

Triplet Matching:

Propensity Score Matching with 3 Groups

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Outline

1. Review of propensity score matching
2. Triplet matching
3. Alternative approaches

Propensity Score Review

- **Goal:** causal inference on a treatment/exposure variable X , observational study
- For binary X , PS is “the probability of treatment assignment conditional on observed baseline characteristics” - **Austin 2011**
 - PS typically estimated by logistic regression, although machine learning can be used
- “Balancing score”: conditional on PS, distribution of baseline covariates should be balanced between treatment groups, similar to an RCT

4 main PS methods

Table 2. Advantages and disadvantages of the 4 major techniques used to apply the propensity scores to estimate treatment effect ^{2-4,13-15,19,20,23-27,29,31}

| Methods | Advantages | Disadvantages |
|--|--|---|
| Matching | Superior at reducing bias compared with stratification and covariate adjustment Presentation of analyses and results is very similar to randomized trial* Transparent [†] | Unmatched treated participants, and possibly unmatched control participants, are excluded from the analysis, decreasing precision of the treatment effect estimate and external validity Requires more control participants than treated participants |
| Stratification | Uses all data | Reduces bias less than matching and weighting Does not work well with survival analysis |
| Covariate adjustment | Uses all data | No clear distinction between the design phase and the analysis phase Assessing balance in baseline covariates between treatment groups is more cumbersome compared with the other methods Produces only odds and hazard ratios and leads to biased estimates of these ratios Requires the specification of a regression model for the relationship between the outcome and the propensity score Outcome always in sight, so temptations toward an anticipated model is always present |
| Inverse probability of treatment weighting | Superior at reducing bias compared with stratification and covariate adjustment Presentation of analyses and results is very similar to randomized trial* Uses all data | May be more sensitive to mis-specification of the propensity-score model and extreme propensity-score values |

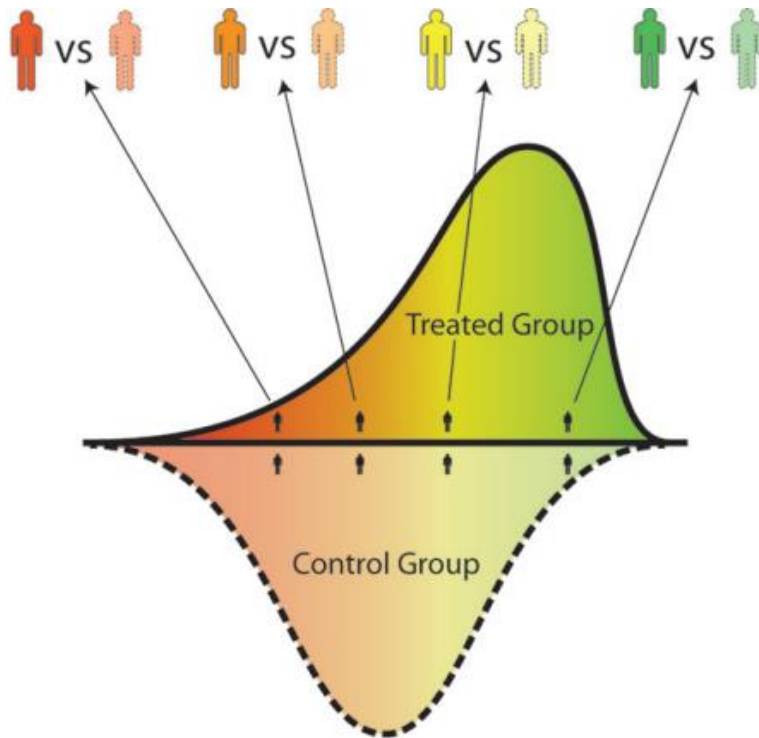
* Similar to randomized trials in that simple absolute and relative measures of effect can be reported. Similarly, the baseline covariates of the treated and control samples can be easily described and presented.

[†] Transparent (ie, easy to follow).

For review:

- Deb, Saswata, et al. "A review of propensity-score methods and their use in cardiovascular research." *Canadian Journal of Cardiology* 32.2 (2016): 259-265.
- Austin, Peter C. "An introduction to propensity score methods for reducing the effects of confounding in observational studies." *Multivariate behavioral research* 46.3 (2011): 399-424.

