

# Quantitative genetics using the sommer package

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The sommer package was developed to provide R users a powerful and reliable multivariate mixed model solver for different genetic and non-genetic analysis in diploid and polyploid organisms. This package allows the user to estimate variance components for a mixed model with the advantage of specifying the variance-covariance structure of the random effects, specify heterogeneous variances, and obtain other parameters such as BLUPs, BLUEs, residuals, fitted values, variances for fixed and random effects, etc. The core algorithms of the package are coded in C++ using the Armadillo library to optimize dense matrix operations common in the direct-inversion algorithms.

The package is focused on problems of the type  $p > n$  related to genomic prediction (hybrid prediction & genomic selection) and GWAS analysis, although any general mixed model can be fitted as well. The package provides kernels to estimate additive (**A.mat**), dominance (**D.mat**), and epistatic (**E.mat**) relationship matrices that have been shown to increase prediction accuracy under certain scenarios or simply to estimate the variance components of such. The package provides flexibility to fit other genetic models such as full and half diallel models as well.

Vignettes aim to provide several examples in how to use the sommer package under different scenarios. We will spend the rest of the space providing examples for:

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## SECTION 1: Introduction

### Backgrounds in linear algebra

The core of the package the `mmer` function which solve the mixed model equations. The functions are an interface to call the NR Direct-Inversion Newton-Raphson or Average Information (Tunnicliffe 1989; Gilmour et al. 1995; Lee et al. 2016). Since version 2.0 sommer can handle multivariate models. Following Maier et al. (2015), the multivariate (and by extension the univariate) mixed model implemented has the form:

$$y_1 = X_1\beta_1 + Z_1u_1 + \epsilon_1 \quad y_2 = X_2\beta_2 + Z_2u_2 + \epsilon_2 \quad \dots \quad y_i = X_i\beta_i + Z_iu_i + \epsilon_i$$

where  $y_i$  is a vector of trait phenotypes,  $\beta_i$  is a vector of fixed effects,  $u_i$  is a vector of random effects for individuals and  $e_i$  are residuals for trait 'i' ( $i = 1, \dots, t$ ). The random effects ( $u_1 \dots u_t$  and  $e_i$ ) are assumed to be normally distributed with mean zero.  $X$  and  $Z$  are incidence matrices for fixed and random effects respectively. The distribution of the multivariate response and the phenotypic variance covariance ( $V$ ) are:

$$Y = X\beta + ZU + \epsilon_i$$

$$Y \sim \text{MVN}(X\beta, V)$$

$$\mathbf{Y} = \begin{bmatrix} y_1 \\ y_2 \\ \dots \\ y_t \end{bmatrix}$$

$$\mathbf{X} = \begin{bmatrix} X_1 & \dots & \dots \\ \vdots & \ddots & \vdots \\ \dots & \dots & X_t \end{bmatrix}$$

$$\mathbf{V} = \begin{bmatrix} Z_1K\sigma_{g_1}^2Z_1' + H\sigma_{\epsilon_1}^2 & \dots & Z_1K\sigma_{g_{1,t}}Z_t' + H\sigma_{\epsilon_{1,t}}^2 \\ \vdots & \ddots & \vdots \\ Z_1K\sigma_{g_{1,t}}Z_t' + H\sigma_{\epsilon_{1,t}}^2 & \dots & Z_tK\sigma_{g_t}^2Z_t' + H\sigma_{\epsilon_t}^2 \end{bmatrix}$$

where  $K$  is the relationship or covariance matrix for the  $k$ th random effect ( $u=1, \dots, k$ ), and  $R=I$  is an identity matrix for the residual term. The terms  $\sigma_{g_i}^2$  and  $\sigma_{\epsilon_i}^2$  denote the genetic (or any of the  $k$ th random terms) and residual variance of trait 'i', respectively and  $\sigma_{g_{ij}}$  and  $\sigma_{\epsilon_{ij}}$  the genetic (or any of the  $k$ th random terms) and residual covariance between traits 'i' and 'j' ( $i=1, \dots, t$ , and  $j=1, \dots, t$ ). The algorithm implemented optimizes the log likelihood:

$$\log L = 1/2 * \ln(|V|) + \ln(X'VX) + Y'PY$$

where  $| |$  is the determinant of a matrix. And the REML estimates are updated using a Newton optimization algorithm of the form:

$$\theta^{k+1} = \theta^k + (H^k)^{-1} * \frac{dL}{d\sigma_i^2} | \theta^k$$

Where,  $\theta$  is the vector of variance components for random effects and covariance components among traits,  $H^{-1}$  is the inverse of the Hessian matrix of second derivatives for the  $k$ th cycle,  $\frac{dL}{d\sigma_i^2}$  is the vector of first derivatives of the likelihood with respect to the variance-covariance components. The Eigen decomposition of the relationship matrix proposed by Lee and Van Der Werf (2016) was included in the Newton-Raphson algorithm to improve time efficiency. Additionally, the popular `vpredict` function to estimate standard errors for linear combinations of variance components (i.e. heritabilities and genetic correlations) was added to the package as well.

Please refer to the canonical papers listed in the Literature section to check how the algorithms work. We have tested widely the methods to make sure they provide the same solution when the likelihood behaves

well but for complex problems they might lead to slightly different answers. If you have any concern please contact me at [cova\\_ruber@live.com.mx](mailto:cova_ruber@live.com.mx).

In the following section we will go in detail over several examples on how to use mixed models in univariate and multivariate case and their use in quantitative genetics.

## SECTION 2: Topics in quantitative genetics

### 1) Marker and non-marker based heritability calculation

The heritability is one of the most popular parameters among the breeding and genetics community because of the insight that provides in the inheritance of the trait. The heritability is usually estimated as narrow sense ( $h^2$ ; only additive variance in the numerator  $\sigma_A^2$ ), and broad sense ( $H^2$ ; all genetic variance in the numerator  $\sigma_G^2$ ).

In a classical breeding experiment with no molecular markers, special designs are performed to estimate and dissect the additive ( $\sigma_A^2$ ) and non-additive (i.e. dominance  $\sigma_D^2$ ) variance along with environmental variability. Designs such as generation analysis, North Carolina designs are used to dissect  $\sigma_A^2$  and  $\sigma_D^2$  to estimate the narrow sense heritability ( $h^2$ ). When no special design is available we can still dissect the genetic variance ( $\sigma_G^2$ ) and estimate the broad sense heritability. In this first example we will show the broad sense estimation which doesn't use covariance structures for the genotypic effect (i.e. genomic or additive relationship matrices). For big models with no covariance structures, sommer's direct inversion is a bad idea to use but we will show anyways how to do it, but keep in mind that for very sparse models we recommend using the lmer function from the lme4 package or any other package using MME-based algorithms (i.e. asreml-R).

The following dataset has 41 potato lines evaluated in 5 locations across 3 years in an RCBD design. We show how to fit the model and extract the variance components to calculate the  $h^2$ .

```
library(sommer)
data(DT_example)
DT <- DT_example
A <- A_example

ans1 <- mmer(Yield~1,
             random= ~ Name + Env + Env:Name + Env:Block,
             rcov= ~ units,
             data=DT, verbose = FALSE)
summary(ans1)$varcomp
```

##		VarComp	VarCompSE	Zratio	Constraint
##	Name.Yield-Yield	3.718279	1.6959834	2.1924029	Positive
##	Env.Yield-Yield	12.008450	12.2771178	0.9781164	Positive
##	Env:Name.Yield-Yield	5.152643	1.4923912	3.4526091	Positive
##	Env:Block.Yield-Yield	0.000000	0.1156675	0.0000000	Positive
##	units.Yield-Yield	4.366189	0.6573086	6.6425245	Positive

```
(n.env <- length(levels(DT$Env)))

## [1] 3

vpredict(ans1, h2 ~ V1 / ( V1 + (V3/n.env) + (V5/(2*n.env)) ) )

## $Estimate
## [1] 0.6032715
## attr(,"gradient")
##          V1 V2          V3 V4          V5
## [1,] 0.06436714 0 -0.03262589 0 -0.01631295
```

```
##
## $SE
## [1] 0.1344582
##
## attr("class")
## [1] "vpredict.mmer"
## attr("row.names")
## [1] "h2"
```

Recently with markers becoming cheaper, thousand of markers can be run in the breeding materials. When markers are available, an special design is not necessary to dissect the additive genetic variance. The availability of the additive, dominance and epistatic relationship matrices allow us to estimate  $\sigma_A^2$ ,  $\sigma_D^2$  and  $\sigma_I^2$ , although given that A, D and E are not orthogonal the interpretation of models that fit more than A and D become cumbersome.

