```
lme()
```

$$r_{mi} = y_i - x_0'\hat{b}$$

$$r_{ci} = y_i - x_i'\hat{b} - z_i'\hat{\gamma}$$

$$\hat{y}_i$$

$$y_i$$

$$\hat{\epsilon}_i = y_i - \hat{y}_i = y_i - (X_i\hat{\beta} + Z_i\hat{b}_i)$$

$$= \sum_{i=1}^{n} (y_i - \hat{y}_{i,-i})^2$$

$\hat{y}_i =$

$x_i' \hat{\beta}$

x_i'

i

X

lme

JS.roy1

coef.lme

```
> JS.roy1 %>% coef %>% head(5)
methodJ    methodS
74      84.31724   91.08404
36      91.54994   97.05548
3       81.16581   96.48653
62      92.09493   90.89073
31      88.41411  103.38802
```

$\varepsilon_i =$

$y_i -$

$\hat{y}_i$

i

$$\varepsilon_{i(U)} = y_i - x_i' \hat{\beta}_{(U)}$$

$$PRESS = \sum \varepsilon_{i(U)}^2$$

U

qqnorm.lme

```
res_lme=residuals(model_lme)
plot(res_lme)
qqnorm(res_lme)
qqline(res_lme)
plot(model_lme)
plot
plot(JS.roy1, which=c(1) )
R
```

```
qqnorm(resid(JS.roy1),pch="*",col="red")
qqline(resid(JS.roy1),col="blue")
table(dat$method[1:255])
##
##   J   S
## 255   0
table(dat$method[256:510])
##
##   J   S
##   0 255
```

```
plot(roy.NLME, resid(., type = "p") ~ fitted(.) | method,
    abline = 0, id=.05)
CookD
library(predictMeans)
CookD(model, group=method, plot=TRUE, idn=5, newwd=FALSE)
## Cook's Distance


blood.red <- blood[!(blood$subject %in% c(68,78,80)),]
dim(blood.red)
# 27 observations should be removed.

blood.NLME.red <-lme(BP ~ method-1 , random=~1|subject,data = blood.red)
plot(blood.NLME.red, resid(., type = "p") ~ fitted(.) | method, abline = 0, id=.05)
```

leave
one
out
leave
k
out'
analysis
V
V
β
u
$\hat{\mathbf{V}}$
influence()
influence.ME
influence()

```
influence(model, group=NULL, select=NULL, obs=FALSE,
gf="single", count = FALSE, delete=TRUE, ...)
```
\
influence()
estex()

$$PRESS = \sum (y - y^{(k)})^2$$

(1)

$e_{-Q} =$
$y_Q -$
$x_Q \hat{\beta}^{-Q}$
$PRESS_{(U)} =$
$y_i -$
$x \hat{\beta}_{(U)}$

R^2