1:1 PS Matching



- Can think of PS as a univariate composite summary of all baseline covariates
- Matched patients must have similar PS value

Matching: many choices

Austin 2014 performed extensive simulations and made the following **recommendations**:

- Optimal vs **greedy nearest neighbor matching**?
- **Caliper** or no caliper?
- Match with or **without replacement**?
- Order in which treated subjects are selected (e.g. lowest to highest propensity score, highest to lowest propensity score, best match first, or **random order**)

Triplet Matching

Generalized propensity score (GPS)

- Extend propensity score for multcategory, ordinal, or continuous treatments
- I will focus on the unordered 3 group case (A, B, C)
- $\mathbf{GPS}_i = [\Pr(X_i = A|Z_i), \Pr(X_i = B|Z_i), \Pr(X_i = C|Z_i)]$ for baseline covariates Z
 - Can estimate using multinomial logistic regression or machine learning methods
- Matched triplets: all 3 patients must have similar GPS *vectors*. Example:

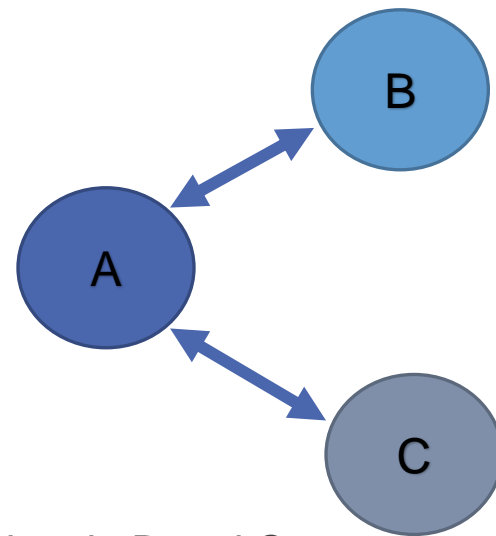
| Subject | True Group | $\Pr(X=A Z)$ | $\Pr(X=B Z)$ | $\Pr(X=C Z)$ |
|---------|------------|--------------|--------------|--------------|
| 1 | A | 0.30 | 0.60 | 0.10 |
| 2 | B | 0.29 | 0.59 | 0.12 |
| 3 | C | 0.31 | 0.61 | 0.08 |

Matching with 3 groups

- See [Lopez 2017](#) for review

Pairwise or “common referent matching” (CRM):

1. Define reference group A (usually smallest group)
 2. Match A to B
 3. Match A to C
 4. Form triplets by only keeping patients in A that had matches in B and C.
- Typically perform pairwise 2-group matching using 2 separate logistic regression models to estimate $\Pr(X = A|Z)$, although one could match on multinomial estimate of $\Pr(X = A|Z)$



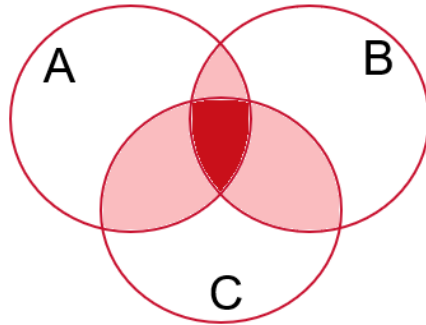
Pairwise matching

Pros:

- Straightforward to implement using existing 2-group matching software (e.g. SAS PSMATCH, or R packages MatchIt, matching)

Cons:

- **Lopez 2017** argues that “transitive property” not guaranteed: even if covariates are balanced for A vs B and A vs C, it’s possible that B vs C is unbalanced



Example

- “Real World Outcomes of TAVR with the SAPIEN-3 Valve in Intermediate Risk Patients: Comparison of Data from the TVT Registry with PARTNER S3 Studies”
2018 <https://www.tctmd.com/slide/real-world-outcomes-tavr-sapien-3-valve-intermediate-risk-patients-comparison-data-tvt>
- Patients with severe aortic stenosis, intermediate surgical risk (IR), treated with SAPIEN 3 TAVR
 - The PARTNER II S3i trial demonstrated safety and efficacy
- It remains unknown whether TAVR with the S3 valve can be performed with similar safety and efficacy in real-world practice
- **Goal:** compare 30-day outcomes in IR patients from 3 data sources: **S3i** trial, S3i continued access registry (**S3iCAP**), ACC/STS Transcatheter Valve Therapeutics Registry (**TVT-R**).

