

432 Class 13

<https://thomaseLove.github.io/432-2023/>

2023-02-28

Today's Agenda

① Evaluation of a Study through Retrospective Design

- Gelman and Carlin
- Type S and Type M errors
- The `retrodesign()` function

② Robust Linear Regression

- The **crimestat** data
- Using Huber weights
- Using bisquare weights (biweights)
- Quantile Regression on the Median

Today's R Setup

```
knitr::opts_chunk$set(comment = NA)

library(janitor)
library(knitr)
library(broom)
library(MASS) ## fitting robust linear models
library(quantreg) ## fitting quantile regressions
library(tidyverse)

theme_set(theme_bw())
```

Section 1

Evaluation through Retrospective Design

Reviewing “The Association Between Men’s Sexist Attitudes and Facial Hair” PubMed 26510427 (*Arch Sex Behavior* May 2016)

Headline Finding: A sample of ~500 men from America and India shows a significant relationship between sexist views and the presence of facial hair.

Excerpt 1:

Since a linear relationship has been found between facial hair thickness and perceived masculinity . . . we explored the relationship between facial hair thickness and sexism. . . . Pearson’s correlation found no significant relationships between facial hair thickness and hostile or benevolent sexism, education, age, sexual orientation, or relationship status.

Facial Hair and Sexist Attitudes

Excerpt 2:

We conducted pairwise comparisons between clean-shaven men and each facial hair style on hostile and benevolent sexism scores. . . . For the purpose of further analyses, participants were classified as either clean-shaven or having facial hair based on their self-reported facial hair style . . . There was a significant Facial Hair Status by Sexism Type interaction . . .

- So their headline finding appeared only because, after their first analysis failed, they shook and shook the data until they found something statistically significant.

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- So their headline finding appeared only because, after their first analysis failed, they shook and shook the data until they found something statistically significant.
- All credit to the researchers for admitting that they did this, but poor practice of them to present their result in the abstract to their paper without making this clear, and too bad that the journal got suckered into publishing this.

How should we react to this?

Gelman:

- Statisticians such as myself should recognize that the point of criticizing a study is, in general, to shed light on statistical errors, maybe with the hope of reforming future statistical education.
- Researchers and policymakers should not just trust what they read in published journals.

Assessing Type S (Sign) and Type M (Magnitude) Errors

- Gelman and Carlin *Psychological Science* 2014 9(6): 641-651.

Specifying effect sizes for power calculations

- ① **Empirical:** assuming an effect size equal to the estimate from a previous study or from the data at hand (if performed retrospectively).
 - generally based on small samples
 - when preliminary results look interesting, they are more likely biased towards unrealistically large effects
 - ② **On the basis of goals:** assuming an effect size deemed to be substantively important or more specifically the minimum effect that would be substantively important.
 - Can also lead to specifying effect sizes that are larger than what is likely to be the true effect.
- Both lead to performing studies that are too small or misinterpretation of findings after completion.

- The idea of a **design analysis** is to improve the design and evaluation of research, when you want to summarize your inference through concepts related to statistical significance.
- Type 1 and Type 2 errors are tricky concepts and aren't easy to describe before data are collected, and are very difficult to use well after data are collected.
- These problems are made worse when you have
 - Noisy studies, where the signal may be overwhelmed,
 - Small Sample Sizes
 - No pre-registered (prior to data gathering) specifications for analysis
- Top statisticians avoid “post hoc power analysis” ...
 - Why? It's usually crummy.

Why not post hoc power analysis?

So you collected data and analyzed the results. Now you want to do an after data gathering (post hoc) power analysis.

- ① What will you use as your “true” effect size?
 - Often, point estimate from data - yuck - results very misleading - power is generally seriously overestimated when computed on the basis of statistically significant results.
 - Much better (but rarer) to identify plausible effect sizes based on external information rather than on your sparkling new result.
- ② What are you trying to do? (too often)
 - get researcher off the hook (I didn't get $p < 0.05$ because I had low power - an alibi to explain away non-significant findings) or
 - encourage overconfidence in the finding.

Gelman and Carlin: Broader Design Ideas

- A broader notion of design, though, can be useful before and after data are gathered.

Gelman and Carlin recommend design calculations to estimate

- 1 Type S (sign) error - the probability of an estimate being in the wrong direction, and
 - 2 Type M (magnitude) error, or exaggeration ratio - the factor by which the magnitude of an effect might be overestimated.
- These can (and should) have value **both** before data collection/analysis and afterwards (especially when an apparently strong and significant effect is found.)
 - The big challenge remains identifying plausible effect sizes based on external information. Crucial to base our design analysis on an external estimate.

The Building Blocks

You perform a study that yields estimate d with standard error s . Think of d as an estimated mean difference, for example.

- Looks significant if $|d/s| > 2$, which roughly corresponds to $p < 0.05$. Inconclusive otherwise.

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- D is hypothesized based on *external* information (Other available data, Literature review, Modeling as appropriate, etc.)
- Define d^{rep} as the estimate that would be observed in a hypothetical replication study with a design identical to our original study.

Design Analysis (Gelman and Carlin)

From external information...

