#### **Section 11 : Sensitivity Analysis**

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## Roadmap

- 1. Sensitivity Analysis
- 2. Bootstrapping
- 3. Homework

Model of an Observational Study

Unit i's probability of treatment is

$$\pi_i = P(T_i = 1)$$

and its probability of control is

$$1-\pi_i=P(T_i=0)$$

So we have

$$P(T_1 = t_1, ..., T_n = t_n) = \prod_{i=1}^n \pi_i^{t_i} (1 - \pi_i)^{1 - t_i}$$

#### Example

Question: Does spending time at the beach improve your health?

 $\pi_i = P(\text{Person } i \text{ Goes to the Beach Regularly})$ 

 $1 - \pi_i = P(Person \ i \ Does \ Not \ Got \ to \ the \ Beach \ Regularly)$ 

Now say that we have information on everyones age and gender.



#### Overt Bias

An observational study is free of hidden bias if every  $\pi_i$  (though unknown) only depends on the observed covariates  $\mathbf{x_i} = (Age_i, Gender_i)$ 

Define the probability that Person i will be a beach person as an unknown function of  $\mathbf{x_i}$ 

$$\pi_i = \lambda(\mathbf{x_i})$$

So the probability of treatment assignment is

$$P(T_1 = t_1, ..., T_n = t_n) = \prod_{i=1}^n \lambda(\mathbf{x_i})^{t_i} (1 - \lambda(\mathbf{x_i}))^{1-t_i}$$

As long as we match exactly on age and gender, our study will be valid. We do not need to know the function  $\lambda$ .

Of course, we rarely believe that a study is free of hidden bias.

So how would our inferences change for different magnitudes of hidden bias?

There is hidden bias if two units have the same observed covariates but different probabilities of treatment assignment.

In other words

 $x_a = x_b$ , but  $\pi_a \neq \pi_b$  for some a and b.

So assume that each person who goes to the beach is matched with exactly one person who doesn't go to the beach.

The treatment odds for Person a and Person b (in the pair) are

$$O_{a}=rac{\pi_{a}}{1-\pi_{a}}$$
 and  $O_{b}=rac{\pi_{b}}{1-\pi_{b}}.$ 

The ratio of these odds,  $\Gamma = O_a/O_b$ , measures bias after matching.

We also have

$$P(T_a = 1 | T_a + T_b = 1) = \frac{\pi_a(1 - \pi_b)}{\pi_a(1 - \pi_b) + \pi_b(1 - \pi_a)}$$



The key parameter in Rosenbaum's sensitivity analysis is the treatment odds ratio  $\Gamma$ .

$$\Gamma = O_a/O_b = rac{\pi_a/(1-\pi_a)}{\pi_b/(1-\pi_b)}$$

Substantively, this is the ratio of the odds of the treated unit going to the beach regularly and the odds of the matched control unit going to the beach regularly.

Sensitivity analysis involves seeing if our results hold for different ranges of  $\Gamma$ . Let  $p_a$  and  $p_b$  be the probability of each unit in the matched pair being treated, conditional on exactly one being treated.

So if  $\Gamma=1$ , the treatment and control unit within each pair has the same value of treatment assignment ( $p_a, p_b=0.5$ ).

If  $1/2 \le \Gamma \le 2$ , no unit can be more than twice as likely as its match to get treated (0.33  $\le p_a, p_b \le 0.66$ ).

If  $1/3 \le \Gamma \le 3$ , no unit can be more than three times as likely as its match to get treated  $(0.25 \le p_a, p_b \le 0.75)$ .

(The quick formula for getting these bounds is  $\frac{1}{\Gamma+1} \leq p_a, p_b \leq \frac{\Gamma}{\Gamma+1}$ )

Question: Imagine that we are doing our beach study and there was no treatment effect. If  $1/2 \le \Gamma \le 2$ , what would be the worst way the odds could go to make it look like there was a treatment effect.

Answer: For every pair, the healthier person was twice as likely to go to the beach regularly, or the less healthy person is twice as likely to go to the beach regularly.

