

Overview of the package LMMstar

Brice Ozenne

May 9, 2022

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 (e.g. time, brain region, ...). Key assumptions are that at the cluster level, observation are independent and identically distributed and that the mean and variance are independent (conditionally on covariates). In particular, in large samples the residuals do not have to be normally distributed.

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 test linear combinations of coefficients (Wald test or Likelihood ratio tests). The output be combined via `rbind`.
 - `coef` to extract the estimates.
 - `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).
 - `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 table containing estimates with the corresponding uncertainty.
 - `plot` to obtain a diagnostic plots, partial residual plots, or a graphical display of the fitted values.
 - `predict` to compute the conditional mean for new observations.
 - `residuals` to extract the observed residuals of the fitted model.
 - `sigma` to extract the modeled residual variance covariance matrix.
 - `summary` to obtain a summary of the input, model fit, and estimated values.
- the `summarize` function to compute summary statistics stratified on a categorical variable.
- 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.

Before going further we need to load the **LMMstar** package in the R session:

```
library(LMMstar)
```

To illustrate the functionalities of the package, we will use the `gastricbypassL` dataset:

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

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

See `?gastricbypassL` for a presentation of the database. We will use a shorter version of the time variable:

```
gastricbypassL$time <- factor(gastricbypassL$time,
  levels = c("3 months before", "1 week before",
    "1 week after", "3 months after" ),
  labels = c("B3_months", "B1_week", "A1_week", "A3_months"))
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
```

Note: the **LMMstar** 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 is:

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

```
[1] '0.6.1'
```

When estimating model coefficients, we will use the internal optimization routine of the **LMMstar** package (instead of relying on the `nlme::gls` function, which is the default option):

```
LMMstar.options(optimizer = "FS")
```

1 Descriptive 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	median	max
1	weight	B3_months	20	0	128.97	20.269	100.90	123.10	173.00
2	weight	B1_week	20	0	121.24	18.910	95.70	114.50	162.20
3	weight	A1_week	20	0	115.70	18.275	89.90	110.60	155.00
4	weight	A3_months	20	0	102.36	17.054	78.80	98.50	148.00
5	glucagon	B3_months	20	0	4.51	0.641	3.61	4.33	6.03
6	glucagon	B1_week	19	1	4.39	0.558	3.58	4.23	5.95
7	glucagon	A1_week	19	1	6.06	1.044	4.52	5.94	8.27
8	glucagon	A3_months	20	0	5.06	0.760	3.95	5.03	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)
```

	outcome	time	observed	missing	mean	sd	min	median	max
1	weight	B3_months	20	0	129	20.3	100.9	123.1	173
2	weight	B1_week	20	0	121	18.9	95.7	114.5	162
3	weight	A1_week	20	0	116	18.3	89.9	110.6	155
4	weight	A3_months	20	0	102	17.1	78.8	98.5	148

Pearson's correlation:

	B3_months	B1_week	A1_week	A3_months
B3_months	1.000	0.990	0.986	0.946
B1_week	0.990	1.000	0.997	0.959
A1_week	0.986	0.997	1.000	0.966
A3_months	0.946	0.959	0.966	1.000

It is possible to compute correlations adjusted for other variables, e.g.:

```
partialCor(list(weight~group, glucagonAUC~group),
  data = gastricbypassL[gastricbypassL$time=="B3_months",])
```

	estimate	se	df	lower	upper	p.value
rho(weight,glucagonAUC)	-0.124	0.236	9.14	-0.576	0.386	0.61

Note: estimates and confidence intervals for rho have been back-transformed.
standard errors are not back-transformed.

2 Linear mixed model

2.1 Classical covariance patterns

Fit a linear model with **identity** structure:

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

Linear regression

```
outcome/cluster/time: weight/id/time
data                  : 78 observations and distributed in 20 clusters
parameters            : 5 mean ((Intercept) timeB1_week timeA1_week timeA3_months glucagon)
                      1 variance (sigma)
log-restr.likelihood: -323.086426918519
convergence           : TRUE (1 iterations)
covariance structure:
      B3_months B1_week A1_week A3_months
B3_months 330.0427 0.0000 0.0000 0.0000
B1_week    0.0000 330.0427 0.0000 0.0000
A1_week    0.0000 0.0000 330.0427 0.0000
A3_months  0.0000 0.0000 0.0000 330.0427
```

Fit a linear model with **independence** structure:

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

Linear regression with heterogeneous residual variance

```
outcome/cluster/time: weight/id/time
data                  : 78 observations and distributed in 20 clusters
parameters            : 5 mean ((Intercept) timeB1_week timeA1_week timeA3_months glucagon)
                      4 variance (sigma k.B1_week k.A1_week k.A3_months)
log-restr.likelihood: -321.457830361849
convergence           : TRUE (9 iterations)
covariance structure:
      B3_months B1_week A1_week A3_months
B3_months 442.6475 0.0000 0.0000 0.0000
B1_week    0.0000 418.9934 0.0000 0.0000
A1_week    0.0000 0.0000 222.8463 0.0000
A3_months  0.0000 0.0000 0.0000 237.2049
```

Fit a linear mixed model with **compound symmetry** structure:

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

Linear Mixed Model with a compound symmetry covariance matrix

```
outcome/cluster/time: weight/id/time
data                  : 78 observations and distributed in 20 clusters
parameters            : 5 mean ((Intercept) timeB1_week timeA1_week timeA3_months glucagon)
                       1 variance (sigma)
                       1 correlation (rho)
log-restr.likelihood: -243.600523870253
convergence            : TRUE (10 iterations)
covariance structure:
      B3_months  B1_week  A1_week  A3_months
B3_months  355.3062 344.6236 344.6236 344.6236
B1_week    344.6236 355.3062 344.6236 344.6236
A1_week    344.6236 344.6236 355.3062 344.6236
A3_months  344.6236 344.6236 344.6236 355.3062
```

Fit a linear mixed model with **stratified compound symmetry** covariance matrix:

```
eSCS.lmm <- lmm(weight ~ time*group,
  repetition = ~time|id, structure = CS(~group),
  data = gastricbypassL)
eSCS.lmm
cat(" covariance structure: \n");sigma(eSCS.lmm)
```

Linear Mixed Model with a block unstructured covariance matrix

```
outcome/cluster/time: weight/id/time
data                  : 80 observations and distributed in 20 clusters
parameters            : 8 mean ((Intercept) timeB1_week timeA1_week timeA3_months group timeB1_week:
                        2 variance (sigma k.1)
                        2 correlation (rho(0) rho(1))
log-restr.likelihood: -233.141302306302
convergence           : TRUE (7 iterations)
covariance structure:
$'0.0'
      B3_months B1_week A1_week A3_months
B3_months 348.0783 334.7404 334.7404 334.7404
B1_week   334.7404 348.0783 334.7404 334.7404
A1_week    334.7404 334.7404 348.0783 334.7404
A3_months  334.7404 334.7404 334.7404 348.0783

$'1.1'
      B3_months B1_week A1_week A3_months
B3_months 345.1388 340.0877 340.0877 340.0877
B1_week   340.0877 345.1388 340.0877 340.0877
A1_week    340.0877 340.0877 345.1388 340.0877
A3_months  340.0877 340.0877 340.0877 345.1388
```

Fit a linear mixed model with **block compound symmetry** covariance matrix¹:

```
eBCS.lmm <- lmm(weight ~ time*group,
  repetition = ~time|id, structure = CS(~baseline, heterogeneous = FALSE),
  data = gastricbypassL)
eBCS.lmm
cat(" covariance structure: \n");sigma(eBCS.lmm)
```

Linear Mixed Model with a block compound symmetry covariance matrix

