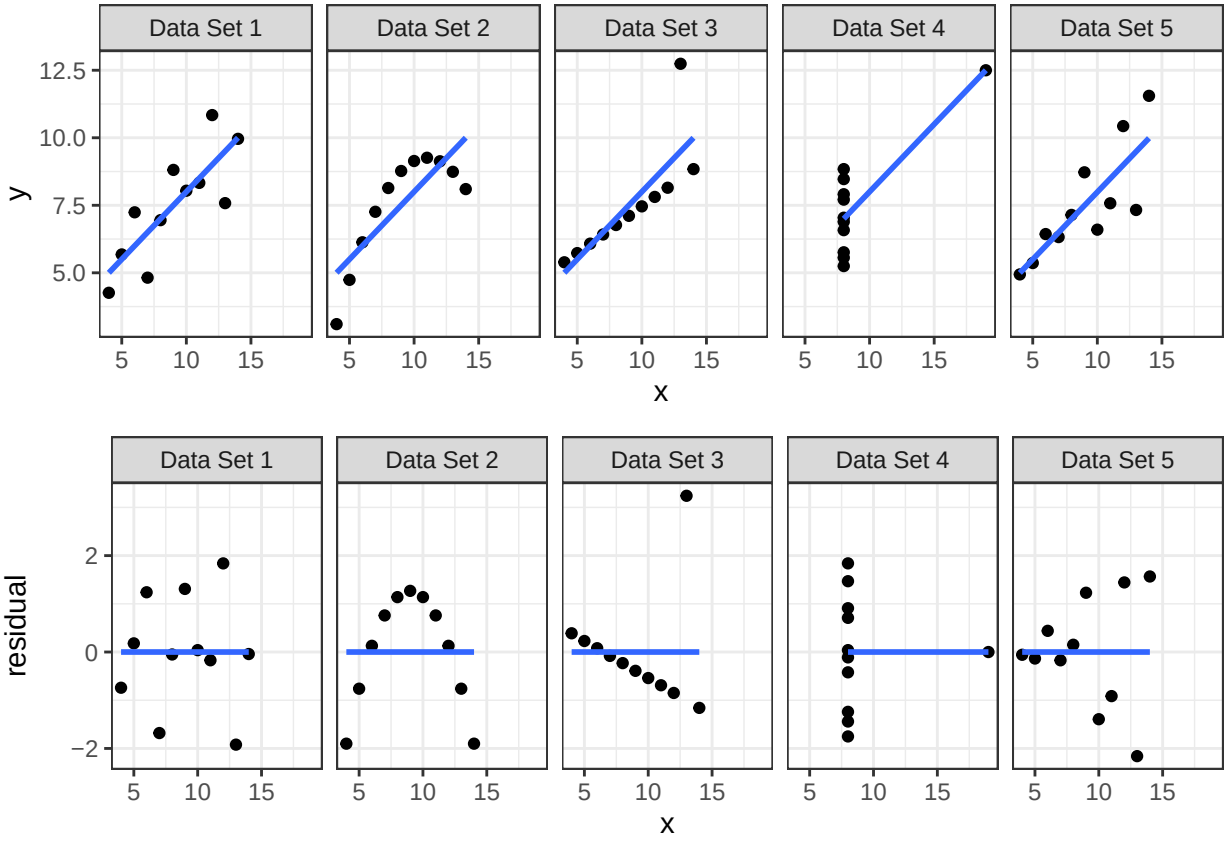
Chapter 11: Outliers and Influential Observations

Nov. 11, 2019

Recall Anscombe's Data



- For today, let's focus on Data Sets 3 and 4. We will see how to identify the problematic observations from the diagnostics.
- In data set 3, observation 3 is the one with a big Y!

```
anscombe$y3[3]
```

```
## [1] 12.74
```

- In data set 4, observation 8 is the one with a big X!

```
anscombe$x4[8]
```

```
## [1] 19
```

