Regression revisited

Regression

- Use regression when one variable is an outcome (*response*, y).
- See if/how response depends on other variable(s), *explanatory*, $x_1, x_2, \ldots$.
- Can have *one* or *more than one* explanatory variable, but always one response.
- Assumes a *straight-line* relationship between response and explanatory.
- Ask:
  - *is there* a relationship between y and x's, and if so, which ones?
  - what does the relationship look like?

Packages

```r
library(MASS, exclude = "select") # for Box-Cox, later
library(tidyverse)
library(broom)
library(marginaleffects)
```

A regression with one x

13 children, measure average total sleep time (ATST, mins) and age (years) for each. See if ATST depends on age. Data in `sleep.txt`, ATST then age. Read in data:

```r
my_url <- "http://ritsokiguess.site/datafiles/sleep.txt"
sleep <- read_delim(my_url, " ")
```

Check data

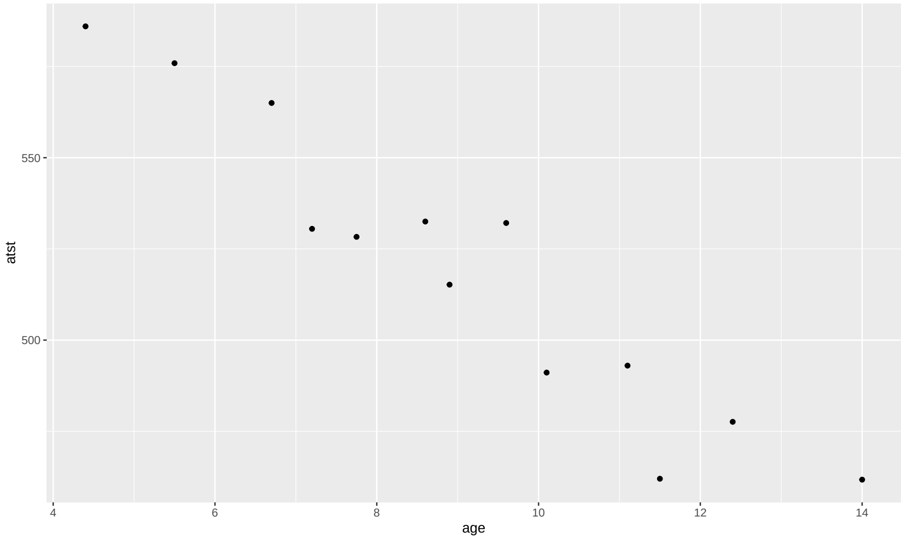
```
sleep
```

```
# A tibble: 13 x 2
    atst   age
   <dbl> <dbl>
 1  586   4.4 
 2  462. 14   
 3  491. 10.1 
 4  565   6.7 
 5  462  11.5 
 6  532.  9.6 
 7  478. 12.4 
 8  515.  8.9 
 9  493  11.1 
10  528.  7.75
11  576.  5.5 
12  532.  8.6 
13  530.  7.2 
```

Make scatter plot of ATST (response) vs. age (explanatory) using code overleaf.

The scatterplot

```
ggplot(sleep, aes(x = age, y = atst)) + geom_point()
```



Correlation

- Measures how well a straight line fits the data:

```
with(sleep, cor(atst, age))
```

```
[1] -0.9515469
```

- 1 is perfect upward trend, -1 is perfect downward trend, 0 is no trend.
- This one close to perfect downward trend.
- Can do correlations of all pairs of variables:

```
cor(sleep)
```

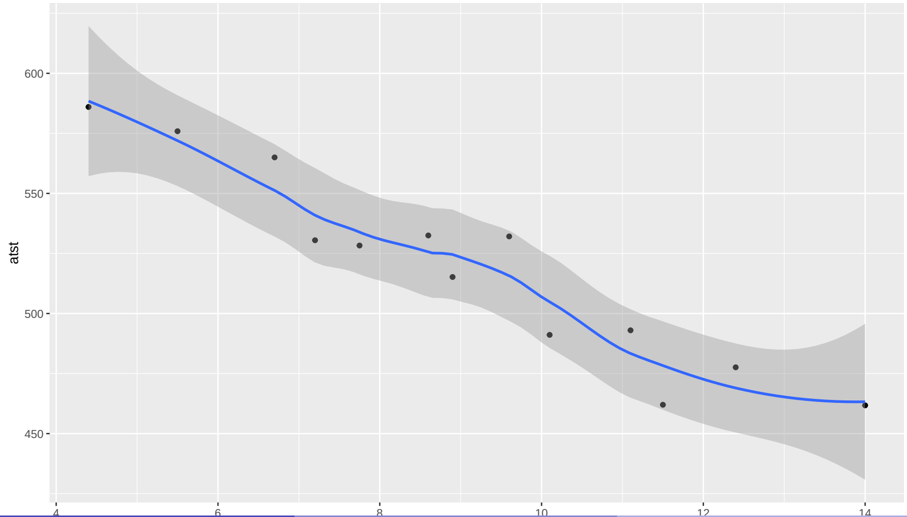
```
           atst        age
atst  1.0000000 -0.9515469
age  -0.9515469  1.0000000
```

Lowess curve

- Sometimes nice to guide the eye: is the trend straight, or not?
- Idea: *lowess curve*. "Locally weighted least squares", not affected by outliers, not constrained to be linear.
- Lowess is a *guide*: even if straight line appropriate, may wiggle/bend a little. Looking for *serious* problems with linearity.
- Add lowess curve to plot using `geom_smooth`:

Plot with lowess curve

```
ggplot(sleep, aes(x = age, y = atst)) + geom_point() +
  geom_smooth()
```



The regression

Scatterplot shows no obvious curve, and a pretty clear downward trend. So we can run the regression:

```r
sleep.1 <- lm(atst ~ age, data = sleep)
```

The output

```r
summary(sleep.1)
```

```

Call:
lm(formula = atst ~ age, data = sleep)

Residuals:
    Min      1Q  Median      3Q     Max 
-23.011  -9.365   2.372   6.770  20.411 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  646.483     12.918   50.05 2.49e-14 ***
age          -14.041      1.368  -10.26 5.70e-07 ***
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Conclusions

- The relationship appears to be a straight line, with a downward trend.
- F-tests for model as a whole and t-test for slope (same) both confirm this (P-value $5.7 \times 10^{-7} = 0.00000057$).
- Slope is -14, so a 1-year increase in age goes with a 14-minute decrease in ATST on average.
- R-squared is correlation squared (when one x anyway), between 0 and 1 (1 good, 0 bad).
- Here R-squared is 0.9054, pleasantly high.

Doing things with the regression output

- Output from regression (and eg. t-test) is all right to look at, but hard to extract and re-use information from.
- Package `broom` extracts info from model output in way that can be used in pipe (later):

