

Quick start for the sommer package

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The sommer package was developed to provide R users with a powerful and reliable multivariate mixed model solver. The package is focused on problems of the type $p > n$ (more effects to estimate than observations) and its core algorithm is coded in C++ using the Armadillo library. This package allows the user to fit mixed models with the advantage of specifying the variance-covariance structure for the random effects, specifying heterogeneous variances, and obtaining other parameters such as BLUPs, BLUEs, residuals, fitted values, variances for fixed and random effects, etc.

The purpose of this quick start guide is to show the flexibility of the package under certain common scenarios:

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SECTION 1: Introduction

1) Background on mixed models

The core of the package is the `mmer` function which solves the mixed model equations. The functions are an interface to call the NR Direct-Inversion Newton-Raphson or Average Information algorithms (Tunnicliffe 1989; Gilmour et al. 1995; Lee et al. 2016). From 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:

$$y_1 = X_1\beta_1 + Z_1u_1 + \epsilon_1$$

$$y_2 = X_2\beta_2 + Z_2u_2 + \epsilon_2$$

...

$$y_i = X_i\beta_i + Z_iu_i + \epsilon_i$$

where y_i is a vector of trait phenotypes, β_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 ($u_1 \dots u_i$ 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:

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

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

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

$$\mathbf{X} = \begin{bmatrix} X_1 & 0 & 0 \\ \vdots & \ddots & \vdots \\ 0 & 0 & X_t \end{bmatrix}$$

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

where K is the relationship or covariance matrix for the k th random effect ($u=1, \dots, k$), and $H=I$ is an identity matrix or a partial 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:

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

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 θ 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`.

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.

2) Background on covariance structures

One of the major strenghts of linear mixed models is the flexibility to specify variance-covariance structures at all levels. In general, variance structures of mixed models can be seen as tensor (kronecker) products of multiple variance-covariance stuctures. For example, a multi-response model (i.e. 2 traits) where “g” individuals (i.e. 100 individuals) are tested in “e” treatments (i.e. 3 environments), the variance-covariance for the random effect “individuals” can be seen as the following multiplicative model:

$$\mathbf{T} \otimes \mathbf{G} \otimes \mathbf{A}$$

where:

$$\mathbf{T} = \begin{bmatrix} \sigma_{g_{t1,t1}}^2 & \sigma_{g_{t1,t2}} \\ \sigma_{g_{t2,t1}} & \sigma_{g_{t2,t2}}^2 \end{bmatrix}$$

is the covariance structure for individuals among traits.

$$\mathbf{G} = \begin{bmatrix} \sigma_{g_{e1,e1}}^2 & \sigma_{g_{e1,e2}} & \sigma_{g_{e1,e3}} \\ \sigma_{g_{e2,e1}} & \sigma_{g_{e2,e2}}^2 & \sigma_{g_{e2,e3}} \\ \sigma_{g_{e3,e1}} & \sigma_{g_{e3,e2}} & \sigma_{g_{e3,e3}}^2 \end{bmatrix}$$

is the covariance structure for individuals among environments.

and \mathbf{A} is a square matrix representing the covariance among the levels of the individuals (any known relationship matrix).

The \mathbf{T} and \mathbf{G} covariance structures shown above are unknown matrices to be estimated whereas \mathbf{A} is known. The \mathbf{T} and \mathbf{G} matrices shown above are called as unstructured (US) covariance matrices, although this type is just one example from several covariance structures that the linear mixed models enable. For example, other popular covariance structures are:

Diagonal (DIAG) covariance structures

$$\mathbf{\Sigma} = \begin{bmatrix} \sigma_{g_{e1,e1}}^2 & 0 & 0 \\ \vdots & \ddots & \vdots \\ 0 & 0 & \sigma_{g_{ei,ei}}^2 \end{bmatrix}$$

Compound simmetry (CS) covariance structures

$$\Sigma = \begin{bmatrix} \sigma_g^2 + \sigma_{ge}^2 & \sigma_g^2 & \sigma_g^2 & \sigma_g^2 \\ \sigma_g^2 & \sigma_g^2 + \sigma_{ge}^2 & \sigma_g^2 & \sigma_g^2 \\ \vdots & \vdots & \ddots & \vdots \\ \sigma_g^2 & \sigma_g^2 & \sigma_g^2 & \sigma_g^2 + \sigma_{ge}^2 \end{bmatrix}$$

First order autoregressive (AR1) covariance structures

$$\Sigma = \sigma^2 \begin{bmatrix} 1 & \rho & \rho^2 & \rho^3 \\ \rho & 1 & \rho & \rho^2 \\ \rho^2 & \rho & 1 & \rho \\ \rho^3 & \rho^2 & \rho & 1 \end{bmatrix}$$

or the already mentioned Unstructured (US) covariance structures

$$\Sigma = \begin{bmatrix} \sigma_{g_{e1,e1}}^2 & \sigma_{g_{e1,e2}} & \sigma_{g_{e1,e3}} \\ \vdots & \ddots & \vdots \\ \sigma_{g_{e3,e1}} & \sigma_{g_{e3,e2}} & \sigma_{g_{e3,e3}}^2 \end{bmatrix}$$

among others. Sommer has the capabilities to fit some of these covariance structures in the mixed model machinery.

