

Overview of the package LMMstar

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This vignette describes the main functionalities of the **LMMstar** package. This package implements specific types of linear mixed models, mainly useful when having repeated observations over a discrete variable: $\mathbf{Y} = (Y_1, \dots, Y_T)$ where T can be for example be time (chronological ordering of the repetitions) or brain region (arbitrary ordering of the repetitions). Denoting by X the associated covariates and $\boldsymbol{\varepsilon} = (\varepsilon_1, \dots, \varepsilon_T)$, the model can be written:

$$\mathbf{Y} = X\boldsymbol{\beta} + \boldsymbol{\varepsilon} \text{ where } \boldsymbol{\varepsilon} \sim \mathcal{N}(0, \Omega)$$

where $\boldsymbol{\beta}$ are the mean parameters and the residual variance-covariance matrix, Ω , depends on a set of variance-covariance parameters (say $\boldsymbol{\gamma}$) distinct of $\boldsymbol{\beta}$. Key assumptions are:

- we observe n independent replicates of $\mathcal{O} = (\mathbf{Y}, X)$, i.e. at the cluster level, observations $(\mathcal{O}_1, \dots, \mathcal{O}_n)$ are independent. The replicates should also be identically distributed up to a categorical variable (called strata variable in the following).
- the residual variance is independent of the mean value.

Additional assumptions are necessary in presence of missing values, typically correct specification of the conditional mean to have consistent estimates of the mean parameters. This case will sometimes be exemplified by considering that only last outcome may be missing: the conditional mean $\mathbb{E}[Y_T | Y_1, Y_2, \dots, Y_{T-1}]$ is then abbreviated as $\mathbb{E}[Y_T | Y_{T-1}]$. Note that we do not require the residuals to be normally distributed to have valid estimates or statistical inference in large samples.

To get start, one should load the **LMMstar** package in the  session:

```
library(LMMstar)
```

This package is under active development. Newer package versions may include additional functionalities and fix previous bugs. The version of the package that is being used for this overview is:

```
utils::packageVersion("LMMstar")
```

[1] '1.0.0'

The user interface of the **LMMstar** package is made of the following functions:

- the function `lmm` is the main function of the package which fits linear mixed models. The user can interact with `lmm` objects using:
 - `anova` to perform Wald tests, i.e. test linear combinations of coefficients ($\hat{\beta}_1 + \hat{\beta}_2 = 0$ or $\hat{\beta}_1 = \hat{\beta}_2 = 0$). The output obtained with different `lmm` can be combined using `rbind`.
 - `coef` to extract the estimated model parameters ($\hat{\beta}$ and possibly $\hat{\gamma}$).
 - `confint` to extract the estimates with their confidence intervals.
 - `dummy.coef` to extract the estimated (marginal) mean for each combination of categorical covariate.
 - `estimate` to test non-linear combinations of coefficients (Wald test via a first order delta method, e.g. $\hat{\beta}_1/\hat{\beta}_2 = 1$).
 - `fitted` to output the fitted mean ($X\hat{\beta}$) or the conditional mean for observations with missing outcome (e.g. $X\hat{\beta} + \hat{\mathbb{E}}[\varepsilon_T|\varepsilon_{-T}]$).
 - `iid` to extract the influence function of the estimated parameters (φ), which satisfies
$$\sqrt{n}(\hat{\beta} - \beta) = \frac{1}{\sqrt{n}} \sum_{i=1}^n \varphi(\mathcal{O}_i) + o_p(1)$$
 - `levels` to extract the reference level for the mean structure. (i.e. what (`Intercept`) refers to in presence of categorical covariates).
 - `logLik` to output the log-likelihood of the estimated model.
 - `model.tables` to extract the estimates, standard errors, p-value, and confidence intervals.
 - `plot` to obtain a diagnostic plots, partial residual plots, or a graphical display of the fitted values.
 - `predict` to compute the mean conditional on covariates and possible outcome values.
 - `profile` to display the likelihood or profile likelihood of the model.
 - `resample` to use non-parametric bootstrap or permutation test for statistical inference.
 - `residuals` to extract the observed residuals of the fitted model, possibly normalized ($\hat{\Omega}^{-\frac{1}{2}}\hat{\varepsilon}$).
 - `sigma` to extract the modeled residual variance covariance matrix ($\hat{\Omega}$).
 - `summary` to obtain a summary of the input, model fit, and estimated values.
 - `vcov` to extract the variance-covariance matrix of the mean parameters ($\hat{\Sigma}_{\hat{\beta}}$).
- the `mlmm` function to fit group-specific linear mixed models and gather the estimated coefficients.
- the `summarize` function to compute summary statistics, possibly stratified on a categorical variable
- the `summarizeNA` function to identify missing data patterns.
- the `partialCor` function to compute partial correlation between two variables.
- the `sampleRem` function to simulate longitudinal data.
- the `LMMstar.options` function enables the user to display the default values used in the **LMMstar** package. The function can also change the default values to better match the user needs.

1 Illustrative dataset

To illustrate the functionalities of the package, we will use the `gastricbypass` dataset. The long format can be imported using:

```
data(gastricbypassL, package = "LMMstar")
head(gastricbypassL)
```

```
  id visit      time weight glucagonAUC
1  1   1 3monthsBefore 127.2    5032.50
2  2   1 3monthsBefore 165.2   12142.50
3  3   1 3monthsBefore 109.7   10321.35
4  4   1 3monthsBefore 146.2    6693.00
5  5   1 3monthsBefore 113.1    7090.50
6  6   1 3monthsBefore 158.8   10386.00
```

See `?gastricbypassL` for a presentation of the dataset. We will shorten the values of the time variable:

```
gastricbypassL$time <- factor(gastricbypassL$time,
                             levels = c("3monthsBefore", "1weekBefore",
                                           "1weekAfter", "3monthsAfter" ),
                             labels = c("B3m","B1w","A1w","A3m"))
gastricbypassL$visit <- as.numeric(gastricbypassL$time) ## convert to numeric
gastricbypassL$baseline <- gastricbypassL$visit<=2
```

rescale the glucagon values

```
gastricbypassL$glucagon <- as.double(scale(gastricbypassL$glucagonAUC))+5
```

and add a group variable:

```
gastricbypassL$group <- as.numeric(gastricbypassL$id)%%2
```

The corresponding wide format is

```
data(gastricbypassW, package = "LMMstar")
head(gastricbypassW)
```

```
  id weight1 weight2 weight3 weight4 glucagonAUC1 glucagonAUC2 glucagonAUC3 glucagonAUC4
1  1  127.2  120.7  115.5  108.1    5032.50    4942.5    20421.0    9249.45
2  2  165.2  153.4  149.2  132.0   12142.50   14083.5    10945.5    7612.50
3  3  109.7  101.6   97.7   87.1   10321.35    6202.5    20121.0   17704.50
4  4  146.2  142.4  136.7  123.0    6693.00    6631.5    13090.5    4551.00
5  5  113.1  105.6   99.9   87.7    7090.50         NA    19155.0   12345.00
6  6  158.8  143.6  134.6  108.7   10386.00    7609.5    11778.0    8014.80
```

for which we can also add the group variable:

```
gastricbypassW$group <- as.numeric(gastricbypassW$id)%%2
```

Finally we will remove observation with missing glucagon values:

```
dfL <- gastricbypassL[!is.na(gastricbypassL$glucagonAUC),]
```

2 Descriptive statistics

2.1 Summary statistics

Mean, standard deviation, and other summary statistic can be computed with respect to a categorical variable (typically time) using the `summarize` function:

```
sss <- summarize(weight+glucagon ~ time, data = gastricbypassL, na.rm = TRUE)
print(sss, digits = 3)
```

	outcome	time	observed	missing	mean	sd	min	q1	median	q3	max
1	weight	B3m	20	0	128.97	20.269	100.90	115.30	123.10	139.82	173.00
2		B1w	20	0	121.24	18.910	95.70	107.78	114.50	134.53	162.20
3		A1w	20	0	115.70	18.275	89.90	102.22	110.60	128.38	155.00
4		A3m	20	0	102.36	17.054	78.80	90.40	98.50	108.25	148.00
5	glucagon	B3m	20	0	4.51	0.641	3.61	4.06	4.33	4.93	6.03
6		B1w	19	1	4.39	0.558	3.58	4.05	4.23	4.55	5.95
7		A1w	19	1	6.06	1.044	4.52	5.30	5.94	6.62	8.27
8		A3m	20	0	5.06	0.760	3.95	4.52	5.03	5.27	7.12

Correlation matrices are also output when a cluster and ordering variable have been specified (here respectively `id` and `time`):

```
sss <- summarize(weight ~ time|id, data = gastricbypassL, na.rm = TRUE)
print(sss, digits = 3)
```

	time	observed	missing	mean	sd	min	q1	median	q3	max
1	B3m	20	0	129	20.3	100.9	115.3	123.1	140	173
2	B1w	20	0	121	18.9	95.7	107.8	114.5	135	162
3	A1w	20	0	116	18.3	89.9	102.2	110.6	128	155
4	A3m	20	0	102	17.1	78.8	90.4	98.5	108	148

Pearson's correlation:

	B3m	B1w	A1w	A3m
B3m	1.000	0.990	0.986	0.946
B1w	0.990	1.000	0.997	0.959
A1w	0.986	0.997	1.000	0.966
A3m	0.946	0.959	0.966	1.000

Alternatively, the `partialCor` function can be used to compute correlation from the wide format, e.g.:

```
partialCor(weight1 + weight4 ~ 1, data = gastricbypassW)
```

	estimate	se	df	lower	upper	p.value
rho(weight1,weight4)	0.946	0.105	31.1	0.867	0.978	8.46e-09

Partial correlations can be also computed, e.g.:

```
partialCor(list(weight1 ~ glucagonAUC1, weight4 ~ glucagonAUC4),
           data = gastricbypassW)
```

```
              estimate    se  df lower upper p.value
rho(weight1,weight4)  0.946 0.109 19.6 0.859  0.98 3.62e-07
```

The `partialCor` function can also be used to obtain group-specific correlations:

```
partialCor(weight + glucagonAUC ~ 1, by = "group", data = gastricbypassL)
```

```
              estimate    se  df lower upper p.value
0: rho(weight,glucagonAUC)  -0.281 0.148 21.1 -0.552  0.0442  0.0858
1: rho(weight,glucagonAUC)  -0.336 0.144 22.2 -0.594 -0.0156  0.0410
```

A p-value for the difference can be obtained specifying the argument `effects`:

```
partialCor(weight + glucagonAUC ~ 1, by = "group", effects = "Dunnett",
           data = gastricbypassL)
```

```
              estimate se df lower upper p.value
1:rho(weight,glucagonAUC) - 0:rho(weight,glucagonAUC)  -0.055 NA NA  NA  NA  0.789
```

2.2 Missing data patterns

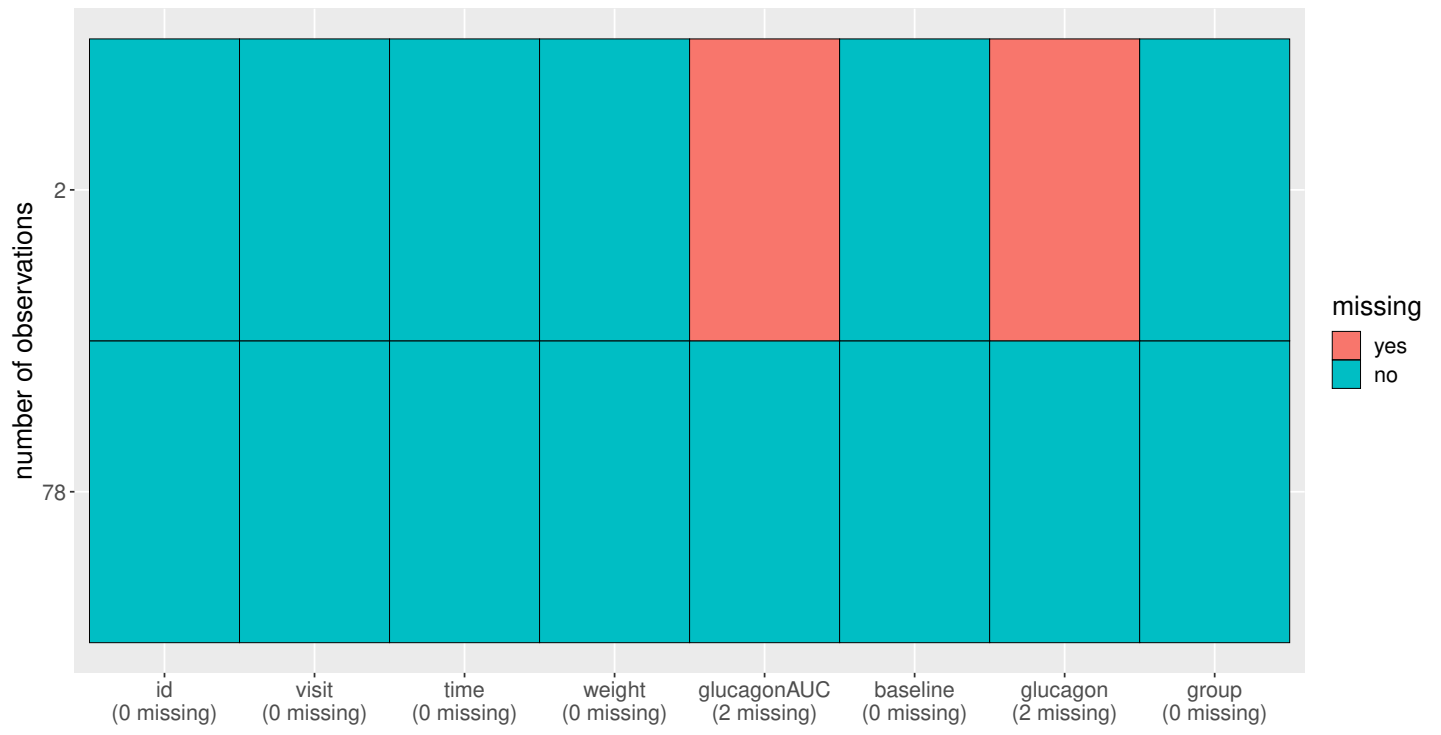
The `summarizeNA` identify the possible combinations of observed/missing data:

```
mp <- summarizeNA(gastricbypassL)
mp
```

```
frequency missing.pattern n.missing id visit time weight glucagonAUC baseline glucagon group
      78      00000000      0 0  0  0  0  0  0  0  0
      2      00001010      2 0  0  0  0  0  1  0  1  0
```

A graphical representation can be obtained using `plot`:

```
plot(mp)
```



3 Linear mixed model (LMM)

3.1 Classical covariance patterns

Several build-in covariance patterns can be used when specifying the linear model. The most basic ones are the **identity** structure:

```
eId.lmm <- lmm(weight ~ time + glucagon, repetition = ~time|id,  
              structure = "ID", data = dfL)  
eId.lmm  
cat(" modeled residual variance-covariance: \n");sigma(eId.lmm)
```

Linear regression

```
outcome/cluster/time: weight/id/time  
data                  : 78 observations from 20 clusters  
parameter             : 5 mean ((Intercept) timeB1w timeA1w timeA3m glucagon)  
                      : 1 variance (sigma)  
log-restr.likelihood: -323.086426918519  
convergence           : TRUE (0 iterations)  
modeled residual variance-covariance:  
      B3m    B1w    A1w    A3m  
B3m 330.0427  0.0000  0.0000  0.0000  
B1w  0.0000 330.0427  0.0000  0.0000  
A1w  0.0000  0.0000 330.0427  0.0000  
A3m  0.0000  0.0000  0.0000 330.0427
```

and the **independence** structure:

```
eInd.lmm <- lmm(weight ~ time + glucagon, repetition = ~time|id,  
              structure = "IND", data = dfL)  
eInd.lmm  
cat(" modeled residual variance-covariance: \n");sigma(eInd.lmm)
```

Linear regression with heterogeneous residual variance

```
outcome/cluster/time: weight/id/time  
data                  : 78 observations from 20 clusters  
parameter             : 5 mean ((Intercept) timeB1w timeA1w timeA3m glucagon)  
                      : 4 variance (sigma k.B1w k.A1w k.A3m)  
log-restr.likelihood: -321.457830361849  
convergence           : TRUE (8 iterations)  
modeled residual variance-covariance:  
      B3m    B1w    A1w    A3m  
B3m 442.6475  0.0000  0.0000  0.0000  
B1w  0.0000 418.9934  0.0000  0.0000  
A1w  0.0000  0.0000 222.8463  0.0000  
A3m  0.0000  0.0000  0.0000 237.2049
```

The most common linear mixed model uses a **compound symmetry** structure:

```
eCS.lmm <- lmm(weight ~ time + glucagon, repetition = ~time|id,
              structure = "CS", data = dfL)
eCS.lmm
cat(" modeled residual variance-covariance: \n");sigma(eCS.lmm)
```

Linear Mixed Model with a compound symmetry covariance matrix

```
outcome/cluster/time: weight/id/time
data                  : 78 observations from 20 clusters
parameter            : 5 mean ((Intercept) timeB1w timeA1w timeA3m glucagon)
                     1 variance (sigma)
                     1 correlation (rho)
log-restr.likelihood: -243.600523870252
convergence          : TRUE (9 iterations)
modeled residual variance-covariance:
      B3m      B1w      A1w      A3m
B3m 355.3062 344.6236 344.6236 344.6236
B1w 344.6236 355.3062 344.6236 344.6236
A1w 344.6236 344.6236 355.3062 344.6236
A3m 344.6236 344.6236 344.6236 355.3062
```

A more flexible model can be obtained with a **toeplitz** covariance matrix:

```
eTOE.lmm <- lmm(weight ~ time*group, repetition = ~time|id,
                structure = "TOEPLITZ", data = dfL)
eTOE.lmm
cat(" modeled residual correlation: \n");cov2cor(sigma(eTOE.lmm))
```

```
outcome/cluster/time: weight/id/time
data                  : 78 observations from 20 clusters
parameter            : 8 mean ((Intercept) timeB1w timeA1w timeA3m group timeB1w:group timeA1w:group)
                     4 variance (sigma k.B1w k.A1w k.A3m)
                     3 correlation (rho(1) rho(2) rho(3))
log-restr.likelihood: -221.152940926053
convergence          : TRUE (21 iterations)
modeled residual correlation:
      B3m      B1w      A1w      A3m
B3m 1.0000000 0.9854133 0.9676223 0.9489216
B1w 0.9854133 1.0000000 0.9854133 0.9676223
A1w 0.9676223 0.9854133 1.0000000 0.9854133
A3m 0.9489216 0.9676223 0.9854133 1.0000000
```


And an even more flexible model can be obtained with an **unstructured** covariance matrix:

```
eUN.lmm <- lmm(weight ~ time + glucagon, repetition = ~time|id,  
              structure = "UN", data = dfL)  
eUN.lmm  
cat(" modeled residual variance-covariance: \n");sigma(eUN.lmm)
```

Linear Mixed Model with an unstructured covariance matrix

```
outcome/cluster/time: weight/id/time  
data                  : 78 observations from 20 clusters  
parameter             : 5 mean ((Intercept) timeB1w timeA1w timeA3m glucagon)  
                      4 variance (sigma k.B1w k.A1w k.A3m)  
                      6 correlation (rho(B3m,B1w) rho(B3m,A1w) rho(B3m,A3m) rho(B1w,A1w) rho(B1w,A3m))  
log-restr.likelihood: -216.318937004306  
convergence           : TRUE (22 iterations)  
modeled residual variance-covariance:  
      B3m      B1w      A1w      A3m  
B3m 411.3114 381.9734 352.6400 318.8573  
B1w 381.9734 362.7326 335.4649 304.6314  
A1w 352.6400 335.4649 311.6921 285.8077  
A3m 318.8573 304.6314 285.8077 280.9323
```

Stratification of the covariance structure on a categorical variable is also possible:

- e.g. to get a **stratified compound symmetry**

```
eSCS.lmm <- lmm(weight ~ time*group,  
               repetition = ~time|id, structure = CS(group~1),  
               data = dfL)  
eSCS.lmm
```

Linear Mixed Model with a stratified compound symmetry covariance matrix

```
outcome/cluster/time: weight/id/time  
data                  : 78 observations from 20 clusters  
parameter             : 8 mean ((Intercept) timeB1w timeA1w timeA3m group timeB1w:group timeA1w:group)  
                      2 variance (sigma:0 sigma:1)  
                      2 correlation (rho:0 rho:1)  
log-restr.likelihood: -229.203435252784  
convergence           : TRUE (6 iterations)
```

- e.g. stratified unstructured covariance matrix:

```
eSUN.lmm <- lmm(weight ~ time*group + glucagon,
               repetition = ~time|id, structure = UN(~group),
               data = dfL)
eSUN.lmm
```

Linear Mixed Model with a stratified unstructured covariance matrix

```
outcome/cluster/time: weight/id/time
data                  : 78 observations from 20 clusters
parameter            : 9 mean ((Intercept) timeB1w timeA1w timeA3m group glucagon timeB1w:group time
                      8 variance (sigma:0 sigma:1 k.B1w:0 k.A1w:0 k.A3m:0 k.B1w:1 k.A1w:1 k.A3m:1)
                      12 correlation (rho(B3m,B1w):0 rho(B3m,A1w):0 rho(B3m,A3m):0 rho(B1w,A1w):0 r
log-restr.likelihood: -197.171312062212
convergence          : TRUE (50 iterations)
```

with modeled residual variance-covariance:

sigma(eSCS.lmm)					sigma(eSUN.lmm)				
\$'1:1'					\$'1:1'				
	B3m	B1w	A1w	A3m		B3m	B1w	A1w	A3m
B3m	348.0783	334.7404	334.7404	334.7404	B3m	417.3374	382.8829	362.5674	301.7430
B1w	334.7404	348.0783	334.7404	334.7404	B1w	382.8829	364.4515	346.4039	292.7507
A1w	334.7404	334.7404	348.0783	334.7404	A1w	362.5674	346.4039	331.1789	282.9301
A3m	334.7404	334.7404	334.7404	348.0783	A3m	301.7430	292.7507	282.9301	253.3324
\$'3:3'					\$'2:2'				
	B3m	B1w	A1w	A3m		B3m	B1w	A1w	A3m
B3m	345.5863	340.1538	340.1538	340.1538	B3m	383.8877	363.6405	336.5771	350.0416
B1w	340.1538	345.5863	340.1538	340.1538	B1w	363.6405	347.9898	321.5908	331.5182
A1w	340.1538	340.1538	345.5863	340.1538	A1w	336.5771	321.5908	297.5329	308.1345
A3m	340.1538	340.1538	340.1538	345.5863	A3m	350.0416	331.5182	308.1345	334.8267

