

PROPENSITY SCORES USING MORE THAN 2 GROUPS: WHAT ARE MY OPTIONS AS A PRACTITIONER?

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Paper overview

- Propensity scores with more than two groups
- Quick review of the packages
- Methods
- Results
- Suggestions for practitioners

Propensity scores with more than 2 groups

- Recent development, despite the fact that Imbens (2000) demonstrated the extension from 2 to > 2 groups
- Very few implementations that can be used to conduct PSA (in R)
 - Trimatch (Bryer, 2013)
 - Twang (McCaffrey et.al., 2012)
- Very different implementations, with very different goals in mind
- As a practitioner, what are my options?

TriMatch (Bryer, 2013)

- PS matching for 3 groups using a measure of distance in a multidimensional space
 - PS estimation using 3 separate logistic regressions (Tr1-C, Tr2-C, Tr1-Tr2)
 - Estimation of 3 distances (one for each pair). The triplets with the smallest distances (next slide) are kept
 - Since distances are estimated across all groups, matches across all 3 groups are possible

TriMatch (cont)

- Options to generate different number of matches across all three groups
 - **MaximumTreat**: matching without replacement with some limitations; **Caliper** includes all units within a specified caliper (multiple duplicates); **one to N** user sets how many times each T1 and T2 can be reused
 - Number of non-used cases or duplicates in an analysis, dependent on these options
- Balance is assessed by the package through plots
- Either RM ANOVA or Friedman's Rank Sum test to estimate the outcome.
 - Follow up tests using paired-t-tests

twang (McCaffrey et. al. 2012)

- Creates multiple propensity scores (one for every pair) using Generalized Boosted Models (GBM)
 - Iterations fitting many simple regression trees combined to create an overall piecewise constant function
- Originally designed for 2 groups, but extended in 2013 to more than 2 groups
 - The package applies propensity scores through weights to the group participants

twang (cont)

- Given that the algorithm can overfit the data, some stopping rules
 - Based on summary statistics (absolute standardized mean difference) or Kolmogorov–Smirnov (KS)
 - Parameters such as number of trees, the stopping method (means, KS), and the estimation approach (ATE, ATT) can be defined
 - Balance is assessed by the package through plots, pairwise standardized differences
 - All cases are included
- Outcome model estimated through weighted regression

Research questions

- Questions tested with both twang (weighted regression) and TriMatch (matching):
 - Effect of **distributional characteristics** (normal, positive skewness) of the variables included in the **selection model**
 - Effect of the **Degree of correlation** (no, small, large) between the variables in the **selection model** and between the variables in the **outcome model**
 - Effect of the selection bias defined as the correlation between one of the variables in the **selection model** and the error term for the **outcome model** (low, high)