D : the true effect size

From the data (or model if prospective design)...

d : the observed effect

s : SE of the observed effect

p : the resulting p-value

Hypothetical replicated data

d^{rep} : the effect that would be observed in a hypothetical replication study with a design like the one used in the original study (so assumed also to have $\text{SE} = s$)



Design calculations:

- **Power**: the probability that the replication d^{rep} is larger (in absolute value) than the critical value that is considered to define “statistical significance” in this analysis.
- **Type S error rate**: the probability that the replicated estimate has the incorrect sign, if it is statistically significantly different from zero.
- **Exaggeration ratio (expected Type M error)**: expectation of the absolute value of the estimate divided by the effect size, if statistically significantly different from zero.

Figure 1. Diagram of our recommended approach to design analysis. It will typi-

Retrodesign function (shown on next slide)

Inputs to the function:

- D , the hypothesized true effect size (actually called A in the function)
- s , the standard error of the estimate
- α , the statistical significance threshold (default 0.05)
- df , the degrees of freedom (default assumption: infinite)

Output:

- the power
- the Type S error rate
- the exaggeration ratio

Retrodesign function (Gelman and Carlin)

```
retrodesign <- function(A, s, alpha=.05, df=Inf,
                        n.sims=10000){
  z <- qt(1-alpha/2, df)
  p.hi <- 1 - pt(z-A/s, df)
  p.lo <- pt(-z-A/s, df)
  power <- p.hi + p.lo
  typeS <- p.lo/power
  estimate <- A + s*rt(n.sims,df)
  significant <- abs(estimate) > s*z
  exaggeration <- mean(abs(estimate)[significant])/A
  return(list(power=power, typeS=typeS,
              exaggeration=exaggeration))
}
```

What if we have a beautiful, unbiased study?

Suppose the true effect that is 2.8 standard errors away from zero, in a study built to have 80% power for that effect with 95% confidence.

```
set.seed(201803161)
retrodesign(A = 28, s = 10, alpha = 0.05)
```

```
$power
[1] 0.7995569
```

```
$typeS
[1] 1.210843e-06
```

```
$exaggeration
[1] 1.12875
```

What if we have a beautiful, unbiased study?

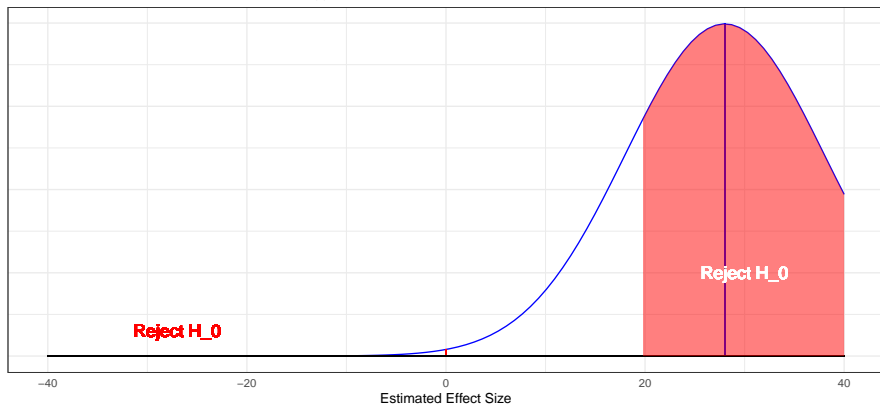
power	typeS	exaggeration
0.79956	1.2×10^{-6}	1.13

- With the power this high (80%), we have a type S error rate of 1.2×10^{-6} and an expected exaggeration factor of 1.13.
- Nothing to worry about with either direction of a statistically significant estimate and the overestimation of the magnitude of the effect will be small.
- What does this look like?

80% power; large effect (2.8 SE above H_0)

True Effect 2.8 SE above Null Hypothesis (Strong Effect)

Power = 80%, Risk of Type S error near zero, Exaggeration Ratio near 1



retrodesign for Zero Effect

```
set.seed(201803162)  
retrodesign(A = 0, s = 10)
```

```
$power  
[1] 0.05
```

```
$typeS  
[1] 0.5
```

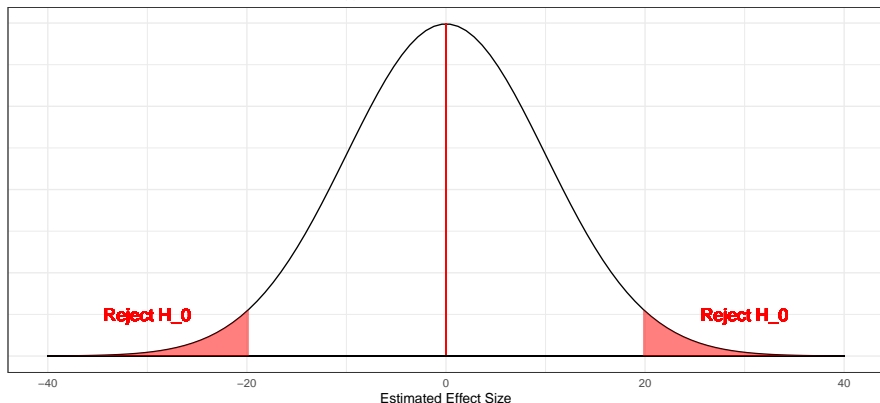
```
$exaggeration  
[1] Inf
```

- Power = 0.05, $\Pr(\text{Type S error}) = 0.5$, Exaggeration Ratio is infinite.