```
tidy(sleep.1)
```

```
# A tibble: 2 x 5
  term        estimate std.error statistic  p.value
  <chr>          <dbl>     <dbl>     <dbl>    <dbl>
1 (Intercept)    646.      12.9       50.0 2.49e-14
2 age            -14.0      1.37     -10.3 5.70e- 7
```

also one-line summary of model:

```
glance(sleep.1)
```

```
# A tibble: 1 x 12
  r.squared adj.r.squared sigma statistic     p.value    df
      <dbl>         <dbl> <dbl>     <dbl>       <dbl> <dbl>
1     0.905         0.897  13.2      105. 0.000000570     1
# i 6 more variables: logLik <dbl>, AIC <dbl>, BIC <dbl>,
#   deviance <dbl>, df.residual <int>, nobs <int>
```

Broom part 2

```
sleep.1 %>% augment(sleep)
```

```
# A tibble: 13 x 8
    atst   age .fitted .resid   .hat .sigma .cooksd
   <dbl> <dbl>   <dbl>  <dbl>  <dbl>  <dbl>   <dbl>
 1  586   4.4     585.   1.30 0.312    13.8 0.00320
 2  462. 14       450.  11.8  0.341    13.0 0.319
 3  491. 10.1     505. -13.6  0.0887   13.0 0.0568
 4  565   6.7     552.  12.6  0.137    13.1 0.0844
 5  462  11.5     485. -23.0  0.141    11.3 0.294
 6  532.  9.6     512.  20.4  0.0801   12.0 0.114
 7  478. 12.4     472.   5.23 0.198    13.7 0.0243
 8  515.  8.9     522.  -6.32 0.0772   13.6 0.0105
 9  493  11.1     491.   2.37 0.122    13.8 0.00258
10  528.  7.75    538.  -9.37 0.0954   13.4 0.0296
11  576.  5.5     569.   6.64 0.214    13.6 0.0441
12  532.  8.6     526.   6.77 0.0792   13.6 0.0124
13  530.  7.2     545. -14.9  0.114    12.9 0.0933
# i 1 more variable: .std.resid <dbl>
```

Useful for plotting residuals against an x-variable.

CI for mean response and prediction intervals

Once useful regression exists, use it for prediction:

- To get a single number for prediction at a given x, substitute into regression equation, eg. age 10: predicted ATST is $646.48 - 14.04(10) = 506$ minutes.
- To express uncertainty of this prediction:
- *CI for mean response* expresses uncertainty about mean ATST for all children aged 10, based on data.
- *Prediction interval* expresses uncertainty about predicted ATST for a new child aged 10 whose ATST not known. More uncertain.
- Also do above for a child aged 5.

The marginaleffects package 1/2

To get predictions for specific values, set up a dataframe with those values first:

```
new <- datagrid(model = sleep.1, age = c(10, 5))
new
```

```
  age rowid
1  10     1
2   5     2
```

Any variables in the dataframe that you don't specify are set to their mean values (quantitative) or most common category (categorical).

The marginaleffects package 2/2

Then feed into newdata in predictions. This contains a lot of columns, so you probably want only to display the ones you care about:

```
cbind(predictions(sleep.1, newdata = new)) %>%
  select(estimate, conf.low, conf.high, age)
```

```
  estimate conf.low conf.high age
1 506.0729 498.4899  513.6558  10
2 576.2781 563.2588  589.2974   5
```

The confidence limits are a 95% confidence interval for the mean response at that age.

Prediction intervals

These are obtained (instead) with predict as below. Use the same dataframe new as before:

```
pp <- predict(sleep.1, new, interval = "p")
pp
```

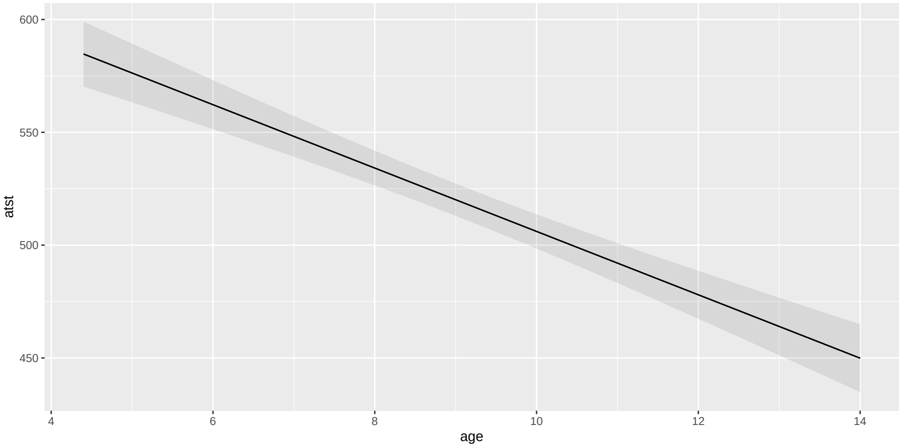
```
       fit      lwr      upr
1 506.0729 475.8982 536.2475
2 576.2781 543.8474 608.7088
```

```
cbind(new, pp)
```

```
  age rowid      fit      lwr      upr
1  10     1 506.0729 475.8982 536.2475
2   5     2 576.2781 543.8474 608.7088
```

Plotting the confidence intervals for mean response again:

```
plot_predictions(sleep.1, condition = "age")
```



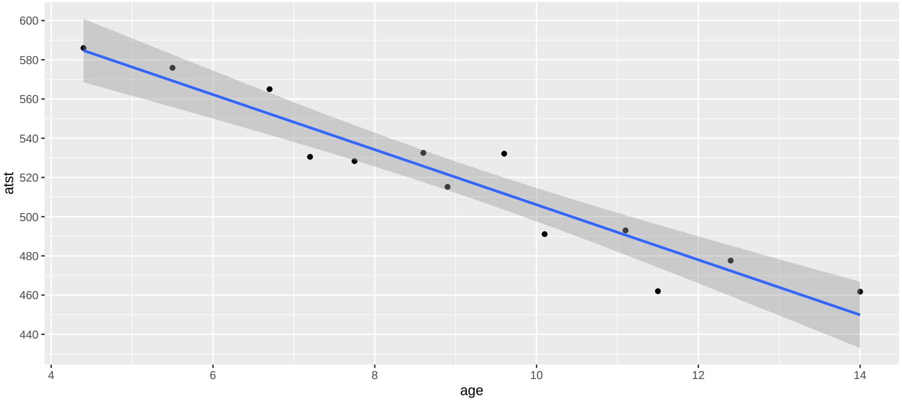
Comments

- Age 10 closer to centre of data, so intervals are both narrower than those for age 5.
- Prediction intervals bigger than CI for mean (additional uncertainty).
- Technical note: output from `predict` is R `matrix`, not data frame, so Tidyverse `bind_cols` does not work. Use base R `cbind`.

That grey envelope

Marks confidence interval for mean for all x:

```
ggplot(sleep, aes(x = age, y = atst)) + geom_point() +
  geom_smooth(method = "lm") +
  scale_y_continuous(breaks = seq(420, 600, 20))
```



Diagnostics

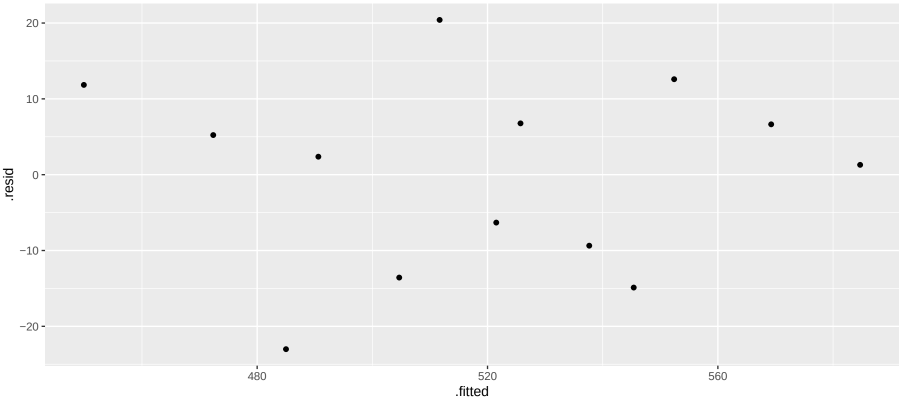
How to tell whether a straight-line regression is appropriate?

- Before: check scatterplot for straight trend.
- After: plot *residuals* (observed minus predicted response) against predicted values. Aim: a plot with no pattern.

Residual plot

Not much pattern here — regression appropriate.

```
ggplot(sleep.1, aes(x = .fitted, y = .resid)) + geom_point()
```



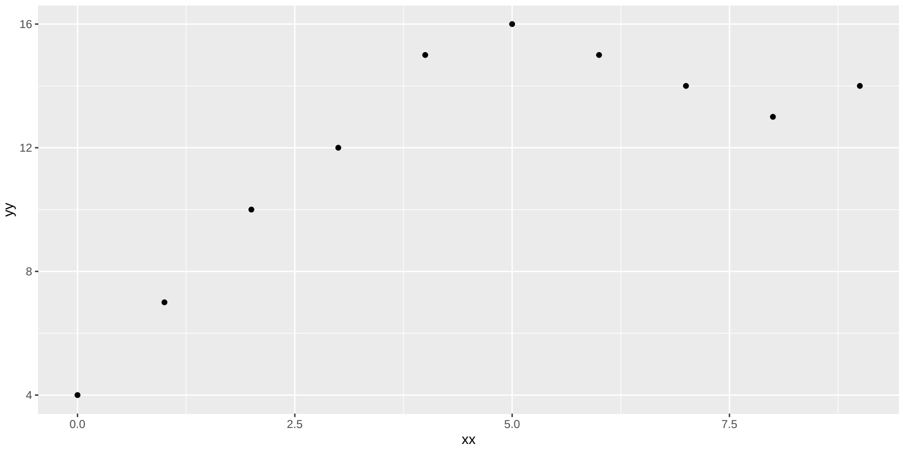
An inappropriate regression

Different data:

```
my_url <- "http://ritsokiguess.site/datafiles/curvy.txt"
curvy <- read_delim(my_url, " ")
```

Scatterplot

```
ggplot(curvy, aes(x = xx, y = yy)) + geom_point()
```



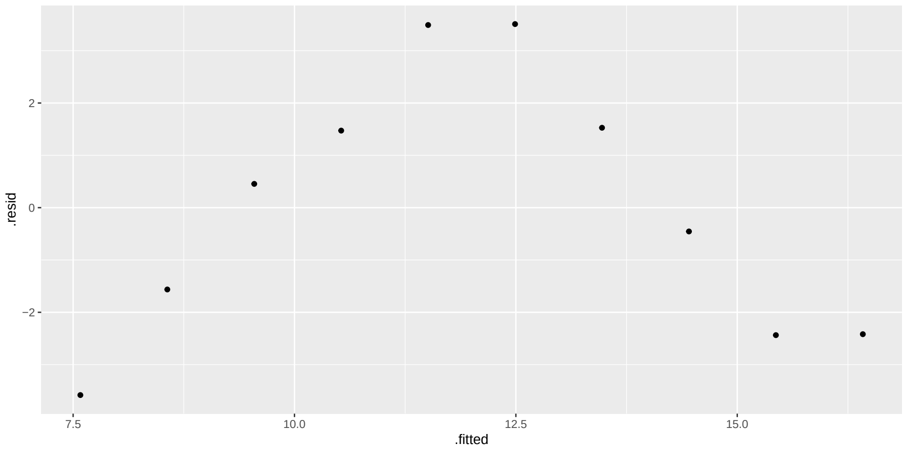
Regression line, anyway

```
curvy.1 <- lm(yy ~ xx, data = curvy)
summary(curvy.1)
```

```
Call:
lm(formula = yy ~ xx, data = curvy)

Residuals:
   Min     1Q Median     3Q    Max 
-3.582 -2.204  0.000  1.514  3.509 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)   
(Intercept)   7.5818     1.5616   4.855  0.00126 **
xx            0.9818     0.2925   3.356  0.00998 **
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.657 on 8 degrees of freedom
Multiple R-squared:  0.5848,	Adjusted R-squared:  0.5329 
F-statistic: 11.27 on 1 and 8 DF,  p-value: 0.009984
```

Residual plot

```
ggplot(curvy.1, aes(x = .fitted, y = .resid)) + geom_point()
```



No good: fixing it up

- Residual plot has *curve*: middle residuals positive, high and low ones negative. Bad.
- Fitting a curve would be better. Try this:

```
curvy.2 <- lm(yy ~ xx + I(xx^2), data = curvy)
```

- Adding xx-squared term, to allow for curve.
- Another way to do same thing: specify how model *changes*:

```
curvy.2a <- update(curvy.1, . ~ . + I(xx^2))
```

Regression 2

```
summary(curvy.2)
```

```

Call:
lm(formula = yy ~ xx + I(xx^2), data = curvy)