Finally the some covariance patterns like the compound symmetry structure may depend on covariates:

- e.g. to obtain a **block compound symmetry** structure¹:

```
eBCS.lmm <- lmm(weight ~ time*group, repetition = ~time|id,  
               structure = CS(~baseline, type = "homogeneous"), data = dfL)  
eBCS.lmm  
cat(" modeled residual variance-covariance: \n");sigma(eBCS.lmm)
```

Linear Mixed Model with a block compound symmetry covariance matrix

```
outcome/cluster/time: weight/id/time  
data                  : 78 observations from 20 clusters  
parameter             : 8 mean ((Intercept) timeB1w timeA1w timeA3m group timeB1w:group timeA1w:group  
                      1 variance (sigma)  
                      2 correlation (rho(baseline) rho(id))  
log-restr.likelihood: -230.532819632968  
convergence           : TRUE (6 iterations)  
modeled residual variance-covariance:  
      B3m      B1w      A1w      A3m  
B3m 346.7441 339.3256 336.1825 336.1825  
B1w 339.3256 346.7441 336.1825 336.1825  
A1w 336.1825 336.1825 346.7441 339.3256  
A3m 336.1825 336.1825 339.3256 346.7441
```

- e.g. to obtain a **block unstructured** covariance matrix:

```
eBUN.lmm <- lmm(weight ~ time*group, repetition = ~time|id,  
               structure = CS(~baseline, type = "heterogeneous"), data = dfL)  
eBUN.lmm  
cat(" modeled residual variance-covariance: \n");sigma(eBUN.lmm)
```

Linear Mixed Model with a block unstructured covariance matrix

```
outcome/cluster/time: weight/id/time  
data                  : 78 observations from 20 clusters  
parameter             : 8 mean ((Intercept) timeB1w timeA1w timeA3m group timeB1w:group timeA1w:group  
                      2 variance (sigma k.TRUE)  
                      3 correlation (rho(FALSE) rho(FALSE,TRUE) rho(TRUE))  
log-restr.likelihood: -227.461008305704  
convergence           : TRUE (6 iterations)  
modeled residual variance-covariance:  
      B3m      B1w      A1w      A3m  
B3m 378.0328 372.8100 336.3064 336.3064  
B1w 372.8100 378.0328 336.3064 336.3064  
A1w 336.3064 336.3064 315.6358 306.0647  
A3m 336.3064 336.3064 306.0647 315.6358
```

¹similar to nested random effects

3.2 User-specific covariance patterns

It is possible input user-specific covariance patterns under the following model for the residuals:

$$\Omega = \sigma^\top R \sigma$$

where:

- $\sigma = f(\theta_\sigma, Z_\sigma)$ is a vector of residual standard errors depending on a vector of parameters θ_σ and possible covariates via the design matrix Z_σ .
- $R = g(\theta_R, Z_R)$ is a matrix of residual correlations depending on a vector of parameters θ_R and possible covariates via the design matrix Z_R .

To be more concrete, consider the following correlation matrix

```
rho.2block <- function(p,n.time,X){
  rho <- matrix(1, nrow = n.time, ncol = n.time)
  rho[1,2] <- rho[2,1] <- rho[4,5] <- rho[5,4] <- p["rho1"]
  rho[1,3] <- rho[3,1] <- rho[4,6] <- rho[6,4] <- p["rho2"]
  rho[2,3] <- rho[3,2] <- rho[5,6] <- rho[6,5] <- p["rho3"]
  rho[4:6,1:3] <- rho[1:3,4:6] <- p["rho4"]
  return(rho)
}
Rho <- rho.2block(p = c(rho1=0.25,rho2=0.5,rho3=0.4,rho4=0.1),
  n.time = 6)
Rho
```

```
      [,1] [,2] [,3] [,4] [,5] [,6]
[1,] 1.00 0.25  0.5 0.10 0.10  0.1
[2,] 0.25 1.00  0.4 0.10 0.10  0.1
[3,] 0.50 0.40  1.0 0.10 0.10  0.1
[4,] 0.10 0.10  0.1 1.00 0.25  0.5
[5,] 0.10 0.10  0.1 0.25 1.00  0.4
[6,] 0.10 0.10  0.1 0.50 0.40  1.0
```

and the corresponding dataset:

```
set.seed(11)
n <- 1000
Y <- rmvnorm(n, mean = rep(0,6), sigma = Rho)
dfL2 <- reshape2::melt(cbind(id = 1:n, as.data.frame(Y)), id.vars = "id")
dfL2$time <- dfL2$variable
dfL2 <- dfL2[order(dfL2$id),]
dfL2[1:8,]
```

```
      id variable      value time
1      1      V1 -0.9842079    V1
```

```

1001 1      V2 -0.3681245  V2
2001 1      V3 -1.6174652  V3
3001 1      V4 -1.4994103  V4
4001 1      V5  0.7493107  V5
5001 1      V6 -1.0719657  V6
2     2      V1  1.2402726  V1
1002 2      V2  0.6494215  V2

```

To estimate the corresponding mixed model we first define a new covariance structure:

```

myStruct <- CUSTOM(~variable,
  FCT.sigma = function(p,n.time,X){rep(p,n.time)}, ## function f
  init.sigma = c("sigma"=1),
  FCT.rho = rho.2block, ## function g
  init.rho = c("rho1"=0.25,"rho2"=0.25,"rho3"=0.25,"rho4"=0.25))

```

and then call `lmm` with this structure structure:

```

e.lmmCUSTOM <- lmm(value~time,
  repetition=~time|id,
  structure = myStruct,
  data=dfL2,
  df = FALSE) ## df = FALSE to save computation time
logLik(e.lmmCUSTOM)

```

```
[1] -7962.243
```

The optimization procedure may be slow but should eventually reaches an optimum. We can then output the estimated correlation matrix:

```
cov2cor(sigma(e.lmmCUSTOM))
```

```

      V1      V2      V3      V4      V5      V6
V1 1.0000000 0.24898095 0.50058994 0.09053785 0.09053785 0.09053785
V2 0.24898095 1.0000000 0.36110943 0.09053785 0.09053785 0.09053785
V3 0.50058994 0.36110943 1.0000000 0.09053785 0.09053785 0.09053785
V4 0.09053785 0.09053785 0.09053785 1.0000000 0.24898095 0.50058994
V5 0.09053785 0.09053785 0.09053785 0.24898095 1.0000000 0.36110943
V6 0.09053785 0.09053785 0.09053785 0.50058994 0.36110943 1.0000000

```

Comparison to build-in structure: consider the following model using a build-in compound symmetry structure:

```
system.time(  
  e.lmmDEFAULT.CS <- lmm(value~time,  
                        repetition = ~time|id,  
                        structure = "CS",  
                        data = dfL2, df = FALSE)  
)
```

```
bruger    system forløbet  
0.15      0.00      0.15
```

Using instead CUSTOM to specifying this structure:

```
myCS <- CUSTOM(~1,  
              FCT.sigma = function(p,n.time,X){rep(p,n.time)},  
              init.sigma = c("sigma"=1),  
              FCT.rho = function(p,n.time,X){p+diag(1-p,n.time,n.time)},  
              init.rho = c("rho"=0.5))
```

is considerably slower than using the pre-specified structure:

```
system.time(  
  e.lmmCUSTOM.CS <- lmm(value~time,  
                        repetition = ~time|id,  
                        structure = myCS,  
                        data = dfL2, df = FALSE  
  )  
)
```

```
bruger    system forløbet  
1.13      0.02      1.20
```

but will lead to the same estimates:

```
logLik(e.lmmDEFAULT.CS)  
logLik(e.lmmCUSTOM.CS)
```

```
[1] -8186.859
```

```
[1] -8186.859
```

There are two reasons for the slower execution time: slower evaluation of the derivatives (since they are obtained by numerical differentiation) and worse starting point, as reflected by the larger number of iterations needed to reach convergence:

```
e.lmmDEFAULT.CS$opt$n.iter  
e.lmmCUSTOM.CS$opt$n.iter
```

```
[1] 1
```

```
[1] 4
```

Faster execution time can be obtained by specifying the first and second derivative regarding each parameter:

```
myCS.wD <- CUSTOM(~1,
  FCT.sigma = function(p,n.time,X){rep(p,n.time)},
  dFCT.sigma = function(p,n.time,X){list(sigma = rep(1,n.time))},
  d2FCT.sigma = function(p,n.time,X){list(sigma = rep(0,n.time))},
  init.sigma = c("sigma"=1),
  FCT.rho = function(p,n.time,X){p+diag(1-p,n.time,n.time)},
  dFCT.rho = function(p,n.time,X){list(rho = 1-diag(1,n.time,n.time))},
  d2FCT.rho = function(p,n.time,X){list(rho = matrix(0,n.time,n.time))},
  init.rho = c("rho"=0.5))

system.time(
  e.lmmCUSTOMwD.CS <- lmm(value~time,
    repetition = ~time|id,
    structure = myCS.wD,
    data = dfL2, df = FALSE
  )
)
```

```
bruger    system forløbet
 0.89     0.00     0.89
```

3.3 Estimation procedure

Initialization: by default the mean parameters are initialized using Ordinary Least Squares (OLS) and the variance and correlation parameters are initialized by minimizing the difference between the observed and residuals variance-covariance matrix. These values can be visualized by specifying the argument `control`:

```
eCS.lmm.bis <- update(eCS.lmm, control = list(trace = 2))
```

Initialization:

```
(Intercept)    timeB1w    timeA1w    timeA3m    glucagon    sigma    rho
159.1349871   -7.7137607   -2.3202963 -22.9747234 -6.6820191  18.1670760  0.8960476
```

Loop:

```
(Intercept)    timeB1w    timeA1w    timeA3m    glucagon    sigma    rho
125.2601602   -7.6194918 -14.4951323 -27.0514694  0.8217879  18.8495686  0.9699341
```

Convergence after 9 iterations: max score=3.680809e-06 | max change in coefficient=1.877273e-06

It is possible to input user-defined value:

- for all parameters (vector)

```
init.all <- coef(eCS.lmm, effects = "all")
eCS.lmm.bis <- update(eCS.lmm, control = list(init = init.all, trace = 2))
```

Initialization:

```
(Intercept)    timeB1w    timeA1w    timeA3m    glucagon    sigma    rho
125.2601602   -7.6194918 -14.4951323 -27.0514694  0.8217879  18.8495686  0.9699341
```

Loop:

```
(Intercept)    timeB1w    timeA1w    timeA3m    glucagon    sigma    rho
125.2601602   -7.6194918 -14.4951323 -27.0514694  0.8217879  18.8495686  0.9699341
```

Convergence after 0 iteration: max score=3.680809e-06

- the mean parameters only (vector)

```
init.mean <- coef(eCS.lmm, effects = "mean")
eCS.lmm.bis <- update(eCS.lmm, control = list(init = init.mean, trace = 2))
```

Initialization:

```
(Intercept)    timeB1w    timeA1w    timeA3m    glucagon    sigma    rho
125.2601602   -7.6194918 -14.4951323 -27.0514694  0.8217879  19.0853249  0.9737808
```

Loop:

```
(Intercept)    timeB1w    timeA1w    timeA3m    glucagon    sigma    rho
125.2601601   -7.6194918 -14.4951323 -27.0514694  0.8217879  18.8495690  0.9699341
```

Convergence after 5 iterations: max score=2.820304e-06 | max change in coefficient=4.171839e-06

- a full data variance-covariance matrix (matrix).

```
init.vcov <- sigma(eCS.lmm)
eCS.lmm.bis <- update(eSCS.lmm, control = list(init = init.vcov, trace = 2))
```

Initialization:

(Intercept)	timeB1w	timeA1w	timeA3m	group	timeB1w:group	timeA1w:group
134.2700000	-8.2800000	-14.1100000	-29.6100000	-10.6000000	1.0505605	1.7562258
timeA3m:group	sigma:0	sigma:1	rho:0	rho:1		
6.0100000	18.8495686	18.8495686	0.9699341	0.9699341		

Loop:

(Intercept)	timeB1w	timeA1w	timeA3m	group	timeB1w:group	timeA1w:group
134.2700000	-8.2800000	-14.1100000	-29.6100000	-10.6000000	1.0444208	1.7525468
timeA3m:group	sigma:0	sigma:1	rho:0	rho:1		
6.0100000	18.6568561	18.5899521	0.9616812	0.9842804		

Convergence after 7 iterations: max score=2.208526e-05 | max change in coefficient=6.343994e-06

Optimizer: by default the optimizer is a Newton Raphson algorithm with backtracking. At each iteration:

- it computes the first two moments (score, information) according to the current parameters values.
- it updates the variance-covariance parameters according to the gradient multiplied by the inverse of the information.
- it updates the mean parameters by generalized least squares (using the updated variance-covariance parameters).
- it checks whether the log-likelihood at the updated estimates is well defined and higher than at the previous estimates. If this is not the case, the step is re-run with half the update of the variance-covariance parameters (backtracking).

One can modify the maximum number of iterations (`n.iter`), maximum number of backtracking steps (`n.backtracking`), the maximum score (absolute) value over all parameters (`tol.score`) and (absolute) maximum difference in parameter value between two iterations (`tol.param`) used to declare convergence. It is also possible to use another optimizer (`optimizer`). All these elements should be passed to the argument `control` of `lmm` using a list.

3.4 Model output

The `summary` method can be used to display the main information relative to the model fit:

```
summary(eUN.lmm)
```

Linear Mixed Model

Dataset: `dfL`

- 20 clusters
- 78 observations
- between 3 and 4 observations per cluster

Summary of the outcome and covariates:

```
$ weight : num 127 165 110 146 113 ...
$ time    : Factor w/ 4 levels "B3m","B1w","A1w",...: 1 1 1 1 1 1 1 1 1 1 ...
$ glucagon: num 4.03 5.24 4.93 4.32 4.38 ...
reference level: time=B3m
```

Estimation procedure

- Restricted Maximum Likelihood (REML)
- log-likelihood :-216.3189
- parameters: mean = 5, variance = 4, correlation = 6
- convergence: TRUE (22 iterations)
- largest `|score|` = 7.034659e-05 for `k.A1w`
|change|= 1.09738491005373e-06 for (Intercept)

Residual variance-covariance: unstructured

- correlation structure: `~0 + time`

	B3m	B1w	A1w	A3m
B3m	1.000	0.989	0.985	0.938
B1w	0.989	1.000	0.998	0.954
A1w	0.985	0.998	1.000	0.966
A3m	0.938	0.954	0.966	1.000
- variance structure: `~time`

	standard.deviation	ratio
sigma.B3m	20.3	1.000
sigma.B1w	19.0	0.939
sigma.A1w	17.7	0.871
sigma.A3m	16.8	0.826

Fixed effects: weight ~ time + glucagon

```
              estimate    se    df   lower   upper  p.value
(Intercept)   132.98 4.664 19.8 123.243 142.717 < 2e-16 ***
timeB1w       -7.882 0.713 19.2  -9.374  -6.39 9.27e-10 ***
timeA1w      -11.788 1.018 21.6  -13.9  -9.676 9.55e-11 ***
timeA3m      -26.122 1.656 18.8 -29.591 -22.654 2.62e-12 ***
glucagon      -0.888 0.242 13.7  -1.408  -0.369 0.00257 **
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1.

Columns lower and upper contain 95% pointwise confidence intervals for each coefficient.

Model-based standard errors are derived from the observed information (column se).

Degrees of freedom were computed using a Satterthwaite approximation (column df).

Note: the calculation of the degrees of freedom, especially when using the observed information can be quite slow. Setting the arguments `df` to `FALSE` and `type.information` to `"expected"` when calling `lmm` should lead to a more reasonable computation time.

3.5 Extract estimated coefficients

The value of the estimated coefficients can be output using `coef`:

```
coef(eUN.lmm)
```

```
(Intercept)   timeB1w   timeA1w   timeA3m   glucagon
132.9801355  -7.8822331 -11.7879545 -26.1223908 -0.8883081
```

Variance coefficients can be output by specifying the `effects` argument:

```
coef(eUN.lmm, effects = "variance")
```

```
      sigma    k.B1w    k.A1w    k.A3m
20.2808131  0.9390916  0.8705176  0.8264480
```

It is possible to apply specific transformation on the variance coefficients, for instance to obtain the residual variance relative to each outcome:

```
coef(eUN.lmm, effects = "variance", transform.k = "sd")
```

```
sigma.B3m sigma.B1w sigma.A1w sigma.A3m
20.28081  19.04554  17.65480  16.76104
```

The marginal means at each timepoint can be obtained using `dummy.coef`:

```
dummy.coef(eUN.lmm)
```

```
time estimate    se    df   lower   upper
1  B3m 128.5386 4.536445 18.97584 119.04289 138.0343
2  B1w 120.6564 4.261691 19.04078 111.73783 129.5749
3  A1w 116.7506 3.956964 19.04925 108.47007 125.0312
4  A3m 102.4162 3.747908 19.05531  94.57328 110.2591
```

3.6 Extract estimated coefficient and associated uncertainty

The uncertainty about the mean coefficients can be obtained using the `model.tables` method ²:

```
model.tables(eUN.lmm)
```

	estimate	se	df	lower	upper	p.value
(Intercept)	132.9801355	4.6642475	19.75815	123.243045	142.7172256	0.000000e+00
timeB1w	-7.8822331	0.7131797	19.17147	-9.374032	-6.3904339	9.273644e-10
timeA1w	-11.7879545	1.0175135	21.64404	-13.900162	-9.6757467	9.552470e-11
timeA3m	-26.1223908	1.6564077	18.84049	-29.591280	-22.6535021	2.617462e-12
glucagon	-0.8883081	0.2416081	13.70759	-1.407545	-0.3690712	2.571605e-03

Values for the all correlation parameters can be displayed too, by specifying `effect="all"`:

```
model.tables(eUN.lmm, effect = "all")
```

	estimate	se	df	lower	upper	p.value
(Intercept)	132.9801355	4.664247e+00	19.75815	123.2430454	142.7172256	0.000000e+00
timeB1w	-7.8822331	7.131797e-01	19.17147	-9.3740323	-6.3904339	9.273644e-10
timeA1w	-11.7879545	1.017513e+00	21.64404	-13.9001622	-9.6757467	9.552470e-11
timeA3m	-26.1223908	1.656408e+00	18.84049	-29.5912795	-22.6535021	2.617462e-12
glucagon	-0.8883081	2.416081e-01	13.70759	-1.4075449	-0.3690712	2.571605e-03
sigma	20.2808131	1.042207e+08	17.94875	14.4225149	28.5187002	NA
k.B1w	0.9390916	8.746246e-02	19.25090	0.8742815	1.0087060	8.159292e-02
k.A1w	0.8705176	9.733113e-02	20.32066	0.7996375	0.9476805	2.778018e-03
k.A3m	0.8264480	1.820402e-01	19.48030	0.6997216	0.9761257	2.692889e-02
rho(B3m,B1w)	0.9889048	9.815766e-02	32.79091	0.9719687	0.9956310	7.778223e-13
rho(B3m,A1w)	0.9848800	9.911546e-02	26.28819	0.9614535	0.9941119	5.780221e-11
rho(B3m,A3m)	0.9380157	1.061121e-01	23.56848	0.8470249	0.9755995	1.153943e-07
rho(B1w,A1w)	0.9976791	9.925175e-02	27.01628	0.9939113	0.9991163	3.730349e-14
rho(B1w,A3m)	0.9542904	1.035349e-01	24.72225	0.8860968	0.9820453	1.782701e-08
rho(A1w,A3m)	0.9658511	1.015050e-01	27.88668	0.9147964	0.9865286	1.450022e-09

Because these parameters are constrained (e.g. strictly positive), their uncertainty is by default computed after transformation (e.g. `log`) and then backtransformed. The `columns` argument can be used to extract more or less information, e.g.:

```
model.tables(eUN.lmm, columns = c("estimate","p.value"))
```

	estimate	p.value
(Intercept)	132.9801355	0.000000e+00
timeB1w	-7.8822331	9.273644e-10
timeA1w	-11.7879545	9.552470e-11
timeA3m	-26.1223908	2.617462e-12
glucagon	-0.8883081	2.571605e-03

²it is equivalent to `confint` method except that by default it also outputs `se` and `p.value`

The functions `add` (resp. `remove`) can be used to add (resp. remove) one or several columns from the default display, e.g.:

```
model.tables(eUN.lmm, columns = add("statistic"))
```

	estimate	se	statistic	df	lower	upper	p.value
(Intercept)	132.9801355	4.6642475	28.510523	19.75815	123.243045	142.7172256	0.000000e+00
timeB1w	-7.8822331	0.7131797	-11.052240	19.17147	-9.374032	-6.3904339	9.273644e-10
timeA1w	-11.7879545	1.0175135	-11.585060	21.64404	-13.900162	-9.6757467	9.552470e-11
timeA3m	-26.1223908	1.6564077	-15.770508	18.84049	-29.591280	-22.6535021	2.617462e-12
glucagon	-0.8883081	0.2416081	-3.676648	13.70759	-1.407545	-0.3690712	2.571605e-03

3.7 Extract estimated residual variance-covariance structure

The method `sigma` can be used to output the modeled residual covariance structure:

```
Sigma <- sigma(eUN.lmm)
Sigma
```

	B3m	B1w	A1w	A3m
B3m	411.3114	381.9734	352.6400	318.8573
B1w	381.9734	362.7326	335.4649	304.6314
A1w	352.6400	335.4649	311.6921	285.8077
A3m	318.8573	304.6314	285.8077	280.9323

and then converted to a correlation matrix using `cov2cor`:

```
cov2cor(Sigma)
```

	B3m	B1w	A1w	A3m
B3m	1.0000000	0.9889048	0.9848800	0.9380157
B1w	0.9889048	1.0000000	0.9976791	0.9542904
A1w	0.9848800	0.9976791	1.0000000	0.9658511
A3m	0.9380157	0.9542904	0.9658511	1.0000000

The method can also be used to extract the residual covariance relative to a "known" individual:

```
sigma(eUN.lmm, cluster = 5)
```

	B3m	A1w	A3m
B3m	411.3114	352.6400	318.8573
A1w	352.6400	311.6921	285.8077
A3m	318.8573	285.8077	280.9323

or for a new individual:

```
newdata <- data.frame(id = "X", time = c("B3m", "B1w", "A1w", "A3m"))
sigma(eUN.lmm, cluster = newdata)
```

	B3m	B1w	A1w	A3m
B3m	411.3114	381.9734	352.6400	318.8573
B1w	381.9734	362.7326	335.4649	304.6314
A1w	352.6400	335.4649	311.6921	285.8077
A3m	318.8573	304.6314	285.8077	280.9323

3.8 Random effects

Mixed model having a compound symmetry structure with positive correlation parameters may be equivalent to random intercept models, possibly with nested random effects. Indeed in some case the residual variance-covariance matrix can then be decomposed as:

$$\Omega = Z\Psi Z^T + \Delta$$

where:

- Z is the design matrix associated to the random effect (e.g. patient id)
- Ψ is the variance-covariance of the random effects
- Δ the residual variance covariance conditional to the random effects.

One can use the `lme4` syntax to fit random intercept models with `lmm`:

```
eRI.lmm <- eCS.lmm <- lmm(weight ~ time + glucagon + (1|id), data = dfL)
eRI.lmm
```

Linear Mixed Model with a random intercept

```
outcome/cluster/time: weight/id/XXtimeXX
data                  : 78 observations from 20 clusters
parameter             : 5 mean ((Intercept) timeB1w timeA1w timeA3m glucagon)
                      1 variance (sigma)
                      1 correlation (rho)
log-restr.likelihood: -243.600523870252
convergence           : TRUE (9 iterations)
```

It is also possible to specify cross or nested random effects, e.g.:

```
eNRI.lmm <- lmm(weight ~ time*group + (1|id/baseline), data = dfL)
eNRI.lmm
```

Linear Mixed Model with nested random intercepts

```
outcome/cluster/time: weight/id/XXtimeXX
data                  : 78 observations from 20 clusters
parameter             : 8 mean ((Intercept) timeB1w timeA1w timeA3m group timeB1w:group timeA1w:group)
                      1 variance (sigma)
                      2 correlation (rho(baseline) rho(id))
log-restr.likelihood: -230.532819632968
convergence           : TRUE (6 iterations)
```

We obtain the same log-likelihood as, respectively, `eCS.lmm` and `eBCS.lmm`. Indeed, as previously mentioned, with positive residual correlation the random effect structure is equivalent to a compound symmetry structure.

⚠ random slopes are not currently supported in LMMstar.

⚠ the proposed implementation can be very inefficient compared to `lme4`.

The joint distribution between the outcome \mathbf{Y} and the random effects $\boldsymbol{\eta}$ can be explicit as:

$$\begin{bmatrix} \mathbf{Y} \\ \boldsymbol{\eta} \end{bmatrix} \sim \mathcal{N} \left(\begin{bmatrix} \boldsymbol{\mu} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \Omega & Z\Psi \\ \Psi Z^\top & \Psi \end{bmatrix} \right)$$

Denote by $\varepsilon_i = \mathbf{Y}_i - \boldsymbol{\mu}_i$ the vector of marginal residuals relative to individual i , Ω_i its variance-covariance matrix, and $\psi_j = (\Psi)_{jj}$ the variance of the j -th random effect. We can re-express the expected value of the j -th random effect for individual i as:

$$\eta_{ij} = \psi_j Z_{ij} \Omega_i^{-1} \varepsilon_i$$

This is what the `ranef` method returns:

head(ranef(eCS.lmm, format = "wide"))			head(ranef(eNRI.lmm, format = "wide"))			
	<code>id</code>	<code>estimate</code>	<code>id</code>	<code>estimate</code>	<code>estimate.0</code>	<code>estimate.1</code>
1	1	0.9036038	1	4.931442	0.52901983	-0.4829138
2	2	32.5542378	2	28.390660	-0.09204109	0.3574766
3	3	-18.3099658	3	-13.728389	0.18951039	-0.3178625
4	4	20.2561307	4	15.645550	0.82309894	-0.6768225
5	5	-15.4258816	5	-11.246852	-0.30658155	0.2014303
6	6	19.3751847	6	15.002108	-2.64303027	2.7832909

It is also possible to extract the variance decomposition by setting the argument `effects` to `"variance"`:

ranef(eCS.lmm, effects = "variance", format = "wide", simplify = FALSE)				
	<code>variable</code>	<code>strata</code>	<code>variance</code>	<code>relative</code>
1	<code>total</code>	1	355.30623	1.00000000
2	<code>id</code>	1	344.62363	0.96993408
3	<code>residual</code>	1	10.68261	0.03006592

ranef(eNRI.lmm, effects = "variance", format = "wide", simplify = FALSE)				
	<code>variable</code>	<code>strata</code>	<code>variance</code>	<code>relative</code>
1	<code>total</code>	1	346.744085	1.00000000
2	<code>id</code>	1	336.182537	0.969540799
3	<code>baseline</code>	1	3.143104	0.009064622
4	<code>residual</code>	1	7.418444	0.021394579

3.9 Sum of squares

⚠ The definition of the sum of squares is not straightforward with mixed models. Intuitively summing residuals across several outcomes will be hard to interpret unless all outcomes have the same variance. This is why LMMstar does not provide them. Nevertheless for specific covariance structure, namely independence and compound symmetry (with positive correlation) structure, sum of squares can be deduced from the `lmm` object - see appendix C for the theoretical derivations. Importantly, with these structures the residuals can be reparametrised as random effects plus independent residuals, i.e. $\Omega = Z\Psi Z^\top + \delta I$ where I is the identity matrix and δ the variance of these independent residuals.

Appendix C illustrate how to extract the sum of squares for univariate linear regression (i.e. independence structure) and here we illustrate the case of a compound symmetry structure. A key step is to extract from the `lmm` object the conditional variance δ :

```
sigma2 <- coef(eCS.lmm, effect = "variance")^2
tau <- coef(eCS.lmm, effect = "correlation")*sigma2
delta <- unname(sigma2 - tau)
```

This step will typically depend on the covariance structure. The residual sum of squares (SSE) equals the residual degrees of freedom times the conditional variance:

```
df.res <- df.residual(eCS.lmm)
SSE <- df.res * delta
c(df.res = df.res, SSE = SSE)
```

```
df.res      SSE
73.0000 779.8304
```

For the regression sum of squares (SSR), we first extract the mean parameters and their variance-covariance based on the expected information:

```
eBeta.lmm <- coef(eCS.lmm)
eVcov.lmm <- vcov(eCS.lmm, type.information = "expected")
```

Parameters are grouped with respect to the original variable:

```
attr(model.matrix(eCS.lmm), "assign")
```

```
[1] 0 1 1 1 2
```


So we respect this grouping when computing the normalized SSR:

```
SSRstar.time <- eBeta.lmm[2:4] %*% solve(eVcov.lmm[2:4,2:4]) %*% eBeta.lmm[2:4]
SSRstar.glucagon <- eBeta.lmm[5] %*% solve(eVcov.lmm[5,5]) %*% eBeta.lmm[5]
```

The SSR is obtained by multiplying the normalized SSR by the conditional variance:

```
SSR.time <- as.double(SSRstar.time * delta)
SSR.glucagon <- as.double(SSRstar.glucagon * delta)
c(time = SSR.time, glucagon = SSR.glucagon)
```

```
      time  glucagon
6986.78351  18.83074
```

3.10 Proportion of explained variance and partial correlation

⚠ The definition of explained variance is not straightforward with mixed models. Intuitively considering the variance across several outcomes will be hard to interpret unless all outcomes have the same variance. Similar consideration holds for partial correlation. This is why LMMstar does not output these quantities by default. Nevertheless for specific covariance structure, namely independence and compound symmetry (with positive correlation) structure, explained variance and partial correlation can be deduced from the `lmm` object. Importantly, with these structures the residuals can be reparametrised as random effects plus independent residuals, i.e. $\Omega = Z\Psi Z^\top + \delta I$ where I is the identity matrix and δ the variance of these independent residuals.

The proportion of explained variance, also called partial R^2 or partial η^2 , is defined as the ratio between sum of squares (e.g. [Lakens \(2013\)](#), equation 12):

$$R^2 = \frac{SSR}{SSR + SSE}$$

```
c(SSR.time/ (SSR.time + SSE),
  SSR.glucagon/ (SSR.glucagon + SSE))
```

```
[1] 0.89959197 0.02357789
```

Computing the SSR for each individual coefficients, taking its squared root, and multiplying by the sign of the corresponding coefficient leads to the partial correlation

```
eCS.R2 <- partialCor(eCS.lmm, R2 = TRUE)
summary(eCS.R2)
```

Partial correlation

```
      estimate    se  df  lower  upper  p.value
timeB1w   -0.646 0.055 18.6 -0.762  -0.53 5.11e-10
timeA1w   -0.765 0.035  9.5 -0.845 -0.686 2.07e-09
```

```
timeA3m    -0.946 0.006  2.4 -0.969 -0.923 6.80e-06
glucagon   0.154 0.114 45.3 -0.076  0.383   0.184
-----
```

Columns lower and upper contain 95% pointwise confidence intervals for each coefficient. Degrees of freedom were computed using a Satterthwaite approximation (column df).

Coefficient of determination (R2)

```
      estimate    se    df  lower upper  p.value
time          0.9 0.011  2.4  0.857 0.942 4.09e-05
glucagon      0.024 0.035 45.3 -0.047 0.094   0.503
global        0.906 0.011  2.3  0.866 0.946 4.51e-05
-----
```

Columns lower and upper contain 95% pointwise confidence intervals for each coefficient. Degrees of freedom were computed using a Satterthwaite approximation (column df).

Here the line "global" refer to the R2 for all covariates, computed based on the SSR relative to all mean parameters but the intercept.

⚠ `partialCor` will compute values for all types of mixed models. But their interpretation as partial correlation and proportion of explained variance outside the covariance structures mentioned in this section is questionable.

Note: Other software packages like `effectsize::eta_squared` uses another formula to estimate the partial R2:

$$R^2 = \frac{F df_{num}}{F df_{num} + df_{denom}}$$

where F denote the F-statistic, df_{num} (resp. df_{denom}) the degrees of freedom of the numerator (resp. denominator) of this statistic. However since the calculation of degrees of freedom in LMM is approximate, I would expect this approach to be less reliable than the one of `partialCor` based on the SSR and SSE.

```
aCS.aov <- anova(eCS.lmm)$multivariate
setNames(with(aCS.aov, statistic*df.num/(statistic*df.num+df.denom)), aCS.aov$test)
```

```
      time  glucagon
0.92380363 0.03162017
```

3.11 Model diagnostic

The method `residuals` returns the residuals in the wide format:

```
eUN.diagW <- residuals(eUN.lmm, type = "normalized", format = "wide")
colnames(eUN.diagW) <- gsub("normalized.", "", colnames(eUN.diagW))
head(eUN.diagW)
```

	cluster	r.B3m	r.B1w	r.A1w	r.A3m
1	1	-0.1082872	0.4283943	0.7477306	0.91794015
2	2	1.8182348	-0.3516996	1.5698307	-0.98743171
3	3	-0.9318737	-0.7728221	0.6315751	0.16549699
4	4	0.8408969	1.8695564	0.3485784	-0.09662565
5	5	-0.7882340	NA	-0.6128276	0.09933842
6	6	1.4896141	-1.9727358	-1.9672939	-1.37068983

or in the long format:

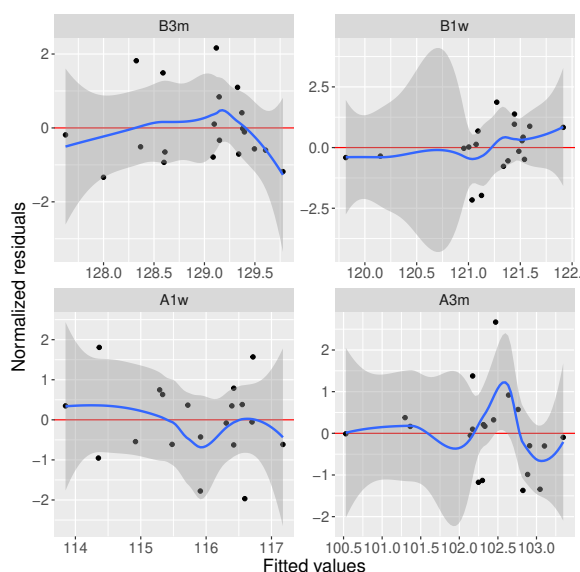
```
eUN.diagL <- residuals(eUN.lmm, type = "normalized", format = "long", keep.data = TRUE)
head(eUN.diagL)
```

	id	visit	time	weight	glucagonAUC	baseline	glucagon	group	fitted	r.normalized
1	1	1	B3m	127.2	5032.50	TRUE	4.034616	1	129.3962	-0.1082872
2	2	1	B3m	165.2	12142.50	TRUE	5.240766	0	128.3247	1.8182348
3	3	1	B3m	109.7	10321.35	TRUE	4.931824	1	128.5992	-0.9318737
4	4	1	B3m	146.2	6693.00	TRUE	4.316306	0	129.1459	0.8408969
5	5	1	B3m	113.1	7090.50	TRUE	4.383738	1	129.0860	-0.7882340
6	6	1	B3m	158.8	10386.00	TRUE	4.942791	0	128.5894	1.4896141

Various type of residuals can be extract but the normalized one are recommended when doing model checking. Diagnostic plots can then be generated by the user, or directly from the `lmm` object via the method `plot` (which internally calls the `residuals` method):

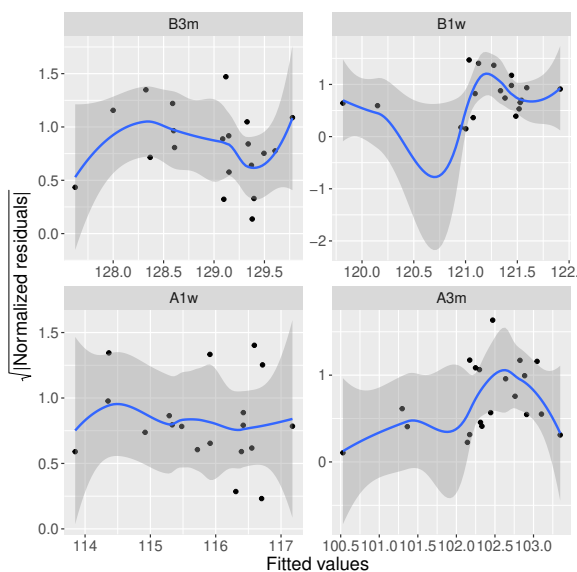
- misspecification of the mean structure

```
plot(eUN.lmm, type = "scatterplot")
```



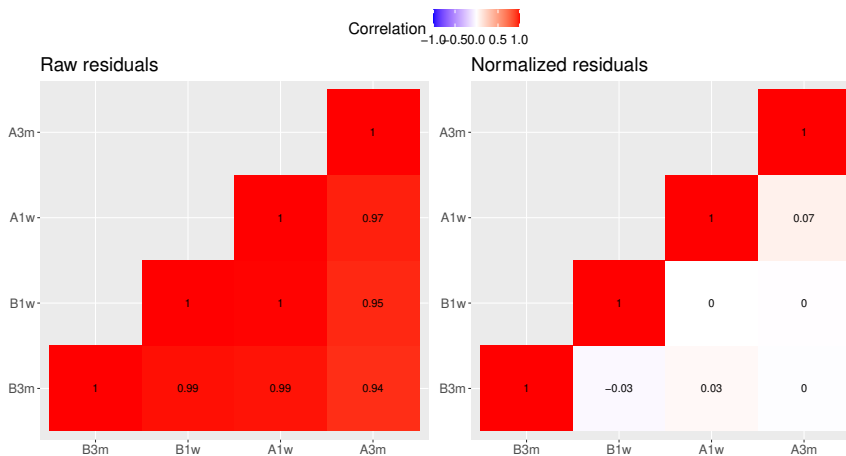
- misspecification of the variance structure

```
plot(eUN.lmm, type = "scatterplot2")
```



- misspecification of the correlation structure

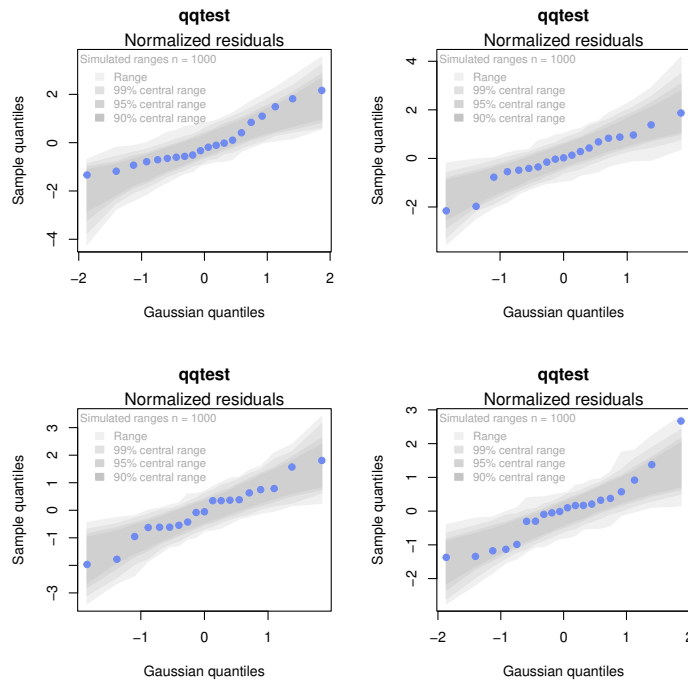
```
plot(eUN.lmm, type = "correlation", type.residual = "response")
plot(eUN.lmm, type = "correlation", type.residual = "normalized")
```



- residual distribution vs. normal distribution ³:

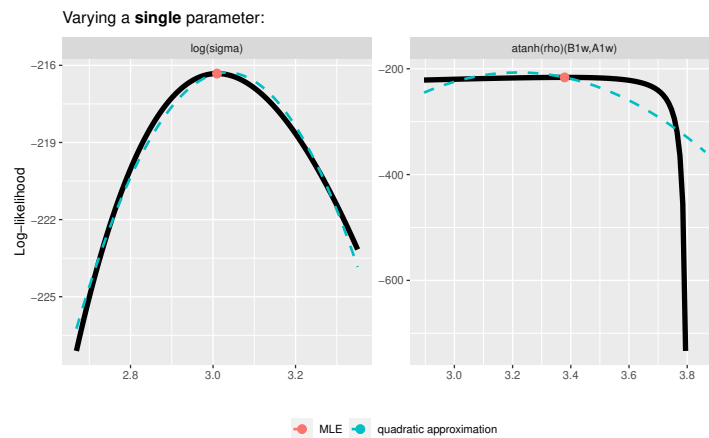
```
plot(eUN.lmm, type = "qqplot", engine.qqplot = "qqtest")
## Note: the qqtest package to be installed to use the argument engine.plot = "qqtest"
```

³see Oldford (2016) for guidance about how to read quantile-quantile plots.



⚠ Deviation from the normal distribution does not necessarily question the validity of the statistical inference. Moreover, for variance and correlation parameters, normally distributed data is not enough to ensure valid statistical inference. Instead one could assess whether the log-likelihood is locally quadratic as this ensures normally distributed estimates in finite samples (Geyer, 2013). Since the likelihood function is a multi-dimensional function this is not an easy task but one can look at specific 'slices' using the `profile` method:

```
plot(profile(eUN.lmm, effects = c("sigma", "rho(B1w,A1w)")))
```

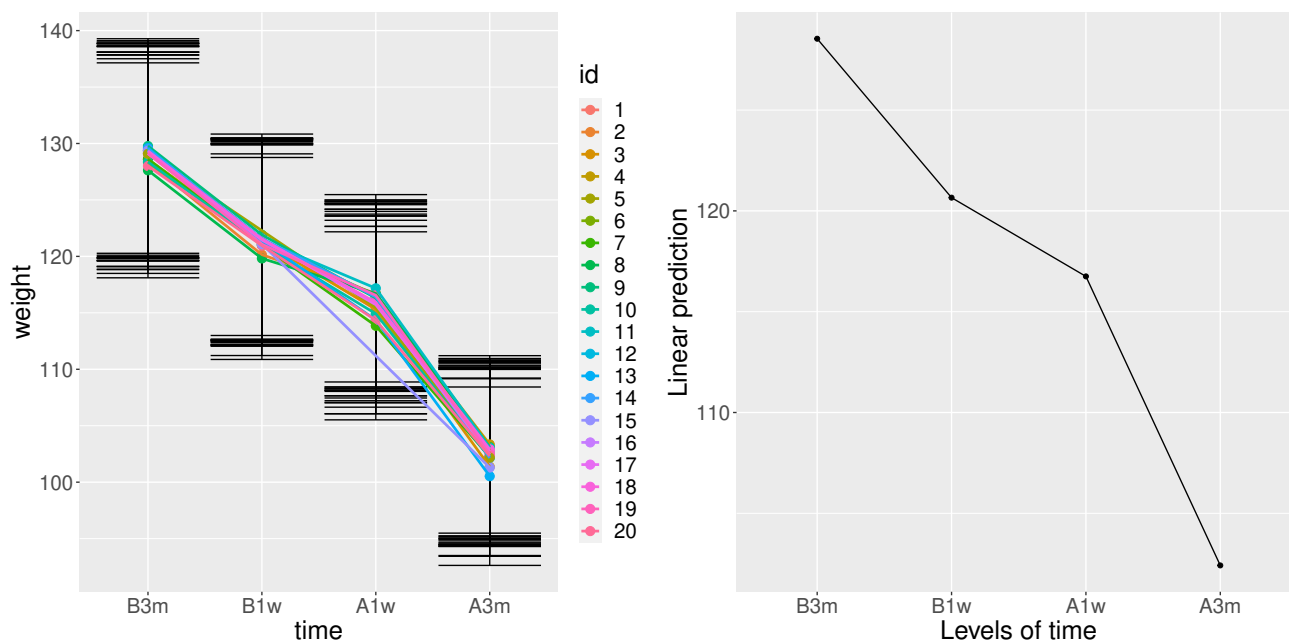


3.12 Model fit

The fitted values can be displayed via the `plot` method or using the `emmeans` package:

```
library(ggplot2) ## left panel
plot(eUN.lmm, type = "fit", color = "id", ci.alpha = NA, size.text = 20)
```

```
library(emmeans) ## right panel
emmip(eUN.lmm, ~time) + theme(text = element_text(size=20))
```

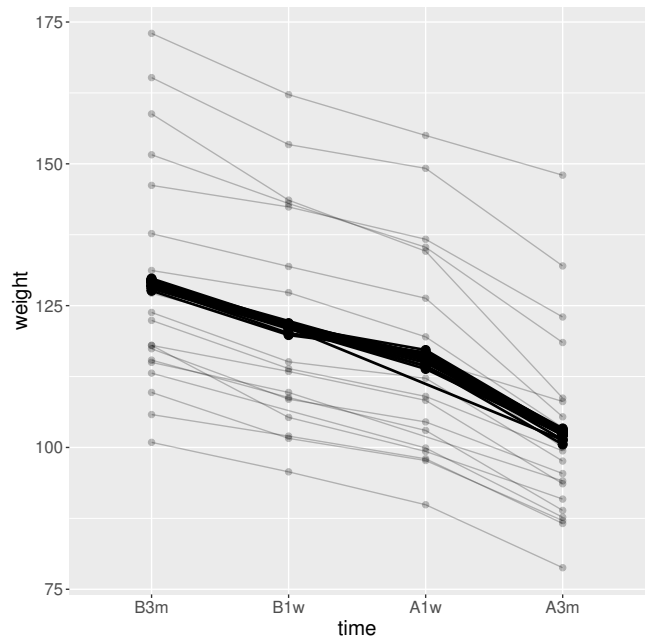
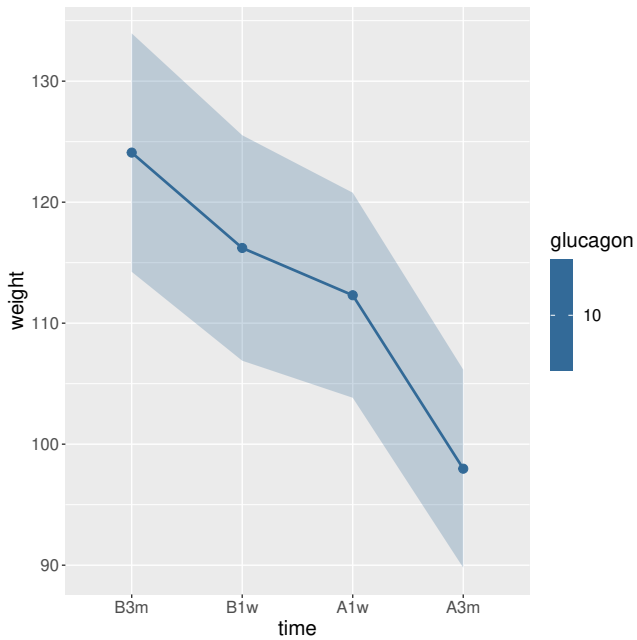


In the first case each possible curve is displayed while in the latter the average curve (over glucagon values). With the `plot` method, it is possible to display a curve specific to a glucagon value via the argument `at`:

```
## left panel
plot(eUN.lmm, type = "fit", at = data.frame(glucagon = 10), color = "glucagon")
```

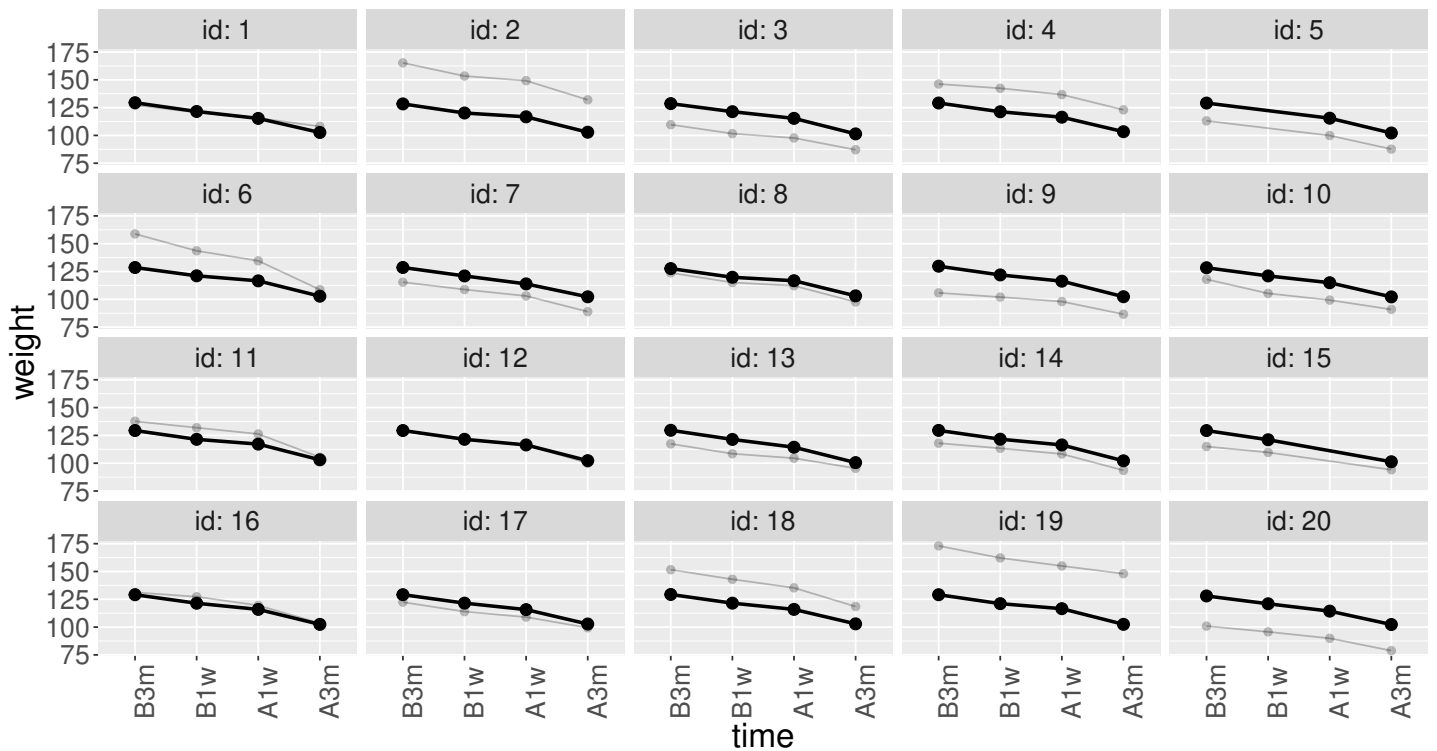
It is also possible to display the observed values along with the fitted values by setting the argument `obs.alpha` to a strictly positive value below or equal to 1. This argument controls the transparency of the color used to display the observed values:

```
## right panel
gg.spafit <- plot(eUN.lmm, type = "fit", obs.alpha = 0.25, ci = FALSE)$plot
```



The `plot` element output by the `plot` method can be manipulated as a `ggplot` object to modify the visual appearance, e.g. to compare each individual trajectory to the model fit:

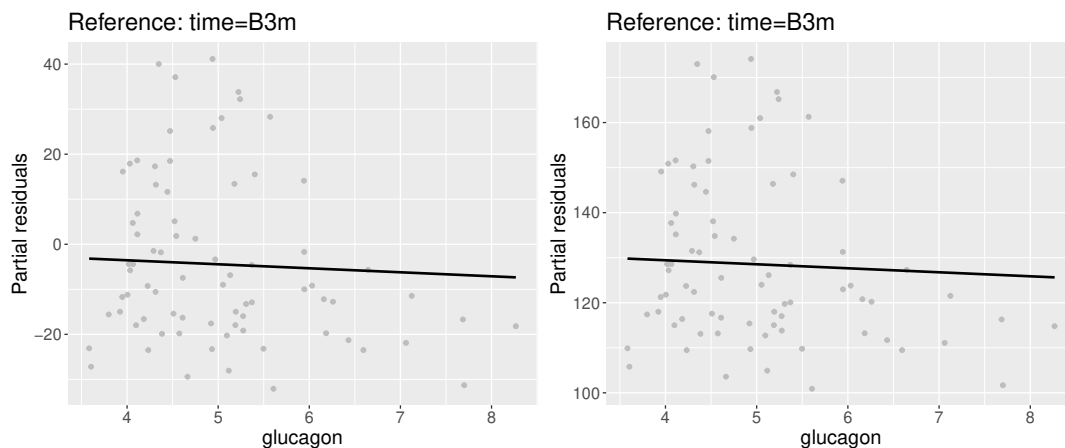
```
gg.traj <- gg.spafit + facet_wrap(~id, labeller = label_both)
gg.traj <- gg.traj + theme(axis.text.x=element_text(angle = 90, hjust = 0))
gg.traj
```



3.13 Partial residuals

Partial residuals can also be displayed via the plot method:

```
gg1 <- plot(eUN.lmm, type = "partial", var = "glucagon")$plot
gg2 <- plot(eUN.lmm, type = "partial", var = c("(Intercept)", "glucagon"))$plot
ggarrange(gg1, gg2)
```



Their value can be extracted via the `residuals` method, e.g.:

```
df.pres <- residuals(eUN.lmm, type = "partial", var = "glucagon", keep.data = TRUE)
head(df.pres)
```

```
  id visit time weight glucagonAUC baseline glucagon group fitted r.partial
1  1     1  B3m 127.2   5032.50     TRUE 4.034616     1 -3.583982 -5.780136
2  2     1  B3m 165.2  12142.50     TRUE 5.240766     0 -4.655415 32.219864
3  3     1  B3m 109.7  10321.35     TRUE 4.931824     1 -4.380979 -23.280136
4  4     1  B3m 146.2   6693.00     TRUE 4.316306     0 -3.834209 13.219864
5  5     1  B3m 113.1   7090.50     TRUE 4.383738     1 -3.894110 -19.880136
6  6     1  B3m 158.8  10386.00     TRUE 4.942791     0 -4.390721 25.819864
NULL
```

This matches manual calculation:

```
m.pres <- dfL$weight - model.matrix(~time, dfL) %*% coef(eUN.lmm)[1:4]
range(df.pres$r.partial - m.pres, na.rm = TRUE)

m.pfit <- model.matrix(~0+glucagon, dfL) %*% coef(eUN.lmm)["glucagon"]
range(df.pres$fitted - m.pfit, na.rm = TRUE)
```

```
[1] -1.421085e-14 1.421085e-14
[1] 0 0
```

The `plot` methods can handle one continuous and one categorical covariate (in addition to the intercept) to display interaction plots. In that case each observation/fitted line is colored according to the categorical covariate.

3.14 Statistical inference (linear)

The `anova` method can be used to test one or several linear combinations of the model coefficients using Wald tests. By default, it will simultaneously test all parameters associated to a variable:

```
anova(eUN.lmm)
```

Multivariate Wald test

	F-statistic	df	p.value
mean: time	86.743 (3,19.0)	2.84e-11	***
: glucagon	13.518 (1,13.7)	0.00257	**

Note that here the p-values are not adjusted for multiple comparisons over variables. It is possible to specify a null hypothesis to be tested: e.g. is there a change in average weight just after taking the treatment:

```
anova(eUN.lmm, effects = c("timeA1w-timeB1w=0"))
```

Multivariate Wald test

	F-statistic	df	p.value
all: 1	43.141 (1,17.9)	3.72e-06	***

One can also simultaneously test several null hypotheses:

```
e.anova <- anova(eUN.lmm, effects = c("timeA1w-timeB1w=0", "timeA3m-timeB1w=0"))
summary(e.anova)
```

Multivariate Wald test

	F-statistic	df	p.value
all: 1	98.651 (2,18.6)	1.23e-10	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1.

Degrees of freedom were computed using a Satterthwaite approximation (column df).

Univariate Wald test

	estimate	se	df	lower	upper	p.value
timeA1w - timeB1w	-3.906	0.595	17.9	-5.329	-2.482	<1e-05 ***
timeA3m - timeB1w	-18.24	1.323	19	-21.407	-15.073	<1e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1.

Columns lower/upper/p.value adjusted for multiple comparisons -- max-test.

(1e+05 samples have been used)

Model-based standard errors are derived from the observed information (column se).

Degrees of freedom were computed using a Satterthwaite approximation (column df).

or return all pairwise comparisons for a given factor using the `mcp` function of the `multcomp` package:

```
library(multcomp)
summary(anova(eUN.lmm, effects = mcp(time = "Tukey")))
```

Singular contrast matrix: contrasts "A1w - B1w" "A3m - B1w" "A3m - A1w" have been removed.

Multivariate Wald test

	F-statistic	df	p.value
all: time	86.743	(3,19.0)	2.84e-11 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1.

Degrees of freedom were computed using a Satterthwaite approximation (column df).

Univariate Wald test

	estimate	se	df	lower	upper	p.value
B1w - B3m	-7.882	0.713	19.2	-9.821	-5.944	<1e-05 ***
A1w - B3m	-11.788	1.018	21.6	-14.554	-9.022	<1e-05 ***
A3m - B3m	-26.122	1.656	18.8	-30.625	-21.62	<1e-05 ***
A1w - B1w	-3.906	0.595	17.9	-5.522	-2.289	<1e-05 ***
A3m - B1w	-18.24	1.323	19	-21.836	-14.644	<1e-05 ***
A3m - A1w	-14.334	1.057	20.3	-17.206	-11.463	<1e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1.

Columns lower/upper/p.value adjusted for multiple comparisons -- max-test.

(1e+05 samples have been used)

Model-based standard errors are derived from the observed information (column se).

Degrees of freedom were computed using a Satterthwaite approximation (column df).

Here the `summary` method prints not only the global test but also the result associated to each hypothesis. When testing transformed variance or correlation parameters, parentheses (as in `log(k).B1w`) cause problem for recognizing parameters:

```
try(
  anova(eUN.lmm,
    effects = c("log(k).B1w=0", "log(k).A1w=0", "log(k).A3m=0"))
)
```

Error in `.anova_Wald(object, effects = effects, robust = robust, rhs = rhs, :`

Possible misspecification of the argument 'effects' as running `multcomp::glht` lead to the following

Error in `parse(text = ex[i])` : <text>:1:7: uventet symbol

1: `log(k).B1w`

~

It is then advised to build a contrast matrix, e.g.:

```
name.coef <- rownames(confint(eUN.lmm, effects = "all"))
name.varcoef <- grep("^k",name.coef, value = TRUE)
C <- matrix(0, nrow = 3, ncol = length(name.coef), dimnames = list(name.varcoef, name.coef))
diag(C[name.varcoef,name.varcoef]) <- 1
C[,1:9]
```

```
      (Intercept) timeB1w timeA1w timeA3m glucagon sigma k.B1w k.A1w k.A3m
k.B1w           0         0         0         0         0         0         1         0         0
k.A1w           0         0         0         0         0         0         0         1         0
k.A3m           0         0         0         0         0         0         0         0         1
```

And then call the `anova` method specifying the null hypothesis via the contrast matrix:

```
anova(eUN.lmm, effects = C)
```

Multivariate Wald test

```
      F-statistic      df p.value
all: 1          6.203 (3,18.0) 0.00442 **
```

Note that using the approach of [Pipper et al. \(2012\)](#) it is also possible to adjust for multiple testing across several `lmm` objects. To do so, one first fit the mixed models, then use the `anova` method to indicate which hypotheses are being tested, and combine them using `rbind`. Here is an (artificial) example:

```
Manova <- rbind(anova(eInd.lmm, effects = "glucagon = 0"),
               anova(eCS.lmm, effects = "glucagon = 0"),
               anova(eUN.lmm, effects = "glucagon = 0"),
               name = c("Ind", "CS", "UN"))
summary(Manova)
```

Multivariate Wald test

```
      Chi2-statistic      df p.value
all: 1          6.393 (3,Inf) 0.000251 ***
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1.

Univariate Wald test

```
      estimate      se      df      lower      upper p.value
Ind: glucagon   -8.27  2.574  34.2 -14.403  -2.137 0.00395 **
CS: glucagon     0.822  0.59  53.8  -0.584   2.228 0.40724
UN: glucagon   -0.888  0.353  13.7  -1.729  -0.047 0.03475 *
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1.

Columns lower/upper/p.value adjusted for multiple comparisons -- max-test.

(error when computing the adjusted columns lower/upper/p.value by numerical integration: 6.6e-05)

Robust standard errors are derived from the observed information (column se).

3.15 Statistical inference (non-linear)

The `estimate` function can be used to test one or several non-linear combinations of model coefficients, using a first order delta method to quantify uncertainty. The combination has to be specified via a function (argument `f`). To illustrate its use consider an ANCOVA analysis:

$$Y_{i1} = \alpha + \beta Y_{i,0} + \gamma X_i + e_i$$

```
e.ANCOVA <- lm(weight4 ~ weight1 + group, data = gastricbypassW)
summary(e.ANCOVA)$coef
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-5.9285136	8.78006389	-0.6752244	5.086140e-01
weight1	0.8236279	0.06411563	12.8459772	3.524665e-10
group	4.1404554	2.53335466	1.6343765	1.205604e-01

We can replicate this analysis by first fitting a mixed model:

$$Y_{ij} = \alpha_j + \gamma_j X_i + \varepsilon_{i,j} \text{ where } \varepsilon_i \sim \mathcal{N} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_1^2 & \rho\sigma_1\sigma_2 \\ \rho\sigma_1\sigma_2 & \sigma_2^2 \end{bmatrix} \right)$$

```
dfL14 <- dfL[dfL$visit %in% c(1,4),]
dfL14$time <- droplevels(dfL14$time)
e.lmmANCOVA <- lmm(weight ~ time+time:group, repetition = ~time|id,
  data = dfL14)
```

and then perform a first order delta-method:

```
lava::estimate(e.lmmANCOVA, f = function(p){
  c(Y1 = as.double(p["rho(B3m,A3m)"]*p["k.A3m"]),
    X1 = as.double(p["timeA3m:group"]-p["rho(B3m,A3m)"]*p["k.A3m"]*p["timeB3m:group"]))
})
```

	estimate	se	df	lower	upper	p.value
Y1	0.8236279	0.06230919	9.874633	0.6845551	0.9627007	1.332743e-07
X1	4.1404554	2.46197819	15.161269	-1.1022695	9.3831803	1.130927e-01

Indeed:

$$\begin{aligned} \mathbb{E}[Y_{i2}|Y_{i1}, X_i] &= \alpha_2 + \gamma_2 X_i + \rho \frac{\sigma_2}{\sigma_1} (Y_{i1} - \alpha_1 - \gamma_1 X_i) \\ &= \alpha_2 - \rho \frac{\sigma_2}{\sigma_1} \alpha_1 + \rho \frac{\sigma_2}{\sigma_1} Y_{i1} + \left(\gamma_2 - \rho \frac{\sigma_2}{\sigma_1} \gamma_1 \right) X_i \end{aligned}$$

We obtain identical estimate but different standard-errors/degrees of freedom compared to the univariate linear model approach. The later is to be prefer as it does not rely on approximation. The former is nevertheless useful as it can handle missing data in the outcome variable.

