Program Evaluation (b)- Matching

Chris Conlon

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Applied Econometrics

Suppose we ran a RCT

- Imagine we ran a randomized controlled trial
- Flip a coin and assign $T_i = 1$ or $T_i = 0$
  - In treated schools we monitor teacher attendance with a camera each day.
  - In control schools we don't.
- By construction it should be that $E[u_i|T_i = 1] - E[u_i|T_i = 0]$
- But did our randomization work? We might have randomized all of the large classes into the treatment group and the small classes into the control group.
- We want to know if $f(x|T_i = 1) = f(x|T_i = 0)$?

Checking Covariate Balance

- One easy thing to do is to construct a covariate balance table.
  - Not exactly the same as $f(x|T_i = 1) = f(x|T_i = 0)$.
  - But if means don't match, we're probably in trouble!
- Compare $E[x|T_i = 1]$ to $E[x|T_i = 0]$.
- Is the difference statistically signficant?
- Just look at regression coefficient (and SE) of

$$x_i = \gamma_0 + \gamma_1 T_i + \varepsilon_i$$

Checking Covariate Balance

TABLE 1—BASELINE DATA

	Treatment (1)	Control (2)	Difference (3)
Panel A. Teacher attendance			
School open	0.66	0.64	0.02
			(0.11)
	41	39	80
Panel B. Student participation (random check)			
Number of students present	17.71	15.92	1.78
			(2.31)
	27	25	52
Panel C. Teacher qualifications			
Teacher test scores	34.99	33.54	1.44
			(2.02)
	53	54	107
Panel D. Teacher performance measures (random check)			
Percentage of children sitting within classroom	0.83	0.84	0.00
			(0.09)
	27	25	52
Percent of teachers interacting with students	0.78	0.72	0.06
			(0.12)
	27	25	52
Blackboards utilized	0.85	0.89	−0.04
			(0.11)
	20	19	39
F-stat (1,110)			1.21
p-value			(0.27)

Checking Covariate Balance in R

https://cran.r-project.org/web/packages/cobalt/vignettes/cobalt_A0_basic_use.html

Now let's try in R

```
library("cobalt")
data("lalonde", package = "cobalt")
covs0 <- subset(lalonde, select = -c(treat, re78, nodegree, married))
tab<-bal.tab(covs0, treat = lalonde$treat)

# output
print(tab)
love.plot(tab, binary = "std", threshold = .1)
bal.plot(covs0, treat = lalonde$treat, var.name='age')
bal.plot(covs0, treat = lalonde$treat, var.name='educ')
bal.plot(covs0, treat = lalonde$treat, var.name='race')
```

Why do we care?

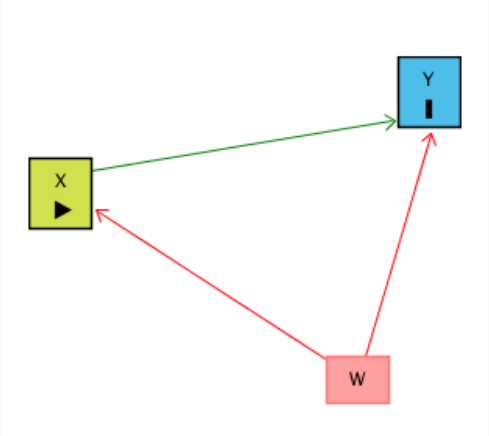
- The same reason we include controls in the regression of

$$y_i = \beta_0 + \beta_1 x_i + \beta_2 w_i + u_i$$

- We are interested in effect of x_i (training) on y_i (wages).
- But if w_i(ability, age, race, etc.) is correlated with both x_i and y_i then we need to include it our regression.
- Easy to see this as a Directed Acyclic Graph (DAG)
  - Think of $x \to y$ as "causes".