```
outcome/cluster/time: weight/id/time
data                  : 80 observations and distributed in 20 clusters
parameters           : 8 mean ((Intercept) timeB1_week timeA1_week timeA3_months group timeB1_week:
                        1 variance (sigma)
                        2 correlation (rho(TRUE) rho(TRUE,FALSE))
log-restr.likelihood: -234.971305082514
convergence           : TRUE (7 iterations)
covariance structure:
      B3_months B1_week A1_week A3_months
B3_months 346.6085 339.4747 336.3836 336.3836
B1_week   339.4747 346.6085 336.3836 336.3836
A1_week   336.3836 336.3836 346.6085 339.4747
A3_months 336.3836 336.3836 339.4747 346.6085
```

Fit a linear mixed model with **block unstructured** covariance matrix:

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

Linear Mixed Model with a block unstructured covariance matrix

```
outcome/cluster/time: weight/id/time
data                  : 80 observations and distributed in 20 clusters
parameters           : 8 mean ((Intercept) timeB1_week timeA1_week timeA3_months group timeB1_week:
                        2 variance (sigma k.TRUE)
                        3 correlation (rho(TRUE) rho(TRUE,FALSE) rho(FALSE))
log-restr.likelihood: -231.80588606934
convergence           : TRUE (7 iterations)
covariance structure:
      B3_months B1_week A1_week A3_months
B3_months 377.4267 372.4602 336.3836 336.3836
B1_week   372.4602 377.4267 336.3836 336.3836
A1_week   336.3836 336.3836 315.7904 306.4892
A3_months 336.3836 336.3836 306.4892 315.7904
```

¹same as nested random effects

Fit a linear mixed model with **unstructured** covariance matrix:

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

Linear Mixed Model with an unstructured covariance matrix

```
outcome/cluster/time: weight/id/time
data                  : 78 observations and distributed in 20 clusters
parameters            : 5 mean ((Intercept) timeB1_week timeA1_week timeA3_months glucagon)
                       4 variance (sigma k.B1_week k.A1_week k.A3_months)
                       6 correlation (rho(B3_months,B1_week) rho(B3_months,A1_week) rho(B3_months,A3_months))
log-restr.likelihood: -216.318937004305
convergence            : TRUE (23 iterations)
covariance structure:
               B3_months  B1_week  A1_week  A3_months
B3_months    411.3114 381.9734 352.6400  318.8573
B1_week       381.9734 362.7326 335.4649  304.6314
A1_week       352.6400 335.4649 311.6921  285.8077
A3_months     318.8573 304.6314 285.8077  280.9323
```


Fit a linear mixed model with **stratified unstructured** covariance matrix:

```
eSUN.lmm <- lmm(weight ~ time*group + glucagon,
  repetition = ~time|id, structure = UN(~group),
  data = gastricbypassL)
eSUN.lmm
cat(" covariance structure: \n");sigma(eSUN.lmm)
```

Linear Mixed Model with a stratified unstructured covariance matrix

```
outcome/cluster/time: weight/id/time
data                  : 78 observations and distributed in 20 clusters
parameters            : 9 mean ((Intercept) timeB1_week timeA1_week timeA3_months group glucagon tim
                        8 variance (sigma:0 sigma:1 k.B1_week:0 k.A1_week:0 k.A3_months:0 k.B1_week:
                        12 correlation (rho(B3_months,B1_week):0 rho(B3_months,A1_week):0 rho(B3_mon
log-restr.likelihood: -197.171312062212
convergence            : TRUE (51 iterations)
covariance structure:
$'0'
      B3_months  B1_week  A1_week  A3_months
B3_months  417.3374 382.8829 362.5674  301.7430
B1_week     382.8829 364.4515 346.4039  292.7507
A1_week     362.5674 346.4039 331.1789  282.9301
A3_months   301.7430 292.7507 282.9301  253.3324

$'1'
      B3_months  B1_week  A1_week  A3_months
B3_months  383.8877 363.6405 336.5771  350.0416
B1_week     363.6405 347.9898 321.5908  331.5182
A1_week     336.5771 321.5908 297.5329  308.1345
A3_months   350.0416 331.5182 308.1345  334.8267
```

2.2 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: `gastricbypassL`

- 20 clusters
- 78 observations were analyzed, 2 were excluded because of missing values
- 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 "B3_months","B1_week",...: 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=B3_months
```

Estimation procedure

- Restricted Maximum Likelihood (REML)
- log-likelihood : -216.3189
- parameters: mean = 5, variance = 4, correlation = 6
- convergence: TRUE (23 iterations)
- largest |score| = 7.034631e-05 for `k.A1_week`
|change| = 1.097373342418e-06 for (Intercept)

Residual variance-covariance: unstructured

- correlation structure: `~time`

	B3_months	B1_week	A1_week	A3_months
B3_months	1.000	0.989	0.985	0.938
B1_week	0.989	1.000	0.998	0.954
A1_week	0.985	0.998	1.000	0.966
A3_months	0.938	0.954	0.966	1.000
- variance structure: `~time`

	standard.deviation	ratio
B3_months	20.28081	1.0000000
B1_week	19.04554	0.9390916
A1_week	17.65480	0.8705176
A3_months	16.76104	0.8264480

Fixed effects: weight ~ time + glucagon

	estimate	se	df	lower	upper	p.value
(Intercept)	132.98	4.664	19.758	123.243	142.717	< 0.001 ***
timeB1_week	-7.882	0.713	19.171	-9.374	-6.39	< 0.001 ***
timeA1_week	-11.788	1.018	21.644	-13.9	-9.676	< 0.001 ***
timeA3_months	-26.122	1.656	18.84	-29.591	-22.654	< 0.001 ***
glucagon	-0.888	0.242	13.708	-1.408	-0.369	0.00257 **

Uncertainty was quantified using model-based standard errors (column se).

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

The columns lower and upper indicate a 95% confidence interval for each coefficient.

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.

2.3 Extract estimated coefficients

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

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

(Intercept)	timeB1_week	timeA1_week	timeA3_months	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.B1_week	k.A1_week	k.A3_months
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:B3_months	sigma:B1_week	sigma:A1_week	sigma:A3_months
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	B3_months	128.5386	4.536445	18.97584	119.04289	138.0343
2	B1_week	120.6564	4.261691	19.04078	111.73783	129.5749
3	A1_week	116.7506	3.956964	19.04925	108.47007	125.0312
4	A3_months	102.4162	3.747908	19.05531	94.57328	110.2591

2.4 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)	132.980	4.664	19.8	123.24	142.717	0.00e+00
timeB1_week	-7.882	0.713	19.2	-9.37	-6.390	9.27e-10
timeA1_week	-11.788	1.018	21.6	-13.90	-9.676	9.55e-11
timeA3_months	-26.122	1.656	18.8	-29.59	-22.654	2.62e-12
glucagon	-0.888	0.242	13.7	-1.41	-0.369	2.57e-03

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

```
model.tables(eUN.lmm, effect = "all") ## not shown
```

Because these parameters are constrained (e.g. strictly positive), they uncertainty is by default computed after transformation (e.g. log) and then backtransformed.

