

第9講 マッチング手法

先に述べたように、政策を実施した処理群のデータはあるが、対照群のデータは不在であり、外部情報から対処群をみつけてマッチングさせる必要が出てくる場合には次のような手法を用いる。

実際に外部データが十分にあり、処理群に含まれる個別サンプルの全ての変数、属性にぴったり一致するような対照群サンプルを選ぶことが出来れば、これを**完全一致マッチング (exact matching)**と呼ぶが、分析に用いる変数が増えるに従って、個別変数をマッチングさせることは難しくなる。このような場合、変数一つ一つをマッチングさせるのではなく、ある程度変数を集約して表現した条件付き確率（これを傾向スコア；**propensity score**と呼ぶ）を処理群と対照群でマッチングさせるという方法が考えられる¹。

具体的な考え方は、処理群に選ばれる確率 $[\Pr[d_i = 1 | x]]$ を全サンプルを用いたロジット推定によって求め、それを処理群と対照群に分け、さらに確率を均等な階層に分け、同じ階層に入るもの同士をマッチングさせ、処理効果の平均を求めるというものである。ここでマッチングをどうするかということが問題になる。すなわち、一度マッチングに使った対照サンプルを再び使うことを認めるかどうか、比較対照するために処理サンプルに対していくつの対照サンプルを割り当てるのか。最も propensity score が近いもの一つを選ばばいいのか (**caliper matching** と言う)、それともその周辺の対照サンプルを複数割り当てるのがいいのか、また、具体的なマッチングの方法としてどのようなものを用いるのか、といった問題がある²。

マッチングの詳細な手法はかなり技術的に高度になるので、ここでは扱わないが、主要な手法の基本的な考え方を紹介しておきたい³。一般に処理効果は次のように表すことが出来る。

$$\Delta^M = \frac{1}{N_T} \sum_{i \in \{d=1\}} [y_{i1} - \sum_j w(i, j) y_{j0}]$$

¹この方法は Rosenbaum and Rubin (1983) によって開発され、現在では以下で紹介するように沢山の拡張が行われている。

²実際にこれらの問題にどう対処するかということは研究者の判断にゆだねられている。逆に、決定的に正しい方法が知られているわけではなく、試行錯誤するしかない。

³最新のマッチング手法のアルゴリズムに関しては、Abadie et al (2004)、Becker and Ichino (2002)、Becker and Caliendo (2007) 等を参照されたい。

ここで $\sum w(i, j) = 1$ 、 $0 < w(i, j) \leq 1$ となるマッチング・ウェイトである。 N_T は処理群のサンプル数を表す。

対照群としてどのようなサンプルを処理群にマッチさせるかという事であるが次のようなマッチング手法が提案されている。(1) **最近傍マッチング (nearest-neighbor matching)** の考え方では、全ての処理サンプル i に対して、次のような条件を満たす集合 $A_i(x) = \{j | \min_j \|x_i - x_j\|\}$ を対照群として選択する⁴。(2) **カーネル・マッチング (kernel matching)** では、ウェイトを次のように定義する $w(i, j) = K(x_j - x_i) / \sum_{j=1}^{N_{ic}} K(x_j - x_i)$ 、ここで K はカーネル関数を表す。(3) **層化マッチング (stratification matching)** とは propensity score を均等に層化し、層内で処理群と対照群が同じスコアになるようにした後で、処理効果を推定する。同じスコアのペアが組めない場合には、その層内での処理効果は計算されない。(4) **半径マッチング (radius matching)** では対照群集合を次のように定義する。 $A_i(p(x)) = \{p_j | \|p_i - p_j\| < r\}$ すなわち、 propensity score の差が半径 r 以内であればペアとしてマッチングするという方法である。

マッチング手法⁵

I_0 the index for non-participant

I_1 the index for participant

The effect of treatment for each treated observation $i \in I$

$$\Delta^{MAT} = \frac{1}{N_1} \sum_{i \in Z_1} \left[Y_i^1 - \sum_{j \in Z_0} W_{N_0}(i, j) Y_j^0 \right]$$

$\sum_j W_{N_0}(i, j) = 1$ ∇_i the total weight of all

controls sums up to one for each treated neighbourhood individual.

