Rosenbaum-Style p-Values for Matched Observational Studies with Unmeasured Confounding

Hanyu Wu

Department of Biostatistics, Peking University

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1. Matched Data Sensitivity Model
2. FRT under Rosenbaum's Sensitivity Model
3. Application

Model Setting

- Consider exactly matched pairs from an observational study, with (i,j) indexing unit j in pair $i (i = 1, \ldots, n; j = 1, 2)$.
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- Let $\mathbb{S}_i = \{Y_{i1}(1), Y_{i1}(0), Y_{i2}(1), Y_{i2}(0)\}$ denote the set of all potential outcomes within pair i.

Conditional Assignment Probability

Conditioning on the event that $Z_{i1} + Z_{i2} = 1$, consider

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Define $o_{ij} = e_{ij} / \left(1 - e_{ij}\right)$ as the odds of the treatment for unit (i, j), we have

$$\begin{aligned}
\pi_{i1} &= \frac{\mathrm{pr}\left\{Z_{i1} = 1, Z_{i2} = 0 \mid X_i, \mathbb{S}_i\right\}}{\mathrm{pr}\left\{Z_{i1} + Z_{i2} = 1 \mid X_i, \mathbb{S}_i\right\}} \\
&= \frac{\mathrm{pr}\left\{Z_{i1} = 1, Z_{i2} = 0 \mid X_i, \mathbb{S}_i\right\}}{\mathrm{pr}\left\{Z_{i1} = 1, Z_{i2} = 0 \mid X_i, \mathbb{S}_i\right\} + \mathrm{pr}\left\{Z_{i1} = 0, Z_{i2} = 1 \mid X_i, \mathbb{S}_i\right\}} \\
&= \frac{e_{i1}\left(1 - e_{i2}\right)}{e_{i1}\left(1 - e_{i2}\right) + \left(1 - e_{i1}\right) e_{i2}} = \frac{o_{i1}}{o_{i1} + o_{i2}}.
\end{aligned}$$

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- The treatment assignment is identical to the MPE conditioning on the covariates and the event that each pair has a treated and control units.
- So we can analyze the exactly matched observational study as if it is a MPE, using either the FRT or the Neymanian approach in Chapter 7.

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- Without ignorability, $e_{ij} \not\perp\!\!\!\perp \{Y_{ij}(1), Y_{ij}(0)\} | X_i$, so $o_{i1} \neq o_{i2}$. We introduce Rosenbaum (1987b)'s model for sensitivity analysis imposes bounds on the odds ratio o_{i1}/o_{i2}.

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Assumption 19.1 (Rosenbaum's sensitivity model)

The odds ratios are bounded by

$$o_{i1}/o_{i2} \leq \Gamma, \quad o_{i2}/o_{i1} \leq \Gamma$$

for some pre-specified $\Gamma \geq 1$. Equivalently,

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- When $\Gamma = 1$, we have $\pi_{i1} = \frac{1}{2}$ and thus a standard MPE.
- $\Gamma > 1$ measures the deviation from the ideal MPE due to the omitted variables in matching.

FRT Setting

- Consider testing the sharp null hypothesis

$$H_{0\mathrm{F}} : Y_{ij}(1) = Y_{ij}(0) \text{ for } i = 1, \ldots, n \text{ and } j = 1, 2$$

based on within-pair differences $\hat{\tau}_i = (2Z_{i1} - 1)(Y_{i1} - Y_{i2})$ $(i = 1, \ldots, n)$.

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  - Specificlly, $\hat{\tau}_i$ takes value from $Y_{i1}(1) - Y_{i2}(0)$ and $Y_{i2}(1) - Y_{i1}(0)$. Under $H_{0\mathrm{F}}$, $|\hat{\tau}_i|$ is constant.

Test Statictics

- Consider the following class of test statistics:

$$T = \sum_{i=1}^{n} S_i q_i$$

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- Special cases include the sign statistic, the pair t statistic (up to some constant shift), and the Wilcoxon sign rank statistic:

$$T_1 = \sum_{i=1}^{n} S_i, \quad T_2 = \sum_{i=1}^{n} S_i |\hat{\tau}_i|, \quad T_3 = \sum_{i=1}^{n} S_i R_i,$$

where $(R_1, \ldots, R_n)$ are the ranks of $(|\hat{\tau}_1|, \ldots, |\hat{\tau}_n|)$.

