

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

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## Contents

<b>1</b>	<b>GL Co-subscription network</b>	<b>2</b>
<b>2</b>	<b>GL Referrals network</b>	<b>3</b>
<b>3</b>	<b>Robustness check</b>	<b>4</b>

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 GL Co-subscription network

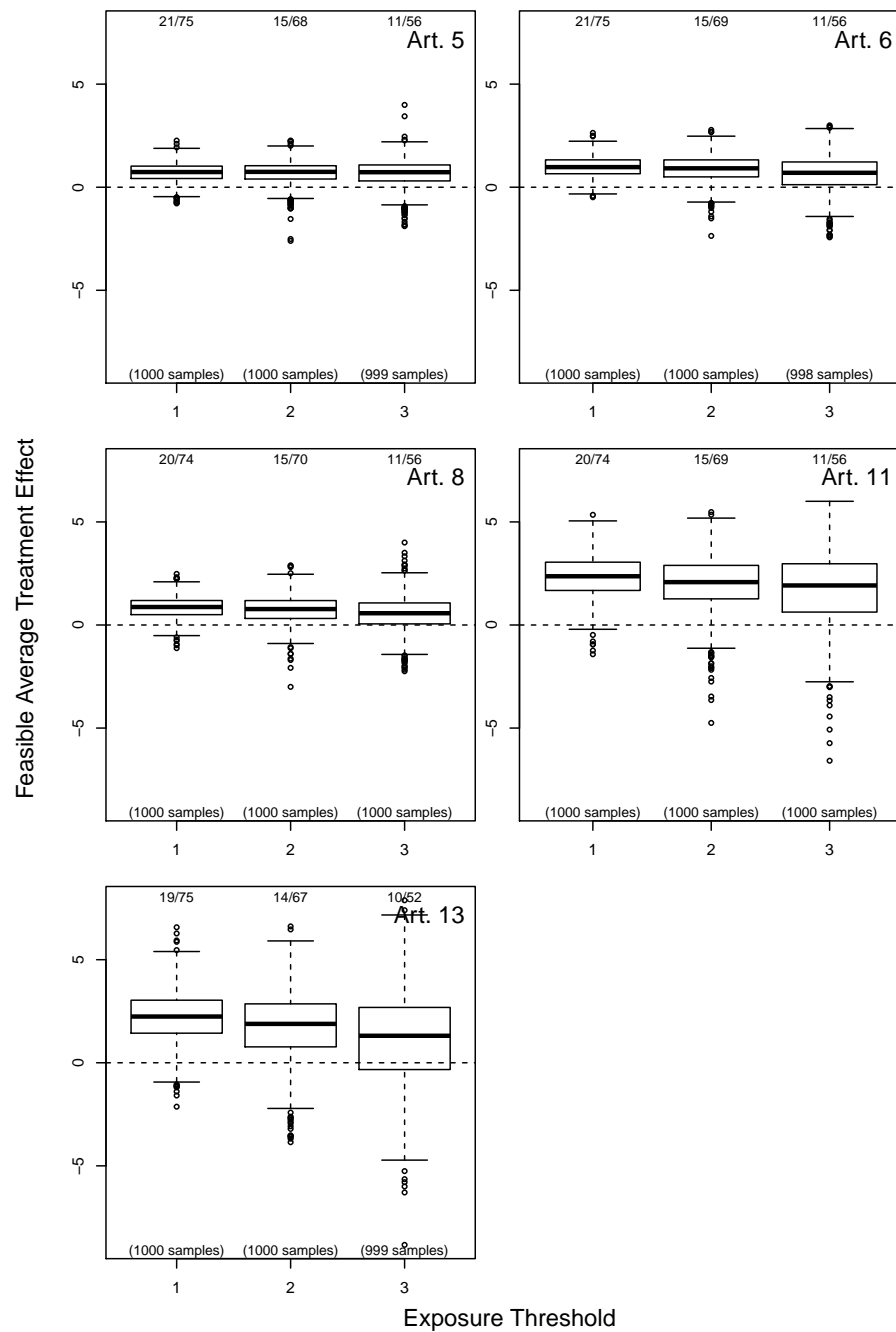


Figure 1: Distribution of Feasible Average Treatment Effect on the Treated using the GlobalLink posts network. Each box represents 2,000 bootstrap versions of the estimator.

