

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

The **LMMstar** package contains four main 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 combinations of coefficients (Wald test or Likelihood ratio tests).
 - `coef` to extract the estimates.
 - `dummy.coef` to extract the estimated (marginal) mean for each combination of categorical covariate.
 - `levels` to extract the reference level for the mean structure (i.e. what (**Intercept**) refers to in presence of categorical covariates).
 - `getVarCov` to extract the modeled residual variance covariance matrix.
 - `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.
 - `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 (typically time).
- 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 `gastricbypass` dataset:

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

```
  id visit          time weight glucagon
1  1     1 3 months before surgery 127.2 5032.50
2  2     1 3 months before surgery 165.2 12142.50
3  3     1 3 months before surgery 109.7 10321.35
4  4     1 3 months before surgery 146.2  6693.00
5  5     1 3 months before surgery 113.1  7090.50
6  6     1 3 months before surgery 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 surgery", "1 week before surgery",
    "1 week after surgery", "3 months after surgery" ),
  labels = c("B3_months", "B1_week", "A1_week", "A3_months"))
```

and rescale the glucagon values

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

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] '0.4.3'
```

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	128.9700	20.269	100.900	123.1000	173.000
2	weight	B1_week	20	0	121.2400	18.910	95.700	114.5000	162.200
3	weight	A1_week	20	0	115.7000	18.275	89.900	110.6000	155.000
4	weight	A3_months	20	0	102.3650	17.054	78.800	98.5000	148.000
5	glucagon	B3_months	20	0	-0.4856	0.641	-1.395	-0.6679	1.030
6	glucagon	B1_week	19	1	-0.6064	0.558	-1.416	-0.7669	0.946
7	glucagon	A1_week	19	1	1.0569	1.044	-0.478	0.9408	3.267
8	glucagon	A3_months	20	0	0.0576	0.760	-1.047	0.0319	2.124

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

2 Linear mixed model

2.1 Modeling tools

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");getVarCov(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 (6 iterations)
covariance structure:
      B3_months B1_week A1_week A3_months
B3_months 330.0426 0.0000 0.0000 0.0000
B1_week    0.0000 330.0426 0.0000 0.0000
A1_week    0.0000 0.0000 330.0426 0.0000
A3_months  0.0000 0.0000 0.0000 330.0426
```

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");getVarCov(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");getVarCov(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 **unstructured** covariance matrix:

```
eUN.lmm <- lmm(weight ~ time + glucagon,
  repetition = ~time|id, structure = "UN",
  data = gastricbypassL)
eUN.lmm
cat(" covariance structure: \n");getVarCov(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,A
log-restr.likelihood: -216.318937004305
convergence          : TRUE (26 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:

```
gastricbypassL$group <- as.numeric(gastricbypassL$id)%%2
eSUN.lmm <- lmm(weight ~ time*group,
  repetition = group~time|id, structure = "UN",
  data = gastricbypassL)
eSUN.lmm
cat(" covariance structure: \n");getVarCov(eSUN.lmm)
```

Linear Mixed Model with an 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:
                        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: -205.26832084513
convergence           : TRUE (15 iterations)
covariance structure:
$`0`
      B3_months  B1_week  A1_week  A3_months
B3_months  421.2046 384.4930 373.1531 308.0198
B1_week    384.4930 363.6010 353.4851 296.0184
A1_week    373.1531 353.4851 346.9516 293.2727
A3_months  308.0198 296.0184 293.2727 260.5560

$`1`
      B3_months  B1_week  A1_week  A3_months
B3_months  383.7179 360.4274 345.6647 354.9368
B1_week    360.4274 341.1832 326.9782 332.8130
A1_week    345.6647 326.9782 313.9293 319.7058
A3_months  354.9368 332.8130 319.7058 341.7246
```

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 -0.9654 0.2408 -0.0682 -0.6837 -0.6163 ...
reference level: time=B3_months
```

Estimation procedure

- Restricted Maximum Likelihood (REML)
- log-restricted likelihood :-216.3189
- parameters: mean = 5, variance = 4, correlation = 6
- convergence: TRUE (26 iterations, largest $|\text{score}|=4.315158e-06$ is for `k.A1_week`)

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  1.000000
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)	128.539	4.536	18.976	119.043	138.034	< 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	13.707	-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
128.5385950	-7.8822331	-11.7879541	-26.1223907	-0.8883083

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 ¹:

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

	estimate	se	df	lower	upper	p.value
(Intercept)	128.539	4.536	19.0	119.04	138.034	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), their uncertainty is by default computed after transformation (e.g. `log`) and then backtransformed.

2.5 Extract estimated residual variance-covariance structure

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