Simulation model

Every model was simulated 100 times
Sample size: 500

Models generated for the simulation

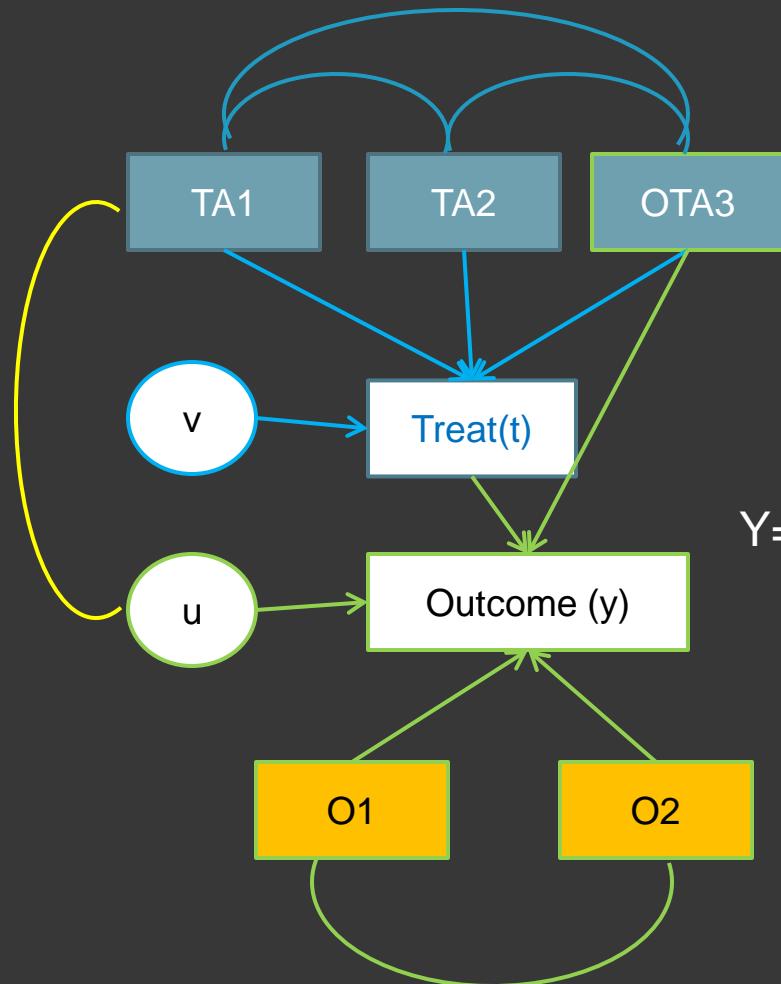
$$D1=0.7(TA1)+0.4(TA2)+0.1(OTA3)+v$$

$$D2=0.8(TA1)+0.5(TA2)+0.15(OTA3)+v$$

$$Y=0.4(O1)+0.7(O2)+0.3(OTA3)+5(D1)+10(D2)+u$$

$$r(TA1, u) = 0.3, 0.6$$

OTA₃ is part of both Treatment (T) and Outcome (Y)



Simulation conditions

- Selection bias. 2 conditions:
 - $r(u, TA1) = 0.3, 0.6$
- Distributional characteristics. 3 conditions:
 - Normal, Positive Skewness, Mixed (Normal, Positive Skewness)
- Correlation between IV's (selection model). 3 conditions:
 - No, small(0.3), large(0.6)
- Initial sample size: 500 cases

Results

Preliminary results

- ◎ twang:
 - Need a reference group (*control*; *treatment*). If you want a different reference, you need to reorganize the file
 - Group 3 in the file is the reference group
 - The analysis assumes independence between groups
 - Twang can estimate either ATE or ATT
 - Runs a weighted regression model (dummy variables)

Preliminary results

○ TriMatch

- Assumes dependency among the matched observations
 - RM-ANOVA, Friedman test for non-parametric
- Matches all groups in every combination
 - Post-hoc analyses using matched-test
- Cases may be lost due to matching (ways to increase/decrease sample size)
 - Observations can be used more than once in some instances
- Cannot account for covariates

Results: twang vs. TriMatch

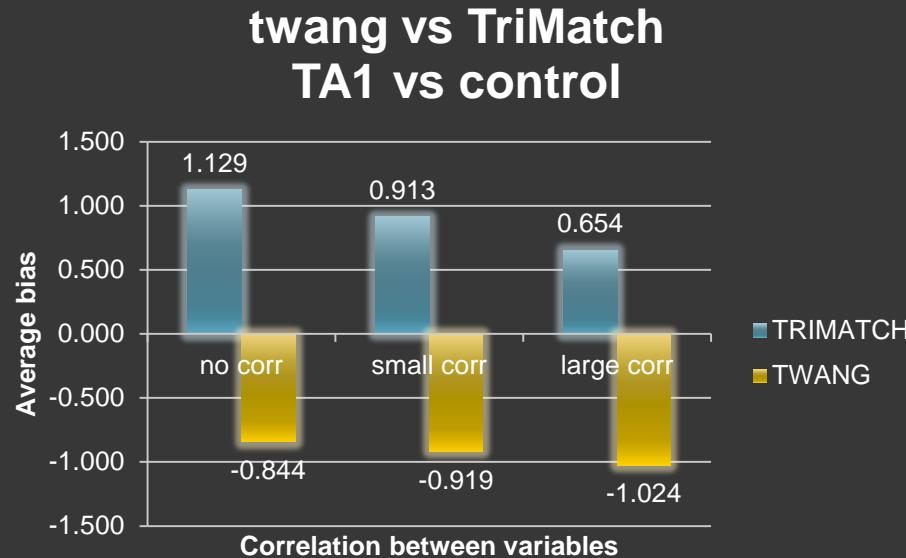
General

- Comparison TA1 vs control: twang bias ($\underline{M}=-0.929$) always larger than TriMatch ($\underline{M}=0.899$)
 - KW(1) = 26.27, p < 0.01*
- Comparison TA2 vs. control: twang bias was always larger than for TriMatch ($\underline{M}=0.555$ vs. $\underline{M}=0.141$)
 - KW(1) = 26.27, p < 0.01*
- 2-way interactions (not statistically tested)

