Supplementary Information for "Is the Tea Party Libertarian, Authoritarian, or Something Else?"

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Additional information on Factor Analysis

We used an oblique rotation which allows for factors to be correlated. This is appropriate here because, while we argue that moral statism and anti-governmentalism are unique and distinct, they are likely to be correlated. We use maximum likelihood as the factoring method because it has a more formal statistical basis than other methods and is widely seen as one of the optimal methods. See Fabrigar et al. (1999). We estimate two factors, which a scree plot (below) suggests to be the optimal number.

For N equal to 5914, a chi-square test of the hypothesis that two factors is sufficient is equal to 900.727 with a p-value of 0, suggesting that two factors are not sufficient, as we would expect. That said, the root mean square of the residuals is 0.044 and the Tucker-Lewis Index for factor reliability score is 0.869, both of which are near the conventional cutoffs of .05 and .9, respectively.

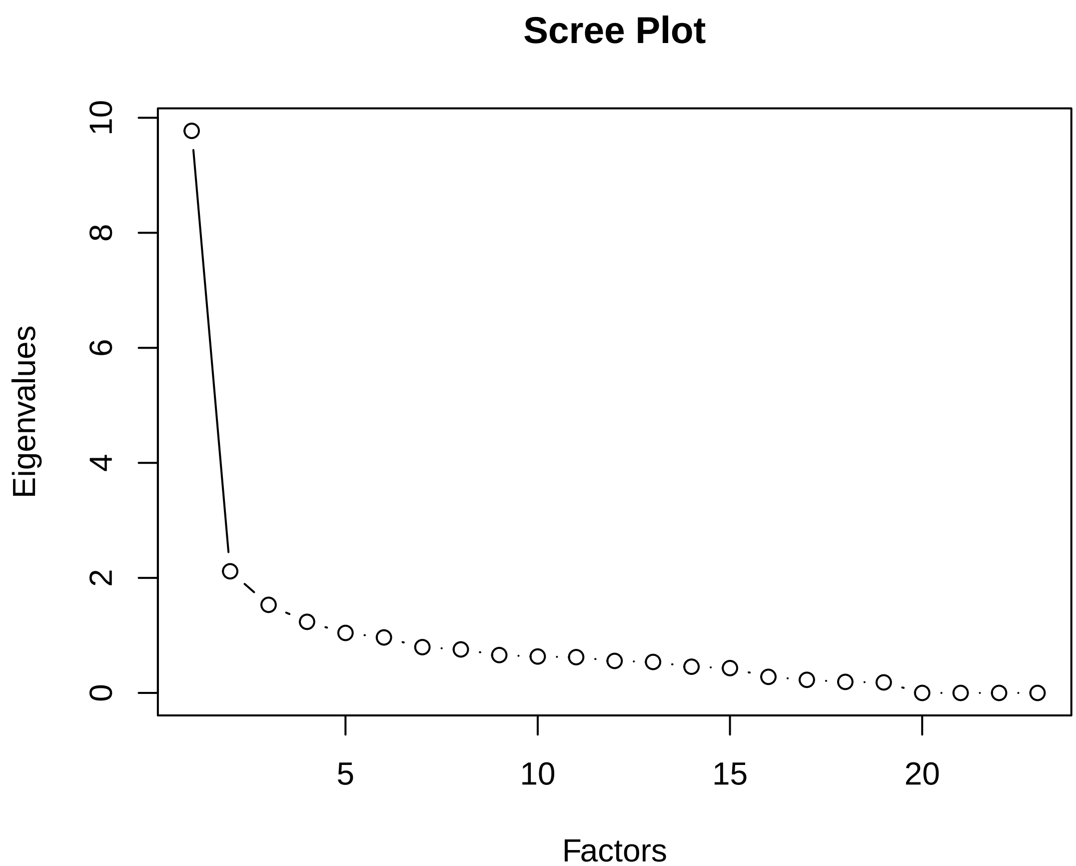

Figure 1: Scree plot shows elbow at two factors

	Moral Statism	Governmentalism
Conservatism	0.56	-0.26
Family	0.64	0.08
GunControl	-0.06	0.39
Intolerant	0.42	-0.12
Morals	0.35	-0.21
Wiretapping	0.37	0.24
DefenseSpending	0.54	0.08
Services	-0.00	0.77
ImmigrationChecks	0.39	-0.21
JobGuarantee	-0.06	0.60

