Residuals, diagnostics, variation

Regression

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The linear model

- Specified as $Y_i = \sum_{k=1}^{p} X_{ik} \beta_j + \epsilon_i$

  remember: epsilon is the true error,
  whereas e is the observed error.

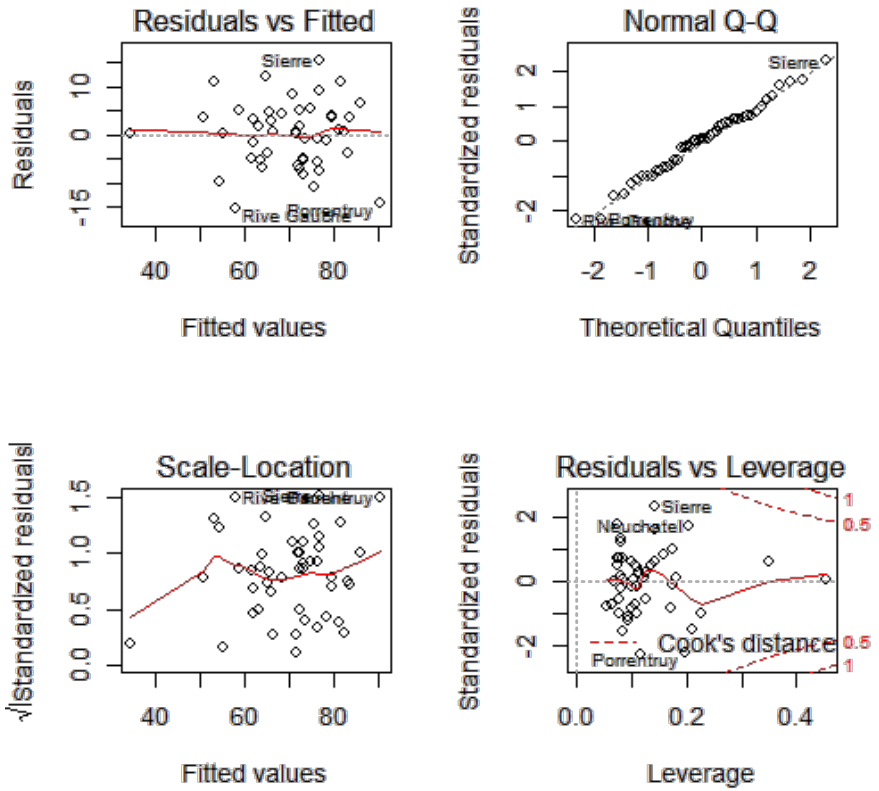
- We'll also assume here that $\epsilon_i \overset{iid}{\sim} N(0, \sigma^2)$
- Define the residuals as $e_i = Y_i - \hat{Y}_i = Y_i - \sum_{k=1}^{p} X_{ik} \hat{\beta}_j$

  e_i = observed.values - fitted.values
  (fitted.values := predicted values)

- Our estimate of residual variation is $\hat{\sigma}^2 = \frac{\sum_{i=1}^{n} e_i^2}{n-p}$, the $n - p$ so that $E[\hat{\sigma}^2] = \sigma^2$