3.16 Baseline adjustment

In clinical trial the group and intervention variable often do not coincide, e.g., in presence of baseline measurement. In our running example, the first two measurement are pre-treatment (i.e. treatment should be "none") while the last two measurements are post-treatment (i.e. treatment should be 1 or 2). The `baselineAdjustment` function can be helpful to:

- define the treatment variable from the time and allocation variable, where baseline has its specific value

```
gastricbypassL$treat <- baselineAdjustment(gastricbypassL, variable = "group",
                                          repetition = ~time|id, constrain = c("B3m","B1w"),
                                          new.level = "none")
table(treat = gastricbypassL$treat, time = gastricbypassL$time, group = gastricbypassL$group)
```

```
, , group = 0
```

```
      time
treat  B3m B1w A1w A3m
  none  10  10  0  0
    0    0  0  10  10
    1    0  0  0  0
```

```
, , group = 1
```

```
      time
treat  B3m B1w A1w A3m
  none  10  10  0  0
    0    0  0  0  0
    1    0  0  10  10
```

- define the treatment variable from the time and allocation variable, where baseline corresponds to the reference group

```
gastricbypassL$treat2 <- baselineAdjustment(gastricbypassL, variable = "group",
                                           repetition = ~time|id, constrain = c("B3m","B1w")
                                           )
table(treat = gastricbypassL$treat2, time = gastricbypassL$time, group = gastricbypassL$group)
```

```
, , group = 0
```

```
      time
treat  B3m B1w A1w A3m
    1  10  10  0  0
    0  0  0  10  10
```

```
, , group = 1
```

```
      time
treat B3m B1w A1w A3m
     1  10  10  10  10
     0   0   0   0   0
```

- define a time varying treatment variable from the time and allocation variable

```
gastricbypassL$timeXtreat <- baselineAdjustment(gastricbypassL, variable = "group",
                                                repetition = ~time|id, constrain = c("B3m", "
B1w"),
                                                collapse.time = ".")

table(treat = gastricbypassL$timeXtreat, time = gastricbypassL$time, group = gastricbypassL$
group)
```

```
, , group = 0
```

```
      time
treat  B3m B1w A1w A3m
  B3m   10  0  0  0
  B1w   0  10  0  0
  A1w.0 0  0  10  0
  A3m.0 0  0  0  10
  A1w.1 0  0  0  0
  A3m.1 0  0  0  0
```

```
, , group = 1
```

```
      time
treat  B3m B1w A1w A3m
  B3m   10  0  0  0
  B1w   0  10  0  0
  A1w.0 0  0  0  0
  A3m.0 0  0  0  0
  A1w.1 0  0  10  0
  A3m.1 0  0  0  10
```

We would then typically like to model group differences only after baseline (i.e. only at 1 week and 3 months after). This can be performed using the time varying treatment variable, e.g.:

```
eC.lmm <- lmm(weight ~ timeXtreat, data = gastricbypassL,
              repetition = ~time|id, structure = "UN")
coef(eC.lmm) ## change from baseline
```

```
(Intercept)    timeXtreatB1w timeXtreatA1w.0 timeXtreatA3m.0 timeXtreatA1w.1 timeXtreatA3m.1
128.97000      -7.73000      -13.38978      -28.52130      -13.15022      -24.68870
```

or

```
eC2.lmm <- lmm(weight ~ 0 + timeXtreat, data = gastricbypassL,
               repetition = ~time|id, structure = "UN")
coef(eC2.lmm) ## absolute value
```

```
timeXtreatB3m    timeXtreatB1w timeXtreatA1w.0 timeXtreatA3m.0 timeXtreatA1w.1 timeXtreatA3m.1
128.9700         121.2400         115.5802         100.4487         115.8198         104.2813
```

The parametrization however does not (directly) output treatment effects. Instead one may be tempted to use a formula like `treatment*time`. However this will lead to a non-identifiable model. Indeed we are only able to estimate a total of 6 means when constraining the expected baseline value between the two groups to be the same. Therefore can at most identify 6 effects. However the design matrix for the interaction model:

```
colnames(model.matrix(weight ~ treat*time, data = gastricbypassL))
```

```
[1] "(Intercept)"      "treat0"           "treat1"           "timeB1w"          "timeA1w"
[6] "timeA3m"          "treat0:timeB1w"  "treat1:timeB1w"  "treat0:timeA1w"  "treat1:timeA1w"
[11] "treat0:timeA3m"  "treat1:timeA3m"
```

contains 12 parameters (i.e. 6 too many). Fortunately, the `lmm` will drop non-identifiable effects from the model and fit the resulting simplified model:

```
eC3.lmm <- lmm(weight ~ treat2*time, data = gastricbypassL,
               repetition = ~time|id, structure = "UN")
```

Constant values in the design matrix for the mean structure.
Coefficients "treat20" "treat20:timeB1w" relative to interactions "treat2:time" have been removed.

with the following coefficients:

```
model.tables(eC3.lmm)
```

	estimate	se	df	lower	upper	p.value
(Intercept)	128.9700000	4.5323695	18.98130	119.483009	138.4569911	0.000000e+00
timeB1w	-7.7300000	0.6974427	18.97552	-9.189892	-6.2701082	9.938186e-10
timeA1w	-13.1502219	0.8970429	22.87334	-15.006465	-11.2939786	4.058975e-13
timeA3m	-24.6886957	1.7751662	22.25061	-28.367762	-21.0096290	1.863398e-12
treat20:timeA1w	-0.2395562	0.6484895	17.66860	-1.603816	1.1247037	7.162149e-01
treat20:timeA3m	-3.8326086	2.1066817	17.60613	-8.265691	0.6004734	8.592047e-02

One can visualize the baseline adjustment via the `plot` function:

```
plot(eC3.lmm, color = "group", ci = FALSE, size.text = 20, obs.alpha = 0.1)
```

3.17 Marginal means

The `emmeans` package can be used to output marginal means. Consider the following model:

```
dfL$group2 <- as.numeric(dfL$id) %% 3 == 0
e.group <- lmm(glucagon ~ time*group2, data = dfL,
              repetition = ~time|id, structure = "UN")
```

We can for instance compute the average value over time *assuming balanced groups*:

```
emmeans(e.group, specs=~time)
```

NOTE: Results may be misleading due to involvement in interactions

time	emmean	SE	df	lower.CL	upper.CL
B3m	4.45	0.156	18.0	4.12	4.78
B1w	4.32	0.131	18.0	4.05	4.60
A1w	5.95	0.262	18.4	5.40	6.50
A3m	5.12	0.187	18.0	4.73	5.51

Results are averaged over the levels of: group2

Confidence level used: 0.95

This differs from the average value over time over the whole sample:

```
df.pred <- predict(e.group, newdata = dfL, keep.newdata = TRUE)
summarize(formula = estimate~time, data = df.pred)
```

	time	observed	missing	mean	sd	min	q1	median	q3	max
1	B3m	20	0	4.514352	0.1502565	4.290643	4.290643	4.610227	4.610227	4.610227
2	B1w	19	0	4.384638	0.1643256	4.149209	4.149209	4.493298	4.493298	4.493298
3	A1w	19	0	6.060587	0.2030009	5.729961	5.954314	6.178668	6.178668	6.178668
4	A3m	20	0	5.057642	0.1465315	4.964144	4.964144	4.964144	5.275805	5.275805

as the groups are not balanced:


```
table(group = dfL$group2, time = dfL$time)
```

```
      time
group  B3m B1w A1w A3m
FALSE  14  13  14  14
TRUE   6   6   5   6
```

The "emmeans" approach gives equal "weight" to the expected value of both group:

```
mu.group1 <- as.double(coef(e.group)[ "(Intercept)" ])
mu.group2 <- as.double(coef(e.group)[ "(Intercept)" ] + coef(e.group)[ "group2TRUE" ])
p.group1 <- 14/20 ; p.group2 <- 6/20
c(emmeans = (mu.group1+mu.group2)/2, predict = mu.group1 * p.group1 + mu.group2 * p.group2)
```

```
emmeans predict
4.450435 4.514352
```

Which one is relevant depends on the application. The `emmeans` function can also be used to display expected value in each group over time:

```
emmeans.group <- emmeans(e.group, specs = ~group2|time)
emmeans.group
```

```
time = B3m:
group2 emmean SE df lower.CL upper.CL
FALSE  4.61 0.171 18.0 4.25 4.97
TRUE   4.29 0.262 18.0 3.74 4.84
```

```
time = B1w:
group2 emmean SE df lower.CL upper.CL
FALSE  4.49 0.145 18.4 4.19 4.80
TRUE   4.15 0.219 17.9 3.69 4.61
```

```
time = A1w:
group2 emmean SE df lower.CL upper.CL
FALSE  6.18 0.277 17.8 5.60 6.76
TRUE   5.73 0.446 18.6 4.80 6.66
```

```
time = A3m:
group2 emmean SE df lower.CL upper.CL
FALSE  4.96 0.205 18.0 4.53 5.39
TRUE   5.28 0.313 18.0 4.62 5.93
```

Confidence level used: 0.95

Using the pair function displays the differences:

```
epairs.group <- pairs(emmeans.group, reverse = TRUE)
epairs.group
```

```
time = B3m:
  contrast      estimate    SE   df t.ratio p.value
TRUE - FALSE  -0.320 0.313 18.0  -1.022  0.3202
```

```
time = B1w:
  contrast      estimate    SE   df t.ratio p.value
TRUE - FALSE  -0.344 0.262 18.0  -1.311  0.2062
```

```
time = A1w:
  contrast      estimate    SE   df t.ratio p.value
TRUE - FALSE  -0.449 0.525 18.4  -0.855  0.4034
```

```
time = A3m:
  contrast      estimate    SE   df t.ratio p.value
TRUE - FALSE   0.312 0.374 18.0   0.834  0.4153
```

One can adjust for multiple comparison via the `adjust` argument and display confidence intervals setting the argument `infer` to `TRUE`:

```
summary(epairs.group, by = NULL, adjust = "mvt", infer = TRUE)
```

```
contrast      time estimate    SE   df lower.CL upper.CL t.ratio p.value
TRUE - FALSE B3m   -0.320 0.313 18.0   -1.16   0.518  -1.022  0.6928
TRUE - FALSE B1w   -0.344 0.262 18.0   -1.05   0.359  -1.311  0.5066
TRUE - FALSE A1w   -0.449 0.525 18.4   -1.86   0.958  -0.855  0.7961
TRUE - FALSE A3m    0.312 0.374 18.0   -0.69   1.314   0.834  0.8085
```

```
Confidence level used: 0.95
Conf-level adjustment: mvt method for 4 estimates
P value adjustment: mvt method for 4 tests
```

This should also work when doing baseline adjustment (because of baseline adjustment no difference is expected at the first two timepoints):

```
summary(pairs(emmeans(eC3.lmm , specs = ~treat2|time), reverse = TRUE), by = NULL)
```

```
Note: adjust = "tukey" was changed to "sidak"
because "tukey" is only appropriate for one set of pairwise comparisons
```

```
contrast      time estimate    SE   df t.ratio p.value
treat20 - treat21 B3m      0.00 0.000 Inf     NaN     NaN
treat20 - treat21 B1w      0.00 0.000 Inf     NaN     NaN
treat20 - treat21 A1w     -0.24 0.648  18   -0.369  0.9935
treat20 - treat21 A3m     -3.83 2.107  18   -1.819  0.3019
```

```
P value adjustment: sidak method for 4 tests
```

3.18 Predictions

Two types of predictions can be performed with the `predict` method:

- **static predictions** that are only conditional on the covariates:

```
news <- dfL[dfL$id==1,]
news$glucagon <- 0
predict(eUN.lmm, newdata = news)
```

```
      estimate      se      df      lower      upper
1 132.9801 4.664247 19.75815 123.24305 142.7172
2 125.0979 4.388294 19.91418 115.94155 134.2543
3 121.1922 4.214230 20.55331 112.41660 129.9678
4 106.8577 3.942058 20.95499  98.65871 115.0568
```

which can be computed by creating a design matrix:

```
X.12 <- model.matrix(formula(eUN.lmm), news)
X.12
```

```
      (Intercept) timeB1w timeA1w timeA3m glucagon
1             1         0         0         0         0
21            1         1         0         0         0
41            1         0         1         0         0
61            1         0         0         1         0
attr(,"assign")
[1] 0 1 1 1 2
attr(,"contrasts")
attr(,"contrasts")$time
[1] "contr.treatment"
```

and then multiplying it with the regression coefficients:

```
X.12 %*% coef(eUN.lmm)
```

```
      [,1]
1 132.9801
21 125.0979
41 121.1922
61 106.8577
```

- **dynamic predictions** that are conditional on the covariates and the outcome measured at other timepoints. Consider two subjects for who we would like to predict the weight 1 week before the intervention based on the weight 3 months before the intervention:

```
newd <- rbind(
  data.frame(id = 1, time = "B3m", weight = coef(eUN.lmm)["(Intercept)"], glucagon = 0),
  data.frame(id = 1, time = "B1w", weight = NA, glucagon = 0),
  data.frame(id = 2, time = "B3m", weight = 100, glucagon = 0),
  data.frame(id = 2, time = "B1w", weight = NA, glucagon = 0)
)
predict(eUN.lmm, newdata = newd, type = "dynamic", keep.newdata = TRUE)
```

	id	time	weight	glucagon	estimate	se	df	lower	upper
1	1	B3m	132.9801	0	NA	NA	Inf	NA	NA
2	1	B1w	NA	0	125.09790	0.6362754	Inf	123.85083	126.3450
3	2	B3m	100.0000	0	NA	NA	Inf	NA	NA
4	2	B1w	NA	0	94.47017	7.2279385	Inf	80.30367	108.6367

The first subjects has the average weight while the second has a much lower weight. The predicted weight for the first subject is then the average weight one week before while it is lower for the second subject due to the positive correlation over time. The predicted value is computed using the formula of the conditional mean for a Gaussian vector:

```
mu1 <- coef(eUN.lmm)[1]
mu2 <- sum(coef(eUN.lmm)[1:2])
Omega_11 <- sigma(eUN.lmm)["B3m","B3m"]
Omega_21 <- sigma(eUN.lmm)["B1w","B3m"]
as.double(mu2 + Omega_21 * (100 - mu1) / Omega_11)
```

```
[1] 94.47017
```

4 Equivalence with other statistical methods

4.1 T-test

A t-test:

```
t.test(weight4 ~ group, data = gastricbypassW)
```

Welch Two Sample t-test

```
data: weight4 by group
t = 0.59144, df = 17.679, p-value = 0.5617
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
95 percent confidence interval:
 -11.73582  20.91582
sample estimates:
mean in group 0 mean in group 1
    104.66      100.07
```

is equivalent to an independent covariance pattern with a different variable for each group:

```
e.tttest4 <- lmm(weight4 ~ group, structure = IND(~group),
                data = gastricbypassW, trace = FALSE)
model.tables(e.tttest4)
```

	estimate	se	df	lower	upper	p.value
(Intercept)	104.66	5.104469	9.00180	93.11324	116.20676	7.270954e-09
group	-4.59	7.760674	17.68244	-20.91558	11.73558	5.617090e-01

Multiple t-tests:

```
e.tttest1 <- lmm(weight1 ~ group, structure = IND(~group),
                data = gastricbypassW, trace = FALSE)
e.tttest2 <- lmm(weight2 ~ group, structure = IND(~group),
                data = gastricbypassW, trace = FALSE)
e.tttest3 <- lmm(weight3 ~ group, structure = IND(~group),
                data = gastricbypassW, trace = FALSE)
```

can be adjusted for multiple comparison by first using the `anova` function to specify the parameter of interest and combining the results using `rbind`:

```
e.mttest <- rbind(anova(e.tttest1, effects = "group=0"),
                 anova(e.tttest2, effects = "group=0"),
                 anova(e.tttest3, effects = "group=0"),
                 anova(e.tttest4, effects = "group=0"))
model.tables(e.mttest, method = "bonferroni")
```

	estimate	se	df	lower	upper	p.value
weight1: group	-10.60	8.971747	17.96464	-35.49775	14.29775	1
weight2: group	-9.50	8.395143	17.98540	-32.79464	13.79464	1
weight3: group	-8.92	8.129458	17.95876	-31.48110	13.64110	1
weight4: group	-4.59	7.760674	17.68244	-26.16472	16.98472	1

⚠ efficient adjustment for multiple comparisons (like "single-step") will not be valid as the correlation structure has not been specified. To do so it is more convenient to work with the long format:

```
e.mttest2 <- mlmm(weight ~ group, structure = IND(~group),
  data = gastricbypassL, trace = FALSE,
  effects = "group=0", by = "time", repetition = ~time|id)
model.tables(e.mttest2, method = "single-step2")
```

	by parameter	estimate	se	df	lower	upper	p.value
1	B3m group	-10.60	8.971747	17.96464	-30.89407	9.694068	0.3155368
2	B1w group	-9.50	8.395143	17.98540	-28.48979	9.489791	0.3387166
3	A1w group	-8.92	8.129458	17.95876	-27.30881	9.468813	0.3554664
4	A3m group	-4.59	7.760674	17.68244	-22.14462	12.964624	0.6640334

or call the dedicated function `mt.test`:

```
mt.test(weight1+weight2+weight3+weight4~group, data = gastricbypassW)
```

	by parameter	estimate	se	df	lower	upper	p.value
1	weight1 group	-10.60	8.971747	17.96464	-30.97670	9.776698	0.3197968
2	weight2 group	-9.50	8.395143	17.98540	-28.56711	9.567110	0.3423566
3	weight3 group	-8.92	8.129458	17.95876	-27.38368	9.543685	0.3584364
4	weight4 group	-4.59	7.760674	17.68244	-22.21610	13.036099	0.6649434

4.2 Linear regression on the change

A widely spread approach to analyze longitudinal data is to reduce the number of repetitions to 1 by working on the change and then apply 'usual' statistical methods. For instance one could compare the pre- and post- operation values using:

```
gastricbypassW$changeG41 <- gastricbypassW$glucagonAUC4-gastricbypassW$glucagonAUC1
e.change41 <- lm(changeG41 ~ weight1, data = gastricbypassW)
summary(e.change41)$coef
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	17865.953	9292.61106	1.922598	0.07050076
weight1	-113.696	71.22173	-1.596367	0.12781371

This turns out to be equivalent to the following mixed model:

```
gastricbypassL41 <- gastricbypassL[gastricbypassL$visit %in% c(1,4),]
gastricbypassL41$time <- droplevels(gastricbypassL41$time)
gastricbypassL41$weight1 <- gastricbypassW$weight1[gastricbypassL41$id]

e.lmm41 <- lmm(glucagonAUC ~ time + time*weight1,
              repetition =~ time|id, structure = "UN",
              data = gastricbypassL41)
model.tables(e.lmm41)
```

	estimate	se	df	lower	upper	p.value
(Intercept)	7730.051990	5737.22268	18.00298	-4323.26268	19783.36666	0.19458155
timeA3m	17865.953183	9292.61106	18.00104	-1657.01749	37388.92385	0.07049983
weight1	1.011014	43.97202	18.00298	-91.36968	93.39171	0.98190941
timeA3m:weight1	-113.695981	71.22173	18.00104	-263.32666	35.93469	0.12781271

This equivalence only holds as there is no missing data.

```
index.missing41 <- which(is.na(gastricbypassW$changeG41))
index.missing41
```

```
integer(0)
```

4.3 Correlation between changes

In some studies, one is interested in studying the relation between two evolutions. Say weight and glucagon before and after the operation:

```
gastricbypassW$changeG41 <- gastricbypassW$glucagonAUC4-gastricbypassW$glucagonAUC1
gastricbypassW$changeW41 <- gastricbypassW$weight4-gastricbypassW$weight1
```

One can evaluate their correlation:

```
cor.test(gastricbypassW$changeW41, gastricbypassW$changeG41)
```

Pearson's product-moment correlation

```
data: gastricbypassW$changeW41 and gastricbypassW$changeG41
t = 1.8667, df = 18, p-value = 0.07831
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.0484149  0.7174011
sample estimates:
      cor
0.4027343
```

or regress one against the other:

```
e2.change41 <- lm(changeG41 ~ changeW41, data = gastricbypassW)
summary(e2.change41)$coef
```

```
              Estimate Std. Error t value Pr(>|t|)
(Intercept) 13321.9427  5592.8058  2.381978 0.02845909
changeW41    380.3556   203.7541  1.866738 0.07831464
```

This problem can be recast using all measurement as outcomes:

```
keep.col <- c("id", "weight1", "weight4", "glucagonAUC1", "glucagonAUC4")
gastricbypassL4 <- reshape(gastricbypassW[,keep.col], direction = "long",
                          idvar = "id", varying = 2:5, timevar = "type", v.names = "value")
gastricbypassL4$type <- factor(gastricbypassL4$type, labels = keep.col[-1])
gastricbypassL4 <- gastricbypassL4[order(gastricbypassL4$id),]
head(gastricbypassL4)
```

```
   id   type  value
1.1  1 weight1 127.20
1.2  1 weight4 108.10
1.3  1 glucagonAUC1 5032.50
1.4  1 glucagonAUC4 9249.45
2.1  2 weight1 165.20
2.2  2 weight4 132.00
```

fitting an unstructured mixed model:

```
e.lmm4 <- lmm(value ~ type,
              repetition = ~type|id, structure = "UN",
              data = gastricbypassL4)
```

extract the residual covariance matrix:


```
sigma.lmm4 <- sigma(e.lmm4)
sigma.lmm4
```

```
          weight1      weight4 glucagonAUC1 glucagonAUC4
weight1    410.8475    326.8357      415.3727    -46296.33
weight4    326.8357    290.8350     -5983.5871   -34434.03
glucagonAUC1 415.3727 -5983.5871 14299430.9269 -4229230.69
glucagonAUC4 -46296.3339 -34434.0320 -4229230.6877 20065722.32
```

Deduce the residual covariance matrix for the change:

```
Mcon <- cbind(c(-1,1,0,0),c(0,0,-1,1))
sigmeChange.lmm4 <- t(Mcon) %*% sigma.lmm4 %*% Mcon
dimnames(sigmeChange.lmm4) <- list(c("d.weight","d.glucagonAUC"),
                                   c("d.weight","d.glucagonAUC"))
sigmeChange.lmm4
```

```
          d.weight d.glucagonAUC
d.weight    48.01103      18261.26
d.glucagonAUC 18261.26175  42823614.62
```

and the correlation or covariance:

```
cov2cor(sigmeChange.lmm4)[1,2]
sigmeChange.lmm4[1,2]/sigmeChange.lmm4[1,1]
```