Table 1: Factor Loadings

Table 2: Alternative Dependent Variables for Model 2

	Dependent variable:	
	PartyID (Republican)	Conservatism
	(1)	(2)
Gender (Male)	-0.005	0.005
	(0.013)	(0.011)
Income	0.033^{**}	-0.002
	(0.015)	(0.013)
Age	-0.068^{***}	-0.029^{**}
	(0.014)	(0.012)
Race (White)	0.066^{***}	-0.053^{***}
	(0.016)	(0.013)
Education	0.047^{***}	0.005
	(0.015)	(0.013)
Obama	-0.549^{***}	0.068^{***}
	(0.020)	(0.020)
Authoritarianism	-0.037^{**}	-0.031^{**}
	(0.015)	(0.013)
BornAgain	0.014	-0.007
	(0.014)	(0.012)
Religion	0.002	0.003
	(0.015)	(0.013)
PartyID (Republican)		0.172^{***}
		(0.017)
FoxNews	0.043^{***}	0.014
	(0.015)	(0.013)
MoralStatism	0.198^{***}	0.748^{***}
	(0.026)	(0.022)
Government	-0.131^{***}	-0.089^{***}
	(0.024)	(0.021)
MoralStatism*Government	0.022	0.060^{***}
	(0.027)	(0.023)
Constant	-0.045^{**}	0.036^{**}
	(0.020)	(0.017)
Observations	2,406	2,406
R^2	0.661	0.712
Adjusted R^2	0.659	0.710
Residual Std. Error	0.311 (df = 2392)	0.266 (df = 2391)
F Statistic	359.000^{***} (df = 13; 2392)	422.000^{***} (df = 14; 2391)
Note:		*p<0.1; **p<0.05; ***p<0.01

Table 3: Including Party ID as a Covariate

	Dependent variable:
	Tea Party Support
Gender (Male)	0.132
	(0.129)
Income	−0.322**
	(0.148)
Conservatism	0.785***
	(0.255)
Age	−0.354**
	(0.145)
Race (White)	−0.419**
	(0.168)
Education	0.057
	(0.159)
Obama	−1.350***
	(0.224)
Authoritarianism	0.052
	(0.148)
BornAgain	0.288**
	(0.135)
Religion	−0.027
	(0.156)
PartyID (Republican)	0.313
	(0.202)
FoxNews	0.682***
	(0.134)
MoralStatism	0.093
	(0.337)
Government	−0.670**
	(0.265)
MoralStatism*Government	−1.510***
	(0.321)
Constant	−2.570***
	(0.208)
Observations	2,406
Log Likelihood	−828.000
Akaike Inf. Crit.	1,688.000
Note:	*p<0.1; **p<0.05; ***p<0.01

Additional information on Bayesian Model Averaging

A version of the R package *BMA* modified by Mongtomery and Nyhan was used to search over the entire model space of Model 2. The analysis was conducted using the *bic.glmMN()* function, which is a version of the *bic.glm()* function in the R package *BMA*. See Raftery et al. (2015) and Montgomery and Nyhan (2010). The analysis uses uniform priors for all independent variables and the only restriction is that the interaction term and its two component variables are required to enter or not enter models together. Options were set to be least restrictive. No Occam's Window was used to narrow the models selected by the initial leap algorithm run over the entire model space and, following Montgomery and Nyhan (pp. 21), the number of best models of each size returned by the leaps algorithm was set to 100,000. In the end, 4,096 models were selected.