Assume you have a population (even unreplicated) in the field but in addition we have genetic markers. Now we can fit the model and estimate the genomic heritability that explains a portion of the additive genetic variance (with high marker density  $\sigma_A^2 = \sigma_g^2$ )

```
data(DT_cpdata)
DT <- DT_cpdata
GT <- GT_cpdata
MP <- MP_cpdata
DT$idd <-DT$id; DT$ide <-DT$id
### look at the data
A <- A.mat(GT) # additive relationship matrix
D <- D.mat(GT) # dominance relationship matrix
E <- E.mat(GT) # epistatic relationship matrix
ans.ADE <- mmer(color~1,
                 random=~vs(id,Gu=A) + vs(idd,Gu=D),
                 rcov=~units,
                 data=DT,verbose = FALSE)
(summary(ans.ADE)$varcomp)
```

```
##                               VarComp   VarCompSE   Zratio Constraint
## u:id.color-color   0.003662313 0.0012194780 3.003181   Positive
## u:idd.color-color  0.001295013 0.0005269670 2.457485   Positive
## units.color-color  0.002106905 0.0002864668 7.354794   Positive
```

```
vpredict(ans.ADE, h2 ~ (V1) / ( V1+V3) )
```

```
## $Estimate
## [1] 0.6348024
## attr("gradient")
##           V1 V2           V3
## [1,] 63.30106  0 -110.0327
##
## $SE
## [1] 0.08840597
##
## attr("class")
## [1] "vpredict.mmer"
## attr("row.names")
## [1] "h2"
```

```
vpredict(ans.ADE, h2 ~ (V1+V2) / ( V1+V2+V3) )
```

```
## $Estimate
## [1] 0.7017503
## attr("gradient")
##          V1          V2          V3
## [1,] 42.21969 42.21969 -99.33853
##
## $SE
## [1] 0.06057814
##
## attr("class")
## [1] "vpredict.mmer"
## attr("row.names")
## [1] "h2"
```

In the previous example we showed how to estimate the additive ( $\sigma_A^2$ ), dominance ( $\sigma_D^2$ ), and epistatic ( $\sigma_I^2$ ) variance components based on markers and estimate broad ( $H^2$ ) and narrow sense heritability ( $h^2$ ). Notice that we used the `vs()` function which indicates that the random effect inside the parenthesis (i.e. id, idd or ide) has a covariance matrix (A, D, or E), that will be specified in the `Gu` argument of the `vs()` function. Please DO NOT provide the inverse but the original covariance matrix.

## 2) Specifying heterogeneous variances in univariate models

Very often in multi-environment trials, the assumption that genetic variance is the same across locations may be too naive. Because of that, specifying a general genetic component and a location specific genetic variance is the way to go.

We estimate variance components for  $GCA_2$  and  $SCA$  specifying the variance structure.

```
data(DT_cornhybrids)
DT <- DT_cornhybrids
DTi <- DTi_cornhybrids
GT <- GT_cornhybrids
### fit the model
modFD <- mmer(Yield~1,
              random=~ vs(at(Location,c("3","4")),GCA2),
              rcov= ~ vs(ds(Location),units),
              data=DT, verbose = FALSE)
summary(modFD)

## =====
##           Multivariate Linear Mixed Model fit by REML
## ***** sommer 4.1 *****
## =====
##           logLik          AIC          BIC Method Converge
## Value -164.6839 331.3677 335.3592      NR      TRUE
## =====
## Variance-Covariance components:
##           VarComp VarCompSE Zratio Constraint
## 3:GCA2.Yield-Yield    62.48    53.45  1.169   Positive
## 4:GCA2.Yield-Yield    97.99    79.56  1.232   Positive
## 1:units.Yield-Yield   216.82    30.77  7.047   Positive
## 2:units.Yield-Yield   216.82    30.77  7.047   Positive
## 3:units.Yield-Yield   493.05    77.27  6.381   Positive
## 4:units.Yield-Yield   711.98   111.63  6.378   Positive
## =====
```

```
## Fixed effects:
##   Trait      Effect Estimate Std.Error t.value
## 1 Yield (Intercept)    138.1    0.9442   146.3
## =====
## Groups and observations:
##      Yield
## 3:GCA2    20
## 4:GCA2    20
## =====
## Use the '$' sign to access results and parameters
```

In the previous example we showed how the `at()` function is used in the `mmer` solver. By using the `at` function you can specify that i.e. the GCA2 has a different variance in different Locations, in this case locations 3 and 4, but also a main GCA variance. This is considered a CS + DIAG (compound symmetry + diagonal) model.

In addition, other functions can be added on top to fit models with covariance structures, i.e. the `Gu` argument from the `vs()` function to indicate a covariance matrix (A, pedigree or genomic relationship matrix)

```
data(DT_cornhybrids)
DT <- DT_cornhybrids
DTi <- DTi_cornhybrids
GT <- GT_cornhybrids
GT[1:4,1:4]

##           A258      A634      A641      A680
## A258  2.23285528 -0.3504778 -0.04756856 -0.32239362
## A634 -0.35047780  1.4529169  0.45203869 -0.02293680
## A641 -0.04756856  0.4520387  1.96940221 -0.09896791
## A680 -0.32239362 -0.0229368 -0.09896791  1.65221984

### fit the model
modFD <- mmer(Yield~1,
              random=~ vs(at(Location,c("3","4")),GCA2,Gu=GT),
              rcov= ~ vs(ds(Location),units),
              data=DT, verbose = FALSE)
summary(modFD)
```

```
## =====
##           Multivariate Linear Mixed Model fit by REML
## ***** sommer 4.1 *****
## =====
##           logLik      AIC      BIC Method Converge
## Value -165.2286 332.4571 336.4486      NR      TRUE
## =====
## Variance-Covariance components:
##           VarComp VarCompSE Zratio Constraint
## 3:GCA2.Yield-Yield    26.64    26.16 1.0185    Positive
## 4:GCA2.Yield-Yield    37.51    37.78 0.9927    Positive
## 1:units.Yield-Yield   216.77    30.75 7.0489    Positive
## 2:units.Yield-Yield   216.77    30.75 7.0489    Positive
## 3:units.Yield-Yield   503.62    77.87 6.4673    Positive
## 4:units.Yield-Yield   738.86   114.17 6.4715    Positive
## =====
## Fixed effects:
##   Trait      Effect Estimate Std.Error t.value
## 1 Yield (Intercept)    138.1    0.9147   151
```

```
## =====
## Groups and observations:
##      Yield
## 3:GCA2    40
## 4:GCA2    40
## =====
## Use the '$' sign to access results and parameters
```

### 3) Using the vpredict calculator

Sometimes the user needs to calculate ratios or functions of specific variance-covariance components and obtain the standard error for such parameters. Examples of these are the genetic correlations, heritabilities, etc. Using the CPdata we will show how to estimate the heritability and the standard error using the vpredict function that uses the delta method to come up with these parameters. This can be extended for any linear combination of the variance components.

```
data(DT_cpdata)
DT <- DT_cpdata
GT <- GT_cpdata
MP <- MP_cpdata
### look at the data
A <- A.mat(GT) # additive relationship matrix
ans <- mmer(color~1,
             random=~vs(id,Gu=A),
             rcov=~units,
             data=DT, verbose = FALSE)
(summary(ans.ADE)$varcomp)
```

