

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) # for Box-Cox, later  
library(tidyverse)  
library(broom)  
library(marginaleffects)  
library(conflicted)  
conflict_prefer("select", "dplyr")
```

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

```
summary(sleep)
```

atst	age
Min. :461.8	Min. : 4.400
1st Qu.:491.1	1st Qu.: 7.200
Median :528.3	Median : 8.900
Mean :519.3	Mean : 9.058
3rd Qu.:532.5	3rd Qu.:11.100
Max. :586.0	Max. :14.000

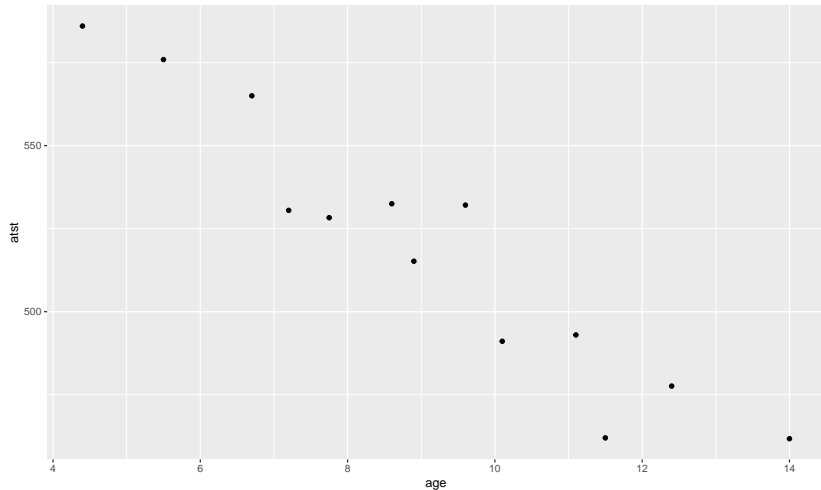
```
sleep
```

```
# A tibble: 13 x 2
```

	atst	age
	<dbl>	<dbl>
1	586	4.4
2	462.	14
3	491.	10.1
4	565	6.7

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)
```

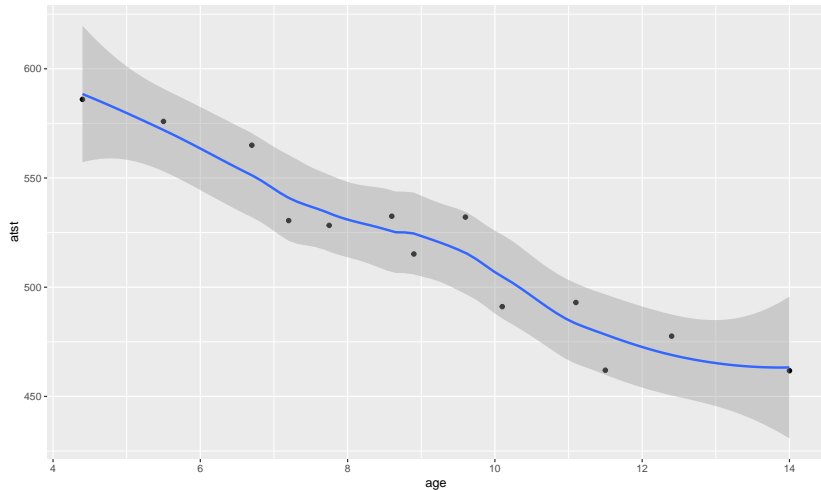
	atst	age
atst	1.0000000	-0.9515469
age	-0.9515469	1.0000000

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

Residual standard error: 12.15 on 11 degrees of freedom

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

```
#> #1: 1 new variable: .std.resid <dbl>
```

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
```

	atst	age
1	519.3038	10
2	519.3038	5

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	576.2781	563.2588	589.2974	5
2	506.0729	498.4899	513.6558	10

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) %>% select(-atst)
```