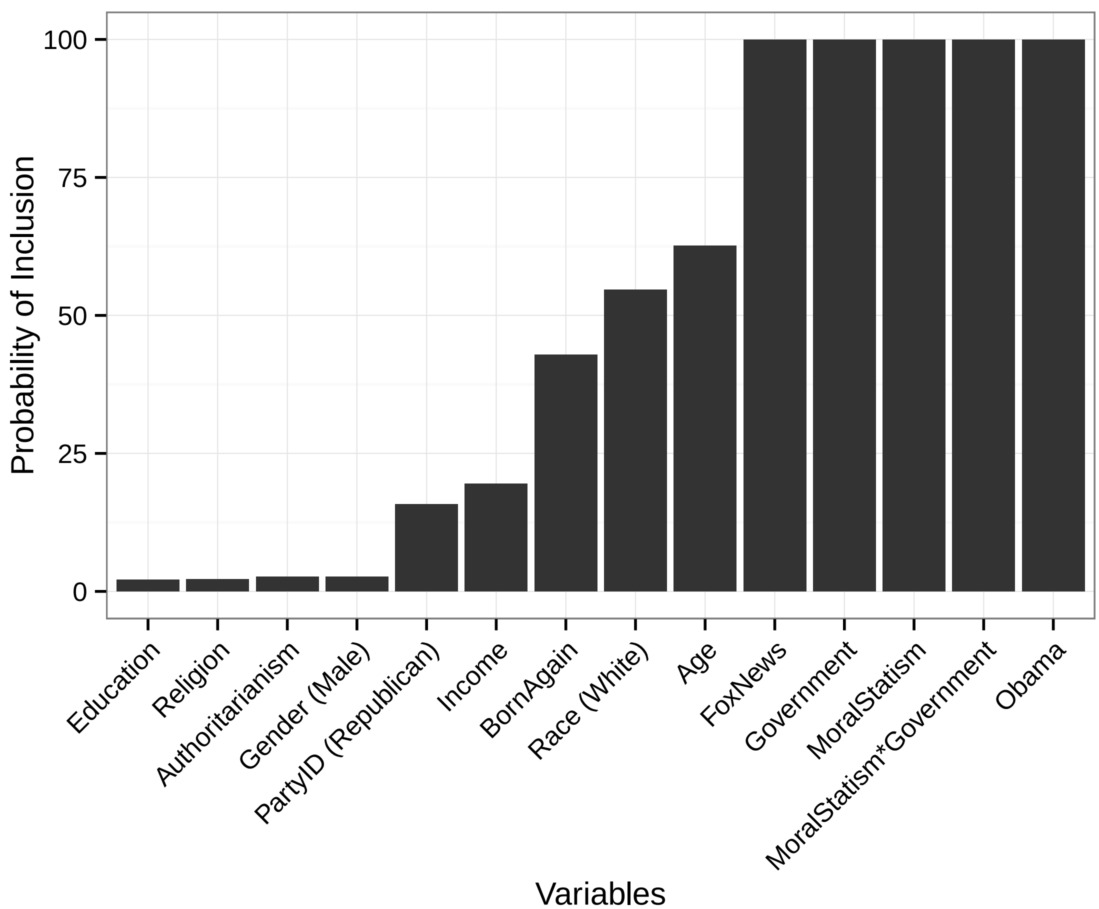

Figure 2: Inclusion Probabilites from Bayesian Model Averaging

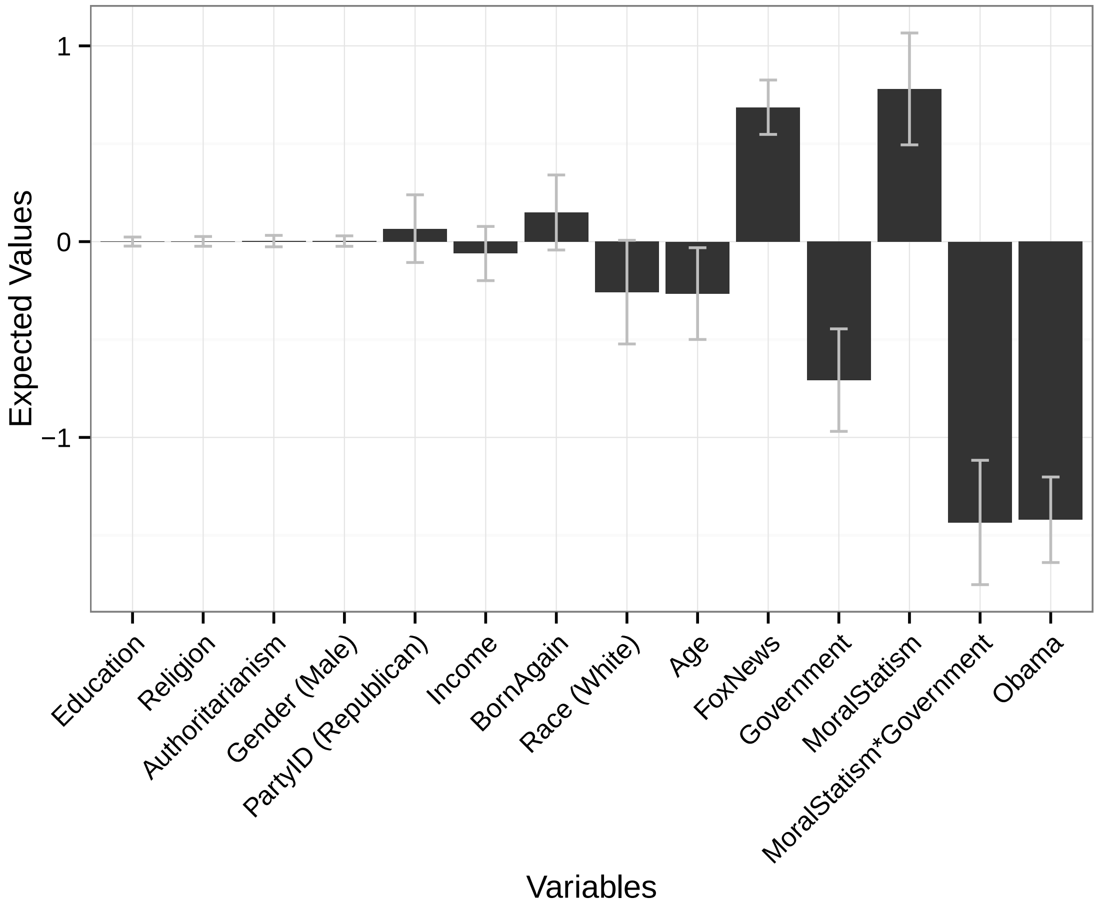

Figure 3: Expected Values from Bayesian Model Averaging

Additional information on Multiple Imputation

We use the R package *Amelia* (Honaker, King, and Blackwell 2008) to generate 10 versions of the ANES dataset with missing values imputed and *Zelig* (Imai, King, and Lau 2009) to obtain pooled regression results via "Rubin's rules." The multiple imputation algorithm only assumes that missing values are "missing at random," not necessarily "missing completely at random." In this context, "missing at random" only means that missingness is dependent on the observed variables. Full numerical results are provided below. Graphical diagnostics for overimputation, dispersion, and comparing pre- and post-imputation densities for our main variables suggest no problems or anomolies in the imputation procedures (see below the numerical results).

	Value	Std. Error	t-stat	p-value
(Intercept)	-2.08	0.12	-18.04	0.00
Gender (Female)	-0.10	0.09	-1.12	0.26
Income	-0.33	0.10	-3.33	0.00
Age	-0.30	0.09	-3.38	0.00
Race (White)	-0.30	0.11	-2.68	0.01
Education	-0.04	0.10	-0.43	0.66
Obama	-0.99	0.14	-7.04	0.00
Authoritarianism	0.06	0.11	0.60	0.55
BornAgain	-0.21	0.12	-1.77	0.08
Religion	0.02	0.09	0.19	0.85
PartyID (Republican)	0.23	0.13	1.75	0.08
FoxNews	0.66	0.10	6.90	0.00
MoralStatism	0.98	0.18	5.35	0.00
Government	-0.67	0.17	-4.03	0.00
MoralStatism*Government	-1.34	0.20	-6.76	0.00