#### 3.1) Standar error for heritability

```
##              VarComp   VarCompSE   Zratio Constraint
## u:id.color-color 0.003662313 0.0012194780 3.003181   Positive
## u:idd.color-color 0.001295013 0.0005269670 2.457485   Positive
## units.color-color 0.002106905 0.0002864668 7.354794   Positive
```

```
vpredict(ans, h2 ~ (V1) / ( V1+V2) )
```

```
## $Estimate
## [1] 0.6512157
## attr(,"gradient")
##      V1      V2
## [1,] 44.34212 -82.79123
##
## $SE
## [1] 0.06107574
##
## attr(,"class")
## [1] "vpredict.mmer"
## attr(,"row.names")
## [1] "h2"
```

The same can be used for multivariate models. Please check the documentation of the vpredict function to see more examples.

```

data(DT_btdata)
DT <- DT_btdata
mix3 <- mmer(cbind(tarsus, back) ~ sex,
             random = ~ vs(dam, Gtc=unsm(2)) + vs(fosternest, Gtc=diag(2)),
             rcov=~vs(units, Gtc=unsm(2)),
             data = DT, verbose = FALSE)
summary(mix3)

```

### 3.2) Standar error for genetic correlation

```

## =====
##           Multivariate Linear Mixed Model fit by REML
## ***** sommer 4.1 *****
## =====
##           logLik      AIC      BIC Method Converge
## Value -651.5865 1315.173 1347.646      NR      TRUE
## =====
## Variance-Covariance components:
##           VarComp VarCompSE Zratio Constraint
## u:dam.tarsus-tarsus      0.21847   0.04743  4.606   Positive
## u:dam.tarsus-back      -0.03618   0.02644 -1.369   Unconstr
## u:dam.back-back        0.05973   0.03073  1.944   Positive
## u:fosternest.tarsus-tarsus 0.07304   0.02891  2.526   Positive
## u:fosternest.back-back   0.13158   0.03890  3.383   Positive
## u:units.tarsus-tarsus    0.56699   0.03082 18.397   Positive
## u:units.tarsus-back     -0.03004   0.02581 -1.164   Unconstr
## u:units.back-back       0.80494   0.04361 18.459   Positive
## =====
## Fixed effects:
##      Trait      Effect Estimate Std.Error t.value
## 1 tarsus (Intercept) -0.40631   0.06720 -6.0466
## 2 back (Intercept) -0.01459   0.06489 -0.2248
## 3 tarsus sexMale 0.76905   0.05711 13.4670
## 4 back sexMale 0.01057   0.06704  0.1577
## 5 tarsus sexUNK 0.21231   0.12665  1.6763
## 6 back sexUNK 0.09976   0.14794  0.6743
## =====
## Groups and observations:
##           tarsus back
## u:dam      106 106
## u:fosternest 104 104
## =====
## Use the '$' sign to access results and parameters
#### calculate the genetic correlation
vpredict(mix3, gen.cor ~ V2 / sqrt(V1*V3))

## $Estimate
## [1] -0.3167271
## attr(,"gradient")
##           V1      V2      V3 V4 V5 V6 V7 V8
## [1,] 0.7248694 8.753917 2.65128 0 0 0 0 0
##
## $SE

```



```
## [1] 0.2228247
##
## attr(,"class")
## [1] "vpredict.mmer"
## attr(,"row.names")
## [1] "gen.cor"
```

#### 4) Half and full diallel designs (use of the overlay)

When breeders are looking for the best single cross combinations, diallel designs have been by far the most used design in crops like maize. There are 4 types of diallel designs depending if reciprocal and self cross (omission of parents) are performed (full diallel with parents  $n^2$ ; full diallel without parents  $n(n-1)$ ; half diallel with parents  $1/2 * n(n+1)$ ; half diallel without parents  $1/2 * n(n-1)$ ). In this example we will show a full diallel design (reciprocal crosses are performed) and half diallel designs (only one of the directions is performed).

In the first data set we show a full diallel among 40 lines from 2 heterotic groups, 20 in each. Therefore 400 possible hybrids are possible. We have phenotypic data for 100 of them across 4 locations. We use the data available to fit a model of the form:

$$y = X\beta + Zu_1 + Zu_2 + Zu_S + \epsilon$$

We estimate variance components for  $GCA_1$ ,  $GCA_2$  and  $SCA$  and use them to estimate heritability. Additionally BLUPs for GCA and SCA effects can be used to predict crosses.

```
data(DT_cornhybrids)
DT <- DT_cornhybrids
DTi <- DTi_cornhybrids
GT <- GT_cornhybrids

modFD <- mmer(Yield-Location,
              random=~GCA1+GCA2+SCA,
              rcov=~units,
              data=DT, verbose = FALSE)
(suma <- summary(modFD)$varcomp)
```

##		VarComp	VarCompSE	Zratio	Constraint
##	GCA1.Yield-Yield	0.000000	16.50337	0.0000000	Positive
##	GCA2.Yield-Yield	7.412226	18.94200	0.3913116	Positive
##	SCA.Yield-Yield	187.560303	41.59428	4.5092817	Positive
##	units.Yield-Yield	221.142463	18.14716	12.1860656	Positive

```
Vgca <- sum(suma[1:2,1])
Vsca <- suma[3,1]
Ve <- suma[4,1]
Va = 4*Vgca
Vd = 4*Vsca
Vg <- Va + Vd
(H2 <- Vg / (Vg + (Ve)) )
```

```
## [1] 0.7790856
```

```
(h2 <- Va / (Vg + (Ve)) )
```

```
## [1] 0.02961832
```

Don't worry too much about the small  $h^2$  value, the data was simulated to be mainly dominance variance, therefore the  $V_a$  was simulated extremely small leading to such value of narrow sense  $h^2$ .

In this second data set we show a small half diallel with 7 parents crossed in one direction.  $n(n-1)/2$  crosses are possible  $7(6)/2 = 21$  unique crosses. Parents appear as males or females indistinctly. Each with two replications in a CRD. For a half diallel design a single GCA variance component for both males and females can be estimated and an SCA as well ( $\sigma_G^2 CA$  and  $\sigma_S^2 CA$  respectively), and BLUPs for GCA and SCA of the parents can be extracted. We would show first how to use it with the `mmer` function using the `overlay()` function. The specific model here is:

$$y = X\beta + Zu_g + Zu_s + \epsilon$$

```
data("DT_halfdiallel")
DT <- DT_halfdiallel
head(DT)
```

```
##   rep geno male female    sugar
## 1    1  12    1      2 13.950509
## 2    2  12    1      2  9.756918
## 3    1  13    1      3 13.906355
## 4    2  13    1      3  9.119455
## 5    1  14    1      4  5.174483
## 6    2  14    1      4  8.452221
```

```
DT$femalef <- as.factor(DT$female)
DT$malef <- as.factor(DT$male)
DT$genof <- as.factor(DT$geno)
#### model using overlay
modh <- mmer(sugar~1,
             random=~vs(overlay(femalef,malef))
             + genof,
             data=DT, verbose = FALSE)
summary(modh)$varcomp
```

```
##                               VarComp VarCompSE   Zratio Constraint
## u:femalef.sugar-sugar  5.507899 3.5741151 1.541052   Positive
## genof.sugar-sugar      1.815784 1.3629575 1.332238   Positive
## units.sugar-sugar      3.117538 0.9626094 3.238632   Positive
```

Notice how the `overlay()` argument makes the overlap of incidence matrices possible making sure that male and female are joint into a single random effect.

