Quantitative genetics using the sommer package

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2019-03-25

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 ($\text{A.mat}$), dominance ($\text{D.mat}$), and epistatic ($\text{E.mat}$) 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:

1) Heritability ($h^2$) calculation
2) Specifying heterogeneous variances in mixed models
3) Using the pin calculator
4) Half and full diallel designs (using the overlay)
5) Genomic selection (predicting mendelian sampling)
   • GBLUP
   • rrBLUP
6) Single cross prediction (hybrid prediction)
7) Spatial modeling (using the 2-dimensional splines)
8) Multivariate genetic models and genetic correlations
9) Final remarks

Background

The core of the package the \texttt{mmer} function which solve the mixed model equations. The functions are an interface to call the \texttt{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:

$$y_1 = X_1 \beta_1 + Z_1 u_1 + \epsilon_1 \quad y_2 = X_2 \beta_2 + Z_2 u_2 + \epsilon_2 \quad \ldots \quad y_i = X_i \beta_i + Z_i u_i + \epsilon_i$$

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 $\epsilon_i$ are residuals for trait 'i' ($i = 1, \ldots, t$). The random effects ($u_1 \ldots u_i$ and $\epsilon_i$) 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:

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

$Y \sim \text{MVN}(X\beta, V)$
\[ Y = \begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_t \end{bmatrix} \]
\[ X = \begin{bmatrix} X_1 & \cdots & \cdots \\ \vdots & \ddots & \vdots \\ \cdots & \cdots & X_t \end{bmatrix} \]
\[ V = \begin{bmatrix} Z_1K\sigma^2_{g_{1,1}}Z_1' + H\sigma^2_{e_{1,1}} & \cdots & Z_1K\sigma_{g_{1,t}}Z_t' + H\sigma_{e_{1,t}} \\ \vdots & \ddots & \vdots \\ Z_tK\sigma_{g_{t,1}}Z_1' + H\sigma_{e_{t,1}} & \cdots & Z_tK\sigma^2_{g_{t,t}}Z_t' + H\sigma^2_{e_{t,t}} \end{bmatrix} \]

where \( K \) is the relationship or covariance matrix for the \( k \)th random effect (\( u=1,\ldots,k \)), and \( R=I \) is an identity matrix for the residual term. The terms \( \sigma^2_{g_{ij}} \) and \( \sigma^2_{e_{ij}} \) denote the genetic (or any of the \( k \)th random terms) and residual variance of trait ‘i’, respectively and \( \sigma_{g_{ij}} \) and \( \sigma_{e_{ij}} \) the genetic (or any of the \( k \)th random terms) and residual covariance between traits ‘i’ and ‘j’ (\( i=1,\ldots,t \), and \( j=1,\ldots,t \)).

The algorithm implemented optimizes the log likelihood:
\[
\log L = \frac{1}{2} \ln(||V||) + \ln(X'VX) + Y'PY
\]

where || is the determinant of a matrix. And the REML estimates are updated using a Newton optimization algorithm of the form:
\[
\theta^{k+1} = \theta^k + (H^k)^{-1} \frac{dL}{d\sigma^2_i} \theta^k
\]

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, \( \frac{dL}{d\sigma^2_i} \) 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 pin 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.

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.

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 \( \sigma^2_A \)), and broad sense (\( H^2 \); all genetic variance in the numerator \( \sigma^2_G \)).

In a classical breeding experiment with no molecular markers, special designs are performed to estimate and dissect the additive (\( \sigma^2_A \)) and non-additive (i.e. dominance \( \sigma^2_D \)) variance along with environmental variability. Designs such as generation analysis, North Carolina designs are used to dissect \( \sigma^2_A \) and \( \sigma^2_D \) to estimate the narrow sense heritability (\( h^2 \)). When no special design is available we can still dissect the genetic variance (\( \sigma^2_G \)) 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 genotipic 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 $h^2$.

```r
library(sommer)
data(DT_example)
head(DT)
```

<table>
<thead>
<tr>
<th>#</th>
<th>Name</th>
<th>Env</th>
<th>Loc</th>
<th>Year</th>
<th>Block</th>
<th>Yield</th>
<th>Weight</th>
</tr>
</thead>
<tbody>
<tr>
<td>33</td>
<td>Manistee(MSL292-A)</td>
<td>CA.2013</td>
<td>CA</td>
<td>2013</td>
<td>CA.2013.1</td>
<td>-1.904711</td>
<td></td>
</tr>
<tr>
<td>66</td>
<td>Manistee(MSL292-A)</td>
<td>CA.2013</td>
<td>CA</td>
<td>2013</td>
<td>CA.2013.2</td>
<td>-1.516271</td>
<td></td>
</tr>
<tr>
<td>67</td>
<td>MSL007-B</td>
<td>CA.2011</td>
<td>CA</td>
<td>2011</td>
<td>CA.2011.2</td>
<td>-1.435510</td>
<td></td>
</tr>
<tr>
<td>103</td>
<td>AC05153-1W</td>
<td>CA.2013</td>
<td>CA</td>
<td>2013</td>
<td>CA.2013.1</td>
<td>-1.307167</td>
<td></td>
</tr>
</tbody>
</table>

```r
ans1 <- mmer(Yield ~ 1,
random  = Name + Env + Env:Name + Env:Block,
    rcov = ~ units,
data=DT)
```

```r
summary(ans1)$varcomp
```