2.5 Extract estimated residual variance-covariance structure

The method `sigma` can be used to output the covariance structure of the residuals:

```
sigma(eUN.lmm)
```

	B3_months	B1_week	A1_week	A3_months
B3_months	411.3114	381.9734	352.6400	318.8573
B1_week	381.9734	362.7326	335.4649	304.6314
A1_week	352.6400	335.4649	311.6921	285.8077
A3_months	318.8573	304.6314	285.8077	280.9323

It can also be specific to a "known" individual:

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

	B3_months	A1_week	A3_months
B3_months	411.3114	352.6400	318.8573
A1_week	352.6400	311.6921	285.8077
A3_months	318.8573	285.8077	280.9323

or for a new individual:

```
newdata <- data.frame(id = "X", time = c("B3_months", "B1_week", "A1_week", "A3_months"))
sigma(eUN.lmm, cluster = newdata)
```

	B3_months	B1_week	A1_week	A3_months
B3_months	411.3114	381.9734	352.6400	318.8573
B1_week	381.9734	362.7326	335.4649	304.6314
A1_week	352.6400	335.4649	311.6921	285.8077
A3_months	318.8573	304.6314	285.8077	280.9323

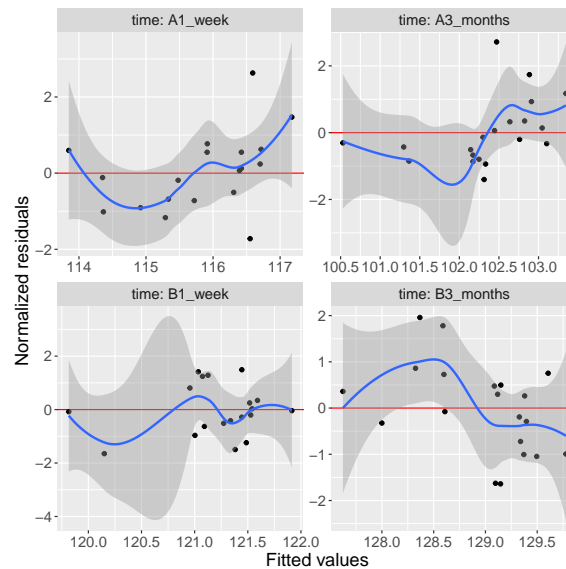
²it is equivalent to `confint` method except that by default it also outputs `se` and `p.value`

2.6 Model diagnostic

The method `plot` can be used to display diagnostic plots about:

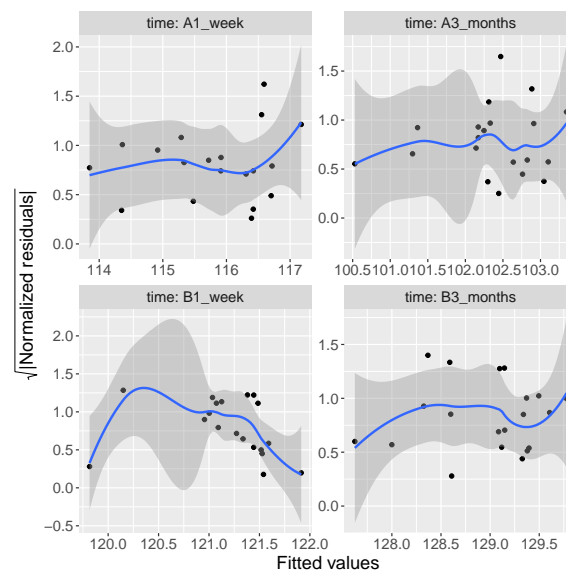
- misspecification of the mean structure

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



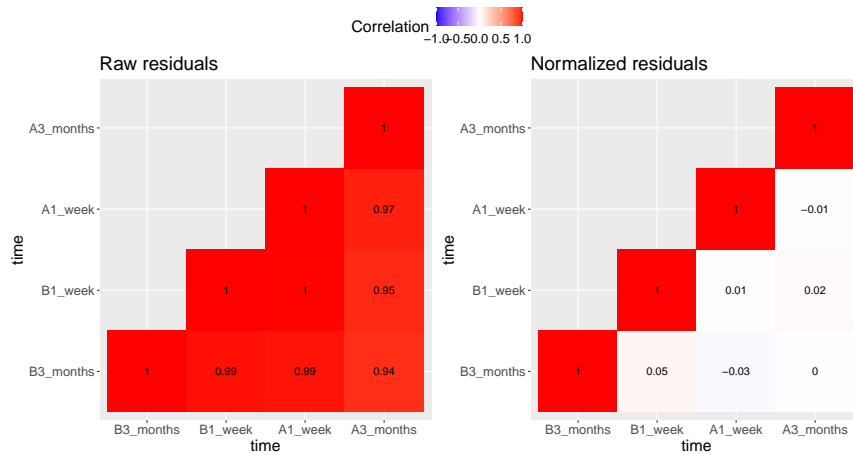
- misspecification of the variance structure

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



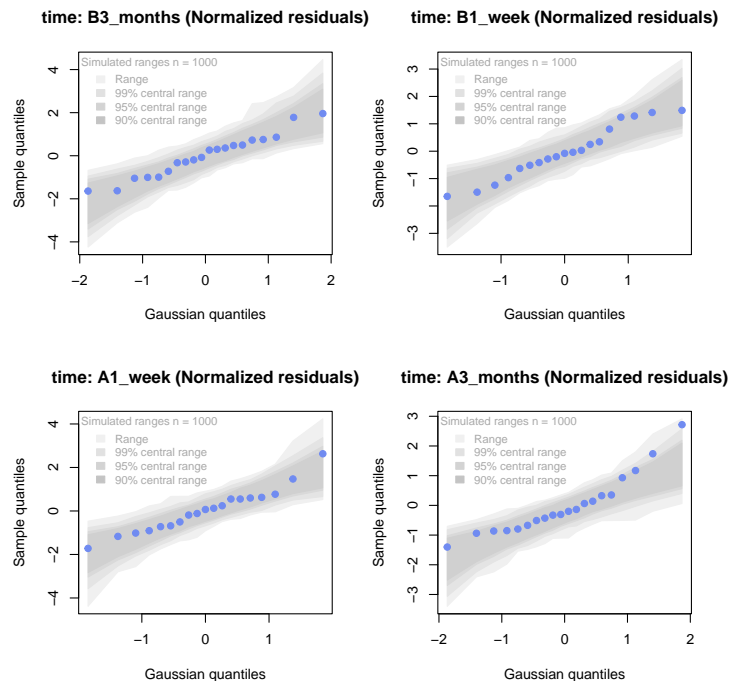
- misspecification of the correlation structure

```
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.

The method `residuals` returns the residulas 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.B3_months r.B1_week r.A1_week r.A3_months
1        1 -0.2897365 -0.2027622 -1.16864038  0.3258573
2        2  0.8603117 -1.6492164  0.62578801  1.7370660
3        3  0.7273066 -0.4155171 -0.68266741 -0.8510316
4        4 -1.6403082 -0.5128368  0.06806206  1.1725813
5        5  0.4755409          NA -0.18736415 -0.8634200
6        6  1.7801675  1.2847703  2.63004812  0.3505542
```

or in the long format:

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

```
[1] -0.2897365  0.8603117  0.7273066 -1.6403082  0.4755409  1.7801675
```

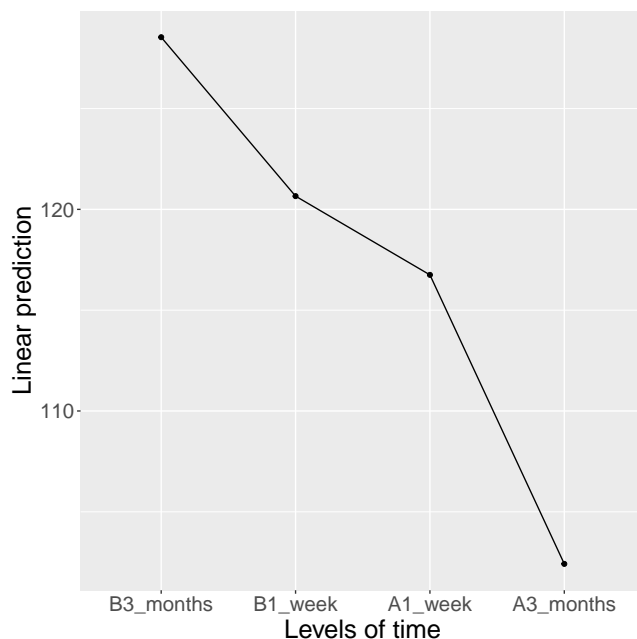
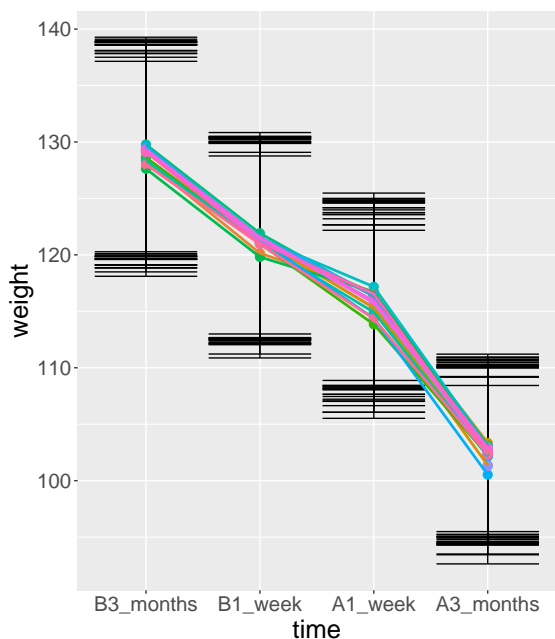
Various type of residuals can be extract but the normalized one are recommanded when doing model checking.