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- Among all null distributions, we aim to find "the worst case", under which T has the largest p-value.
- Since FRT is right-tailed test, the worst case is $E(S_i) = \max(\pi_{i1})$, i.e.

$$S_i \overset{\text{IID}}{\sim} \text{Bernoulli}\left(\frac{\Gamma}{1+\Gamma}\right).$$

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- Under "the worst case",

$$E_\Gamma(T) = \frac{\Gamma}{1+\Gamma}\sum_{i=1}^{n} q_i, \quad \mathrm{var}_\Gamma(T) = \frac{\Gamma}{(1+\Gamma)^2}\sum_{i=1}^{n} q_i^2$$

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- The Normal approximation is

$$\frac{T - \frac{\Gamma}{1+\Gamma} \sum_{i=1}^{n} q_i}{\sqrt{\frac{\Gamma}{(1+\Gamma)^2} \sum_{i=1}^{n} q_i^2}} \xrightarrow{\mathrm{d}} \mathrm{N}(0,1).$$

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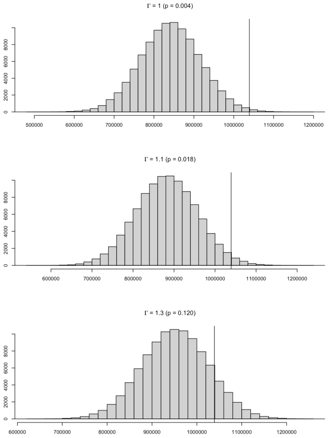
- In practice, we can report a sequence of p-values as a function of Γ.

Matched Lalonde Data Analysis

```r
# Match
library("car")
library("Matching")
data(lalonde)
lalonde$u74 <- as.numeric(lalonde$re74 ==0)
lalonde$u75 <- as.numeric(lalonde$re75 ==0)
y = lalonde$re78
z = lalonde$treat
x = as.matrix(lalonde[, c("age", "educ", "black",
                          "hisp", "married", "nodegr",
                          "re74", "re75", "u74", "u75")])
matchest.adj = Match(Y = y, Tr = z, X = x, BiasAdjust = TRUE)
```

```r
# Rosenbaum's Sensitivity Analysis
tre = lalonde$re78[matchest.adj$index.treated]
con = lalonde$re78[matchest.adj$index.control]
tau = tre-con
T = sum(tau*(tau>0))
ga = 1  # Gamma = 1
Mean1 = ga/(1+ga)*sum(abs(tau))
Var1 = ga/(1+ga)^2*sum((tau)^2)
hist(rnorm(100000, Mean1, sqrt(Var1)),
     main = expression(paste(Gamma, " = 1 (p = 0.004)")),
     xlab = NULL, ylab = NULL)
abline(h=0,v=T)p1 = pnorm(T, Mean1, sqrt(Var1))
```



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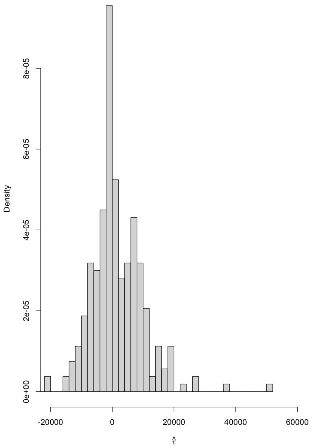

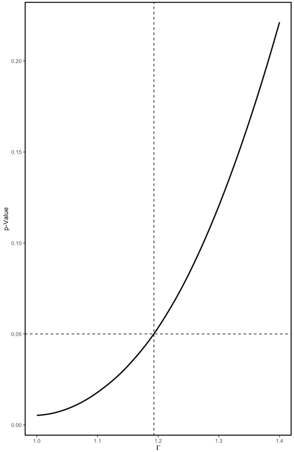

Thanks!