```
[1] 0.4027343
[1] 380.3556
```

The uncertainty can be quantified using a delta method:

```
estimate(e.lmm4, function(p){
  Sigma.change <- t(Mcon) %*% sigma(e.lmm4, p = p) %*% Mcon
  c(cor = cov2cor(Sigma.change)[1,2],
    beta = Sigma.change[1,2]/Sigma.change[1,1])
})
```

```
      estimate      se      df      lower      upper  p.value
cor    0.4027343  0.1922078  2.660595  -0.2555602  1.061029  0.1386265
beta 380.3555798 198.3453360  2.798661 -277.3518013 1038.062961  0.1575655
```

The standard errors and degrees of freedom do not match the univariate analysis, suggesting probably poor small sample properties of this technic.

5 Missing values and imputation

We reconsider the example of the previous section, but now in presence of missing values. The `summarize` function can be used to describe the amount of missing data at each repetition:

```
sss <- summarize(glucagon ~ time, data = gastricbypassL, na.rm = TRUE)
cbind(sss[,1:4], pc = paste0(100 * sss$missing / (sss$missing + sss$observed), "%"))
```

```
  outcome time observed missing pc
1 glucagon  B3m      20       0 0%
2 glucagon  B1w      19       1 5%
3 glucagon  A1w      19       1 5%
4 glucagon  A3m      20       0 0%
```

For more detail about the missing data patters, see the `summarizeNA` function:

```
summarizeNA(data = gastricbypassL, repetition = ~ time|id)
```

```
  variable frequency missing.pattern n.missing id B3m B1w A1w A3m
  visit          20          00000          0 0 0 0 0 0
  weight          20          00000          0 0 0 0 0 0
glucagonAUC      18          00000          0 0 0 0 0 0
              1           00100          1 0 0 1 0 0
              1           00010          1 0 0 0 1 0
  baseline       20          00000          0 0 0 0 0 0
  glucagon       18          00000          0 0 0 0 0 0
              1           00100          1 0 0 1 0 0
              1           00010          1 0 0 0 1 0
  group          20          00000          0 0 0 0 0 0
```

To begin with we will only consider 1 week before and 1 week after surgery:

```
## long format
gastricbypassL32 <- gastricbypassL[gastricbypassL$visit %in% c(3,2),]
gastricbypassL32$time <- droplevels(gastricbypassL32$time)
gastricbypassL32$weight1 <- gastricbypassW$weight1[gastricbypassL32$id]
## wide format
gastricbypassW$changeG32 <- gastricbypassW$glucagonAUC3-gastricbypassW$glucagonAUC2
```

5.1 Full information approach

LMM uses a full information approach:

```
e.lmm32 <- lmm(glucagonAUC ~ time + time*weight1,
              repetition =~ time|id, structure = "UN",
              data = gastricbypassL32)
model.tables(e.lmm32)
```

	estimate	se	df	lower	upper	p.value
(Intercept)	2226.30678	4973.21491	17.01148	-8265.72037	12718.33393	0.6600471546
timeA1w	37469.89400	8950.26818	17.88948	18657.74792	56282.04008	0.0005612515
weight1	37.90933	37.87004	17.01113	-41.98548	117.80414	0.3308362562
timeA1w:weight1	-213.20181	68.15807	17.71309	-356.56304	-69.84058	0.0058968630

whereas a linear model would perform a complete case approach:

```
e.change32 <- lm(changeG32 ~ weight1, data = gastricbypassW)
summary(e.change32)$coef
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	38101.9400	9417.61506	4.045816	0.0009373023
weight1	-217.2672	71.25218	-3.049271	0.0076504030

In the former the likelihood is evaluated using all observations, even those from individuals with some (but not all) missing outcome values: baseline is used even if follow-up is missing. In the later the likelihood is only evaluated on individuals with no missing outcome values: if follow-up is missing then baseline is not used. Indeed:


```
coef(lm(changeG32 ~ weight1, data = gastricbypassW[-c(5,15),]))
```

(Intercept)	weight1
38101.9400	-217.2672

The estimates of the LMM can be retrieved using a linear model where we have imputed the conditional expectation of the missing values given the observed value and the estimated model parameters: (see section 5.3 for a graphical representation)

```
gastricbypassWA <- fitted(e.lmm32, impute = TRUE, format = "wide")
gastricbypassWA$change32 <- gastricbypassWA$glucagonAUC_A1w - gastricbypassWA$glucagonAUC_B1w
gastricbypassWA$weight1 <- gastricbypassW$weight1[match(gastricbypassW$id,gastricbypassWA$id)]
coef(lm(change32 ~ weight1, data = gastricbypassWA))
```

(Intercept)	weight1
37469.8940	-213.2018

 Standard errors, confidence intervals, and p-values from this linear model should not be trusted as they do not account for the uncertainty in the imputed values.

5.2 Complete case approach

The `lmmCC` can be used to obtain the LMM that is equivalent to a linear regression. In the case of the comparing the change between groups, the `repetition` argument should indicate how the change has been computed:

```
e.lmmCC <- lmmCC(e.change32, repetition = changeG32 ~ glucagonAUC3-glucagonAUC2|id)
model.tables(e.lmmCC)
```

Remove 2 clusters (4 observations)

- 2 observations with missing data (2 clusters)

- 0 missing repetitions (0 clusters)

	estimate	se	df	lower	upper	p.value
(Intercept)	-36283.0356	12841.66795	15.99997	-63506.15929	-9059.91191	0.0121849728
time	38101.9400	9417.61506	16.00030	18137.51789	58066.36212	0.0009372705
weight1	257.7767	97.15802	15.99997	51.81085	463.74249	0.0173566171
time:weight1	-217.2672	71.25218	16.00030	-368.31484	-66.21956	0.0076502759

As output, the data from two clusters (i.e. 4 observations) has been excluded before fitting the LMM (instead of just the 2 observations with missing values for the full information approach). The interaction term of the LMM matches the regression coefficient of the linear model:

```
summary(e.change32)$coef
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	38101.9400	9417.61506	4.045816	0.0009373023
weight1	-217.2672	71.25218	-3.049271	0.0076504030

In the case of regressing two changes:

```
gastricbypassW$changeW32 <- gastricbypassW$weight3 - gastricbypassW$weight2
```

```
e2g.change32 <- lm(changeG32 ~ changeW32 + group, data = gastricbypassW)
```

```
summary(e2g.change32)$coef
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2720.5540	6930.588	0.3925430	0.7001787
changeW32	-783.8895	1122.541	-0.6983171	0.4956633
group	6059.7378	3525.140	1.7190062	0.1061756

the `repetition` argument should indicate how each change has been computed:

```
e2.lmmCC <- lmmCC(e2g.change32, repetition = list(changeG32 ~ glucagonAUC3-glucagonAUC2|id,
                                                changeW32 ~ weight3-weight2|id))
```

```
model.tables(e2.lmmCC)
```

Remove 2 clusters (8 observations)

- 2 observations with missing data (2 clusters)
- 0 missing repetitions (0 clusters)

	estimate	se	df	lower	upper	p.value
cor	-0.1774435	0.2416113	1.714523	-1.401851	1.046964	0.5499188
beta	-783.8895353	1081.5567036	2.338122	-4848.482516	3280.703446	0.5342415

We retrieve the same estimate for the effect of change in weights but the uncertainty (standard error, confidence intervals, p.value) do not match. They should be asymptotically correct but may not have very good small sample properties.

5.3 Imputation

When fitting a linear mixed model on a dataset with missing values:

```
eUN.lmmNA <- lmm(glucagon ~ time, repetition = ~time|id, data = gastricbypassL)
nobs(eUN.lmmNA)
```

obs	cluster	missing.obs	missing.cluster
78	20	2	0

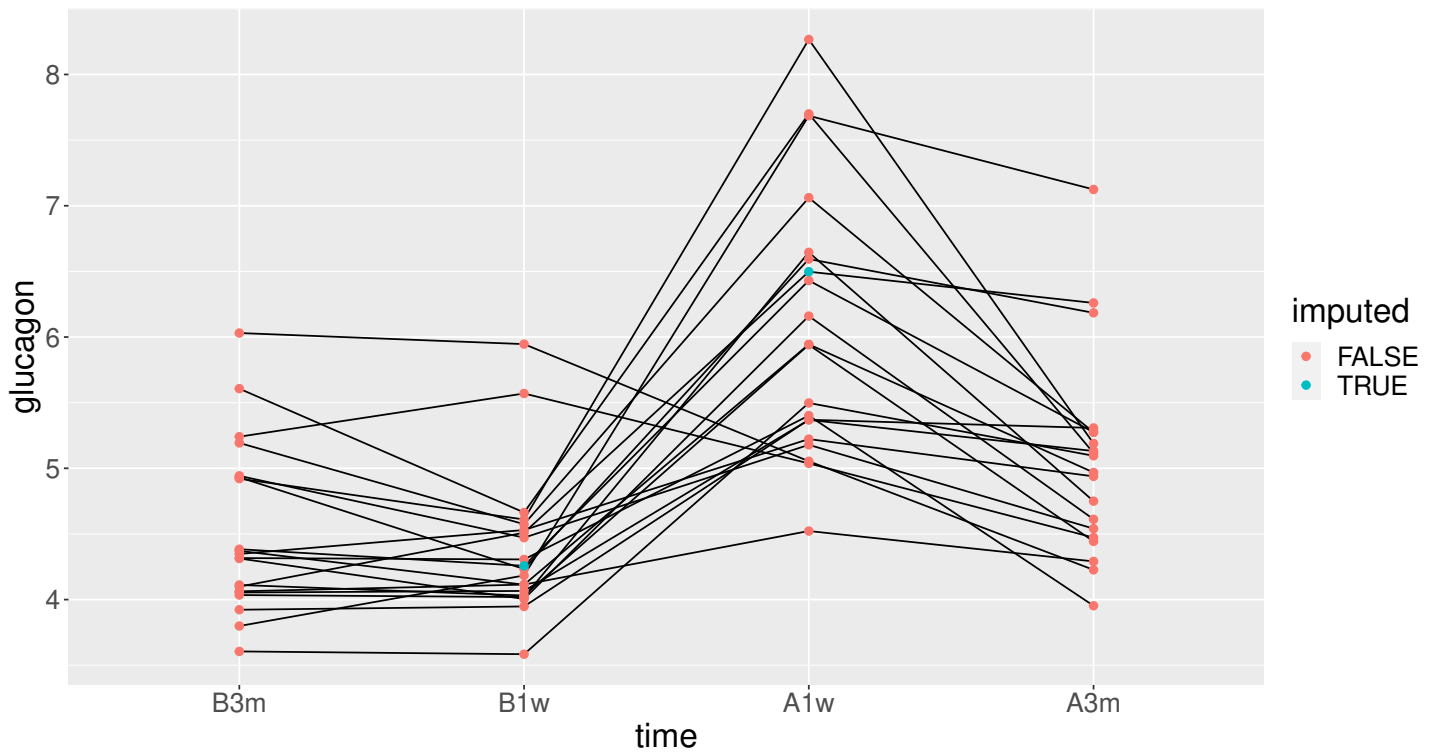
It is possible to extract the most likely value for these missing observations using the fitted function with argument `impute=TRUE`:

```
eData <- fitted(eUN.lmmNA, impute = TRUE, keep.newdata = TRUE)
eData$treat <- eData$treat2 <- eData$timeXtreat <- NULL
eData[eData$id %in% eData[eData$imputed, "id"],]
```

	id	visit	time	weight	glucagonAUC	baseline	glucagon	group	group2	imputed
5	5	1	B3m	113.1	7090.5	TRUE	4.383738	1	FALSE	FALSE
15	15	1	B3m	115.0	5410.5	TRUE	4.098741	1	TRUE	FALSE
25	5	2	B1w	105.6	NA	TRUE	4.256984	1	FALSE	TRUE
35	15	2	B1w	109.7	7833.0	TRUE	4.509697	1	TRUE	FALSE
45	5	3	A1w	99.9	19155.0	FALSE	6.430376	1	FALSE	FALSE
55	15	3	A1w	103.5	NA	FALSE	6.497856	1	TRUE	TRUE
65	5	4	A3m	87.7	12345.0	FALSE	5.275118	1	FALSE	FALSE
75	15	4	A3m	94.1	18148.5	FALSE	6.259632	1	TRUE	FALSE

Missing outcome values in the dataset have been replaced by its most likely value (which is the same as the dynamic prediction, described previously). A column `imputed` has also been added to differentiate between the modeled and observed value. Visually:

```
ggplot(eData, aes(x=time,y=glucagon, group=id)) + geom_line() + geom_point(aes(color=imputed))
```



It is possible to sample from the estimated distribution of the missing value instead of using the most likely value, e.g. accounting for residual variance and uncertainty related to parameter estimation:

```

set.seed(10)
fitted(eUN.lmmNA, impute = TRUE, se = "total")
fitted(eUN.lmmNA, impute = TRUE, se = "total")
fitted(eUN.lmmNA, impute = TRUE, se = "total")

```

```

[1] 4.262434 6.305287
[1] 3.858267 5.871642
[1] 4.342624 6.905246

```

5.4 Multiple imputation

The `mlmm` function can be used to perform stratified analyses, typically useful when performing multiple imputations. Consider the wide format of the dataset where a few values are missing:

```
data(gastricbypassW, package = "LMMstar")
colSums(is.na(gastricbypassW))
```

```
      id      weight1      weight2      weight3      weight4 glucagonAUC1 glucagonAUC2
      0           0           0           0           0           0           1
glucagonAUC3 glucagonAUC4
      1           0
```

We use `mice` to generate a number of imputed datasets (here 5):

```
library(mice)
set.seed(10)
gastricbypassW.mice <- mice(gastricbypassW, m = 5, printFlag = FALSE)
gastricbypassW.NNA <- complete(gastricbypassW.mice, action = "long")
table(gastricbypassW.NNA$.imp)
```

```
Advarselsbesked:
Number of logged events: 110
```

```
 1  2  3  4  5
20 20 20 20 20
```

We can then use `mlmm` to perform a separate linear regression per dataset:

```
e.mlmm <- mlmm(glucagonAUC3~glucagonAUC2+weight2, data=gastricbypassW.NNA,
              by = ".imp", effects = "weight2=0", trace = FALSE)
model.tables(e.mlmm)
```

```
  by parameter estimate      se      df      lower      upper      p.value
1  1  weight2 -204.6291 62.88617 17.0034 -337.3053 -71.95289 0.004670840
2  2  weight2 -194.4004 62.31006 17.0034 -325.8611 -62.93968 0.006231893
3  3  weight2 -211.9042 65.51654 17.0034 -350.1299 -73.67848 0.004872354
4  4  weight2 -199.8417 62.12071 17.0034 -330.9029 -68.78041 0.005058119
5  5  weight2 -199.9269 62.16057 17.0034 -331.0722 -68.78152 0.005065662
```

and pool the results using Rubin's rule:

```
model.tables(e.mlmm, method = "pool.rubin")
```

```
      estimate      se      df      lower      upper      p.value
<1, 5> -202.1404 63.4192 15.09811 -337.2388 -67.04208 0.006078676
```

This matches⁴ the results obtained with the `mice` package:

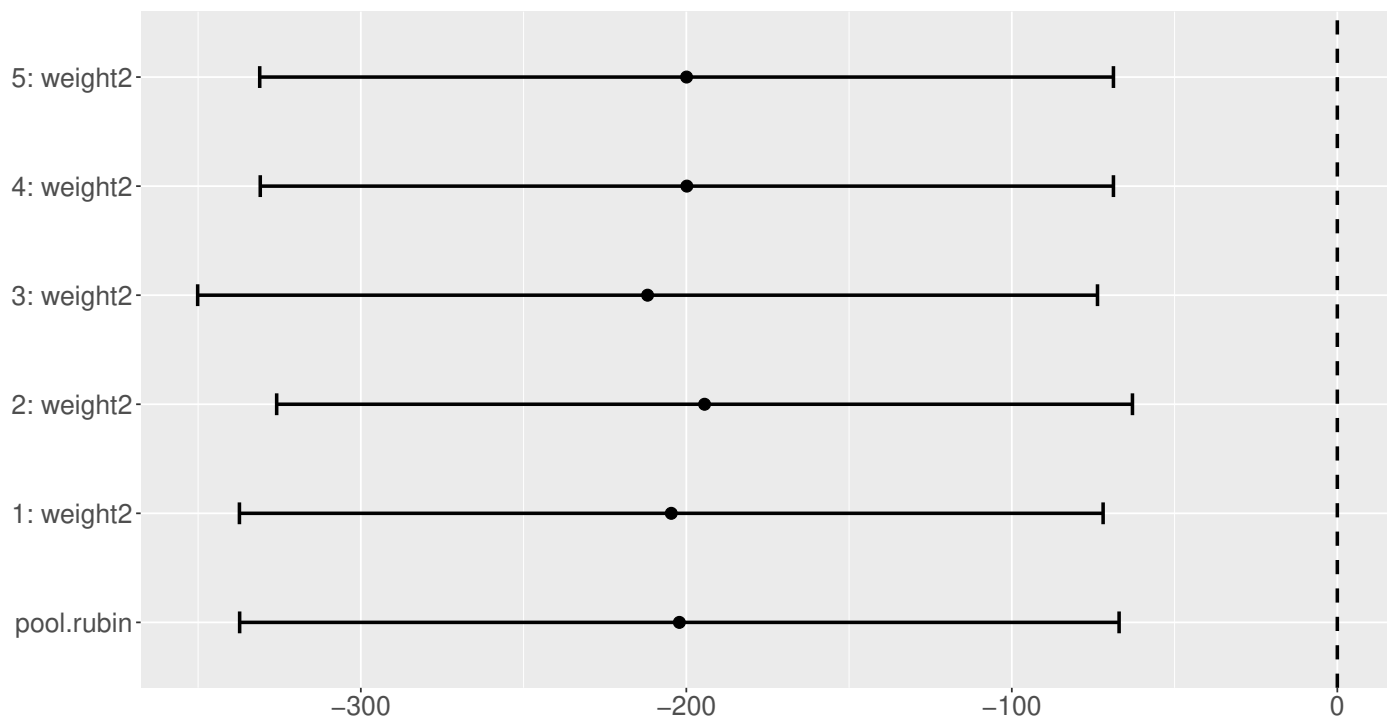
⁴almost exactly, only the degrees of freedom are a little different

```
e.mice <- with(data=gastricbypassW.mice,exp=lm(glucagonAUC3~glucagonAUC2+weight2))
summary(pool(e.mice))
```

	term	estimate	std.error	statistic	df	p.value
1	(Intercept)	4.119699e+04	7674.2675772	5.3681988	15.08457	7.675819e-05
2	glucagonAUC2	7.038742e-02	0.3689445	0.1907805	15.23549	8.512165e-01
3	weight2	-2.021404e+02	63.4191998	-3.1873698	15.09481	6.080058e-03

One can use the `plot` function to obtain a forest plot of the individual estimates along with the pooled estimate:

```
plot(e.mlmm, method = c("pool.rubin", "none"))
```



6 Data generation

Simulate some data in the wide format:

```
set.seed(10) ## ensure reproductibility
n.obs <- 100
n.times <- 4
mu <- rep(0,4)
gamma <- matrix(0, nrow = n.times, ncol = 10) ## add interaction
gamma[,6] <- c(0,1,1.5,1.5)
dW <- sampleRem(n.obs, n.times = n.times, mu = mu, gamma = gamma, format = "wide")
head(round(dW,3))
```

	id	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	Y1	Y2	Y3	Y4
1	1	1	0	1	1	0	-0.367	1.534	-1.894	1.729	0.959	1.791	2.429	3.958	2.991
2	2	1	0	1	2	0	-0.410	2.065	1.766	0.761	-0.563	2.500	4.272	3.002	2.019
3	3	0	0	2	1	0	-1.720	-0.178	2.357	1.966	1.215	-3.208	-5.908	-4.277	-5.154
4	4	0	0	0	1	0	0.923	-2.089	0.233	1.307	-0.906	-2.062	0.397	1.757	-1.380
5	5	0	0	2	1	0	0.987	5.880	0.385	0.028	0.820	7.963	7.870	7.388	8.609
6	6	0	0	1	1	2	-1.075	0.479	2.202	0.900	-0.739	0.109	-1.602	-1.496	-1.841

Simulate some data in the long format:

```
set.seed(10) ## ensure reproductibility
dL <- sampleRem(n.obs, n.times = n.times, mu = mu, gamma = gamma, format = "long")
head(dL)
```

	id	visit	Y	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
1	1	1	1.791444	1	0	1	1	0	-0.3665251	1.533815	-1.894425	1.7288665	0.9592499
2	1	2	2.428570	1	0	1	1	0	-0.3665251	1.533815	-1.894425	1.7288665	0.9592499
3	1	3	3.958350	1	0	1	1	0	-0.3665251	1.533815	-1.894425	1.7288665	0.9592499
4	1	4	2.991198	1	0	1	1	0	-0.3665251	1.533815	-1.894425	1.7288665	0.9592499
5	2	1	2.500179	1	0	1	2	0	-0.4097541	2.065413	1.765841	0.7613348	-0.5630173
6	2	2	4.272357	1	0	1	2	0	-0.4097541	2.065413	1.765841	0.7613348	-0.5630173

7 Modifying default options

The `LMMstar.options` method enable to get and set the default options used by the package. For instance, the default option for the information matrix is:

```
LMMstar.options("type.information")
```

```
$type.information  
[1] "observed"
```

To change the default option to "expected" (faster to compute but less accurate p-values and confidence intervals in small samples) use:

```
LMMstar.options(type.information = "expected")
```

To restore the original default options do:

```
LMMstar.options(reinitialise = TRUE)
```

