P2

November 6, 2021

[11]:
```
#2
```

(a)

[12]:
```
data_bac <- read.table("Table6.2.txt",
                       head = TRUE,
                       sep = "\t")
#data_bac
```

[13]:
```
mod_bac1 <- lm(N_t ~ t, data_bac)
print(summary(mod_bac1))
```

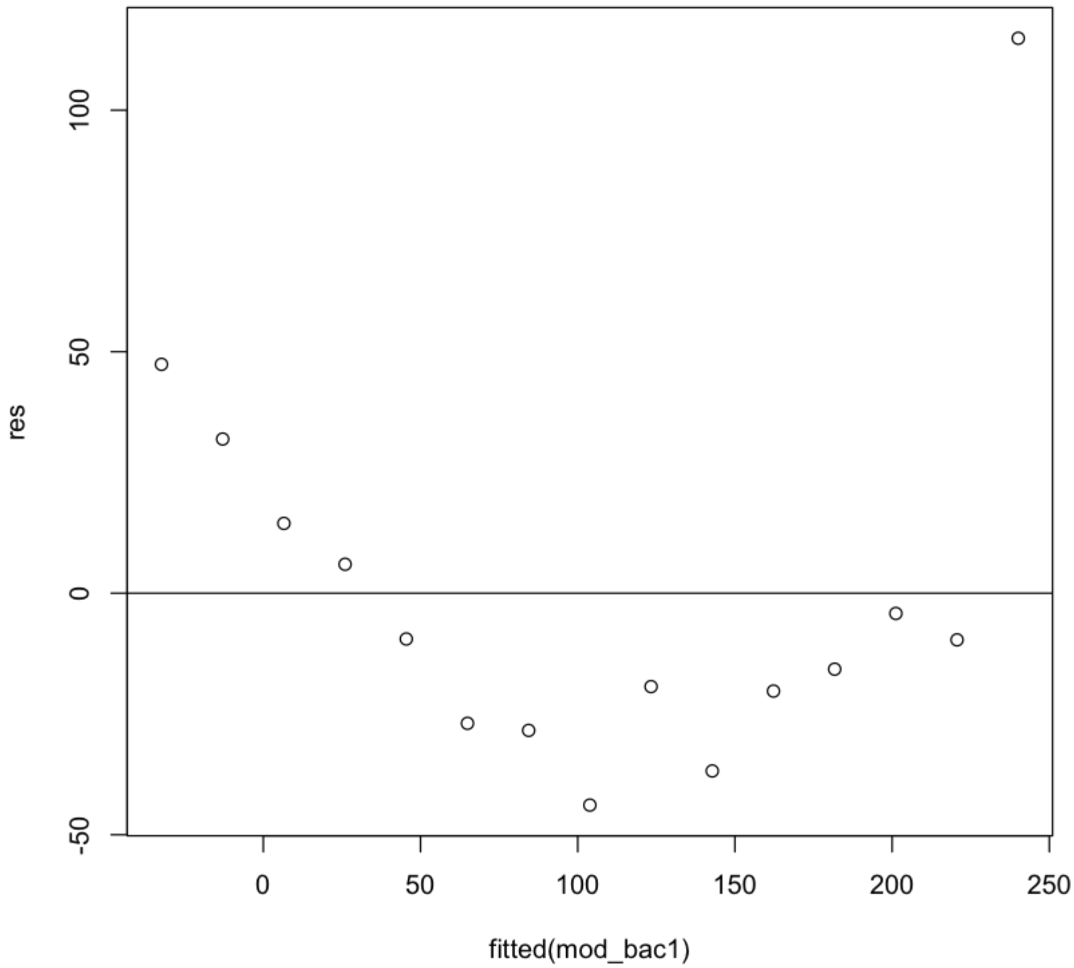
```
Call:
lm(formula = N_t ~ t, data = data_bac)

Residuals:
    Min      1Q  Median      3Q     Max
-43.867 -23.599  -9.652  10.223 114.883

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   259.58      22.73  11.420 3.78e-08 ***
t             -19.46       2.50  -7.786 3.01e-06 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 41.83 on 13 degrees of freedom
Multiple R-squared:  0.8234,	Adjusted R-squared:  0.8098
F-statistic: 60.62 on 1 and 13 DF,  p-value: 3.006e-06
```

[14]:
```
res <- resid(mod_bac1)
plot(fitted(mod_bac1), res)
abline(0,0)
```



No. Generally, when the regression model satisfies the "L" assumption, the points on the residual plot are irregular and randomly distributed around the horizontal line 0. However, in situation problem 2 (1), the points on the residual plot are curved.