```
getVarCov(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:

```
getVarCov(eUN.lmm, individual = 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"))  
getVarCov(eUN.lmm, individual = 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

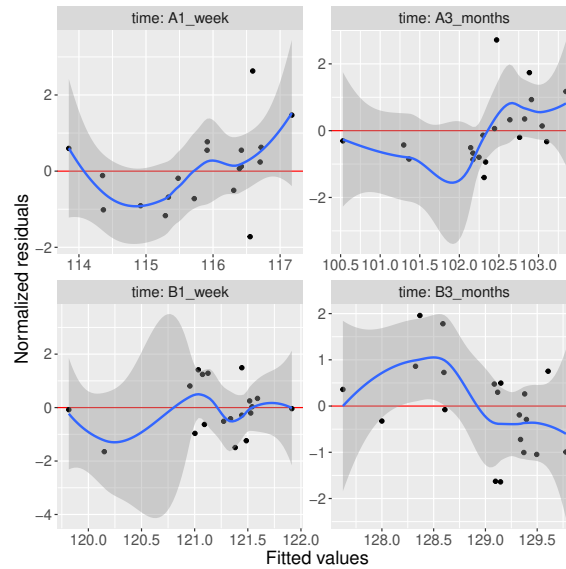
¹it is equivalent to `confint` method except that by default it also outputs `se` and `p.value`

2.6 Model diagnostic

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

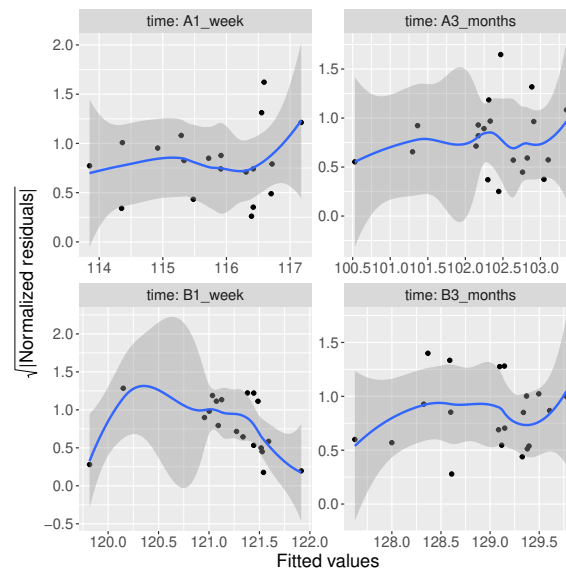
- misspecification of the mean structure

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



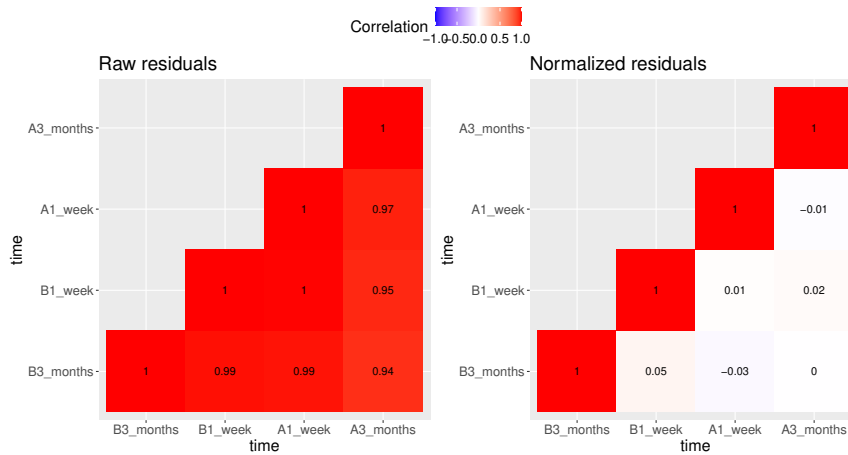
- misspecification of the variance structure

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



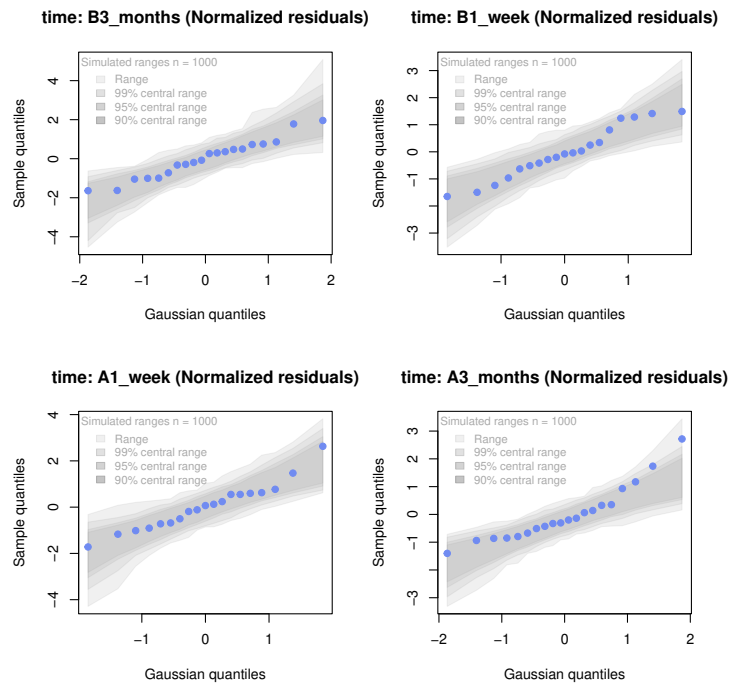
- misspecification of the correlation structure

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



- residual distribution vs. normal distribution ²:

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



²see Oldford (2016) for guidance about how to read quantile-quantile plots.

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.B3_months r.B1_week r.A1_week r.A3_months
1        1 -0.2897364 -0.2027622 -1.16864032  0.3258573
2        2  0.8603118 -1.6492167  0.62578804  1.7370660
3        3  0.7273066 -0.4155168 -0.68266746 -0.8510316
4        4 -1.6403081 -0.5128371  0.06806212  1.1725813
5        5  0.4755409          NA -0.18736417 -0.8634200
6        6  1.7801675  1.2847698  2.63004809  0.3505542
```