8 R session

Details of the R session used to generate this document:

```
sessionInfo()
```

```
R version 4.2.0 (2022-04-22 ucrt)
```

```
Platform: x86_64-w64-mingw32/x64 (64-bit)
```

```
Running under: Windows 10 x64 (build 19045)
```

```
Matrix products: default
```

```
locale:
```

```
[1] LC_COLLATE=Danish_Denmark.utf8 LC_CTYPE=Danish_Denmark.utf8 LC_MONETARY=Danish_Denmark.utf8
```

```
[4] LC_NUMERIC=C LC_TIME=Danish_Denmark.utf8
```

```
attached base packages:
```

```
[1] stats graphics grDevices utils datasets methods base
```

```
other attached packages:
```

```
[1] mice_3.14.0 lme4_1.1-29 Matrix_1.5-1 LMMstar_0.8.10
```

```
[5] nlme_3.1-158 ggpubr_0.4.0 multcomp_1.4-20 TH.data_1.1-1
```

```
[9] MASS_7.3-57 survival_3.3-1 mvtnorm_1.1-3 qqtest_1.2.0
```

```
[13] emmeans_1.8.1-90002 ggplot2_3.4.0
```

```
loaded via a namespace (and not attached):
```

```
[1] tidyr_1.2.0 splines_4.2.0 carData_3.0-5 datawizard_0.6.1
```

```
[5] assertthat_0.2.1 stats4_4.2.0 bayestestR_0.13.0 globals_0.16.1
```

```
[9] numDeriv_2016.8-1.1 pillar_1.8.1 backports_1.4.1 lattice_0.20-45
```

```
[13] glue_1.6.2 digest_0.6.29 ggsignif_0.6.3 minqa_1.2.4
```

```
[17] colorspace_2.0-3 sandwich_3.0-2 cowplot_1.1.1 plyr_1.8.7
```

```
[21] pcaPP_2.0-2 pkgconfig_2.0.3 broom_0.8.0 listenv_0.8.0
```

```
[25] purrr_0.3.4 xtable_1.8-4 scales_1.2.1 copula_1.1-0
```

```
[29] lava_1.6.10 tibble_3.1.8 ADGofTest_0.3 mgcv_1.8-40
```

```
[33] generics_0.1.2 farver_2.1.1 car_3.1-0 withr_2.5.0
```

```
[37] cli_3.4.1 effectsize_0.7.0.5 magrittr_2.0.3 estimability_1.4.1
```

```
[41] future_1.28.0 fansi_1.0.3 parallelly_1.32.1 gsl_2.1-7.1
```

```
[45] rstatix_0.7.0 textshaping_0.3.6 tools_4.2.0 lifecycle_1.0.3
```

```
[49] pspline_1.0-19 stringr_1.4.0 munsell_0.5.0 stabledist_0.7-1
```

```
[53] compiler_4.2.0 systemfonts_1.0.4 rlang_1.0.6 grid_4.2.0
```

```
[57] nloptr_2.0.3 parameters_0.18.2 labeling_0.4.2 boot_1.3-28
```

```
[61] lmerTest_3.1-3 gtable_0.3.1 codetools_0.2-18 abind_1.4-5
```

```
[65] DBI_1.1.3 reshape2_1.4.4 R6_2.5.1 zoo_1.8-11
```

```
[69] dplyr_1.0.9 future.apply_1.9.1 utf8_1.2.2 insight_0.18.4
```

```
[73] ragg_1.2.2 stringi_1.7.6 parallel_4.2.0 Rcpp_1.0.8.3
```

```
[77] vctrs_0.5.1 tidyselect_1.1.2 coda_0.19-4
```

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Appendix A Likelihood in a linear mixed model

Denote by \mathbf{Y} a vector of m outcomes, \mathbf{X} a vector of p covariates, $\mu(\boldsymbol{\Theta}, \mathbf{X})$ the modeled mean, and $\Omega(\boldsymbol{\Theta}, \mathbf{X})$ the modeled residual variance-covariance. We consider n replicates (i.e. $\mathbf{Y}_1, \dots, \mathbf{Y}_n$) and $VX_1, \dots, \mathbf{X}_n$) along with a vector of weights $\omega = (w_1, \dots, w_n)$, which are by default all equal to 1.

A.1 Log-likelihood

The restricted log-likelihood in a linear mixed model can then be written:

$$\begin{aligned} \mathcal{L}(\boldsymbol{\Theta}|\mathbf{Y}, \mathbf{X}) &= \frac{p}{2} \log(2\pi) - \frac{1}{2} \log \left(\left| \sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top \right| \right) \\ &\quad + \sum_{i=1}^n w_i \left(-\frac{m}{2} \log(2\pi) - \frac{1}{2} \log |\Omega_i(\boldsymbol{\Theta})| - \frac{1}{2} (\mathbf{Y}_i - \mu(\boldsymbol{\Theta}, \mathbf{X}_i)) \Omega_i(\boldsymbol{\Theta})^{-1} (\mathbf{Y}_i - \mu(\boldsymbol{\Theta}, \mathbf{X}_i))^\top \right) \end{aligned} \quad (\text{A})$$

This is what the `logLik` method is computing for the REML criteria. The red term is specific to the REML criteria and prevents from computing individual contributions to the likelihood⁵. The blue term is what `logLik` outputs for the ML criteria when setting the argument `indiv` to `TRUE`.

A.2 Score

Using that $\partial \log(\det(X)) = \text{tr}(X^{-1} \partial(X))$, the score is obtained by derivating once the log-likelihood, i.e., for $\theta \in \boldsymbol{\Theta}$:

$$\begin{aligned} \mathcal{S}(\theta) &= \frac{\partial \mathcal{L}(\boldsymbol{\Theta}|\mathbf{Y}, \mathbf{X})}{\partial \theta} = \frac{1}{2} \text{tr} \left(\left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top \right)^{-1} \left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta} \Omega_i(\boldsymbol{\Theta})^{-1} \mathbf{X}_i^\top \right) \right) \\ &\quad + \sum_{i=1}^n w_i \left(-\frac{1}{2} \text{tr} \left(\Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta} \right) + \frac{\partial \mu(\boldsymbol{\Theta}, \mathbf{X}_i)}{\partial \theta} \Omega_i(\boldsymbol{\Theta})^{-1} (\mathbf{Y}_i - \mu(\boldsymbol{\Theta}, \mathbf{X}_i))^\top \right. \\ &\quad \left. + \frac{1}{2} (\mathbf{Y}_i - \mu(\boldsymbol{\Theta}, \mathbf{X}_i)) \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta} \Omega_i(\boldsymbol{\Theta})^{-1} (\mathbf{Y}_i - \mu(\boldsymbol{\Theta}, \mathbf{X}_i))^\top \right). \end{aligned}$$

This is what the `score` method is computing for the REML criteria. The red term is specific to the REML criteria and prevents from computing the score relative to each cluster. The blue term is what `score` outputs for the ML criteria when setting the argument `indiv` to `TRUE`.

⁵The REML is the likelihood of the observations divided by the prior on the estimated mean parameters $\hat{\boldsymbol{\Theta}}_\mu \sim \mathcal{N}(\mu, (\mathbf{X} \Omega^{-1}(\boldsymbol{\Theta}) \mathbf{X}^\top)^{-1})$. This corresponds to $\frac{1}{\sqrt{2\pi^p} \left| (\sum_{i=1}^n \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top)^{-1} \right|} \exp \left(-(\hat{\boldsymbol{\Theta}}_\mu - \mu) (2 \sum_{i=1}^n \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top)^{-1} (\hat{\boldsymbol{\Theta}}_\mu - \mu)^\top \right)$. Since μ will be estimated to be $\boldsymbol{\Theta}_\mu$, the exponential term equals 1 and thus does not contribute to the log-likelihood. One divided by the other term gives $\sqrt{2\pi^p} \left(\left| \sum_{i=1}^n \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top \right| \right)^{-1}$. The log of this term equals the red term

A.3 Hessian

Derivating a second time the log-likelihood gives the hessian, $\mathcal{H}(\Theta)$, with element⁶:

$$\begin{aligned}
\mathcal{H}(\theta, \theta') &= \frac{\partial^2 \mathcal{L}(\Theta | \mathbf{Y}, \mathbf{X})}{\partial \theta \partial \theta'} = \frac{\partial \mathcal{S}(\theta)}{\partial \theta'} \\
&= \frac{1}{2} \text{tr} \left(\left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \mathbf{X}_i^\top \right)^{-1} \left\{ \sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \left(\frac{\partial^2 \Omega_i(\Theta)}{\partial \theta \partial \theta'} - 2 \frac{\partial \Omega_i(\Theta)}{\partial \theta} \Omega_i^{-1}(\Theta) \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \right) \Omega_i(\Theta)^{-1} \mathbf{X}_i^\top \right. \right. \\
&\quad \left. \left. + \left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \frac{\partial \Omega_i(\Theta)}{\partial \theta} \Omega_i(\Theta)^{-1} \mathbf{X}_i^\top \right) \left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \mathbf{X}_i^\top \right)^{-1} \left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \mathbf{X}_i^\top \right) \right\} \right) \\
&\quad + \sum_{i=1}^n w_i \left(\frac{1}{2} \text{tr} \left(\Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta} - \Omega_i(\Theta)^{-1} \frac{\partial^2 \Omega_i(\Theta)}{\partial \theta \partial \theta'} \right) \right. \\
&\quad \left. - \frac{\partial \mu(\Theta, \mathbf{X}_i)}{\partial \theta} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \boldsymbol{\varepsilon}_i(\Theta)^\top - \frac{\partial \mu(\Theta, \mathbf{X}_i)}{\partial \theta} \Omega_i(\Theta)^{-1} \frac{\partial \mu(\Theta, \mathbf{X}_i)^\top}{\partial \theta'} \right. \\
&\quad \left. + \frac{1}{2} \boldsymbol{\varepsilon}_i(\Theta) \Omega_i(\Theta)^{-1} \left(\frac{\partial^2 \Omega_i(\Theta)}{\partial \theta \partial \theta'} - \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta} - \frac{\partial \Omega_i(\Theta)}{\partial \theta} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \right) \Omega_i(\Theta)^{-1} \boldsymbol{\varepsilon}_i(\Theta)^\top \right).
\end{aligned}$$

where $\boldsymbol{\varepsilon}_i(\Theta) = \mathbf{Y}_i - \mu(\Theta, \mathbf{X}_i)$.

The `information` method will (by default) return the (observed) information which is the opposite of the hessian. So multiplying the previous formula by -1 gives what `information` output for the REML criteria. The red term is specific to the REML criteria and prevents from computing the information relative to each cluster. The blue term is what `information` outputs for the ML criteria (up to a factor -1) when setting the argument `indiv` to `TRUE`.

A possible simplification is to use the expected hessian at the maximum likelihood. Indeed for any deterministic matrix A :

- $\mathbb{E}[A(\mathbf{Y}_i - \mu(\Theta, \mathbf{X}_i))^\top | \mathbf{X}_i] = 0$
- $\mathbb{E}[(\mathbf{Y}_i - \mu(\Theta, \mathbf{X}_i))A(\mathbf{Y}_i - \mu(\Theta, \mathbf{X}_i))^\top | \mathbf{X}_i] = \text{tr}(A \text{Var}(\mathbf{Y}_i - \mu(\Theta, \mathbf{X}_i)))$

when $\mathbb{E}[\mathbf{Y}_i - \mu(\Theta, \mathbf{X}_i)] = 0$. This leads to:

$$\begin{aligned}
\mathbb{E}[\mathcal{H}(\theta, \theta') | \mathbf{X}] &= \frac{1}{2} \text{tr} \left(\left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \mathbf{X}_i^\top \right)^{-1} \left\{ \sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \left(\frac{\partial^2 \Omega_i(\Theta)}{\partial \theta \partial \theta'} - 2 \frac{\partial \Omega_i(\Theta)}{\partial \theta} \Omega_i^{-1}(\Theta) \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \right) \Omega_i(\Theta)^{-1} \mathbf{X}_i^\top \right. \right. \\
&\quad \left. \left. + \left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \frac{\partial \Omega_i(\Theta)}{\partial \theta} \Omega_i(\Theta)^{-1} \mathbf{X}_i^\top \right) \left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \mathbf{X}_i^\top \right)^{-1} \left(\sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \mathbf{X}_i^\top \right) \right\} \right) \\
&\quad + \sum_{i=1}^n w_i \left(-\frac{1}{2} \text{tr} \left(\Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta} \right) - \frac{\partial \mu(\Theta, \mathbf{X}_i)}{\partial \theta} \Omega_i(\Theta)^{-1} \frac{\partial \mu(\Theta, \mathbf{X}_i)^\top}{\partial \theta'} \right) \quad (\text{B})
\end{aligned}$$

This is what `information` output when the argument `type.information` is set to "expected" (up to a factor -1).

⁶if one is relative to the mean and the other to the variance then they are respectively θ and θ'

A.4 Degrees of freedom

Degrees of freedom are computed using a Satterthwaite approximation, i.e. for an estimate coefficient $\hat{\beta} \in \widehat{\Theta}$ with standard error $\sigma_{\hat{\beta}}$, the degree of freedom is:

$$df(\sigma_{\hat{\beta}}) = \frac{2\sigma_{\hat{\beta}}^4}{\text{Var}[\hat{\sigma}_{\hat{\beta}}]}$$

Using a first order Taylor expansion we can approximate the variance term as:

$$\begin{aligned} \text{Var}[\hat{\sigma}_{\hat{\beta}}] &\approx \frac{\partial \hat{\sigma}_{\hat{\beta}}}{\partial \Theta} \Sigma_{\Theta} \frac{\partial \hat{\sigma}_{\hat{\beta}}}{\partial \Theta}^{\top} \\ &\approx c_{\beta} (\widehat{\mathcal{I}}_{\widehat{\Theta}})^{-1} \frac{\partial \widehat{\mathcal{I}}_{\widehat{\Theta}}}{\partial \Theta} (\widehat{\mathcal{I}}_{\widehat{\Theta}})^{-1} c_{\beta}^{\top} \Sigma_{\Theta} c_{\beta} (\widehat{\mathcal{I}}_{\widehat{\Theta}})^{-1} \frac{\partial \widehat{\mathcal{I}}_{\widehat{\Theta}}}{\partial \Theta}^{\top} (\widehat{\mathcal{I}}_{\widehat{\Theta}})^{-1} c_{\beta} \end{aligned}$$

where Σ_{Θ} is the variance-covariance matrix of all model coefficients, \mathcal{I}_{Θ} the information matrix for all model coefficients, c_{β} a matrix used to select the element relative to β in the first derivative of the information matrix, and $\frac{\partial}{\partial \Theta}$ denotes the vector of derivatives with respect to all model coefficients.

The derivative of the information matrix (i.e. negative hessian) can then be computed using numerical derivatives or using analytical formula. To obtain the later we first notice that:

$$\begin{aligned} \mathcal{H}(\theta, \theta') &= \mathbb{E}[\mathcal{H}(\theta, \theta') | \mathbf{X}] \\ &+ \sum_{i=1}^n w_i \left(\text{tr} \left(\Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta} - \Omega_i(\Theta)^{-1} \frac{\partial^2 \Omega_i(\Theta)}{\partial \theta \partial \theta'} \right) \right. \\ &\quad \left. - \frac{\partial \mu(\Theta, \mathbf{X}_i)}{\partial \theta} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \varepsilon_i(\Theta)^{\top} \right. \\ &\quad \left. + \frac{1}{2} \varepsilon_i(\Theta) \Omega_i(\Theta)^{-1} \left(\frac{\partial^2 \Omega_i(\Theta)}{\partial \theta \partial \theta'} - \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta} - \frac{\partial \Omega_i(\Theta)}{\partial \theta} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \right) \Omega_i(\Theta)^{-1} \varepsilon_i(\Theta)^{\top} \right) \end{aligned} \quad (\text{C})$$

where

$$\begin{aligned} \mathbb{E}[\mathcal{H}(\theta, \theta') | \mathbf{X}] &= \frac{1}{2} \text{tr} \left(A(\Theta)^{-1} \left(\sum_{i=1}^n w_i b_i(\Theta) B_i(\Theta) b_i^{\top}(\Theta) + C(\Theta) A(\Theta)^{-1} C^{\top}(\Theta) \right) \right) + \sum_{i=1}^n w_i E_i(\Theta) \\ E_i(\Theta) &= \frac{1}{2} \text{tr} \left(\Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \Omega_i(\Theta)^{-1} \frac{\partial \Omega_i(\Theta)}{\partial \theta} \right) - \frac{\partial \mu(\Theta, \mathbf{X}_i)}{\partial \theta} \Omega_i(\Theta)^{-1} \frac{\partial \mu(\Theta, \mathbf{X}_i)}{\partial \theta'}^{\top} \\ A(\Theta) &= \sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \mathbf{X}_i^{\top} \\ B(\Theta) &= \frac{\partial^2 \Omega_i(\Theta)}{\partial \theta \partial \theta'} - 2 \frac{\partial \Omega_i(\Theta)}{\partial \theta} \Omega_i^{-1}(\Theta) \frac{\partial \Omega_i(\Theta)}{\partial \theta'} \\ b_i(\Theta) &= \mathbf{X}_i \Omega_i^{-1} \\ C(\Theta) &= \sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\Theta) \frac{\partial \Omega_i(\Theta)}{\partial \theta} \Omega_i(\Theta)^{-1} \mathbf{X}_i^{\top} \end{aligned}$$

So we will first derive the derivative of $\mathbb{E}[\mathcal{H}(\theta, \theta') | \mathbf{X}]$ and then the one of the blue term in Equation C. To simplify the derivation of the formula we will only derive them at the maximum likelihood, i.e. when

$\mathbb{E} \left[\frac{\partial \mathcal{H}(\theta, \theta' | \mathbf{X})}{\partial \theta''} \right] = \frac{\partial \mathbb{E}[\mathcal{H}(\theta, \theta' | \mathbf{X})]}{\partial \theta''}$ where the expectation is taken over \mathbf{X} . We first notice that the derivative with respect to the mean parameters is 0. So we just need to compute the derivative with respect to a variance parameter θ'' :

$$\begin{aligned} & \frac{\partial A(\boldsymbol{\Theta})^{-1} \left(\sum_{i=1}^n w_i b_i(\boldsymbol{\Theta}) B_i(\boldsymbol{\Theta}) b_i^\top(\boldsymbol{\Theta}) + C(\boldsymbol{\Theta}) A(\boldsymbol{\Theta})^{-1} C^\top(\boldsymbol{\Theta}) \right)}{\partial \theta''} \\ = & A(\boldsymbol{\Theta})^{-1} \frac{\partial A(\boldsymbol{\Theta})}{\partial \theta''} A(\boldsymbol{\Theta})^{-1} \left(\sum_{i=1}^n w_i b_i(\boldsymbol{\Theta}) B_i(\boldsymbol{\Theta}) b_i^\top(\boldsymbol{\Theta}) + C(\boldsymbol{\Theta}) A(\boldsymbol{\Theta})^{-1} C^\top(\boldsymbol{\Theta}) \right) \\ & + A(\boldsymbol{\Theta})^{-1} \left(\sum_{i=1}^n w_i \left(\frac{\partial b_i(\boldsymbol{\Theta})}{\partial \theta''} B_i(\boldsymbol{\Theta}) b_i^\top(\boldsymbol{\Theta}) + b_i(\boldsymbol{\Theta}) \frac{\partial B_i(\boldsymbol{\Theta})}{\partial \theta''} b_i^\top(\boldsymbol{\Theta}) + b_i(\boldsymbol{\Theta}) B_i(\boldsymbol{\Theta}) \frac{\partial b_i^\top(\boldsymbol{\Theta})}{\partial \theta''} \right. \right. \\ & \left. \left. + \frac{\partial C(\boldsymbol{\Theta})}{\partial \theta''} A^{-1}(\boldsymbol{\Theta}) C^\top(\boldsymbol{\Theta}) + C(\boldsymbol{\Theta}) A^{-1} \frac{\partial A(\boldsymbol{\Theta})}{\partial \theta''} A^{-1} C^\top(\boldsymbol{\Theta}) + C(\boldsymbol{\Theta}) A^{-1}(\boldsymbol{\Theta}) \frac{\partial C^\top(\boldsymbol{\Theta})}{\partial \theta''} \right) \right) \end{aligned}$$

and

$$\begin{aligned} \frac{\partial E(\boldsymbol{\Theta})}{\partial \theta''} = & \sum_{i=1}^n w_i \left(-\frac{1}{2} \text{tr} \left(-2 \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta''} \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta'} \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta} \right. \right. \\ & \left. \left. + \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial^2 \Omega_i(\boldsymbol{\Theta})}{\partial \theta' \partial \theta''} \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta} + \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta'} \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial^2 \Omega_i(\boldsymbol{\Theta})}{\partial \theta \partial \theta''} \right) \right. \\ & \left. + \frac{\partial \mu(\boldsymbol{\Theta}, \mathbf{X}_i)}{\partial \theta} \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta''} \Omega_i(\boldsymbol{\Theta})^{-1} \frac{\partial \mu(\boldsymbol{\Theta}, \mathbf{X}_i)^\top}{\partial \theta'} \right) \end{aligned}$$

where:

$$\begin{aligned} \frac{\partial A(\boldsymbol{\Theta})}{\partial \theta''} &= \sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta''} \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top \\ \frac{\partial b_i(\boldsymbol{\Theta})}{\partial \theta''} &= \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta''} \Omega_i^{-1}(\boldsymbol{\Theta}) \\ \frac{\partial B_i(\boldsymbol{\Theta})}{\partial \theta''} &= \frac{\partial^3 \Omega_i(\boldsymbol{\Theta})}{\partial \theta' \theta''} \\ & - 2 \left(\frac{\partial^2 \Omega_i(\boldsymbol{\Theta})}{\partial \theta \partial \theta''} \Omega_i^{-1}(\boldsymbol{\Theta}) \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta'} + \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta} \Omega_i^{-1}(\boldsymbol{\Theta}) \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta''} \Omega_i^{-1}(\boldsymbol{\Theta}) \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta'} + \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta} \Omega_i^{-1}(\boldsymbol{\Theta}) \frac{\partial^2 \Omega_i(\boldsymbol{\Theta})}{\partial \theta' \partial \theta''} \right) \\ \frac{\partial C(\boldsymbol{\Theta})}{\partial \theta''} &= \sum_{i=1}^n w_i \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \left(\frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta''} \Omega_i^{-1}(\boldsymbol{\Theta}) \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta} + \frac{\partial^2 \Omega_i(\boldsymbol{\Theta})}{\partial \theta \partial \theta''} + \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta} \Omega_i^{-1}(\boldsymbol{\Theta}) \frac{\partial \Omega_i(\boldsymbol{\Theta})}{\partial \theta''} \right) \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top \end{aligned}$$

Appendix B Likelihood ratio test with the REML criterion

The blue term of Equation A in the log-likelihood is invariant to re-parameterisation while the red term is not. This means that a re-parametrisation of X into $\tilde{X} = BX$ with B invertible would not change the likelihood when using ML but would decrease the log-likelihood by $\log(|B|)$ when using REML.