## 2 GL Referrals network

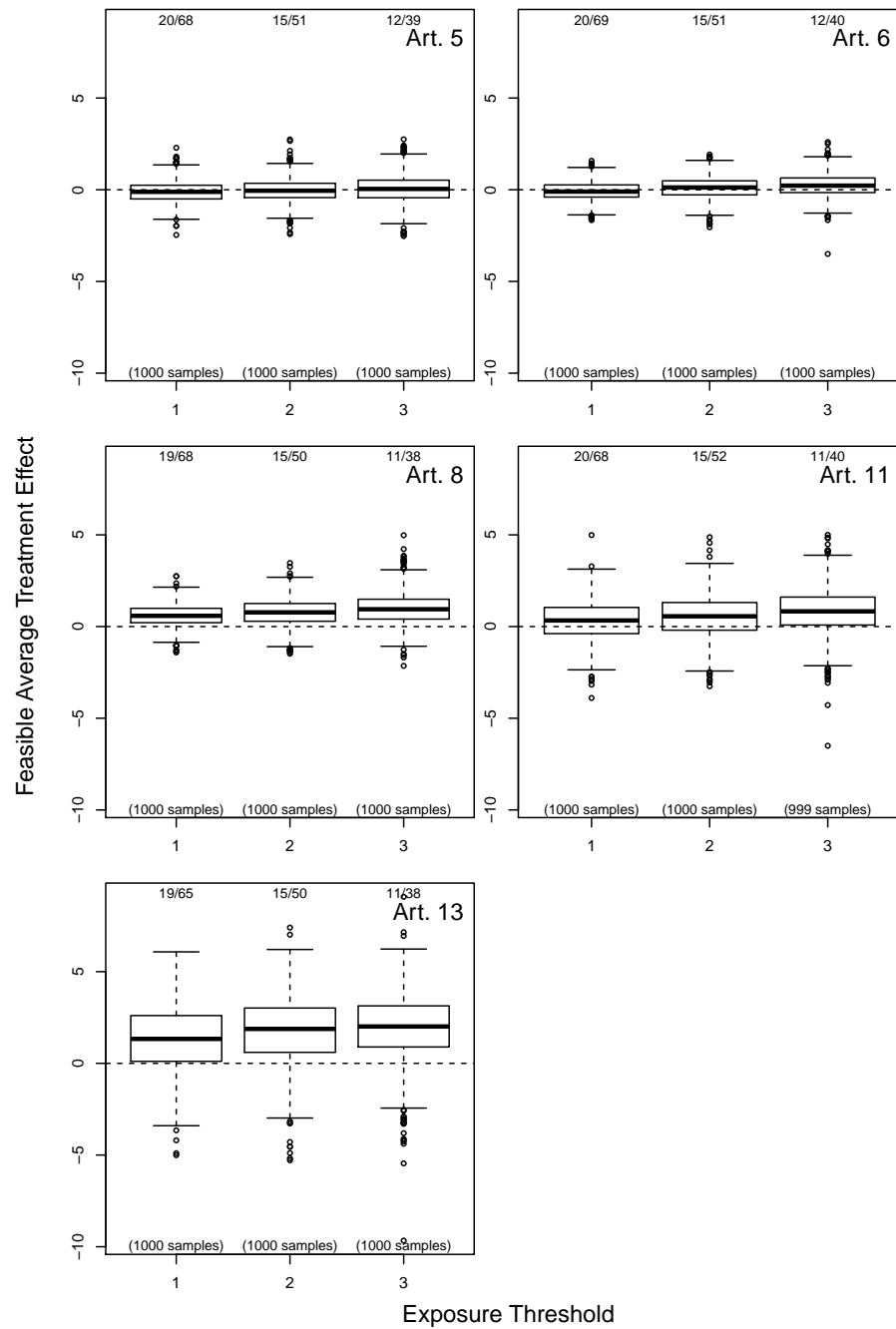


Figure 2: Distribution of Feasible Average Treatment Effect on the Treated using the GlobalLink posts network. Each box represents 2,000 bootstrap versions of the estimator.

