

Online Appendix

The formula for calculating the weighted defection rate

Let s_i and v_i be the total number of defections and the total number of votes cast (i.e. not including abstentions and absences) by the i_{th} MP, respectively; P_i be MP i 's party; x_{in} be MP i 's choice during vote n (equal to zero if MP i did not cast a vote during vote n); V_{pn} be the mode of the frequency distribution of party P_i votes during vote n (equal to zero if the distribution is multimodal); w_n be the percent difference between the alternative obtaining the most votes and the second most voted alternative during vote n ; A_n be an indicator function that is equal to 1 iff $x_n \neq V_{pn}$, $x_n = 0$, and $V_{pn} \neq 0$, and zero otherwise; F_{pn} be a function that returns the fraction of party P_i membership present and voting during vote n ; let M_{pn} be an indicator function equal to 1 iff $F_{pn} \geq 0.5$, and zero otherwise; and t be the total number of votes taken during a legislature. Then

$$s_i = \sum_{n=1} w_n(A_n M_{pn})$$

and

$$d_i = \frac{s_i}{v_i}$$

is the defection rate for the i_{th} MP.

Estimation Results Using *Difference in Defection Rate* as the Outcome Variable

Table 1A. The effect of mandate change on change in defection rate, Linear Multi-level Model

Explanatory Variables	Outcome: Change (difference) in Defection Rate Estimate (s.d.)
Random Effects	
Mandate Change	
From SMD to PR	0.147 (0.183)
From PR to SMD	0.470 (0.221)*
Intercept	
Intercept SMD	-1.616 (0.238)*
Intercept PR	-1.374 (0.275)*
Fixed Effects	
Party	
Fidesz	-1.112 (0.367)*
MDF	0.579 (0.261)*
MSZP	-0.889 (0.118)*
SZDSZ	-0.949 (0.219)
Parliamentary Term	
2002-2006	0.933 (0.145)*
2006-2010	1.842 (0.146)*
Double Nomination (at time t)	0.445 (0.146)*
Electoral Security	-0.281 (0.562)
Principal Distance	-0.007(0.011)
Data level Standard Deviation: σ_y	1.209
Mandate Change Standard Deviation: σ_θ	0.671
Intercept Standard Deviation σ_α	0.500
Data level R^2	0.372
N	588

Note: Table entries are means of posterior sampling distributions of regression coefficients, with the respective distribution's standard deviation in parentheses. Response variable is *Change (difference) in defection rate*. The reference category for *Party* is FKGP and for *Parliamentary term* 1998-2002. * $p < 0.1$

**Estimation Results of Aggregated Model Using REML (i.e. vanilla)
Method**

Table 2A. The effect of mandate change on percent change in defection rate, Linear Multilevel Model

Explanatory Variables	Outcome: Percent Change in Defection Rate Estimate (s.d.)
Random Effects	
Mandate Change	
From SMD to PR	-4.154 (6.073)
From PR to SMD	45.931 (6.819)*
Intercept	
Intercept SMD	-99.104 (1.933)*
Intercept PR	-83.163 (2.170)*
Fixed Effects	
Party	
Fidesz	115.113 (23.288)*
MDF	156.665 (27.195)*
MSZP	40.547 (22.241)*
SZDSZ	47.911 (24.274)*
Parliamentary Term	
2002-2006	-27.437 (9.700)*
2006-2010	26.617 (9.792)*
Double Nomination (at time t)	22.635 (11.022)*
Electoral Security	8.665 (28.533)
Principal Distance	0.125 (0.704)
Data level Standard Deviation: σ_y	81.514
Mandate Change Standard Deviation: σ_θ	35.998
Intercept Standard Deviation σ_α	11.457
AIC	6788
N	587

Note: Table entries are MLEs of regression coefficients, with the respective standard errors in parentheses. Response variable is *Percent Change in defection rate*. The reference category for *Party* is FKGP and for *Parliamentary term* 1998-2002. * $p < 0.1$

Matching: Treatment and Control Group Balance and Power Functions

Matching is a data preprocessing technique that works with the existing dataset to create one in which treatment and control groups are as similar as possible with respect to all variables we believe to affect the outcome of interest. This provides us with data that can be used to make inferences about the counterfactual claim that is implicit in any causal statement: “what would have happened, had the treatment not been present in this particular observation?” We use GenMatch,¹ an R programme which uses a genetic algorithm to search for the optimal balance in the independent variables included in the original models that could theoretically confound the effect of the treatment, and on a propensity score (i.e., a probability of being treated), which is estimated using a logistic regression. Optimal balance is searched using a “one-to-one with replacement” matching scheme.²

Figure 1A shows balance in the covariates after matching for the respective datasets as indicated in the headings of the different panels. The solid black dots represent the difference in proportions/means (depending on the measurement scale of the corresponding covariate) between the treatment and control groups for each categorical variable. The black bands around each dot correspond to the 90% confidence interval of these differences. In other words, a difference for which the corresponding band includes the zero point is not statistically distinct from zero. The fact that the differences are close to zero in all cases indicates that balance is achieved in all confounding variables. Balance is formally understood as a situation in which *all* moments of the distributions of the random variables conditional on the different values of the treatment variable are identical, not simply the mean. As such, it is almost impossible to insure. Equal means, however, should provide a good empirical approximation.