Power, Type S and Type M Errors: Zero Effect

True Effect At the Null Hypothesis

Power = 0.05, Type S error rate = 50% and infinite Exaggeration Ratio



Retrodesign for a true effect 1.2 SE above H_0

```
set.seed(201803163)  
retrodesign(A = 12, s = 10)
```

\$power

[1] 0.224427

\$typeS

[1] 0.003515367

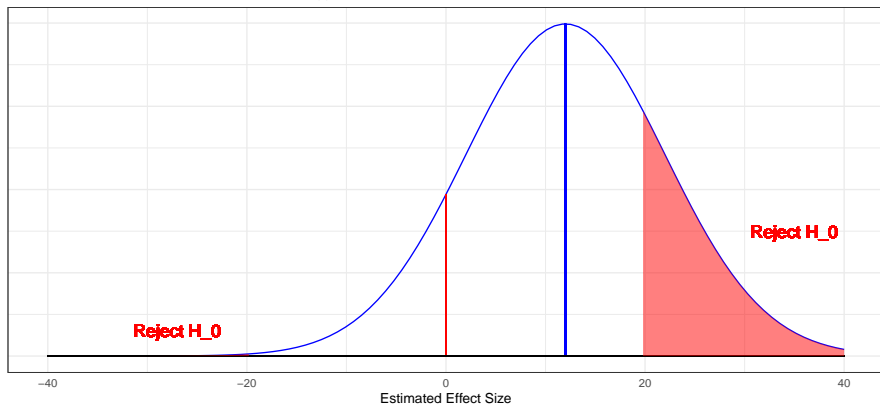
\$exaggeration

[1] 2.117846

What 22.4% power looks like...

True Effect 1.2 SE above Null Hypothesis

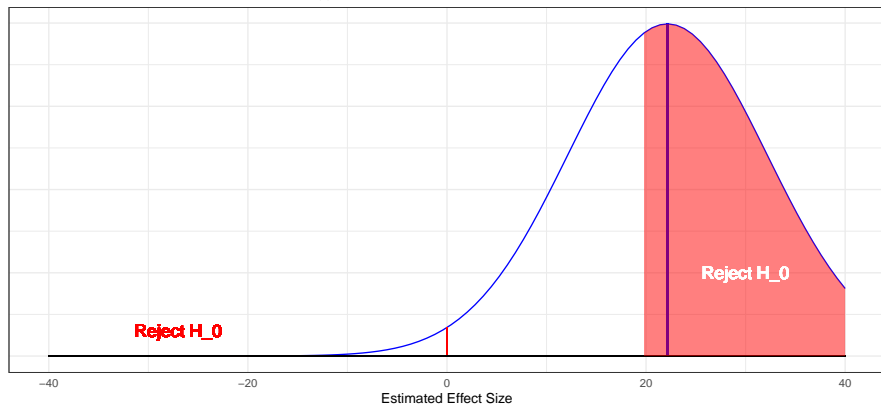
Power = 22.4%, Risk of Type S error is 0.004, Exaggeration Ratio is 2.12



What 60% Power Looks Like

True Effect 2.215 SE above Null Hypothesis

Power = 0.60, Risk of Type S error is <0.01%, Exaggeration Ratio is about 1.3



Gelman & Carlin, Figure 2

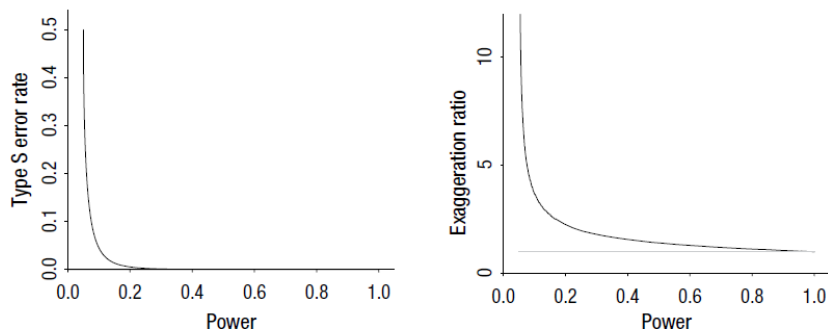


Figure 2. Type S error rate and exaggeration ratio as a function of statistical power for unbiased estimates that are normally distributed. If the estimate is unbiased, the power must be between 0.05 and 1.0, the Type S error rate must be less than 0.5, and the exaggeration ratio must be greater than 1. For studies with high power, the Type S error rate and the exaggeration ratio are low. But when power gets much below 0.5, the exaggeration ratio becomes high (that is, statistically significant estimates tend to be much larger in magnitude than true effect sizes). And when power goes below 0.1, the Type S error rate becomes high (that is, statistically significant estimates are likely to be the wrong sign).

