

SAR results for FCTC implementation Articles 5, 6, 8, 11, and 13

December 16, 2016

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This document presents the results from implementing an adjusted version of Aral et al. (2012) propensity score matching estimator for evaluating contagion effects in the context of the implementation of the FCTC.

Roughly, the method can be described as follows:

1. Define a treatment variable Z_i which will be equal to 1 if and only if individual i is exposed to at least some percentage or number of neighbors in the network that implemented at least one item of a particular article,
2. With Z defined, via the MatchIt R package, we use the Coarsened Exact Matching method (which maximizes balance). This returns a vector of weights W that indicate whether an individual j was matched, hence $w_j > 0$, or not, in which case $w_j = 0$ and compute an Average Treatment Effect on the Treated (ATT).
3. Finally, we estimated distributions for the ATT using bootstrapping as described in Snijders and Borgatti (1999).

1 Posts network

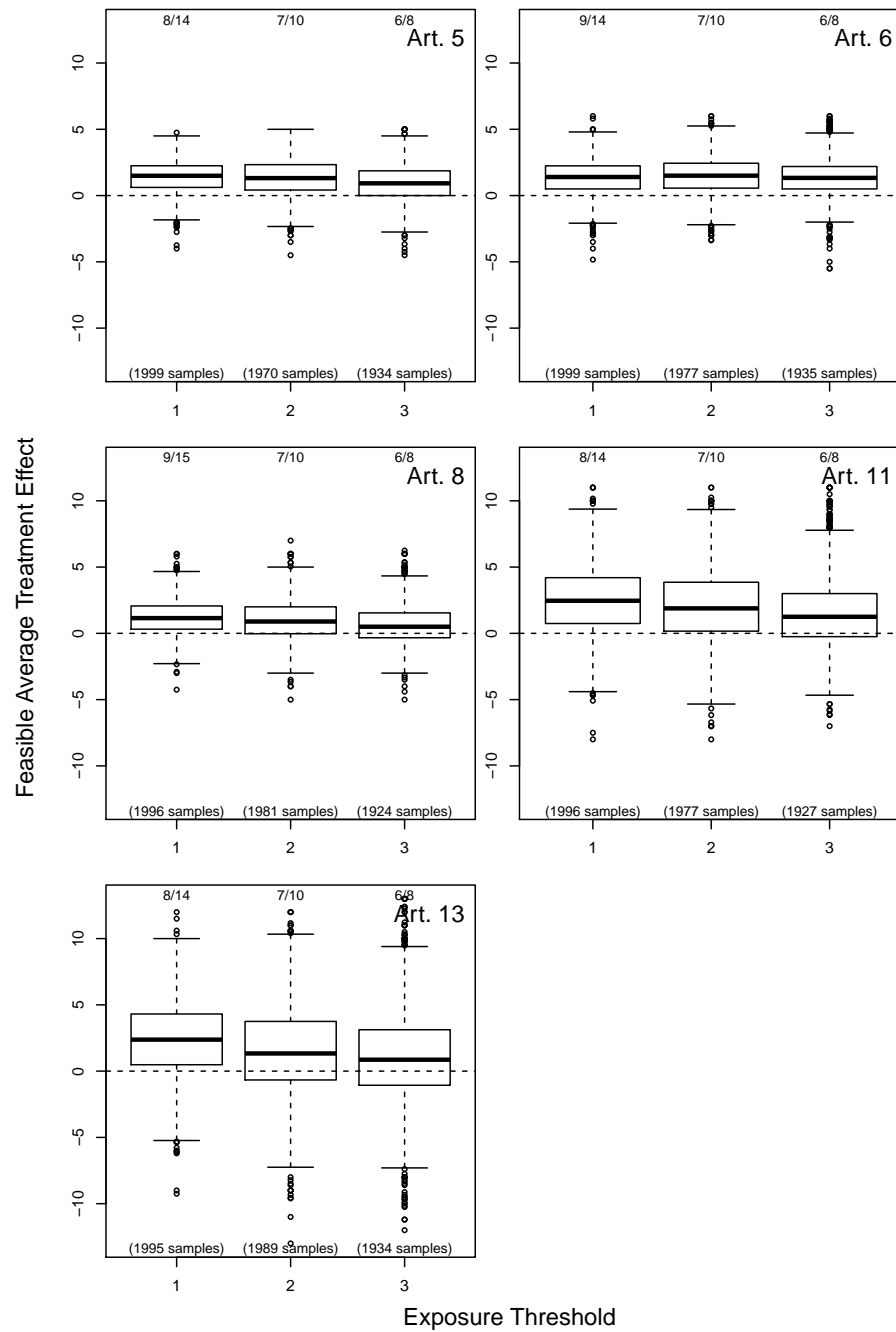


Figure 1: Distribution of Feasible Average Treatment Effect on the Treated using the GlobalLink posts network. Each box represents 2,000 bootstrap versions of the estimator.

