253 11.442
## as.factor(tempdis2)17 0.25472 0.02284 11.153
## as.factor(tempdis2)18 0.25837 0.02326 11.110
## as.factor(tempdis2)19 0.25663 0.02424 10.588
## as.factor(tempdis2)20 0.25880 0.02645 9.785
```

```
##
## Correlation matrix not shown by default, as p = 41 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x) if you need it
```

Time shift (uncorrected data) with and without Block effect

```
ts2<-lmer(cOD~-1+as.factor(tempdis2)+(1|Haplo2)+(1|locmo),data=data)
summary(ts2)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: cOD ~ -1 + as.factor(tempdis2) + (1 | Haplo2) + (1 | locmo)
##   Data: data
##
## REML criterion at convergence: -23206.3
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -9.0328 -0.4612 -0.0359  0.4406  9.6470
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Haplo2   (Intercept) 0.017531 0.13240
##   locmo    (Intercept) 0.002075 0.04555
##   Residual           0.007001 0.08367
## Number of obs: 11264, groups: Haplo2, 43; locmo, 32
##
## Fixed effects:
##             Estimate Std. Error t value
## as.factor(tempdis2)-20  0.15847   0.02570  6.165
## as.factor(tempdis2)-19  0.18253   0.02387  7.647
## as.factor(tempdis2)-18  0.18861   0.02322  8.123
## as.factor(tempdis2)-17  0.18882   0.02292  8.237
## as.factor(tempdis2)-16  0.18895   0.02269  8.329
## as.factor(tempdis2)-15  0.19852   0.02253  8.812
## as.factor(tempdis2)-14  0.19588   0.02241  8.742
## as.factor(tempdis2)-13  0.19568   0.02232  8.769
## as.factor(tempdis2)-12  0.20227   0.02237  9.041
## as.factor(tempdis2)-11  0.20558   0.02246  9.151
## as.factor(tempdis2)-10  0.22169   0.02262  9.802
## as.factor(tempdis2)-9   0.22253   0.02278  9.769
## as.factor(tempdis2)-8   0.21781   0.02313  9.418
## as.factor(tempdis2)-7   0.23213   0.02268 10.233
## as.factor(tempdis2)-6   0.23730   0.02251 10.544
## as.factor(tempdis2)-5   0.24621   0.02252 10.935
## as.factor(tempdis2)-4   0.24793   0.02224 11.148
## as.factor(tempdis2)-3   0.24532   0.02213 11.083
## as.factor(tempdis2)-2   0.23719   0.02206 10.750
## as.factor(tempdis2)-1   0.24310   0.02201 11.046
## as.factor(tempdis2)0    0.24450   0.02197 11.129
## as.factor(tempdis2)1    0.24233   0.02201 11.009
## as.factor(tempdis2)2    0.24198   0.02207 10.963
## as.factor(tempdis2)3    0.23825   0.02216 10.749
## as.factor(tempdis2)4    0.23332   0.02229 10.467
## as.factor(tempdis2)5    0.24173   0.02235 10.818
## as.factor(tempdis2)6    0.24665   0.02260 10.914
## as.factor(tempdis2)7    0.25739   0.02257 11.402
## as.factor(tempdis2)8    0.28498   0.02309 12.343
## as.factor(tempdis2)9    0.28924   0.02280 12.686
## as.factor(tempdis2)10   0.27457   0.02260 12.147
## as.factor(tempdis2)11   0.26532   0.02246 11.814
## as.factor(tempdis2)12   0.27306   0.02239 12.196
## as.factor(tempdis2)13   0.27604   0.02237 12.342

```

```
## as.factor(tempdis2)14 0.27727 0.02246 12.347
## as.factor(tempdis2)15 0.27953 0.02272 12.302
## as.factor(tempdis2)16 0.27220 0.02276 11.960
## as.factor(tempdis2)17 0.26909 0.02306 11.667
## as.factor(tempdis2)18 0.27252 0.02348 11.605
## as.factor(tempdis2)19 0.27085 0.02447 11.069
## as.factor(tempdis2)20 0.27288 0.02668 10.226
```

```
##
## Correlation matrix not shown by default, as p = 41 > 12.
## Use print(x, correlation=TRUE) or
## vcov(x) if you need it
```