Example: Beauty and Sex Ratios

Kanazawa study of 2972 respondents from the National Longitudinal Study of Adolescent Health

- Each subject was assigned an attractiveness rating on a 1-5 scale and then, years later, had at least one child.
- Of the first-born children with parents in the most attractive category, 56% were girls, compared with 48% girls in the other groups.
- So the estimated difference was 8 percentage points with a reported $p = 0.015$
- Kanazawa stopped there, but Gelman and Carlin don't.

Beauty and Sex Ratios

We need to postulate an effect size, which will not be 8 percentage points. Instead, Gelman and colleagues hypothesized a range of true effect sizes using the scientific literature.

There is a large literature on variation in the sex ratio of human births, and the effects that have been found have been on the order of 1 percentage point (for example, the probability of a girl birth shifting from 48.5 percent to 49.5 percent). Variation attributable to factors such as race, parental age, birth order, maternal weight, partnership status and season of birth is estimated at from less than 0.3 percentage points to about 2 percentage points, with larger changes (as high as 3 percentage points) arising under economic conditions of poverty and famine. (There are) reliable findings that male fetuses (and also male babies and adults) are more likely than females to die under adverse conditions.

So, what is a reasonable effect size?

- Small observed differences in sex ratios in a multitude of studies of other issues (much more like 1 percentage point, tops)
- Noisiness of the subjective attractiveness rating (1-5) used in this particular study

So, Gelman and colleagues hypothesized three potential effect sizes (0.1, 0.3 and 1.0 percentage points) and under each effect size, considered what might happen in a study with sample size equal to Kanazawa's study.

How big is the standard error?

- From the reported estimate of 8 percentage points and p value of 0.015, the standard error of the difference is 3.29 percentage points.
 - If p value = 0.015 (two-sided), then Z score = $\text{qnorm}(p = 0.015/2, \text{lower.tail}=\text{FALSE}) = 2.432$
 - $Z = \text{estimate}/\text{SE}$, and if estimate = 8 and $Z = 2.432$, then $\text{SE} = 8/2.432 = 3.29$

Retrodesign Results: Option 1

- Assume true difference $D = 0.1$ percentage point (probability of girl births differing by 0.1 percentage points, comparing attractive with unattractive parents).
- Standard error assumed to be 3.29, and $\alpha = 0.05$

```
set.seed(201803164)
retrodesign(A = 0.1, s = 3.29, alpha = 0.05)
```

```
$power
[1] 0.05010584
```

```
$typeS
[1] 0.4645306
```

```
$exaggeration
[1] 76.93614
```


Option 1 Conclusions

Assuming the true difference is 0.1 means that probability of girl births differs by 0.1 percentage points, comparing attractive with unattractive parents.

If the estimate is statistically significant, then:

- 1 There is a 46% chance it will have the wrong sign (from the Type S error rate).
- 2 The power is 5% and the Type S error rate of 46%. Multiplying those gives a 2.3% probability that we will find a statistically significant result in the wrong direction.
- 3 We thus have a power - 2.3% = 2.7% probability of showing statistical significance in the correct direction.
- 4 In expectation, a statistically significant result will be 78 times too high (the exaggeration ratio).

Retrodesign Results: Options 2 and 3

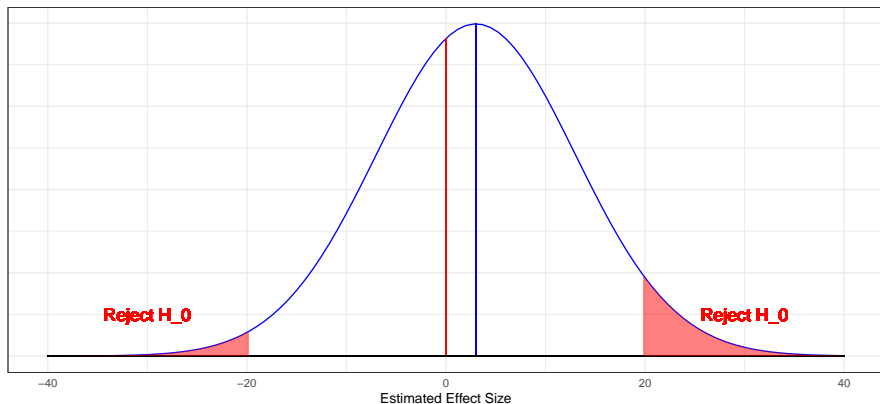
Assumption	Power	Type S	Exaggeration Ratio
$D = 0.1$	0.05	0.46	78
$D = 0.3$	0.05	0.39	25
$D = 1.0$	0.06	0.19	7.8

- Under a true difference of 1.0 percentage point, there would be
 - a 4.9% chance of the result being statistically significantly positive and a 1.1% chance of a statistically significantly negative result.
 - A statistically significant finding in this case has a 19% chance of appearing with the wrong sign, and
 - the magnitude of the true effect would be overestimated by an expected factor of 8.

What 6% power looks like...

