

`lme()`

$$\begin{aligned} r_{mi} &= \\ y_i - & \\ x_0' \hat{b} & \\ r_{ci} &= \\ y_i - & \\ x_i' \hat{b} - & \\ z_i' \hat{\gamma} & \\ y_i & \end{aligned}$$

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

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

```

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

```

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

$U$

```
      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  
 $\beta$   
 $y$   
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)

$$e_{-Q} = y_Q - x_Q \hat{\beta}_{-Q}$$

$$PRESS_{(U)} = y_i - x \hat{\beta}_{(U)}$$

$$R^2$$