## 5) Genomic selection: predicting mendelian sampling

In this section we will use wheat data from CIMMYT to show how is genomic selection performed. This is the case of prediction of specific individuals within a population. It basically uses a similar model of the form:

$$y = X\beta + Zu + \epsilon$$

and takes advantage of the variance covariance matrix for the genotype effect known as the additive relationship matrix ( $A$ ) and calculated using the `A.mat` function to establish connections among all individuals and predict the BLUPs for individuals that were not measured. The prediction accuracy depends on several factors such as the heritability ( $h^2$ ), training population used (TP), size of TP, etc.

```
data(DT_wheat)
DT <- DT_wheat
GT <- GT_wheat
colnames(DT) <- paste0("X",1:ncol(DT))
```

```
DT <- as.data.frame(DT);DT$id <- as.factor(rownames(DT))
# select environment 1
rownames(GT) <- rownames(DT)
K <- A.mat(GT) # additive relationship matrix
colnames(K) <- rownames(K) <- rownames(DT)
# GBLUP pedigree-based approach
set.seed(12345)
y.trn <- DT
vv <- sample(rownames(DT),round(nrow(DT)/5))
y.trn[vv,"X1"] <- NA
head(y.trn)
```

```
##           X1           X2           X3           X4    id
## 775    1.6716295 -1.72746986 -1.89028479  0.0509159  775
## 2166 -0.2527028  0.40952243  0.30938553 -1.7387588 2166
## 2167           NA -0.64862633 -0.79955921 -1.0535691 2167
## 2465  0.7854395  0.09394919  0.57046773  0.5517574 2465
## 3881  0.9983176 -0.28248062  1.61868192 -0.1142848 3881
## 3889  2.3360969  0.62647587  0.07353311  0.7195856 3889
```

```
## GBLUP
ans <- mmer(X1~1,
            random=~vs(id,Gu=K),
            rcov=~units,
            data=y.trn, verbose = FALSE) # kinship based
ans$U$`u:id`$X1 <- as.data.frame(ans$U$`u:id`$X1)
rownames(ans$U$`u:id`$X1) <- gsub("id","",rownames(ans$U$`u:id`$X1))
cor(ans$U$`u:id`$X1[vv,],DT[vv,"X1"], use="complete")
```

```
## [1] 0.5737594
```

```
## rrBLUP
ans2 <- mmer(X1~1,
             random=~vs(list(GT), buildGu = FALSE),
             rcov=~units, getPEV = FALSE,
             data=y.trn, verbose = FALSE) # kinship based

u <- GT %*% as.matrix(ans2$U$`u:GT`$X1) # BLUPs for individuals
rownames(u) <- rownames(GT)
cor(u[vv,],DT[vv,"X1"]) # same correlation
```

```
## [1] 0.5737681
```

```
# the same can be applied in multi-response models in GBLUP or rrBLUP
```

Please notice that when specifying the marker matrix as a random effect we used the argument ‘buildGu=FALSE’ to inform the ‘mmer’ function that a covariance matrix for the levels of the random effect shouldn’t be built. Imagine a model with 100,000 markers, that would imply a relationship matrix of 100,000 x 100,000. If that matrix is a diagonal it would only compromise the speed and memory of the function. By setting ‘buildGu=FALSE’ the mmer solver will avoid the matrix multiplications using that huge diagonal matrix. If you want to specify a relationship matrix for the marker matrix then you cannot use that ‘buildGu’ argument.

## 6) Indirect genetic effects

General variance structures can be used to fit indirect genetic effects. Here, we use an example dataset to show how we can fit the variance and covariance components between two or more different random effects.

We first fit a direct genetic effects model:

```
data(DT_ige)
DT <- DT_ige
Af <- A_ige
An <- A_ige

## Direct genetic effects model
modDGE <- mmer(trait ~ block,
               random = ~ focal,
               rcov = ~ units,
               data = DT, verbose=FALSE)
summary(modDGE)$varcomp
```

	VarComp	VarCompSE	Zratio	Constraint
focal.trait-trait	19894.45	3118.3474	6.379806	Positive
units.trait-trait	10134.22	477.9483	21.203584	Positive

We now fit the indirect genetic effects model without covariance between DGE and IGE:

```
data(DT_ige)
DT <- DT_ige
A <- A_ige

## Indirect genetic effects model
modDGE <- mmer(trait ~ block,
               random = ~ focal + neighbour,
               rcov = ~ units,
               data = DT, verbose=FALSE)
summary(modDGE)$varcomp
```

	VarComp	VarCompSE	Zratio	Constraint
focal.trait-trait	20550.511	3148.6833	6.526700	Positive
neighbour.trait-trait	2926.704	607.4191	4.818261	Positive
units.trait-trait	7301.084	363.8236	20.067649	Positive

We now fit the indirect genetic effects model with covariance between DGE and IGE for which we will use the `gvs()` function:

```
### Indirect genetic effects model
modIGE <- mmer(trait ~ block,
               random = ~ gvs(focal, neighbour),
               rcov = ~ units,
               data = DT, verbose=FALSE)
summary(modIGE)$varcomp
```

	VarComp	VarCompSE	Zratio	Constraint
focal:focal.trait-trait	21014.516	3212.3586	6.541772	Positive
focal:neighbour.trait-trait	-7469.401	1246.1105	-5.994173	Unconstr
neighbour:neighbour.trait-trait	2964.707	576.9991	5.138149	Positive
units.trait-trait	7297.715	357.8869	20.391120	Positive

On top of that we can a relationship matrix for the two random effects that are being forced to covary

```
### Indirect genetic effects model
modIGE <- mmer(trait ~ block,
               random = ~ gvs(focal, neighbour, Gu=list(Af,An)),
               rcov = ~ units,
               data = DT, verbose=FALSE)
summary(modIGE)$varcomp
```

##	VarComp	VarCompSE	Zratio	Constraint
## focal:focal.trait-trait	27806.797	4162.7014	6.679988	Positive
## focal:neighbour.trait-trait	-9901.351	1532.8048	-6.459630	Unconstr
## neighbour:neighbour.trait-trait	3638.534	611.4065	5.951089	Positive
## units.trait-trait	7409.998	359.9827	20.584320	Positive

## 7) Genomic selection: single cross prediction

When doing prediction of single cross performance the phenotype can be dissected in three main components, the general combining abilities (GCA) and specific combining abilities (SCA). This can be expressed with the same model analyzed in the diallel experiment mentioned before:

$$y = X\beta + Zu_1 + Zu_2 + Zu_s + \epsilon$$

with:

$$u_1 \sim N(0, K_1\sigma_u^2 1)$$

$$u_2 \sim N(0, K_2\sigma_u^2 2)$$

$$u_s \sim N(0, K_3\sigma_u^2 s)$$

And we can specify the K matrices. The main difference between this model and the full and half diallel designs is the fact that this model will include variance covariance structures in each of the three random effects (GCA1, GCA2 and SCA) to be able to predict the crosses that have not occurred yet. We will use the data published by Technow et al. (2015) to show how to do prediction of single crosses.

```
data(DT_technow)
DT <- DT_technow
Md <- Md_technow
Mf <- Mf_technow
Ad <- Ad_technow
Af <- Af_technow
# RUN THE PREDICTION MODEL
y.trn <- DT
vv1 <- which(!is.na(DT$GY))
vv2 <- sample(vv1, 100)
y.trn[vv2,"GY"] <- NA
anss2 <- mmer(GY~1,
               random=~vs(dent,Gu=Ad) + vs(flint,Gu=Af),
               rcov=~units,
               data=y.trn, verbose = FALSE)
summary(anss2)$varcomp
```

##	VarComp	VarCompSE	Zratio	Constraint
## u:dent.GY-GY	16.06423	2.5737578	6.241548	Positive
## u:flint.GY-GY	11.42070	2.1591718	5.289390	Positive
## units.GY-GY	16.81801	0.7689509	21.871368	Positive

```

zu1 <- model.matrix(~dent-1,y.trn) %*% anss2$U$`u:dent`$GY
zu2 <- model.matrix(~flint-1,y.trn) %*% anss2$U$`u:flint`$GY
u <- zu1+zu2+anss2$Beta[1,"Estimate"]
cor(u[vv2,], DT$GY[vv2])

```

```
## [1] 0.7756383
```

In the previous model we only used the GCA effects (GCA1 and GCA2) for practicality, although it's been shown that the SCA effect doesn't actually help that much in increasing prediction accuracy and increase a lot the computation intensity required since the variance covariance matrix for SCA is the kronecker product of the variance covariance matrices for the GCA effects, resulting in a 10578x10578 matrix that increases in a very intensive manner the computation required.