SECTION 2: Different models enabled in sommer

1) Univariate homogeneous variance models

This type of model refers to single response models where a variable of interest (i.e. genotypes) needs to be analyzed as interacting with a 2nd random effect (i.e. environments), but you assume that across environments the genotypes have the same variance component. This is the so-called compound symmetry (CS) model.

```
library(sommer)
data(DT_example)
DT <- DT_example
## solving for r records
ans1r <- mmer(Yield~Env,
              random= ~ Name + Env:Name,
              rcov= ~ units,
              data=DT, verbose = FALSE)
summary(ans1r)$varcomp

##           VarComp VarCompSE  Zratio Constraint
## Name.Yield-Yield  3.681877 1.6909561 2.177394   Positive
## Env:Name.Yield-Yield 5.173062 1.4952313 3.459707   Positive
## units.Yield-Yield  4.366285 0.6470458 6.748031   Positive

## solving for c coefficients
ans1c <- mmec(Yield~Env,
              random= ~ Name + Env:Name,
              rcov= ~ units,
              data=DT, verbose = FALSE)
summary(ans1c)$varcomp
```

```
##                VarComp VarCompSE  Zratio Constraint
## Name:isc:isc    3.702831  1.883592  1.965835  Positive
## Env:Name:isc:isc 5.132119  2.428131  2.113609  Positive
## units:isc:isc   4.465685  2.295313  1.945567  Positive
```

2) Univariate heterogeneous variance models

Very often in multi-environment trials, the assumption that the genetic variance or the residual 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. This requires a CS+DIAG model (also called heterogeneous CS model).

```
data(DT_example)
DT <- DT_example

ans2r <- mmer(Yield~Env,
              random= ~Name + vsr(dsr(Env),Name),
              rcov= ~ vsr(dsr(Env),units),
              data=DT, verbose = FALSE)
summary(ans2r)$varcomp
```

```
##                VarComp VarCompSE  Zratio Constraint
## Name.Yield-Yield      2.962851  1.4962000  1.980251  Positive
## CA.2011:Name.Yield-Yield 10.146369  4.5073271  2.251083  Positive
## CA.2012:Name.Yield-Yield  1.877530  1.8697568  1.004158  Positive
## CA.2013:Name.Yield-Yield  6.629152  2.5028114  2.648682  Positive
## CA.2011:units.Yield-Yield 4.942450  1.5245057  3.242001  Positive
## CA.2012:units.Yield-Yield 5.724963  1.3123015  4.362536  Positive
## CA.2013:units.Yield-Yield 2.559880  0.6399685  4.000010  Positive
```

```
DT=DT[with(DT, order(Env)), ]
ans2c <- mmec(Yield~Env,
              random= ~Name + vsc(dsc(Env),isc(Name)),
              rcov= ~ vsc(dsc(Env),isc(units)),
              data=DT, verbose = FALSE)
summary(ans2c)$varcomp
```

```
##                VarComp VarCompSE  Zratio Constraint
## Name:isc:isc          2.961895  1.4528410  2.038692  Positive
## Env:Name:CA.2011:CA.2011 10.148219  4.5621703  2.224428  Positive
## Env:Name:CA.2012:CA.2012  1.878507  1.8883210  0.994803  Positive
## Env:Name:CA.2013:CA.2013  6.629521  2.4890927  2.663429  Positive
## Env:units:CA.2011:CA.2011 4.942517  1.5201273  3.251384  Positive
## Env:units:CA.2012:CA.2012 5.724702  1.3326002  4.295888  Positive
## Env:units:CA.2013:CA.2013 2.559825  0.6395342  4.002640  Positive
```

As you can see the special function `atr` or `diag` can be used to indicate that there's a different variance for the genotypes in each environment. The same was done for the residual. The difference between `atr` and `diag` is that the `atr` function can be used to specify the levels or specific environments where the variance is different.

3) Unstructured variance models

A more relaxed assumption than the CS+DIAG model is the unstructured model (US) which assumes that among the levels of certain factor (i.e. Environments) there's a covariance structure of a second random effect