Residuals:
    Min      1Q  Median      3Q     Max 
-1.2091 -0.3602 -0.2364  0.8023  1.2636 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  3.90000    0.77312   5.045 0.001489 ** 
xx           3.74318    0.40006   9.357 3.31e-05 ***
I(xx^2)     -0.30682    0.04279  -7.170 0.000182 ***
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9833 on 7 degrees of freedom
Multiple R-squared:  0.9502,	Adjusted R-squared:  0.936 
```

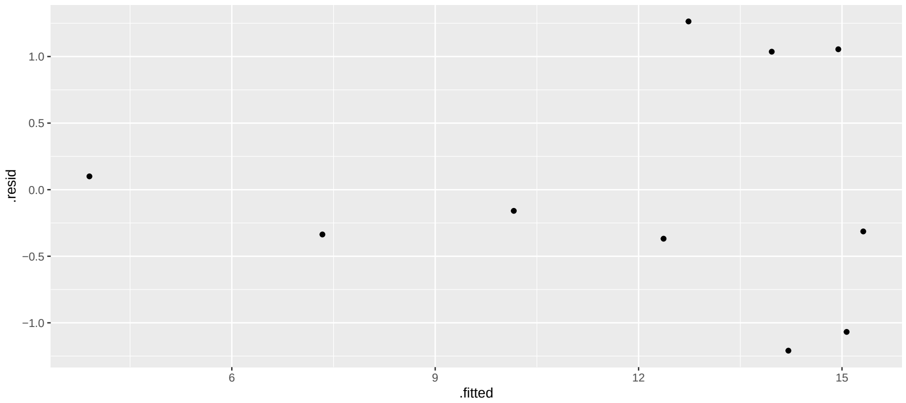
Comments

- `xx`-squared term definitely significant (P-value 0.000182), so need this curve to describe relationship.
- Adding squared term has made R-squared go up from 0.5848 to 0.9502: great improvement.
- This is a definite curve!

The residual plot now

No apparent problems any more:

```
ggplot(curvy.2, aes(x = .fitted, y = .resid)) + geom_point()
```



Another way to handle curves

- Above, saw that changing x (adding x^2) was a way of handling curved relationships.
- Another way: change y (transformation).
- Can guess how to change y, or might be theory:
- example: relationship $y = ae^{bx}$ (exponential growth):
- take logs to get $\ln y = \ln a + bx$.
- Taking logs has made relationship linear ($\ln y$ as response).
- Or, *estimate* transformation, using Box-Cox method.

Box-Cox

- Install package `MASS` via `install.packages("MASS")` (only need to do *once*)
- Every R session you want to use something in `MASS`, type `library(MASS)`

Some made-up data

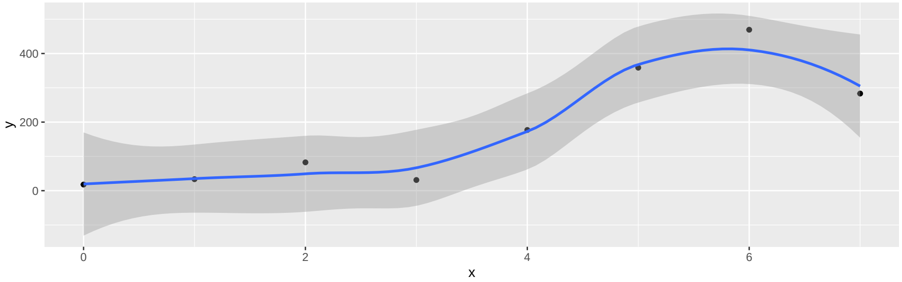
```
my_url <- "http://ritsokiguess.site/datafiles/madeup2.csv"
madeup <- read_csv(my_url)
madeup
```

```
# A tibble: 8 x 3
   ...1     x     y
  <dbl> <dbl> <dbl>
1     1     0  17.9
2     2     1  33.6
3     3     2  82.7
4     4     3  31.2
5     5     4 177. 
6     6     5 359. 
7     7     6 469. 
8     8     7 283. 
```

Seems to be faster-than-linear growth, maybe exponential growth.

Scatterplot: faster than linear growth

```
ggplot(madeup, aes(x = x, y = y)) + geom_point() +
  geom_smooth()
```

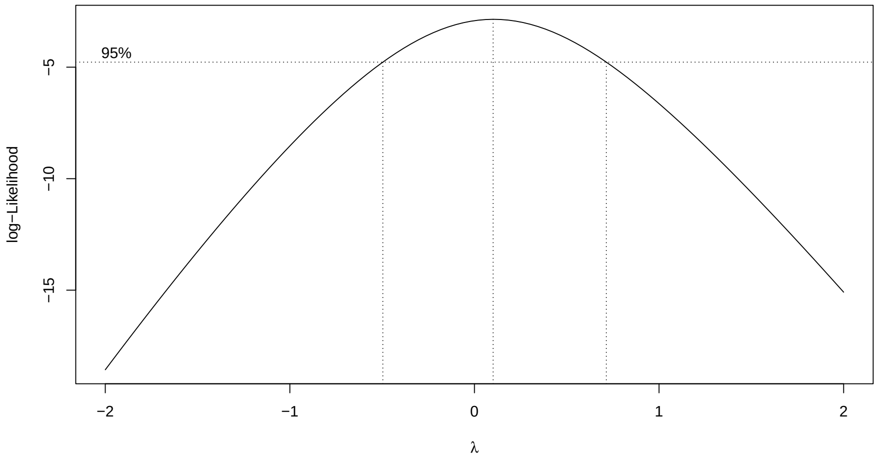


Running Box-Cox

- `library(MASS)` first.
- Feed `boxcox` a model formula with a squiggle in it, such as you would use for `lm`.
- Output: a graph (next page):

```
boxcox(y ~ x, data = madeup)
```

The Box-Cox output



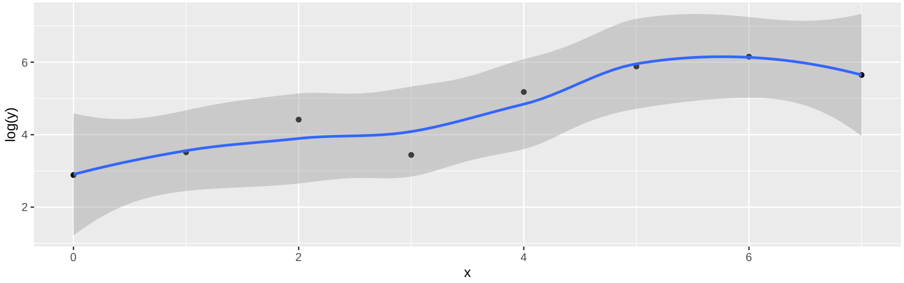
Comments

- λ (lambda) is the power by which you should transform y to get the relationship straight (straighter). Power 0 is "take logs"
- Middle dotted line marks best single value of λ (here about 0.1).
- Outer dotted lines mark 95% CI for λ, here -0.3 to 0.7, approx. (Rather uncertain about best transformation.)
- Any power transformation within the CI supported by data. In this case, log ($\lambda = 0$) and square root ($\lambda = 0.5$) good, but no transformation ($\lambda = 1$) not.
- Pick a "round-number" value of λ like $2, 1, 0.5, 0, -0.5, -1$. Here 0 and 0.5 good values to pick.

Did transformation straighten things?

- Plot transformed y against x. Here, log:

```
ggplot(madeup, aes(x = x, y = log(y))) + geom_point() +
  geom_smooth()
```



Looks much straighter.

Regression with transformed y

```
madeup.1 <- lm(log(y) ~ x, data = madeup)
summary(madeup.1)
```

```
Call:
lm(formula = log(y) ~ x, data = madeup)

Residuals:
    Min      1Q  Median      3Q     Max 
-0.9688 -0.2577  0.1663  0.3881  0.5534 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  3.02884    0.37935   7.984 0.000206 ***
x            0.46006    0.09068   5.073 0.002281 ** 
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.5877 on 6 degrees of freedom
Multiple R-squared:  0.811, Adjusted R-squared:  0.7794
```

Multiple regression

- What if more than one x? Extra issues:
  - Now one intercept and a slope for each x: how to interpret?
  - Which x-variables actually help to predict y?
  - Different interpretations of "global" F-test and individual t-tests.
  - R-squared no longer correlation squared, but still interpreted as "higher better".
  - In `lm` line, add extra xs after `~`.
  - Interpretation not so easy (and other problems that can occur).

Multiple regression example

Study of women and visits to health professionals, and how the number of visits might be related to other variables:

timedrs:	number of visits to health professionals (over course of study)
phyheal:	number of physical health problems
menheal:	number of mental health problems
stress:	result of questionnaire about number and type of life changes

`timedrs` response, others explanatory.

The data

```
my_url <-
  "http://ritsokiguess.site/datafiles/regressx.txt"
visits <- read_delim(my_url, " ")
```

Check data

```
visits
```

```
# A tibble: 465 x 5
   subjno timedrs phyheal menheal stress
    <dbl>   <dbl>   <dbl>   <dbl>  <dbl>
 1      1       1       5       8    265
 2      2       3       4       6    415
 3      3       0       3       4     92
 4      4      13       2       2    241
 5      5      15       3       6     86
 6      6       3       5       5    247
 7      7       2       5       6     13
 8      8       0       4       5     12
 9      9       7       5       4    269
10     10       4       3       9    391
# i 455 more rows
```

Fit multiple regression

```r
visits.1 <- lm(timedrs ~ phyheal + menheal + stress,
  data = visits)
summary(visits.1)
```

```

Call:
lm(formula = timedrs ~ phyheal + menheal + stress, data = visits)

Residuals:
    Min      1Q  Median      3Q     Max 
-14.792  -4.353  -1.815   0.902  65.886 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept) -3.704848   1.124195  -3.296 0.001058 ** 
phyheal      1.786948   0.221074   8.083  5.6e-15 ***
menheal     -0.009666   0.129029  -0.075 0.940318    
stress       0.013615   0.003612   3.769 0.000185 ***
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 9.708 on 461 degrees of freedom
Multiple R-squared:  0.2188,	Adjusted R-squared:  0.2137 
F-statistic: 43.03 on 3 and 461 DF,  p-value: < 2.2e-16
```

The slopes

- Model as a whole strongly significant even though R-sq not very big (lots of data). At least one of the x's predicts `timedrs`.
- The physical health and stress variables definitely help to predict the number of visits, but *with those in the model* we don't need `menheal`. However, look at prediction of `timedrs` from `menheal` by itself:

Just menheal

```r
visits.2 <- lm(timedrs ~ menheal, data = visits)
summary(visits.2)
```

```

Call:
lm(formula = timedrs ~ menheal, data = visits)

Residuals:
    Min      1Q  Median      3Q     Max
-13.826  -5.150  -2.818   1.177  72.513

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   3.8159     0.8702   4.385 1.44e-05 ***
menheal       0.6672     0.1173   5.688 2.28e-08 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 10.6 on 463 degrees of freedom
Multiple R-squared:  0.06532,   Adjusted R-squared:  0.0633
```

`menheal` by itself

- `menheal` by itself *does* significantly help to predict `timedrs`.
- But the R-sq is much less (6.5% vs. 22%).
- So other two variables do a better job of prediction.
- With those variables in the regression (`phyheal` and `stress`), don't need `menheal` *as well*.

Investigating via correlation

Leave out first column (`subjno`):

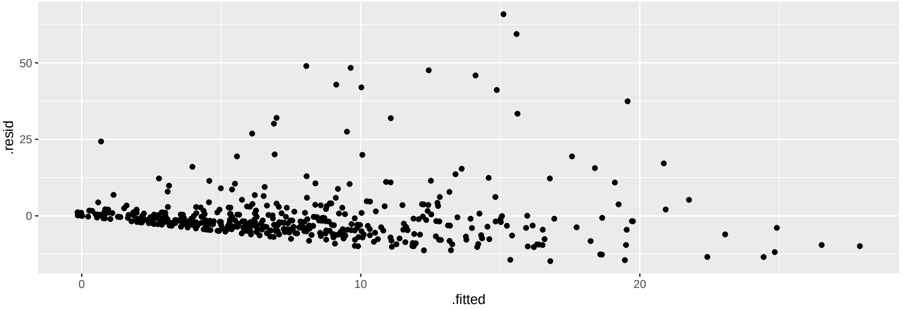
```
visits %>% select(-subjno) %>% cor()
```

```
          timedrs   phyheal   menheal    stress
timedrs 1.0000000 0.4395293 0.2555703 0.2865951
phyheal 0.4395293 1.0000000 0.5049464 0.3055517
menheal 0.2555703 0.5049464 1.0000000 0.3697911
stress  0.2865951 0.3055517 0.3697911 1.0000000
```

- `phyheal` most strongly correlated with `timedrs`.
- Not much to choose between other two.
- But `menheal` has higher correlation with `phyheal`, so not as much to *add* to prediction as `stress`.
- Goes to show things more complicated in multiple regression.

Residual plot (from timedrs on all)

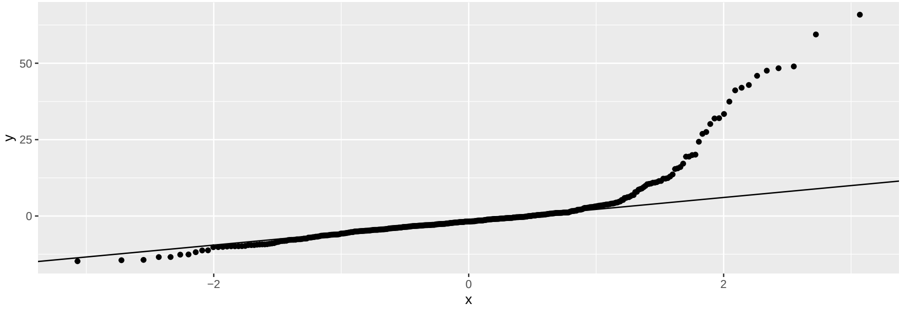
```
ggplot(visits.1, aes(x = .fitted, y = .resid)) + geom_point()
```



Apparently random. But...

Normal quantile plot of residuals

