HW3_kmg0122

Mingang Kim

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1.

2.

3.

```
library(data.table)
```

```
## Warning:    'data.table' R   4.1.1
```

```
covid_raw <- fread("https://opendata.ecdc.europa.eu/covid19/casedistribution/csv")
us <- covid_raw[covid_raw$countriesAndTerritories == 'United_States_of_America',]
us_filtered <- us[us$month %in% c(6:7),]
us_filtered$index <- rev(1:dim(us_filtered)[1])
fit<-lm(`Cumulative_number_for_14_days_of_COVID-19_cases_per_100000`~index, data=us_filtered)
```

```
library("broom")
```

```
## Warning:    'broom' R   4.1.1
```
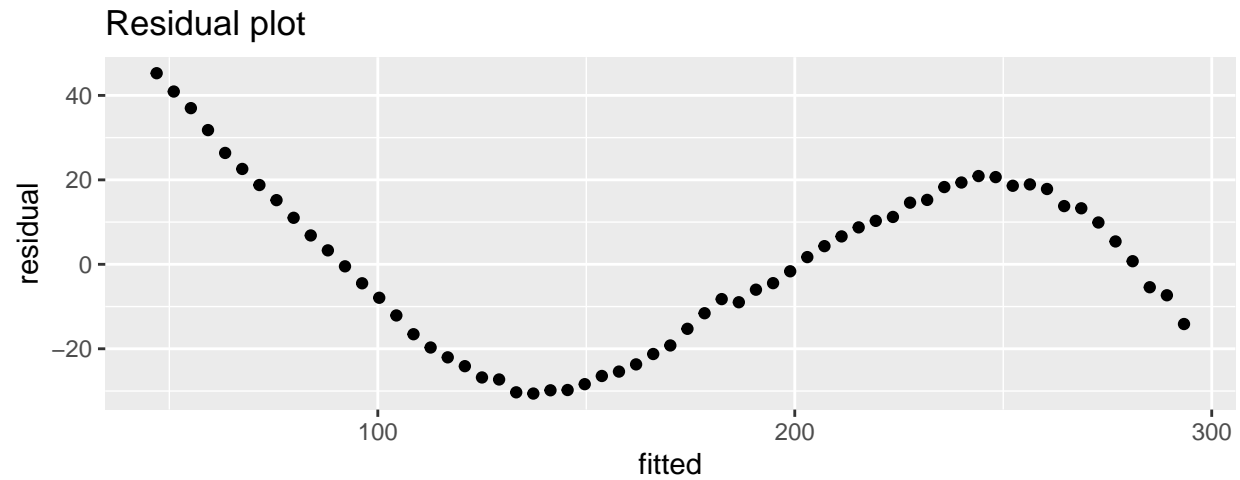
```
fit.diags <- broom::augment(fit)
```

1. residuals vs fitted

```
library(ggplot2)
```

```
## Warning:    'ggplot2' R   4.1.1
```

```
plot1 <- ggplot(fit.diags, aes(x = .fitted, y = .resid)) +

geom_point() + xlab("fitted") + ylab("residual") +

ggtitle("Residual plot", subtitle = waiver())

plot1
```
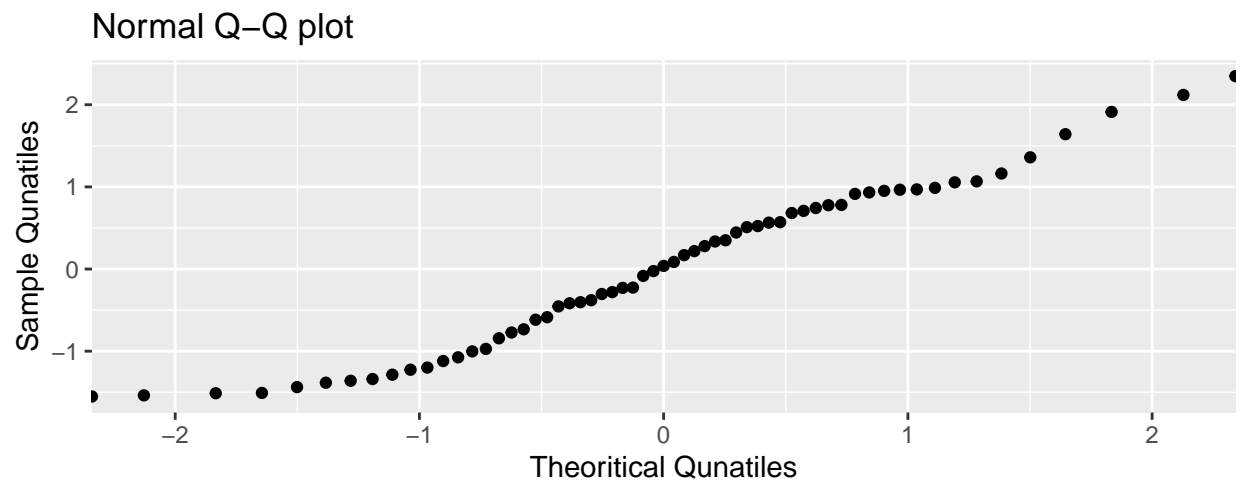
Residual plot