```
ts2b<-lmer(cOD~-1+as.factor(tempdis2)+(1|Haplo2)+(1|locmo)+(1|Block),data=data)
summary(ts2b)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: cOD ~ -1 + as.factor(tempdis2) + (1 | Haplo2) + (1 | locmo) +
##           (1 | Block)
## Data: data
##
## REML criterion at convergence: -23223
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -8.9827 -0.4598 -0.0359  0.4406  9.6855
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Haplo2   (Intercept) 1.753e-02 0.132409
##   locmo    (Intercept) 2.117e-03 0.046013
##   Block    (Intercept) 2.828e-05 0.005318
##   Residual            6.988e-03 0.083592
## Number of obs: 11264, groups: Haplo2, 43; locmo, 32; Block, 2
##
## Fixed effects:
##             Estimate Std. Error t value
## as.factor(tempdis2)-20  0.15828   0.02600  6.088
## as.factor(tempdis2)-19  0.18236   0.02419  7.539
## as.factor(tempdis2)-18  0.18844   0.02355  8.002
## as.factor(tempdis2)-17  0.18866   0.02326  8.112
## as.factor(tempdis2)-16  0.18880   0.02302  8.201
## as.factor(tempdis2)-15  0.19838   0.02287  8.675
## as.factor(tempdis2)-14  0.19575   0.02275  8.605
## as.factor(tempdis2)-13  0.19556   0.02266  8.631
## as.factor(tempdis2)-12  0.20215   0.02271  8.900
## as.factor(tempdis2)-11  0.20547   0.02280  9.010
## as.factor(tempdis2)-10  0.22159   0.02296  9.653
## as.factor(tempdis2)-9   0.22244   0.02312  9.623
## as.factor(tempdis2)-8   0.21772   0.02346  9.282
## as.factor(tempdis2)-7   0.23201   0.02302  10.078
## as.factor(tempdis2)-6   0.23717   0.02285  10.381
## as.factor(tempdis2)-5   0.24607   0.02286  10.767
## as.factor(tempdis2)-4   0.24781   0.02258  10.973
## as.factor(tempdis2)-3   0.24517   0.02248  10.906
## as.factor(tempdis2)-2   0.23708   0.02241  10.579
## as.factor(tempdis2)-1   0.24300   0.02236  10.869
## as.factor(tempdis2)0    0.24441   0.02232  10.951
## as.factor(tempdis2)1    0.24225   0.02236  10.834
## as.factor(tempdis2)2    0.24190   0.02242  10.790
## as.factor(tempdis2)3    0.23819   0.02251  10.581
## as.factor(tempdis2)4    0.23327   0.02264  10.305
## as.factor(tempdis2)5    0.24172   0.02269  10.654
## as.factor(tempdis2)6    0.24660   0.02294  10.751
## as.factor(tempdis2)7    0.25732   0.02291  11.230
## as.factor(tempdis2)8    0.28488   0.02342  12.165
## as.factor(tempdis2)9    0.28915   0.02314  12.498
## as.factor(tempdis2)10   0.27441   0.02294  11.961
## as.factor(tempdis2)11   0.26524   0.02280  11.633

```

```
## as.factor(tempdis2)12 0.27299 0.02273 12.010
## as.factor(tempdis2)13 0.27599 0.02271 12.153
## as.factor(tempdis2)14 0.27722 0.02280 12.160
## as.factor(tempdis2)15 0.27948 0.02306 12.120
## as.factor(tempdis2)16 0.27216 0.02310 11.784
## as.factor(tempdis2)17 0.26907 0.02340 11.501
## as.factor(tempdis2)18 0.27263 0.02381 11.451
## as.factor(tempdis2)19 0.27085 0.02478 10.931
## as.factor(tempdis2)20 0.27291 0.02696 10.121
```

```
##
## Correlation matrix not shown by default, as p = 41 > 12.
## Use print(x, correlation=TRUE) or
##   vcov(x) if you need it
```

Time shift excluding low quality environments with and without Block effect