Use pairwise triplet matching to adjust for baseline covariates

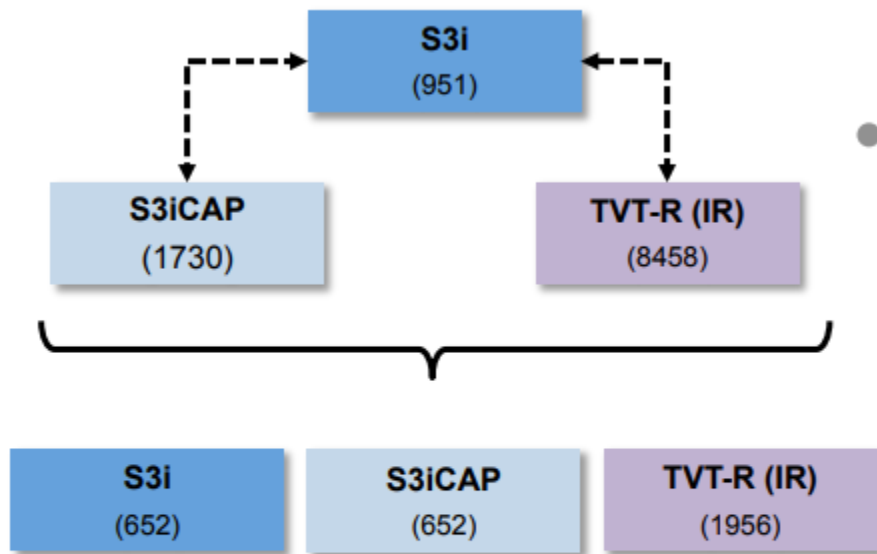
Baseline characteristics

| | S3i N = 1077 | S3iCAP N = 1814 | TVT-R (IR) N = 8781 | Overall P-value |
|----------------------------------|-----------------|--------------------|------------------------|--------------------|
| Age years | 81.9 ± 6.60 | 80.7 ± 6.02 | 79.6 ± 7.66 | <0.001 |
| Sex % female | 38.3 | 43.3 | 43.3 | 0.006 |
| * STS Score % ± std. dev. | 5.3 ± 1.29 | 4.4 ± 1.21 | 4.4 ± 1.49 | <0.001 |
| NYHA III/IV % | 72.5 | 62.4 | 68.6 | <0.001 |
| Prior MI % | 16.0 | 13.8 | 18.9 | <0.001 |
| Prior Stroke % | 9.0 | 7.2 | 9.2 | 0.029 |
| Chronic Lung Disease % | 30.0 | 31.9 | 33.4 | 0.050 |
| LVEF % ± std. dev. | 58.6 ± 13.37 | 59.4 ± 10.73 | 57.6 ± 11.44 | <0.001 |
| MR % Mod/Sev | 8.8 | 22.6 | 23.9 | <0.001 |
| TR % Mod/Sev | 6.6 | 13.9 | 16.3 | <0.001 |
| Transfemoral Access % | 88.3 | 95.4 | 96.3 | <0.001 |

* did not match on STS Score, since one of the outcomes of interest was 30 day O:E ratio (observed 30 day mortality rate / STS score)

<https://www.tctmd.com/slide/real-world-outcomes-tavr-sapien-3-valve-intermediate-risk-patients-comparison-data-tvt>

Pairwise Triplet Matching



Propensity Matched Analysis

- 1:1:3 subject selection
- Transfemoral population
- 24 baseline covariates
 - Missing values: imputed using Markov Chain Monte Carlo method
- Logistic regression model
- S3i used as control