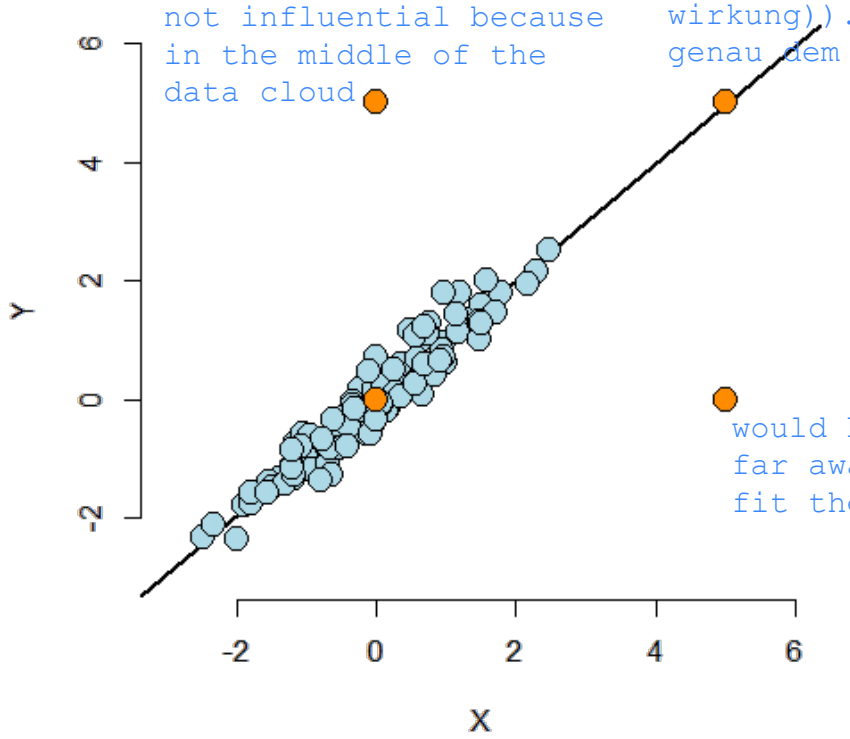
resid.var = averaged squared residuals, but instead of deviding by n,
we devide by n-p to get unbiasedness

```
data(swiss); par(mfrow = c(2, 2))
fit <- lm(Fertility ~ . , data = swiss); plot(fit)
```



Influential, high leverage and outlying points

if there were four points like these…



Summary of the plot

Calling a point an outlier is vague.

- Outliers can be the result of spurious or real processes.
- Outliers can have varying degrees of influence.
- Outliers can conform to the regression relationship (i.e being marginally outlying in X or Y, but not outlying given the regression relationship).
    - Upper left hand point has low leverage, low influence, outlies in a way not conforming to the regression relationship.
    - Lower left hand point has low leverage, low influence and is not to be an outlier in any sense.
    - Upper right hand point has high leverage, but chooses not to extert it and thus would have low actual influence by conforming to the regresison relationship of the other points.
    - Lower right hand point has high leverage and would exert it if it were included in the fit.

Influence measures

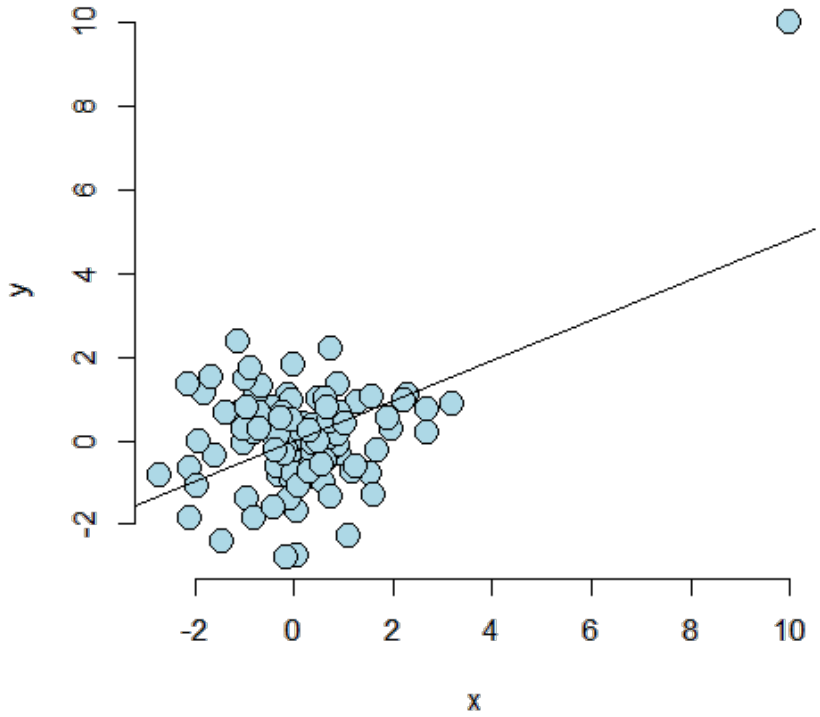
- Do `?influence.measures` to see the full suite of influence measures in stats. The measures include
  - `rstandard` - standardized residuals, residuals divided by their standard deviations)
  - `rstudent` - standardized residuals, residuals divided by their standard deviations, where the ith data point was deleted in the calculation of the standard deviation for the residual to follow a t distribution
  - `hatvalues` - measures of leverage
  - `dffits` - change in the predicted response when the i^{th} point is deleted in fitting the model.
  - `dfbetas` - change in individual coefficients when the i^{th} point is deleted in fitting the model.
  - `cooks.distance` - overall change in teh coefficients when the i^{th} point is deleted.
  - `resid` - returns the ordinary residuals

neat:
  - `resid(fit) / (1 - hatvalues(fit))` where `fit` is the linear model fit returns the PRESS residuals, i.e. the leave one out cross validation residuals - the difference in the response and the predicted response at data point i, where it was not included in the model fitting.