True Effect 0.3 SE above Null Hypothesis

Power = 6%, Risk of Type S error is 20%, Exaggeration Ratio is 7.9



Gelman's Chief Criticism: 6% Power = D.O.A.

Their effect size is tiny and their measurement error is huge. My best analogy is that they are trying to use a bathroom scale to weigh a feather ... and the feather is resting loosely in the pouch of a kangaroo that is vigorously jumping up and down.



What to do?

In advance, **and** after the fact, think hard about what a plausible effect size might be.

Then...

- Analyze *all* your data.
- Present *all* your comparisons, not just a select few.
 - A big table, or even a graph, is what you want.
- Make your data public.
 - If the topic is worth studying, you should want others to be able to make rapid progress.

But I do studies with 80% power?

Based on some reasonable assumptions regarding main effects and interactions (specifically that the interactions are half the size of the main effects), you need **16 times** the sample size to estimate an interaction that you need to estimate a main effect.

And this implies a major, major problem with the usual plan of designing a study with a focus on the main effect, maybe even preregistering, and then looking to see what shows up in the interactions.

Or, even worse, designing a study, not finding the anticipated main effect, and then using the interactions to bail you out. The problem is not just that this sort of analysis is “exploratory”; it's that these data are a lot noisier than you realize, so what you think of as interesting exploratory findings could be just a bunch of noise.

- Gelman [2018-03-15](#)

Section 2

A New Topic: Introducing Robust Linear Regression Methods

The crimestat data

For each of 51 states (including the District of Columbia), we have the state's ID number, postal abbreviation and full name, as well as:

- **crime** - the violent crime rate per 100,000 people
- **poverty** - the official poverty rate (% of people living in poverty in the state/district) in 2014
- **single** - the percentage of households in the state/district led by a female householder with no spouse present and with her own children under 18 years living in the household in 2016

The crimestat data set

```
crimestat <- read_csv("c13/data/crimestat.csv",  
                      show_col_types = FALSE)  
  
crimestat
```

A tibble: 51 x 6

	sid	state	crime	poverty	single	state.full
	<dbl>	<chr>	<dbl>	<dbl>	<dbl>	<chr>
1	1	AL	427.	19.2	9.02	Alabama
2	2	AK	636.	11.4	7.63	Alaska
3	3	AZ	400.	18.2	8.31	Arizona
4	4	AR	480.	18.7	9.41	Arkansas
5	5	CA	396.	16.4	7.25	California
6	6	CO	309.	12.1	6.75	Colorado
7	7	CT	237.	10.8	8.04	Connecticut
8	8	DE	489.	13	6.52	Delaware
9	9	DC	1244.	18.4	8.41	District of Columbia
10	10	FL	540.	16.6	8.29	Florida

Modeling crime with poverty and single

Our main goal will be to build a linear regression model to predict **crime** using centered versions of both **poverty** and **single**.

```
crimestat <- crimestat |>
  mutate(pov_c = poverty - mean(poverty),
         single_c = single - mean(single))
```

Our original (OLS) model

Note the sneaky trick with the outside parentheses...

```
(mod1 <- lm(crime ~ pov_c + single_c, data = crimestat))
```

Call:

```
lm(formula = crime ~ pov_c + single_c, data = crimestat)
```

Coefficients:

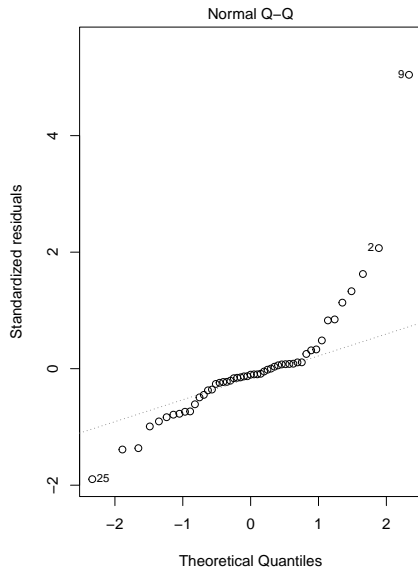
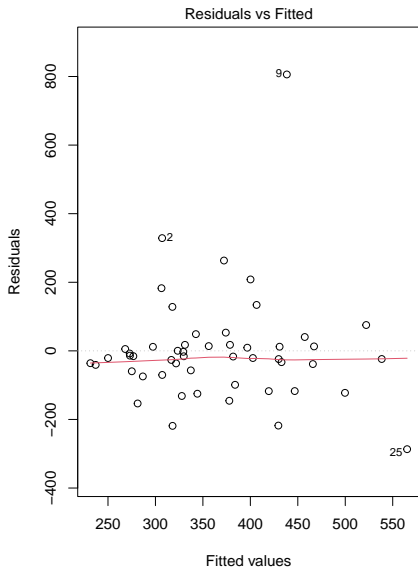
(Intercept)	pov_c	single_c
364.41	16.11	23.84

Coefficients?