(i.e. Genotypes). This can be done in sommer using the `usr(.)` function:

```
data(DT_example)
DT <- DT_example

ans3r <- mmer(Yield~Env,
             random=~ vsr(usr(Env),Name),
             rcov=~vsr(dsr(Env),units),
             data=DT, verbose = FALSE)
summary(ans3r)$varcomp

##                               VarComp VarCompSE   Zratio Constraint
## CA.2011:Name.Yield-Yield      15.6650010  5.4206906  2.8898534   Positive
## CA.2012:CA.2011:Name.Yield-Yield  6.1101600  2.4850649  2.4587527   Unconstr
## CA.2012:Name.Yield-Yield       4.5296090  1.8208107  2.4876881   Positive
## CA.2013:CA.2011:Name.Yield-Yield  6.3844808  3.0658977  2.0824181   Unconstr
## CA.2013:CA.2012:Name.Yield-Yield  0.3929997  1.5233985  0.2579757   Unconstr
## CA.2013:Name.Yield-Yield       8.5972750  2.4837814  3.4613654   Positive
## CA.2011:units.Yield-Yield       4.9698460  1.5322540  3.2434870   Positive
## CA.2012:units.Yield-Yield       5.6729333  1.3007862  4.3611574   Positive
## CA.2013:units.Yield-Yield       2.5570940  0.6392821  3.9999462   Positive

DT=DT[with(DT, order(Env)), ]
ans3c <- mmec(Yield~Env,
             random=~ vsc(usc(Env),isc(Name)),
             rcov=~vsc(dsc(Env),isc(units)),
             data=DT, verbose = FALSE)
summary(ans3c)$varcomp
```

```
##                               VarComp VarCompSE   Zratio Constraint
## Env:Name:CA.2011:CA.2011      14.1130508  3.4147828  4.1329278   Positive
## Env:Name:CA.2011:CA.2012       5.5944492  1.9635238  2.8491883   Unconstr
## Env:Name:CA.2012:CA.2012       4.5127684  2.4324072  1.8552685   Positive
## Env:Name:CA.2011:CA.2013       5.3289701  1.6025432  3.3253206   Unconstr
## Env:Name:CA.2012:CA.2013       0.4846585  1.4944492  0.3243058   Unconstr
## Env:Name:CA.2013:CA.2013       8.0187930  2.0739979  3.8663457   Positive
## Env:units:CA.2011:CA.2011      4.9579597  1.5264964  3.2479342   Positive
## Env:units:CA.2012:CA.2012      5.6456207  1.3068683  4.3199615   Positive
## Env:units:CA.2013:CA.2013      2.5572308  0.6385923  4.0044812   Positive
```

As can be seen the `usr(Env)` indicates that the genotypes (Name) can have a covariance structure among environments (Env).

4) Multivariate homogeneous variance models

Currently there's a great push for multi-response models. This is motivated by the correlation that certain variables hide and that could benefit in the prediction perspective. In sommer to specify multivariate models the response requires the use of the `cbind()` function in the response, and the `usr(trait)`, `diag(trait)`, or `atr(trait)` functions in the random part of the model.

```
data(DT_example)
DT <- DT_example
DT$EnvName <- paste(DT$Env,DT$Name)

DT$Yield <- as.vector(scale(DT$Yield))
DT$Weight <- as.vector(scale(DT$Weight))
```

```

ans4r <- mmer(cbind(Yield, Weight) ~ Env,
             random= ~ vsr(Name, Gtc=unsm(2)),
             rcov= ~ vsr(units, Gtc=diag(2)),
             data=DT, verbose = FALSE)
summary(ans4r)$varcomp

##              VarComp  VarCompSE  Zratio Constraint
## u:Name.Yield-Yield  0.2448029  0.07278135  3.363540   Positive
## u:Name.Yield-Weight  0.3177637  0.07457957  4.260733   Unconstr
## u:Name.Weight-Weight  0.2813217  0.08054357  3.492789   Positive
## u:units.Yield-Yield  0.3725767  0.04331247  8.602066   Positive
## u:units.Weight-Weight  0.3586951  0.04189443  8.561882   Positive

DT2 <- reshape(DT, idvar = c("Name", "Env", "Block"), varying = list(6:7),
               v.names = "y", direction = "long", timevar = "trait", times = colnames(DT)[6:7])
DT2$trait <- as.factor(DT2$trait)

# ans4c <- mmec(y ~ Env:trait,
#              random= ~ vsc(usc(trait),isc(Name)),
#              rcov= ~ vsc(dsc(trait),isc(units)), returnParam = T,
#              data=DT2, verbose = T)
# summary(ans4c)$varcomp

```

You may notice that we have added the `usr(trait)` behind the random effects. This is to indicate the structure that should be assumed in the multivariate model. The `diag(trait)` used behind a random effect (i.e. Name) indicates that for the traits modeled (Yield and Weight) there's no covariance component and should not be estimated, whereas `usr(trait)` assumes that for such a random effect, there's a covariance component to be estimated (i.e. covariance between Yield and Weight for the random effect Name). The same applies for the residual part (rcov).

Any number of random effects can be specified with different structures.

5) Details on special functions for variance models

the `vsr()` function for special variance models and its auxiliaries The sommer function `vsr()` allows constructing complex variance models that are passed to the `mmer()` function which constitutes one of the most important features of the sommer package. The specification of the `vsr()` function has the form:

```
random=~vsr(..., Gu, Gti, Gtc)
```

The idea is that the `vsr()` function reflects the special variance structure that each random effect could have in the matrix notation:

$$var(u) = T \otimes E \otimes \dots \otimes A$$

where the `...` argument in the `vsr()` function is used to specify the kronecker products from all matrices that form the variance for the random effect, where the auxiliary functions `dsc()`, `usr()`, `csr()`, `atr()`, can be used to define such structured variance structures. The idea is that a variance model for a random effect `x` (i.e. individuals) might require a more flexible model than just:

```
random=~x
```

For example, if individuals are tested in different time-points and environments, we can assume a different variance and covariance components among the individuals in the different environment-timepoint combinations. An example of variance structure of the type:

$$var(u) = T \otimes E \otimes S \otimes A$$

would be specified in the `vsr()` function as:

```
random=~vsr(usr(e),usr(s),x, Gu=A, Gtc=T)
```

where the `e` would be a column vector in a data frame for the environments, `s` a column vector in the dataframe for the time points, `x` is the vector in the dataframe for the identifier of individuals, `A` is a known square variance covariance matrix among individuals (usually an identity matrix; default if not specified), and `T` is a square matrices with as many rows and columns as the number of traits that specifies the trait covariance structure.

