Monte Carlo Simulation and Resampling

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Resampling

- Resampling methods share many similarities to Monte Carlo simulations – in fact, some refer to resampling methods as a type of Monte Carlo simulation.
- Resampling methods use a computer to generate a large number of simulated samples.
- Patterns in these samples are then summarized and analyzed.
- However, in resampling methods, the simulated samples are drawn from the existing sample of data you have in your hands and NOT from a theoretically defined (researcher defined) DGP.
- Thus, in resampling methods, the researcher DOES NOT know or control the DGP, but the goal of learning about the DGP remains.

Resampling Principles

- Begin with the assumption that there is some population DGP that remains unobserved.
- That DGP produced the one sample of data you have in your hands.
- Now, draw a new "sample" of data that consists of a different mix of the cases in your original sample. Repeat that many times so you have a lot of new simulated "samples."
- The fundamental assumption is that all information about the DGP contained in the original sample of data is also contained in the distribution of these simulated samples.
- If so, then resampling from the one sample you have is equivalent to generating completely new random samples from the population DGP.

Resampling Principles (2)

- Another way to think about this is that if the sample of data you have in your hands is a reasonable representation of the population, then the distribution of parameter estimates produced from running a model on a series of resampled data sets will provide a good approximation of the distribution of that statistics in the population.
- Resampling methods can be parametric or non-parametric.
- In either type, but especially in the non-parametric case, yet another way to justify resampling methods according to Mooney (1993) is that sometimes it is, "$\cdots$ better to draw conclusions about the characteristics of a population strictly from teh sample at hand, rather than by making perhaps unrealistic assumptions about that population (p. 1)."

Common Resampling Techniques

- Bootstrap
- Jackknife
- Permutation/randomization tests
- Posterior sampling
- Cross-validation

The Bootstrap

- Formally introduced by Efron (1979).
- There are a variety of bootstrap methods, but at their core is a common process:
  - Begin with an observed sample of size N
  - Generate a simulated sample of size N by drawing observations from your observed sample independently and with replacement.
  - Compute and save the statistic of interest
  - Repeat this process many times (e.g. 1,000)
  - Treat the distribution of your estimated statistics of interest as an estimate of the population distribution of that statistic.

Key Features of the Bootstrap

- The draws must be independent – each observation in your observed sample must have an equal chance of being selected.
  - If observations in the original sample are NOT independent, then the resampling must accommodate that – more later.
- The simulated samples must be of size N to take full advantage of the information in the sample.
- Resampling must be done with replacement. If not, then every simulated sample of size N would be identical to each other and to the original sample.
- Resampling with replacement means that in any give simulated sample, some cases might appear more than once while others will not appear at all.

Sampling With/Without Replacement

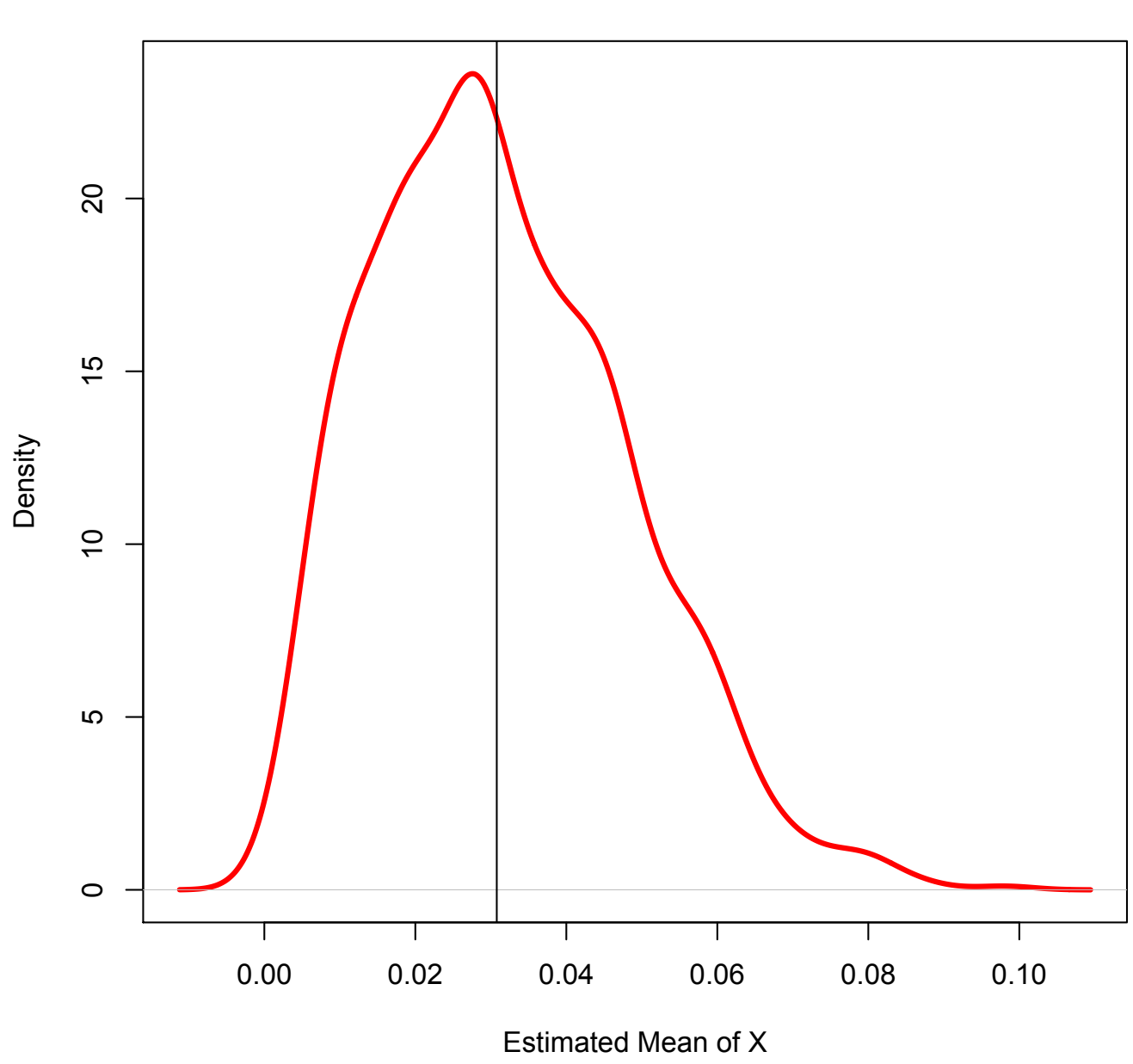
```
> set.seed(61893)
> Names <- c("Jeffrey","Sung-Geun","William","Andrew",
 "Michael","Kate","Rosie","Ahmed","Jeff","Tom")
> N <- length(Names)
>
> sample(Names,N,replace=FALSE)
 [1] "Sung-Geun" "William"   "Tom"       "Michael"   "Jeffrey"
 [6] "Andrew"    "Rosie"     "Jeff"      "Kate"      "Ahmed"
>
> sample(Names,N,replace=FALSE)
 [1] "Jeffrey"   "Andrew"    "Tom"       "William"   "Ahmed"
 [6] "Jeff"      "Sung-Geun" "Michael"   "Rosie"     "Kate"
>
> sample(Names,N,replace=TRUE)
 [1] "Tom"       "Tom"       "Kate"      "Jeff"      "Sung-Geun"
 [6] "Sung-Geun" "Michael"   "Andrew"    "Sung-Geun" "Ahmed"
>
> sample(Names,N,replace=TRUE)
 [1] "Sung-Geun" "Kate"      "William"   "Andrew"    "Kate"
 [6] "Jeff"      "Jeff"      "Sung-Geun" "William"   "Tom"
```

What to Resample?

- In the single variable case, you must resample from the data itself.
- However, in something like OLS, you have a choice.
- Remember the "X's fixed in repeated samples" assumption?
  - So, you can resample from the data, thus getting a new mix of X's and Y each time for your simulations.
  - Or you can leave the X's fixed, resample from the residuals of the model, and use those to generate simulated samples of Y to regress on the same fixed X's every time.
- As before, it depends on the validity of the "fixed in repeated samples" assumption, but also it is unlikely to matter in practice.
- Most folks resample from the data.

Simple Example

- Let's suppose I draw a sample of 10 folks and compute a mean.
- I could make a distributional assumption about that mean, compute a standard error, and treat that as my best guess of the population mean and its variance.
- Or In can draw lots of resamples, compute a mean for each one of them, and then plot that distribution


Bootstrap Sim of Mean, N=10
Density
0
5
10
15
20
0.00
0.02
0.04
0.06
0.08
0.10
Estimated Mean of X

What Did We Learn?

- The distribution of simulated sample means is close to centered on our original sample estimate.
- But the distribution is not normal, and not even symmetric.
- A Bootstrap standard error would probably be better to use than an analytic one that assumed a normal distribution.
- So, how do we compute a Bootstrap standard error – and more importantly, a Bootstrap confidence interval?
- There are multiple ways

Standard Normal Bootstrap CI

- This is the simplest method, mirrors the fully analytic method of computing confidene intervals, and is parametric.
- It is parametric because it assumes that the statistic of interest is distributed normally.
- You generate a large simulated sample of the parameter of interest (e.g. a mean, a regression coefficient, etc.)
- Since the SE of a parameter is defined as the standard deviation of that parameter in multiple samples, you compute a simulated SE as just the the standard deviation of your simulated parameters.
- A 95% CI is just your original sample parameter estimate plus/minus 1.96 times your estimated SE.

