

Proposal of a general macro framework for propensity-score matching (RW03)

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Introduction

Very Short Introduction to Propensity-Score Matching

Procedure Overview

Suggested Framework

Conclusion

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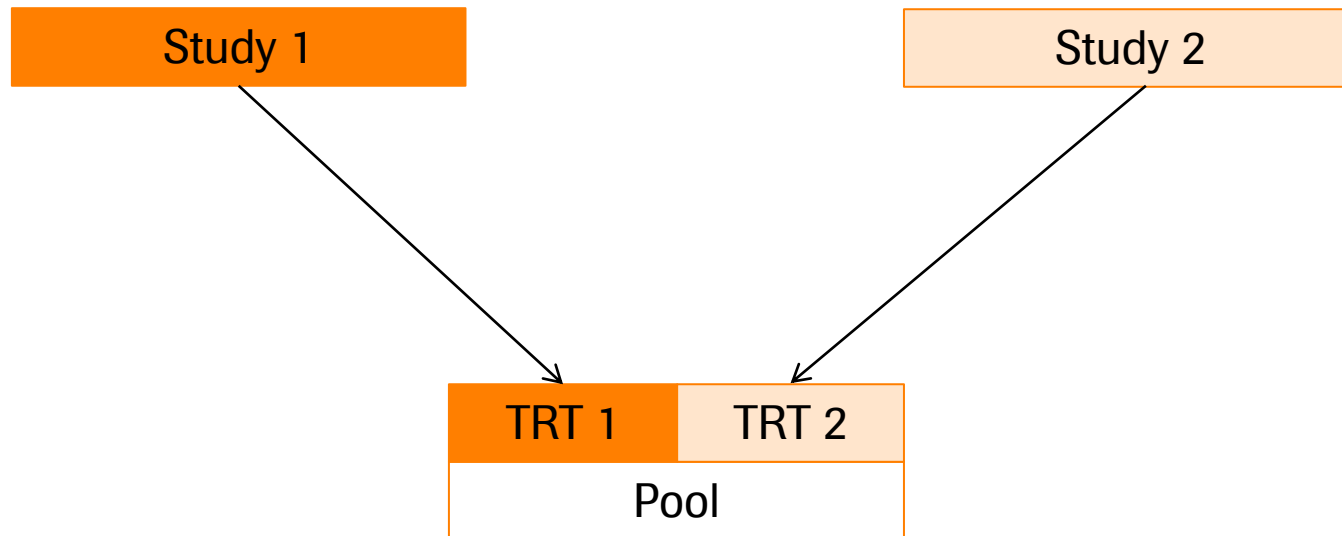
What do you need propensity-score matching for?

Scenario 1

Randomized Controlled Trial	Non-Interventional Study (NIS)
Random treatment assignment	Self-selection into treatment and control group
Subject characteristics balanced across groups	Between-group imbalances due to self-selection
→ Naïve estimate unbiased	→ Naïve estimate potentially biased

