

# Regression revisited

# Regression

- Use regression when one variable is an outcome (*response*,  $y$ ).
- See if/how response depends on other variable(s), *explanatory*,  $x_1, x_2, \dots$
- 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

```
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:

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

# Check data

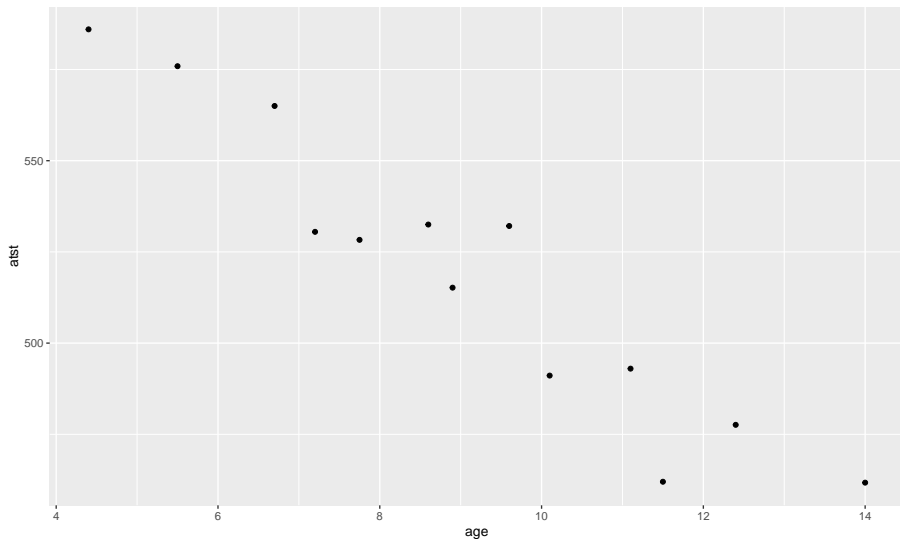
```
sleep
```

```
# 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

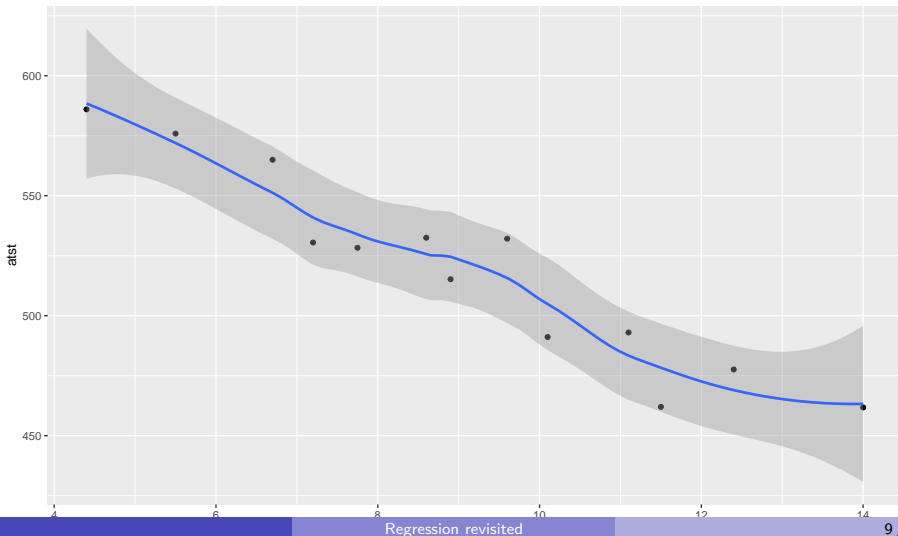
## Lowess curve

- 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:

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

# The output

```
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 marginalesffects 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 marginalesffects 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
```