2. normal Q-Q

```
probs<-seq(0,1,length.out=length(fit.diags$.std.resid))
y<-fit.diags$.std.resid[order(fit.diags$.std.resid)]
norm<-qnorm(probs, lower.tail = TRUE, log.p = FALSE)

plot2 <- ggplot(fit.diags, aes(x = norm, y = y)) +

geom_point() + xlab("Theoritical Qunatiles") + ylab("Sample Qunatiles") +

ggtitle("Normal Q-Q plot", subtitle = waiver())

plot2
```
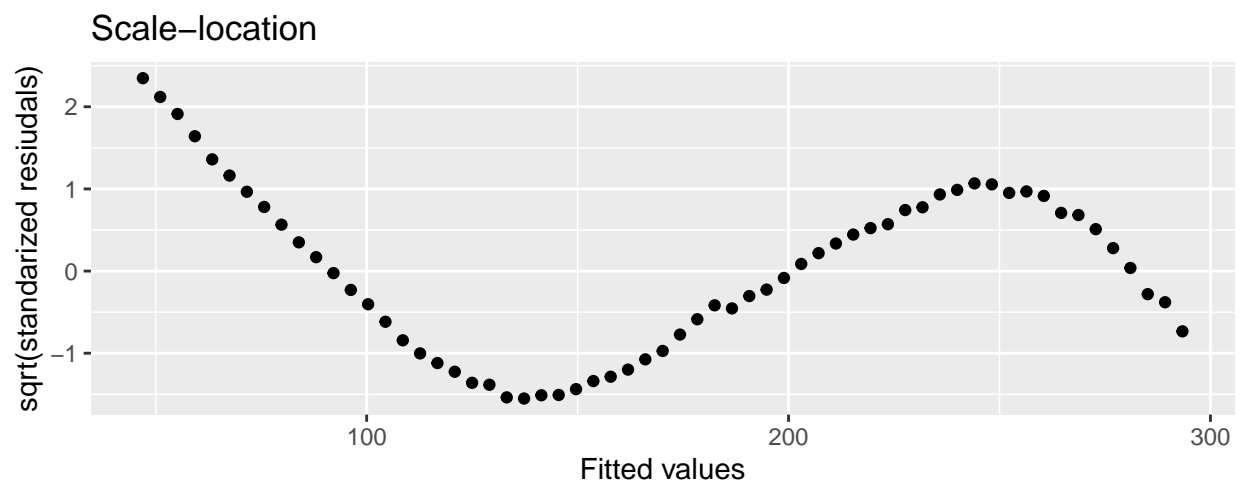
Normal Q–Q plot

3. scale-location

```
plot3 <- ggplot(fit.diags, aes(x = .fitted, y = .std.resid)) +

geom_point() + xlab("Fitted values") + ylab("sqrt(standarized resiudals)") +

ggtitle("Scale-location", subtitle = waiver())

plot3
```
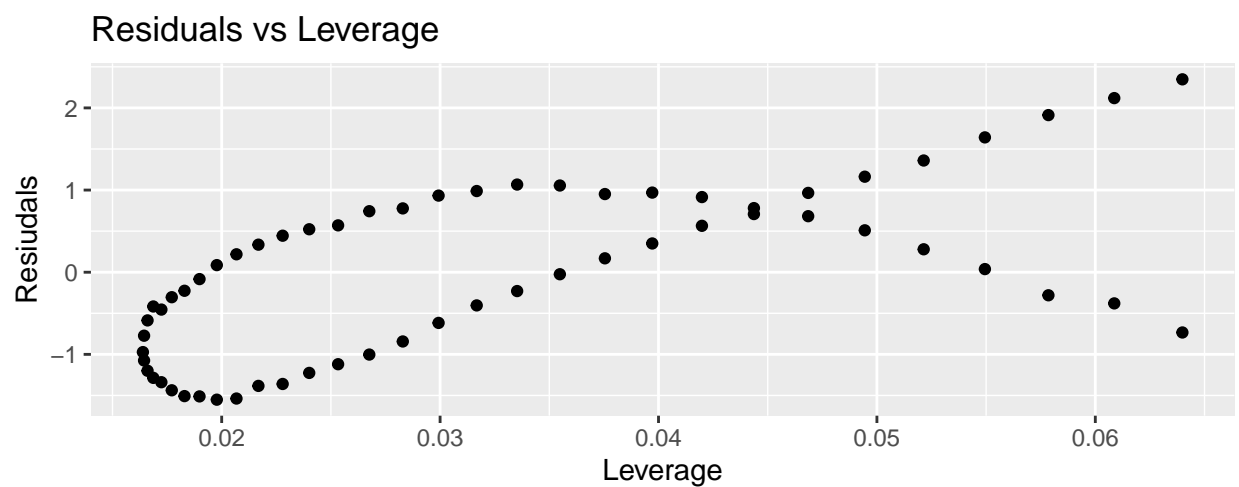
Scale−location

4. residuals vs leverage

```
plot4 <- ggplot(fit.diags, aes(x = .hat, y = .std.resid)) +

geom_point() + xlab("Leverage") + ylab("Resiudals") +

ggtitle("Residuals vs Leverage", subtitle = waiver())

plot4
```

Residuals vs Leverage

4.

```
library("ggpubr")
```

```
## Warning:    'ggpubr' R    4.1.1
```

```
ggarrange(plot1, plot2, plot3, plot4, ncol = 2, nrow = 2)
```