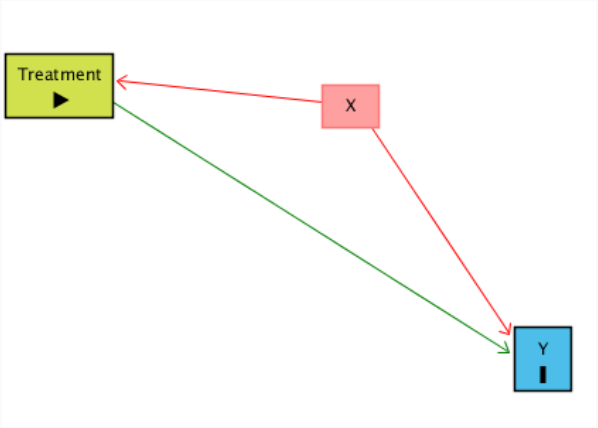
Control DAG: http://nickchk.com/causalgraphs.html

- We want the $x \rightarrow y$ path
- We do not want the $x \leftarrow w \rightarrow y$ path (Backdoor Path).
- Close the backdoor path by removing part of X and Y that depends on W.



Matching DAG: http://nickchk.com/causalgraphs.html

- We want the $T \rightarrow y$ path
- We do not want the $T \leftarrow x \rightarrow y$ path (Backdoor Path).
- Same idea as controls in OLS!



Nonparametric Matching (k-NN)

For each observation T_i, we observe $Y_i(T_i)$ compute a counterfactual $\hat{Y}_i(1-T_i)$:

$$\widehat{Y}_i(0) = \begin{cases} Y_i & \text{if } T_i = 0 \\ \frac{1}{\#\mathcal{J}_M(i)} \sum_{l \in \mathcal{J}_M(i)} Y_l & \text{if } T_i = 1 \end{cases}$$

$$\widehat{Y}_i(1) = \begin{cases} \frac{1}{\#\mathcal{J}_M(i)} \sum_{l \in \mathcal{J}_M(i)} Y_l & \text{if } T_i = 0 \\ Y_i & \text{if } T_i = 1 \end{cases}$$

- $\#\mathcal{J}_M(i)$ is the number of matches for i of opposite treatment assignment $T_l = 1 - T_i$.
- M is the "number of matches" within some distance of $|X_l - X_i| < d_M$.
- If there are ties $\#\mathcal{J}_M(i) > M$.
- This is just k-NN matching.

Matching

- Compare treated individuals to un-treated individuals with identical observable characteristics X_i.
- Key assumption: everything about $Y_i(1) - Y_i(0)$ is captured in X_i; or u_i is randomly assigned conditional on X_i.
- Basic idea: The treatment group and the control group don't have the same distribution of observed characteristics as one another.
- Re-weight the un-treated population so that it resembles the treated population.
- Once distribution of X_i is the same for both groups $X_i|T_i \sim X_i$ then we assume all other differences are irrelevant and can just compare means.
- Matching assumes all selection is on observables.

Matching

- Formally the key assumption is the Conditional Independence Assumption (CIA)

$$\{Y_i(1), Y_i(0)\} \perp T_i | X_i$$

- Once we know X_i allocation to treatment T_i is as if it is random.
- The only difference between treatment and control is composition $f(X_i)$ of the sample.

Matching

Let $F^1(x)$ be the distribution of characteristics in the treatment group, we can define the ATE as

$$\begin{aligned} & E[Y(1) - Y(0)|T = 1] = E_{F^1(x)}[E(Y(1) - Y(0)|T = 1, X)] \\ = \quad & E_{F^1(x)}[E(Y(1)|T = 1, X)] - E_{F^1(x)}[E(Y(0)|T = 1, X)] \text{ linearity} \end{aligned}$$

The first part we observe directly:

$$= \quad E_{F^1(x)}[E(Y(1)|T = 1, X)]$$

But the counterfactual mean is not observed!

$$= \quad E_{F^1(x)}[E(Y(0)|T = 1, X)]$$

But conditional independence does this for us:

$$E_{F^1(x)}[E(Y(0)|T = 1, X)] = E_{F^1(x)}[E(Y(0)|T = 0, X)]$$

Matching in Practice: Caliper Matching

How do we actually do this?