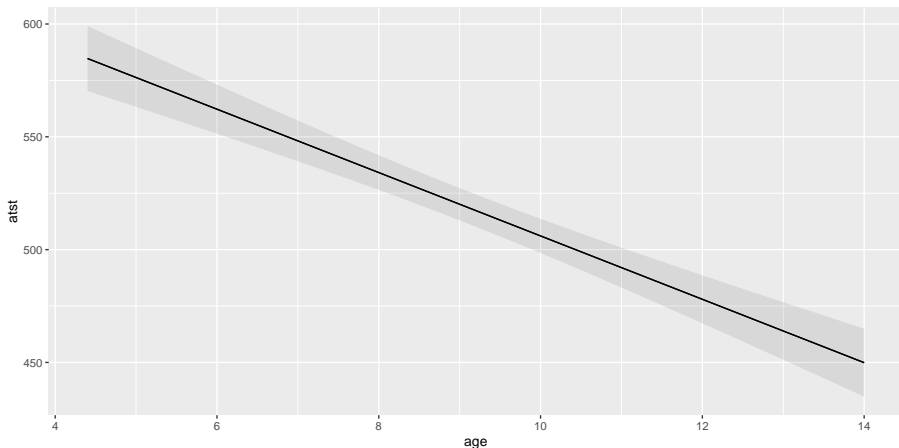
	fit	lwr	upr
1	506.0729	475.8982	536.2475
2	576.2781	543.8474	608.7088

```
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")
```



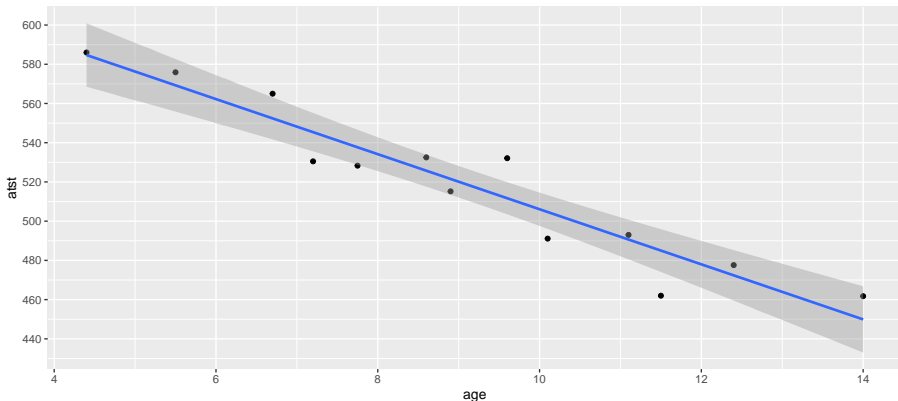
# Comments

- 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

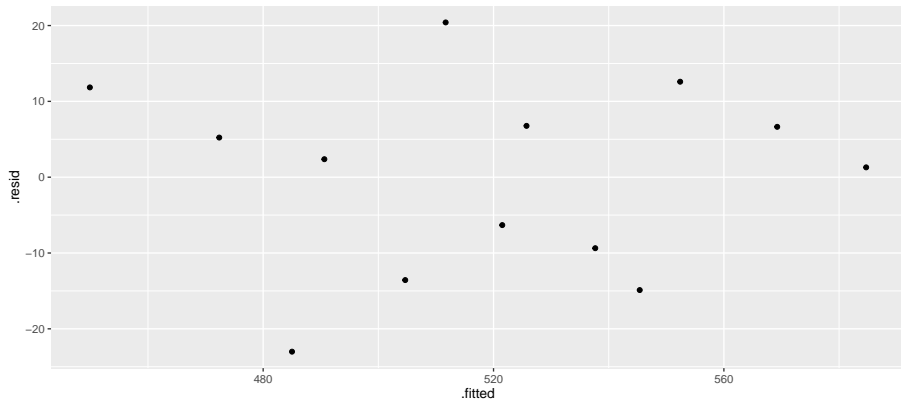
How to tell whether a straight-line regression is appropriate?