Standard Normal Bootstrap CI (2)

- The advantage is its simplicity.
- The disadvantage is that it makes a distributional assumption that may not be appropriate. If normality is a good assumption, the analytic calculation may be appropriate.
- This also implicitly assumes that your estimate of the parameter of interest is unbiased.

Percentile Bootstrap CI

- The Percentile version of the Bootstrap CI is noparametric.
- This approach uses the large number of simulated parameters of interest (e.g. means, medians, slope coefficients) and orders them from smallest to largest.
- A 95% CI is then computed by just identifying the lower CI as the 2.5^{th} percentile and the upper CI as the 97.5^{th} percentile.
- This leaves 95% of the simulated parameter estimates within this range while dividing the remaining 5% of the simulated values equally into the upper and lower tails.

Percentile Bootstrap CI (2)

- The advantage of this method is it does not make any distributional assumption – it does not even require the distribution (or the CI) to be symmetric.
- Of course, if a distributional assumption is appropriate and you don't use it, this approach uses less information.
- In addition, this method has been shown to be less accurate than it could be.
- Still, this is the most common way to compute a Bootstrap CI.
- Side Note: This approach parallels what Bayesians do when the compute what they call "Credible Intervals."

Other Bootstrap CI Methods

- The Basic Bootstrap CI: The simulated parameters are adjusted by subtracting out the observed statistic, and then the percentile method is applied.
- The Bootstrap t CI: for each simulation you compute the sample t statistic each time. Select the 2.5^{th} and 97.5^{th} percentile t-scores. Use those to multiply by the simulated SE (instead of $\pm$ 1.96).
- The BCa Bootstrap CI: This method modifies the percentile CI to correct for bias and for skewness. Simulation works suggests better performance than the unadjusted percentile CI.
- Which to use? How to compute them?

Which CI Method to Use?

- All five are available in the `boot` package in `R` by first computing the simulated parameters and then using the `boot.ci()` function. See the Lab.
- The first two are pretty simple to program yourself.
- They all converge toward toward the true population distribution of the parameter in question as:
  - the original sample size increases toward infinity
  - the number of resamples you draw increases toward infinity (If the original sample is "large enough")
- Rules of Thumb: Replications of 1,000, sample size of 30-50 is no problem, but smaller can work if the sample is not too "odd."

Does this Always Work?

- To some, the bootstrap seems like magic.
- However, it is still fundamentally dependent on the quality of the original sample you have in your hands.
- If the original sample is not representative of the population, the simulated distribution of any statistics computed from that sample will also probably not accurately reflect the population. (Small samples, biased samples, or bad luck)
- Also, the bootstrap simulated distribution of a sample statistic is necessarily discrete, whereas often the underlying population PDF is continuous. They converge as sample size increases, but the simulated distribution remains discrete.
- Nothing is perfect!

Bootstrapping Complex Data

- Resampling one observation at a time with replacement assumes the data points in your observed sample are independent. If they are not, the simple bootstrap will not work.
- Fortunately the bootstrap can be adjusted to accommodate the dependency structure in the original sample.
- If the data is clustered (spatially correlated, multi-level, etc.) the solution is to resample clusters of observations one at a time with replacement rather than individual observations.
- If the data is time-serial dependent, this is harder because any sub-set you select still "breaks" the dependency in the sample, but methods are being developed.

When Does it Not Work Well?

- Data with serial correlation in the residual (as noted in the last slide).
- Models with heteroskedasticity (other than unit-specific a la clustered data) when the form of the heteroskedasticity is unknown. One approach here is to sample pairs (on Y and X) rather than leaving X fixed in repeated samples.
- Simultaneous equation models (because you have to bootstrap all of the endogenous variables in the model).

An Example

- Londregan and Snyder (1994) compare the preferences of legislative committees with the entire legislative chamber to test if committees are preference outliers.
- Competing theories:
  - Committees will be preference outliers due to self-selection and candidate-centered incentive to win re-election.
  - Committees will NOT be preference outliers because the floor assigns members to develop expertise for the floor to follow.
- Empirical work is mixed – What are the problems?
- Ideology scores are measured with error, but that error is ignored.
- Too many use analytic tests on two-sample differences of means when they should use non-parametric tests (e.g. bootstraps) on differences of medians.

Londregan and Snyder (cont.)

- Two-sample tests fail when there are more than two groups and some people are part of more than one group.
- Two-sample tests treat all heterogeneity on a committee as sampling error.
- Theory is about the median voter, but sample means tests do not fit that theory.
- Between measurement error issues and concerns about the statistical properties of medians, the resampled among legislators to estimate committee and floor medians, and then how far apart they'd have to be to be considered "significantly" different.
- Results

FIGURE 1
Comparison of Committee and Floor Medians in the U.S. House, 82d-98th Congress, for the Heterogeneous Preferences and Two-Type Models
(preferences measured with Poole-Rosenthal NOMINATE scores)

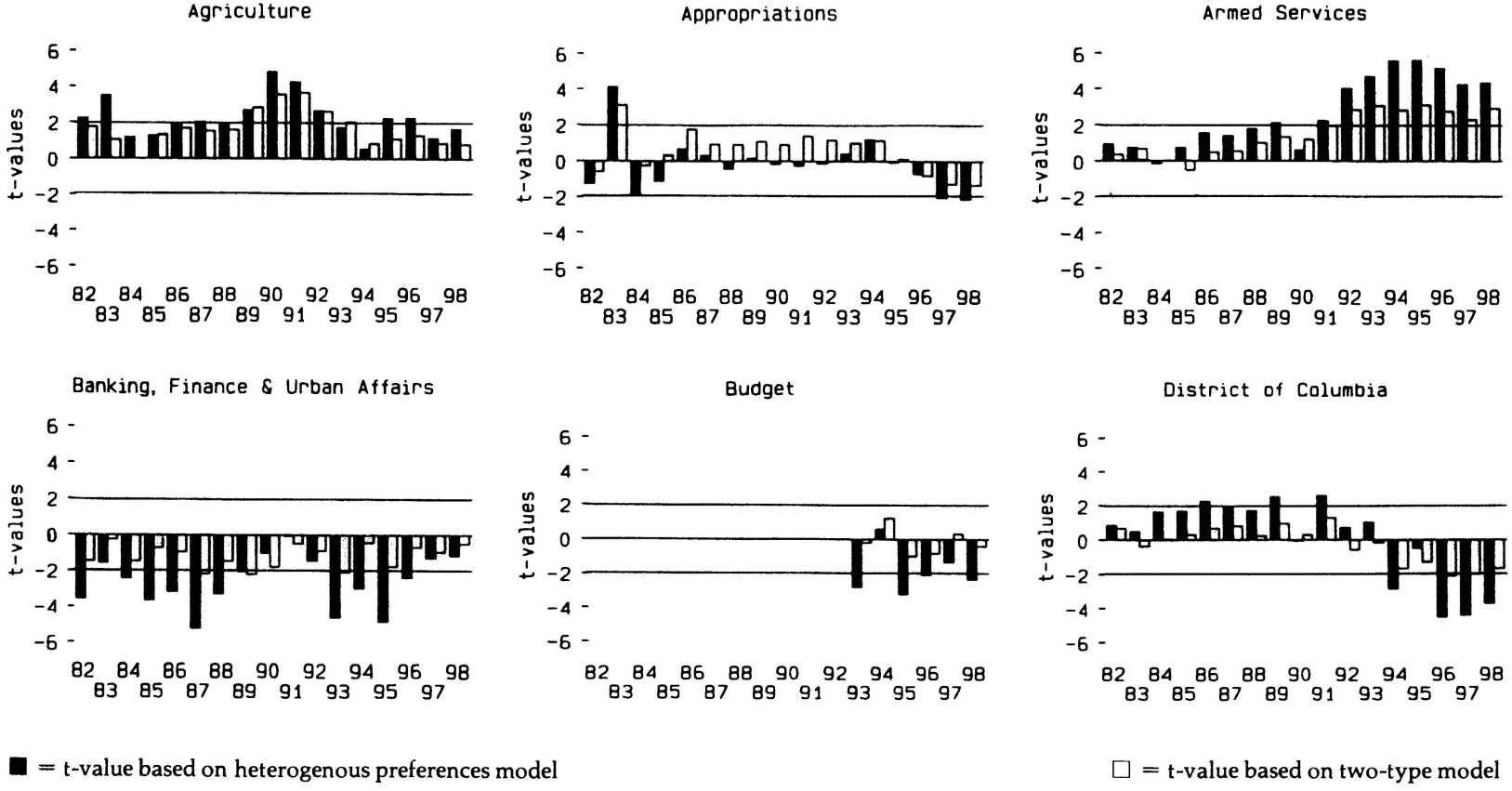


Fig1.pdf

One More Example

- Benoit, Laver, and Mikhaylov (2009) analyze texts of the Comparative Manifesto Project (CMP), which uses party manifestos to measure ideological locations.
- Current methods fail to consider measurement error in these types of measures.
- Use bootstraps to estimate this variability so it can be accounted for in subsequent regression models.
- The CMP data is extremely influential.