or in the long format:

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

```
[1] -0.2897364  0.8603118  0.7273066 -1.6403081  0.4755409  1.7801675
```

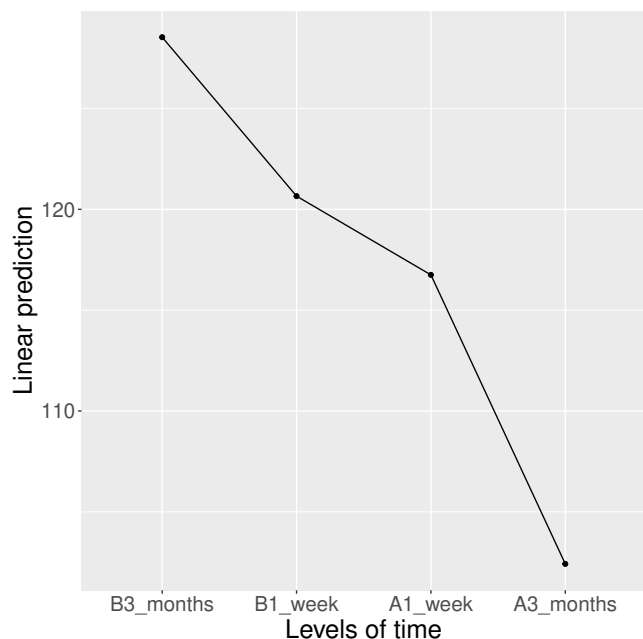
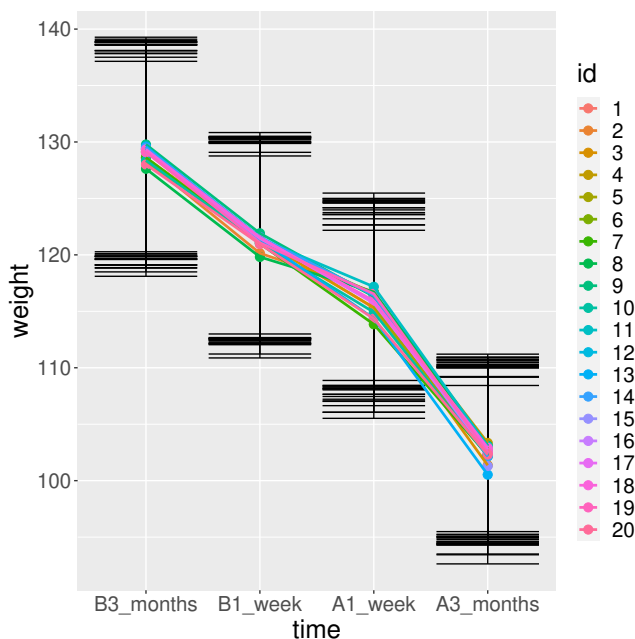
Various type of residuals can be extract but the normalized one are recommended when doing model checking.