The auxiliary functions to build the variance models for the random effect are: `+ dsr()` diagonal covariance structure `+ usr()` unstructured covariance `+ atr()` specific levels heterogeneous variance structure `+ csr()` customized covariance structure

the `vsc()` function for special variance models and its auxiliaries The sommer function `vsc()` allows constructing complex variance models that are passed to the `mmec()` function which constitutes one of the most important features of the sommer package. The specification of the `vsc()` function has the form:

```
random=~vsc(..., Gu)
```

where the different variance structures are input as before but the constraints are specified within the auxiliary function with the argument `theta` and `thetaC`. Please notice that all functions for `c` coefficients end in the letter `c` instead of `r`.

`dsr()` and `dsc()` to specify a diagonal (DIAG) covariance structures A diagonal covariance structure looks like this:

$$\Sigma = \begin{bmatrix} \sigma_{g_{e1,e1}}^2 & 0 & 0 \\ \vdots & \ddots & \vdots \\ 0 & 0 & \sigma_{g_{ei,ei}}^2 \end{bmatrix}$$

Considering an example for one random effect (`g`; indicating i.e. individuals) evaluated in different treatment levels (`e`; indicating i.e. the different treatments) the model would look like:

```
random=~vsr(dsr(e),g) for r records random=~vsc(dsc(e),isc(g)) for c coefficients
```

`usr()` and `usc()` to specify an unstructured (US) covariance An unstructured covariance looks like this:

$$\mathbf{G} = \begin{bmatrix} \sigma_{g_{e1,e1}}^2 & \sigma_{g_{e1,e2}} & \sigma_{g_{e1,e3}} \\ \sigma_{g_{e2,e1}} & \sigma_{g_{e2,e2}}^2 & \sigma_{g_{e2,e3}} \\ \sigma_{g_{e3,e1}} & \sigma_{g_{e3,e2}} & \sigma_{g_{e3,e3}}^2 \end{bmatrix}$$

Considering same example for one random effect (`g`; indicating i.e. individuals) evaluated in different treatment levels (`e`; indicating i.e. the different treatments) the model would look like:

```
random=~vsr(usr(e),g) for r records random=~vsc(usc(e),isc(g)) for c coefficients
```

`atr()` and `atc()` to specify a level-specific heterogeneous variance A diagonal covariance structure for specific levels of the second random effect looks like this:

$$\Sigma = \begin{bmatrix} \sigma_{g_{e1,e1}}^2 & 0 & 0 \\ \vdots & \ddots & \vdots \\ 0 & 0 & \sigma_{g_{ei,ei}}^2 \end{bmatrix}$$

Considering the same example for one random effect (*g*; indicating i.e. individuals) evaluated in different treatment levels (*e*; indicating i.e. the different treatments A,B,C) the model would look like:

```
random=~vsr(atr(e,c("A","B")),g) random=~vsc(atc(e,c("A","B")),isc(g))
```

where the variance component for *g* is only fitted at levels A and B.

csr() and csc() to specify a level-specific variance-covariance structure A customized covariance structure for specific levels of the second random effect (variance and covariances) looks i.e. like this:

$$\Sigma = \begin{bmatrix} \sigma_{g_{e1,e1}}^2 & \sigma_{g_{e1,e2}} & 0 \\ \vdots & \ddots & \vdots \\ 0 & 0 & \sigma_{g_{ei,ei}}^2 \end{bmatrix}$$

Considering same example for one random effect (*g*; indicating i.e. individuals) evaluated in different treatment levels (*e*; indicating i.e. the different treatments A,B,C) the model would look like:

```
random=~vsr(csr(e,c("A","B")),g) random=~vsc(csc(e,c("A","B")),isc(g))
```

where *mm* indicates which variance and covariance components are estimated for *g*.

6) The specification of multi-trait constraints in the variance components for the vsr function (Gtc argument)

One of the major strengths of sommer is its extreme flexibility to specify variance-covariance structures in the multi-trait framework. Since sommer 3.7 this is easily achieved by the use of the `vsr()` function and its argument `Gtc`. The `Gtc` argument expects a matrix of constraints for the variance-covariance components for the random effect filled with numbers according to the following rules:

- 0: parameter not to be estimated
- 1: estimated and constrained to be positive
- 2: estimated and unconstrained
- 3: not to be estimated but fixed value provided in `Gti`

Some useful functions to specify quickly the constraint matrices are `unsm()` for unstructured, `fixm()` for fixed constraint, and `fcm()` for fixed effect constraints.