Data Set 3

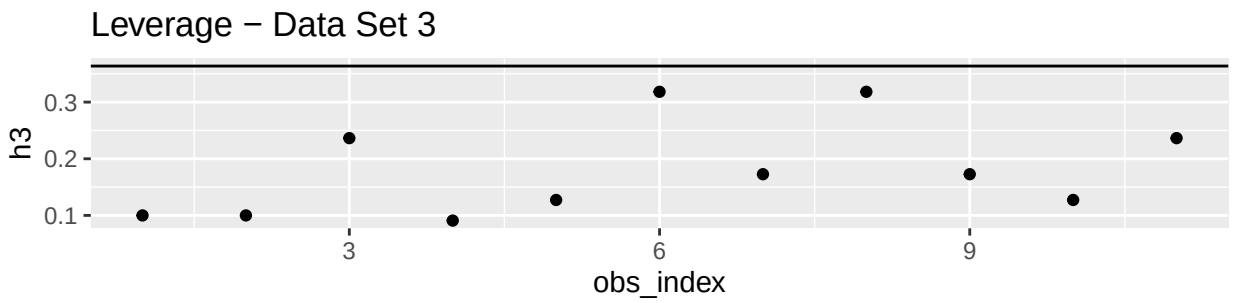
- Every statistical software package will give you different plots by default. Here is my preferred option:

```
fit3 <- lm(y3 ~ x3, data = anscombe)
anscombe <- anscombe %>%
  mutate(
    obs_index = row_number(),
    h3 = hatvalues(fit3),
    studres3 = rstudent(fit3),
    D3 = cooks.distance(fit3)
  )

# 2p/n; p = 2 since we have beta_0 and beta_1 in our simple linear regression model
2 * 2 / nrow(anscombe)
```

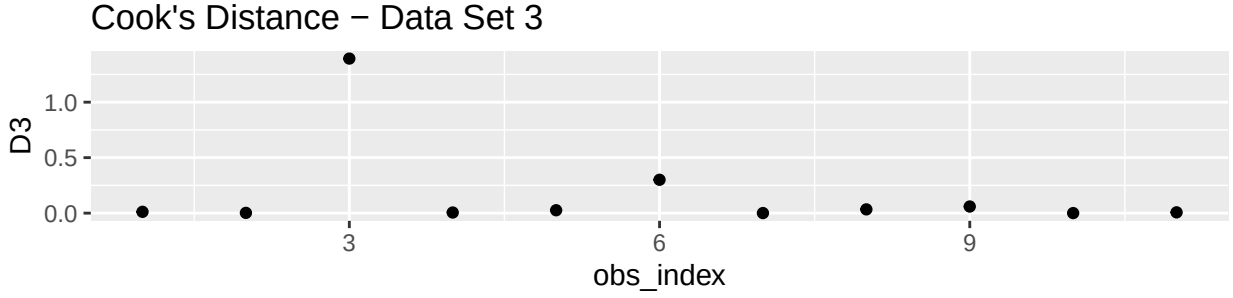
```
## [1] 0.3636364
```

```
ggplot(data = anscombe, mapping = aes(x = obs_index, y = h3)) +
  geom_point() +
  geom_hline(yintercept = 2 * 2 / nrow(anscombe)) +
  ggtitle("Leverage - Data Set 3")
```




```
ggplot(data = anscombe, mapping = aes(x = obs_index, y = studres3)) +
  geom_point() +
  ggtitle("Studentized Residuals - Data Set 3")
```


```
ggplot(data = anscombe, mapping = aes(x = obs_index, y = D3)) +
  geom_point() +
  ggtitle("Cook's Distance - Data Set 3")
```