How do I use all of these things?

- Be wary of simplistic rules for diagnostic plots and measures. The use of these tools is context specific. It's better to understand what they are trying to accomplish and use them judiciously.
- Not all of the measures have meaningful absolute scales. You can look at them relative to the values across the data. `what does that mean???`
- They probe your data in different ways to diagnose different problems.
- Patterns in your residual plots generally indicate some poor aspect of model fit. These can include:
  - Heteroskedasticity (non constant variance).
  - Missing model terms.
  - Temporal patterns (plot residuals versus collection order).
- Residual QQ plots investigate normality of the errors.
  `quantile-quantile plots: plot obs quantiles against theoretical, quantils of norm distr.`
- Leverage measures (hat values) can be useful for diagnosing data entry errors. `depend only on x values`
- Influence measures get to the bottom line, 'how does deleting or including this point impact a particular aspect of the model'.

Case 1



no relationship betw x and y but this single point has huge influence!

The code

```
n <- 100; x <- c(10, rnorm(n)); y <- c(10, c(rnorm(n)))
plot(x, y, frame = FALSE, cex = 2, pch = 21, bg = "lightblue", col = "black")
abline(lm(y ~ x))
```

- The point `c(10, 10)` has created a strong regression relationship where there shouldn't be one.

Showing a couple of the diagnostic values

```
fit <- lm(y ~ x)
round(dfbetas(fit)[1 : 10, 2], 3)
```

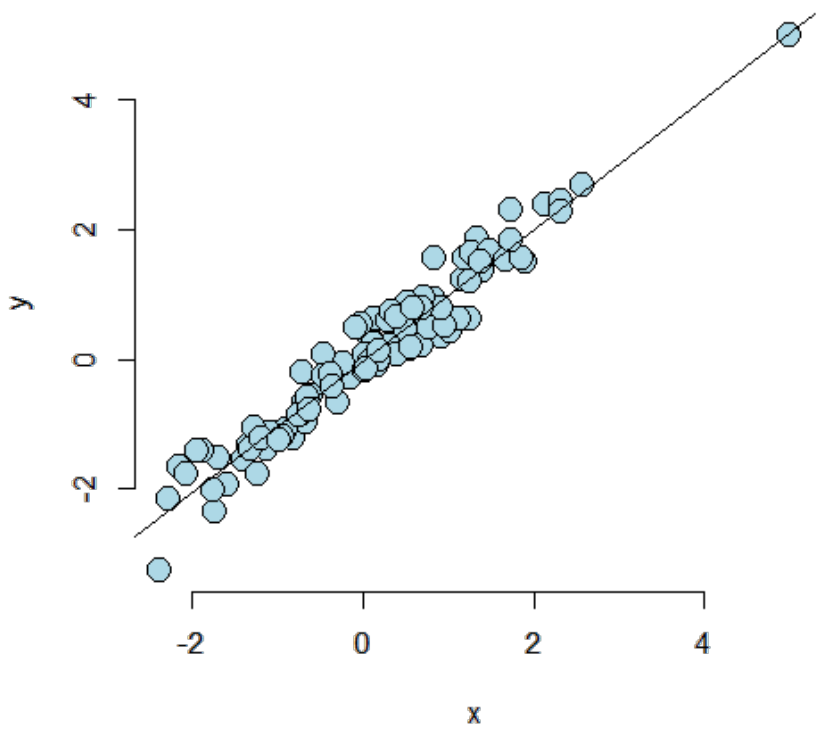
```
diff in coefficients between with and without a datapoint
```

```
     1      2      3      4      5      6      7      8      9     10
 6.007 -0.019 -0.007  0.014 -0.002 -0.083 -0.034 -0.045 -0.112 -0.008
```

```
round(hatvalues(fit)[1 : 10], 3)
```

```
    1     2     3     4     5     6     7     8     9    10
0.445 0.010 0.011 0.011 0.030 0.017 0.012 0.033 0.021 0.010
```