Consider a multi-trait model with 4 traits (y_1, \dots, y_4) and 1 random effect (*u*) and 1 fixed effect (*x*)

```
fixed=cbind(y1,y2,y3,y4)~x
```

```
random= ~vsr(u, Gtc=?)
```

The constraint for the 4 x 4 matrix of variance covariance components to be estimated can be an:

- a) unstructured (variance components have to be positive and covariances either positive or negative)
`random= ~vsr(u, Gtc=unsm(4))` and `random= ~vsr(dsc(x,thetaC=unsm(4)),isc(u))`

```
unsm(4)
```

```
##      [,1] [,2] [,3] [,4]
## [1,]   1   2   2   2
## [2,]   2   1   2   2
## [3,]   2   2   1   2
## [4,]   2   2   2   1
```

c) fixed (variance or covariance components indicated with a 3 are considered fixed and values are provided in the Gti argument) `random= ~vsr(u, Gtc=fixm(4), Gti=mm)` and `random= ~vsr(dsc(x,thetaC=fixm(4)),isc(u))`

```
fixm(4)
```

```
##      [,1] [,2] [,3] [,4]
## [1,]   3   3   3   3
## [2,]   3   3   3   3
## [3,]   3   3   3   3
## [4,]   3   3   3   3
```

where mm is a 4 x 4 matrix with initial values for the variance components.

d) constraints for fixed effects `fixed= cbind(y1,y2,y3,y4)~vsr(x, Gtc=fcm(c(1,0,1,0)))`

```
fcm(c(1,0,1,0))
```

```
##      [,1] [,2]
## [1,]   1   0
## [2,]   0   0
## [3,]   0   1
## [4,]   0   0
```

where 1's and 0's indicate the traits where the fixed effect will be estimated (1's) and where it won't (0's).

7) Special functions for special models

Random regression models In order to fit random regression models the user can use the `leg()` function to fit Legendre polynomials. This can be combined with other special covariance structures such as `dsc()` / `dsc()`, `usr()` / `usc()`, etc.

```
library(orthopolynom)
data(DT_legendre)
DT <- DT_legendre
```

```
mRR2r<-mmer(Y~ 1 + Xf
, random=~ vsr(usr(leg(X,1)),SUBJECT)
, rcov=~vsr(units)
, data=DT, verbose = FALSE)
summary(mRR2r)$varcomp
```

##	VarComp	VarCompSE	Zratio	Constraint
## leg0:SUBJECT.Y-Y	2.5782969	0.6717242	3.838326	Positive
## leg1:leg0:SUBJECT.Y-Y	0.4765431	0.2394975	1.989763	Unconstr
## leg1:SUBJECT.Y-Y	0.3497299	0.2183229	1.601893	Positive
## u:units.Y-Y	2.6912226	0.3825197	7.035513	Positive

```
mRR2c<-mmec(Y~ 1 + Xf
, random=~ vsc(usc(leg(X,1)),isc(SUBJECT))
, rcov=~vsc(isc(units))
```

```
, data=DT, verbose = FALSE)
summary(mRRR2c)$varcomp
```

```
##                VarComp VarCompSE  Zratio Constraint
## X:SUBJECT:leg0:leg0 2.5615527 0.4925762 5.200317   Positive
## X:SUBJECT:leg0:leg1 0.4675469 0.1908303 2.450067   Unconstr
## X:SUBJECT:leg1:leg1 0.3473523 0.2828763 1.227930   Positive
## units:isc:isc      2.6919055 0.4614647 5.833394   Positive
```

Here, a numeric covariate X is used to explain the trajectory of the SUBJECTs and combined with an unstructured covariance matrix. The details can be found in the theory.

GWAS models Although genome-wide association studies can be conducted through a variety of approaches, the use of mixed models to find associations between markers and phenotypes still one of the most popular approaches. One of the most classical and popular approaches is to test marker by marker through mixed modeling (1 model by marker) to obtain the marker effect and a statistic reflecting the level of association usually provided as the $-\log_{10}$ p-value. The second most popular approach is to assume that the genetic variance component is similar for all markers and therefore the variance components are only estimated once (1 model for all markers) and use the inverse of the phenotypic variance matrix (V^{-1}) to test all markers in the generalized linear model $b = (X'V - X) - XV - y$. This makes the GWAS much faster and efficient without major losses. Given the straightforward extension, sommer provides the GWAS function which can fit both type of approaches (be aware that these are two methods among many existing in the literature) in univariate and multivariate models, that way genetically correlated traits can be tested together to increase the power of detection. In summary the GWAS model implemented in sommer to obtain marker effect is a generalized linear model of the form:

$$b = (X'V - X)X'V^{-1}y$$

with $X = ZM_i$

where: - b is the marker effect (dimensions 1 x mt) - y is the response variable (univariate or multivariate) (dimensions 1 x nt) - V^{-1} is the inverse of the phenotypic variance matrix (dimensions nt x nt) - Z is the incidence matrix for the random effect selected (gTerm argument) to perform the GWAS (dimensions nt x ut) M_i is the ith column of the marker matrix (M argument) (dimensions u x m)

for t traits, n observations, m markers and u levels of the random effect. Depending if P3D is TRUE or FALSE the V- matrix will be calculated once and used for all marker tests (P3D=TRUE) or estimated through REML for each marker (P3D=FALSE).