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))
```

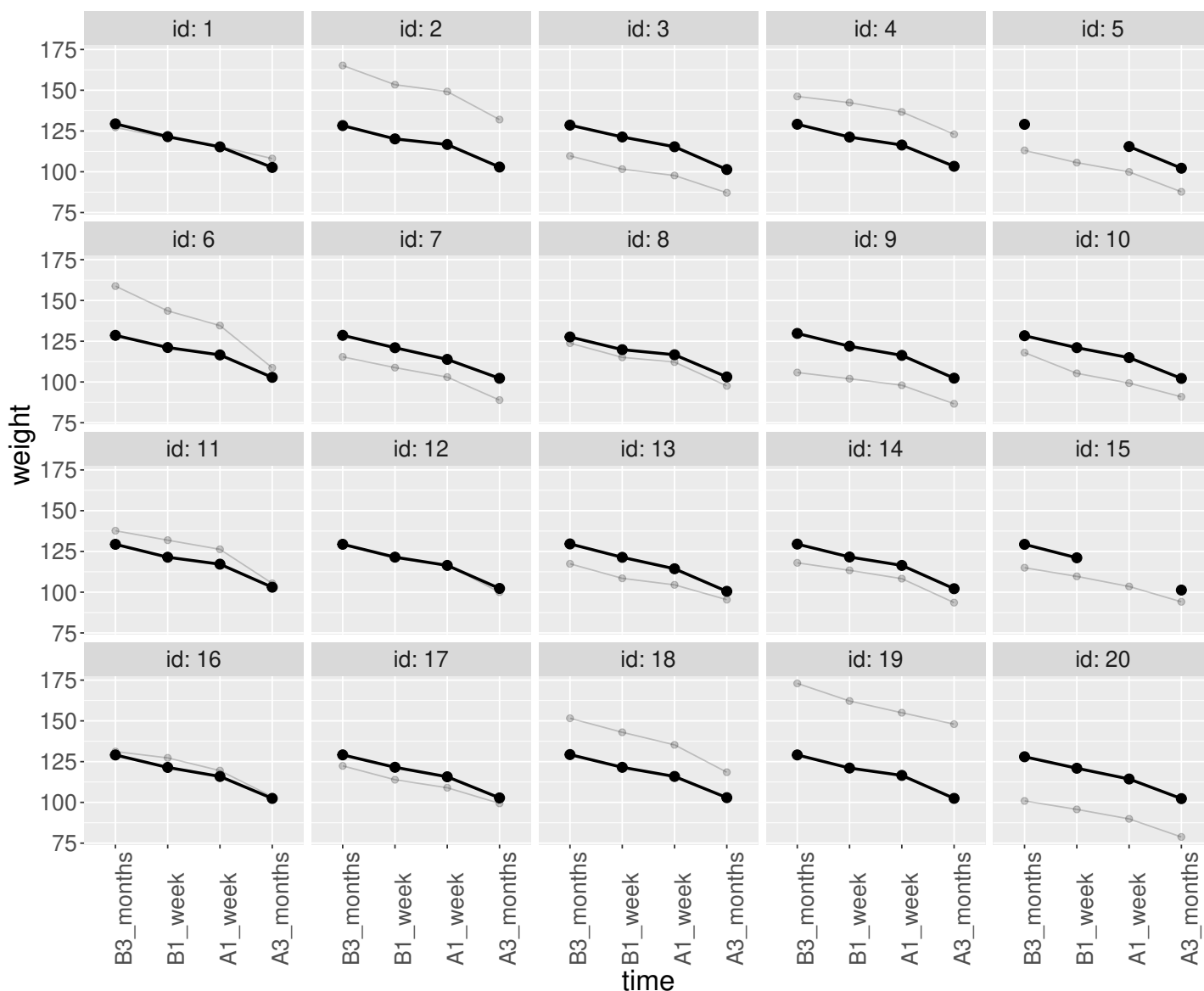


In the first case each possible curve is displayed while in the latter the average curve (over glucagon values). With the `plot` method, it is possible to display a curve specific to a glucagon value via the argument `at`:

```
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
```



2.8 Statistical inference

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 **  
- F-test:  
      statistic df.num df.denom      p.value  
time      86.74279      3 19.00520 2.842460e-11  
glucagon  13.51775      1 13.70749 2.571625e-03
```