- 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()
```





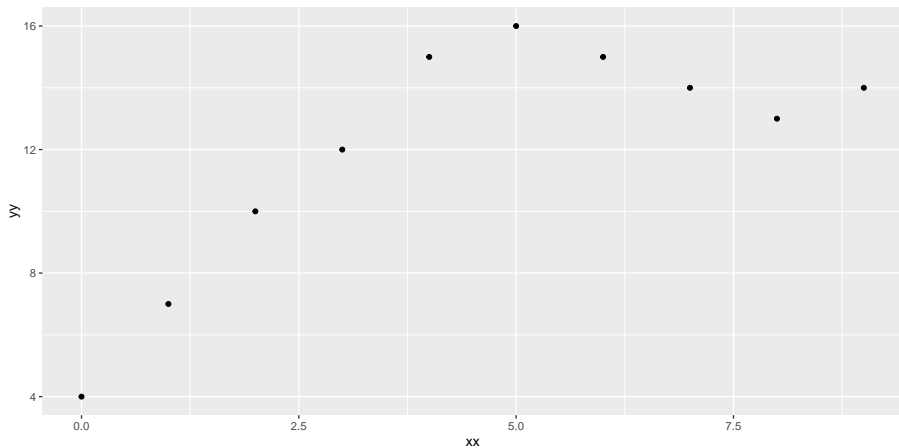
# An inappropriate regression

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

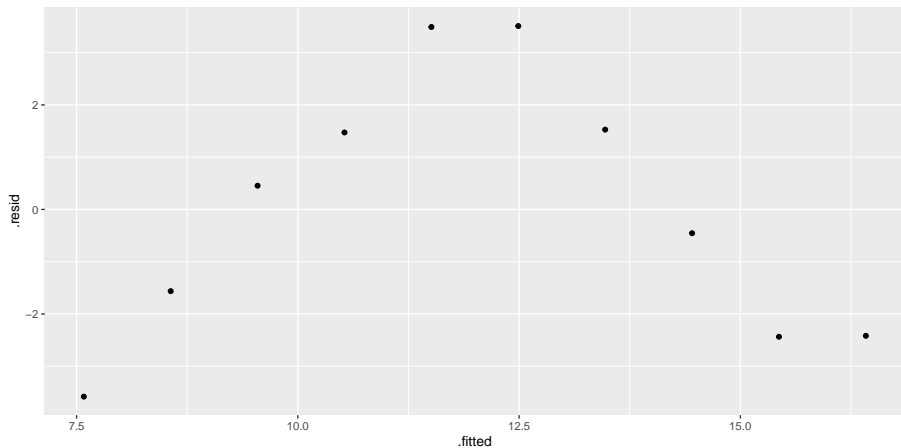
Residual standard error: 2.657 on 8 degrees of freedom

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

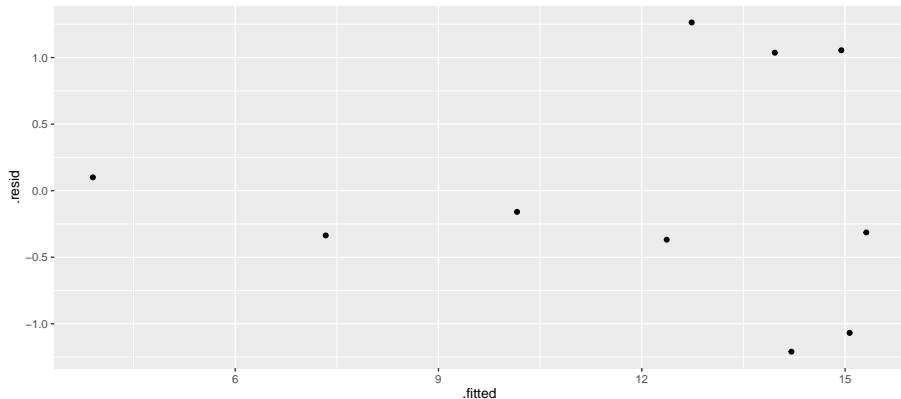
## Comments

- $xx$ -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

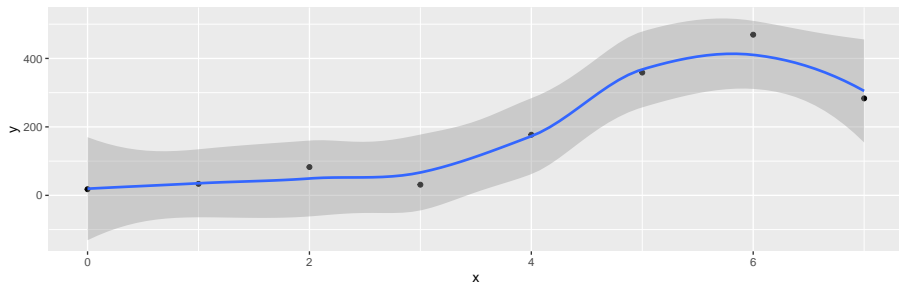
```
my_url <- "http://ritsokiguess.site/datafiles/madeup2.csv"
madeup <- read_csv(my_url)
madeup
```