(b)

[15]:
```
mod_bac2 <- lm(log(N_t) ~ t, data_bac)
print(summary(mod_bac2))
```

```
Call:
lm(formula = log(N_t) ~ t, data = data_bac)

Residuals:
```

```
     Min       1Q   Median       3Q      Max
-0.18445 -0.06189  0.01253  0.05201  0.20021

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  5.973160   0.059778   99.92  < 2e-16 ***
t           -0.218425   0.006575  -33.22 5.86e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.11 on 13 degrees of freedom
Multiple R-squared:  0.9884,	Adjusted R-squared:  0.9875
F-statistic:  1104 on 1 and 13 DF,  p-value: 5.86e-14
```

Regression line equation:

$$\log(n_t) = \beta_0 + \beta_1 t + \varepsilon$$

That is

$$Log(n_t) = 5.97 - 0.22t + \varepsilon$$

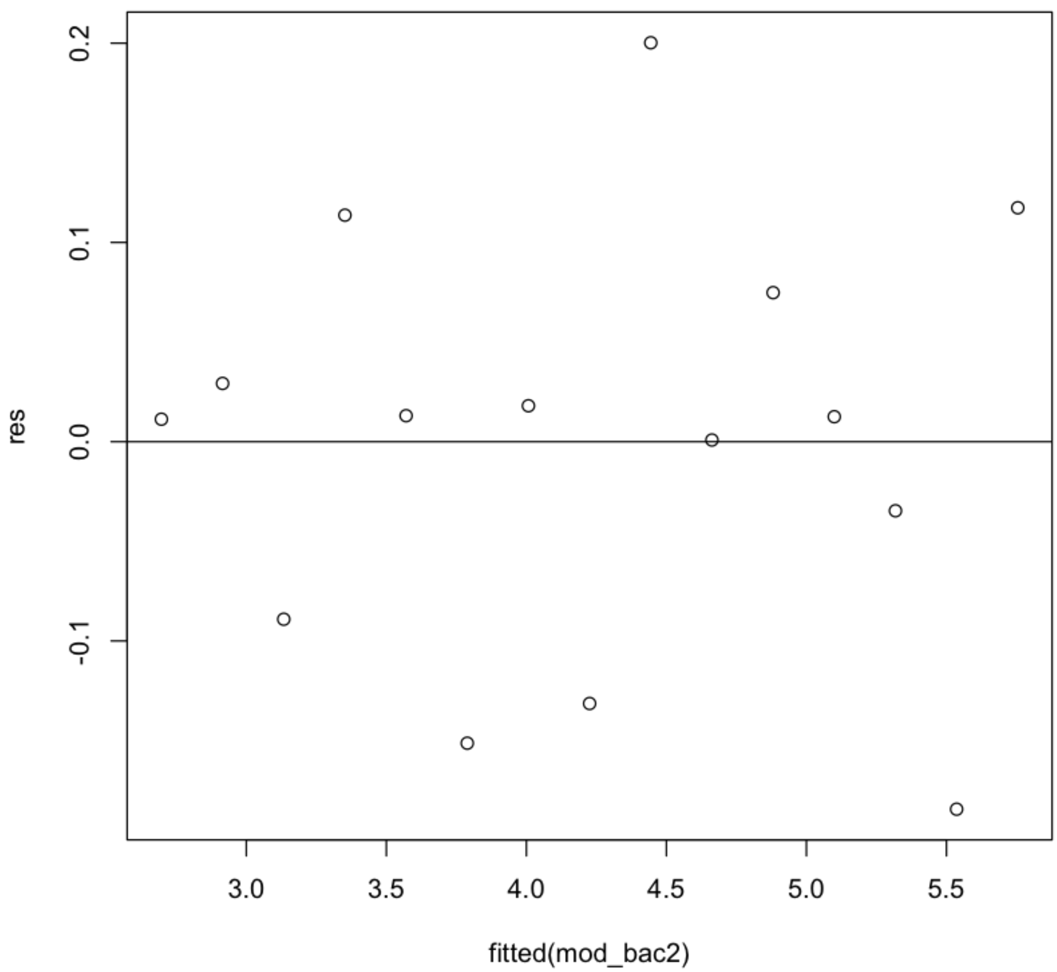
OR

$$n_t = \exp(\beta_0 + \beta_1 t) + \varepsilon$$

That is

$$n_t = \exp(5.97 - 0.22t) + \varepsilon$$

[10]:
```
res <- resid(mod_bac2)
plot(fitted(mod_bac2), res)
abline(0,0)
```



The “L” assumption is no longer violated.