So say that these are our four matched pairs. Let's start with  $\Gamma=1. \label{eq:gamma}$ 

#### > data

	Y1	Y2	T1	T2	Age1	Age2	Gender1	Gender2	P(T1=1 T1+T2=1)	Min Gamma	Max	Gamma
1	6	5	1	0	13	13	1	1	0.5	1		1
2	3	7	1	0	22	22	1	1	0.5	1		1
3	4	7	1	0	45	45	0	0	0.5	1		1
4	7	14	1	0	70	70	0	0	0.5	1		1

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Reminder: Wilcoxon Signed Rank Test

- 1. Drop pairs where the matches have the same outcome
- 2. Calculate the difference in outcomes within each pair
- 3. Rank the pairs (Smallest Difference=1)
- 4. Take the sum of the ranks where the treated unit had the higher outcome

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	Y1	<b>Y2</b>	T1	T2	Age1	Age2	Gender1	Gender2	P(T1=1 T1+T2=1)	Min Gamma	Max Gamma
1	6	5	1	0	13	13	1	1	0.5	1	1
2	3	7	1	0	22	22	1	1	0.5	1	1
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The Wilcoxon Signed-Rank test statistic W is 1.

Sum of the ranks=1+2+3+4=10

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Sum of the ranks=
$$1+2+3+4=10$$

p-value= 
$$P(W \in \{0, 1, 9, 10\} | Randomization)$$

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p-value= 
$$\frac{1}{16} + \frac{1}{16} + \frac{1}{16} + \frac{1}{16} = \frac{1}{4}$$

In an experimental setting, we compute our p-values by assuming randomness and asking how rare our test statistic would be if there was no treatment effect.

Specifically, we look at the distribution of the test statistic under random assignment and no treatment effect.

If we believe that there is some degree of hidden bias, we cannot compute exact p-values. But we can find the p-value for the worst case scenario (given a maximum  $\Gamma$ ).

Let's look at the case where  $\frac{1}{2} \le \Gamma \le 2$  (no one is more than twice as likely to go to the beach as their matched partner).

#### > data

	Y1	Y2	T1	T2	Age1	Age2	Gender1	Gender2	P(T1=1 T1+T2=1)	Min Gamma	Max Gamma
1	6	5	1	0	13	13	1	1	0.667	0.5	2
2	3	7	1	0	22	22	1	1	0.333	0.5	2
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$$Sum(Ranks)=1+2+3+4=10$$

p-value= 
$$P(W \in \{0, 1, 9, 10\} | \text{This Randomization})$$

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$$Sum(Ranks)=1+2+3+4=10$$

p-value= 
$$P(W \in \{0, 1, 9, 10\}|This Randomization)$$

$$\text{p-value} = (\tfrac{1}{3} \cdot \tfrac{1}{3} \cdot \tfrac{1}{3} \cdot \tfrac{1}{3}) + (\tfrac{2}{3} \cdot \tfrac{1}{3} \cdot \tfrac{1}{3} \cdot \tfrac{1}{3}) + (\tfrac{1}{3} \cdot \tfrac{2}{3} \cdot \tfrac{2}{3} \cdot \tfrac{2}{3}) + (\tfrac{2}{3} \cdot \tfrac{2}{3} \cdot \tfrac{2}{3} \cdot \tfrac{2}{3})$$

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4	7	14	1	0	70	70	0	0	0.333	0.5	2

$$Sum(Ranks)=1+2+3+4=10$$

p-value= 
$$P(W \in \{0, 1, 9, 10\}|This Randomization)$$

$$p-value = (\frac{1}{3} \cdot \frac{1}{3} \cdot \frac{1}{3} \cdot \frac{1}{3}) + (\frac{2}{3} \cdot \frac{1}{3} \cdot \frac{1}{3} \cdot \frac{1}{3}) + (\frac{1}{3} \cdot \frac{2}{3} \cdot \frac{2}{3} \cdot \frac{2}{3} \cdot \frac{2}{3}) + (\frac{2}{3} \cdot \frac{2}{3} \cdot \frac{2}{3} \cdot \frac{2}{3})$$

p-value= 
$$\frac{3}{9}$$

So we can say that our maximum p-value is 3/9 as long as no person was more than twice as likely to go to the beach as their matched control.