```
data<-subset(data,SoilID!="C1-8")
data<-subset(data,SoilID!="C12-July")
data<-subset(data,SoilID!="N1-Sep")
ts3<-lmer(corOD~-1+as.factor(tempdis2)+(1|Haplo2)+(1|locmo),data=data)
summary(ts3)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ -1 + as.factor(tempdis2) + (1 | Haplo2) + (1 | locmo)
##   Data: data
##
## REML criterion at convergence: -24507.2
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -7.1820 -0.4655 -0.0457  0.4119 10.7559
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   Haplo2   (Intercept) 0.0193406 0.13907
##   locmo    (Intercept) 0.0003998 0.01999
##   Residual           0.0055411 0.07444
## Number of obs: 10688, groups: Haplo2, 43; locmo, 32
##
## Fixed effects:
##             Estimate Std. Error t value
## as.factor(tempdis2)-20  0.15267  0.02472  6.176
## as.factor(tempdis2)-19  0.17750  0.02321  7.646
## as.factor(tempdis2)-18  0.18324  0.02268  8.077
## as.factor(tempdis2)-17  0.18474  0.02244  8.231
## as.factor(tempdis2)-16  0.18561  0.02225  8.341
## as.factor(tempdis2)-15  0.19517  0.02213  8.820
## as.factor(tempdis2)-14  0.19188  0.02203  8.710
## as.factor(tempdis2)-13  0.19169  0.02197  8.725
## as.factor(tempdis2)-12  0.19636  0.02202  8.916
## as.factor(tempdis2)-11  0.20165  0.02210  9.123
## as.factor(tempdis2)-10  0.21245  0.02224  9.552
## as.factor(tempdis2)-9   0.20854  0.02239  9.314
## as.factor(tempdis2)-8   0.20489  0.02272  9.018
## as.factor(tempdis2)-7   0.22169  0.02231  9.938
## as.factor(tempdis2)-6   0.23470  0.02215  10.595
## as.factor(tempdis2)-5   0.23938  0.02213  10.819
## as.factor(tempdis2)-4   0.24135  0.02192  11.013
## as.factor(tempdis2)-3   0.24208  0.02184  11.087
## as.factor(tempdis2)-2   0.22990  0.02177  10.558
## as.factor(tempdis2)-1   0.23594  0.02173  10.860
## as.factor(tempdis2)0   0.23781  0.02170  10.961
## as.factor(tempdis2)1   0.23501  0.02173  10.813
## as.factor(tempdis2)2   0.23609  0.02179  10.836
## as.factor(tempdis2)3   0.23343  0.02186  10.676
## as.factor(tempdis2)4   0.23349  0.02198  10.623
## as.factor(tempdis2)5   0.23525  0.02203  10.677
## as.factor(tempdis2)6   0.23742  0.02223  10.682
## as.factor(tempdis2)7   0.25237  0.02224  11.349
## as.factor(tempdis2)8   0.27874  0.02267  12.296
## as.factor(tempdis2)9   0.28174  0.02240  12.579
## as.factor(tempdis2)10  0.27571  0.02226  12.386
## as.factor(tempdis2)11  0.25857  0.02212  11.687
## as.factor(tempdis2)12  0.26242  0.02205  11.899
## as.factor(tempdis2)13  0.26975  0.02203  12.246

```

```
## as.factor(tempdis2)14 0.26886 0.02211 12.161
## as.factor(tempdis2)15 0.27046 0.02233 12.112
## as.factor(tempdis2)16 0.26204 0.02235 11.722
## as.factor(tempdis2)17 0.25573 0.02263 11.303
## as.factor(tempdis2)18 0.26767 0.02290 11.689
## as.factor(tempdis2)19 0.26655 0.02370 11.248
## as.factor(tempdis2)20 0.27016 0.02552 10.588
```

```
##
## Correlation matrix not shown by default, as p = 41 > 12.
## Use print(x, correlation=TRUE) or
## vcov(x) if you need it
```

```
ts3b<-lmer(corOD~-1+as.factor(tempdis2)+(1|Haplo2)+(1|locmo)+(1|Block),data=data)
summary(ts3b)
```