$C(P_i)$ for each i in the participant sample and denote as neighbours for i those non-participants

$$j \in A_i \quad \text{where} \quad A_i = \{j \in I_0 | P_j \in C(P_i)\}$$

Nearest-Neighbour-Matching 最近傍マッチング (NN マッチング)

$$C^{NN}(p_i) = \min_j \|p_i - p_j\| \cdot j \in N_0$$

$$W_{N_0}^{NN}(i, j) = \begin{cases} 1 & \text{if } \|p_i - p_j\| = \min_j \|p_i - p_j\| \\ 0 & \text{otherwise} \end{cases}$$

NN matching with replacement and without replacement

If we allow replacement(再利用可) the average quality of matching will **increase** and the bias will **decrease**.

⁴ $\|\cdot\|$ はベクトル間のユークリッド距離を表す。

⁵ 以下は Cameron and Trevedi (2005, pp.874-878) を参照。

When using oversampling, one has to decide how many matching partners m should be chosen for each individual i and which weight should be assigned to them. One possibility is to use *uniform weights*. $(1/m)$

All the m control individuals within set A_i receive the weight $1/m$ whereas all other individuals from the control group receive the weight zero

$$W^{NN^0}(i, j) = \begin{cases} 1 & \frac{1}{m} \text{ if } j \in A_i \\ 0 & \text{otherwise} \end{cases}$$

Triangular weights, the m individuals with set A_i has to be ranked where $\rho = 1$ is the closest neighbour. $\rho = 2$ the next closest.

Caliper and Radius Matching

NN matching faces the risk of bad matches, if the closest neighbour is far away. This can be avoided by imposing a *tolerance level* on the maximum distance $\|p_i - p_j\|$ allowed.

$$w^{CM}(i, j) = \begin{cases} 1 & \text{if } \|p_i - p_j\| = \min_j \|p_i - p_j\| \wedge \|p_i - p_j\| < \varepsilon \\ 0 & \text{otherwise} \end{cases}$$

Stratification and Interval Matching

To implement STM, the propensity score is used to divide the full sample into M blocks of units of approximately equal probability of treatment.

Let J is be an indicator for unit i being in blocks. One way of implementing this is to divide the unit interval into ξ blocks with boundary values equal to $\frac{s}{\xi}$ for $s = 1, \dots, s - 1$.

$$J_{is} = \left\{ \frac{s-1}{\xi} < p(x_i) \leq \frac{s}{\xi} \right\}$$

$$N_{1s}(\text{treated}) = \sum_i \{D_i = 1, J_{is} = 1\}$$

$$N_{0s}(\text{untreated}) = \sum_i \{D_i = 0, J_{is} = 1\}$$

Average Treatment effect within each block

$$\Delta_s^{STM} = \frac{1}{N_{1s}} \sum_{i=1}^N J_{is} D_i Y_i - \frac{1}{N_{0s}} \sum_{i=1}^N J_{is} (1 - D_i) Y_i$$

overall average treatment effect

$$\Delta_{ATE}^{STM} = \sum_{s=1}^S \Delta_s^{STM} \frac{N_{1s} + N_{0s}}{N}$$

$$\Delta_{ATT}^{STM} = \sum_{s=1}^S \Delta_s^{STM} \frac{N_{1s}}{N_1}$$

The within block average treatment effects by the number of treated units.

Kernel and Local Polynomial Matching

Kernel Matching (KMA) and local linear matching (LLM) and non-parametric matching estimates that were all units in the control group to constructed a match for each programme participant.

And advantage is the lower variance is head for constructing counterfactual outcomes.

If weights from symmetric, non-negative, unimodal Kernel and Wed , then the average places higher weight on persons close in terms of P_i and lower weight on more distant observations. Kernel matching set $A_i = I_0$ and s uses the following weights:

$$W_{ND}^{KM}(i,j) = \frac{G_{ij}}{\sum_{K \in Z_0} G_{iK}}$$

when $G_{iK} = G[(P_i - P_k)/GN_0]$ is a Kernel

that downweights distant observations from P_i and aN_0 is a bandwidth parameter.