2 Robustness check

In order to evaluate if the method reaches coherent results, we use it on a network that, according to the SAR model, does show contagion effects, the centroid distance network. Furthermore, we also performed the test on 2,000 permuted versions of this network expecting to find no contagion effect.

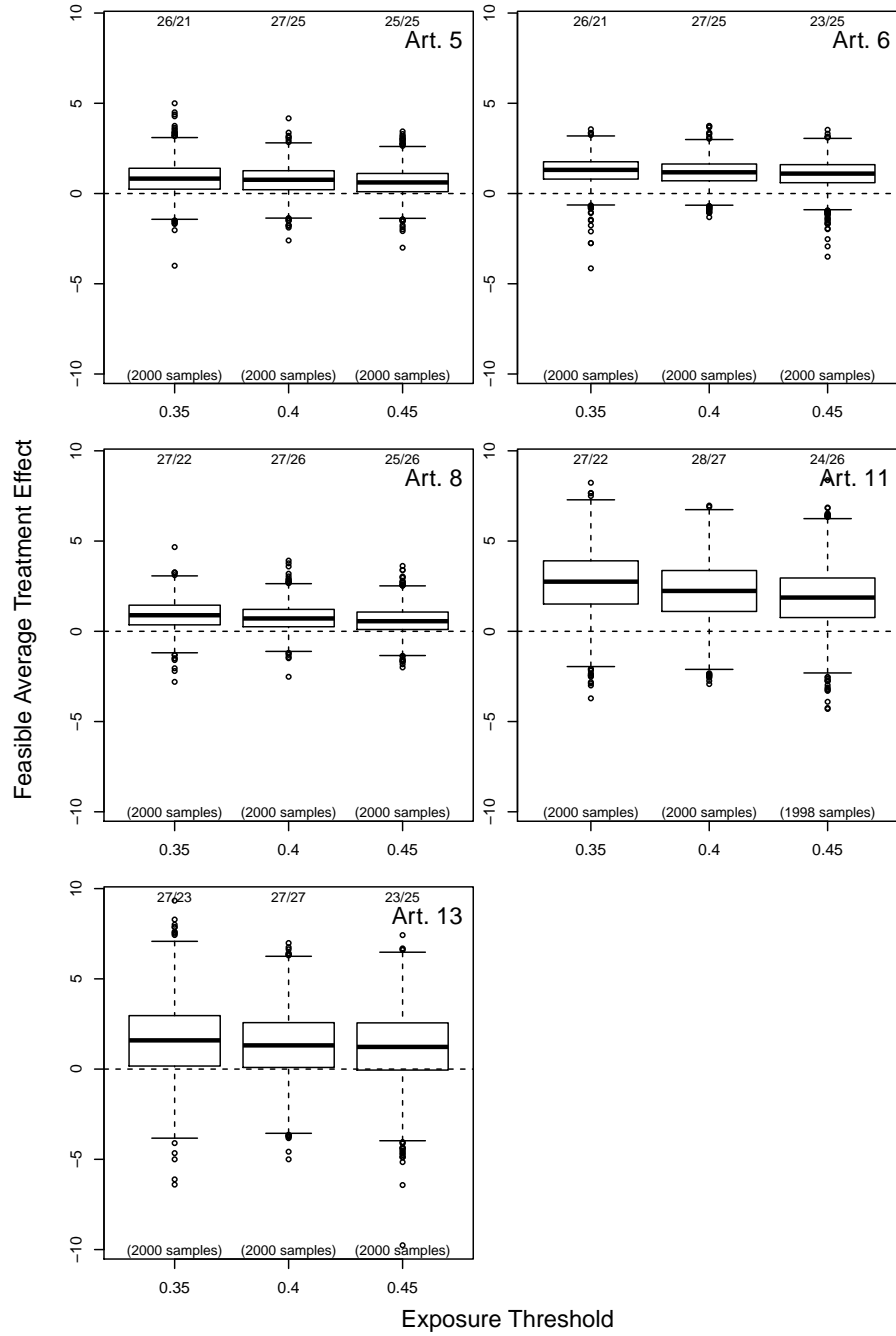


Figure 2: Distribution of Sample Average Treatment Effect on the Treated using the Centroid Network. Each box represents 2,000 bootstrap versions of the estimator.