Case 2



Looking at some of the diagnostics

```
round(dfbetas(fit2)[1 : 10, 2], 3)
```

```
    1     2     3     4     5     6     7     8     9    10
-0.072 -0.041 -0.007  0.012  0.008 -0.187  0.017  0.100 -0.059  0.035
```

doesn't make a big difference to model params

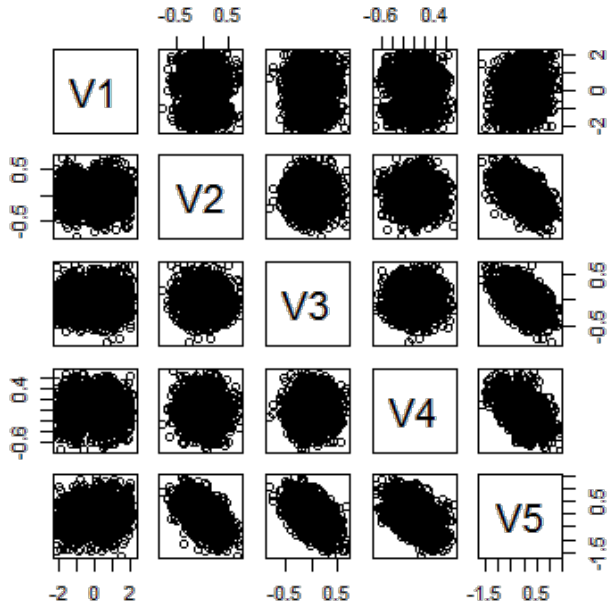
```
round(hatvalues(fit2)[1 : 10], 3)
```

```
    1     2     3     4     5     6     7     8     9    10
0.164 0.011 0.014 0.012 0.010 0.030 0.017 0.017 0.013 0.021
```

but hatvalue is much bigger than for the rest

Example described by Stefanski TAS 2007 Vol 61.

```
## Don't everyone hit this server at once.  Read the paper first.
dat <- read.table('http://www4.stat.ncsu.edu/~stefanski/NSF_Supported/Hidden_Images/orly_owl_files/orly
pairs(dat)
```



Got our P-values, should we bother to do a residual plot?

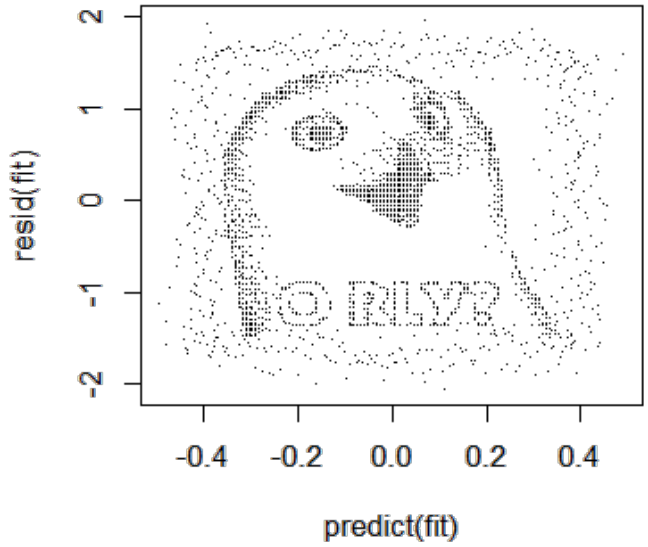
```
summary(lm(V1 ~ . -1, data = dat))$coef
```

```
   Estimate Std. Error t value  Pr(>|t|)
V2   0.9856    0.12798   7.701 1.989e-14
V3   0.9715    0.12664   7.671 2.500e-14
V4   0.8606    0.11958   7.197 8.301e-13
V5   0.9267    0.08328  11.127 4.778e-28  all very significant, but…
```

Residual plot

P-values significant, O RLY?

```
fit <- lm(V1 ~ . - 1, data = dat); plot(predict(fit), resid(fit), pch = '.')
```



Back to the Swiss data