### 3 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.

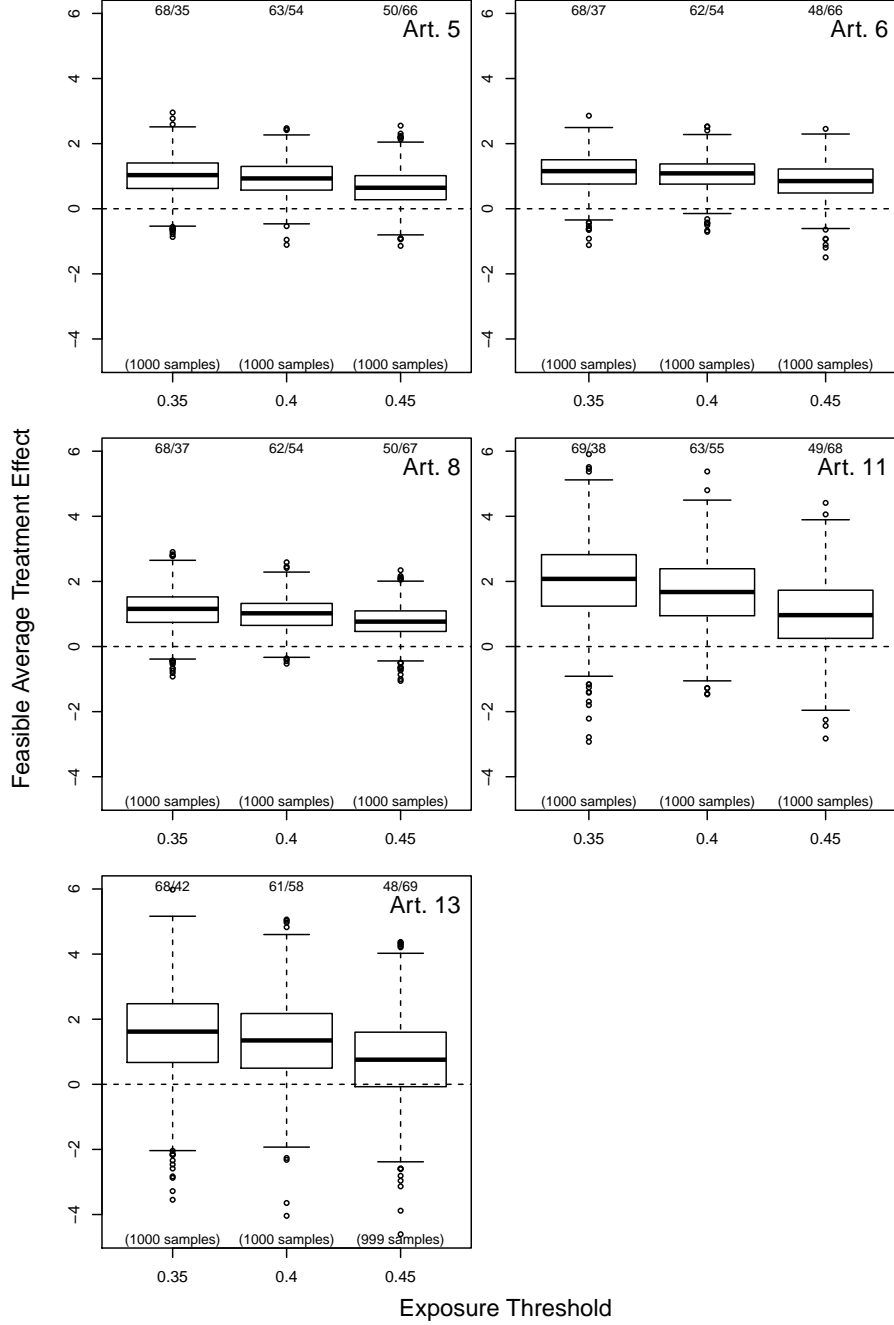


Figure 3: Distribution of Sample Average Treatment Effect on the Treated using the Centroid Network. Each box represents 2,000 bootstrap versions of the estimator.