Here we show a simple GWAS model for an univariate example.

```
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
head(DT,3)
```

```
##      id Row Col Year      color  Yield FruitAver Firmness Rowf Colf
## P003 P003  3  1 2014 0.10075269 154.67    41.93  588.917    3    1
## P004 P004  4  1 2014 0.13891940 186.77    58.79  640.031    4    1
## P005 P005  5  1 2014 0.08681502  80.21    48.16  671.523    5    1
```

```
head(MP,3)
```

```
##                Locus Position Chrom
```

```
## 1 scaffold_77830_839      0      1
## 2 scaffold_39187_895     0      1
## 3 scaffold_50439_2379    0      1
```

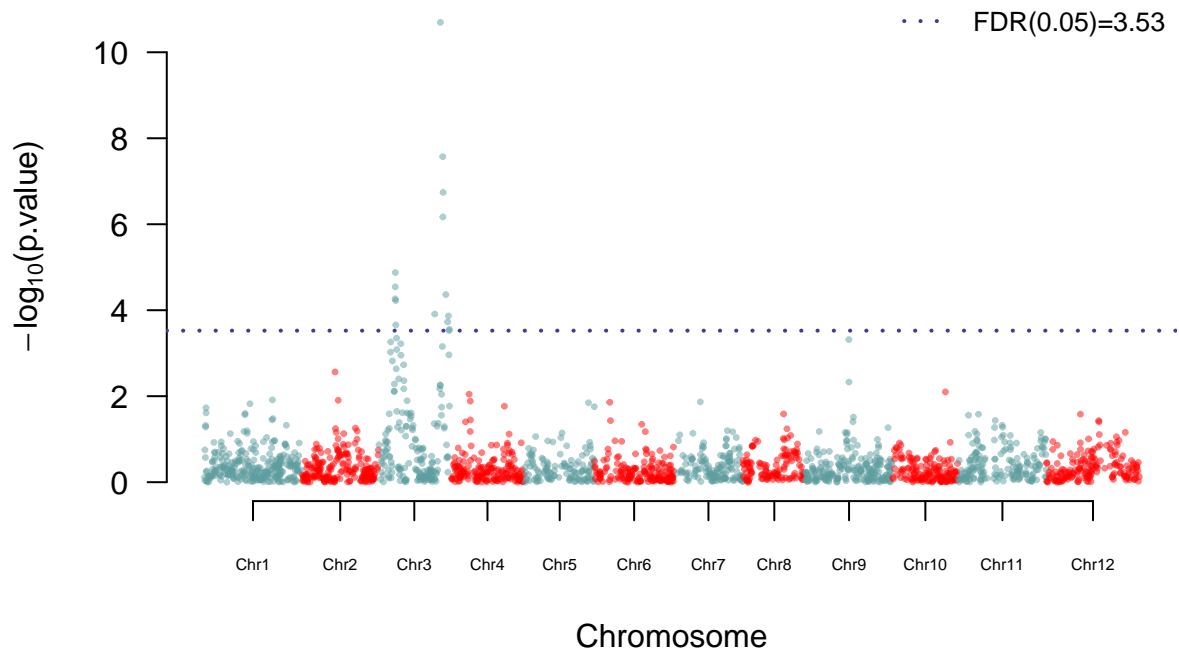
```
GT[1:3,1:4]
```

```
##      scaffold_50439_2381 scaffold_39344_153 uneak_3436043 uneak_2632033
## P003                0                0                0                1
## P004                0                0                0                1
## P005                0                -1                0                1
```

```
mix1 <- GWAS(color~1,
             random=~vsr(id,Gu=A)
             + Rowf + Colf,
             rcov=~units,
             data=DT, nIters=3,
             M=GT, gTerm = "u:id",
             verbose = FALSE)
```

```
## Performing GWAS evaluation
```

```
ms <- as.data.frame(mix1$scores)
ms$Locus <- rownames(ms)
MP2 <- merge(MP,ms,by="Locus",all.x = TRUE);
manhattan(MP2, pch=20,cex=.5, PVCN = "color")
```



Be aware that the marker matrix M has to be imputed (no missing data allowed) and make sure that the number of rows in the M matrix is equivalent to the levels of the $gTerm$ specified (i.e. if the $gTerm$ is “id” and has 300 levels or in other words 300 individuals, then M has dimensions 300 x m , where m is the number of markers).

Overlaid models [the `overlay()` function] Another very useful function is the `overlay` function, which allows for the overlay of matrices of different random effects and estimate a single variance component for the overlaid terms.

```

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
modhr <- mmer(sugar~1,
              random=~vsr(overlay(femalef,malef))
              + genof, data=DT,verbose = FALSE)

modhc <- mmec(sugar~1,
              random=~vsc(isc(overlay(femalef,malef, sparse = TRUE)))
              + genof,data=DT,verbose = FALSE)

```

here the `femalef` and `malef` random effects are overlaid becoming a single random effect that has the same variance component.

Spatial models (using the 2-dimensional spline) We will use the CPdata to show the use of 2-dimensional splines for accomodating spatial effects in field experiments. In early generation variety trials the availability of seed is low, which makes the use of an unreplicated design a neccesity more than anything else. Experimental designs such as augmented designs and partially-replicated (p-rep) designs have become 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 accomodate 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 usr 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=~vsr(id, Gu=A) +
            vsr(Rowf) +
            vsr(Colf) +
            spl2Da(Row,Col),
            rcov=~vsr(units), nIters=3,
            data=DT,verbose = FALSE)

```