<table>
<thead>
<tr>
<th>#</th>
<th>Name.Yield-Yield</th>
<th>VarComp</th>
<th>VarCompSE</th>
<th>Zratio</th>
<th>Constraint</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3.718279</td>
<td>3.718279</td>
<td>1.6959834</td>
<td>2.1924029</td>
<td>Positive</td>
</tr>
<tr>
<td>2</td>
<td>12.008450</td>
<td>12.008450</td>
<td>12.277118</td>
<td>0.9781164</td>
<td>Positive</td>
</tr>
<tr>
<td>3</td>
<td>5.152643</td>
<td>5.152643</td>
<td>1.4923912</td>
<td>3.4526091</td>
<td>Positive</td>
</tr>
<tr>
<td>4</td>
<td>0.000000</td>
<td>0.000000</td>
<td>0.1156675</td>
<td>0.0000000</td>
<td>Positive</td>
</tr>
<tr>
<td>5</td>
<td>4.366189</td>
<td>4.366189</td>
<td>0.6573086</td>
<td>6.6425245</td>
<td>Positive</td>
</tr>
</tbody>
</table>

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

```r
## [1] 3
pin(ans1, h2 ~ V1 / (V1 + (V3/n.env) + (V5/(2*n.env)) ) )
```

```r
## Estimate  SE
## h2 0.6032715 0.1344582
```

Recently with markers becoming cheaper, thousand of markers can be run in the breeding materials. When markers are available, an special design is not necesary to disect 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$idd <- DT$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)

### iteration LogLik wall cpu(sec) restrained
## 1 -123 20:13:52 1 0
## 2 -107.864 20:13:52 1 0
## 3 -103.867 20:13:52 1 0
## 4 -103.315 20:13:53 2 0
## 5 -103.294 20:13:53 2 0
## 6 -103.293 20:13:53 2 0

(summary(ans.ADE)$varcomp)

## VarComp VarCompSE Zratio Constraint
## u:id.color-color 0.003662202 0.0012194130 3.003250 Positive
## u:idd.color-color 0.001820079 0.0007406216 2.457502 Positive
## units.color-color 0.002106929 0.0002864724 7.354736 Positive

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

## Estimate SE
## h2 0.6347926 0.08840488

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

## Estimate SE
## h2 0.7223783 0.05563774

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 GCA2 and SCA specifying the variance structure.

data("DT_cornhybrids")
### fit the model
modFD <- mmer(Yield ~ 1,
               random = vs(at(Location, c("3", "4")), GCA2),
               rcov = vs(ds(Location), units),
               data = DT)
## iteration LogLik wall cpu(sec) restrained
## 1 -190.104 20:13:54 0 0
## 2 -171.543 20:13:55 1 0
## 3 -165.319 20:13:55 1 0
## 4 -164.691 20:13:56 2 0
## 5 -164.684 20:13:56 2 0
## 6 -164.684 20:13:57 3 0

summary(modFD)

## Multivariate Linear Mixed Model fit by REML
## ********************** sommer 3.8 **********************
## 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")

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 0.45203867 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)

### iteration LogLik wall cpu(sec) restrained
## 1 -191.286 20:13:57 0 0
## 2 -172.247 20:13:58 1 0
## 3 -165.948 20:13:58 1 0
## 4 -165.248 20:13:59 2 0
## 5 -165.23 20:13:59 2 0
## 6 -165.229 20:13:59 2 0
## 7 -165.229 20:14:0 3 0

summary(modFD)

### Multivariate Linear Mixed Model fit by REML
### ********************** sommer 3.8 **********************
### 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 20
## 4:GCA2 20

### Use the '$' sign to access results and parameters

3) Using the pin 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 pin 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")

### look at the data
A <- A.mat(GT) # additive relationship matrix
ans <- mmer(color = 1,
random = vs(id, Gu=A),  
rcov = units,  
data = DT)

## iteration LogLik wall cpu(sec) restrained
## 1   -137.304 20:14:1 0 0
## 2   -115.507 20:14:1 0 0
## 3   -111.236 20:14:1 0 0
## 4   -110.755 20:14:2 1 0
## 5   -110.741 20:14:2 1 0
## 6   -110.741 20:14:2 1 0

(summary(ans.ADE)$varcomp)

## VarComp VarCompSE Zratio Constraint
## u:id.color-color 0.003662202 0.001219413 3.003250 Positive
## u:idd.color-color 0.001820079 0.000740621 2.457502 Positive
## units.color-color 0.002106929 0.000286472 7.354736 Positive

pin(ans, h2 ~ (V1) / (V1 + V2))