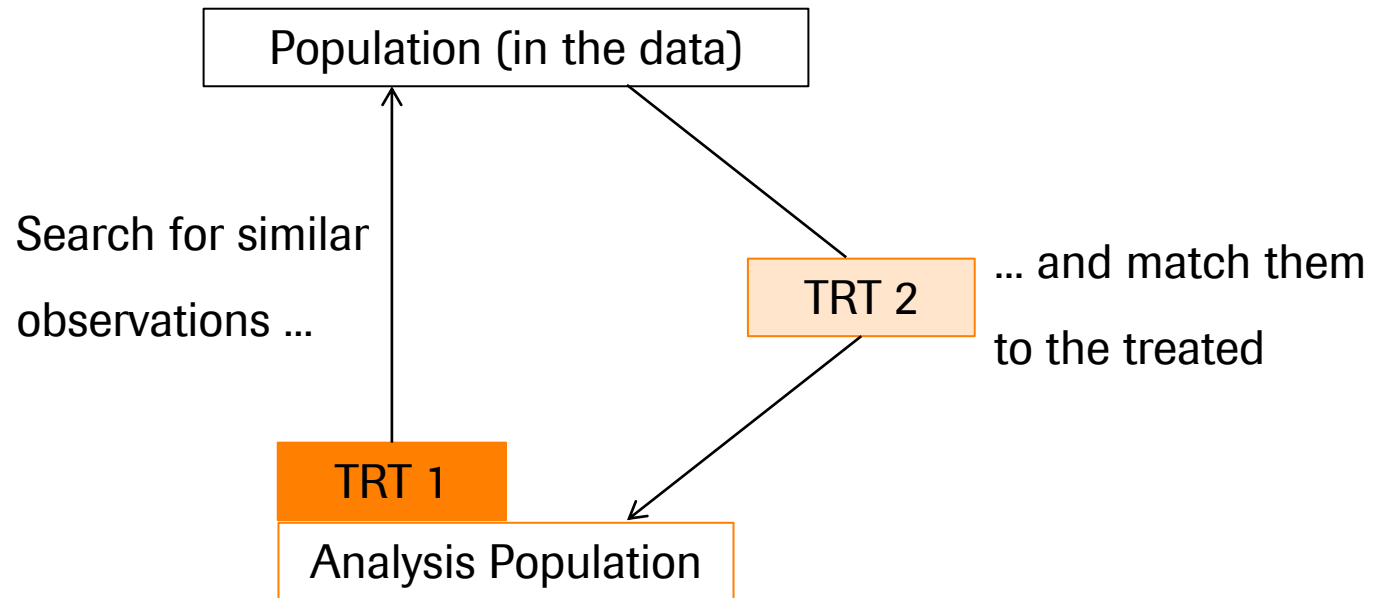
What do you need propensity-score matching for?

Scenario 2



- → Naïve estimate potentially biased

Solution to the Evaluation Problem



- Matching can be done on the (full) vector of covariates (high-dimensional!)
- or on the propensity score (one-dimensional!).

What is the propensity score?

- The propensity score is the conditional probability of being in the treatment group given a specific set of covariables:

$$P(T = 1|X)$$

- Estimated via probit/logit model or other

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Main Steps of Propensity-Score Matching

- (1) Check for imbalances between control and treatment group.
- (2) Estimate the propensity model and predict individual propensity scores.
- (3) Match controls on treated subjects.
- (4) Check if propensity-score matching reduced the imbalances.
- (5) Estimate the treatment effect.

Step (1): Pre-Matching Balance Assessment

Available measures to be compared:

- Mean
- Standard deviation
- Median and other quantiles
- Proportions
- Boxplot
- Histogram
- ...

The use of statistical tests is generally discouraged.

Step (2): Model Estimation and Prediction of Propensity Scores

- Use a binary response model (e.g. probit or logit model).
- Prediction easy from the programmer's perspective:

```
OUTPUT OUT=SAS-data-set PREDICTED=name;
```

Step (3): Matching

Available algorithms:

- k -nearest-neighbor matching
- Caliper matching
- Block-wise matching
- Kernel matching
- Combinations of the above
- Whatever you might come up with ...

Step (4): Post-Matching Balance Assessment

Same as Step (1)

Step (5): Treatment-Effect Estimation

- Depends on the matching algorithm applied.
- Might be very easy.
- Might be very complicated.