A model without covariance structures would show that the SCA variance component is insignificant compared to the GCA effects. This is why including the third random effect doesn't increase the prediction accuracy.

## 8) Spatial modeling: using the 2-dimensional spline

We will use the CPdata to show the use of 2-dimensional splines for accommodating spatial effects in field experiments. In early generation variety trials the availability of seed is low, which makes the use of unreplicated design a necessity more than anything else. Experimental designs such as augmented designs and partially-replicated (p-rep) designs become every day more common these days.

In order to do a good job modeling the spatial trends happening in the field special covariance structures have been proposed to accommodate such spatial trends (i.e. autoregressive residuals; ar1). Unfortunately, some of these covariance structures make the modeling rather unstable. More recently other research groups have proposed the use of 2-dimensional splines to overcome such issues and have a more robust modeling of the spatial terms (Lee et al. 2013; Rodríguez-Álvarez et al. 2018).

In this example we assume an unreplicated population where row and range information is available which allows us to fit a 2 dimensional spline model.

```

data(DT_cpdata)
DT <- DT_cpdata
GT <- GT_cpdata
MP <- MP_cpdata
### mimic two fields
A <- A.mat(GT)
mix <- mmer(Yield~1,
            random=~vs(id, Gu=A) +
              vs(Rowf) +
              vs(Colf) +
              vs(spl2D(Row,Col)),
            rcov=~vs(units),
            data=DT, verbose = FALSE)
summary(mix)

```

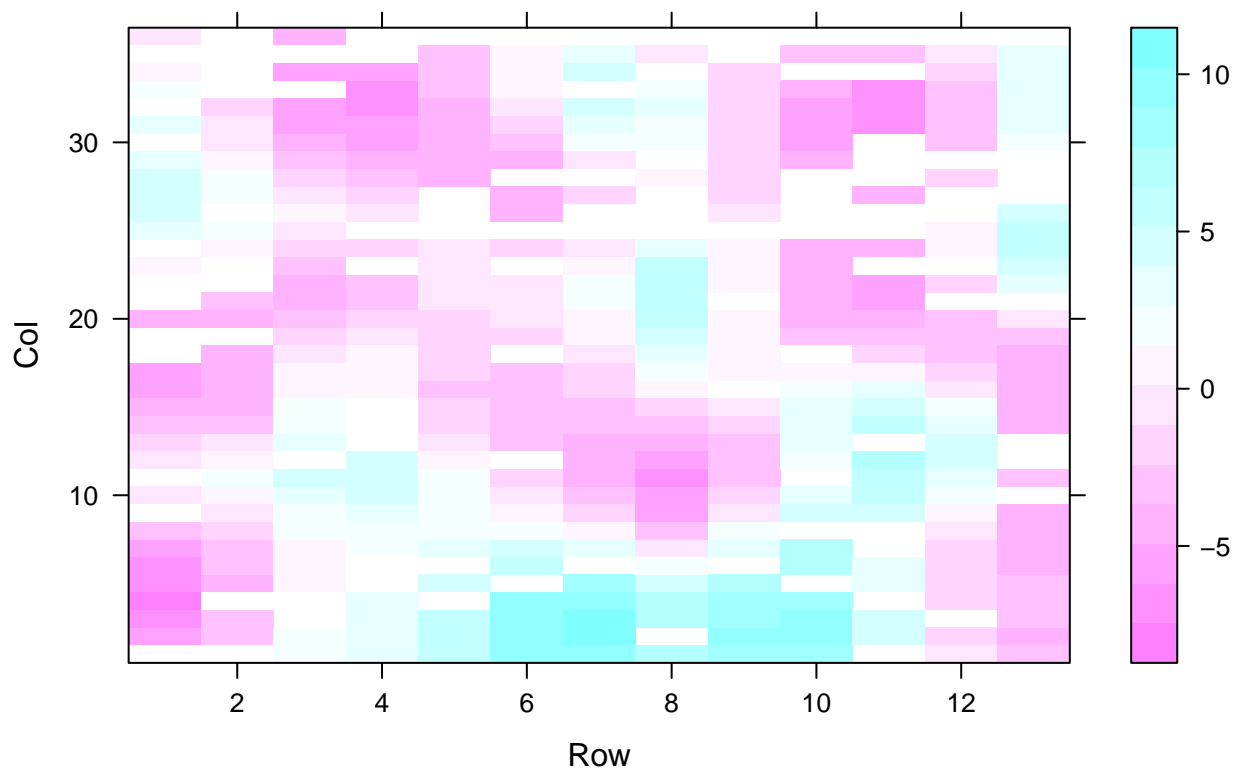
```

## =====
##           Multivariate Linear Mixed Model fit by REML
## ***** sommer 4.1 *****
## =====
##           logLik      AIC      BIC Method Converge
## Value -151.2011 304.4021 308.2938      NR      TRUE
## =====
## Variance-Covariance components:
##           VarComp VarCompSE Zratio Constraint

```

```
## u:id.Yield-Yield      783.4      319.3 2.4536   Positive
## u:Rowf.Yield-Yield    814.7      390.5 2.0863   Positive
## u:Colf.Yield-Yield    182.2      129.7 1.4053   Positive
## u:Row.Yield-Yield     513.6      694.7 0.7393   Positive
## u:units.Yield-Yield   2922.6      294.1 9.9368   Positive
## =====
## Fixed effects:
##   Trait      Effect Estimate Std.Error t.value
## 1 Yield (Intercept)    132.1      8.791   15.03
## =====
## Groups and observations:
##      Yield
## u:id      363
## u:Rowf     13
## u:Colf     36
## u:Row     168
## =====
## Use the '$' sign to access results and parameters
```

```
# make a plot to observe the spatial effects found by the spl2D()
W <- with(DT,spl2D(Row,Col)) # 2D spline incidence matrix
DT$spatial <- W%*%mix$U$`u:Row`$Yield # 2D spline BLUPs
lattice::levelplot(spatial~Row*Col, data=DT) # plot the spatial effect by row and column
```



Notice that the job is done by the `spl2D()` function that takes the Row and Col information to fit a spatial kernel.