Benoit et al (cont.)

- Use a bootstrap to estimate uncertainty, then use methods that accommodate uncertainty.
- They find that many reported differences between parties are probably not real differences, but rather due to random noise in the measures that others Failed to consider.
- Example of French Parties: You find out that the Communist, Socialist, Green, and Union for a Popular Movement parties are probably not statistically significantly different from each other. Only the far-right National Front is clearly different.

FIGURE 3 **Left-Right Placement of the Major French Parties in 2002. Bars Indicate 95% Confidence Intervals**

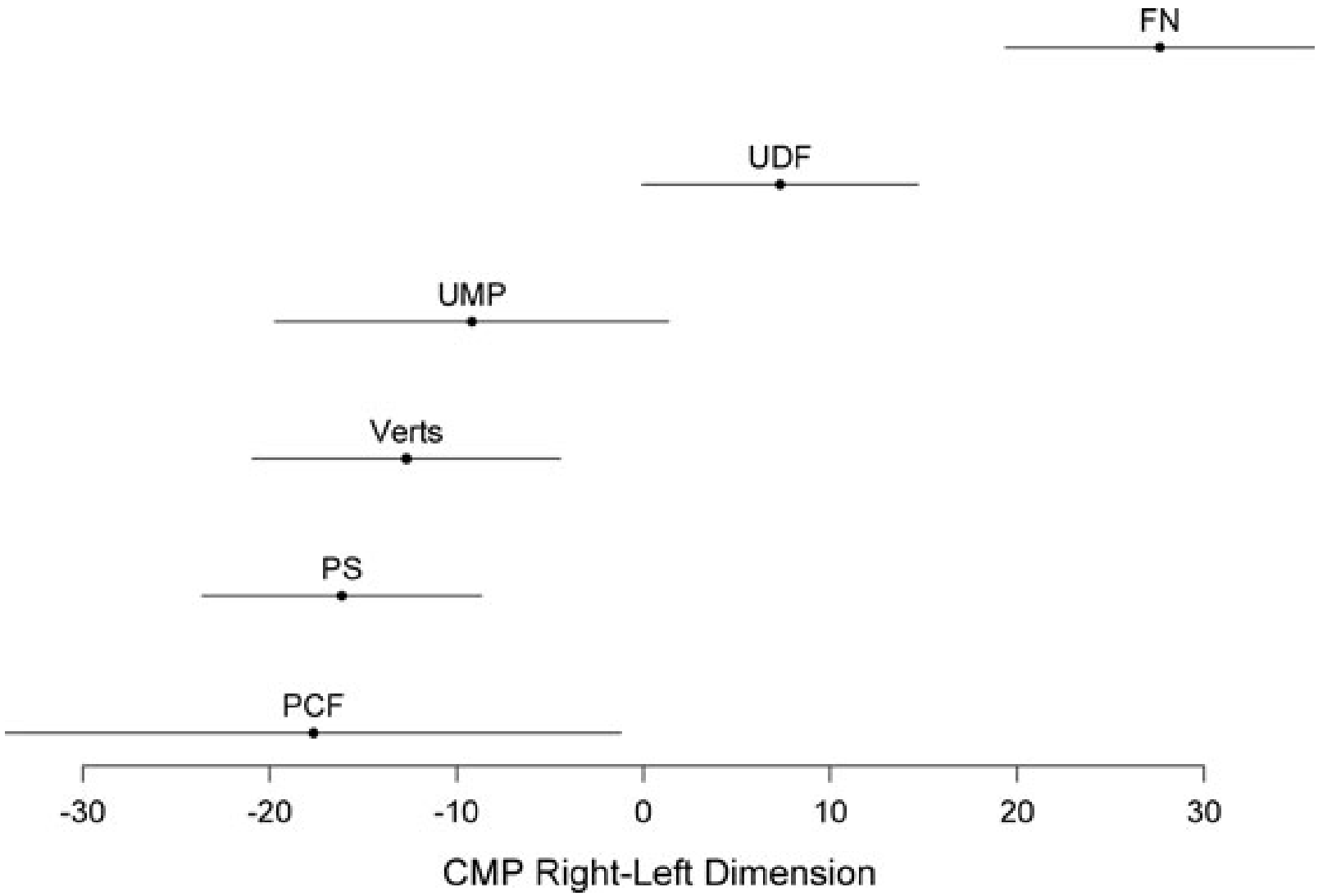


Fig1.pdf

The Jackknife

- The Jackknife emerged before the bootstrap.
- It's primary use has been to compute standard error and confidence intervals just like the bootstrap.
- It is a resampling method, but it is based on drawing n resamples each of size n-1 because each time you drop out a different observation.
- The notion is that each sub-sample provides an estimate of the parameter of interest on a sample that can easily be viewed as a random sample from the population (if the original sample was) since it only drops won case at a time.
- NOTE: You can leave out groups rather than individual observations if the sampling/data structure is complex (e.g. clustered data).

Jackknife (2)

- The jackknife is less general than the bootstrap, and thus, used less frequently.
- It does not perform well if the statistic under consideration does not change "smoothly" across simulated samples.
- It does not perform well in small samples because you don't end up generating many resamples.
- However, it is good at detecting outliers/influential cases. Those sub-sample estimates that differ most from the rest indicate those cases that has the most influence on those estimates in the original full sample analysis.

A Digression to Cook's D

- The jackknife works very similarly to Cook's Distance (or Cook's D), which is a measure of how influential individual observations are on statistical estimates (in OLS).

$$D_i = \frac{\sum(\hat{Y}_j - \hat{Y}_{ji})^2}{k \cdot \sigma^2} \tag{1}$$

- Where:
  - k = the number of parameters in the model
  - $\hat{Y}_j$ for j^{th} observation for full model
  - $\hat{Y}_{ji}$ for j^{th} observation after i^{th} observation has been dropped.
- Large values of D indicate influential points.
- "Large" = values greater than $4/(n-k-1)$ [n=sample size and k=number of parameters estimated in the model].
- Ler's see an example.