```
summary(mix)
```

```
## =====
##           Multivariate Linear Mixed Model fit by REML
## ***** sommer 4.1 *****
## =====
##           logLik      AIC      BIC Method Converge
## Value -151.2647 304.5293 308.421      NR      FALSE
## =====
## Variance-Covariance components:
##           VarComp VarCompSE Zratio Constraint
## u:id.Yield-Yield      792.6      317.6 2.4959 Positive
## u:Rowf.Yield-Yield     807.6      371.3 2.1750 Positive
## u:Colf.Yield-Yield     183.2      139.7 1.3121 Positive
## A:all.Yield-Yield      515.8      701.3 0.7354 Positive
## u:units.Yield-Yield   2918.4      292.8 9.9667 Positive
## =====
## Fixed effects:
##   Trait      Effect Estimate Std.Error t.value
## 1 Yield (Intercept)      132.1      8.761  15.08
## =====
## Groups and observations:
##      Yield
## u:id      363
## u:Rowf     13
## u:Colf     36
## A:all     168
## =====
## Use the '$' sign to access results and parameters
```

Notice that the job is done by the `spl2Da()` function that takes the `Row` and `Col` information to fit a spatial kernel.

Customized random effects One of the most powerful features of `sommer` is the ability to provide any customized matrix and estimate any random effect. For example:

```
data(DT_cpdata)
DT <- DT_cpdata
GT <- GT_cpdata
MP <- MP_cpdata

#### look at the data and fit the model
mix1 <- mmer(Yield~1,
             random=~vsr(list(GT)),
             rcov=~units, nIters=3,
             data=DT, verbose = FALSE)
```

the matrix `GT` is provided as a random effect by encapsulating the matrix in a list and provided in the `vsr()` function.

10) Genomic selection

In this section I decided to show the way you can fit an `rrBLUP` and `GBLUP` model in `sommer` using some wheat example data from `CIMMYT` in the genomic selection framework. 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. In case the interest is to get BLUPs for markers the random effect is the actual marker matrix and the relationship among markers can be specified as well but in this example is assumed to be diagonal.

```
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

## GBLUP
ans <- mmer(X1~1,
            random=~vsr(id,Gu=K),
            rcov=~units, nIters=3,
            data=y.trn,verbose = FALSE) # kinship based
ans$US$`u:id`$X1 <- as.data.frame(ans$US$`u:id`$X1)
rownames(ans$US$`u:id`$X1) <- gsub("id","",rownames(ans$US$`u:id`$X1))
cor(ans$US$`u:id`$X1[vv,],DT[vv,"X1"], use="complete")

## [1] 0.5733721

## rrBLUP
ans2 <- mmer(X1~1,
             random=~vsr(list(GT), buildGu = FALSE),
             rcov=~units, getPEV = FALSE, nIters=3,
             data=y.trn,verbose = FALSE) # kinship based

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

## [1] 0.5771181

# the same can be applied in multi-response models in GBLUP or rrBLUP
# same can be achieved with the mmec function (see ?DT_wheat)
```

11) Likelihood ratio tests

The Likelihood ratio test (LRT) is a good way to investigate the significance of random effects or specific variance-covariance components.

11.1) Testing the significance of a variance component For example, imagine that a researcher would like to know if his model improves when adding the effect of a spatial kernel to capture the spatial trend in the field, his base model may look like this:

```
data(DT_cpdata)
DT <- DT_cpdata
GT <- GT_cpdata
MP <- MP_cpdata
### mimic two fields
A <- A.mat(GT)

mix1 <- mmer(Yield~1,
             random=~vsr(id, Gu=A) +
               vsr(Rowf) +
               vsr(Colf),
             rcov=~vsr(units), nIters=3,
             data=DT, verbose = FALSE)
```

And the model with the spatial kernel is the following:

```
mix2 <- mmer(Yield~1,
             random=~vsr(id, Gu=A) +
               vsr(Rowf) +
               vsr(Colf) +
               spl2Da(Row,Col),
             rcov=~vsr(units), nIters=3,
             data=DT, verbose = FALSE)
```

Then to test if the second model brings value let us fit the likelihood ratio test as follows:

```
lrt <- anova(mix1, mix2)

## Likelihood ratio test for mixed models
## =====
##      Df      AIC      BIC      loLik      Chisq ChiDf PrChisq
## mod2  8 304.5293 308.4210 -151.2647
## mod1  7 305.1825 309.0741 -151.5912 0.65315      1 0.41899
## =====
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

As can be seen the test turns out to not be very significant despite the increase in the likelihood.

11.2) Testing the significance of a covariance component Sometimes the researcher is more interested in knowing if a covariance structure is relevant or not. Assume we have two multi-trait models, 1) fitting no-covariance (independent) among traits, and 2) one fitting the genetic covariance among yield and color in the following population:

```
data(DT_example)
DT <- DT_example

DT$EnvName <- paste(DT$Env,DT$Name)
modelBase <- mmer(cbind(Yield, Weight) ~ Env,
                 random= ~ vsr(Name, Gtc=diag(2)), # here is diag()
                 rcov= ~ vsr(units, Gtc=unsm(2)), nIters=3,
                 data=DT, verbose = FALSE)

modelCov <- mmer(cbind(Yield, Weight) ~ Env,
```



```

random= ~ vsr(usr(Env),Name, Gtc=unsm(2)), # here is unsm()
rcov= ~ vsr(dsr(Env),units, Gtc=unsm(2)), nIters=3,
data=DT,verbose = FALSE)