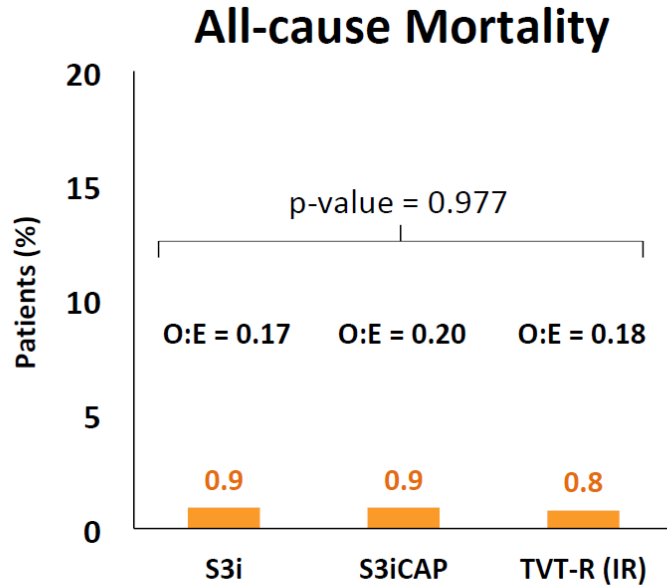
Baseline characteristics after matching

| | S3i N = 652 | S3iCAP N = 652 | TVT-R (IR) N = 1956 | Overall P-value |
|----------------------------------|----------------|-------------------|------------------------|--------------------|
| Age years | 81.3 ± 6.91 | 81.4 ± 5.61 | 81.1 ± 6.72 | 0.480 |
| Sex % female | 41.1 | 36.3 | 40.5 | 0.129 |
| * STS Score % ± std. dev. | 5.2 ± 1.30 | 4.5 ± 1.21 | 4.4 ± 1.46 | <0.001 |
| NYHA III/IV % | 69.2 | 68.1 | 69.7 | 0.745 |
| Prior MI % | 14.3 | 13.7 | 15.4 | 0.510 |
| Prior Stroke % | 8.6 | 8.3 | 8.4 | 0.980 |
| Chronic Lung Disease % | 31.1 | 29.0 | 30.2 | 0.696 |
| LVEF % ± std. dev. | 58.9 ± 13.45 | 59.1 ± 10.63 | 58.5 ± 10.69 | 0.414 |
| MR % Mod/Sev | 13.4 | 13.8 | 14.6 | 0.729 |
| TR % Mod/Sev | 9.6 | 10.0 | 8.7 | 0.573 |

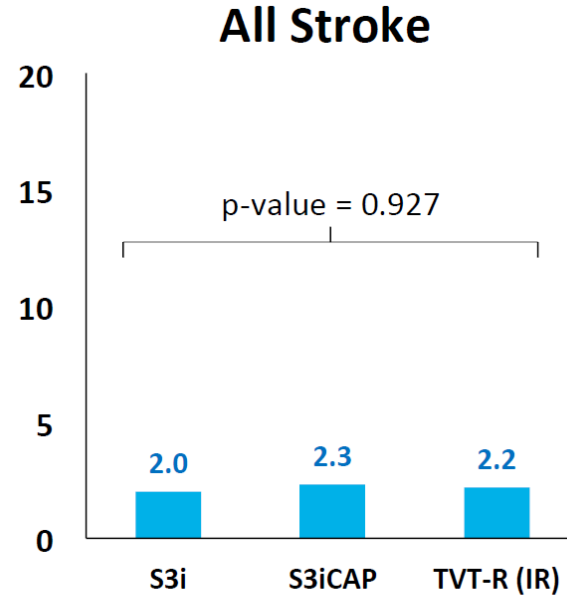
* did not match on STS Score, since one of the outcomes of interest was 30 day O:E ratio (observed 30 day mortality rate / STS score)

<https://www.tctmd.com/slide/real-world-outcomes-tavr-sapien-3-valve-intermediate-risk-patients-comparison-data-tvt>

Results



| | | | |
|------------|------|------|------|
| STS | 5.19 | 4.47 | 4.44 |
| # Patients | 652 | 652 | 1956 |
| # Sites | 51 | 60 | 453 |



| | | | |
|------------|-----|-----|------|
| # Patients | 652 | 652 | 1956 |
| # Sites | 51 | 60 | 453 |

Conclusion: after propensity matching, the 3 data sources (clinical and real world data) are comparable for the outcomes of interest

Simultaneous matching

- Simultaneously form triplets that are close on all 3 elements of GPS vector

How to define “close”?