2.7 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))
```

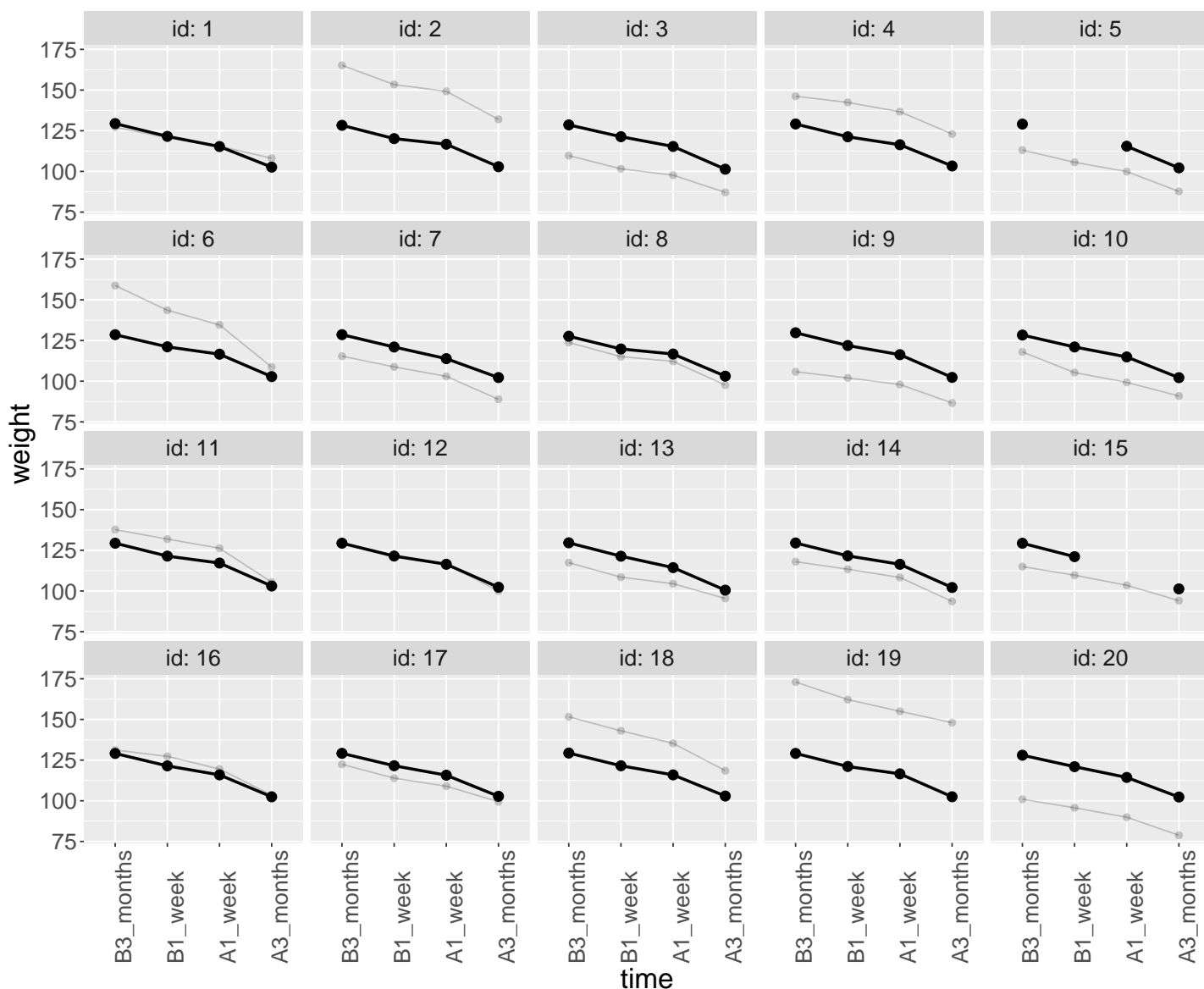


In the first case each possible curve is displayed while in the latter the average curve (over glucagon values). With the `plot` method, it is possible to display a curve specific to a glucagon value via the argument `at`:

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

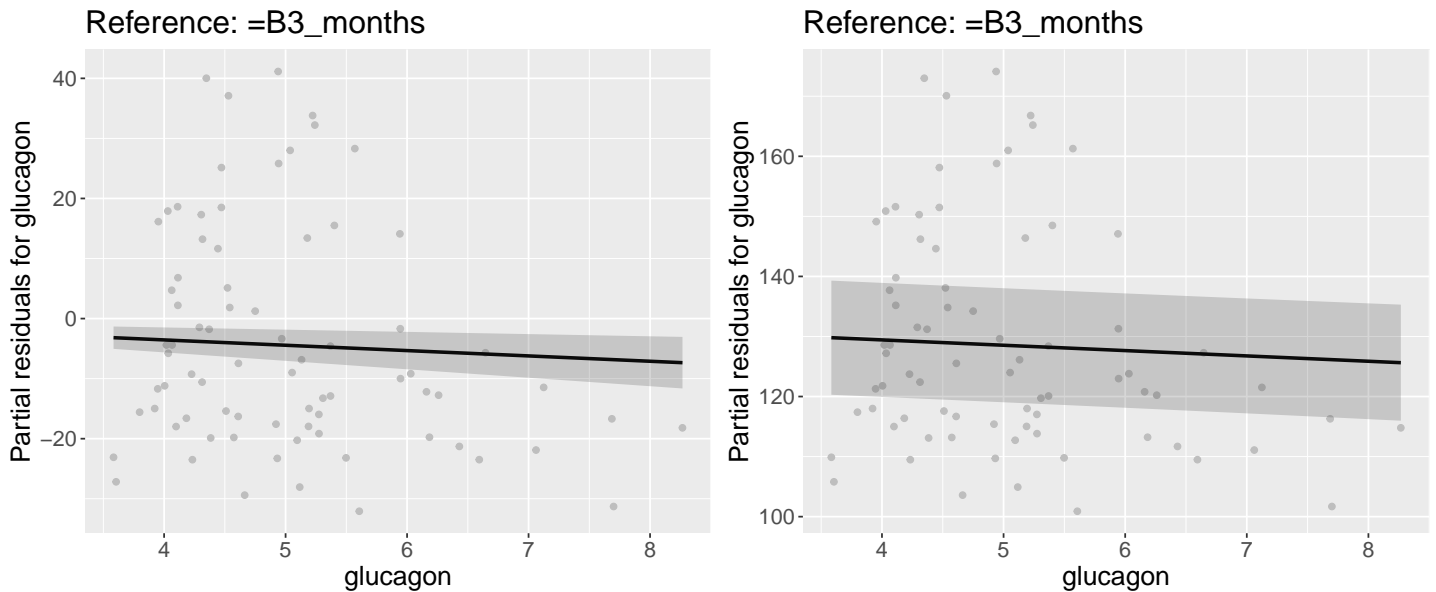
It is also possible to display the observed values along with the fitted values by setting the argument `obs.alpha` to a strictly positive value below or equal to 1. This argument controls the transparency of the color used to display the observed values:

```
gg <- plot(eUN.lmm, type = "fit", obs.alpha = 0.2, ci = FALSE, plot = FALSE)$plot
gg <- gg + facet_wrap(~id, labeller = label_both)
gg <- gg + theme(axis.text.x=element_text(angle = 90, hjust = 0))
gg
```



Partial residuals can also be displayed via the plot method:

```
gg1 <- plot(eUN.lmm, type = "partial", var = "glucagon", plot = FALSE)$plot
gg2 <- plot(eUN.lmm, type = "partial", var = c("(Intercept)", "glucagon"), plot = FALSE)$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)
m.pres <- gastricbypassL$weight - model.matrix(~time, gastricbypassL) %*% coef(eUN.lmm)[1:4]
range(df.pres$r.partial - m.pres, na.rm = TRUE)
```

```
[1] -1.065814e-14  1.154632e-14
```

2.8 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)
```

```
|| mean coefficients ||

- Multivariate Wald test (global null hypothesis)
      statistic df.num df.denom    p.value
time      86.743     3   19.005 2.8424e-11 ***
glucagon   13.518     1   13.708 0.0025716 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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("timeA1_week-timeB1_week=0"))
```

```
|| User-specified linear hypotheses ||

- Multivariate Wald test (global null hypothesis)
      statistic df.num df.denom    p.value
      43.141      1   17.875 3.7234e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

One can also simultaneously test several null hypotheses:

```
e.anova <- anova(eUN.lmm, effects = c("timeA1_week-timeB1_week=0",
                                     "timeA3_months-timeB1_week=0"))
summary(e.anova)
```

```
|| User-specified linear hypotheses ||

- Multivariate Wald test (global null hypothesis)
      statistic df.num df.denom    p.value
      98.651      2   18.62 1.2338e-10 ***

- Univariate Wald test (individual null hypotheses)
               estimate      se      df      lower      upper p.value
timeA1_week - timeB1_week   -3.90572  0.59464  17.00000  -5.32750  -2.4839 < 1e-05 ***
timeA3_months - timeB1_week -18.24016  1.32283  19.00000 -21.40304 -15.0773 < 1e-05 ***
```

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Standard errors: model-based
(CIs/p-values adjusted for multiple comparisons -- max-test adjustment)
CIs/p-values computed using 1e+05 samples.

```

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 "A1_week - B1_week" "A3_months - B1_week" "A3_months - A1_week"

```

|| User-specified linear hypotheses ||

```

- Multivariate Wald test (global null hypothesis)

```

statistic df.num df.denom    p.value
  86.743      3    19.005 2.8424e-11 ***

```

- Univariate Wald test (individual null hypotheses)

	estimate	se	df	lower	upper	p.value	
B1_week - B3_months	-7.88223	0.71318	19.00000	-9.82885	-5.9356	<1e-05	***
A1_week - B3_months	-11.78795	1.01751	21.00000	-14.56525	-9.0107	<1e-05	***
A3_months - B3_months	-26.12239	1.65641	18.00000	-30.64354	-21.6012	<1e-05	***
A1_week - B1_week	-3.90572	0.59464	17.00000	-5.52879	-2.2827	2e-05	***
A3_months - B1_week	-18.24016	1.32283	19.00000	-21.85081	-14.6295	<1e-05	***
A3_months - A1_week	-14.33444	1.05650	20.00000	-17.21814	-11.4507	<1e-05	***

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
Standard errors: model-based
(CIs/p-values adjusted for multiple comparisons -- max-test adjustment)
CIs/p-values computed using 1e+05 samples.

```

When testing transformed variance or correlation parameters, parentheses (as in `log(k).B1_week`) cause problem for recognizing parameters:

```

try(
  anova(eUN.lmm,
    effects = c("log(k).B1_week=0","log(k).A1_week=0","log(k).A3_months=0"))
)

```

```

Error in .anova_Wald(object, effects = effects, robust = robust, rhs = rhs, :
Possible misspecification of the argument 'effects' as running mulcomp::glht lead to the following
Error in parse(text = ex[i]) : <text>:1:7: uventet symbol
1: log(k).B1_week
      ^

```

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

```

```

      (Intercept) timeB1_week timeA1_week timeA3_months glucagon sigma k.B1_week k.A1_week
k.B1_week      0          0          0          0          0          0          1          0
k.A1_week      0          0          0          0          0          0          0          1
k.A3_months    0          0          0          0          0          0          0          0
      k.A3_months rho(B3_months,B1_week) rho(B3_months,A1_week) rho(B3_months,A3_months)
k.B1_week      0          0          0          0          0
k.A1_week      0          0          0          0          0
k.A3_months    1          0          0          0          0
      rho(B1_week,A1_week) rho(B1_week,A3_months) rho(A1_week,A3_months)
k.B1_week      0          0          0
k.A1_week      0          0          0
k.A3_months    0          0          0

```

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

```

anova(eUN.lmm, effects = C)

```

```

|| User-specified linear hypotheses ||

```

```

- Multivariate Wald test (global null hypothesis)

```

```

statistic df.num df.denom  p.value
  6.2032      3    17.995 0.0044171 **

```

```

---

```

```

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

```

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 a (very artificial) example:

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

|| User-specified linear hypotheses ||

- Multivariate Wald test (global null hypothesis)

statistic	df.num	df.denom	p.value
8.8925	3	Inf	6.8788e-06 ***

- Univariate Wald test (individual null hypotheses)

	estimate	se	df	lower	upper	p.value	
[1,]	-8.27006	2.57880	34.00000	-14.90551	-1.6346	0.01222	*
[2,]	0.82179	0.61997	53.00000	-0.77344	2.4170	0.47409	
[3,]	-0.88831	0.24161	13.00000	-1.50998	-0.2666	0.00408	**

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

Standard errors: model-based

(CIs/p-values adjusted for multiple comparisons -- max-test adjustment)

CIs/p-values computed using 1e+05 samples.

2.9 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:

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

```
gastricbypassW <- reshape(gastricbypassL[,c("id","time","weight","group")],
  direction = "wide",
  timevar = "time", idvar = c("id","group"))
e.ANCOVA <- lm(weight.A1_week ~ weight.B1_week + group, data = gastricbypassW)
summary(e.ANCOVA)$coef
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-1.4823022	2.31781138	-0.6395267	5.310047e-01
weight.B1_week	0.9654917	0.01803988	53.5198489	2.156258e-20
group	0.2521714	0.66499945	0.3792054	7.092302e-01

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

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

```
e.lmmANCOVA <- lmm(weight ~ time+time:group, repetition = ~time|id,
  data = gastricbypassL[gastricbypassL$visit %in% 2:3,])
```

and then perform a delta-method:

```
lava::estimate(e.lmmANCOVA, f = function(p){
  c(Y1 = as.double(p["rho(B1_week,A1_week)"]*p["k.A1_week"]),
    X1 = as.double(p["timeA1_week:group"]-p["rho(B1_week,A1_week)"]*p["k.A1_week"]*p["timeB1_
week:group"])))
})
```

	estimate	se	df	lower	upper	p.value
Y1	0.9654917	0.01753161	15.96769	0.9283203	1.002663	0.0000000
X1	0.2521714	0.64626331	15.00349	-1.1252784	1.629621	0.7018731

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.

2.10 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$treat <- baselineAdjustment(gastricbypassL, variable = "group",
  repetition = ~time|id, constrain = c("B3_months", "B1_week"),
  new.level = "none")
table(treat = gastricbypassL$treat, time = gastricbypassL$time, group = gastricbypassL$group)
```

```
, , group = 1
```

```
      time
treat B3_months B1_week A1_week A3_months
none      14      14      0        0
1         0       0      14       14
2         0       0       0        0
```

```
, , group = 2
```

```
      time
treat B3_months B1_week A1_week A3_months
none      6       6       0        0
1         0       0       0        0
2         0       0       6        6
```