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"), ci = TRUE)
```

```
          ** User-specified hypotheses **  
- F-test:  
      statistic df.num df.denom      p.value  
      43.14135      1 17.87455 3.723358e-06  
  
- P-values and confidence interval  
              estimate      se      df      lower      upper      p.value  
timeA1_week - timeB1_week -3.905721 0.5946403 17.87455 -5.155643 -2.655799 3.723358e-06
```

One can also simultaneously test several null hypotheses:

```
anova(eUN.lmm, effects = c("timeA1_week-timeB1_week=0",  
                          "timeA3_months-timeB1_week=0"), ci = TRUE)
```

```
          ** User-specified hypotheses **  
- F-test:  
      statistic df.num df.denom      p.value  
      98.65053      2 18.61992 1.233819e-10  
  
- P-values and confidence interval (adjusted for multiplicity)  
              estimate      se df      lower      upper      p.value  
timeA1_week - timeB1_week   -3.905721 0.5946403 20  -5.306911  -2.504531 4.080425e-06  
timeA3_months - timeB1_week -18.240158 1.3228299 20 -21.357228 -15.123087 2.195177e-11
```

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

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

Singular contrast matrix: contrasts "A1_week - B1_week" "A3_months - B1_week" "A3_months - A1_week"

**** User-specified hypotheses ****

- F-test:

statistic	df.num	df.denom	p.value
86.74279	3	19.0052	2.84246e-11

- P-values and confidence interval (adjusted for multiplicity)

	estimate	se	df	lower	upper	p.value
B1_week - B3_months	-7.882233	0.7131797	22	-9.784489	-5.979977	8.137047e-12
A1_week - B3_months	-11.787954	1.0175135	22	-14.501956	-9.073953	4.271916e-12
A3_months - B3_months	-26.122391	1.6564077	22	-30.540507	-21.704274	0.000000e+00
A1_week - B1_week	-3.905721	0.5946403	22	-5.491798	-2.319644	4.898696e-06
A3_months - B1_week	-18.240158	1.3228299	22	-21.768526	-14.711789	4.718448e-14
A3_months - A1_week	-14.334437	1.0565002	22	-17.152427	-11.516446	4.263256e-14

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, rhs = rhs, df = df, ci = ci, :
Possible misspecification of the argument 'effects' as running mulcomp::glht lead to the following
Error in parse(text = ex[i]) : <text>:1:7: unexpected 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", backtransform = FALSE))
name.varcoef <- grep("log(k)", name.coef, value = TRUE, fixed = 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	log(sigma)
log(k).B1_week	0	0	0	0	0	0
log(k).A1_week	0	0	0	0	0	0
log(k).A3_months	0	0	0	0	0	0
	log(k).B1_week	log(k).A1_week	log(k).A3_months	atanh(rho(B3_months, B1_week))		
log(k).B1_week	1	0	0			0
log(k).A1_week	0	1	0			0
log(k).A3_months	0	0	1			0
	atanh(rho(B3_months, A1_week))		atanh(rho(B3_months, A3_months))			
log(k).B1_week		0				0

```

log(k).A1_week          0          0
log(k).A3_months       0          0
                        atanh(rho(B1_week,A1_week)) atanh(rho(B1_week,A3_months))
log(k).B1_week         0          0
log(k).A1_week         0          0
log(k).A3_months       0          0
                        atanh(rho(A1_week,A3_months))
log(k).B1_week         0
log(k).A1_week         0
log(k).A3_months       0

```

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

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

```

** User-specified hypotheses **

```

```
- F-test:
```

```

statistic df.num df.denom    p.value
6.203161    3 17.99456 0.004417117

```


2.9 Baseline adjustment

The `lmm` contains an "experimental" feature to drop non-identifiable effects from the model. For instance, let us define two (artificial) groups of patients:

```
gastricbypassL$group <- c("1","2")[as.numeric(gastricbypassL$id) %in% 15:20 + 1]
```

We would like to model group differences only after baseline (i.e. only at 1 week and 3 months after). For this we will define a treatment variable being the group variable except before baseline where it is "none":

```
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
```

Here we will be able to estimate a total of 6 means and 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). The `lmm` function will internally remove the one that cannot be identified and fit a simplified model:

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

Constant values in the design matrix in interactions "treat:time"

Coefficients "treat1" "treat2" "timeA1_week" "timeA3_months" "treat1:timeB1_week" "treat2:timeB1_w

with the following coefficients:

```
coef(eC.lmm, effects = "mean")
```

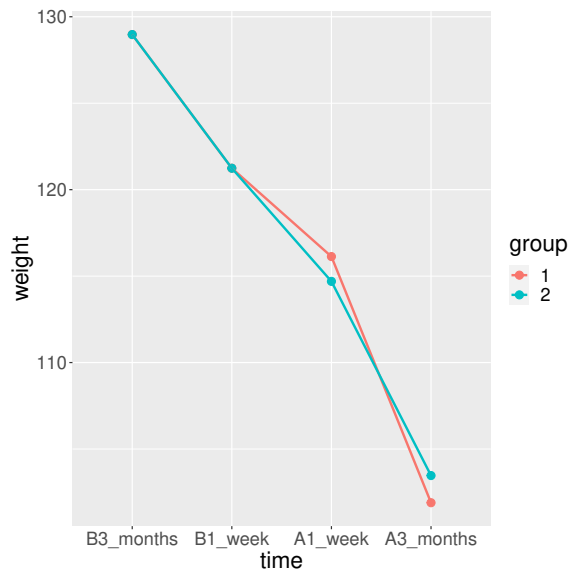
```

(Intercept)          timeB1_week  treat1:timeA1_week  treat2:timeA1_week
  128.97000          -7.73000        -12.83949          -14.27452
treat1:timeA3_months  treat2:timeA3_months
 -27.07620          -25.50553

```

One can visualize the baseline adjustment via the autoplot function:

```
autoplot(eC.lmm, color = "group", ci = FALSE, size.text = 20)
```



To more easily compare the two groups, one could set the baseline treatment to the treatment in the control arm by omitting the argument `new.level`:

```

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

```

Fitting the model

```
eC2.lmm <- suppressWarnings(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.

will directly output group differences (last two coefficients):

```
model.tables(eC2.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

It is also possible to get the estimated mean at each timepoint, using an equivalent mean structure:

```
eC3.lmm <- suppressWarnings(lmm(weight ~ 0+treat2:time, data = gastricbypassL,  
  repetition = ~time|id, structure = "UN"))  
model.tables(eC3.lmm) ## equivalent to dummy.coef(eC2.lmm)
```

Constant values in the design matrix in interactions "treat2:time"
Coefficients "treat22:timeB3_months" "treat22:timeB1_week" have been removed.

	estimate	se	df	lower	upper	p.value
treat21:timeB3_months	129	4.53	19.0	119.5	138	0
treat21:timeB1_week	121	4.23	19.0	112.4	130	0
treat21:timeA1_week	116	4.11	19.1	107.5	125	0
treat22:timeA1_week	115	4.13	19.4	106.1	123	0
treat21:timeA3_months	102	3.87	20.2	93.8	110	0
treat22:timeA3_months	103	4.17	25.2	94.9	112	0

or the baseline mean and the change since baseline:

```
eC4.lmm <- suppressWarnings(lmm(weight ~ treat2:time, data = gastricbypassL,  
  repetition = ~time|id, structure = "UN"))  
model.tables(eC4.lmm)
```

Constant values in the design matrix in interactions "treat2:time"
Coefficients "treat22:timeB3_months" "treat22:timeB1_week" have been removed.

	estimate	se	df	lower	upper	p.value
(Intercept)	128.97	4.532	19.0	119.48	138.46	0.00e+00
treat21:timeB1_week	-7.73	0.697	19.0	-9.19	-6.27	1.00e-09
treat21:timeA1_week	-12.84	0.865	20.5	-14.64	-11.04	2.02e-12
treat22:timeA1_week	-14.27	0.950	26.3	-16.23	-12.32	2.02e-14
treat21:timeA3_months	-27.08	1.724	21.4	-30.66	-23.50	3.20e-13
treat22:timeA3_months	-25.51	2.323	22.6	-30.32	-20.69	1.60e-10

2.10 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	-18.0	27.6	0.478	0.7499
2 - 1	B1_week	5.80	9.38	18.0	-15.4	27.0	0.618	0.6476
2 - 1	A1_week	4.29	9.11	18.0	-16.3	24.9	0.471	0.7553
2 - 1	A3_months	6.69	8.40	18.1	-12.3	25.7	0.797	0.5279

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

2.11 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	128.5386	4.536445	18.97584	119.04289	138.0343
2	120.6564	4.261691	19.04078	111.73783	129.5749
3	116.7506	3.956964	19.04925	108.47007	125.0312
4	102.4162	3.747908	19.05531	94.57328	110.2591

which can be computed 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]
1 128.5386
21 120.6564
41 116.7506
61 102.4162
```