Table 4: Pooled Logistic Regression Results From 10 Multiple Imputations

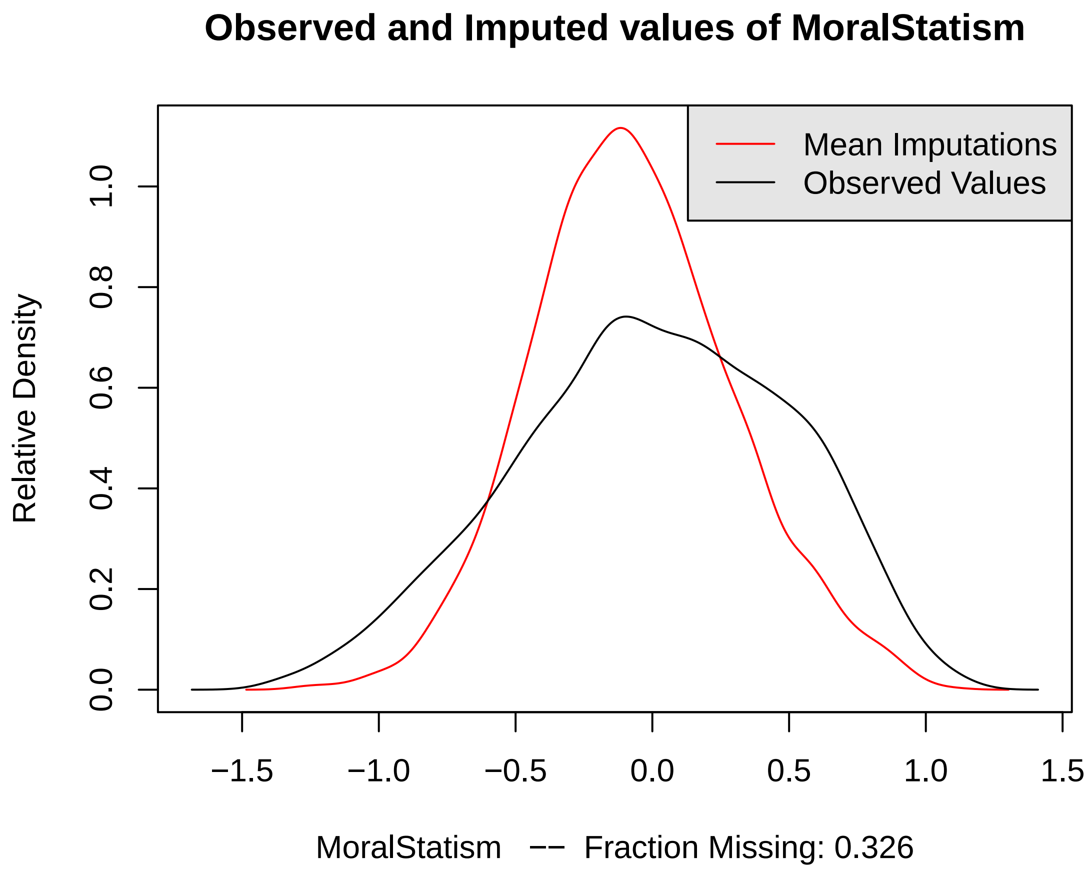

Figure 4: Distributions before and after multiple imputation