- For each entry in the treatment (y_t, x_t)
  - Find all x_s from the control group that is "close enough" $\|x_s - x_t\| < b_w$.
  - For each treated observation compute $\beta(x_t) = y_t - E[y_s | I(\|x_s - x_t\| < b_w)]$.
  - Compute the mean of $\beta(x_t)$
- Some pitfalls
  - Variance can be unpredictable: some (y_t, x_t) have many of matches, others have none
  - For some (y_t, x_t) may have nothing within $\|x_s - x_t\| < b_w$? Drop these?
- Can also use k-nearest neighbors instead.

Matching in Practice: Inverse Probability Weighting

How do we actually do this?

- Calculate a smoothed estimate of the treatment probability $\pi(x) = Pr(T_i = 1|x)$.

$$\frac{1}{n} \sum_{t \in \text{Treatment}} \frac{y_t}{\pi(x_t)} - \frac{1}{n} \sum_{s \in \text{Control}} \frac{y_s}{1 - \pi(x_s)}$$

- How to get $\pi(x)$? Run a logit or probit.
- We can stabilize the weights replace $w(x) = \frac{1}{\pi(x)}$ with:

$$w(x) = \frac{Pr(T = 1)}{\pi(x)} \text{ for } T_i = 1 \quad w(x) = \frac{Pr(T = 0)}{1 - \pi(x)} \text{ for } T_i = 0$$

- This sometimes helps crazy big weights when treated group is small.

A Matching Example

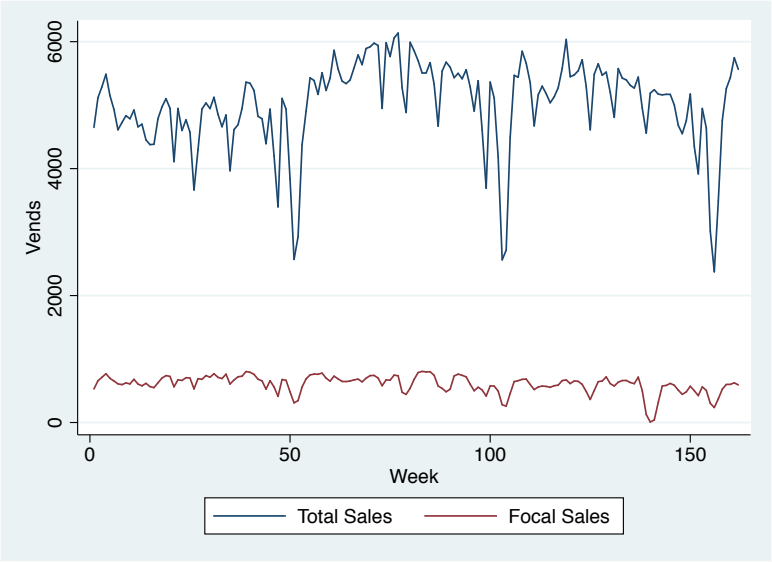
Here is an example where I found that matching was helpful in my own work with Julie Mortimer:

- We ran a randomized experiment where we removed Snickers bars from around 60 vending machines in office buildings in downtown Chicago.
- We have a few possible control groups:
  1. Same vending machine in other weeks (captures heterogeneous tastes in the cross section)
  2. Other vending machines in the same week (might capture aggregate shocks, ad campaigns, etc.)
- We went with #1 as #2 was not particularly helpful.

A Matching Example

Major problem was that there was a ton of heterogeneity in the overall level of (potential) weekly sales which we call M_t.

- Main source of heterogeneity is how many people are in the office that week, or how late they work.
- Based on total sales our average over treatment weeks was in the 74th percentile of all weeks.
- This was after removing a product, so we know sales should have gone down!
- How do we fix this without running the experiment for an entire year!
- Can't use shares instead of quantities. Why?


