An example of using likelihood contrasts

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17.01.2019

The method of likelihood contrasts is very general. We have chosen to provide it here for longitudinal data where there is only one grouping factor, e.g. individual or experimental batch.

This manual shows you how to analyze the data 'prothro' in R package JM by using the method of likelihood contrasts.

Data in etc.

```
library(JM)

data(prothro)

source("Likelihood_contrasts.R")
```

Picking relevant things from data

```
dat = prothro[,c("id","pro","time","treat","death")]

dlt = dat$death # this is the binary label
```

Splitting data into training data and test data

```
X = dat[which(dat$id<300),]

testx = dat[which(dat$id>=300),]

testdlt = dlt[which(dat$id>=300)]
```

```
dlt = dlt[which(dat$id<300)]
```

Analyzing by likelihood contrasts

```
mod = lcont(X, dlt, "pro~time+treat", id.name="id") # one option

mod = lcont(X, dlt, "pro~treat", id.name="id") # another option

mod = lcont(X, dlt, "pro~time", id.name="id") # yet another option

# The model in fact assumes that the name of the ID column is "id",
so you can equally well type:

mod = lcont(X, dlt, "pro~time+treat")

mod = lcont(X, dlt, "pro~treat")

mod = lcont(X, dlt, "pro~time")
```

Prediction for individual 300

```
x300 = testx[which(testx$id==300),]

predict.multiple(mod, x300, id.name="id")
```

Prediction for multiple individuals

```
probs = predict.multiple(mod, testx, id.name="id")
```

ROC curve for the last model

```
true_labels = NULL

for( u in unique(testx$id) ){ # picking the true labels

     totake = which(testx$id==u)[1]

     true_labels = c(true_labels, testdlt[totake])

}

library(pROC)

plot.roc(true_labels, probs)
```