Let's take an example:

```
## data(dfL, package = "LMMstar")
dfTest <- dfL
dfTest$glucagon2 <- dfTest$glucagon*2
```

where we multiply one column of the design matrix by 2. As mentioned previously this does not affect the log-likelihood when using ML:

```
eML.lmmUN <- lmm(weight ~ time+glucagon, data = dfTest, repetition = ~time|id, method = "ML")
eML.lmmUN2 <- lmm(weight ~ time+glucagon2, data = dfTest, repetition = ~time|id, method = "ML")
```

```
logLik(eML.lmmUN)
logLik(eML.lmmUN2)
```

```
[1] -218.71
[1] -218.71
```

but it does when using REML:

```
eREML.lmmUN <- lmm(weight ~ time + glucagon, data = dfTest, repetition = ~time|id, method = "REML")
eREML.lmmUN2 <- lmm(weight ~ time + glucagon2, data = dfTest, repetition = ~time|id, method = "REML")
```

```
logLik(eREML.lmmUN)-logLik(eREML.lmmUN2)
log(2)
```

```
[1] 0.6931472
[1] 0.6931472
```

Therefore, when comparing models with different mean effects there is a risk that the difference (or part of it) in log-likelihood is due to a new parametrisation and not only to a difference in model fit. This would typically be the case when adding an interaction where we can have a smaller restricted log-likelihood when considering a more complex model:

```
set.seed(5)
dfTest$ff <- rbinom(NROW(dfTest), size = 1, prob = 0.5)
logLik(lmm(weight ~ time+glucagon, data = dfTest, repetition = ~time|id, method = "REML"))
logLik(lmm(weight ~ time+glucagon*ff, data = dfTest, repetition = ~time|id, method = "REML"))
```

```
[1] -216.3189
[1] -216.8425
```

This is quite counter-intuitive as more complex model should lead to better fit and would never happen when using ML:

```
logLik(lmm(weight ~ time + glucagon, data = dfTest, repetition = ~time|id, method = "ML"))  
logLik(lmm(weight ~ time + glucagon*ff, data = dfTest, repetition = ~time|id, method = "ML"))
```

```
[1] -218.71
```

```
[1] -218.6259
```

This is why, unless one knows what he/she is doing, it is not recommended to use likelihood ratio test to assess relevance of mean parameters in mixed models estimated with REML.

Appendix C Sum of squares in a linear mixed model

All mixed models implemented in LMMstar can be written as:

$$Y_{it} = X_{it}\beta + \varepsilon_{it} \text{ where } \varepsilon_i \sim \mathcal{N}(0, \Omega)$$

where Y denote the outcome repeatedly measured within each cluster i where t indexes the repetitions. X denotes the covariates, β the mean parameters, ε the residuals, and Ω the residual variance-covariance matrix. Ω must be positive definite so there must exist a square positive definite matrix $\Omega^{1/2}$ such that $\Omega^{1/2}\Omega^{1/2} = \Omega$. Therefore the previous model is equivalent to:

$$Y_{it}^* = X_{it}^*\beta + \varepsilon_{it}^* \text{ where } \varepsilon_i \sim \mathcal{N}(0, I_T)$$

where $Y_i^* = \Omega^{-1/2}Y_i$, $X_i^* = \Omega^{-1/2}X_i$, $\varepsilon_i^* = \Omega^{-1/2}\varepsilon_i$, and I_x is the identity matrix with x rows and columns. One can then introduce the projectors $H = X(X^\top\Omega^{-1}X)^{-1}X^\top\Omega^{-1}$ and $H^* = X^*(X^{*\top}X^*)^{-1}X^{*\top}$ onto the space spanned by X and X^* respectively. We can now define the "normalized" residual sum of squares as the squared sum of the normalized residuals:

$$\begin{aligned} SSE^* &= \varepsilon^{*\top}\varepsilon^* = Y^{*\top}(I_{nT} - H^*)Y^* \\ &= Y^\top\Omega^{-1}Y - Y^\top\Omega^{-1}X(X^\top\Omega^{-1}X)^{-1}X^\top\Omega^{-1}Y \\ &= Y^\top(I_{nT} - H^\top)\Omega^{-1}(I_{nT} - H)Y \end{aligned}$$

The previous to last line uses that: $(I_{nT} - H^\top)\Omega^{-1}(I_{nT} - H) = \Omega^{-1} - H^\top\Omega^{-1} - \Omega^{-1}H + H^\top\Omega^{-1}H = \Omega^{-1} - H^\top\Omega^{-1}$ as $H^\top\Omega^{-1}H = \Omega^{-1}HH = \Omega^{-1}H$ since H is a projector. Note that compared to the "traditional" SSE defined for linear regression and random effect models (e.g. see [Christensen \(2011\)](#) section 2.7), $SSE = \delta SSE^*$ where δ is the residual variance conditional on any random effects, i.e. SSE^* are the residual degrees of freedom. This is because the same definition for the sum of squares is used except that $\varepsilon_i \sim \mathcal{N}(0, \delta\Omega)$.

We can also define the "normalized" regression sum of squares:

$$\begin{aligned} SSR^* &= (X^*\beta)^\top X^*\beta = (H^*Y^*)^\top H^*Y^* = Y^{*\top}H^*Y^* \\ &= Y^\top H^\top\Omega^{-1}Y^* = Y^\top H^\top H^\top\Omega^{-1}Y^* = Y^\top H^\top\Omega^{-1}HY^* \\ &= \hat{\beta}X^\top\Omega^{-1}X\hat{\beta} \end{aligned}$$

where $\hat{\beta} = (X^\top\Omega^{-1}X)^{-1}X^\top\Omega^{-1}Y$. Note that when using the expected information $SSR^* = \hat{\beta}\Sigma_{\hat{\beta}}^{-1}\hat{\beta}$, i.e. it is the F-statistics times the number of parameters. Again the "traditional" SSR defined for linear regression and random effect models is proportional to this normalized SSR: $SSR = \delta SSR^*$.

The proportion of explained variance of p parameters can thus be re-expressed as:

$$R^2 = \frac{SSR}{SSR + SSE} = \frac{SSR^*}{SSR^* + SSE^*} = \frac{Fp}{Fp + df}$$

where df denotes the residual degrees of freedom, typically $n - p$ in a univariate linear model fitted with n observations.

⚠ In practice df is estimated using the Satterthwaite approximation of the degrees of freedom of the regression coefficient. This is only equivalent to the "SSR/SSE" formula in univariate linear regression.

Illustration for a univariate linear model:

Data without missing values:

```
df.aov <- dfL[!is.na(dfL$glucagon),]
```

Traditional anova decomposition:

```
e.lm <- lm(weight ~ time + glucagon, data = df.aov)
car::Anova(e.lm, type = "II")
```

Anova Table (Type II tests)

```
Response: weight
          Sum Sq Df F value    Pr(>F)
time      6367.3  3  6.4308 0.0006329 ***
glucagon  1964.8  1  5.9531 0.0171207 *
Residuals 24093.1 73
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Fit lmm:

```
e.lmm <- lmm(weight ~ time + glucagon, data = df.aov)
```

Residual sum of squares (SSE):

```
SSEstar <- crossprod(residuals(e.lmm, type = "normalized"))
c(SSEstar = SSEstar, SSE = SSEstar * sigma(e.lmm))
```

```
SSEstar    SSE
 73.00 24093.11
```

The normalized SSE can also be obtained using the `df.residual` method:

```
df.residual(e.lmm)
```

```
[1] 73
```

Regression sum of squares (SSR):

```
eBeta.lmm <- coef(e.lmm)
eVcov.lmm <- vcov(e.lmm, type.information = "expected")

SSRstar.glucagon <- eBeta.lmm[5] %*% solve(eVcov.lmm[5,5]) %*% eBeta.lmm[5]
SSRstar.time <- eBeta.lmm[2:4] %*% solve(eVcov.lmm[2:4,2:4]) %*% eBeta.lmm[2:4]
c(SSR.glucagon = SSRstar.glucagon * sigma(e.lmm),
  SSR.time = SSRstar.time * sigma(e.lmm),
  F.glucagon = SSRstar.glucagon,
  F.time = SSRstar.time/3)
```

```
SSR.glucagon    SSR.time    F.glucagon    F.time
1964.764452    6367.324429    5.953062     6.430810
```

So the proportion of explained variance is:

```
R2.glucagon <- SSRstar.glucagon/(SSRstar.glucagon+SSEstar)
R2.glucagon
```

```
      [,1]
[1,] 0.07540002
```

and the corresponding partial correlation is:

```
sign(coef(e.lmm)["glucagon"])*sqrt(R2.glucagon)
```

```
      [,1]
[1,] -0.2745906
```

which matches the output of `partialCor`:

```
summary(partialCor(e.lmm, R2 = TRUE))
```

Partial correlation

	estimate	se	df	lower	upper	p.value
timeB1w	-0.153	0.113	73	-0.378	0.072	0.1796
timeA1w	-0.038	0.117	73	-0.27	0.195	0.7475
timeA3m	-0.413	0.088	73	-0.589	-0.236	1.36e-05
glucagon	-0.275	0.104	73	-0.482	-0.067	0.0102

Columns lower and upper contain 95% pointwise confidence intervals for each coefficient. Degrees of freedom were computed using a Satterthwaite approximation (column df).

Coefficient of determination (R2)

	estimate	se	df	lower	upper	p.value
time	0.209	0.075	73	0.059	0.359	0.006976
glucagon	0.075	0.057	73	-0.038	0.189	0.191156
global	0.285	0.076	73	0.134	0.435	0.000328

Columns lower and upper contain 95% pointwise confidence intervals for each coefficient. Degrees of freedom were computed using a Satterthwaite approximation (column df).

Appendix D Equivalent with other R packages

D.1 nlme package

The model class obtained with the `lmm` function overlaps the model class of the `lme` and `gls` functions from the `nlme` package.

```
library(nlme)
```

For instance, the compound symmetry is equivalent to `corCompSymm` correlation structure, or to a random intercept model (when the within subject correlation is positive):

```
eCS.gls <- gls(weight ~ time + glucagon, correlation = corCompSymm(form=~time|id),
              data = dfL, na.action = na.omit)
eCS.lme <- lme(weight ~ time + glucagon, random = ~1|id,
              data = dfL, na.action = na.omit)
logLik(eCS.lme)
logLik(eCS.gls)
logLik(eCS.lmm)
```

```
'log Lik.' -243.6005 (df=7)
'log Lik.' -243.6005 (df=7)
[1] -243.6005
```

The estimated random effect also match:

```
range(coef(eCS.lmm, effects = "ranef")-ranef(eCS.lme))
```

```
[1] -3.136988e-08 2.384361e-08
```

Unstructured residual covariance matrix can also be obtained with `gls`:

```
eUN.gls <- gls(weight ~ time + glucagon,
              correlation = corSymm(form=~as.numeric(time)|id),
              weights = varIdent(form=~1|time),
              data = dfL, na.action = na.omit)
logLik(eUN.gls)
logLik(eUN.lmm)
```

```
'log Lik.' -216.3189 (df=15)
[1] -216.3189
```

D.2 lme4 package

The model class obtained with the `lmm` function overlaps the model class of the `lmer` function from the `lme4` package.

```
library(lme4)
library(lmerTest)
```

For instance, the compound symmetry is equivalent to a random intercept model (when the within subject correlation is positive):

```
eCS.lmer <- lmer(weight ~ time + glucagon + (1|id),
                data = dfL)
logLik(eCS.lmer)
logLik(eCS.lmm)
```

```
'log Lik.' -243.6005 (df=7)
[1] -243.6005
```

The estimated random effects match:

```
range(coef(eCS.lmm, effects = "ranef")-ranef(eCS.lmer)$id)
```

```
[1] -3.167863e-08  2.406745e-08
```

Nested random effects correspond to block unstructured:

```
eBCS.lmer <- lmer(weight ~ time*group + (1|id/baseline),
                data = dfL)
logLik(eBCS.lmer)
logLik(eBCS.lmm)
```

```
'log Lik.' -230.5328 (df=11)
[1] -230.5328
```

And the estimated random effects still match:

```
eRanefBCS.lmm <- coef(eBCS.lmm, effects = "ranef")
eRanefBCS.lmer <- ranef(eBCS.lmer)
## id
range(eRanefBCS.lmm[, "id"]-eRanefBCS.lmer$id)
## baseline
range(c(eRanefBCS.lmm[, "baseline1"], eRanefBCS.lmm[, "baseline2"])-ranef(eBCS.lmer)$'baseline:id'
      ')
```

```
[1] -7.457484e-05  1.182242e-04
[1] -0.0001493705  0.0001080902
```


An unstructure residual covariance matrix can also be obtained using random slopes:

```
eUN.lmer <- lmer(weight ~ time + glucagon + (0 + time|id),
                data = dfL, control = lmerControl(check.nobs.vs.nRE = "ignore"))
logLik(eUN.lmer)
logLik(eUN.lmm)
```

```
'log Lik.' -216.3189 (df=16)
[1] -216.3189
```

Note that however the uncertainty is quantified in a slightly different way, e.g.:

```
anova(eUN.lmm)
```

Multivariate Wald test

	F-statistic	df	p.value
mean: time	86.743 (3,19.0)	2.84e-11	***
: glucagon	13.518 (1,13.7)	0.00257	**

do not match

```
anova(eUN.lmer)
```

Type III Analysis of Variance Table with Satterthwaite's method

	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
time	114.275	38.092	3	20.483	87.242	7.784e-12 ***
glucagon	10.125	10.125	1	16.784	23.191	0.0001671 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

I think this is because lmer base uncertainty computation on the expected information (instead of the observed information). Doing so leads to more similar results:

```
eUN2.lmm <- lmm(weight ~ time + glucagon, repetition = ~time|id,
               structure = "UN", data = dfL, type.information = "expected")
suppressWarnings(anova(eUN2.lmm))
```

Multivariate Wald test

	F-statistic	df	p.value
mean: time	87.253 (3,22.5)	1.48e-12	***
: glucagon	23.198 (1,19.4)	0.000114	***

It is also possible to fit cross-random effects such as:

```
data("Penicillin")
fm03 <- lmer(diameter ~ 1 + (1|plate) + (1|sample), Penicillin)
logLik(fm03)
```

```
'log Lik.' -165.4303 (df=4)
```

using `lmm` with a small hack: using a block compound symmetry structure with heterogeneous set to -1 to remove the correlation coefficient for pairs that have none of the covariate defining the blocks in common:

```
Penicillin$index <- paste(Penicillin$sample, Penicillin$plate, sep=".")
Penicillin$id <- 1

e.lmm <- lmm(diameter ~ 1,
             repetition = ~index|id,
             structure = CS(list(~1, ~plate+sample), heterogeneous = -1),
             data = Penicillin)
logLik(e.lmm)
```

```
[1] -165.4303
```

D.3 mmrm package

The package `mmrm` is an alternative implementation of mixed models specified via covariance structures:

```
library(mmrm)
e.mmrm <- mmrm(
  formula = FEV1 ~ RACE + SEX + ARMCD * AVISIT + us(AVISIT | USUBJID),
  data = fev_data
)
```

It leads nearly identical results compared to `lmm`:

```
e.lmm <- lmm(
  formula = FEV1 ~ RACE + SEX + ARMCD * AVISIT,
  repetition = ~ AVISIT | USUBJID, structure = "UN",
  data = fev_data, type.information = "expected"
)
```

```
logLik(e.mmrm) - logLik(e.lmm)
range(coef(e.mmrm) - coef(e.lmm))
range(vcov(e.mmrm) - vcov(e.lmm))
```

```
[1] -2.541298e-06
```

```
[1] -0.0001830095  0.0001626755
```

```
[1] -0.0003971008  0.0002047941
```

The main differences are:

- `mmrm` uses the expected information matrix to quantify uncertainty instead of the observed information matrix.

- `mrmr` implements the Kenward and Roger method for computing the degrees of freedom and not only the Satterthwaite approximation
- `mrmr` implements different covariance patterns
- `mrmr` is faster and probably more memory efficient
- `mrmr` have fewer post-processing methods (e.g. no `residuals` function in the current CRAN version 0.2.2)

D.4 effectsize package (R^2 or η^2)

Partial η^2 can be computed based on `lmer` using the `effectsiz` package:

```
library(effectsiz)
eta_squared(eCS.lmer)
cat("\n")
```

```
# Effect Size for ANOVA (Type III)
```

```
Parameter | Eta2 (partial) |          95% CI
-----|-----|-----
time      |          0.92 | [0.89, 1.00]
glucagon  |          0.03 | [0.00, 1.00]
```

```
- One-sided CIs: upper bound fixed at [1.00].>
```

and are approximately equal to what one can compute "manually":

```
eCS.Wald <- anova(eCS.lmm)$multivariate
eCS.Wald$df.num*eCS.Wald$statistic/(eCS.Wald$df.num*eCS.Wald$statistic+eCS.Wald$df.denom)
```

```
[1] 0.92380363 0.03162017
```

This will not be true for heteroschedastic models:

```
eUN.Wald <- anova(eUN.lmm)$multivariate
eUN.Wald$df.num*eUN.Wald$statistic/(eUN.Wald$df.num*eUN.Wald$statistic+eUN.Wald$df.denom)
```

```
[1] 0.9319379 0.4965135
```

compared to:

```
eta_squared(eUN.lmer)
cat("\n")
```

```
# Effect Size for ANOVA (Type III)
```

```
Parameter | Eta2 (partial) |          95% CI  
-----  
time      |                | 0.93 | [0.87, 1.00]  
glucagon  |                | 0.58 | [0.29, 1.00]
```

```
- One-sided CIs: upper bound fixed at [1.00].>
```

But in that case both may be misleading as the proportion of explained variance is not clearly defined.

D.5 MuMIn package (R^2)

```
library(MuMIn)  
r.squaredGLMM(eCS.lmer)  
cat("\n")
```

```
          R2m      R2c  
[1,] 0.2163302 0.9764382
```

To reproduce these R^2 , we extract from the random intercept model:

- the residual variance

```
sigmaW <- sigma(eCS.lmm)[1,1]-sigma(eCS.lmm)[1,2]
```

- the variance of the random effect

```
sigmaB <- sigma(eCS.lmm)[1,2]
```

- the variance of the fitted values:

```
sigma2_XB <- var(fitted(eCS.lmm))
```

and evaluate the ratios:

```
c(R2m = sigma2_XB/(sigmaW + sigmaB + sigma2_XB),  
  R2c = (sigma2_XB + sigmaB)/(sigmaW + sigmaB + sigma2_XB))
```

```
          R2m      R2c  
0.2163302 0.9764382
```

D.6 stats package (partial residuals)

The function `residuals.lm` can be used to extract partial residuals from `lm` objects:

```
eIID.lm <- lm(weight ~ time + glucagon, data = dfL)
pRes.lm <- residuals(eIID.lm, type = "partial")
head(pRes.lm)
```

```
      time  glucagon
1  3.359543  1.475108
2 49.419060 39.475108
3 -8.145299 -16.024892
4 24.241798 20.475108
5 -8.407618 -12.624892
6 41.027985 33.075108
```

Those generally differ (by a constant) from the one provided by `residuals.lmm`:

```
eIID.lmm <- lmm(weight ~ time + glucagon, data = dfL)
head(residuals(eIID.lmm, type = "partial", var = "glucagon"))
```

```
[1] -31.9349871  6.0650129 -49.4349871 -12.9349871 -46.0349871  -0.3349871
```

Indeed, `residuals.lm` centers the design matrix of the variable relative to which the partial residuals are computed:

```
m.pres2 <- dfL$weight - cbind(model.matrix(~time,dfL), mean(dfL$glucagon)) %*% coef(eIID.lmm)
range(pRes.lm[, "glucagon"] - m.pres2, na.rm = TRUE)
```

```
[1] -3.348433e-13  4.654055e-13
```

For continuous variable with a linear effect, these residuals can be obtained by setting the `type` argument to `"partial-center"`:

```
eIID.lmm <- lmm(weight ~ time + glucagon, data = dfL)
pRes.lmm <- residuals(eIID.lmm, type = "partial-center", var = "glucagon")
range(pRes.lm[, "glucagon"] - pRes.lmm)
```

```
[1] -3.330669e-13  4.725109e-13
```

⚠ When evaluating the partial residuals relative to categorical variables, interactions, or non-linear terms, the output obtained with `partial-center` will not match the one of `residuals.lm`. Indeed `partial-center` will, when numeric, center the original variable whereas `residuals.lm` will center the column relative to the coefficient in the design matrix.