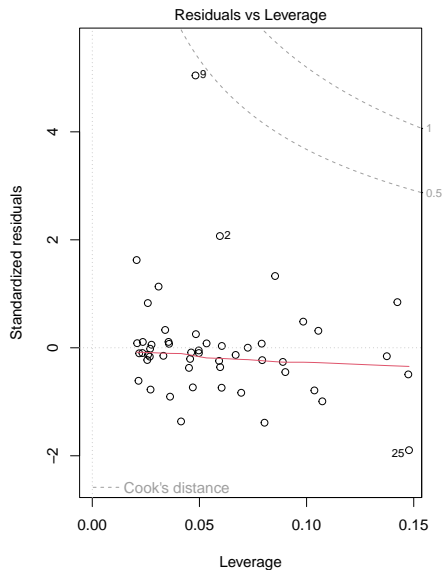
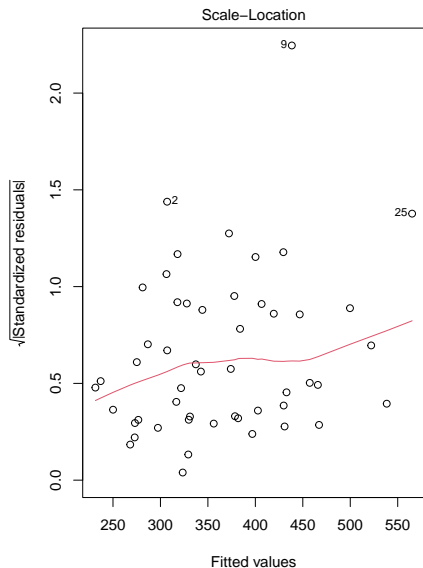
```
tidy(mod1, conf.int = TRUE) |>  
  select(term, estimate, std.error,  
         p.value, conf.low, conf.high) |>  
  kable(digits = 3)
```

term	estimate	std.error	p.value	conf.low	conf.high
(Intercept)	364.406	22.933	0.000	318.297	410.515
pov_c	16.115	9.616	0.100	-3.219	35.448
single_c	23.843	18.384	0.201	-13.121	60.807

OLS Residuals



Remaining Residual Plots from OLS



Which points are of special interest?

Several points show up in the residual plots.

```
crimestat |>  
  slice(c(2, 9, 25))
```

A tibble: 3 x 8

	sid	state	crime	poverty	single	state.full	pov_c
	<dbl>	<chr>	<dbl>	<dbl>	<dbl>	<chr>	<dbl>
1	2	AK	636.	11.4	7.63	Alaska	-3.47
2	9	DC	1244.	18.4	8.41	District of Columbia	3.53
3	25	MS	278.	21.9	11.4	Mississippi	7.03

Robust Linear Regression with Huber weights

There are several ways to do robust linear regression using M-estimation, including weighting using Huber and bisquare strategies.

- Robust linear regression here will make use of a method called iteratively re-weighted least squares (IRLS) to estimate models.
- M-estimation defines a weight function which is applied during estimation.
- The weights depend on the residuals and the residuals depend on the weights, so an iterative process is required.

We'll fit the model, using the default weighting choice: what are called Huber weights, where observations with small residuals get a weight of 1, and the larger the residual, the smaller the weight.

Our robust model (using MASS::rlm)

```
rob.huber <-  
  rlm(crime ~ pov_c + single_c, data = crimestat)
```

Summary of the robust (Huber weights) model

```
tidy(rob.huber) |>  
  kable(digits = 3)
```

term	estimate	std.error	statistic
(Intercept)	343.798	13.131	26.182
pov_c	11.910	5.506	2.163
single_c	30.987	10.527	2.944

Now, *both* predictors appear to have estimates that exceed twice their standard error. So this is a very different result than ordinary least squares gave us.

Glance at the robust model (vs. OLS)

```
glance(mod1)
```

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

	r.squ~1	adj.r~2	sigma	stati~3	p.value	df	logLik	AIC	BIC
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	0.197	0.163	164.	5.88	0.00518	2	-331.	670.	677.

```
# ... with 1 more variable: nobs <int>, and abbreviated variable names  
#   1: r.squared, 2: adj.r.squared, 3: statistic, 4: deviance.
```

```
glance(rob.huber)
```

```
# A tibble: 1 x 7
```

	sigma	converged	logLik	AIC	BIC	deviance	nobs
	<dbl>	<lgl>	<logLik>	<dbl>	<dbl>	<dbl>	<int>
1	59.1	TRUE	-331.3785	671.	678.	1314784.	51

Understanding the Huber weights a bit

Let's augment the data with results from this model, including the weights.

```
crime_with_huber <- augment(rob.huber, crimestat) |>
  mutate(w = rob.huber$w) |> arrange(w)

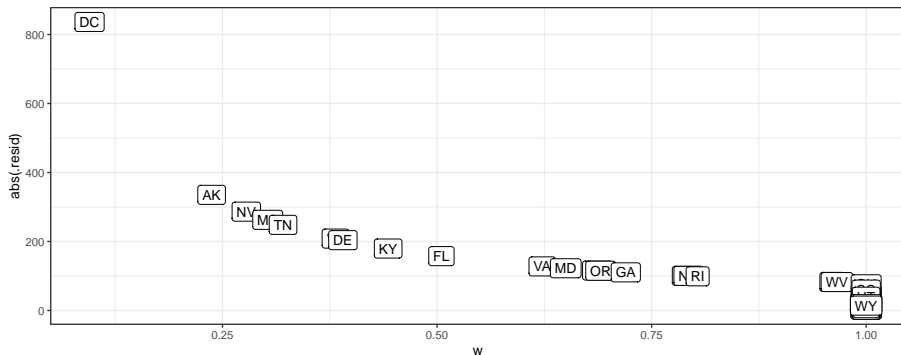
crime_with_huber |>
  select(sid, state, w, crime,
         pov_c, single_c, everything()) |>
  head()
```

