R language and data analysis: diagnostics of linear model

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Symbols

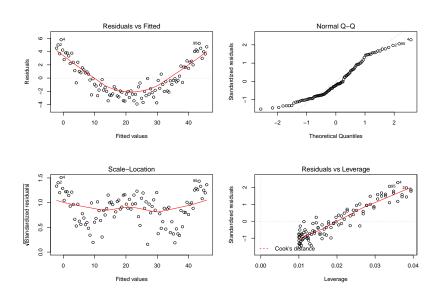
Symbol	Usage
~	Separates response variables on the left from the explanatory variables on the right. For example, a prediction of y from x, z, and w would be coded y \sim x + z + w.
+	Separates predictor variables.
:	Denotes an interaction between predictor variables. A prediction of y from x, z, and the interaction between x and z would be coded y \sim x + z + x:z.
•	A shortcut for denoting all possible interactions. The code $y \sim x * z * w$ expands to $y \sim x + z + w + x : z + x : w + z : w + x : z : w$.
^	Denotes interactions up to a specified degree. The code $y \sim (x + z + w)^2$ expands to $y \sim x + z + w + x : z + x : w + z : w$.
	A placeholder for all other variables in the data frame except the dependent variable. For example, if a data frame contained the variables x , y , z , and w , then the code $y \sim x$ would expand to $y \sim x + z + w$.
-	A minus sign removes a variable from the equation. For example, $y \sim (x + z + w)^2 - x \cdot w$ expands to $y \sim x + z + w + x \cdot z + z \cdot w$.
-1	Suppresses the intercept. For example, the formula $y \sim x$ -1 fits a regression of y on x , and forces the line through the origin at x =0.

Figure 1:

Classical linear regression

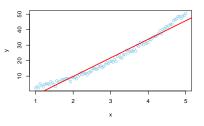
- Linearity: $Y = X\beta_0 + \epsilon$
- ▶ Full rank: rank(X) = K
- Exogeneity: $E(\epsilon|X) = 0$
- ▶ Spherical disturbance: $E(\epsilon \epsilon' | X) = \sigma^2 I_n$
- ▶ Normality: $\epsilon \sim N(0, \sigma^2 I_n)$

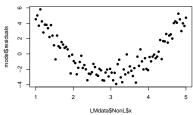
Diagnostics plot in R.



Linearity

```
## df AIC
## model 3 478.4558
## model2 4 269.2121
## model3 3 267.2736
```





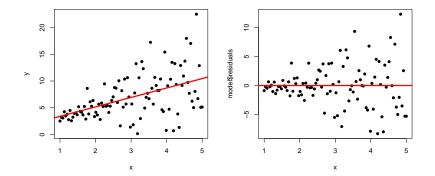


Multicollinearity

```
data(LMdata,package='rinds')
model <-lm(y~x1+x2+x3,data=LMdata$Mult)
summary(model)$coefficients
library(car);vif(model)#variance inflation factor
model1<-step(model)
model1
summary(model1)$coe</pre>
```

Heteroskedasticity

```
par(mfrow=c(1,2))
model<-lm(y~x,data=LMdata$Hetero)
plot(y~x,data=LMdata$Hetero,pch=16)
abline(model,col='red',lwd=3)
with(LMdata$Hetero,plot(x,model$residuals,pch=16))
abline(h=0,,col='red',lwd=3)</pre>
```



Standard error

Standard error

$$var(\hat{\beta}) = \sigma_{\mu}^2 (X'X)^{-1}$$

```
library(foreign)
children<- read.dta("fertil2.dta")
r1 <- lm(ceb ~ age + agefbrth + usemeth,
          data=children)
X <- model.matrix(r1)</pre>
n \leftarrow dim(X)[1]
k \leftarrow dim(X)[2]
se <- sqrt(diag(solve(crossprod(X)) *</pre>
as.numeric(crossprod(resid(r1))/(n-k))))
se
```

```
## (Intercept) age agefbrth usemeth
## 0.173782844 0.003448024 0.008795350 0.055429804
```

Robust standard error

$$(X'X)^{-1}X'\Sigma_{\mu}X(X'X)^{-1}$$

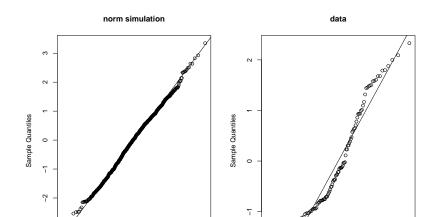
```
library(foreign)
children<- read.dta("data/fertil2.dta")
r1 <- lm(ceb ~ age + agefbrth + usemeth,
         data=children)
u <- matrix(resid(r1))</pre>
meat1 <- t(X) %*% diag(diag(crossprod(t(u)))) %*% X</pre>
dfc <- n/(n-k)
se <- sqrt(dfc*diag(solve(crossprod(X)) %*%
        meat1 %*% solve(crossprod(X))))
se
```

Robust standard error

```
library(foreign)
library(sandwich)
library(lmtest)
children<- read.dta("data/fertil2.dta")
model = lm( ceb ~ age + agefbrth + usemeth,data=children)
summary(model)
coeftest(model, vcov = vcovHC(model, "HC1"))#vs. Stata. ##
##https://cran.r-project.org/web/packages/sandwich/vignette</pre>
```

Normality

```
##
## Shapiro-Wilk normality test
##
## data: res1
## W = 0.93524, p-value = 1e-04
```



Autocorrelation

```
data(LMdata,package='rinds')
model<-lm(y~x,data=LMdata$AC)
suppressMessages(library(lmtest))
dwtest(model)##Durbin-Watson test
##
##
    Durbin-Watson test
##
## data: model
## DW = 0.65556, p-value = 2.683e-12
## alternative hypothesis: true autocorrelation is greater
```

Clustered standard error