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

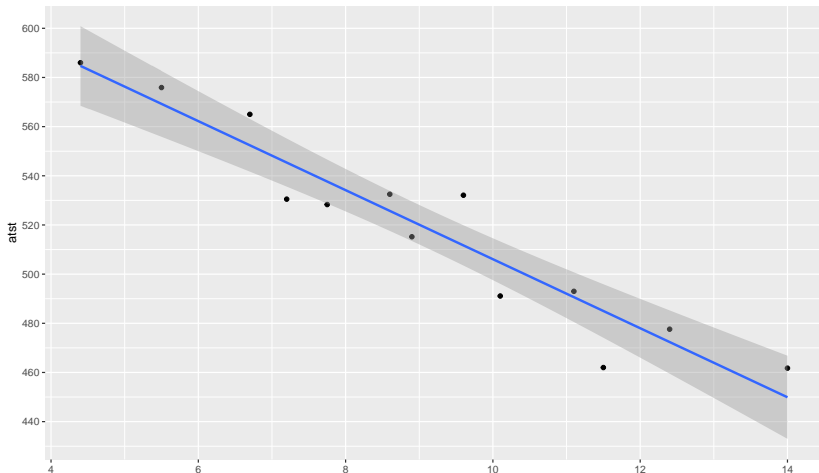
Comments

- ▶ 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

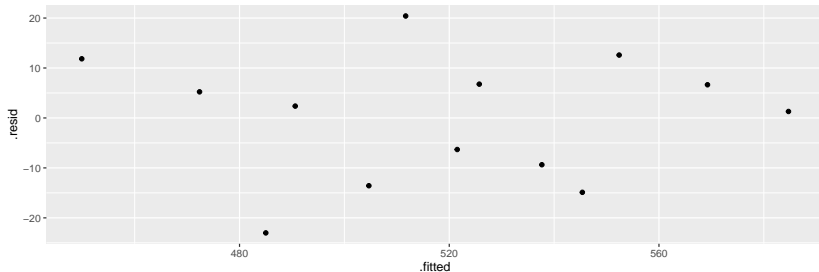
How to tell whether a straight-line regression is appropriate?

- ▶ 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
```



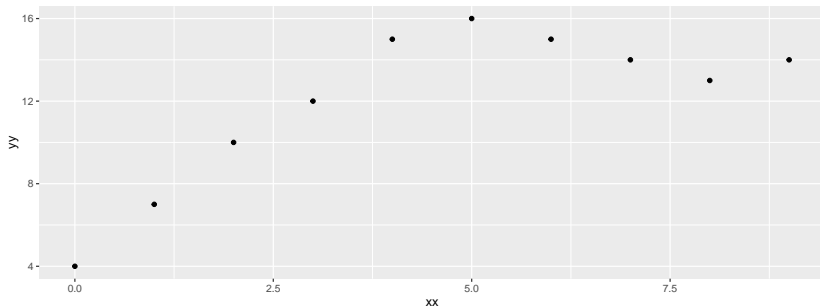
An inappropriate regression

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

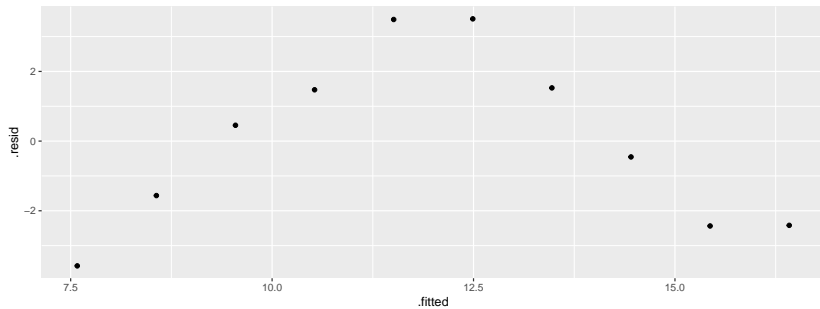
Residual standard error: 2.657 on 8 degrees of freedom

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

```
tidy(curvy.2)
```

```
# A tibble: 3 x 5
```

	term <chr>	estimate <dbl>	std.error <dbl>	statistic <dbl>	p.value <dbl>
1	(Intercept)	3.9	0.773	5.04	0.00149
2	xx	3.74	0.400	9.36	0.0000331
3	I(xx^2)	-0.307	0.0428	-7.17	0.000182

```
glance(curvy.2) #
```

```
# A tibble: 1 x 12
```

	r.squared <dbl>	adj.r.squared <dbl>	sigma <dbl>	statistic <dbl>	p.value <dbl>	df <dbl>
1	0.950	0.936	0.983	66.8	0.0000275	2