* Kruskal Wallis, based on ranks

twang vs. TriMatch

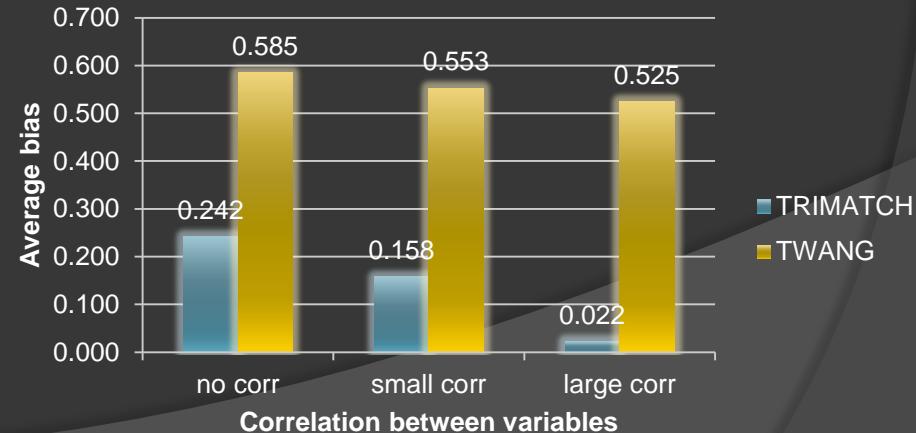
Correlation among IV's in the selection model (no, small, large)



TA1 vs control

- Larger bias for twang
- Bias for TriMatch got smaller for larger correlations among variables

twang vs TriMatch TA2 vs. control

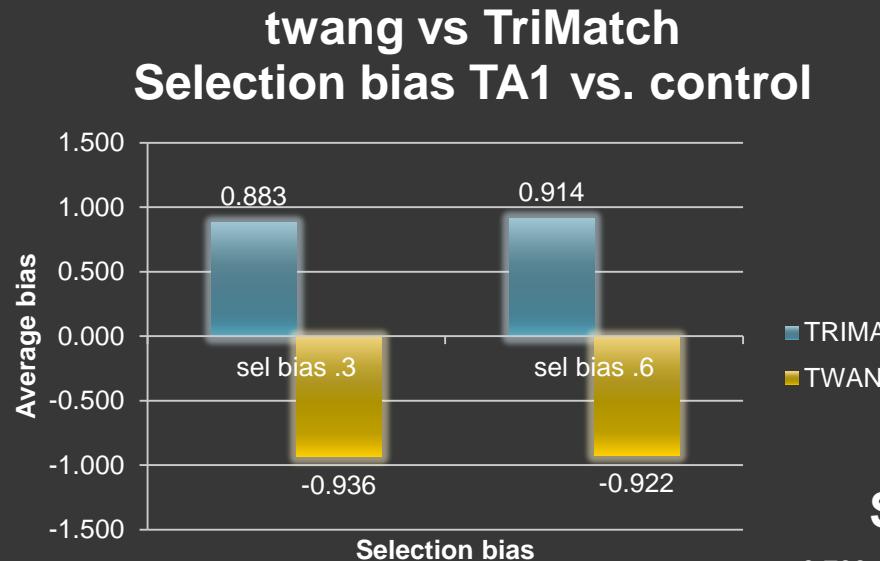


TA2 vs. control

- Larger bias for twang
- Bias for TriMatch got smaller for larger correlations among variables