What if  $\frac{1}{4} \le \Gamma \le 4$  (no one is more than twice as likely to go to the beach as their matched partner).

# > data Y1 Y2 T1 T2 Age1 Age2 Gender1 Gender2 P(T1=1|T1+T2=1) Min Gamma Max Gamma 1 6 5 1 0 13 13 1 1 0.8 0.25 4 2 3 7 1 0 22 22 1 1 0.2 0.25 4 3 4 7 1 0 45 45 0 0 0.2 0.25 4 4 7 14 1 0 70 70 0 0 0 0.2 0.25 4

$$\begin{aligned} & \text{Sum}(\text{Ranks}) \!\!=\!\! 1 \!\!+\!\! 2 \!\!+\!\! 3 \!\!+\!\! 4 \!\!=\!\! 10 \\ & \text{p-value} \!\!=\! P(W \in \{0,1,9,10\} | \text{This Randomization}) \\ & \text{p-value} \!\!=\! (\frac{1}{5} \cdot \frac{1}{5} \cdot \frac{1}{5} \cdot \frac{1}{5}) + (\frac{4}{5} \cdot \frac{1}{5} \cdot \frac{1}{5}) + (\frac{1}{5} \cdot \frac{4}{5} \cdot \frac{4}{5} \cdot \frac{4}{5}) + (\frac{4}{5} \cdot \frac{4}{5} \cdot \frac{4}{5} \cdot \frac{4}{5}) \\ & \text{p-value} \!\!=\! \frac{3}{6} \end{aligned}$$

# Bootstrapping (from Section 5)

#### Motivation

Imagine that we want to study the height of people in the United States, so we take a random sample of 10,000 Americans and measure them.

By the Central Limit Theorem, the sample average  $\hat{\mu}$  will be distributed about N( $\mu$ ,  $\sigma/100$ ), where  $\mu$  is the population mean and  $\sigma$  is the sample variance.

However, what if we are interested in the population median? The CLT does not give us a simple way to estimate its distribution.

# Bootstrapping (from Section 5)

#### Basic Idea

To estimate the distribution of a parameter like the sample median

- 1. Take many random samples (with replacement) from the original sample, each of size n (in this case 10,000)
- 2. Estimate the parameter for each sample
- 3. The distribution of these estimates should be close to the sampling distribution of the estimator

# Bootstrapping (from Section 5)

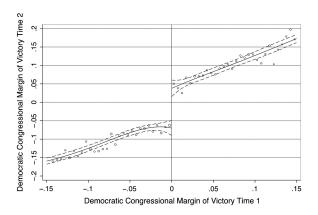
#### Basic Idea

The previous example is a case of non-parametric bootstrapping, because we made no assumptions about the distribution of the heights of Americans. We simply had a random sample of the population, and we resampled from our sample over and over.

- 1. Take many random samples (with replacement) from the original sample, each of size n (in this case 10,000)
- 2. Estimate the parameter for each sample
- 3. The distribution of these estimates should be close to the sampling distribution of the estimator

# Regression Discontinuity (from Section 5)

#### Creating the Graph



## Regression Discontinuity (from Section 5)

#### Estimating the Confidence Interval

- 1. The 95% confidence interval is found by bootstrapping
- 2. Starting with the left side of the cut-point, randomly sample (with replacement) from the points on the left. The size of the new sample should be the same as the number of points on the left.
- 3. Construct a regression line for this new sample
- 4. Repeat this process several thousand times. This will result in thousands of regression lines. Each regression line will be defined by a large number of (x, y) coordinates. Thus, each x will be associated with a large number of y's.
- 5. For each x, find the lower 2.5% and upper 97.5% quantile for the y's. These points will define the lower and upper bounds of the 95% confidence interval.

## Questions

- 1. Lectures
- 2. Readings
- 3. Homework