```
ggplot(visits.1, aes(sample = .resid)) + stat_qq() + stat_qq_l
```

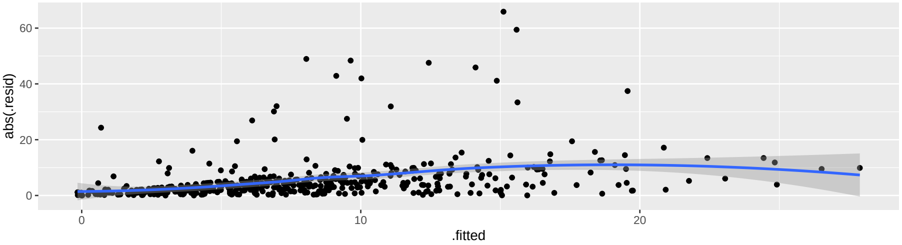


Not normal at all; upper tail is way too long.

Absolute residuals

Is there trend in *size* of residuals (fan-out)? Plot *absolute value* of residual against fitted value:

```r
ggplot(visits.1, aes(x = .fitted, y = abs(.resid))) +
  geom_point() + geom_smooth()
```



Comments

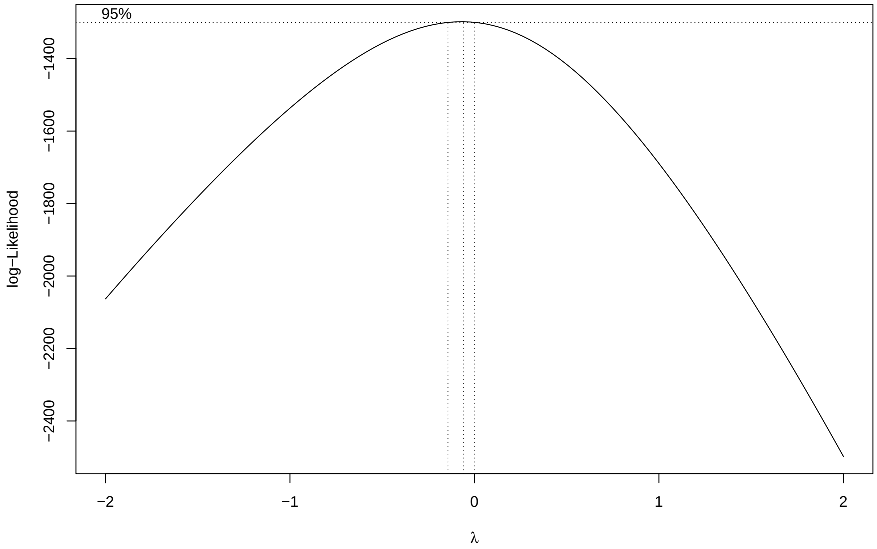
- On the normal quantile plot:
  - highest (most positive) residuals are *way* too high
  - distribution of residuals skewed to right (not normal at all)
- On plot of absolute residuals:
  - size of residuals getting bigger as fitted values increase
  - predictions getting more variable as fitted values increase
  - that is, predictions getting *less accurate* as fitted values increase, but predictions should be equally accurate all way along.
- Both indicate problems with regression, of kind that transformation of response often fixes: that is, predict *function* of response `timedrs` instead of `timedrs` itself.

Box-Cox transformations

- Taking log of timedrs and having it work: lucky guess. How to find good transformation?
- Box-Cox again.
- Extra problem: some of timedrs values are 0, but Box-Cox expects all $+$. Note response for boxcox:

```
boxcox(timedrs + 1 ~ phyheal + menheal + stress, data = visits
```

Try 1



Comments on try 1

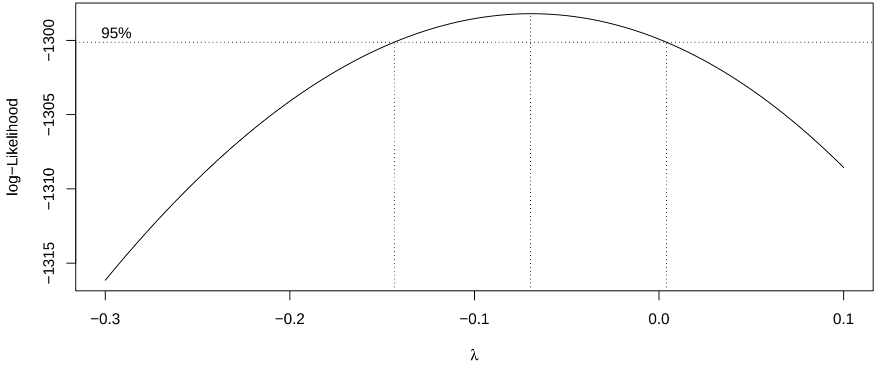
- Best: λ just less than zero.
- Hard to see scale.
- Focus on λ in $(-0.3, 0.1)$:

```
my.lambda <- seq(-0.3, 0.1, 0.01)
my.lambda
```

```
 [1] -0.30 -0.29 -0.28 -0.27 -0.26 -0.25 -0.24 -0.23 -0.22
[10] -0.21 -0.20 -0.19 -0.18 -0.17 -0.16 -0.15 -0.14 -0.13
[19] -0.12 -0.11 -0.10 -0.09 -0.08 -0.07 -0.06 -0.05 -0.04
[28] -0.03 -0.02 -0.01  0.00  0.01  0.02  0.03  0.04  0.05
[37]  0.06  0.07  0.08  0.09  0.10
```

Try 2

```
boxcox(timedrs + 1 ~ phyheal + menheal + stress,
  lambda = my.lambda,
  data = visits
)
```



Comments

- Best: λ just about -0.07.
- CI for λ about $(-0.14, 0.01)$.
- Only nearby round number: $\lambda = 0$, log transformation.

Fixing the problems

- Try regression again, with transformed response instead of original one.
- Then check residual plot to see that it is OK now.