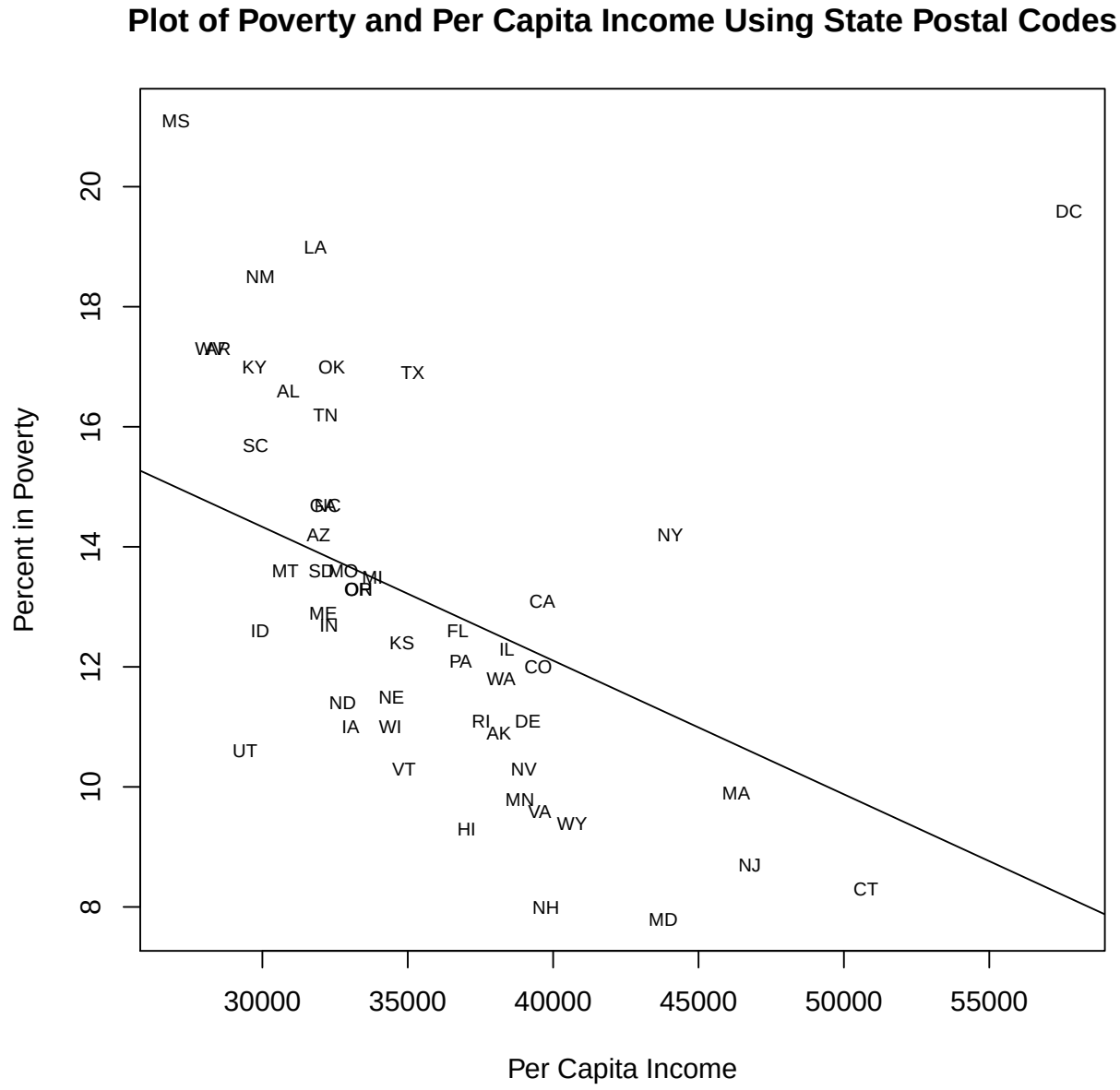


Figure: State Level Poverty Rate as a Function of Per Capita Income

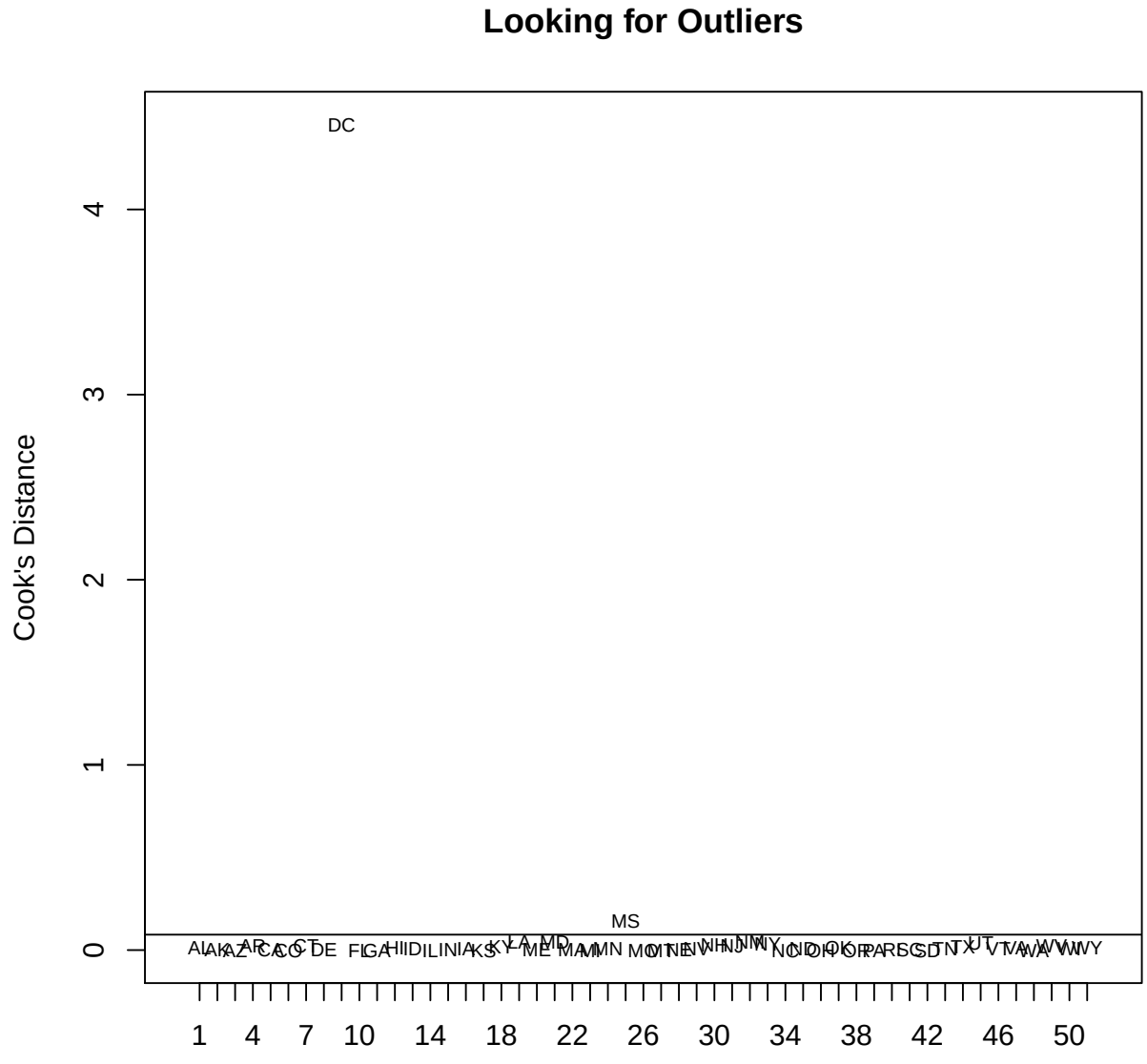


Figure: Cook's Distance Plot from Model of State Level Poverty Rate as a Function of Per Capita Income

Jackknife-after-Bootstrap

- Rizzo (2008, pp. 195-6) suggests combining the bootstrap and jackknife proceedures.
- First, you run the bootstrap to generate your bootstrap estimates of the parameter of interest.
- Then you run a jackkife by dropping all bootstrap samples that include the i^{th} observation, then summarizing across these jackknifed samples.
- The procedure is available in the `boot` package in `R` .

Permutation/Randomization

- Just another form of resampling, but in this case it is done *without replacement*.
- They have been around since Fisher introduced them in the 1930's.
- Often used to conduct hypothesis testing where the Null is zero.
- Rather than assume a distribution for the Null hypothesis, we simulate what it would be by randomly reconfiguring our sample lots of times (e.g. 1,000) in a way that "breaks" the relationship in our sample data.
- The question then is how often do these permutations or randomly reshuffled data sets produce a relationship as large or larger than the one we saw in our original sample?

Running a Permutation Experiment

- Suppose we are testing the difference in means between Men and Women on some variable.
- If we have N_M Men and N_W Women, such that $N = N_M + N_W$, then the total number of possible permutations where the first group equals the number of men and the total sample size stays the same is $\frac{(N_M+N_W)!}{N_M!N_W!}$
- Suppose we have a sample of 14 Men and 12 Women. If so then we have $\frac{(14+12)!}{14!12!} = 9,657,700$ possible permutations.
- Thus, in most settings, we randomly generate some of the possible permutations and call it good.

Additional Considerations

- Randomization tests do assume exchangeability. If the Null of no effect is true, the observed outcomes across individuals should be similar no matter what the level of the treatment (X) variable is.
- This is a weaker assumption than iid.
- If we do examine all possible permutations, that is often called a permutation test, or an exact test.
- If we just simulate a large number, it's called a randomization test.
- What do we reshuffle? Most reshuffle the treatment.

A Simple Example

- I have data on the weight of chicks and what they were fed.
- The samples are small, and the distributions unknown.
- Still, I want to know if their weights differ based on what they were fed.
- In a parametric world, I'd do a two-sample difference of means t-test
- But, that is only appropriate if the distributional assumption holds.

Randomization Example

```
attach(chickwts)

x <- sort(as.vector(weight[feed=="soybean"]))
y <- sort(as.vector(weight[feed=="linseed"]))

> x
 [1] 158 171 193 199 230 243 248 248 250 267 271 316 327 329
> y
 [1] 141 148 169 181 203 213 229 244 257 260 271 309
```

Are the Two Groups Different?

```
Sample.T <- t.test(x,y)
Sample.T

data:  x and y
t = 1.3246, df = 23.63, p-value = 0.198
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -15.48547  70.84262
sample estimates:
mean of x mean of y
 246.4286  218.7500
```