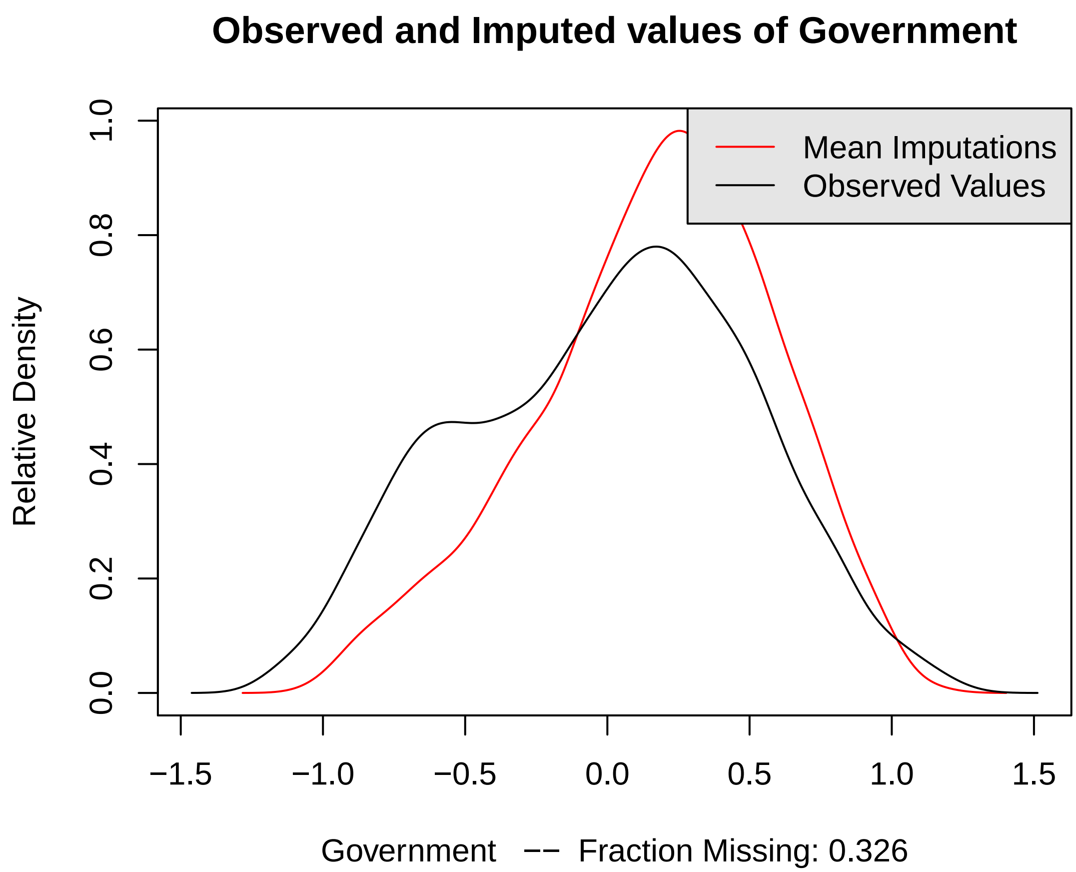

Figure 5: Distributions before and after multiple imputation

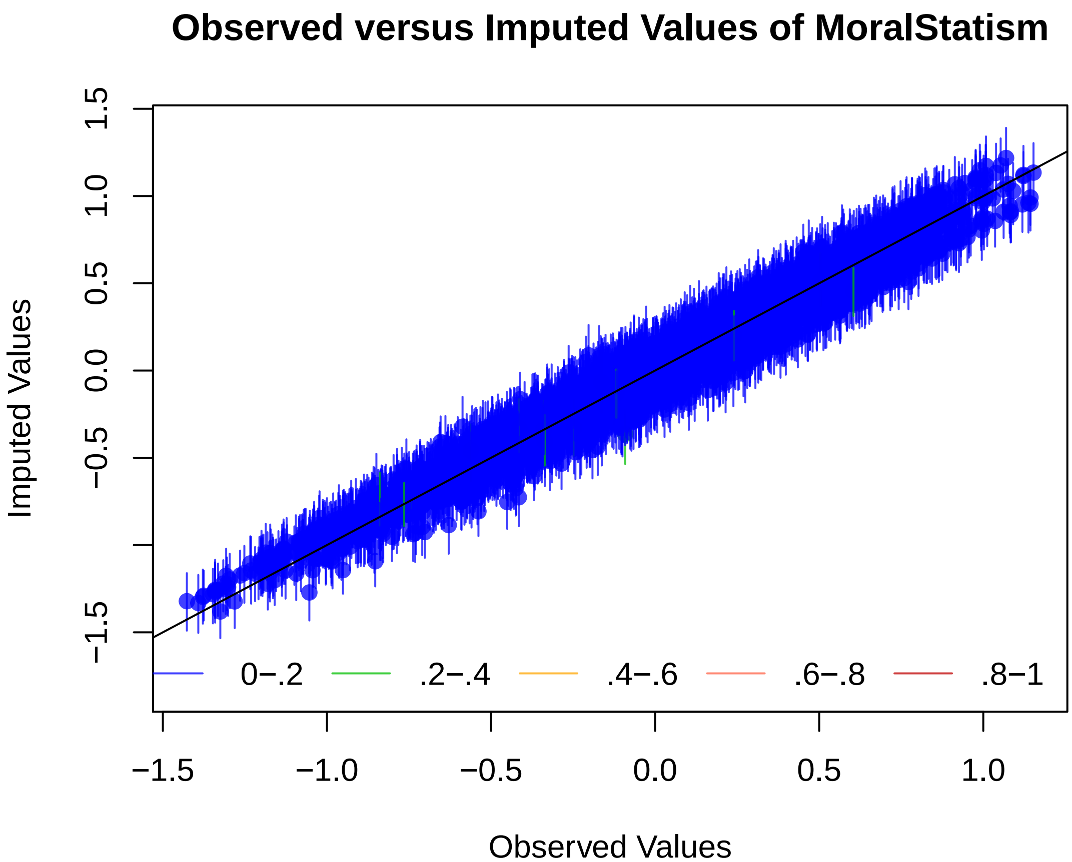