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

```
gastricbypassL$treat2 <- baselineAdjustment(gastricbypassL, variable = "group",
  repetition = ~time|id, constrain = c("B3_months", "B1_week"))
table(treat = gastricbypassL$treat2, time = gastricbypassL$time, group = gastricbypassL$group)
```

```
, , group = 1
```

```
      time
treat B3_months B1_week A1_week A3_months
1      14      14      14       14
2       0       0       0        0
```

```
, , group = 2
```

	time	B3_months	B1_week	A1_week	A3_months
treat					
1		6	6	0	0
2		0	0	6	6

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

```
gastricbypassL$timeXtreat <- baselineAdjustment(gastricbypassL, variable = "group",
  repetition = ~time|id, constrain = c("B3_months", "B1_week"),
  collapse.time = ".")

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

```
, , group = 1
```

	time	B3_months	B1_week	A1_week	A3_months
treat					
B3_months		14	0	0	0
B1_week		0	14	0	0
A1_week.1		0	0	14	0
A3_months.1		0	0	0	14
A1_week.2		0	0	0	0
A3_months.2		0	0	0	0

```
, , group = 2
```

	time	B3_months	B1_week	A1_week	A3_months
treat					
B3_months		6	0	0	0
B1_week		0	6	0	0
A1_week.1		0	0	0	0
A3_months.1		0	0	0	0
A1_week.2		0	0	6	0
A3_months.2		0	0	0	6

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)	timeXtreatB1_week	timeXtreatA1_week.1	timeXtreatA3_months.1
	128.97000	-7.73000	-12.83949	-27.07620
timeXtreatA1_week.2		-14.27452		
timeXtreatA3_months.2			-25.50553	

or

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

```
timeXtreatB3_months      timeXtreatB1_week      timeXtreatA1_week.1 timeXtreatA3_months.1  
      128.9700              121.2400              116.1305              101.8938  
timeXtreatA1_week.2 timeXtreatA3_months.2  
      114.6955              103.4645
```

The parametrization however does (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)"      "treat1"           "treat2"           "timeB1_week"  
[5] "timeA1_week"      "timeA3_months"    "treat1:timeB1_week" "treat2:timeB1_week"  
[9] "treat1:timeA1_week" "treat2:timeA1_week" "treat1:timeA3_months" "treat2:timeA3_months"
```

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

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

Constant values in the design matrix in interactions "treat2:time"
Coefficients "treat22" "treat22:timeB1_week" have been removed.

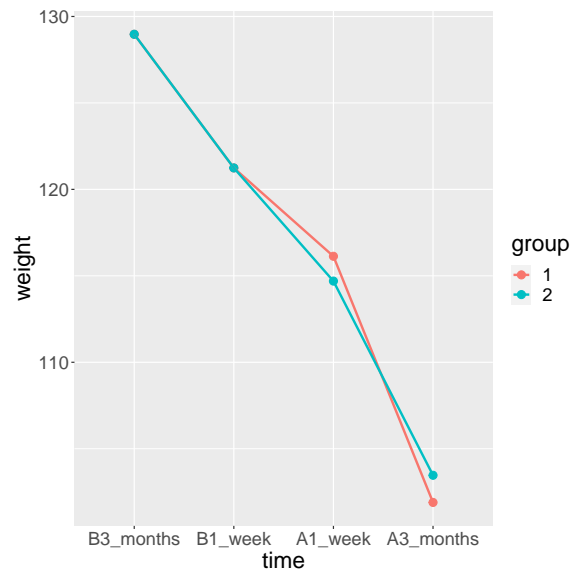
with the following coefficients:

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

	estimate	se	df	lower	upper	p.value
(Intercept)	128.97	4.532	19.0	119.48	138.46	0.00e+00
timeB1_week	-7.73	0.697	19.0	-9.19	-6.27	1.00e-09
timeA1_week	-12.84	0.865	20.5	-14.64	-11.04	2.02e-12
timeA3_months	-27.08	1.724	21.4	-30.66	-23.50	3.20e-13
treat22:timeA1_week	-1.44	0.621	16.3	-2.75	-0.12	3.43e-02
treat22:timeA3_months	1.57	2.463	16.3	-3.64	6.78	5.32e-01

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

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



2.11 Marginal means

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

```
e.group <- lmm(weight ~ time*group, data = gastricbypassL,
  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
B3_months	130	5.05	18.0	119.3	141
B1_week	122	4.69	18.0	112.5	132
A1_week	117	4.55	18.0	107.0	126
A3_months	104	4.20	18.1	94.9	113

Results are averaged over the levels of: group

Confidence level used: 0.95

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

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

	outcome	time	observed	missing	mean	sd	min	median	max
1	estimate	B3_months	20	0	128.970	2.270212	127.5214	127.5214	132.35
2	estimate	B1_week	20	0	121.240	2.726942	119.5000	119.5000	125.30
3	estimate	A1_week	20	0	115.700	2.014981	114.4143	114.4143	118.70
4	estimate	A3_months	20	0	102.365	3.146729	100.3571	100.3571	107.05

as the groups are not balanced:

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

```

time
group B3_months B1_week A1_week A3_months
1      14      14      14      14
2       6       6       6       6

```

The "emmeans" approach gives equal "weight" to the expected value of both group 2:

```

mu.group1 <- as.double(coef(e.group)["(Intercept)"])
mu.group2 <- as.double(coef(e.group)["(Intercept)"] + coef(e.group)["group2"])
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
129.9357 128.9700

```

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 = ~group|time)
emmeans.group

```

```

time = B3_months:
group emmean SE df lower.CL upper.CL
1      128 5.53 18.0    115.9    139
2      132 8.45 18.0    114.6    150

```

```

time = B1_week:
group emmean SE df lower.CL upper.CL
1      120 5.14 18.0    108.7    130
2      125 7.85 18.0    108.8    142

```

```

time = A1_week:
group emmean SE df lower.CL upper.CL
1      114 4.99 18.0    103.9    125
2      119 7.62 18.0    102.7    135

```

```

time = A3_months:
group emmean SE df lower.CL upper.CL
1      100 4.60 18.1     90.7    110
2      107 7.03 18.1     92.3    122

```

Confidence level used: 0.95

Using the `pair` function displays the differences:

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

```
time = B3_months:
  contrast estimate    SE    df t.ratio p.value
2 - 1          4.83 10.10 18.0   0.478  0.6383
```

```
time = B1_week:
  contrast estimate    SE    df t.ratio p.value
2 - 1          5.80  9.38 18.0   0.618  0.5441
```

```
time = A1_week:
  contrast estimate    SE    df t.ratio p.value
2 - 1          4.29  9.11 18.0   0.471  0.6435
```

```
time = A3_months:
  contrast estimate    SE    df t.ratio p.value
2 - 1          6.69  8.40 18.1   0.797  0.4361
```

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
2 - 1    B3_months      4.83 10.10 18.0   -17.9    27.6    0.478  0.7490
2 - 1    B1_week       5.80  9.38 18.0   -15.4    27.0    0.618  0.6482
2 - 1    A1_week       4.29  9.11 18.0   -16.2    24.8    0.471  0.7552
2 - 1    A3_months      6.69  8.40 18.1   -12.3    25.6    0.797  0.5287
```

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(eC2.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
2 - 1    B3_months      0.00 0.000  NaN    NaN    NaN
2 - 1    B1_week       0.00 0.000  NaN    NaN    NaN
2 - 1    A1_week      -1.44 0.621 16.2  -2.311  0.1303
2 - 1    A3_months      1.57 2.463 16.3   0.638  0.9522
```

P value adjustment: sidak method for 4 tests

2.12 Predictions

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

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

```
news <- gastricbypassL[gastricbypassL$id==1,]  
news$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 computing by creating a design matrix:

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