Vends
6000
4000
2000
0
0
50
100
150
Week
Total Sales
Focal Sales

A Matching Example

Ideally we could just observe M_t directly and use that as our matching variable X

- We didn't observe it directly and tried a few different measures:
  - Sales at the soda machine next to the snack machine
  - Sales of salty snacks at the same machine (not substitutes for candy bars).
  - We used k-NN with $k = 4$ to select control weeks – notice we re-weight so that overall sales are approximately same (minus the removed product).
- We also tried a more structured approach:
  - Define controls weeks as valid IFF
  - Overall sales were weakly lower
  - Overall sales were not less than Overall Sales less expected sales less Snickers Sales.

Product	Control Mean	Control %ile	Treatment Mean	Treatment %ile	Mean Difference	% Δ
Vends						
Peanut M&Ms	359.9	73.6	478.3*	99.4	118.4*	32.9
Twix Caramel	187.6	55.3	297.1*	100.0	109.5*	58.4
Assorted Chocolate	334.8	66.7	398.0*	95.0	63.2*	18.9
Assorted Energy	571.9	63.5	616.2	76.7	44.3	7.8
Zoo Animal Cracker	209.1	78.6	243.7*	98.1	34.6*	16.5
Salted Peanuts	187.9	70.4	216.3*	93.7	28.4	15.1
Choc Chip Famous Amos	171.6	71.7	193.1*	95.0	21.5*	12.5
Ruger Vanilla Wafer	107.3	59.7	127.9	78.6	20.6*	19.1
Assorted Candy	215.8	43.4	229.6	60.4	13.7	6.4
Assorted Potato Chips	279.6	64.2	292.4*	66.7	12.8	4.6
Assorted Pretzels	548.3	87.4	557.7*	88.7	9.4	1.7
Raisinets	133.3	66.0	139.4	74.2	6.1	4.6
Cheetos	262.2	60.1	260.5	58.2	-1.8	-0.7
Grandmas Choc Chip	77.9	51.3	72.5	37.8	-5.4	-7.0
Doritos	215.4	54.1	203.1	39.6	-12.3*	-5.7
Assorted Cookie	180.3	61.0	162.4	48.4	-17.9	-10.0
Skittles	100.1	62.9	75.1*	30.2	-25.1*	-25.0
Assorted Salty Snack	1382.8	56.0	1276.2*	23.3	-106.7*	-7.7
Snickers	323.4	50.3	2.0*	1.3	-321.4*	-99.4
Total	5849.6	74.2	5841.3	73.0	-8.3	-0.1

Notes: Control weeks are selected through the-neighbor matching using four control observations for each treatment week. Percentiles are relative to the full distribution of control weeks.

Higher Dimensions

So matching works great in dimension 1. But what if $dim(X) > 1$?

- True high-dimensional matching may be infeasible. There may be no set of weights such that: $f(X_i|T_i = 1) \equiv \int w_i f(X_i|T_i = 0) \partial w_i$.
- One solution is the nearest-neighbor approach in Abadie Imbens (2006).
- This is still cursed in that our nearest neighbors get further away as the dimension grows.
- Suppose instead we had a sufficient statistic

Propensity Score

- Rosenbaum and Rubin propose the propensity score

$$P(T_i = 1|X_i) \equiv P(X_i)$$

- They prove that the propensity score and any function of X, $b(X)$ which is finer serves as a balancing score.
- Finer implies that:

$$\begin{aligned} b(X^1) = b(X^2) &\implies P(X^1) = P(X^2) \\ P(X^1) = P(X^2) &\not\implies b(X^1) = b(X^2) \end{aligned}$$

Propensity Score

- Main result: If treatment assignment is strongly ignorable conditional on X (CIA) then it is strongly ignorable $Y(1), Y(0) \perp T|X$ given any balancing score $b(X)$ including the propensity score:

$$\begin{aligned} Pr(T = 1|Y(1), Y(0), P(X)) &= E[Pr(T = 1|Y(1), Y(0), X)|P(X)] \\ &= E[Pr(T = 1|x)|P(X)] = P(X) \end{aligned}$$

- Also we require that $0 < P(X) < 1$ at each X which is known as the support condition.
- The theorem implies that given $P(X)$ we have as if random assignment.