```
# 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()
```

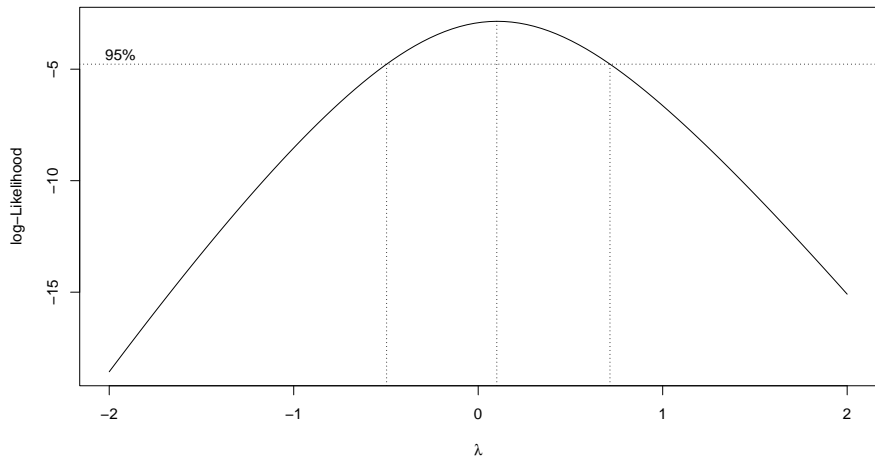


# Running Box-Cox

- `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



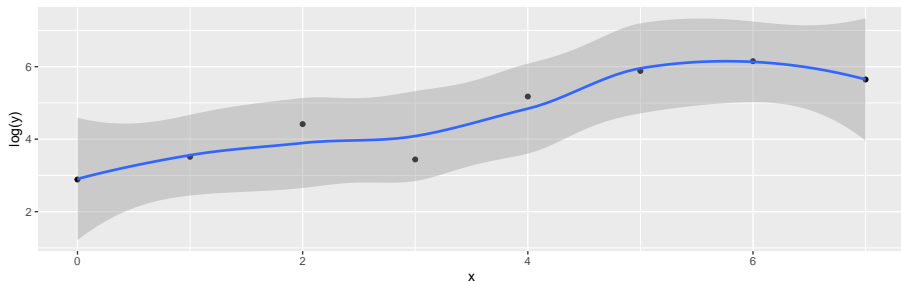
## Comments

- $\lambda$  (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  $\lambda$  (here about 0.1).
- Outer dotted lines mark 95% CI for  $\lambda$ , 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  $\lambda$  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  $x$ s 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:

`timeds`: 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

`timeds` 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