```

## Linear mixed model fit by REML ['lmerMod']
## Formula: corOD ~ -1 + as.factor(tempdis2) + (1 | Haplo2) + (1 | locmo) +
##           (1 | Block)
## Data: data
##
## REML criterion at convergence: -24515
##
## Scaled residuals:
##    Min     1Q Median     3Q    Max
## -7.1538 -0.4652 -0.0457  0.4133 10.7834
##
## Random effects:
##   Groups      Name        Variance Std.Dev.
##   Haplo2    (Intercept) 1.934e-02 0.139075
##   locmo     (Intercept) 4.082e-04 0.020204
##   Block      (Intercept) 1.251e-05 0.003537
##   Residual            5.535e-03 0.074400
## Number of obs: 10688, groups: Haplo2, 43; locmo, 32; Block, 2
##
## Fixed effects:
##                   Estimate Std. Error t value
## as.factor(tempdis2)-20  0.15247  0.02485  6.135
## as.factor(tempdis2)-19  0.17735  0.02335  7.594
## as.factor(tempdis2)-18  0.18309  0.02283  8.020
## as.factor(tempdis2)-17  0.18460  0.02259  8.172
## as.factor(tempdis2)-16  0.18549  0.02240  8.281
## as.factor(tempdis2)-15  0.19506  0.02228  8.757
## as.factor(tempdis2)-14  0.19178  0.02218  8.647
## as.factor(tempdis2)-13  0.19159  0.02212  8.662
## as.factor(tempdis2)-12  0.19628  0.02217  8.853
## as.factor(tempdis2)-11  0.20157  0.02225  9.059
## as.factor(tempdis2)-10  0.21238  0.02239  9.487
## as.factor(tempdis2)-9   0.20848  0.02253  9.252
## as.factor(tempdis2)-8   0.20482  0.02286  8.959
## as.factor(tempdis2)-7   0.22160  0.02245  9.870
## as.factor(tempdis2)-6   0.23459  0.02230 10.520
## as.factor(tempdis2)-5   0.23928  0.02227 10.743
## as.factor(tempdis2)-4   0.24127  0.02206 10.934
## as.factor(tempdis2)-3   0.24199  0.02198 11.007
## as.factor(tempdis2)-2   0.22983  0.02192 10.483
## as.factor(tempdis2)-1   0.23588  0.02188 10.782
## as.factor(tempdis2)0    0.23776  0.02185 10.883
## as.factor(tempdis2)1    0.23497  0.02188 10.737
## as.factor(tempdis2)2    0.23606  0.02194 10.760
## as.factor(tempdis2)3    0.23341  0.02201 10.603
## as.factor(tempdis2)4    0.23347  0.02213 10.551
## as.factor(tempdis2)5    0.23526  0.02218 10.606
## as.factor(tempdis2)6    0.23740  0.02237 10.611
## as.factor(tempdis2)7    0.25233  0.02238 11.273
## as.factor(tempdis2)8    0.27869  0.02281 12.216
## as.factor(tempdis2)9    0.28170  0.02254 12.497
## as.factor(tempdis2)10   0.27564  0.02241 12.302
## as.factor(tempdis2)11   0.25854  0.02227 11.608

```

```
## as.factor(tempdis2)12 0.26241 0.02220 11.819
## as.factor(tempdis2)13 0.26974 0.02217 12.164
## as.factor(tempdis2)14 0.26886 0.02226 12.080
## as.factor(tempdis2)15 0.27047 0.02248 12.034
## as.factor(tempdis2)16 0.26206 0.02250 11.647
## as.factor(tempdis2)17 0.25576 0.02277 11.233
## as.factor(tempdis2)18 0.26778 0.02304 11.622
## as.factor(tempdis2)19 0.26659 0.02383 11.185
## as.factor(tempdis2)20 0.27024 0.02564 10.539
```

```
##
## Correlation matrix not shown by default, as p = 41 > 12.
## Use print(x, correlation=TRUE) or
## vcov(x) if you need it
```

Using phylogenetic relatedness instead of genotype (corOD)

```
tree<-read.tree('/home/susanne/Desktop/rsync/soil_exp2_phylo/GTRGAMMA_haplo/RAXML_bestTree.test')
ctree<-compute.brtime(tree)
Ainv<-inverseA(ctree)$Ainv

fit1<-asreml(corOD~locmo,random=~Haplo2,rcov=~units,data=data)
```

```
## ASReml: Wed Sep 21 17:08:12 2016
##
##      LogLik      S2      DF      wall      cpu
## 21424.9770 0.0064 10656 17:08:12 0.0
## 21576.9288 0.0062 10656 17:08:12 0.0
## 21742.6696 0.0060 10656 17:08:12 0.0
## 21881.0165 0.0058 10656 17:08:12 0.0
## 21942.2120 0.0058 10656 17:08:12 0.0
## 21966.8481 0.0057 10656 17:08:12 0.0
## 21974.8525 0.0057 10656 17:08:12 0.0
## 21976.4836 0.0057 10656 17:08:12 0.0
## 21976.6058 0.0057 10656 17:08:12 0.0
## 21976.6069 0.0057 10656 17:08:12 0.0
## 21976.6069 0.0057 10656 17:08:12 0.0
##
## Finished on: Wed Sep 21 17:08:12 2016
##
## LogLikelihood Converged
```

```
fit2<-
asreml(corOD~locmo,random=~giv(Haplo2),rcov=~units,ginverse=list(Haplo2=sm2asreml(Ainv)),m
xiter=30,data=data)
```