Setting Up the Test

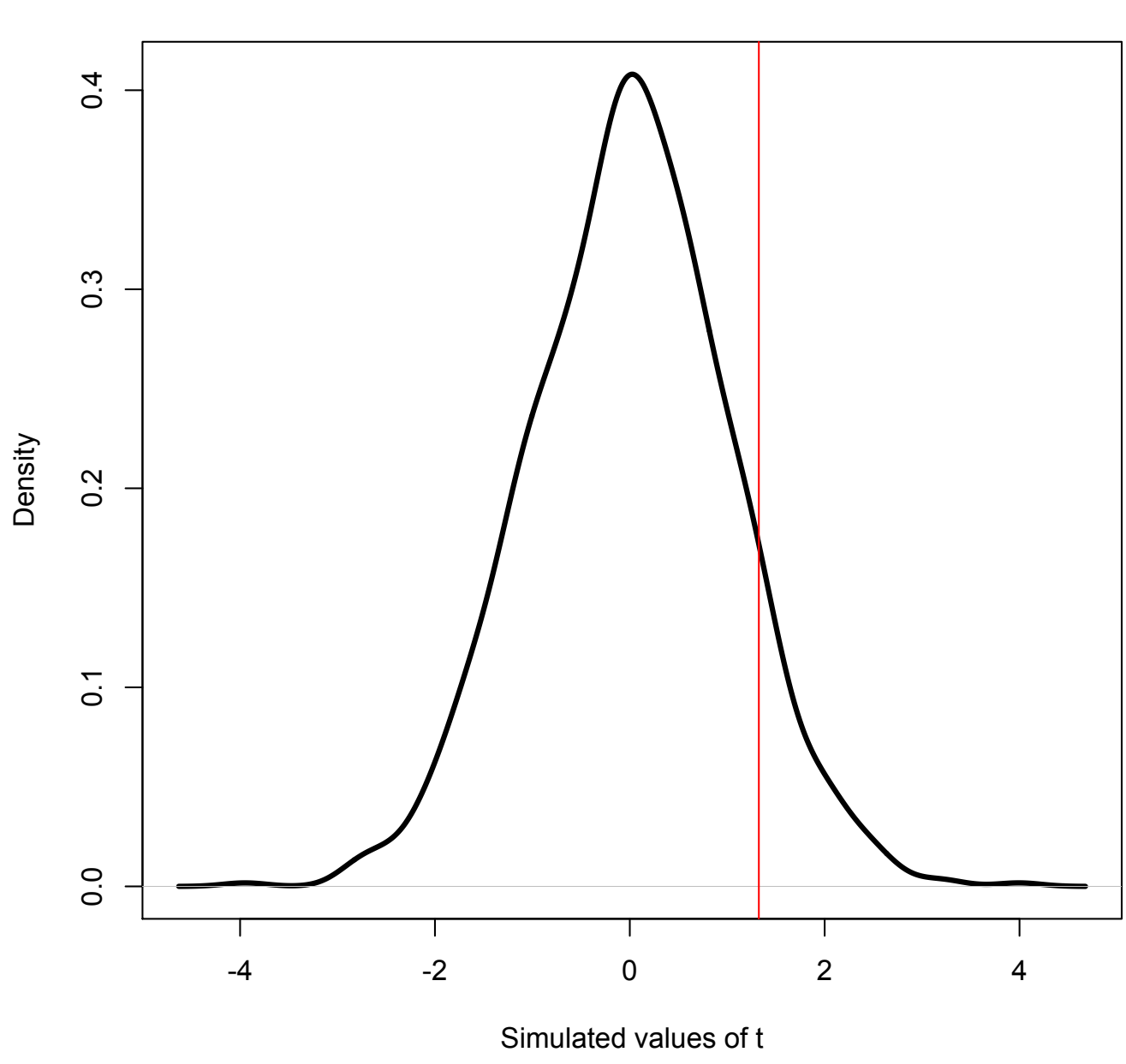
```
set.seed(6198)
R <- 999
z <- c(x,y)
K <- seq(1:length(z))
reps <- numeric(R)
t0 <- t.test(x,y)$statistic

for(i in 2:R) {
k <- sample(K,size=14,replace=FALSE)
x1 <- z[k]
y1 <- z[-k]
reps[i] <- t.test(x1,y1)$statistic
}
```

Results

- What proportion of t-test scores were at or above the one we observed in our sample?

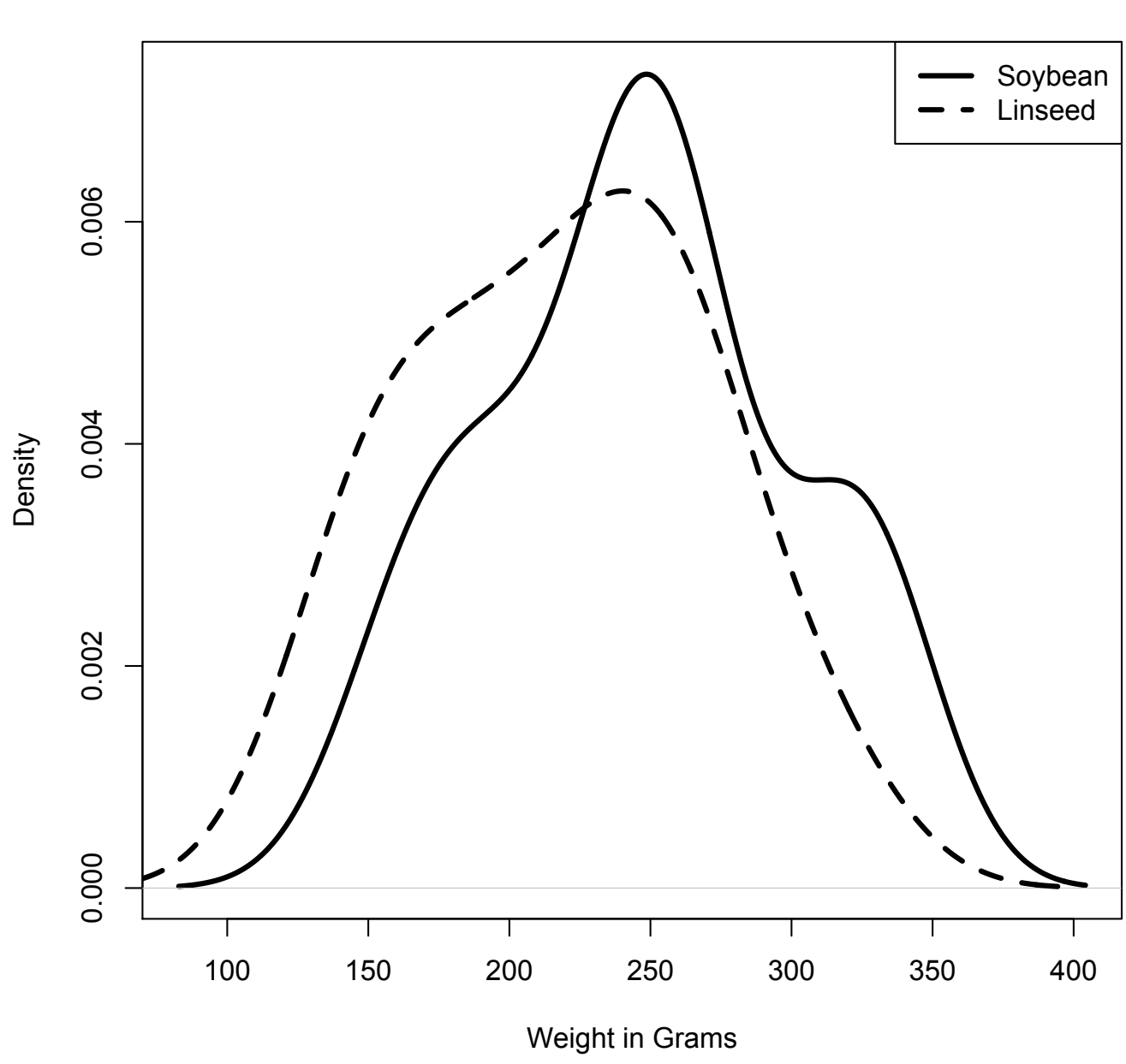
```
> p <- mean(c(t0,reps) >- t0)
> p
[1] 0.903
```

- Note that I included the actual sample estimate in the calculation.
- This p-value is large than .05, so we'd fail to reject the Null of no difference if we were using a 95% cut-off.
- What does the distribution of the t-tests look like?


Density function of simulated t-tests
Density
0.0
0.1
0.2
0.3
0.4
-4
-2
0
2
4
Simulated values of t

What Did We Learn?

- It does not look like the means of these two groups differ significantly (at least at the .05 level of significance).
- We can compare any aspect of these two samples the same way – compute the statistic every time for a thousand replications and then look at their distribution.
- In fact, there are tests to evaluate whether the two distributions are statistically significantly different or not.