```
# i 6 more variables: logLik <dbl>, AIC <dbl>, BIC <dbl>,  
# deviance <dbl>, df.residual <int>, nobs <int>
```

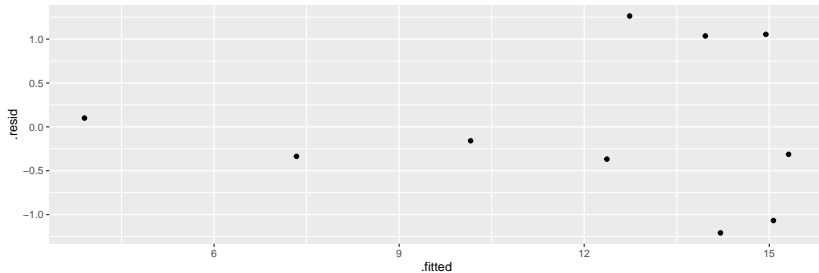
Comments

- ▶ 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 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

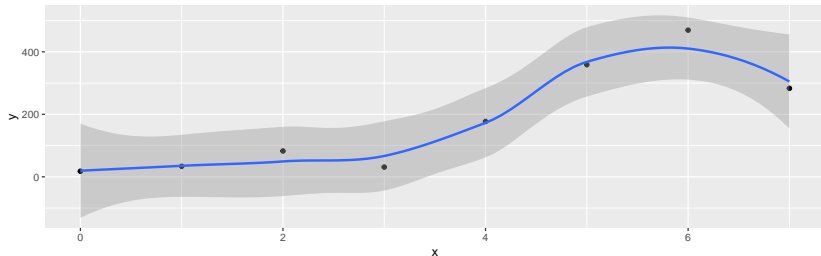
```
my_url <- "http://ritsokiguess.site/datafiles/madeup2.csv"
madeup <- read_csv(my_url)
madeup
```

```
# 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()
```

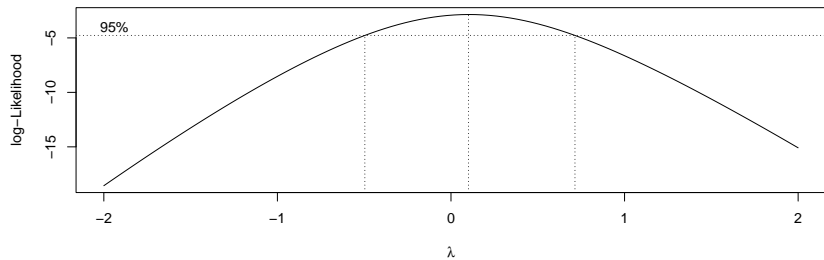


Running Box-Cox

- ▶ `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



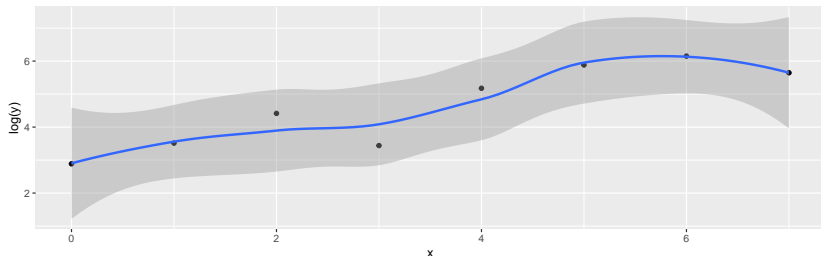
Comments

- ▶ 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)
glance(madeup.1)
```

```
# A tibble: 1 x 12
```

	r.squared	adj.r.squared	sigma	statistic	p.value	df
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	0.811	0.779	0.588	25.7	0.00228	1

```
# i 6 more variables: logLik <dbl>, AIC <dbl>, BIC <dbl>,  
# deviance <dbl>, df.residual <int>, nobs <int>
```

```
tidy(madeup.1)
```

```
# A tibble: 2 x 5
```

	term	estimate	std.error	statistic	p.value
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
1	(Intercept)	3.03	0.379	7.98	0.000206
2	x	0.460	0.0907	5.07	0.00228

R-squared now decently high.

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:

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

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

Call:

```
lm(formula = timedrs ~ phyheal + menheal + stress, data = v
```

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	***

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

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):

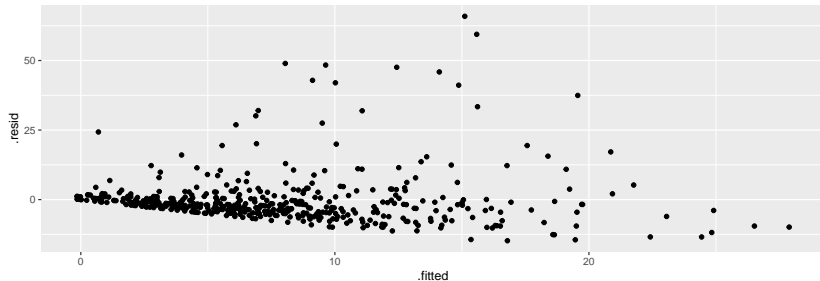
```
visits %>% select(-subjno) %>% cor()
```