```
visits.3 <- lm(log(timedrs + 1) ~ phyheal + menheal + stress,
  data = visits
)
```

- `timedrs+1` because some `timedrs` values 0, can't take log of 0.
- Won't usually need to worry about this, but when response could be zero/negative, fix that before transformation.

Output

```r
summary(visits.3)
```

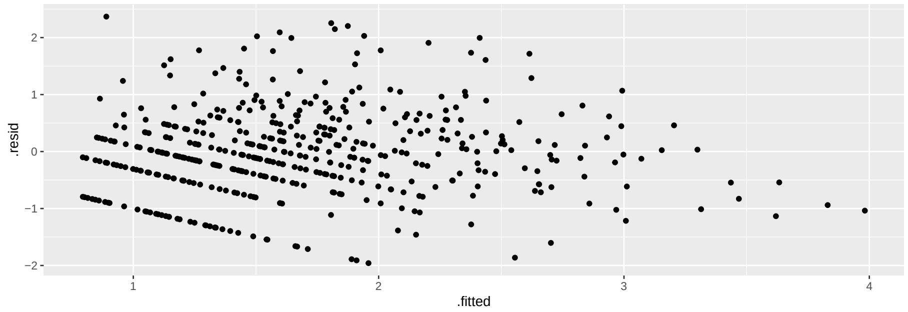
```
Call:
lm(formula = log(timedrs + 1) ~ phyheal + menheal + stress, data = visits)

Residuals:
     Min       1Q   Median       3Q      Max 
-1.95865 -0.44076 -0.02331  0.42304  2.36797 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept) 0.3903862  0.0882908   4.422 1.22e-05 ***
phyheal     0.2019361  0.0173624  11.631  < 2e-16 ***
menheal     0.0071442  0.0101335   0.705    0.481    
stress      0.0013158  0.0002837   4.638 4.58e-06 ***
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.7625 on 461 degrees of freedom
Multiple R-squared:  0.3682,	Adjusted R-squared:  0.3641 
F-statistic: 89.56 on 3 and 461 DF,  p-value: < 2.2e-16
```

Comments

- Model as a whole strongly significant again
- R-sq higher than before (37% vs. 22%) suggesting things more linear now
- Same conclusion re `menheal`: can take out of regression.
- Should look at residual plots (next pages). Have we fixed problems?

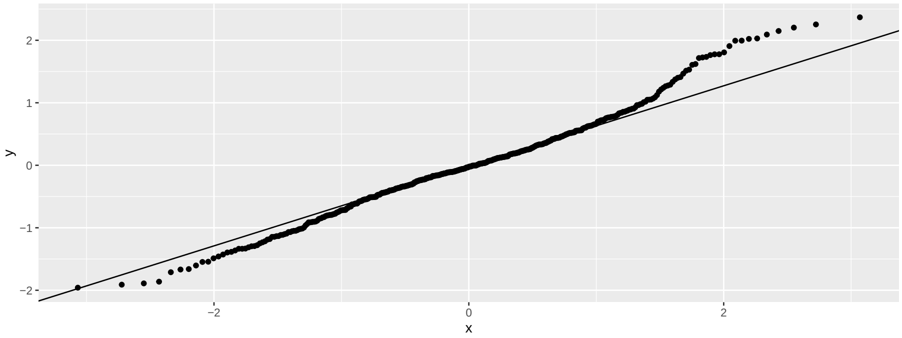
Residuals against fitted values

```
ggplot(visits.3, aes(x = .fitted, y = .resid)) +
  geom_point()
```



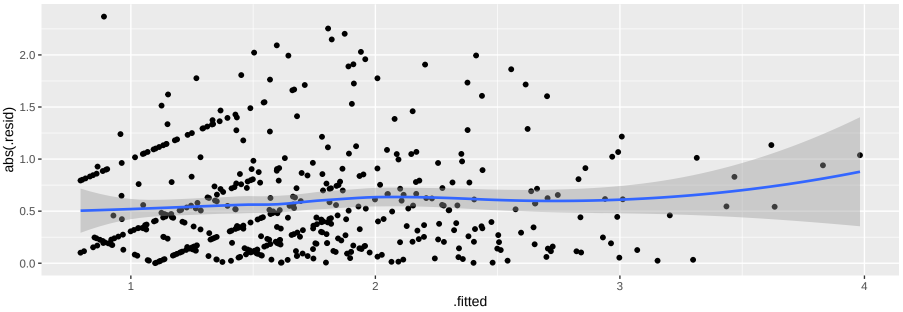
Normal quantile plot of residuals

```
ggplot(visits.3, aes(sample = .resid)) + stat_qq() + stat_qq_l
```



Absolute residuals against fitted

```
ggplot(visits.3, aes(x = .fitted, y = abs(.resid))) +
  geom_point() + geom_smooth()
```



Comments

- Residuals vs. fitted looks a lot more random.
- Normal quantile plot looks a lot more normal (though still a little right-skewness)
- Absolute residuals: not so much trend (though still some).
- Not perfect, but much improved.

Testing more than one x at once

- The t-tests test only whether one variable could be taken out of the regression you're looking at.
- To test significance of more than one variable at once, fit model with and without variables
    - then use `anova` to compare fit of models:

```r
visits.5 <- lm(log(timedrs + 1) ~ phyheal + menheal + stress,
               data = visits)
visits.6 <- lm(log(timedrs + 1) ~ stress, data = visits)
```

Results of tests

```r
anova(visits.6, visits.5)
```

```
Analysis of Variance Table

Model 1: log(timedrs + 1) ~ stress
Model 2: log(timedrs + 1) ~ phyheal + menheal + stress
  Res.Df    RSS Df Sum of Sq      F    Pr(>F)
1    463 371.47
2    461 268.01  2    103.46 88.984 < 2.2e-16 ***
---
Signif. codes:
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Models don't fit equally well, so bigger one fits better.
- Or "taking both variables out makes the fit worse, so don't do it".
- Taking out those x's is a mistake. Or putting them in is a good idea.

The punting data

Data set `punting.txt` contains 4 variables for 13 right-footed football kickers (punters): left leg and right leg strength (lbs), distance punted (ft), another variable called "fred". Predict punting distance from other variables.

Reading in

- Separated by *multiple spaces* with *columns lined up*:

```r
my_url <- "http://ritsokiguess.site/datafiles/punting.txt"
punting <- read_table(my_url)
```

The data

```
punting
```

```
# A tibble: 13 x 4
    left right  punt  fred
   <dbl> <dbl> <dbl> <dbl>
 1   170   170  162.   171
 2   130   140  144    136
 3   170   180  174.   174
 4   160   160  164.   161
 5   150   170  192    159
 6   150   150  172.   151
 7   180   170  162    174
 8   110   110  105.   111
 9   110   120  106.   114
10   120   130  118.   126
11   140   120  140.   129
12   130   140  150.   136
13   150   160  165.   154
```

Regression and output

```r
punting.1 <- lm(punt ~ left + right + fred, data = punting)
summary(punting.1)
```

```

Call:
lm(formula = punt ~ left + right + fred, data = punting)

Residuals:
     Min       1Q   Median       3Q      Max 
-14.9325 -11.5618  -0.0315   9.0415  20.0886 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -4.6855    29.1172  -0.161    0.876
left          0.2679     2.1111   0.127    0.902
right         1.0524     2.1477   0.490    0.636
fred         -0.2672     4.2266  -0.063    0.951

Residual standard error: 14.68 on 9 degrees of freedom
Multiple R-squared:  0.7781,	Adjusted R-squared:  0.7042 
F-statistic: 10.52 on 3 and 9 DF,  p-value: 0.00267
```

Comments

- Overall regression strongly significant, R-sq high.
- None of the x's significant! Why?
- t-tests only say that you could take any one of the x's out without damaging the fit; doesn't matter which one.
- Explanation: look at *correlations*.