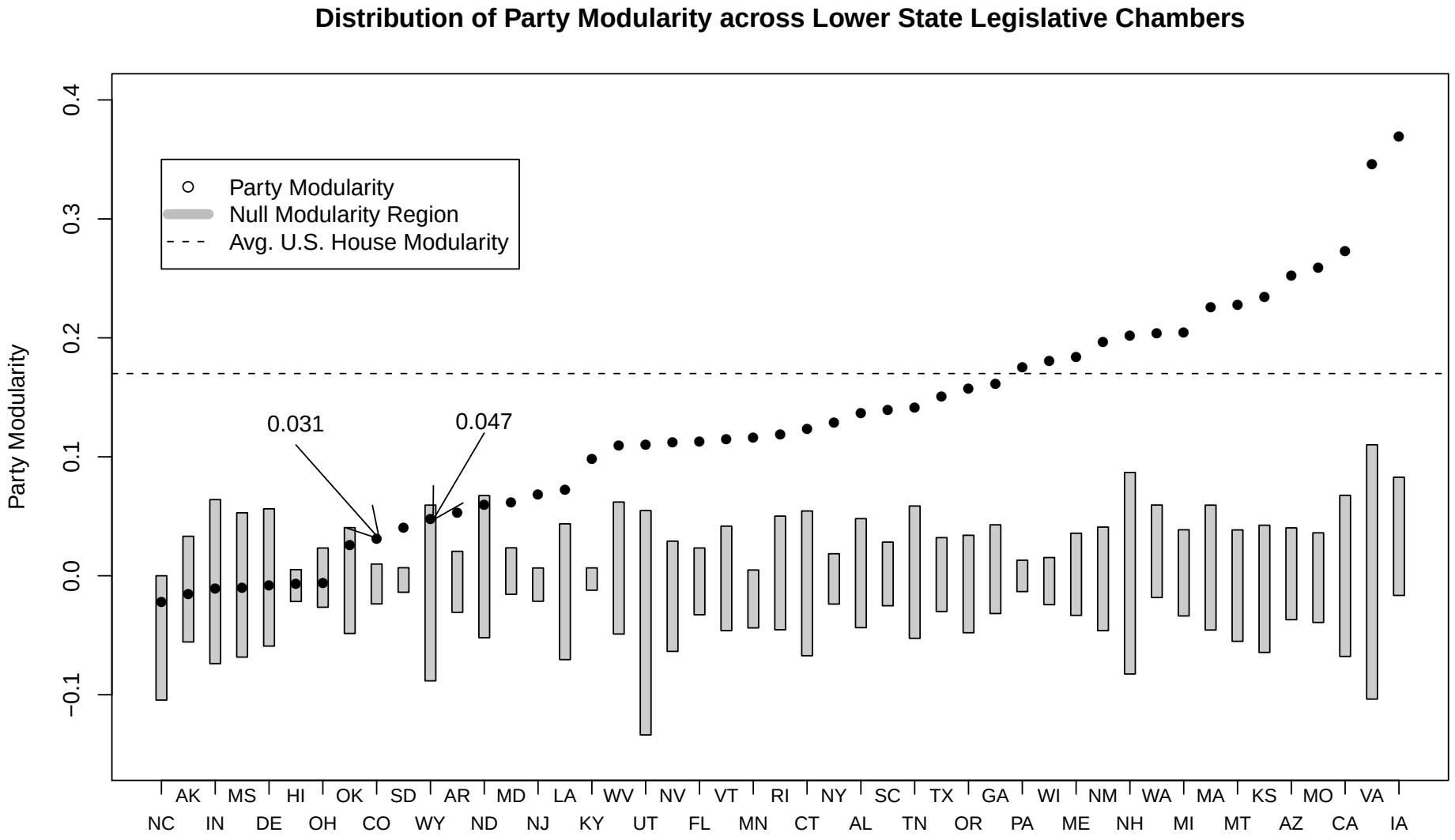

Density functions of Chick Weights
Soybean
Linseed
Density
0.000
0.002
0.004
0.006
100
150
200
250
300
350
400
Weight in Grams

Example: Legislative Networks

- Legislators form networks of cooperation, in this case, via co-sponsorship of bills.
- Those connections are intentional actions that signal relationships.
- Does party structure those relationships? We can measure network modularity due to partisanship.
- Modularity measures how well a division separates a network into distinct groups by measuring the number of ties within a group versus the number of ties between groups.
- But what is the distribution of modularity? Let's estimate it rather than assume it.

Kirkland (2011)

- Modularity is bounded between -1 and 1, but no known distribution.
- Kirkland simulates that distribution by randomly partitioning the network 25,000 times (basically randomly assigning legislators to two "teams")
- The population PDF is then estimated by the 25,000 modularity statistics computed on randomly partitioned networks.
- Use a percentile method to compute 95% confidence interval, and compare the observed modularity in a chamber to this null distribution.
- Party matters


Distribution of Party Modularity across Lower State Legislative Chambers
Party Modularity
Party Modularity
Null Modularity Region
Avg. U.S. House Modularity
0.031
0.047
0.4
0.3
0.2
0.1
0.0
−0.1
AK MS HI OK SD AR MD LA WV NV VT RI NY SC TX GA WI NM WA MA KS MO VA
NC IN DE OH CO WY ND NJ KY UT FL MN CT AL TN OR PA ME NH MI MT AZ CA IA

Comparing Methods

- Bootstrap is the most flexible and most powerful. It can be extended to any statistical or calculation you might make using sample data.
- Bootstraping does NOT make the exchangeability assumption that randomization tests make.
- Jackknife is limited by sample size
- Permutation/Randomization methods break all relationships in data – don't let you produce a covariance matrix.[but what if we reshuffled just on Y?]
- I think Bootstrap confidence intervals, etc. will be standard in empirical social science in 5-10 years.

Posterior Simulation (PS)

- Definition: a simulation-based approach to understanding patterns in our data
- Of course, we want to go beyond our data to draw inference about the population from which it came.
- A straightforward way to go beyond simple tables of regression coefficients
  - Calculate "quantities of interest" (QI)
  - Account for uncertainty
- Uses Bayesian principles, but does not require Bayesian models
- Example: CLARIFY in Stata (King, Tomz, and Wittenberg 2000)

Posterior Simulation (PS)

- Key assumption: coefficients/SEs we estimate are drawn from a probability distribution that describes the larger population
  - Coefficients define the mean, SEs define the variance
- With large enough sample size, according to the central limit theorem this distribution is multivariate normal
  - Instead of a bell curve, imagine a jello mold that can take on different colors, flavors, and textures
- The goal of PS: make random draws from this distribution to simulate many "hypothetical values" of the coefficients
- Instead of drawing one single number, as with `rnorm()`, we draw a vector of numbers (one for each coefficient)

Posterior Simulation (PS)

- The next step: choose a QI
  - Expected value, predicted probability, odds ratio, first difference, change in hazard rate, etc. . .
- Set a key variable in the model to a theoretically interesting value and the rest to their means or modes
- Calculate that QI with each set of simulated coefficients
- Set the variable to a new value
- Calculate that QI with each set of simulated coefficients
- Repeat as appropriate

Posterior Simulation (PS)

- At every value of the variable, we now have many calculations of the QI
- Final step: efficiently summarize the distribution of the computed QI at each value of our variable
- Most common: point estimate and confidence intervals
- Can represent this in a table or graph (we will do a graph example)

Advantages of PS

- Provides more information than a just a table of regression output
- Accounts for uncertainty in the QI
- Flexible to many different types of models, QIs, and variable specifications
- After doing it once, easy to use
- Can be much easier than working with analytic solutions

Limitations of PS

- Relies on CLT to justify asymptotic normality
  - Fully Bayesian model using MCMC could produce exact finite-sample distribution
  - Bootstrapping would require no distributional assumption
- Computational intensity
- Large models can produce lots of uncertainty around quantity of interest

Motivation for Cross-Validation (CV)

- A key component of scientific research is the independent assessment and testing of our theories.
- Lave and March (1979) model of theory building:
  - Observe something in the world
  - Speculate about why it appears the way it does (develop a theory)
  - If your theory were true, what else would you expect to observe?
  - Testing a your theory involves exploring that "what else."
- The "what else" might involve other dependent variables, but it might also involve the same dependent variable in an independently drawn sample of data
- The key is: Data that helps you build your theory cannot also be used as an independent test of theory

Motivation for CV (2)

- Using the same data to build and "test" a theory leads to over-fitting a statistical model to your sample.
- Such over fitting to the sample captures aspects of the true population DGP you care about . . .
- But, it also captures elements that are peculiar to your particular sample that are NOT reflective of the true DGP.
- Thus, over-fitting a model to your sample actually leads to worse/less accurate inference about the population from which it came.

Motivation for CV (3)

- How can you avoid using the same data to build and then "test" your theory?
- Develop your theory, specify your model, etc. before looking at your data, then run the statistical analysis you planned one time and write it up.
- Use the data you have to build your model, then collect fresh data to test it.
- Divide the data you have so you use some of it to build your model and some of it to independently test it.
- This last option is cross-validation

Cross-Validation (CV)

- Definition: a method for assessing a statistical model on a data set that is independent of the data set used to fit the model
- Often used in disciplines like computer science that focus on predictive models
- Goal: guard against "Type III" errors—the testing of hypotheses suggested by the data (i.e., overfitting)
- Many different types based on different ways of constructing the independent data
- Many different fit statistics can be calculated in a CV routine

CV Example: The Netflix Prize

- Key component of Netflix: recommend the right movies to the right people
- Main data source: customers' own ratings of movies they have seen
- 2009: $1 million prize for beating Netflix's current prediction system
- Netflix provided 100 million ratings from 480,000 users of 18,000 movies
- Teams developed models predicting ratings in these data
- Submissions were then evaluated on 2.8 million ratings *not included* in the data given to teams

CV Example: The Netflix Prize

- The winning team beat Netflix's own system by 10% as judged by mean squared error
- Why was it important to set aside the 2.8 million ratings for model evaluation?
- If the evaluation was done on the 100 million, teams could have "gamed the system"
  - Find the odd quirks of that particular sample that came about due to random sampling
  - Overfit the model to account for these odd quirks
  - This would make the model look really good on this one sample, but it wouldn't be generalizable to other samples
- For more information: `http://www.netflixprize.com/assets/GrandPrize2009_BPC_BellKor.pdf`

CV Example: Predicting Divorce

- Psychologist featured in Malcolm Gladwell's book *Blink*
- Research on whether a couple will get divorced based on watching them argue for 15 minutes
- Videotaped 57 couples, coded several variables
- Claims 80-90% accuracy (amazing!)
- But there are problems...