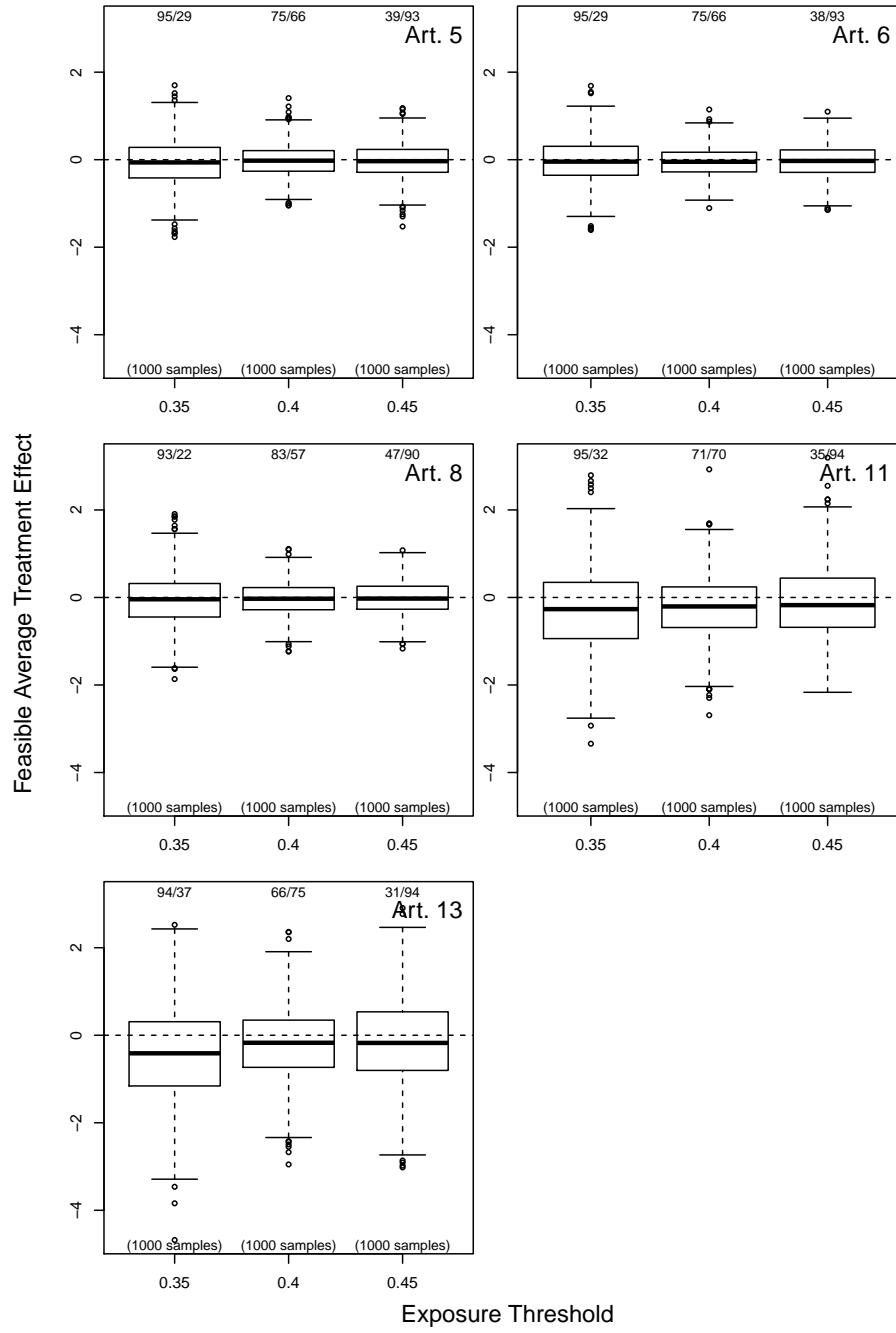


Figure 4: Distribution of Feasible Average Treatment Effect on the Treated using a permuted version of the centroid network. Each box represents 2,000 bootstrap versions of the estimator.