Propensity Score

- Instead of matching on K dimensional X we can now match on a one-dimensional propensity score
- Thus the propensity score provides dimension reduction
- We still have to estimate the propensity score which is a high dimensional problem without *ad-hoc* parametric restrictions.
- Let us begin by assuming a can-opener.
- An easy way would be to use $\pi(x)$ from logit or probit.

Propensity Score

Just like in the matching case the problem arises because we do not observe the counterfactual mean:

$$E_{F^1(x)}[E(Y(0)|T=1,X)]$$

With conditional independence and the propensity score:

$$\begin{aligned} E_{F^1(x)}[E(Y(0)|T=1,X)] &= E_{F^1(x)}[E(Y(0)|T=0,X)] \\ &= E_{F^1(x)}[E(Y(0)|T=0,P(X))] \end{aligned}$$

Kernel Matching

How do we implement?

- Kernels are an obvious choice

$$\widehat{ATT} = \frac{1}{N_1} \sum_{i \in T=1} \left[Y_i - \frac{\sum_{j \in T=0} Y_j K\left(P(X_i) - P(X_j)\right)}{\sum_{s \in T=0} K\left(P(X_i) - P(X_s)\right)} \right]$$

  where N_1 is the sample size of the treatment group
  and $K(u)$ is a valid Kernel weight (people tend to use Gaussian Kernels here)
- As your propensity score gets further away from observation i you get less weight
- As $h \to 0$ (or σ_h) the window gets smaller and we use fewer neighbors.

Kernel Matching

- The usual caveats apply: h determines the bias-variance tradeoff
- Choice of Kernel effects finite-sample properties
- Here the common support is important. We can only learn about cases where $P(X) \neq 1$ and $P(X) \neq 0$. If you always get treated (or not-treated) we cannot learn from this observation.
- We also have to be careful in choosing X so as not to violate CIA (too many X's , too few X's) $\rightarrow$ have to think carefully!
- If you use propensity scores you will need a slide convincing us you have thought about why CIA holds for you!

Gotcha!

Under CIA we know

$$G(Y(1), Y(0)|X, T) = G(Y(1), Y(0)|X)$$

Suppose we add in Z, then we require that:

$$G(Y(1), Y(0)|X, Z, T) = G(Y(1), Y(0)|X, Z)$$

$$\begin{aligned} G(Y(1), Y(0)|X, T) &= \int G(Y(1), Y(0)|X, Z, T) dF(Z|X, T) \\ &= G(Y(1), Y(0)|X) \end{aligned}$$

where the last part follows by CIA.

- Thus each element can depend on T conditional on Z, X but the average may not.
- Mindless applications of matching can give you biased results!

Matching and OLS

- Recall that OLS is a special case of Kernel regression (and hence matching!)
- Think about

$$Y = \alpha + \beta T_i + u$$

- Assume that $E(u|T, X) = E(u|X)$ which is a conditional mean independence assumption
- The we can get β consistently (but not other variables) by running the following:

$$Y = \alpha + \beta T_i + \gamma X + v$$

- Again we are in the homogenous treatment world

Exercises

- This would be a good time to work through the vignette for `cobalt` `https://cran.r-project.org/web/packages/cobalt/vignettes/cobalt_A0_basic_use.html`
- Compare the ATE for the Lalonde data with the IPW, Nearest Neighbor, and Propensity Score estimates.
- Then start the homework

Up next...

Local Average Treatment Effects.