CV Example: Predicting Divorce

- "Predictive formula" developed with knowledge of the couples' marriage outcomes
- Then the formula was applied to *those same couples*
- Are we still amazed that he got 80% right?
- A better test: get a new sample of couples and apply the formula to them
- For more information:
  `http://www.slate.com/id/2246732/`

Stagflation

- The 1970s saw a period thought impossible in a modern economy – high unemployment AND high inflation.
- Most statistical models of the economy at the time fail to predict this. Why?
- Forecasters used massively large models that included hundreds of variables. This resulted in forecasting failure do to:
  - Massive uncertainty in a model that is estimating hundreds/thousands of parameters.
  - Over-fitting the sample data.

CV Examples

- These examples show us the importance of out-of-sample prediction
- There are always oddities in a particular sample
- We don't want to fit our models to those oddities
- CV only rewards models for picking up general patterns that appear across samples
- The problem: where do we get a new sample?

General CV Steps

1. Randomly partition the available data into a *training* set and a *testing* set
2. Fit the model on the training set
3. Take the parameter estimates from that model, use them to calculate a measure of fit on the testing set
4. Can repeat steps 1–3 several times, average to reduce variability

Two Types of CV

- Split-sample CV:
  - Partition into 50% training, 50% testing (could also do 75/25, 80/20, etc. . .)
  - Usually want to maximize size of training set
  - Particularly common in time series analysis where the testing data is generally the most recent years for which data is available.
- Leave-one-out CV:
  - Iterative method with number of iterations = sample size
  - Each observation becomes the training set one time
  - Note the parallel to the Jackknife and Cook's D.

Leave-One-Out CV

1. Delete observation #1 from the data
2. Fit the model on observations #2–n
3. Apply the coefficients from step #2 to observation #1, calculate the chosen fit measure
4. Delete observation #2 from the data
5. Fit the model on observations #1 and #3–n
6. Apply the coefficients from step #5 to observation #2, calculate the chosen fit measure
7. Repeat until all observations have been deleted once

Limitations of CV

- Training and testing data must be random samples from the same population (Why?)
- Will show biggest differences from in-sample measures when n is small (Why?)
- Higher computational demand than calculating in-sample measures
- Subject to researcher's selection of an appropriate fit statistic

Statistics in analyzing elections

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Election polls

An election poll is a survey of "likely voters" used to predict the results of an election.

For an election with two candidates, each respondent to the poll states that they will vote for one candidate or the other.

This can be coded as a Bernoulli trial. The response of the i^{th} person to be polled can be written $X_i = 1$ or $X_i = 0$.

The result of the poll is $\bar{X}$, with standard error $\sqrt{p(1-p)/n}$, estimated as $\sqrt{\bar{X}(1-\bar{X})/n}$.

Election polls

If the poll sample size is $n = 1000$ and the election is close, the standard error is approximately

$$\sqrt{(1/2) \cdot (1 - 1/2)/1000} \approx 0.016.$$

The poll is usually reported as the estimate plus or minus a "margin of error", which should be twice the standard error to correspond to a 95% confidence interval. Thus a poll of 1000 people gives a margin of error of around 3 percentage points.

Sources of bias in polling

The main source of bias in polling is that the people who are willing to participate in polls may not be representative of all voters.

Other possible issues:

People could deliberately misstate their views.

People could be included in the poll, but subsequently not vote.

People could change their mind between the poll and the election.

Bias from non-representative samples

Suppose we anticipate the voting population to have roughly equal numbers of females and males, but our poll respondents consist of 600 females and 400 males.

Suppose that p_f fraction of females prefer candidate X, and p_m fraction of males prefer candidate X. Then the support for candidate X in the election will be

$$(p_f + p_m)/2.$$

But the expected support for candidate X in our poll will be

$$0.6p_f + 0.4p_m.$$

Hence the bias is

$$0.1(p_f - p_m).$$

Bias from non-representative samples

Now let's generalize to a setting in which the voting population contains q_f fraction of females and q_m fraction of males (so $q_f + q_m = 1$).

Then the support for candidate X in the election is

$$
\begin{aligned}
&P(\text{vote for X}|\text{voter is female}) \cdot P(\text{voter is female}) + \\
&\quad P(\text{vote for X}|\text{voter is male}) \cdot P(\text{voter is male}) = \\
&\quad q_f p_f + q_m p_m = \\
&\quad q_f (p_f - p_m) + p_m = \\
&\quad q_m (p_m - p_f) + p_f .
\end{aligned}
$$

Bias from non-representative samples

If the poll respondents consist of q'_f fraction of females and q'_m fracttion of males, then the expected results of the poll are

$$q'_f(p_f - p_m) + p_m = q'_m(p_m - p_f) + p_f.$$

Thus the bias is

$$q'_f(p_f - p_m) + p_m - q_f(p_f - p_m) - p_m = (q'_f - q_f)(p_f - p_m),$$

which also equals $(q_m - q'_m)(p_f - p_m)$.

Bias of the spread

If fraction p of the population supports candidate X, and if there are only two candidates, then fraction $1 - p$ of the population supports the other candidate.

The spread in support between the two candidates is

$$p - (1 - p) = 2p - 1.$$

Thus if we have an estimate $\hat{p}$ of p with bias b, then the bias in the estimated spread is

$$E[2\hat{p} - 1 - (2p - 1)] = 2E[\hat{p} - p] = 2b.$$

Thus the bias is doubled when we work with the spread.

Weighting to reduce bias

Let's return to the setting where $q_f = q_m = 1/2$.

The sample mean from our poll, $\bar{X}$, is equivalent to

$$0.6\hat{p}_f + 0.4\hat{p}_m.$$

We can get an unbiased result using the estimator

$$0.5\hat{p}_f + 0.5\hat{p}_m.$$

This estimator is equivalent to constructing a weighted average of the X_i, with weights for females proportional to $1/0.6$, and weights for males proportional to $1/0.4$.

Weighting to reduce bias

The variance of the adjusted estimator is

$$0.25p_f(1-p_f)/600 + 0.25p_m(1-p_m)/400.$$

The variance of the original (biased) estimator is

$$0.6^2p_f(1-p_f)/600 + 0.4^2p_m(1-p_m)/400.$$

Now suppose we form an arbitrary convex combination

$$w\hat{p}_f + (1-w)\hat{p}_m.$$

The variance of this statistic is

$$w^2v_f/(qN) + (1-w)^2v_m/((1-q)N),$$

where $v_f = p_f(1-p_f)$, $v_m = p_m(1-p_m)$, q is the proportion of females in the original sample, and N is the total sample size.

Weighting to reduce bias

If we differentiate with respect to w we get

$$2wv_f/(qN) - 2(1-w)v_m/((1-q)N),$$

then differentiating again yields

$$2v_f/(qN) + 2v_m/((1-q)N.$$

Since the second derivative is non-negative, the original variance function is convex in w, so the stationary point

$$w = \frac{v_m/(1-q)}{v_f/q + v_m/(1-q)} = \frac{qv_m}{(1-q)v_f + qv_m}$$

is a global minimum. If $v_m \approx v_f$, then $w = q$, which is the same weight used in the original (biased estimate).

Weighting eliminates the bias, but may increase or decrease the variance.

Reducing bias with a likely voter model

Suppose there is a community with n people. Let $V_i = 1$ if the i^{th} person in the community votes for candidate X, and $V_i = 0$ otherwise. Let $I_i = 1$ if the i^{th} person in the community votes in the eletion X, and $I_i = 0$ otherwise.

The proportion of voters in the community who vote for candidate X is:

$$\frac{V_1 I_1 + \cdots V_n I_n}{I_1 + \cdots + I_n}.$$

If we treat the I_i as random, with $P(I_i = 1) = p_i$, then the expected number of people who vote for candiate X is approximately

$$\frac{V_1 p_1 + \cdots V_n p_n}{p_1 + \cdots + p_n}.$$

Reducing bias with a likely voter model

Now suppose we have a sample of $m < n$ people who are represenative of the community. We don't know who will really vote, but we have covariates (age, gender, etc.) that predict whether a person will vote. Suppose that using the covariates we can estimate the probability $p_i = E[I_i]$ of the i^{th} person voting.

Then we can form a weighted average to estimate the support for candidate X:

$$\begin{aligned} E\frac{V_1 p_1 + \cdots + V_m p_m}{p_1 + \cdots + p_m} &= E\frac{V_1 p_1 J_1 + \cdots + V_n p_n J_n}{p_1 J_1 + \cdots + p_n J_n} \\ &\approx \frac{E[V_1 p_1 J_1] + \cdots E[V_n p_n J_n]}{E[p_1 J_1] + \cdots + E[p_n J_n]} \\ &= \frac{V_1 p_1 + \cdots V_n p_n}{p_1 + \cdots + p_n}, \end{aligned}$$

where J_i is the indicator the the i^{th} person is part of the poll, and the J_i are iid.

Poll averaging

If we average two independent polls with standard errors SE_1 and SE_2, then the standard error of the average is

$$\sqrt{\mathrm{SE}_1^2 + \mathrm{SE}_2^2}/2.$$

If the two polls have the same standard error, then the standard error of the average is $\mathrm{SE}/\sqrt{2}$.

We can do better than taking a simple average:

$$\mathrm{var}(wP_1 + (1-2)P_2) = w^2\mathrm{SE}_1^2 + (1-w)^2\mathrm{SE}_2^2,$$

where P_1 and P_2 are the results of the two polls.