```
X.12
```

```
      (Intercept) timeB1_week timeA1_week timeA3_months 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 = "B3_months", weight = coef(eUN.lmm)["(Intercept)"], glucagon = 0),
  data.frame(id = 1, time = "B1_week", weight = NA, glucagon = 0),
  data.frame(id = 2, time = "B3_months", weight = 100, glucagon = 0),
  data.frame(id = 2, time = "B1_week", 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	B3_months	132.9801	0	NA	NA	NA	NA	NA
2	1	B1_week	NA	0	125.09790	0.6362754	Inf	123.85083	126.3450
3	2	B3_months	100.0000	0	NA	NA	NA	NA	NA
4	2	B1_week	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)["B3_months","B3_months"]
Omega_21 <- sigma(eUN.lmm)["B1_week","B3_months"]
as.double(mu2 + Omega_21 * (100 - mu1) / Omega_11)
```

```
[1] 94.47017
```

2.13 Missing values and imputation

We now consider the glucagon level as an outcome. 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 B3_months      20        0 0%
2 glucagon B1_week      19        1 5%
3 glucagon A1_week      19        1 5%
4 glucagon A3_months      20        0 0%
```

Further description of the missing data patterns rely on function outside the LMMstar package, e.g. appropriate call to `tapply` and `table`:

```
vec.pattern <- tapply(as.numeric(is.na(gastricbypassL$glucagon)),
  INDEX = gastricbypassL$id,
  FUN = paste, collapse=".")
table(vec.pattern)
```

```
vec.pattern
0.0.0.0 0.0.1.0 0.1.0.0
      18        1        1
```

Linear mixed model can handle missing value in the outcome variable, assuming that missigness is random conditional on the covariate and observed outcome values. The `lmm` function can be used "as usual":

```
eUN.lmmNA <- lmm(glucagon ~ time,
  repetition = ~time|id, structure = "UN",
  data = gastricbypassL)
summary(eUN.lmmNA, hide.fit = TRUE,
  hide.cor = TRUE, hide.sd = TRUE, hide.mean = TRUE)
```

Linear Mixed Model

Dataset: `gastricbypassL`

- 20 clusters
- 78 observations were analyzed, 2 were excluded because of missing values
- between 3 and 4 observations per cluster

Summary of the outcome and covariates:

```
$ glucagon: num  4.03 5.24 4.93 4.32 4.38 ...
$ time      : Factor w/ 4 levels "B3_months","B1_week",...: 1 1 1 1 1 1 1 1 1 1 ...
reference level: time=B3_months
```


The visible difference in the summary is when describing the dataset: we can see that some repetitions (here 2) have been ignored as the outcome was missing. So for some clusters only 3 values were analyzed instead of 4. It is possible to extract the most likely value for these missing observation using the `fitted` function with argument `impute=TRUE`:

```
fitted(eUN.lmmNA, impute = TRUE)
```

[1] 4.256984 6.497856

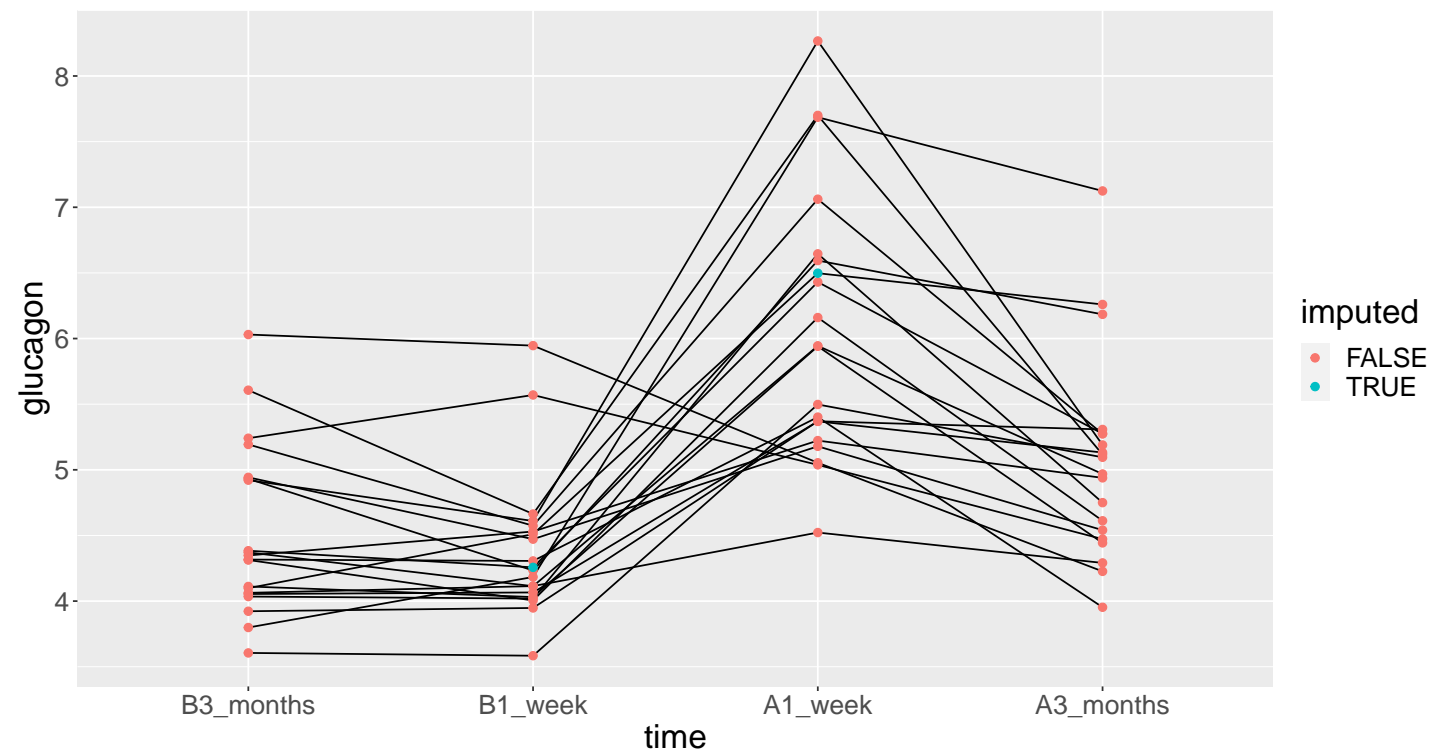
When using the argument `keep.newdata=TRUE`, the missing outcome value has been replaced by its most likely value (which is the same as the dynamic prediction, described previously):

```
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	id2	treatXtime	imputed	estimate
5	5	1 B3_months	113.1	7090.5	TRUE	4.383738	1	C5	B3_months	FALSE	4.514352
15	15	1 B3_months	115.0	5410.5	TRUE	4.098741	2	C15	B3_months	FALSE	4.514352
25	5	2 B1_week	105.6	NA	TRUE	4.256984	1	C5	B1_week	TRUE	4.386762
35	15	2 B1_week	109.7	7833.0	TRUE	4.509697	2	C15	B1_week	FALSE	4.386762
45	5	3 A1_week	99.9	19155.0	FALSE	6.430376	1	C5	A1_week.1	FALSE	6.078985
55	15	3 A1_week	103.5	NA	FALSE	6.497856	2	C15	A1_week.2	TRUE	6.078985
65	5	4 A3_months	87.7	12345.0	FALSE	5.275118	1	C5	A3_months.1	FALSE	5.057642
75	15	4 A3_months	94.1	18148.5	FALSE	6.259632	2	C15	A3_months.2	FALSE	5.057642

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
```