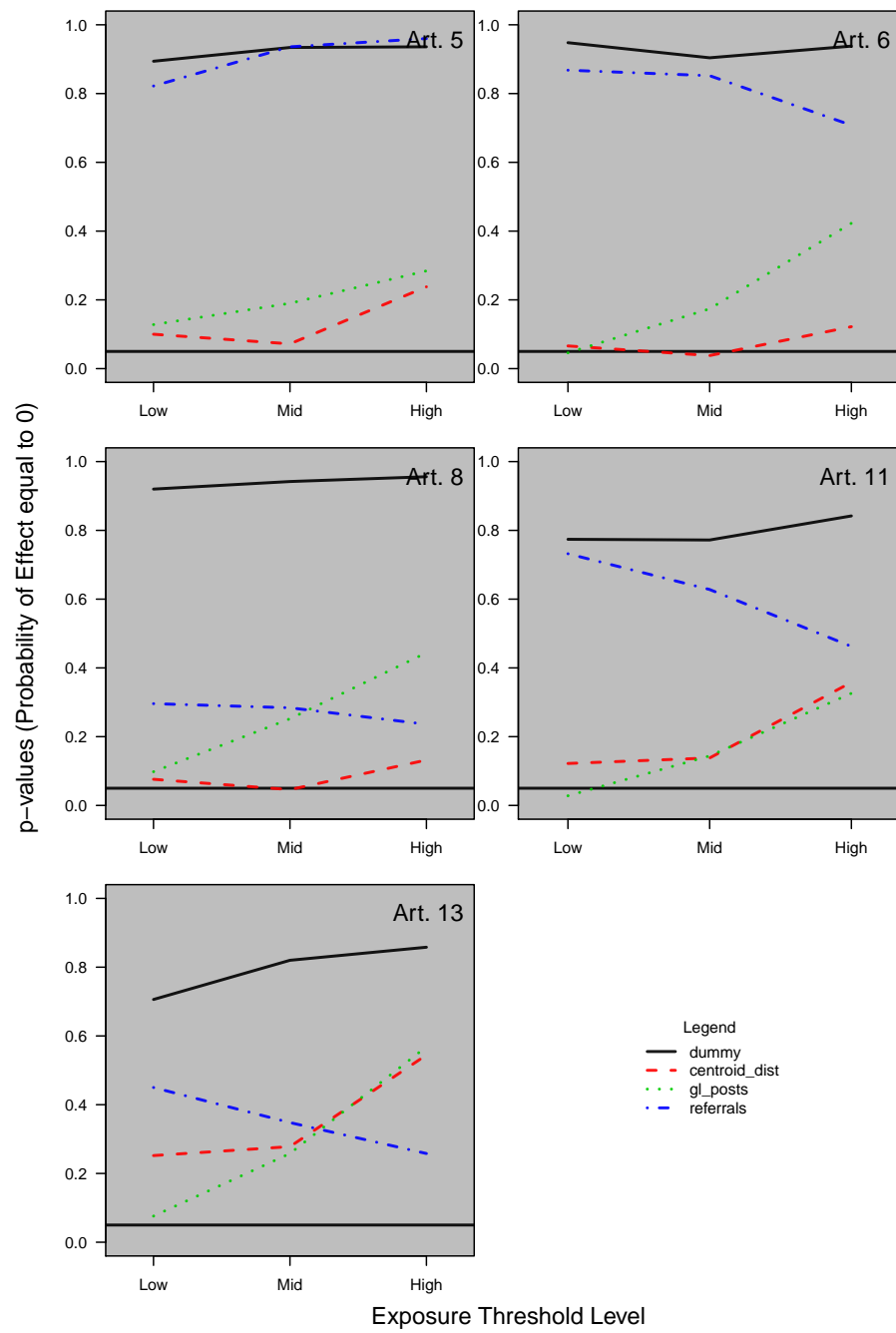


Figure 5: P-values testing treatment effect equal to zero.

Table 1: p-values of NetMatching

Network	Art.	Low Thr.	Mid. Thr.	High Thr.
dummy	5	0.894	0.934	0.9360000
dummy	6	0.948	0.904	0.9380000
dummy	8	0.920	0.942	0.9560000
dummy	11	0.774	0.772	0.8420000
dummy	13	0.706	0.820	0.8580000
adjmat_centroid_dist	5	0.100	0.072	0.2380000
adjmat_centroid_dist	6	0.066	0.038	0.1220000
adjmat_centroid_dist	8	0.076	0.046	0.1320000
adjmat_centroid_dist	11	0.122	0.138	0.3580000
adjmat_centroid_dist	13	0.252	0.278	0.5445445
adjmat_gl_posts	5	0.128	0.190	0.2842843
adjmat_gl_posts	6	0.046	0.174	0.4228457
adjmat_gl_posts	8	0.098	0.252	0.4440000
adjmat_gl_posts	11	0.028	0.144	0.3260000
adjmat_gl_posts	13	0.076	0.258	0.5685686
adjmat_referrals	5	0.822	0.936	0.9600000
adjmat_referrals	6	0.868	0.852	0.7080000
adjmat_referrals	8	0.296	0.284	0.2360000
adjmat_referrals	11	0.732	0.628	0.4624625
adjmat_referrals	13	0.450	0.348	0.2580000