- **dynamic predictions** that are conditional on the covariates and the outcome measured at other timepoints. Consider two subjects for whom 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	128.5386	0	NA	NA	NA	NA	NA
2	1	B1_week	NA	0	120.65636	0.6361009	Inf	119.40963	121.9031
3	2	B3_months	100.0000	0	NA	NA	NA	NA	NA
4	2	B1_week	NA	0	94.15336	6.2597469	Inf	81.88448	106.4222

The first subject 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 <- getVarCov(eUN.lmm)["B3_months","B3_months"]
Omega_21 <- getVarCov(eUN.lmm)["B1_week","B3_months"]
as.double(mu2 + Omega_21 * (100 - mu1) / Omega_11)
```

```
[1] 94.15336
```


2.12 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 missiness 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  -0.9654 0.2408 -0.0682 -0.6837 -0.6163 ...
$ 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] -0.7430158  1.4978616
```

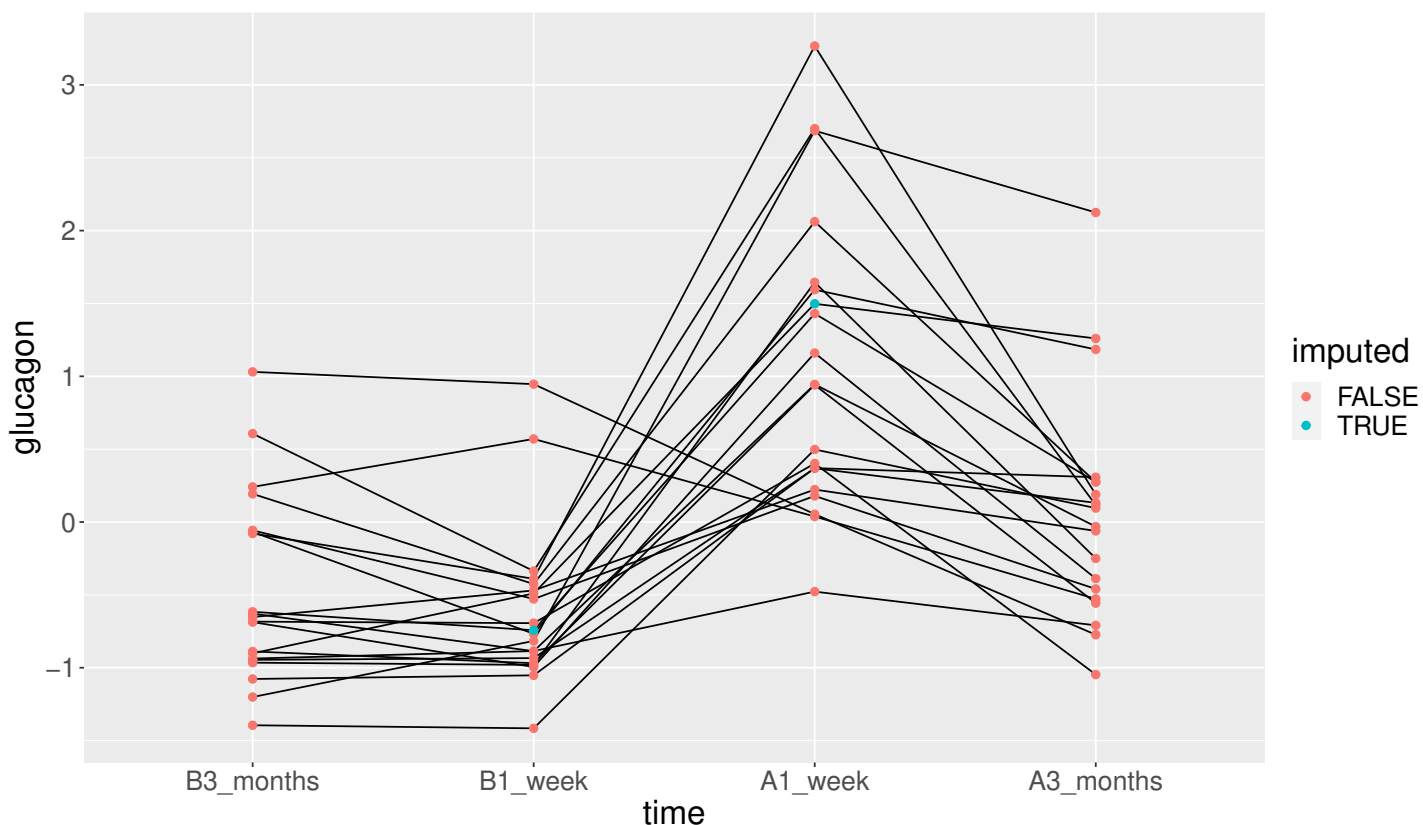
When using the argument `keep.newdata=TRUE`, the missing outcome value has been replaced by its most likely value (which is the same as the dynamic prediction, described previously):