The correlations

```
cor(punting)
```

```
          left     right      punt      fred
left  1.0000000 0.8957224 0.8117368 0.9722632
right 0.8957224 1.0000000 0.8805469 0.9728784
punt  0.8117368 0.8805469 1.0000000 0.8679507
fred  0.9722632 0.9728784 0.8679507 1.0000000
```

- *All* correlations are high: x's with `punt` (good) and with each other (bad, at least confusing).
- What to do? Probably do just as well to pick one variable, say `right` since kickers are right-footed.

Just right

```
punting.2 <- lm(punt ~ right, data = punting)
anova(punting.2, punting.1)
```

```
Analysis of Variance Table

Model 1: punt ~ right
Model 2: punt ~ left + right + fred
  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1     11 1962.5
2      9 1938.2  2    24.263 0.0563 0.9456
```

No significant loss by dropping other two variables.

Comparing R-squareds

- All three x-variables:

```
summary(punting.1)$r.squared
```

```
[1] 0.7781401
```

- Only `right`:

```
summary(punting.2)$r.squared
```

```
[1] 0.7753629
```

- Basically no difference. In regression (over), `right` significant:

Regression results

```
summary(punting.2)
```

```

Call:
lm(formula = punt ~ right, data = punting)

Residuals:
     Min       1Q   Median       3Q      Max 
-15.7576 -11.0611   0.3656   7.8890  19.0423 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  -3.6930    25.2649  -0.146    0.886    
right         1.0427     0.1692   6.162 7.09e-05 ***
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 13.36 on 11 degrees of freedom
Multiple R-squared:  0.7754,	Adjusted R-squared:  0.7549 
F-statistic: 37.97 on 1 and 11 DF,  p-value: 7.088e-05
```

But...

- Maybe we got the *form* of the relationship with `left` wrong.
- Check: plot *residuals* from previous regression (without `left`) against `left`.
- Residuals here are "punting distance adjusted for right leg strength".
- If there is some kind of relationship with `left`, we should include in model.
- Plot of residuals against original variable: `augment` from `broom`.

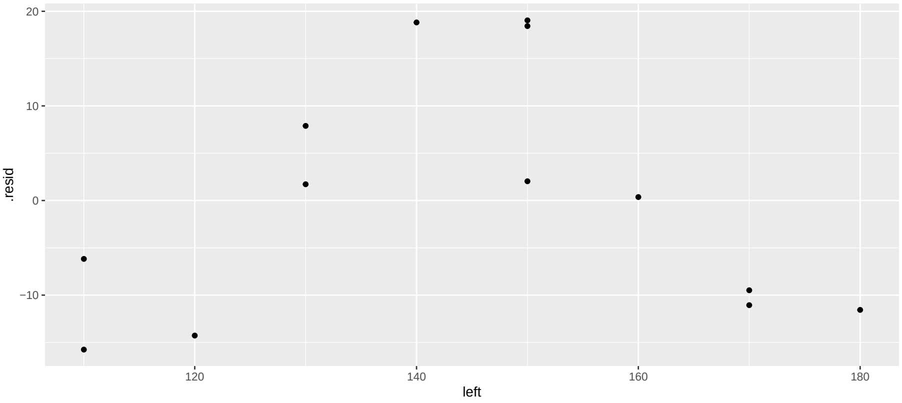
Augmenting punting.2

```
punting.2 %>% augment(punting) -> punting.2.aug
punting.2.aug
```

```
# A tibble: 13 x 10
    left right  punt  fred .fitted  .resid   .hat .sigma
   <dbl> <dbl> <dbl> <dbl>   <dbl>   <dbl>  <dbl>  <dbl>
 1   170   170  162.   171    174. -11.1   0.157    13.5
 2   130   140  144    136    142.   1.72  0.0864   14.0
 3   170   180  174.   174    184.  -9.49  0.244    13.6
 4   160   160  164.   161    163.   0.366 0.101    14.0
 5   150   170  192    159    174.  18.4   0.157    12.5
 6   150   150  172.   151    153.  19.0   0.0778   12.5
 7   180   170  162    174    174. -11.6   0.157    13.4
 8   110   110  105.   111    111.  -6.17  0.305    13.8
 9   110   120  106.   114    121. -15.8   0.2      12.9
10   120   130  118.   126    132. -14.3   0.127    13.1
11   140   120  140.   129    121.  18.8   0.2      12.3
12   130   140  150.   136    142.   7.89  0.0864   13.8
13   150   160  165.   154    163.   2.04  0.101    14.0
# i 2 more variables: .cooksd <dbl>, .std.resid <dbl>
```

Residuals against `left`

```r
ggplot(punting.2.aug, aes(x = left, y = .resid)) +
  geom_point()
```



Comments

- There is a *curved* relationship with `left`.
- We should add `left`-squared to the regression (and therefore put `left` back in when we do that):

```
punting.3 <- lm(punt ~ left + I(left^2) + right,
  data = punting
)
```

Regression with `left-squared`

```
summary(punting.3)
```

```
Call:
lm(formula = punt ~ left + I(left^2) + right, data = punting)

Residuals:
     Min       1Q   Median       3Q      Max 
-11.3777  -5.3599   0.0459   4.5088  13.2669 

Coefficients:
              Estimate Std. Error t value Pr(>|t|)   
(Intercept) -4.623e+02  9.902e+01  -4.669  0.00117 **
left         6.888e+00  1.462e+00   4.710  0.00110 **
I(left^2)   -2.302e-02  4.927e-03  -4.672  0.00117 **
right        7.396e-01  2.292e-01   3.227  0.01038 * 
---
Signif. codes:  
0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 7.931 on 9 degrees of freedom
Multiple R-squared:  0.9352,	Adjusted R-squared:  0.9136 
F-statistic:  43.3 on 3 and 9 DF,  p-value: 1.13e-05
```

Comments

- This was definitely a good idea (R-squared has clearly increased).
- We would never have seen it without plotting residuals from `punting.2` (without `left`) against `left`.
- Negative slope for `leftsq` means that increased left-leg strength only increases punting distance up to a point: beyond that, it decreases again.