```
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

```
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):

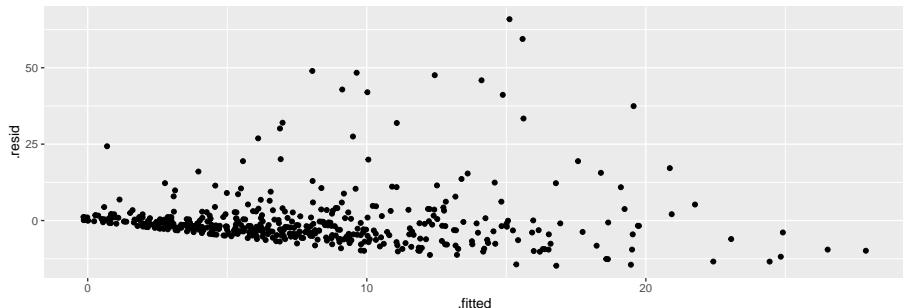
```
visits %>% select(-subjno) %>% cor()
```

	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)

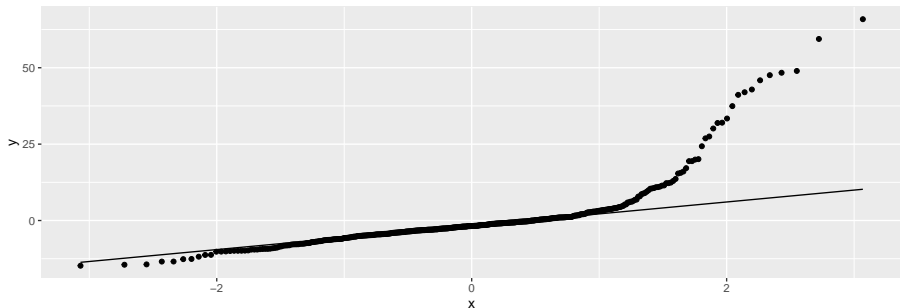
```
ggplot(visits.1, aes(x = .fitted, y = .resid)) + geom_point()
```



Apparently random. But...

## Normal quantile plot of residuals

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

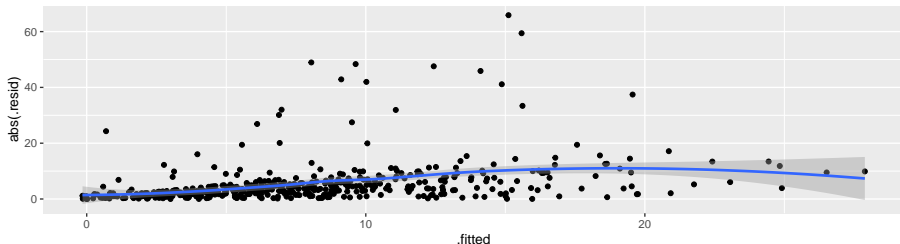


Not normal at all; upper tail is way too long.

# Absolute residuals

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

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



# Comments

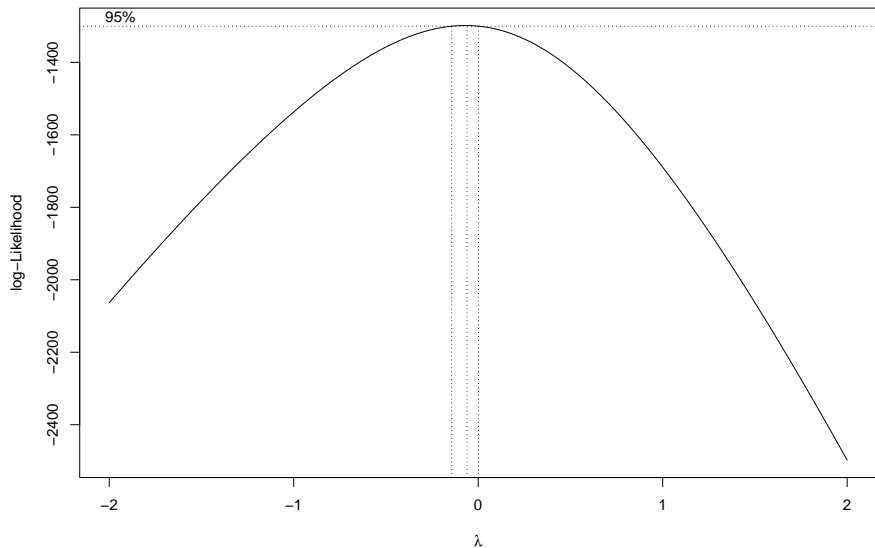
- On the normal quantile plot:
  - ▶ highest (most positive) residuals are way too high
  - ▶ distribution of residuals skewed to right (not normal at all)
- On plot of absolute residuals:
  - ▶ size of residuals getting bigger as fitted values increase
  - ▶ predictions getting more variable as fitted 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

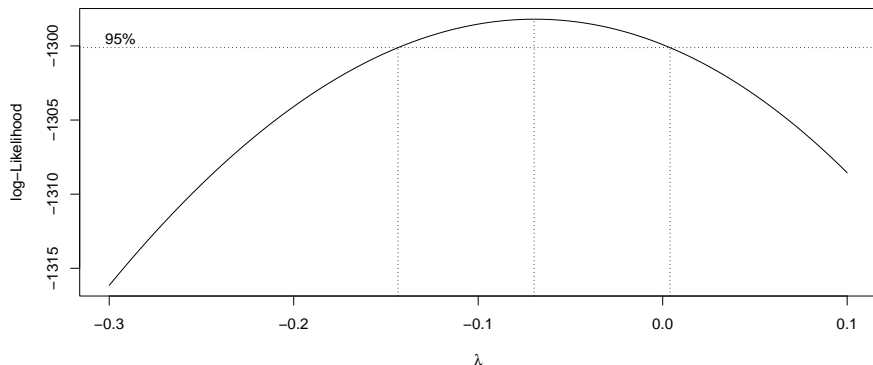
- Best:  $\lambda$  just less than zero.
- Hard to see scale.
- Focus on  $\lambda$  in  $(-0.3, 0.1)$ :