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

id	visit	time	weight	glucagon	group	treat	treat2	imputed	estimate
5	5	1 B3_months	113.1	-0.6162619	1	none	1	FALSE	-0.48564787
15	15	1 B3_months	115.0	-0.9012594	2	none	1	FALSE	-0.48564787
25	5	2 B1_week	105.6	-0.7430158	1	none	1	TRUE	-0.61323797
35	15	2 B1_week	109.7	-0.4903032	2	none	1	FALSE	-0.61323797
45	5	3 A1_week	99.9	1.4303759	1	1	1	FALSE	1.07898563
55	15	3 A1_week	103.5	1.4978616	2	2	2	TRUE	1.07898563
65	5	4 A3_months	87.7	0.2751184	1	1	1	FALSE	0.05764249
75	15	4 A3_months	94.1	1.2596319	2	2	2	FALSE	0.05764249

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] -0.7375653  1.3052918
```

```
[1] -1.1417336  0.8716473
```

```
[1] -0.657376  1.905251
```

3 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

4 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)
```

5 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 19042)
```

```
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] ggpubr_0.4.0 emmeans_1.7.0 LMMstar_0.3.5 nlme_3.1-152 ggplot2_3.3.5
```

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

```
[1] tidyr_1.1.3 splines_4.1.1 carData_3.0-4 assertthat_0.2.1
[5] cellranger_1.1.0 globals_0.14.0 numDeriv_2016.8-1.1 pillar_1.6.4
[9] backports_1.2.1 lattice_0.20-44 glue_1.4.2 digest_0.6.28
[13] ggsignif_0.6.2 colorspace_2.0-2 sandwich_3.0-1 qqtest_1.2.0
[17] cowplot_1.1.1 Matrix_1.3-4 plyr_1.8.6 pkgconfig_2.0.3
[21] broom_0.7.9 listenv_0.8.0 haven_2.4.3 purrr_0.3.4
[25] xtable_1.8-4 mvtnorm_1.1-3 scales_1.1.1 openxlsx_4.2.4
[29] lava_1.6.10 rio_0.5.27 tibble_3.1.5 mgcv_1.8-36
[33] generics_0.1.0 farver_2.1.0 car_3.0-11 ellipsis_0.3.2
[37] TH.data_1.1-0 withr_2.4.2 survival_3.2-13 magrittr_2.0.1
[41] crayon_1.4.2 readxl_1.3.1 estimability_1.3 future_1.23.0
[45] fansi_0.5.0 parallely_1.28.1 MASS_7.3-54 rstatix_0.7.0
[49] forcats_0.5.1 foreign_0.8-81 textshaping_0.3.6 tools_4.1.1
[53] data.table_1.14.2 hms_1.1.0 lifecycle_1.0.1 multcomp_1.4-17
[57] stringr_1.4.0 munsell_0.5.0 zip_2.2.0 compiler_4.1.1
[61] systemfonts_1.0.3 rlang_0.4.12 grid_4.1.1 labeling_0.4.2
[65] gtable_0.3.0 codetools_0.2-18 abind_1.4-5 DBI_1.1.1
[69] curl_4.3.2 reshape2_1.4.4 R6_2.5.1 gridExtra_2.3
[73] zoo_1.8-9 dplyr_1.0.7 future.apply_1.8.1 utf8_1.2.2
[77] ragg_1.1.3 stringi_1.7.5 parallel_4.1.1 Rcpp_1.0.7
[81] vctrs_0.3.8 tidyselect_1.1.1 coda_0.19-4
```

References

Oldford, R. W. (2016). Self-calibrating quantile–quantile plots. *The American Statistician*, 70(1):74–90.

Appendix A Likelihood in a linear mixed model

A.1 Log-likelihood

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

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

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 likelihood³. 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 $\theta \in \boldsymbol{\Theta}$:

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

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`.

³The 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 element⁴:

$$\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 \mathbf{X}_i \Omega_i^{-1}(\Theta) \mathbf{X}_i^\top \right)^{-1} \left\{ \sum_{i=1}^n \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 \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 \mathbf{X}_i \Omega_i^{-1}(\Theta) \mathbf{X}_i^\top \right)^{-1} \left(\sum_{i=1}^n \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 \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:

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

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

⁴if 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:

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

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'' :

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

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.