- One could constrain the total distance between each pair of vectors, or the sum
- Instead, I used 3 separate “caliper widths” to ensure all patients within a triplet are close on each element of the GPS vector
- **Pro:** unlike Pairwise, one can directly control distance between each element of GPS vector, which may lead to better covariate balance
- **Con:** more computationally challenging to implement, limited available software

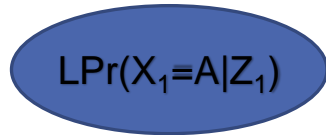
3 calipers widths:

$$W_A = \tau * SD\{\text{logit}[\text{Pr}(X=A|Z)]\}, \quad W_B = \tau * SD\{\text{logit}[\text{Pr}(X=B|Z)]\}, \quad W_C = \tau * \text{logit}[\text{Pr}(X=A|Z)]$$

$\tau=0.2$ as recommended in Austin 2011 and Wang 2013

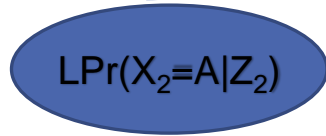
Subject:

1



$<W_A$

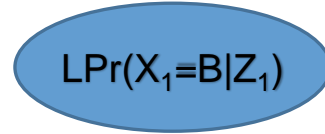
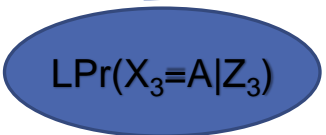
2



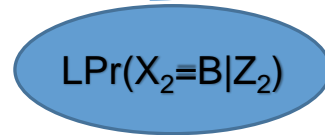
$<W_A$

$<W_A$

3

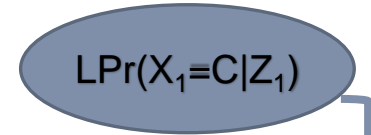
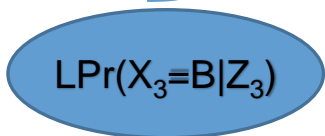


$<W_B$

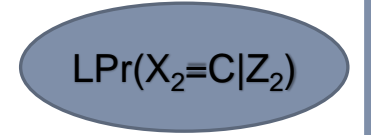


$<W_B$

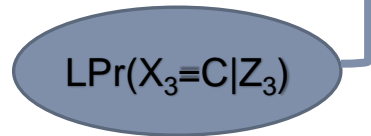
$<W_B$



$<W_C$



$<W_C$



Checking covariate balance

2 groups

- Can use “standardized differences” to assess balance between groups (see Austin 2011 and references therein)

Continuous variable:
$$d = \frac{(\bar{x}_{treatment} - \bar{x}_{control})}{\sqrt{\frac{s_{treatment}^2 + s_{control}^2}{2}}}$$

Binary variable:

$$d = \frac{(\hat{p}_{treatment} - \hat{p}_{control})}{\sqrt{\frac{\hat{p}_{treatment}(1 - \hat{p}_{treatment}) + \hat{p}_{control}(1 - \hat{p}_{control})}{2}}}$$