Figure 6: Diagnostic Plot for Overimputation (1)

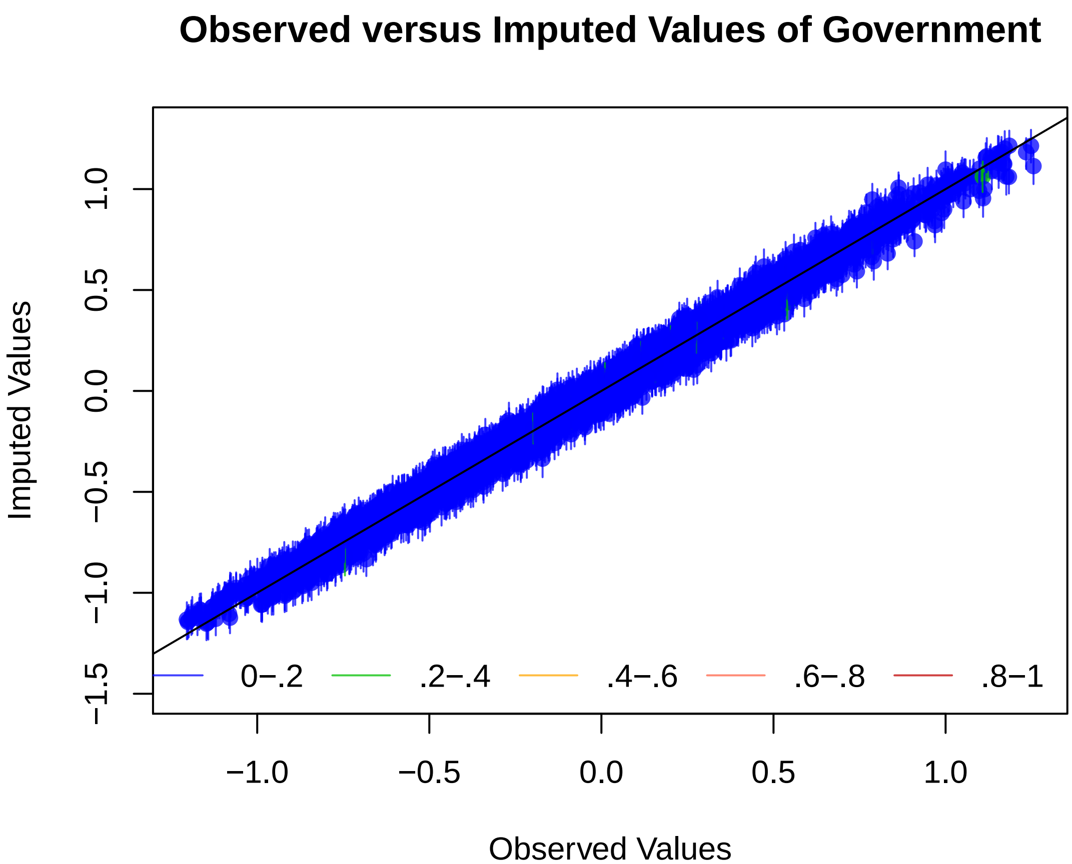

Figure 7: Diagnostic Plot for Overimputation (2)