```

```
lrt <- anova(modelBase, modelCov)
```

```

## Likelihood ratio test for mixed models
## =====
##      Df      AIC      BIC   loLik   Chisq ChiDf      PrChisq
## mod2 45 -340.4760 -316.9949 176.2380
## mod1 23 -205.0695 -181.5885 108.5347 135.40646    22 2.57838297802183e-18 ***
## =====
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

As can be seen, in this case fitting the covariance among the genotypes improves the model fit considerably and the probability of the Chi-square distribution is < 0.05 . Then you the model with the covariance is the preferred model.

SECTION 3: The predict function

1) Background on prediction

In a linear mixed model where y is an $n \times 1$ vector of observations, the linear mixed model can be written as:

$$y = X\tau + Zu + e = W\beta + e$$

where τ is a vector $t \times 1$ of fixed effects, X is an $n \times t$ design matrix which associates observations with the appropriate combinations of fixed effects, u is the $q \times 1$ vector of random effects, Z is the $n \times q$ matrix which associates observations with the appropriate random effects, and e is the $n \times 1$ vector of residual errors. For shorthand W and β represent the combined design matrix and vector of effects, respectively. It is assumed:

$$\begin{bmatrix} u \\ e \end{bmatrix} = N\left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} G(\gamma) & 0 \\ 0 & R(\phi) \end{bmatrix}\right)$$

where the covariance matrices G and R for random effects and residuals are functions of parameters γ and ϕ respectively. The covariance matrix of data can be written as:

$$\text{var}(y) = \sigma^2(ZGZ' + R)$$

The variance parameters γ and ϕ are usually estimated by maximum likelihood or REML (Patterson and Thompson, 1971).

The BLUP of a linear combination for known D , γ , and ϕ is then:

$$D\bar{\beta} = \begin{bmatrix} D_\tau & D_u \end{bmatrix} \begin{bmatrix} \bar{\tau} \\ \bar{u} \end{bmatrix} = D\bar{\tau} + D_u\bar{u}$$

where $\bar{\beta} = (\tau, u)$ is the solution of the mixed model equations:

$$\begin{bmatrix} X^T R^{-1} X & X^T R^{-1} Z \\ Z^T R^{-1} X & Z^T R^{-1} Z + G^{-1} \end{bmatrix} \begin{bmatrix} \tau \\ u \end{bmatrix} = \begin{bmatrix} X^T R^{-1} y \\ Z^T R^{-1} X \end{bmatrix}$$

These can also be written as $C\bar{\beta} = W^T R^{-1} y$. The $\bar{\tau}$ is the best linear unbiased estimator (BLUE) of τ and \bar{u} is the best linear unbiased predictor (BLUP) of u , this with variance $\text{var}(\bar{\beta} - \beta) = C^{-1}$. Consideration of the values required to form the confidence intervals make it clear that is the prediction error variance (PEV

or $var(\bar{\beta} - \beta)$), rather than the variance of the estimator $var(\bar{\beta})$ that is usually of interest. The prediction error variance for a linear combination $D\bar{\beta}$ is then $DC^{-1}D^T$. Since the variance parameters are unknown, we replace the unknown variance parameters by their REML estimates and use the empirical values.

The `predict()` function of the `sommer` package then builds the C^{-1} matrix from the mixed model equations and the D matrix of linear combinations to obtain the PEV and SEs for the predictions. For the means it uses the D matrix of linear combinations times the vector of required fixed and random effects $X\bar{\tau} + Z\bar{u}$ or $D\bar{\beta}$, where the matrix D is a linear combination of specific fixed and/or random effects from matrices X and/or Z .

2) Predicting means

The `sommer` package is equipped with a `predict()` function that can be used to calculate means and standard errors for fixed and random effects specified in the models fitted with the `mmer()` and `mmec` functions. Using the `yatesoats` dataset we will fit some fixed and random effects.

```
library(sommer)
data(DT_yatesoats)
DT <- DT_yatesoats
m3 <- mmer(fixed=Y ~ V + N + V:N,
           random = ~ B + B:MP,
           rcov=~units,
           data = DT, verbose=FALSE)
summary(m3)$varcomp
```

```
##           VarComp VarCompSE  Zratio Constraint
## B.Y-Y      214.4477 168.62790 1.271722  Positive
## B:MP.Y-Y   106.0508  67.83280 1.563415  Positive
## units.Y-Y  177.0883  37.34293 4.742217  Positive
```

Now, the model can be used together with the `classify` argument to obtain means for the `classify` argument. For example, the model includes in the fixed formula the terms “V” for variety, “N” for nitrogen treatments, and “V:N” for the interaction between variety and nitrogen. The `classify` argument can be used to specify the term for which the means are desired. In the following example the means for the nitrogen treatments are obtained as follows:

```
p0 <- predict.mmer(object=m3, classify = "N")
```

```
## iteration   LogLik      wall   cpu(sec)  restrained
##      1      -0.745921 6:22:6      0          0
##      2      -0.745921 6:22:6      0          0
##      3      -0.745921 6:22:6      0          0
##      4      -0.745921 6:22:6      0          0
```

```
p0$pvals
```

```
##  trait  N predicted.value standard.error
## 1    Y  0          79.38889          7.174710
## 2    Y 0.2          98.88889          9.530389
## 3    Y 0.4         114.22222          9.530389
## 4    Y 0.6         123.38889          9.530389
```

Literature

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