A tibble: 6 x 15

	sid	state	w	crime	pov_c	singl~1	poverty	single	stat
	<dbl>	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<chr>
1	9	DC	0.0951	1244.	3.53	0.721	18.4	8.41	Dist
2	2	AK	0.237	636.	-3.47	-0.0588	11.4	7.63	Alas
3	29	NV	0.278	636.	0.527	-0.0288	15.4	7.66	Neva
4	25	MS	0.303	278.	7.03	3.67	21.9	11.4	Miss
5	43	TN	0.321	608.	3.33	-0.749	18.2	6.94	Tenn

Are cases with large residuals down-weighted?

```
ggplot(crime_with_huber, aes(x = w, y = abs(.resid))) +  
  geom_label(aes(label = state))
```



Conclusions from the Plot of Weights

- District of Columbia will be down-weighted the most, followed by Alaska and then Nevada and Mississippi.
- But many of the observations will have a weight of 1.
- In ordinary least squares, all observations would have weight 1.
- So the more cases in the robust regression that have a weight close to one, the closer the results of the OLS and robust procedures will be.

summary(rob.huber)

```
Call: rlm(formula = crime ~ pov_c + single_c, data = crimestat)
```

Residuals:

Min	1Q	Median	3Q	Max
-262.751	-45.641	1.762	36.732	836.244

Coefficients:

	Value	Std. Error	t value
(Intercept)	343.7982	13.1309	26.1823
pov_c	11.9098	5.5058	2.1631
single_c	30.9868	10.5266	2.9437

Residual standard error: 59.14 on 48 degrees of freedom

Robust Linear Regression with the biweight

As mentioned there are several possible weighting functions - we'll next try the **biweight**, also called the bisquare or Tukey's bisquare, in which all cases with a non-zero residual get down-weighted at least a little. Here is the resulting fit...

```
(rob.biweight <- rlm(crime ~ pov_c + single_c,  
                     data = crimestat, psi = psi.bisquare))
```

Call:

```
rlm(formula = crime ~ pov_c + single_c, data = crimestat, psi  
Converged in 13 iterations
```

Coefficients:

(Intercept)	pov_c	single_c
336.17015	10.31578	34.70765

Degrees of freedom: 51 total; 48 residual

Scale estimate: 67.3

Coefficients and Standard Errors

```
tidy(rob.biweight) |> kable(digits = 3)
```

term	estimate	std.error	statistic
(Intercept)	336.170	12.673	26.526
pov_c	10.316	5.314	1.941
single_c	34.708	10.160	3.416

Understanding the biweights weights a bit

Let's augment the data, as above

```
crime_with_biweights <-  
  augment(rob.biweight, newdata = crimestat) |>  
  mutate(w = rob.biweight$w) |>  
  arrange(w)  
  
head(crime_with_biweights, 3)
```

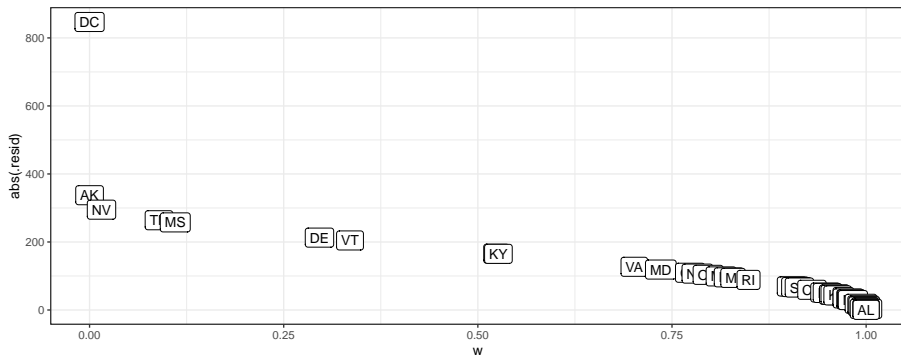
A tibble: 3 x 11

	sid	state	crime	poverty	single	state.~1	pov_c	singl~2	.fi
	<dbl>	<chr>	<dbl>	<dbl>	<dbl>	<chr>	<dbl>	<dbl>	<
1	2	AK	636.	11.4	7.63	Alaska	-3.47	-0.0588	
2	9	DC	1244.	18.4	8.41	Distric~	3.53	0.721	
3	29	NV	636.	15.4	7.66	Nevada	0.527	-0.0288	

... with abbreviated variable names 1: state.full, 2: single

Relationship of Weights and Residuals

```
ggplot(crime_with_biweights, aes(x = w, y = abs(.resid))) +  
  geom_label(aes(label = state))
```



Conclusions from the biweights plot

Again, cases with large residuals (in absolute value) are down-weighted generally, but here, Alaska and Washington DC receive no weight at all in fitting the final model.