## 9) Multivariate genetic models and genetic correlations

Sometimes is important to estimate genetic variance-covariance among traits, multi-reponse models are very useful for such task. Let see an example with 3 traits (color, Yield, and Firmness) and a single random effect (genotype; id) although multiple effects can be modeled as well. We need to use a variance covariance structure for the random effect to be able to obtain the genetic covariance among traits.

```
data(DT_cpdata)
DT <- DT_cpdata
GT <- GT_cpdata
MP <- MP_cpdata
A <- A.mat(GT)
ans.m <- mmer(cbind(Yield,color)~1,
              random=~ vs(id, Gu=A, Gtc=unsm(2))
              + vs(Rowf,Gtc=diag(2))
              + vs(Colf,Gtc=diag(2)),
              rcov=~ vs(units, Gtc=unsm(2)),
              data=DT, verbose = FALSE)
```

Now you can extract the BLUPs using the 'randef' function or simple accesing with the '\$' sign and pick 'u.hat'. Also, genetic correlations and heritabilities can be calculated easily.

```
cov2cor(ans.m$sigma$`u:id`)
```

```
##           Yield      color
## Yield 1.0000000 0.1234441
## color 0.1234441 1.0000000
```

## SECTION 3: Special topics in Quantitative genetics

### 1) Partitioned model

The partitioned model was popularized by () to show that marker effects can be obtained fitting a GBLUP model to reduce the computational burden and then recover them by creating some special matrices MM' for GBLUP and M'(M'M)- to recover marker effects. Here we show a very easy example using the DT\_cpdata:

```
library(sommer)
data("DT_cpdata")
DT <- DT_cpdata
M <- GT_cpdata

#####
# MARKER MODEL
#####
mix.marker <- mmer(color~1,
                  random=~Rowf+vs(M),
                  rcov=~units,data=DT,
                  verbose = FALSE)

me.marker <- mix.marker$U$`u:M`$color

#####
# PARTITIONED GBLUP MODEL
#####
```



```

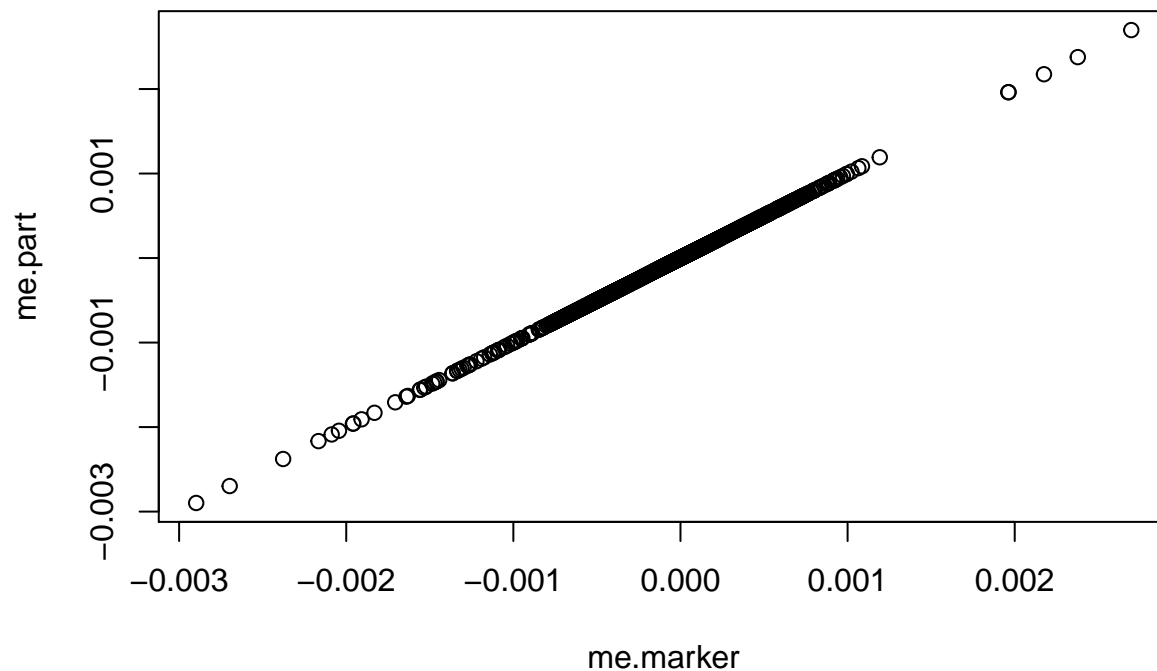
MMT<-M%*%t(M) ## additive relationship matrix
MMTinv<-solve(MMT) ## inverse
MTMMTinv<-t(M)%*%MMTinv # M' %*% (M'M)-

mix.part <- mmer(color~1,
                 random=~Rowf+vs(id, Gu=MMT),
                 rcov=~units,data=DT,
                 verbose = FALSE)

#convert BLUPs to marker effects me=M'(M'M)- u
me.part<-MTMMTinv%*%matrix(mix.part$U$`u:id`$color,ncol=1)

# compare marker effects between both models
plot(me.marker,me.part)

```



As can be seen this two models are equivalent with the exception that the partitioned model is more computationally efficient.

## 2) UDU' decomposition

Lee and Van der Warf (2015) proposed a decomposition of the relationship matrix  $A=UDU'$  together with a transformation of the response and fixed effects  $Uy = Ux + UZ + e$ , to fit a model where the phenotypic variance matrix  $V$  is a diagonal because the relationship matrix is the diagonal matrix  $D$  from the decomposition that can be inverted easily and make multitrait models more feasible.

```

data("DT_wheat")
rownames(GT_wheat) <- rownames(DT_wheat)
G <- A.mat(GT_wheat)
Y <- data.frame(DT_wheat)

# make the decomposition
UD<-eigen(G) # get the decomposition: G = UDU'

```

```

U<-UD$vector
D<-diag(UD$values)# This will be our new 'relationship-matrix'
rownames(D) <- colnames(D) <- rownames(G)
X<-model.matrix(~1, data=Y) # here: only one fixed effect (intercept)
UX<-t(U)%*%X # premultiply X and y by U'
UY <- t(U) %*% as.matrix(Y) # multivariate

# dataset for decomposed model
DTd<-data.frame(id = rownames(G) ,UY, UX =UX[,1])
DTd$id<-as.character(DTd$id)

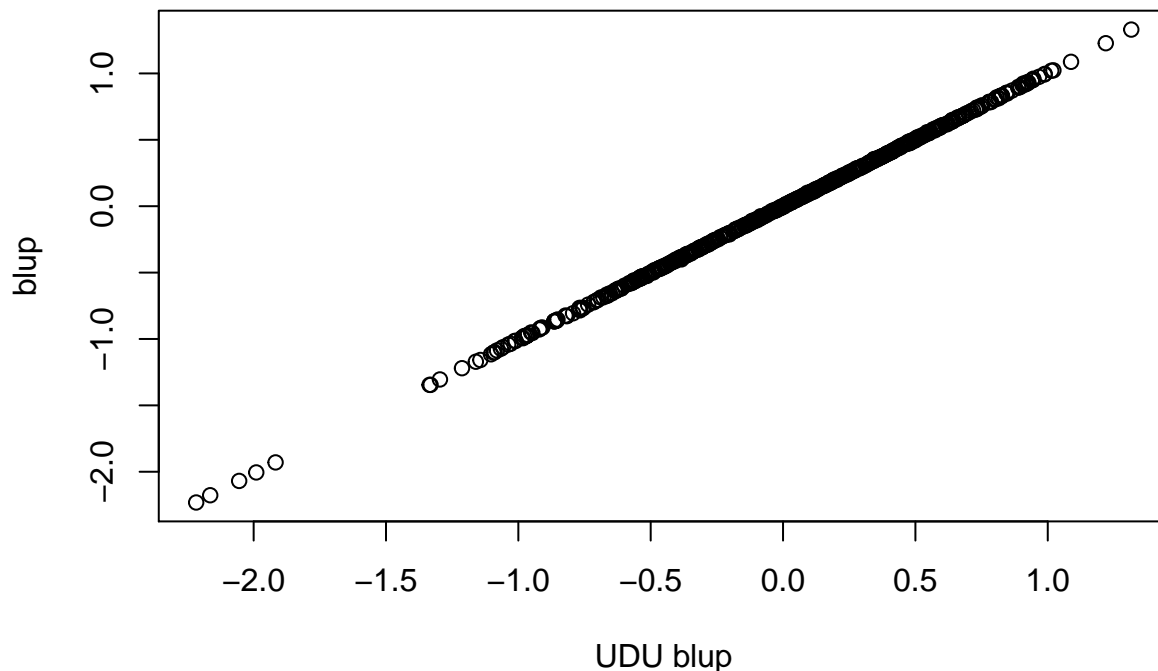
modeld <- mmer(cbind(X1,X2) ~ UX - 1,
               random = ~vs(id,Gu=D),
               rcov = ~vs(units),
               data=DTd, verbose = FALSE)

# dataset for normal model
DTn<-data.frame(id = rownames(G) , DT_wheat)
DTn$id<-as.character(DTn$id)

modeln <- mmer(cbind(X1,X2) ~ 1,
               random = ~vs(id,Gu=G),
               rcov = ~vs(units),
               data=DTn, verbose = FALSE)

## compare regular and transformed blups
plot(x=(solve(t(U))%*%modeld$U$`u:id`$X2[colnames(D)]),
     y=modeln$U$`u:id`$X2[colnames(D)], xlab="UDU blup",
     ylab="blup")