## Estimate SE
## h2 0.6512157 0.06107574

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

### 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 reciprocate 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 \( 1/2 \times n(n+1) \); half diallel without parents \( 1/2 \times n(n-1) \)). In this example we will show a full dialle design (reciprocate 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")

modFD <- lmer(Yield ~ Location,  
random = ~GCA1+GCA2+SCA,  
rcov = units,  
data = DT)

## iteration LogLik wall cpu(sec) restrained
## 1   -149.436 20:14:3 1 0
## 2   -136.475 20:14:3 1 1
## 3   -132.852 20:14:4 2 1
## 4   -132.625 20:14:4 2 1

7
Don’t worry too much about the small h2 value, the data was simulated to be mainly dominance variance, therefore the Va was simulated extremely small leading to such value of narrow sense h2.

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 (\(\sigma^2_G CA\) and \(\sigma^2_S CA\) 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"`

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

```r
modh <- mmer(sugar ~ 1,
             random = vs(overlay(femalef, malef)) + genof,
             data = DT)
```
### iteration LogLik wall cpu(sec) restrained
### 1 -10.425 20:14:6 0 0
### 2 -6.487 20:14:6 0 0
### 3 -5.732 20:14:6 0 0
### 4 -5.67494 20:14:6 0 0
### 5 -5.67441 20:14:6 0 0

summary(modh)$varcomp

<table>
<thead>
<tr>
<th>#</th>
<th>VarComp</th>
<th>VarCompSE</th>
<th>Zratio</th>
<th>Constraint</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>u:femalef.sugar-sugar</strong></td>
<td>5.507899</td>
<td>3.5741151</td>
<td>1.541052</td>
<td>Positive</td>
</tr>
<tr>
<td><strong>genof.sugar-sugar</strong></td>
<td>1.815784</td>
<td>1.3629575</td>
<td>1.332238</td>
<td>Positive</td>
</tr>
<tr>
<td><strong>units.sugar-sugar</strong></td>
<td>3.117538</td>
<td>0.9626094</td>
<td>3.238632</td>
<td>Positive</td>
</tr>
</tbody>
</table>

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

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.

```r
# select environment 1
rownames(GT) <- rownames(DT)
K <- A.mat(GT) # additive relationship matrix
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 -1.72746986 -0.89028479 0.0509159  775
## 2166 -0.25270280 0.40952243 0.30938553 -1.7387588 2166
## 2167 0.34181510 -0.64862633 -0.79955921 -1.0535691 2167
## 2465 0.09394919 0.57046773 0.5517574  2465
## 3881 -0.28248062 1.61868192 -0.1142848 3881
## 3889 2.33609690 0.62647587 0.07353310 0.7195856 3889

# GBLUP
ans <- mmer(X1~1,
    random=-vs(id,Gu=K),
    rcov=-units,
    data=y.trn) # kinship based
```
6) 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:

- \( u_1 \sim N(0, K_1\sigma^2_u) \)
- \( u_2 \sim N(0, K_2\sigma^2_u) \)
- \( u_S \sim N(0, K_3\sigma^2_S) \)

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")

# 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)

## iteration LogLik wall cpu(sec) restrained
## 1 93.142 20:14:25 7 0
## 2 135.18 20:14:32 14 0
## 3 145.517 20:14:39 21 0
## 4 147.085 20:14:47 29 0
## 5 147.178 20:14:54 36 0
## 6 147.184 20:15:1 43 0
## 7 147.184 20:15:8 50 0

summary(anss2)$varcomp

## VarComp VarCompSE Zratio Constraint
## u:dent.GY-GY 16.93639 2.6917284 6.292012 Positive
## u:flint.GY-GY 12.47174 2.3248074 5.364634 Positive
## units.GY-GY 16.75020 0.7662471 21.860045 Positive

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

## [1] 0.8234584

In the previous model we only used the GCA effects (GCA1 and GCA2) for practicty, 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.

### 7) 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 this 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.

```r
data("DT_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)

summary(mix)
```

Notice that the job is done by the `spl2D()` function that takes the Row and Col information to fit a spatial kernel.
8) 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.

```r
library(sommer)

# Load data
data("DT_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)
```

## iteration LogLik wall cpu(sec) restrained
## 1 -375.872 20:15:17 4 0
## 2 -291.932 20:15:22 9 0
## 3 -258.273 20:15:26 13 0
## 4 -253.459 20:15:30 17 0
## 5 -253.291 20:15:34 21 0
## 6 -253.278 20:15:39 26 0
## 7 -253.277 20:15:43 30 0
## 8 -253.277 20:15:48 35 0

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

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

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

9) 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.

Literature


Covarrubias-Pazaran G. 2018. Software update: Moving the R package sommer to multivariate mixed models for genome-assisted prediction. doi: https://doi.org/10.1101/354639