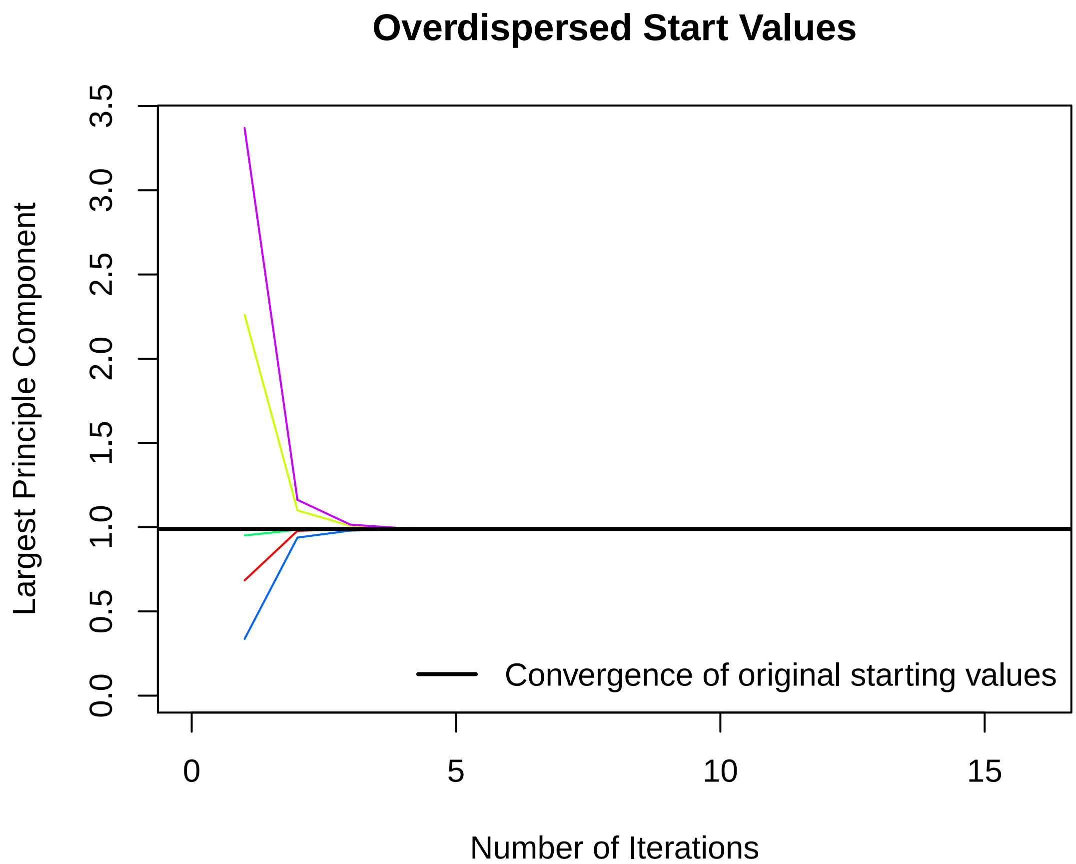

Figure 8: Diagnostic Plot for Dispersion

Additional information on matching estimates and sensitivity bounds

Rosenbaum bounds (1988) for a binary dependent variable are calculated using the *binarysens()* function in the R package *rbounds*. See Keele (2014). We generate matching estimates for each of our three independent variables of interest, one at a time, using one-to-one genetic matching with replacement. In each case, "treatment" is defined as having a value above the sample mean of the variable of interest. For each estimate, we balance on all covariates in Model 2 except the two components of the interaction term and including the treatment variable's propensity scores with respect to those covariates.

References

Fabrigar, Leandre R, Duane T Wegener, Robert C MacCallum, and Erin J Strahan. 1999. "Evaluating the use of exploratory factor analysis in psychological research." *Psychological Methods* 4(3): 272–99.

Keele, Luke J. 2014. "rbounds: Perform Rosenbaum bounds sensitivity tests for matched and unmatched data." https://cran.r-project.org/web/packages/rbounds.

Raftery, Adrian E., Jennifer Hoeting, Chris Volinksy, Ian Painter, and Ka Yee Yeung. 2015. "BMA: Bayesian Model Averaging." https://cran.r-project.org/web/packages/BMA/.