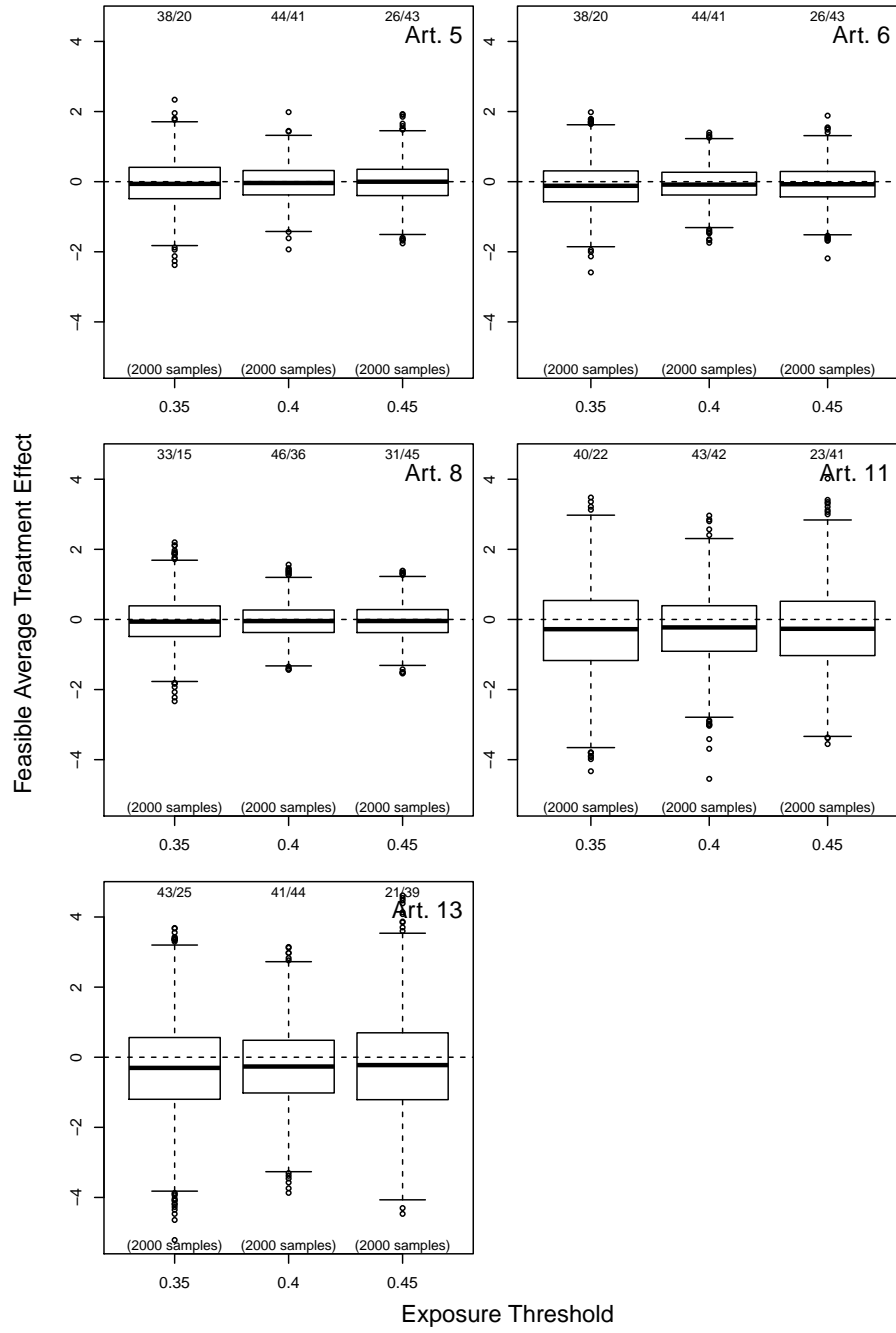


Figure 3: Distribution of Feasible Average Treatment Effect on the Treated using a permuted version of the centroid network. Each box represents 2,000 bootstrap versions of the estimator.