Next to the dot-plots, the Figure also reports the statistical power of the test. Power is particularly important when trying to establish that a null hypothesis is *not* rejected, which is the case here. As Agresti and Finlay state, “when you read that results of a study are insignificant, [you should] be skeptical if no information is given about the power. [It] may be low, especially if n is small.”³ Statistical power of a test is the probability of rejecting the null hypothesis (in our case, that the difference in proportions is zero). This probability is equal to 1 minus the probability of making a type II error – the error made when a false null hypothesis is not rejected. If the power of a test is low, the probability of making a type II error is high. Statistical power always increases for values of difference that are farther from the hypothesized null value (i.e., zero in our case).⁴

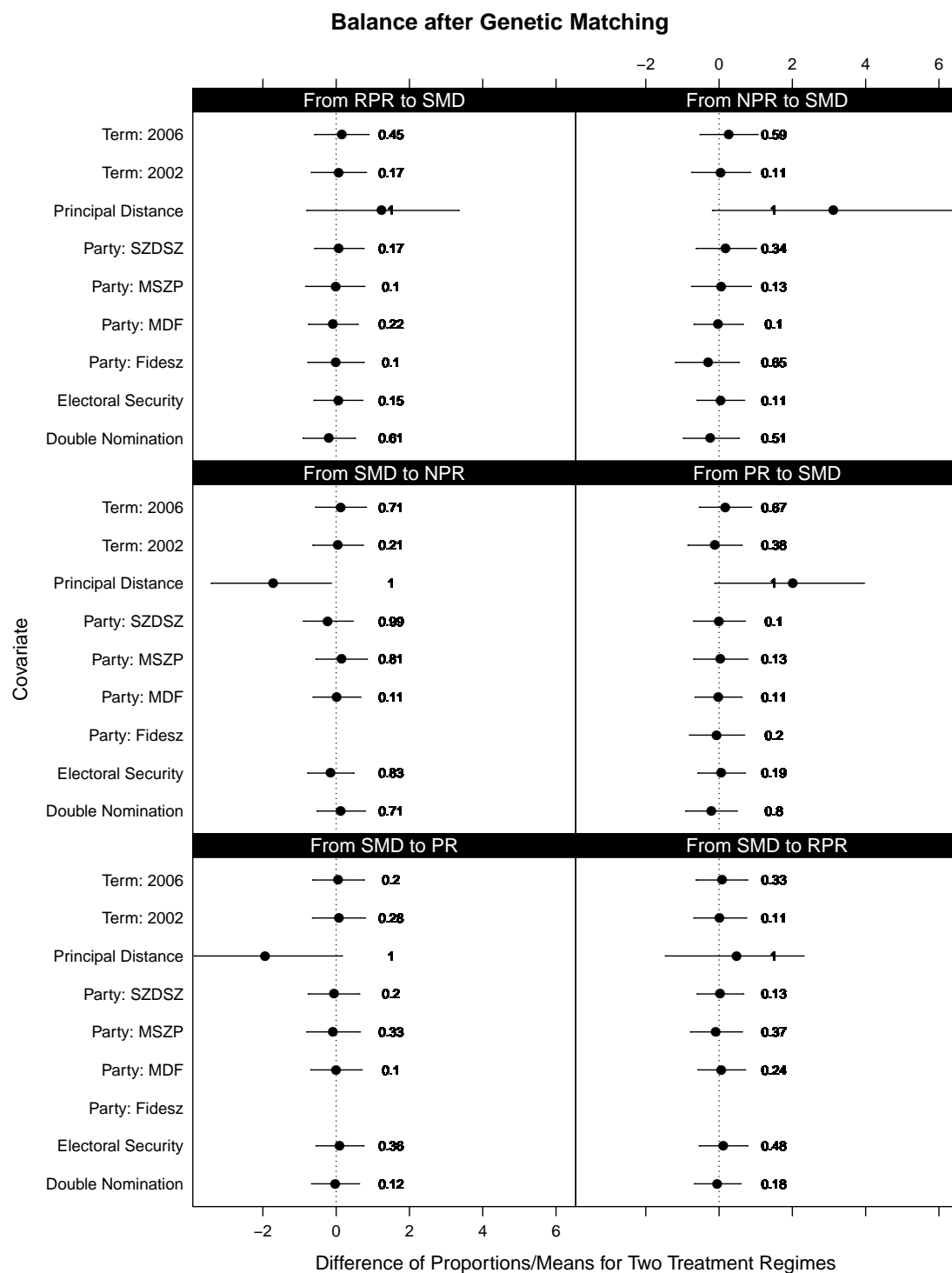
¹ Sekhon 2010.

² Rubin 2006.

³ Agresti and Finlay 2008, 169.

⁴ DeGroot and Schervish 1986.

Figure 1A. Treatment and control groups balance and their corresponding powers



Note: The dotplots present difference in means/proportions across treatment and control groups for each of the six possible mandate change scenarios. The numbers next to each dotplot represent the power of the test.

References

- Agresti, Alan and Barbara Finlay. 2008. *Statistical Methods for the Social Sciences (4th Ed.)* Upper Saddle River, NJ: Prentice Hall.
- DeGroot, Morris H. and Mark Schervish. 1986. *Probability and Statistics*. Reading, MA: Addison-Wesley.
- Rubin, Donald B. 2006. *Matched Sampling for Causal Effects*. Cambridge: Cambridge University Press.
- Sekhon, Jasjeet Singh. 2010. *Matching: Multivariate and Propensity Score Matching with Balance Optimization*. R package version 4.7-9.