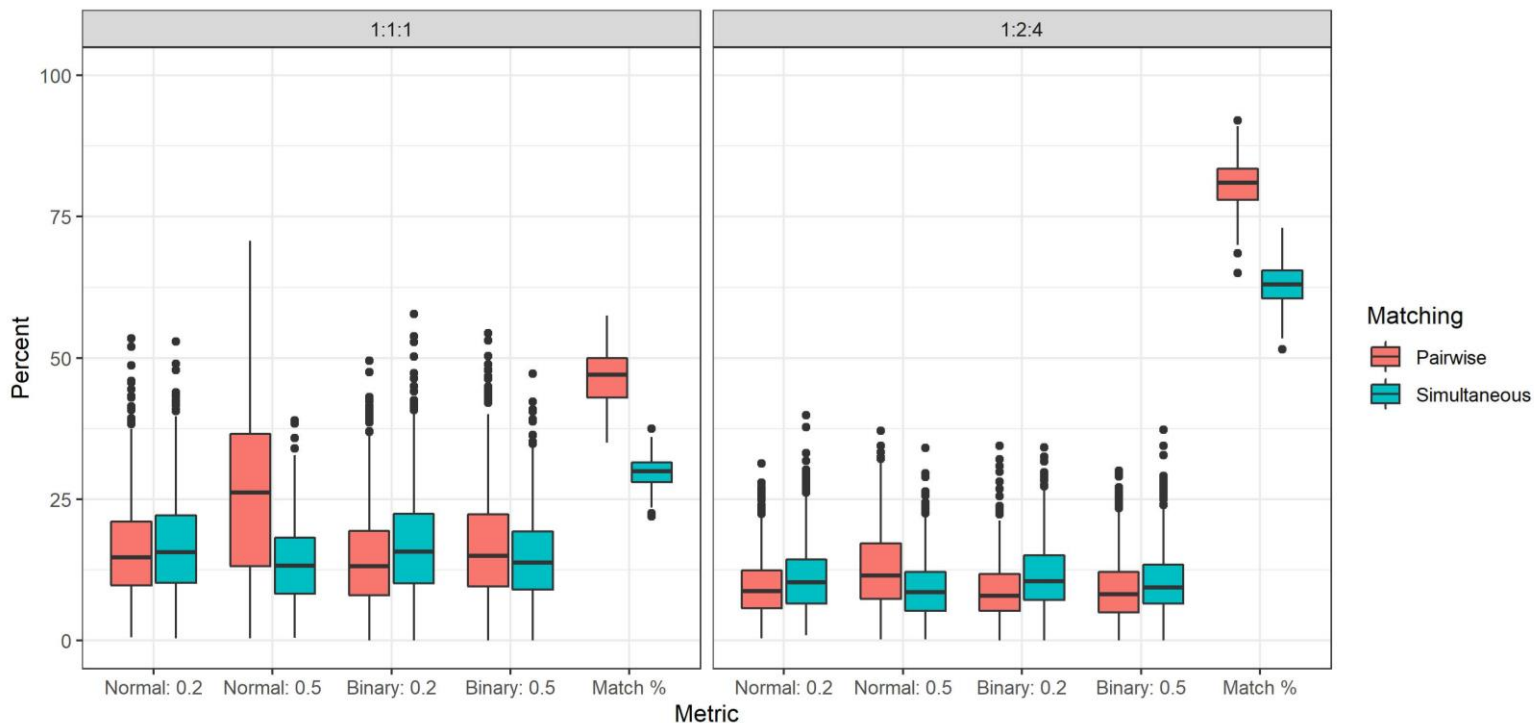
Cutoffs of ≤ 0.1 (Austin 2011) and ≤ 0.25 (Harder 2010) have been used

3+ groups

- Lopez 2017: calculate all pairwise standardized differences, then require the maximum standardized difference to be $\leq C$

cobalt R package: easily check standardized differences before and after matching with ≥ 2 groups (both tabular outputs and plots)

Simulations: Pairwise vs Simultaneous matching



- Pairwise results in better Match % (% matched in smallest group)
- Other boxplots show standardized diffs after matching (lower=better) for Normal & Binary covariates, simulated with standardized diffs of 0.2 or 0.5. Simultaneous is better for Normal 0.5

Alternative approaches

Weighting:

- weightit R package supports 3+ groups and can check covariate balance using cobalt R package
- Lu 2019: “Propensity score inverse weighting and regression approaches... are generally not optimal for use in pre-market medical device applications...”

Stratification:

- How to stratify on a multivariate vector (GPS)? Imai 2004 and Brown 2020
- Lopez 2017 proposes a clustering + stratified pair matching approach (no code)

Conclusion

- One can easily implement pairwise matching in practice and use when covariate balance is achieved (e.g. max standardized pairwise diff < 0.1 or 0.25)
- Simultaneous matching may be better in theory, but need more research and software development
 - Nattino 2021 seems promising

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