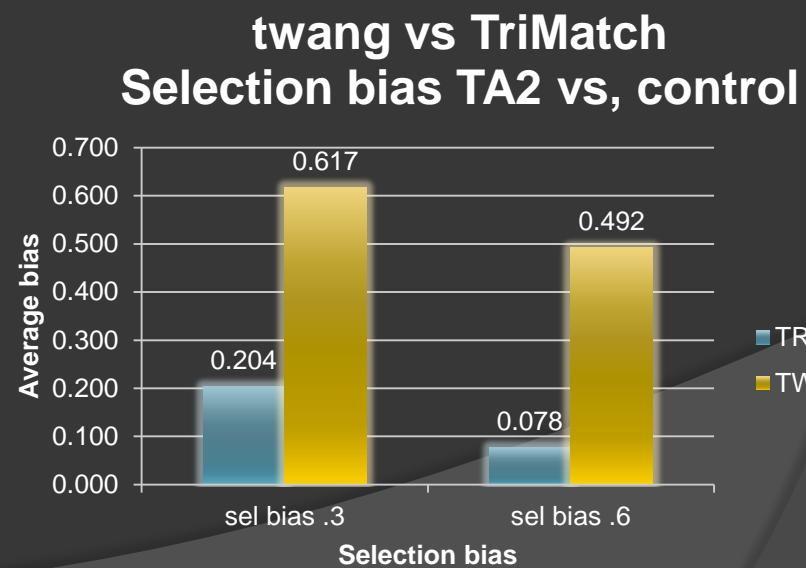
twang vs. TriMatch

Selection bias $r(u, TA1) = 0.3, 0.6$



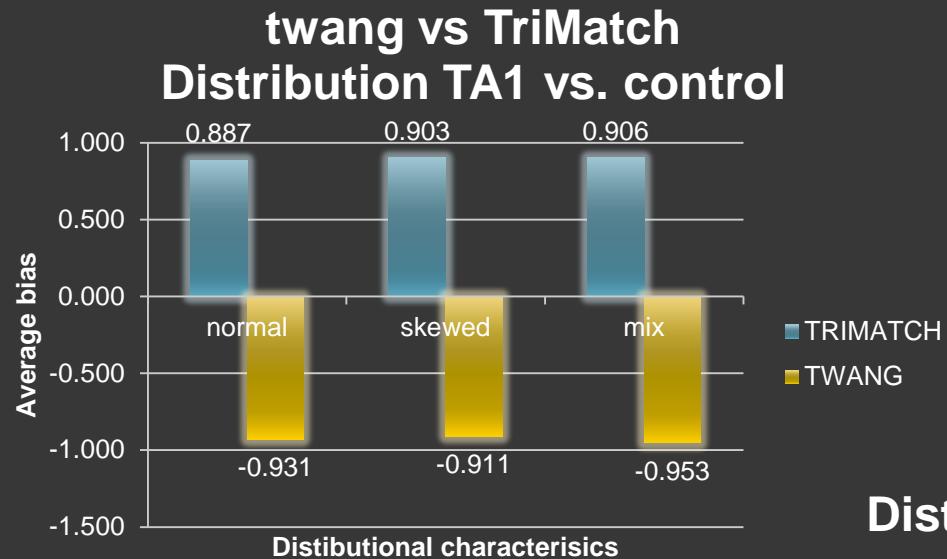
TA2 vs control

- Larger bias for twang
- Bias for TriMatch got smaller for larger selection bias



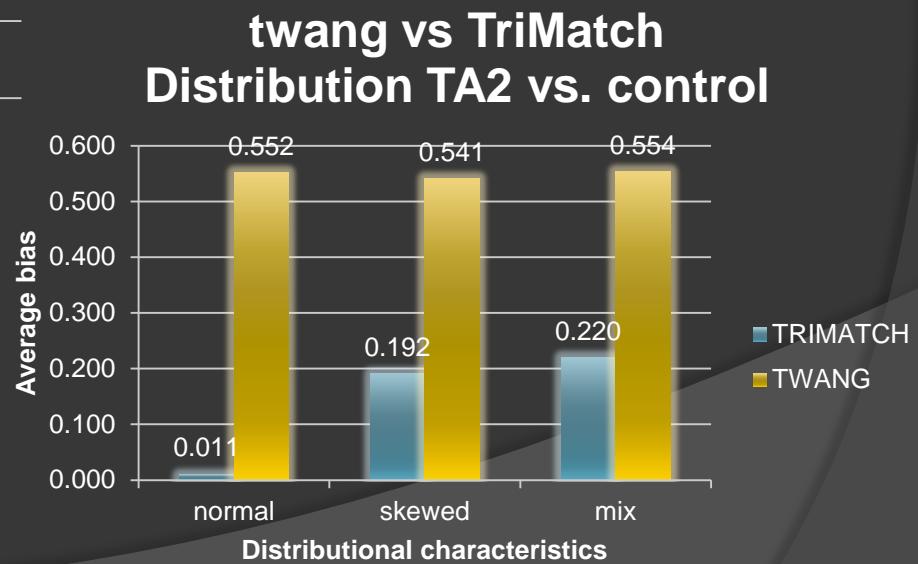
twang vs. TriMatch

Distributional characteristics (normal, positive skew, mix)



TA2 vs control

- Larger bias for twang
- Bias for TriMatch got larger for skewed/mix



Conclusions

- Under the present conditions, TriMatch seems a better choice than twang
 - Overall, less bias than twang
 - More likely to provide an accurate estimate when IV's in the selection model are correlated
 - Better, if distributions are normal
- Only main effects were tested for significance

As a practitioner, what are my choices?

- **TriMatch**, if you have max three groups, and you don't have covariates
- At this point, your only choice if you have more than 3 groups or if you have covariates is limited to **twang**
 - Be aware that twang is very sensitive to correlation between IV's in the selection model, larger selection bias, distributional characteristics of the variables in your selection model

Future work

- Multiple options within each package that were not tested
 - TriMatch: type of match
 - twang: number of trees, stopping method, estimation approach
- Sample size (small, medium, large)
- Effect of hidden bias

Thanks

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