- We can see that the weight given to DC and Alaska is dramatically lower (in fact it is zero) using the bisquare weighting function than the Huber weighting function and the parameter estimates from these two different weighting methods differ.
- The maximum weight (here, for Alabama) for any state using the biweight is still slightly smaller than 1.

summary(rob.biweight)

Call: `rlm(formula = crime ~ pov_c + single_c, data = crimestat`

Residuals:

Min	1Q	Median	3Q	Max
-257.58	-40.53	8.01	45.30	846.81

Coefficients:

	Value	Std. Error	t value
(Intercept)	336.1702	12.6733	26.5259
pov_c	10.3158	5.3139	1.9413
single_c	34.7077	10.1598	3.4162

Residual standard error: 67.27 on 48 degrees of freedom

Comparing OLS and the two weighting schemes

```
glance(mod1) |> select(1:6)
```

```
# A tibble: 1 x 6
```

	r.squared	adj.r.squared	sigma	statistic	p.value	df
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	0.197	0.163	164.	5.88	0.00518	2

```
glance(mod1) |> select(7:12)
```

```
# A tibble: 1 x 6
```

	logLik	AIC	BIC	deviance	df.residual	nobs
	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<int>
1	-331.	670.	677.	1287405.	48	51

Comparing OLS and the two weighting schemes

```
glance(rob.biweight) # biweights
```

```
# A tibble: 1 x 7
```

	sigma	converged	logLik	AIC	BIC	deviance	nobs
	<dbl>	<lgl>	<logLik>	<dbl>	<dbl>	<dbl>	<int>
1	67.3	TRUE	-331.8601	672.	679.	1339850.	51

```
glance(rob.huber) # Huber weights
```

```
# A tibble: 1 x 7
```

	sigma	converged	logLik	AIC	BIC	deviance	nobs
	<dbl>	<lgl>	<logLik>	<dbl>	<dbl>	<dbl>	<int>
1	59.1	TRUE	-331.3785	671.	678.	1314784.	51

Quantile Regression on the Median

We can use the `rq` function in the `quantreg` package to model the **median** of our outcome (violent crime rate) on the basis of our predictors, rather than the mean, as is the case in ordinary least squares.

```
rob.quan <- rq(crime ~ pov_c + single_c, data = crimestat)

glance(rob.quan)
```

```
# A tibble: 1 x 5
   tau logLik      AIC    BIC df.residual
<dbl> <logLik> <dbl> <dbl>         <int>
1   0.5 -315.7569  638.  643.           48
```


summary(rob.quan)

```
Call: rq(formula = crime ~ pov_c + single_c, data = crimestat)
```

```
tau: [1] 0.5
```

Coefficients:

	coefficients	lower bd	upper bd
(Intercept)	344.75658	336.94534	366.23603
pov_c	10.54757	3.06714	28.95962
single_c	32.27249	4.45889	48.18925

Estimating a different quantile ($\tau = 0.70$)

In fact, if we like, we can estimate any quantile by specifying the τ parameter (here $\tau = 0.5$, by default, so we estimate the median.)

```
(rob.quan70 <- rq(crime ~ pov_c + single_c, tau = 0.70,  
                  data = crimestat))
```

Call:

```
rq(formula = crime ~ pov_c + single_c, tau = 0.7, data = crimestat)
```

Coefficients:

(Intercept)	pov_c	single_c
379.72818	19.30376	32.15827

Degrees of freedom: 51 total; 48 residual

Comparing our Four Models

Estimating the Mean

	Fit	Intercept CI	pov_c CI	single_c CI
OLS		(318.6, 410.2)	(-3.13, 35.35)	(-12.92, 60.6)
Robust (Huber)		(320, 367.6)	(0.89, 22.93)	(9.93, 52.05)
Robust (biweight)		(310.7, 361.5)	(-0.3, 20.94)	(14.39, 55.03)

Note: CIs estimated for OLS and Robust methods as point estimate ± 2 standard errors

Estimating the Median

	Fit	Intercept CI	pov_c CI	single_c CI
Quantile (Median) Reg		(336.9, 366.2)	(3.07, 28.96)	(4.46, 48,19)

Comparing AIC and BIC

	Fit	AIC	BIC
OLS		669.7	677.4
Robust (Huber)		670.8	678.5
Robust (biweight)		671.7	679.4
Quantile (median)		637.5	643.3

Some General Thoughts

- ① When comparing the results of a regular OLS regression and a robust regression for a data set which displays outliers, if the results are very different, you will most likely want to use the results from the robust regression.
 - Large differences suggest that the model parameters are being highly influenced by outliers.
- ② Different weighting functions have advantages and drawbacks.
 - Huber weights can have difficulties with really severe outliers.
 - Bisquare weights can have difficulties converging or may yield multiple solutions.
 - Quantile regression approaches have some nice properties, but describe medians (or other quantiles) rather than means.