3 User-specific covariance patterns

From version 0.6.0 and above it is possible to customize the covariance pattern 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,time,...){
  n.time <- length(time)
  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),
  time = 1:6)
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)
dfL <- reshape2::melt(cbind(id = 1:n, as.data.frame(Y)), id.vars = "id")
dfL$time <- dfL$variable
dfL <- dfL[order(dfL$id),]
dfL[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 fit the corresponding mixed model, we call `lmm` using a (non-standard) correlation structure via the `CUSTOM` structure:

```
e.lmmCUSTOM <- lmm(value~time,
  repetition=~time|id,
  structure=CUSTOM(~variable,
    FCT.sigma = function(p,time,X){rep(p,length(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)),
  data=dfL, control = list(optimizer = "FS"),
  df = FALSE) ## df = FALSE to save computation time
logLik(e.lmmCUSTOM)
```

```
[1] -7962.243
```

The optimization procedure is not very fast but eventually reaches an optimum. We can then output the estimated correlation matrix:

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

	V1	V2	V3	V4	V5	V6
V1	1.00000000	0.24898095	0.50058993	0.09053785	0.09053785	0.09053785
V2	0.24898095	1.00000000	0.36110943	0.09053785	0.09053785	0.09053785
V3	0.50058993	0.36110943	1.00000000	0.09053785	0.09053785	0.09053785
V4	0.09053785	0.09053785	0.09053785	1.00000000	0.24898095	0.50058993
V5	0.09053785	0.09053785	0.09053785	0.24898095	1.00000000	0.36110943
V6	0.09053785	0.09053785	0.09053785	0.50058993	0.36110943	1.00000000

Note that specifying a classical structure via `CUSTOM` (e.g. compound symmetry):

```
logLik(lmm(value~time,
  repetition=~time|id,
  structure=CUSTOM(~1,
    FCT.sigma = function(p,time,X){rep(p,length(time))},
    init.sigma = c("sigma"=1),
    FCT.rho = function(p,time,X){matrix(p,length(time),length(time))+diag(1-p,length(time),
length(time))},
    init.rho = c("rho"=0.5)),
  data=dfL, control = list(optimizer = "FS"),
  df = FALSE))
```

```
[1] -8186.859
```

should be the same as using the pre-specified structure (up the certain user-friendly displays):

```
logLik(lmm(value~time,  
  repetition=~time|id,  
  structure="CS",  
  data=dfL, control = list(optimizer = "FS"),  
  df = FALSE))
```

```
[1] -8186.859
```

4 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

5 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)
```

6 R session

Details of the R session used to generate this document:

```
sessionInfo()
```

```
R version 4.1.1 (2021-08-10)
```

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

```
Running under: Windows 10 x64 (build 19044)
```

```
Matrix products: default
```

```
locale:
```

```
[1] LC_COLLATE=Danish_Denmark.1252 LC_CTYPE=Danish_Denmark.1252 LC_MONETARY=Danish_Denmark.1252
```

```
[4] LC_NUMERIC=C LC_TIME=Danish_Denmark.1252
```

```
attached base packages:
```

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

```
other attached packages:
```

```
[1] lme4_1.1-27.1 Matrix_1.4-0 LMMstar_0.5.0 nlme_3.1-153 ggpubr_0.4.0 multcomp_1.4-1
```

```
[7] TH.data_1.1-0 MASS_7.3-54 survival_3.2-13 mvtnorm_1.1-3 qqtest_1.2.0 emmeans_1.7.2
```

```
[13] ggplot2_3.3.5
```

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

```
[1] Rcpp_1.0.8 lattice_0.20-45 tidyr_1.1.4 listenv_0.8.0
[5] zoo_1.8-9 assertthat_0.2.1 digest_0.6.29 utf8_1.2.2
[9] parallelly_1.30.0 R6_2.5.1 plyr_1.8.6 backports_1.4.1
[13] coda_0.19-4 pillar_1.6.5 rlang_0.4.12 minqa_1.2.4
[17] nloptr_1.2.2.3 car_3.0-12 textshaping_0.3.6 labeling_0.4.2
[21] splines_4.1.1 stringr_1.4.0 munsell_0.5.0 broom_0.7.11
[25] compiler_4.1.1 numDeriv_2016.8-1.1 systemfonts_1.0.3 pkgconfig_2.0.3
[29] mgcv_1.8-38 globals_0.14.0 tidyselect_1.1.1 gridExtra_2.3
[33] tibble_3.1.6 codetools_0.2-18 fansi_1.0.2 future_1.23.0
[37] crayon_1.4.2 dplyr_1.0.7 withr_2.4.3 grid_4.1.1
[41] xtable_1.8-4 gtable_0.3.0 lifecycle_1.0.1 DBI_1.1.2
[45] magrittr_2.0.1 scales_1.1.1 estimability_1.3 future.apply_1.8.1
[49] stringi_1.7.6 carData_3.0-5 farver_2.1.0 ggsignif_0.6.3
[53] reshape2_1.4.4 ragg_1.2.1 ellipsis_0.3.2 generics_0.1.1
[57] vctrs_0.3.8 cowplot_1.1.1 boot_1.3-28 sandwich_3.0-1
[61] lava_1.6.10 tools_4.1.1 glue_1.6.1 purrr_0.3.4
[65] abind_1.4-5 parallel_4.1.1 colorspace_2.0-2 rstatix_0.7.0
```


References

- Oldford, R. W. (2016). Self-calibrating quantile–quantile plots. *The American Statistician*, 70(1):74–90.
- Pipper, C. B., Ritz, C., and Bisgaard, H. (2012). A versatile method for confirmatory evaluation of the effects of a covariate in multiple models. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 61(2):315–326.

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:

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

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 likelihood⁴. 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 $\theta \in \boldsymbol{\Theta}$:

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

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`.

⁴The 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 $\frac{1}{\sqrt{2\pi^p} |(\sum_{i=1}^n \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top)^{-1}|} \exp \left(-(\hat{\boldsymbol{\Theta}}_\mu - \mu) (2 \sum_{i=1}^n \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top)^{-1} (\hat{\boldsymbol{\Theta}}_\mu - \mu)^\top \right)$. 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 $\sqrt{2\pi^p} |(\sum_{i=1}^n \mathbf{X}_i \Omega_i^{-1}(\boldsymbol{\Theta}) \mathbf{X}_i^\top)|^{-1}$. 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 element⁵:

$$\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)}{\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:

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

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

⁵if 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 $\sigma_{\widehat{\beta}}$, the degree of freedom is:

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

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

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

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 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 can therefore take the derivative of formula (B). We first note that its derivative with respect to the mean parameters is 0. So we just need to compute the derivative with respect to a variance parameter θ'' :

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

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.

```
LMMstar.options(optimizer = "FS",  
  param.optimizer = c(n.iter = 1000, tol.score = 1e-3, tol.param = 1e-5))
```

Let's take an example:

```
## data(gastricbypassL, package = "LMMstar")  
dfTest <- gastricbypassL  
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:

```
logLik(lmm(weight ~ glucagon, data = dfTest, structure = UN(~time|id), method = "ML"))  
logLik(lmm(weight ~ glucagon2, data = dfTest, structure = UN(~time|id), method = "ML"))
```

```
[1] -245.7909
```

```
[1] -245.7909
```

but it does when using REML:

```
logLik(lmm(weight ~ glucagon, data = dfTest, structure = UN(~time|id), method = "REML"))  
logLik(lmm(weight ~ glucagon2, data = dfTest, structure = UN(~time|id), method = "REML"))  
log(2)
```

```
[1] -245.0382
```

```
[1] -245.7313
```

```
[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(1)  
dfTest$ff <- rbinom(NROW(dfTest), size = 1, prob = 0.5)  
logLik(lmm(weight ~ glucagon, data = dfTest, structure = UN(~time|id), method = "REML"))  
logLik(lmm(weight ~ glucagon*ff, data = dfTest, structure = UN(~time|id), method = "REML"))
```

```
[1] -245.0382
```

```
[1] -245.3555
```

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

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

```
[1] -245.7909
```

```
[1] -245.3593
```

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.