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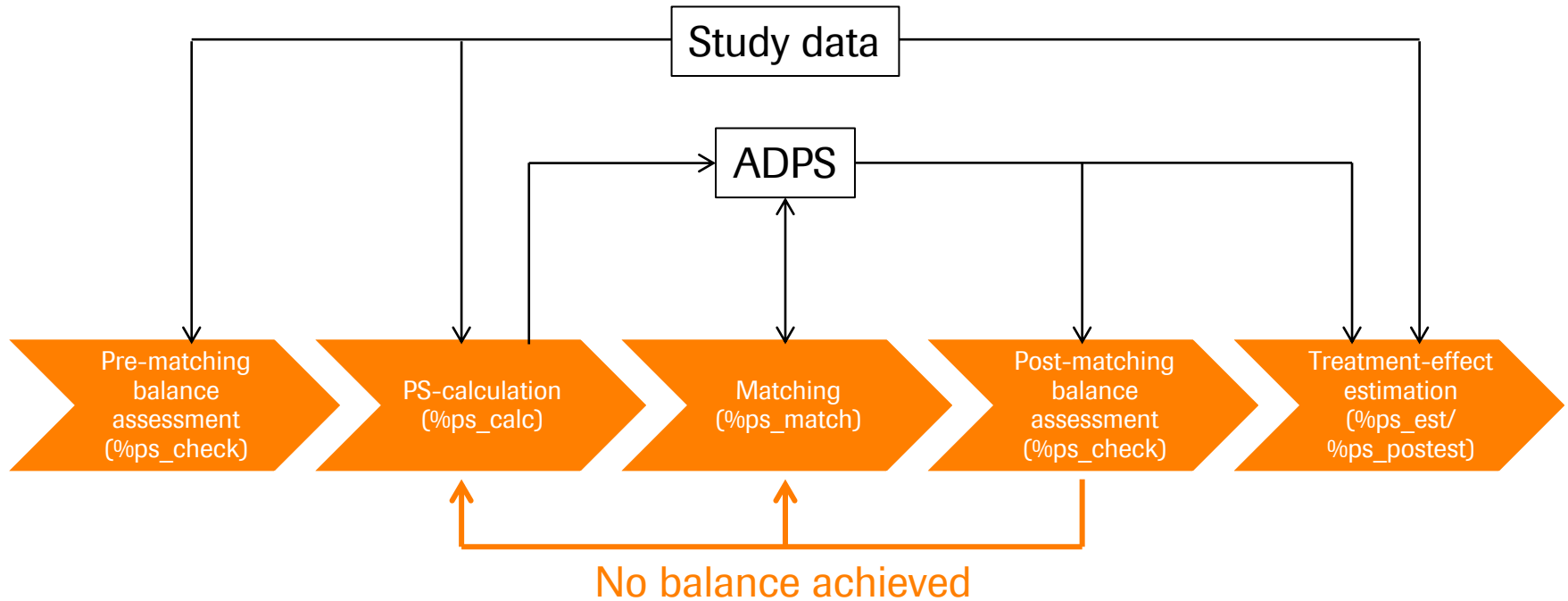
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Overall Process Flow



%ps_check

Proposed example macro call:

```
%ps_check(inds      = adsl  
           , vars      = age basebmi baseweight baseheight  
           , statistics = table boxplot histogram );
```

%ps_calc

Proposed example macro call:

```
%ps_calc(inds          = adsl
          , invars      = age basebmi baseweig baseheig
          , link         = probit
          , outds        = adps1
          , cs_diagnosis = yes );
```

%ps_match

Proposed example macro call for 1-to-1-nearest-neighbor matching with caliper and without replacement:

```
%ps_match_1nn(inds      = adps1
                , outds    = adps2
                , seed      = 12345
                , caliper   = 0.1
                , replacement = off );
```

ADPS-data structure

Minimally required variables

USUBJID	Unique identifier of the observation to which the information applies
TRT	Treatment status of the observation
PS	Predicted propensity score
STRATUM	[For block-wise matching:] Stratum to which the observation was matched
MATCHED	0/1-variable indicating whether the observation was used for matching
ID_MATCH	Unique identifier of the observation which has been matched to the current observation
WEIGHT	[If more than 1 control is matched to a treated observation:] Weight in the set of matched observations

ADPS-data structure

Example for 1-to-1-nearest-neighbor matching

USUBJID	TRT	PS	STRATUM	MATCHED	ID_MATCH	WEIGHT
1234	A	0.186		1	2345	
2345	B	0.259		1	1234	
3456	B	0.846		0		
...	...	...		...	...	

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Doing now what patients need next