	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)

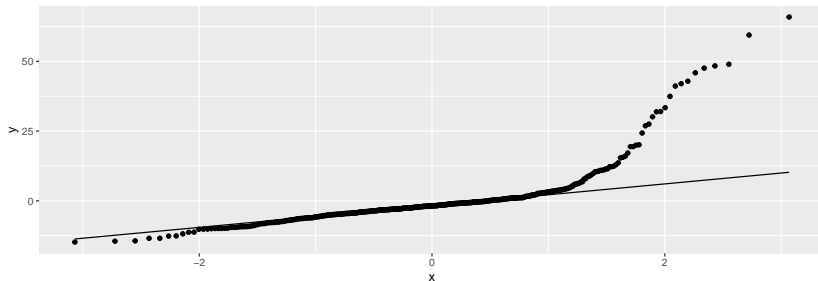
```
ggplot(visits.1, aes(x = .fitted, y = .resid)) + geom_point
```



Apparently random. But...

Normal quantile plot of residuals

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

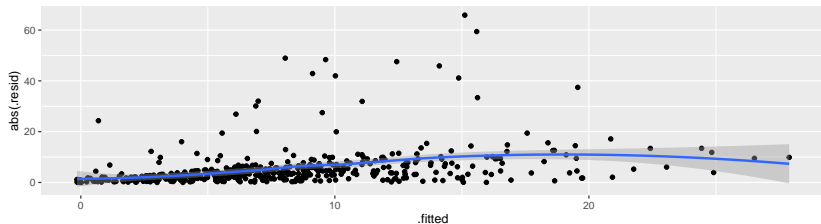


Not normal at all; upper tail is way too long.

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

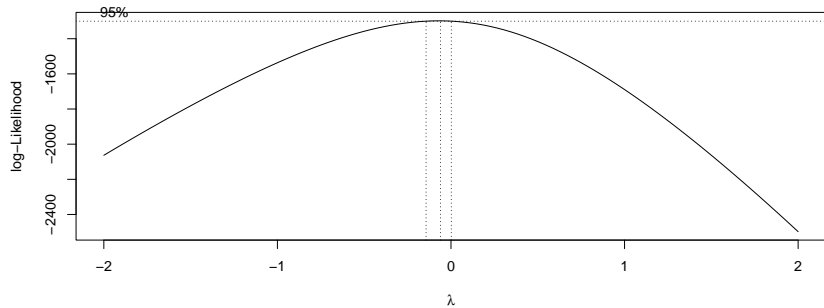
- ▶ On the normal quantile plot:
 - ▶ highest (most positive) residuals are *way* too high
 - ▶ distribution of residuals skewed to right (not normal at all)
- ▶ On plot of absolute residuals:
 - ▶ size of residuals getting bigger as fitted values increase
 - ▶ predictions getting more variable as fitted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