```



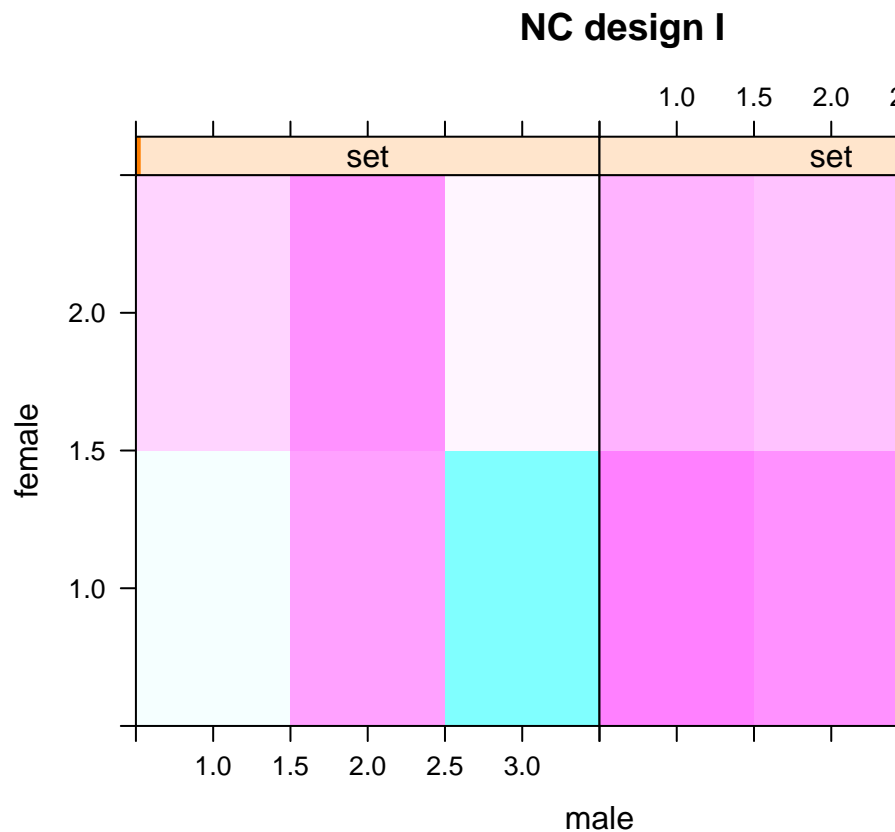
As can be seen the two models are equivalent. Despite that sommer doesn't take a great advantage of this trick because it was built for dense matrices using the Armadillo library other software may be better using

this trick.

### 3) Mating designs

Estimating variance components has been a topic of interest for the breeding community for a long time. Here we show how to calculate additive and dominance variance using the North Carolina Design I (Nested design) and North Carolina Design II (Factorial design) using the classical Expected Mean Squares method and the REML methods from sommer and how these two are equivalent.

```
data(DT_expdesigns)
DT <- DT_expdesigns$car1
DT <- aggregate(yield~set+male+female+rep, data=DT, FUN = mean)
DT$setf <- as.factor(DT$set)
DT$repf <- as.factor(DT$rep)
DT$malef <- as.factor(DT$male)
DT$femalef <- as.factor(DT$female)
levelplot(yield~male*female|set, data=DT, main="NC design I")
```



North Carolina Design I (Nested design)

```
#####
## Expected Mean Square method
#####
mix1 <- lm(yield~ setf + setf:repf + femalef:malef:setf + malef:setf, data=DT)
MS <- anova(mix1); MS

## Analysis of Variance Table
##
```

```
## Response: yield
##
##      Df Sum Sq Mean Sq F value    Pr(>F)
## setf      1 0.1780 0.17796   1.6646 0.226012
## setf:repf    2 0.9965 0.49824   4.6605 0.037141 *
## setf:malef   4 7.3904 1.84759  17.2822 0.000173 ***
## setf:femalef:malef 6 1.6083 0.26806   2.5074 0.095575 .
## Residuals    10 1.0691 0.10691
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ms1 <- MS["setf:malef", "Mean Sq"]
ms2 <- MS["setf:femalef:malef", "Mean Sq"]
mse <- MS["Residuals", "Mean Sq"]
nrep=2
nfem=2
Vfm <- (ms2-mse)/nrep
Vm <- (ms1-mse)/(nrep*nfem)

## Calculate Va and Vd
Va=4*Vm # assuming no inbreeding (4/(1+F))
Vd=4*(Vfm-Vm) # assuming no inbreeding (4/(1+F)^2)
Vg=c(Va,Vd); names(Vg) <- c("Va", "Vd"); Vg
```

```
##      Va      Vd
## 1.579537 -1.257241
```

```
#####
## REML method
#####
mix2 <- mmer(yield~ setf + setf:repf,
             random=~femalef:malef:setf + malef:setf,
             data=DT, verbose = FALSE)
vc <- summary(mix2)$varcomp; vc
```

```
##
##      VarComp  VarCompSE  Zratio Constraint
## femalef:malef:setf.yield-yield 0.08056338 0.08096526 0.9950364    Positive
## malef:setf.yield-yield         0.39480593 0.32832346 1.2024908    Positive
## units.yield-yield              0.10691762 0.04785610 2.2341480    Positive
```

```
Vfm <- vc[1, "VarComp"]
Vm <- vc[2, "VarComp"]
```

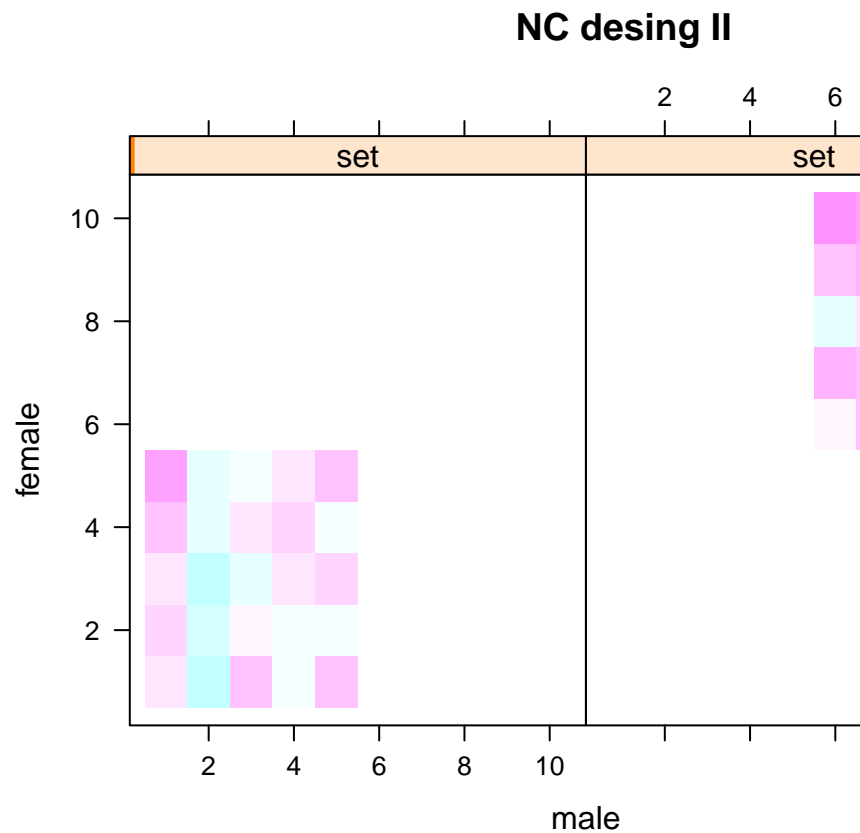
```
## Calculate Va and Vd
Va=4*Vm # assuming no inbreeding (4/(1+F))
Vd=4*(Vfm-Vm) # assuming no inbreeding (4/(1+F)^2)
Vg=c(Va,Vd); names(Vg) <- c("Va", "Vd"); Vg
```

```
##      Va      Vd
## 1.579224 -1.256970
```