```

## ASReml: Wed Sep 21 17:08:12 2016
##
##      LogLik      S2      DF     wall      cpu
## 16666.1766 0.0158 10656 17:08:12 0.0
## 16845.1250 0.0153 10656 17:08:12 0.0
## 17121.8462 0.0145 10656 17:08:12 0.0
## 17683.7508 0.0130 10656 17:08:12 0.0
## 18787.7351 0.0105 10656 17:08:12 0.0
## 20126.8160 0.0081 10656 17:08:12 0.0
## 21100.9717 0.0068 10656 17:08:12 0.0
## 21560.5280 0.0062 10656 17:08:12 0.0
## 21771.1069 0.0059 10656 17:08:12 0.0
## 21866.7002 0.0058 10656 17:08:12 0.0
## 21907.7258 0.0057 10656 17:08:12 0.0
## 21923.0572 0.0057 10656 17:08:12 0.0
## 21927.2868 0.0057 10656 17:08:12 0.0
## 21927.8932 0.0057 10656 17:08:12 0.0
## 21927.9151 0.0057 10656 17:08:12 0.0
## 21927.9152 0.0057 10656 17:08:12 0.0
## 21927.9152 0.0057 10656 17:08:13 0.0
##
## Finished on: Wed Sep 21 17:08:13 2016
##
## LogLikelihood Converged

```

```
AICfit1<-2*32-2*fit1$loglik
AICfit2<-2*32-2*fit2$loglik
```

```
AICfit1
```

```
## [1] -43889.21
```

```
AICfit2
```

```
## [1] -43791.83
```

Using phylogenetic relatedness instead of genotype (cOD)

```

tree<-read.tree('/home/susanne/Desktop/rsync/soil_exp2_phylo/GTRGAMMA_haplo/RAxML_bestTree.test')
ctree<-compute.brtime(tree)
Ainv<-inverseA(ctree)$Ainv

fit1<-asreml(cOD~locmo,random=~Haplo2,rcov=~units,data=data)

```

```

## ASReml: Wed Sep 21 17:08:13 2016
##
##      LogLik      S2      DF     wall      cpu
## 21413.3501 0.0064 10656 17:08:13 0.0
## 21564.9430 0.0062 10656 17:08:13 0.0
## 21730.2999 0.0060 10656 17:08:13 0.0
## 21868.3264 0.0059 10656 17:08:13 0.0
## 21929.3701 0.0058 10656 17:08:13 0.0
## 21953.9351 0.0057 10656 17:08:13 0.0
## 21961.9091 0.0057 10656 17:08:13 0.0
## 21963.5309 0.0057 10656 17:08:13 0.0
## 21963.6518 0.0057 10656 17:08:13 0.0
## 21963.6529 0.0057 10656 17:08:13 0.0
## 21963.6529 0.0057 10656 17:08:13 0.0
## 21963.6529 0.0057 10656 17:08:13 0.0
##
## Finished on: Wed Sep 21 17:08:13 2016
##
## LogLikelihood Converged

```

```

fit2<-asreml(COD~locmo,random=~giv(Haplo2),rcov=~units,ginverse=list(Haplo2=sm2asreml(Ainv)),maxiter=30,data=data)

```

```

## ASReml: Wed Sep 21 17:08:13 2016
##
##      LogLik      S2      DF     wall      cpu
## 16135.9015 0.0175 10656 17:08:13 0.0
## 16437.2711 0.0165 10656 17:08:13 0.0
## 16856.5316 0.0152 10656 17:08:13 0.0
## 17477.2697 0.0135 10656 17:08:13 0.0
## 18353.8773 0.0114 10656 17:08:13 0.0
## 19391.0495 0.0094 10656 17:08:13 0.0
## 20515.1075 0.0076 10656 17:08:13 0.0
## 21273.1353 0.0065 10656 17:08:13 0.0
## 21630.3433 0.0061 10656 17:08:13 0.0
## 21794.7690 0.0059 10656 17:08:13 0.0
## 21868.6555 0.0058 10656 17:08:13 0.0
## 21899.3931 0.0057 10656 17:08:13 0.0
## 21910.1004 0.0057 10656 17:08:13 0.0
## 21912.6370 0.0057 10656 17:08:13 0.0
## 21912.9001 0.0057 10656 17:08:13 0.0
## 21912.9050 0.0057 10656 17:08:13 0.0
## 21912.9050 0.0057 10656 17:08:13 0.0
## 21912.9050 0.0057 10656 17:08:13 0.0
##
## Finished on: Wed Sep 21 17:08:13 2016
##
## LogLikelihood Converged

```

```
AICfit1<-2*32-2*fit1$loglik  
AICfit2<-2*32-2*fit2$loglik
```

```
AICfit1
```

```
## [1] -43863.31
```

```
AICfit2
```

```
## [1] -43761.81
```