```
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:  $\lambda$  just about  $-0.07$ .
- CI for  $\lambda$  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

```
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

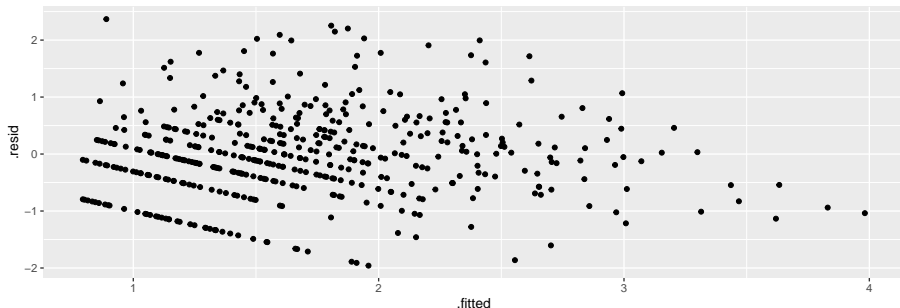
Residual standard error: 0.7625 on 461 degrees of freedom  
Multiple R-squared: 0.3682, Adjusted R-squared: 0.3641  
F-statistic: 89.56 on 3 and 461 DF, p-value: < 2.2e-16

# 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?

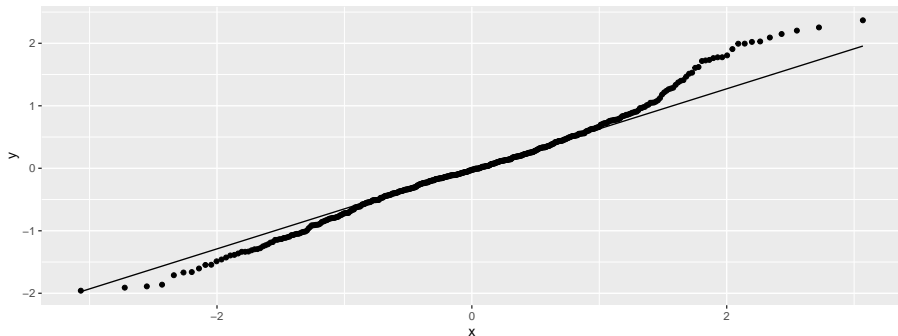
# Residuals against fitted values

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



# Normal quantile plot of residuals

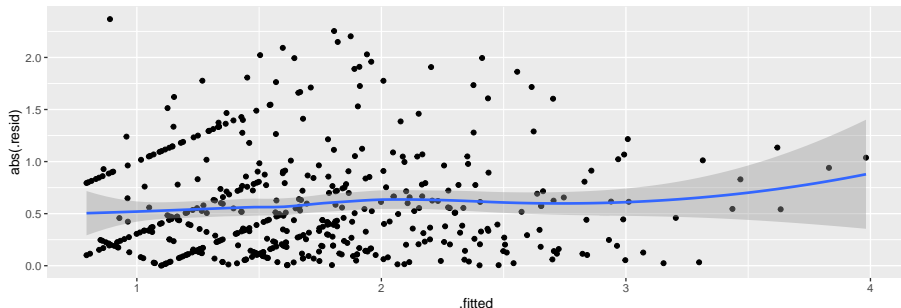
```
ggplot(visits.3, aes(sample = .resid)) + stat_qq() + stat_qq_l
```





# 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:

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

## Results of tests

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

### Analysis of Variance Table

Model 1:  $\log(\text{timedrs} + 1) \sim \text{stress}$

Model 2:  $\log(\text{timedrs} + 1) \sim \text{phyheal} + \text{menheal} + \text{stress}$

	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*:

```
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

```
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
```

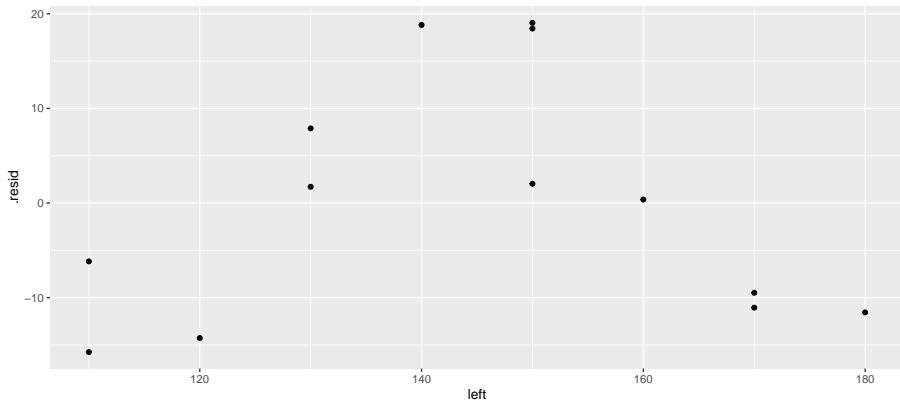
```
# A tibble: 13 x 10
```

	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

```
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.