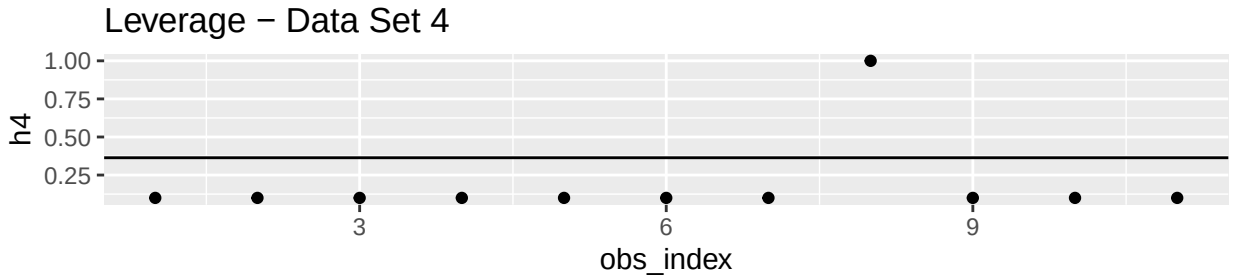
Data Set 4

```
fit4 <- lm(y4 ~ x4, data = anscombe)
anscombe <- anscombe %>%
  mutate(
    obs_index = row_number(),
    h4 = hatvalues(fit4),
    studres4 = rstudent(fit4),
    D4 = cooks.distance(fit4)
  )

# 2p/n; p = 2 since we have beta_0 and beta_1 in our simple linear regression model
2 * 2 / nrow(anscombe)
```

```
## [1] 0.3636364
```

```
ggplot(data = anscombe, mapping = aes(x = obs_index, y = h4)) +
  geom_point() +
  geom_hline(yintercept = 2 * 2 / nrow(anscombe)) +
  ggtitle("Leverage - Data Set 4")
```

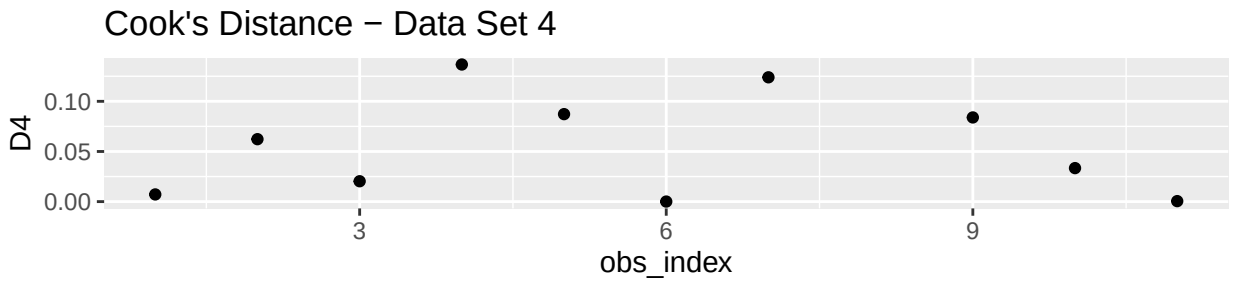



```
ggplot(data = anscombe, mapping = aes(x = obs_index, y = studres4)) +
  geom_point() +
  ggtitle("Studentized Residuals - Data Set 4")
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```


```
ggplot(data = anscombe, mapping = aes(x = obs_index, y = D4)) +
  geom_point() +
  ggtitle("Cook's Distance - Data Set 4")
```

```
## Warning: Removed 1 rows containing missing values (geom_point).
```



The lower two plots look OK... what's up with that warning?

```
anscombe$h4
```

```
##   1   2   3   4   5   6   7   8   9  10  11
## 0.1 0.1 0.1 0.1 0.1 0.1 0.1 1.0 0.1 0.1 0.1
```