Kernel Functions

Rectangular/uniform	$K(x) = \frac{1}{2}$	$ x \leq 1$
Epanchnikov	$K(x) = \frac{3}{4\sqrt{5}}(1 - \frac{1}{5}x^2)$	$ x \leq \sqrt{5}$
	$\{-\frac{3}{4}(1 - x^2)$	$ x \leq 1\}$
Quadratic (biweight)	$K(x) = \frac{15}{16}(1 - x^2)^2$	$ x \leq 1$
Triangular	$K(x) = (1 - x)$	$ x \leq 1$
Normal/Gaussian	$K(x) = \frac{1}{\sqrt{2\pi}}e^{-0.5x^2}$	$-\infty < x < \infty$

A generalized version of KM is local linear matching LLM has a faster rate of convergence near boundary points, and greater robustness to different data design densities.

$$W^{LLM}(i,j) = \frac{G_{ij} \sum_{k \in I_0} G_{ik} (P_k - P_i)^2 - [G_{ij} (P_j - P_i)] [\sum_{K \in I_0} G_{iK} (P_K - P_i)]}{\sum_{j \in I_0} G_{ij} \sum_{K \in I_0} G_{iK} (P_K - P_i)^2 - (\sum_{K \in I_0} G_{iK}) (P_K - P_i)}$$

Weighting on the Propensity Slovic Hirano and Imbens (2002) suggest a straightforward way to implement this estimator by re-weighting treated and control observations to make them representative of the population of interest.

$$\begin{aligned} E \left[\frac{YD}{P(X)} \right] &= E \left[\frac{Y^1 D}{P(X)} \right] = E \left[E \left[\frac{Y^1 D}{P(X)} \middle| X \right] \right] \\ &= E \left[\frac{P(X) E[Y^1 | X]}{P(X)} \right] = E[Y^1] \end{aligned}$$

Unconfoundedness

$$E \left[\frac{(1-D)Y}{1-P(X)} \right] = E[Y^0]$$

The Average Treatment Effect.

$$E \left[\frac{YD}{P(X)} - \frac{(1-D)Y}{1-P(X)} \right] = E[Y^1 - Y^0] = \Delta_{ATE}$$

If the propensity score is known, the estimator can directly be implemented as the difference between a weighted average of the outcomes for the treated individuals and a weighted

Trade-offs in Teams of bias and Efficiency

	<i>Bias</i>	<i>Variance</i>
Nearest neighbour matching:		
multiple neighbour	+/-	-/+
Single neighbour with caliper/without caliper		+/-
Use of Control individuals:		
With replacement/without replacement	-/+	(+)/(-)
Use of Control individuals:		
With replacement/without replacement	(-)/(+)	(+)/(-)
NN-matching/Radical matching	-/+	+/-
KM/LLM/NN method	+/-	-/+
Band width choice with KM small/large	-/+	+/-

average of the outcomes for the non-participants.

The weights can be normalized to unity. The simple weighting estimator is given by

$$\Delta_{ATE}^{WG} = \sum_{i=1}^N \frac{P_i Y_i}{\hat{P}(X_i)} \Big/ \sum_{i=1}^N \frac{D_i}{\hat{P}(X_i)} - \sum_{i=1}^N \frac{(1-D_i) Y_i}{1-\hat{P}(X_i)} \Big/ \sum_{i=1}^N \frac{1-D_i}{1-\hat{P}(X_i)}$$

ATT

$$\Delta_{ATT}^{WG} = \left[\frac{1}{N_1} \sum_{i \in I_1} Y_1 \right] - \left[\sum_{i \in I_0} Y_i \cdot \frac{\hat{P}(X_i)}{1-\hat{P}(X_i)} \Big/ \sum_{i \in I_0} \frac{\hat{P}(X_i)}{1-\hat{P}(X_i)} \right]$$

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