As can be seen the REML method is easier than manipulating the MS and we arrive to the same results.

```
DT <- DT_expdesigns$car2
DT <- aggregate(yield~set+male+female+rep, data=DT, FUN = mean)
DT$setf <- as.factor(DT$set)
```

```
DT$repf <- as.factor(DT$rep)
DT$malef <- as.factor(DT$male)
DT$femalef <- as.factor(DT$female)
levelplot(yield~male*female|set, data=DT, main="NC desing II")
```



North Carolina Design II (Factorial design)

```
head(DT)
```

```
##   set male female rep   yield setf repf malef femalef
## 1   1     1       1   1 831.03   1   1     1         1
## 2   1     2       1   1 1046.55  1   1     2         1
## 3   1     3       1   1 853.33   1   1     3         1
## 4   1     4       1   1 940.00   1   1     4         1
## 5   1     5       1   1 802.00   1   1     5         1
## 6   1     1       2   1 625.93   1   1     1         2
```

```
N=with(DT,table(female, male, set))
nmale=length(which(N[,1,] > 0))
nfemale=length(which(N[,1,1] > 0))
nrep=table(N[,1])
nrep=as.numeric(names(nrep[which(names(nrep) !=0)]))

#####
## Expected Mean Square method
#####

mix1 <- lm(yield~ setf + setf:repf +
           femalef:malef:setf + malef:setf + femalef:setf, data=DT)
MS <- anova(mix1); MS
```

```
## Analysis of Variance Table
##
## Response: yield
##              Df Sum Sq Mean Sq F value    Pr(>F)
## setf           1  847836   847836 45.6296 1.097e-09 ***
## setf:repf       4  144345    36086  1.9421  0.109652
## setf:malef      8  861053   107632  5.7926 5.032e-06 ***
## setf:femalef    8  527023    65878  3.5455  0.001227 **
## setf:femalef:malef 32  807267    25227  1.3577  0.129527
## Residuals      96 1783762    18581
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ms1 <- MS["setf:malef", "Mean Sq"]
ms2 <- MS["setf:femalef", "Mean Sq"]
ms3 <- MS["setf:femalef:malef", "Mean Sq"]
mse <- MS["Residuals", "Mean Sq"]
nrep=length(unique(DT$rep))
nfem=length(unique(DT$female))
nmale=length(unique(DT$male))
Vfm <- (ms3-mse)/nrep;
Vf <- (ms2-ms3)/(nrep*nmale);
Vm <- (ms1-ms3)/(nrep*nfemale);

Va=4*Vm; # assuming no inbreeding (4/(1+F))
Va=4*Vf; # assuming no inbreeding (4/(1+F))
Vd=4*(Vfm); # assuming no inbreeding (4/(1+F)^2)
Vg=c(Va,Vd); names(Vg) <- c("Va","Vd"); Vg
```

```
##          Va          Vd
## 10840.192  8861.659
```

```
#####
## REML method
#####
```

```
mix2 <- mmer(yield~ setf + setf:repf ,
             random=~femalef:malef:setf + malef:setf + femalef:setf,
             data=DT, verbose = FALSE)
vc <- summary(mix2)$varcomp; vc
```

```
##              VarComp VarCompSE    Zratio Constraint
## femalef:malef:setf.yield-yield 2215.618 2284.794 0.9697231    Positive
## malef:setf.yield-yield        5493.338 3610.989 1.5212836    Positive
## femalef:setf.yield-yield      2710.176 2236.621 1.2117280    Positive
## units.yield-yield            18580.739 2681.742 6.9286068    Positive
```

```
Vfm <- vc[1,"VarComp"]
Vm <- vc[2,"VarComp"]
Vf <- vc[3,"VarComp"]
```

```
Va=4*Vm; # assuming no inbreeding (4/(1+F))
Va=4*Vf; # assuming no inbreeding (4/(1+F))
Vd=4*(Vfm); # assuming no inbreeding (4/(1+F)^2)
Vg=c(Va,Vd); names(Vg) <- c("Va","Vd"); Vg
```

```
##          Va          Vd
## 10840.704  8862.471
```

As can be seen the REML method is easier than manipulating the MS and we arrive to the same results.

#### 4) Dominance variance

The estimation of non-additive variance has been proposed to be a challenge since the additive and dominance relationship matrices are not orthogonal. In recent literature it has been proposed that the best practice to fit the dominance component is to fit the additive component first and then fix the value of that variance c

```
data(DT_cpdata)
DT <- DT_cpdata
GT <- GT_cpdata
MP <- MP_cpdata
#### create the variance-covariance matrix
A <- A.mat(GT) # additive relationship matrix
#### look at the data and fit the model
mix1 <- mmer(Yield~1,
             random=~vs(id,Gu=A),
             rcov=~units,
             data=DT, verbose = FALSE)

####=====####
#### adding dominance and forcing the other VC's
####=====####
DT$idd <- DT$id;
D <- D.mat(GT) # dominance relationship matrix
mm <- matrix(3,1,1) ## matrix to fix the var comp

mix2 <- mmer(Yield~1,
             random=~vs(id, Gu=A, Gti=mix1$sigma_scaled~u:id~, Gtc=mm)
             + vs(idd, Gu=D, Gtc=unsm(1)),
             rcov=~vs(units,Gti=mix1$sigma_scaled$units, Gtc=mm),
             data=DT, verbose = FALSE)

# analyze variance components
summary(mix1)$varcomp

##          VarComp VarCompSE    Zratio Constraint
## u:id.Yield-Yield  650.4145  325.5562  1.997856   Positive
## units.Yield-Yield 4031.0153  344.6051 11.697493   Positive

summary(mix2)$varcomp

##          VarComp VarCompSE    Zratio Constraint
## u:id.Yield-Yield  650.4145  504.0820  1.2902950    Fixed
## u:idd.Yield-Yield  156.9553  292.3026  0.5369617   Positive
## u:units.Yield-Yield 4031.0153  360.7273 11.1746898    Fixed
```

#### Final remarks

Keep in mind that sommer uses direct inversion (DI) algorithm which can be very slow for large datasets. The package is focused in problems of the type  $p > n$  (more random effect levels than observations) and models with dense covariance structures. For example, for experiment with dense covariance structures

with low-replication (i.e. 2000 records from 1000 individuals replicated twice with a covariance structure of 1000x1000) sommer will be faster than MME-based software. Also for genomic problems with large number of random effect levels, i.e. 300 individuals (n) with 100,000 genetic markers (p). For highly replicated trials with small covariance structures or  $n > p$  (i.e. 2000 records from 200 individuals replicated 10 times with covariance structure of 200x200) asreml or other MME-based algorithms will be much faster and we recommend you to opt for those software. When datasets are big, the installation of the OpenBLAS library can make sommer quite fast and sometimes faster than asreml given the capability of sommer to take advantage of the multi-processor architecture of some systems.

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