Try 1



Comments on try 1

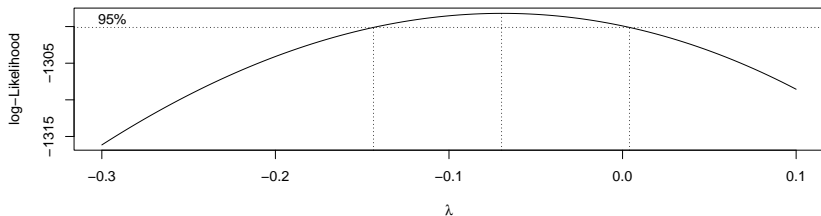
- ▶ Best: λ just less than zero.
- ▶ Hard to see scale.
- ▶ Focus on λ in $(-0.3, 0.1)$:

```
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 + stres  
  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

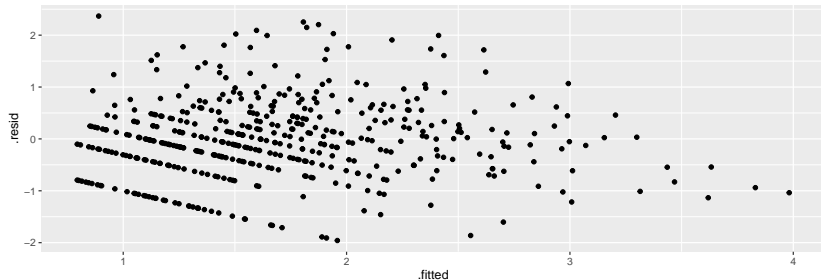
F-statistic: 89.56 on 3 and 461 DF, p-value: < 2.2e-16

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?

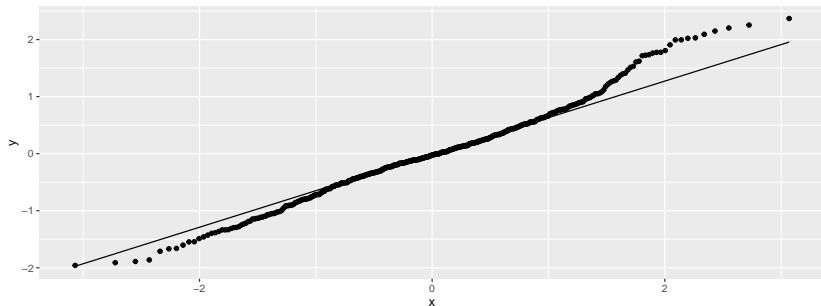
Residuals against fitted values

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



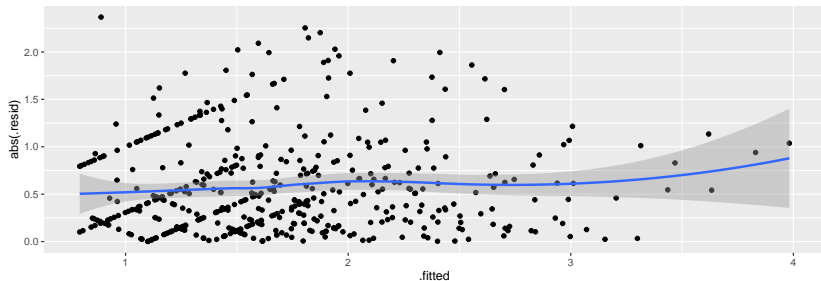
Normal quantile plot of residuals

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



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:

left	right	punt	fred
170	170	162.50	171
130	140	144.0	136
170	180	174.50	174
160	160	163.50	161
150	170	192.0	159
150	150	171.75	151
180	170	162.0	174
110	110	104.83	111
110	120	105.67	114
120	130	117.58	126
140	120	140.25	129
130	140	150.17	136
150	160	165.17	154

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)
glance(punting.1)
```

```
# A tibble: 1 x 12
```

	r.squared	adj.r.squared	sigma	statistic	p.value	df
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	0.778	0.704	14.7	10.5	0.00267	3

```
# i 6 more variables: logLik <dbl>, AIC <dbl>, BIC <dbl>,
# deviance <dbl>, df.residual <int>, nobs <int>
```

```
tidy(punting.1)
```

```
# A tibble: 4 x 5
```

	term	estimate	std.error	statistic	p.value
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>
1	(Intercept)	-4.69	29.1	-0.161	0.876
2	left	0.268	2.11	0.127	0.902
3	right	1.05	2.15	0.490	0.636
4	fred	-0.267	4.23	-0.0632	0.951

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)
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

Comparing R-squareds

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

```
[1] 0.7781401
```

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

```
[1] 0.7753629
```

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

Regression results

```
tidy(punting.2)
```

```
# A tibble: 2 x 5
```

	term <chr>	estimate <dbl>	std.error <dbl>	statistic <dbl>	p.value <dbl>
1	(Intercept)	-3.69	25.3	-0.146	0.886
2	right	1.04	0.169	6.16	0.0000709

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

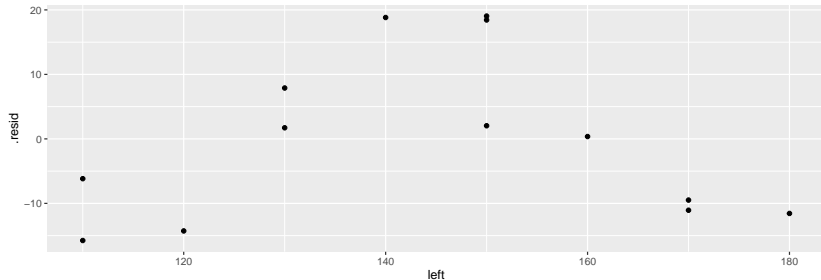
```
punting.2 %>% augment(punting) -> punting.2.aug  
punting.2.aug
```

```
# 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	162.	8.04	0.101	14.0

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.