```
anscombe$studres4
```

```
##           1           2           3           4           5           6
## -0.34104165 -1.06669299  0.58216636  1.73514504  1.30031318  0.03136768
##           7           8           9          10          11
## -1.62381807         NaN -1.27046922  0.75677904 -0.08931624
```

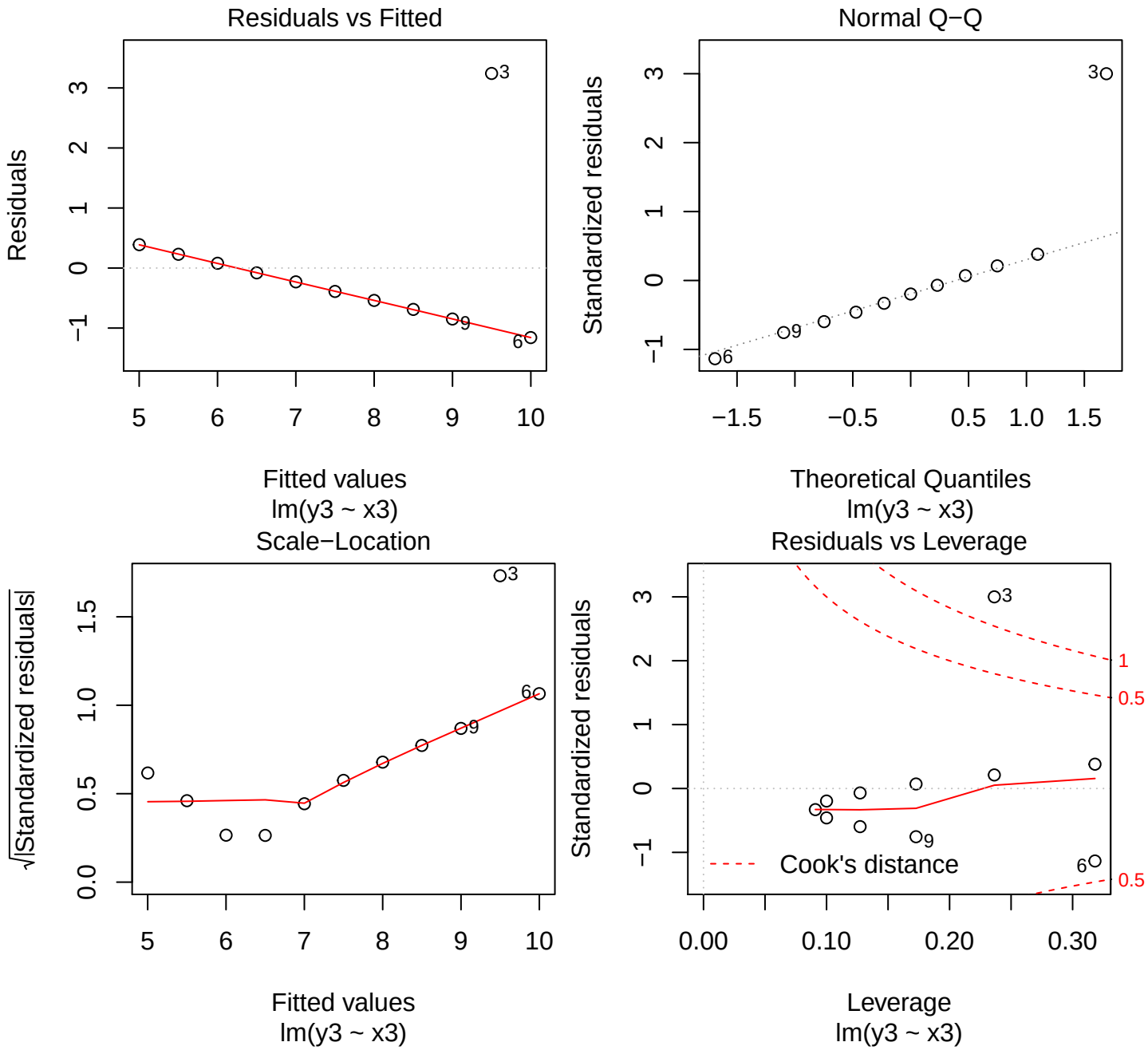
```
anscombe$D4
```

```
##            1            2            3            4            5
## 7.165166e-03 6.225950e-02 2.032144e-02 1.367179e-01 8.723799e-02
##            6            7            8            9           10
## 6.148813e-05 1.239465e-01          NaN 8.394407e-02 3.340334e-02
##           11
## 4.980902e-04
```

R Code: Default Plots

You can get a set of different diagnostic plots more easily, but I find the plot involving Cook's distance and Leverage less intuitive:

```
plot(fit3)
```



Note: to get the plots to all show up in the knitted pdf, I had to set figure height and width in the code chunk declaration:

```
```{r, fig.height = 4, fig.width = 4}
```
```