Poll averaging

This variance expression is convex, so it has a local miniumum.

Differentiate with respect to w to get

$$2w\mathrm{SE}_1^2 - 2(1-w)\mathrm{SE}_2^2 = 0.$$

and solve for w to get

$$w = \frac{\mathrm{SE}_2^2}{\mathrm{SE}_1^2 + \mathrm{SE}_2^2} = \frac{1/\mathrm{SE}_1^2}{1/\mathrm{SE}_1^2 + 1/\mathrm{SE}_2^2}.$$

These are called the "inverse variance weights".

The resulting variance is

$$\frac{1}{1/\mathrm{SE}_1^2 + 1/\mathrm{SE}_2^2}.$$

Poll averaging of dependent polls

Suppose that different polls are subject to a common source of influence, so the results become dependent:

$$\mathrm{cor}(P_1, P_2) = r.$$

Now the variance of the simple average of the two polls is

$$\mathrm{SE}_1^2/4 + \mathrm{SE}_2^2/4 + r\mathrm{SE}_1\mathrm{SE}_2/2$$

which is increasing in r.

Forecasting more complicated elections

In the US Electoral College, each state has a specific number of electoral votes (based on population). In most cases, the candidate who wins the most votes in the state receives all the electoral votes for the state.

The candidate who wins the most votes overall (the "popular vote") may not win the Electoral College.

To see why this is so, suppose there are only two states, one with 100 electoral votes and a population of 100 million people, and one with 50 electoral votes, and a population of 50 million.

In the following situation, candidate X wins the popular vote but loses the election:

Candidate	Big state	Small state	Popular	Electoral
X	49,999,999	50,000,000	99,999,999	50
Y	50,000,001	0	50,000,001	100

Forecasting more complicated elections

The situation doesn't need to be so extreme:

Candidate	Big state	Small state	Popular	Electoral
X	49,999,999	25,000,010	75,000,009	50
Y	50,000,001	24,999,990	74,999,991	100

The general idea is that if you lose the big states by a small amount, but win the small states by a lot, you can win the popular vote but lose the election.

Monte Carlo simulation of elections

Let p_i denote the proportion of voters for candidate X in the i^{th} state, and let N_i denote the number of electoral votes for the i^{th} state.

Candidate X wins the election if and only if

$$\sum_i \mathcal{I}(p_i > 0.5) N_i > \sum_i \mathcal{I}(p_i < 0.5) N_i.$$

Let's treat p_i as being a random variable, with distribution

$$[p_i|\text{polling data}] \propto [\text{polling data}|p_i][p_i].$$

Monte Carlo simulation of elections

Conditioned on p_i, we can model the polling data as a binomial distribution, and we can reduce the polling data to the sufficient statistic $\hat{p}_i$.

Using the central limit theorem, $[\hat{p}_i|p_i]$ is normal with mean p_i and variance $p_i(1-p_i)/m_i$, where m_i is the sample size of the poll.

As a further approximation, we set the variance as $1/(4m_i)$, which is appropriate as long as we are only looking at close races.

We might choose to use the flat prior here, $[p_i] \propto 1$.

So the distribution of p_i is proportional to

$$\exp(-(\hat{p}_i - p_i)^2/(1/(2m_i)))/\sqrt{1/(4m_i)},$$

which is a normal distribution with mean $\hat{p}_i$ and variance $1/(4m_i)$.

Monte Carlo simulation of elections

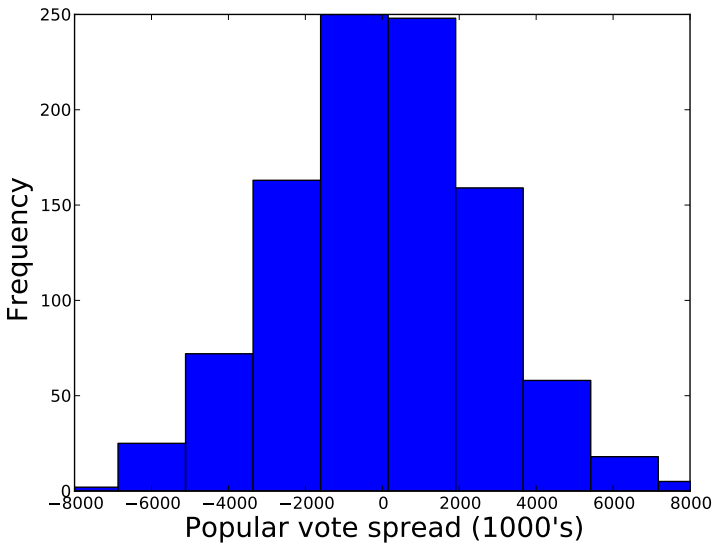
Now the condition

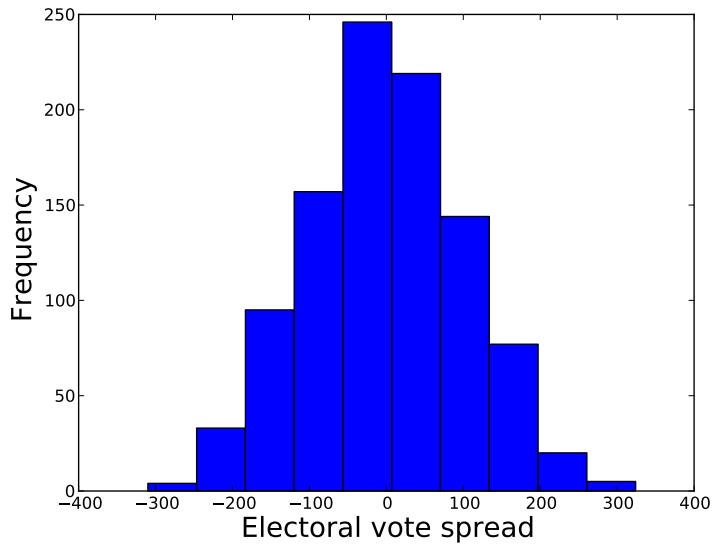
$$\sum_i \mathcal{I}(p_i > 0.5) N_i > \sum_i \mathcal{I}(p_i < 0.5) N_i.$$

is a property of a known distribution. It would be difficult to calculate exactly, but it is easy to approximate using simulation.

Simulation setting 1

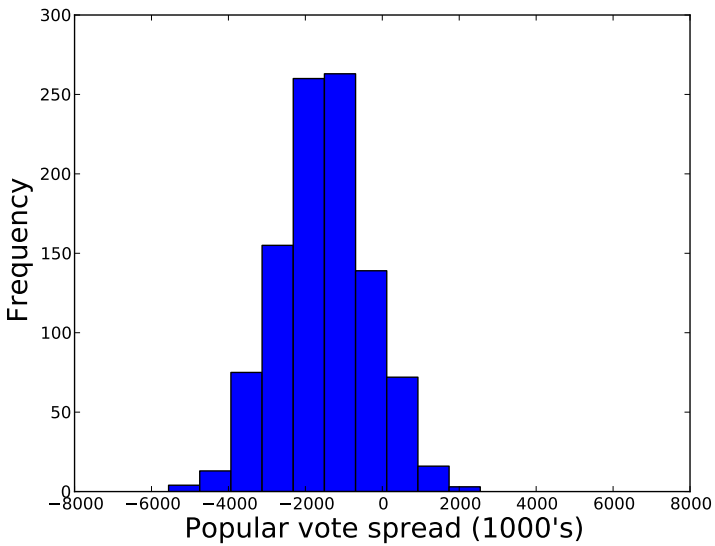
The election is a perfect tie in all states, all polls have margin of error 0.04, and the polls are independent.

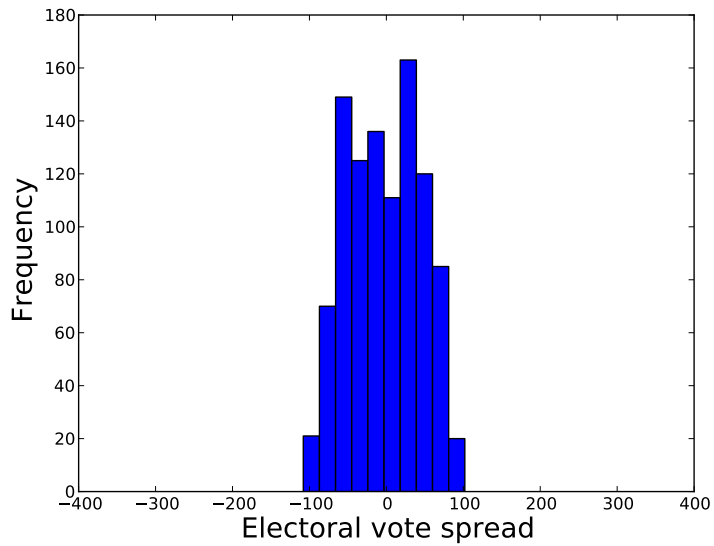




Simulation setting 2

The results are fixed for 41 states, and are a tie in 10 states. The polls for the 10 "in play" states have margin of error 0.04, and the polls are independent.





Simulation setting 3

The results are fixed for 41 states, and are a tie in 10 states. The polls for the 10 "in play" states have margin of error 0.04, and are correlated with ICC=0.4.