

Matching Methods for Causal Inference

Gary King
Institute for Quantitative Social Science
Harvard University

Talk at University of Georgia, 3/3/2011

- Problem: Model dependence (review)

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- Solution: Matching to preprocess data (review)

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- Problem: The most commonly used method can increase imbalance!
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- (Coarsened Exact Matching is usually best)
- \rightsquigarrow Lots of insights revealed in the process

Model Dependence Example

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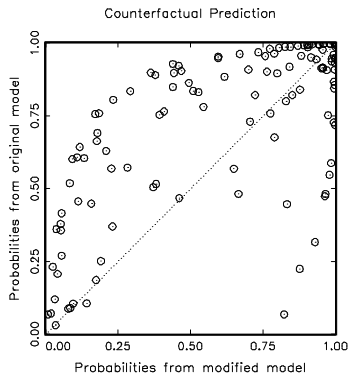
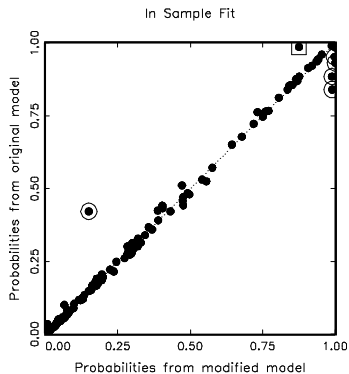
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- **Data analysis:** Logit model
- **The question:** How *model dependent* are the results?

Two Logit Models, Apparently Similar Results

Variables	Original "Interactive" Model			Modified Model		
	Coeff	SE	P-val	Coeff	SE	P-val
Wartype	-1.742	.609	.004	-1.666	.606	.006
Logdead	-.445	.126	.000	-.437	.125	.000
Wardur	.006	.006	.258	.006	.006	.342
Factnum	-1.259	.703	.073	-1.045	.899	.245
Factnum2	.062	.065	.346	.032	.104	.756
Trnsfcap	.004	.002	.010	.004	.002	.017
Develop	.001	.000	.065	.001	.000	.068
Exp	-6.016	3.071	.050	-6.215	3.065	.043
Decade	-.299	.169	.077	-0.284	.169	.093
Treaty	2.124	.821	.010	2.126	.802	.008
UNOP4	3.135	1.091	.004	.262	1.392	.851
Wardur*UNOP4	—	—	—	.037	.011	.001
Constant	8.609	2.157	0.000	7.978	2.350	.000
N		122			122	
Log-likelihood		-45.649			-44.902	
Pseudo R^2		.423			.433	

Doyle and Sambanis: Model Dependence



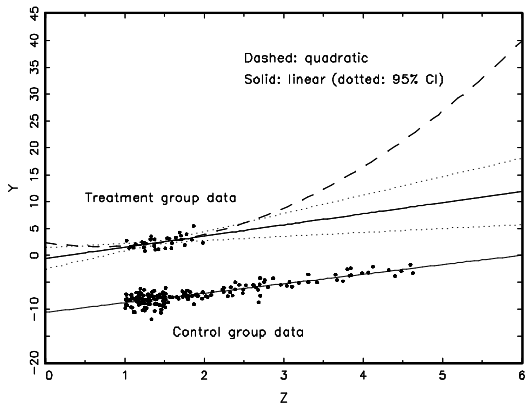
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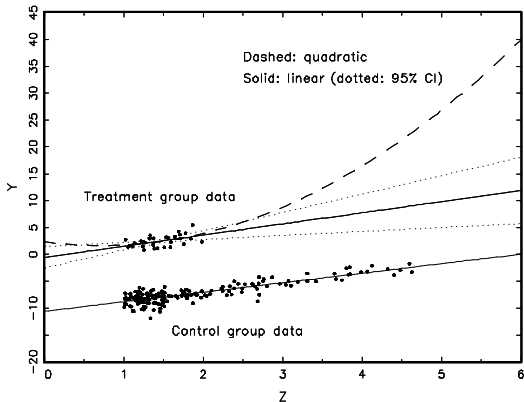
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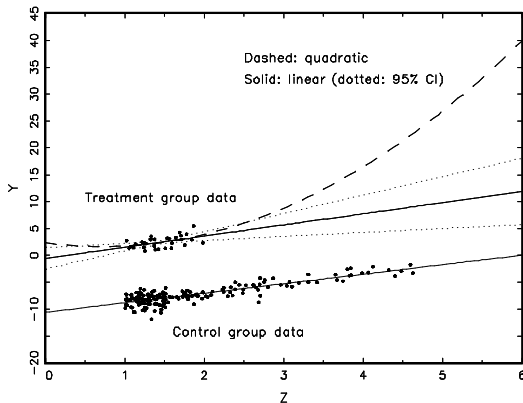
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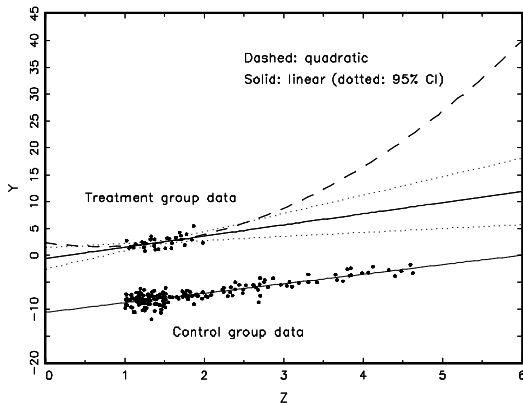


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- Preprocess I: Eliminate extrapolation region

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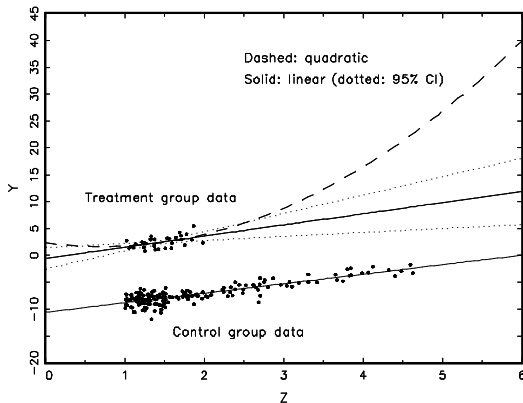


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- Preprocess II: Match (prune bad matches) within interpolation region
- Model remaining imbalance

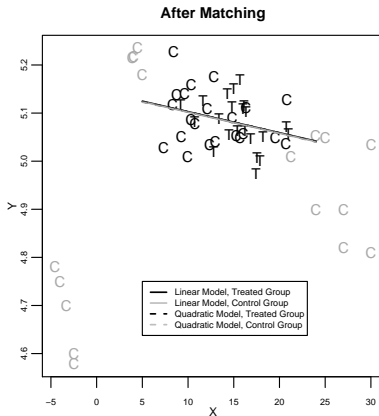
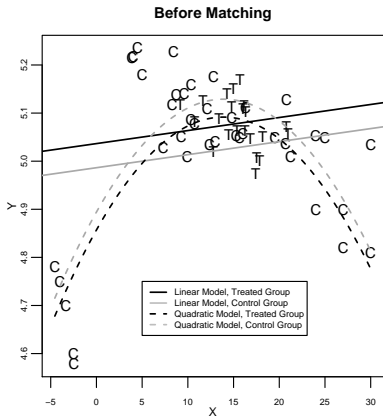
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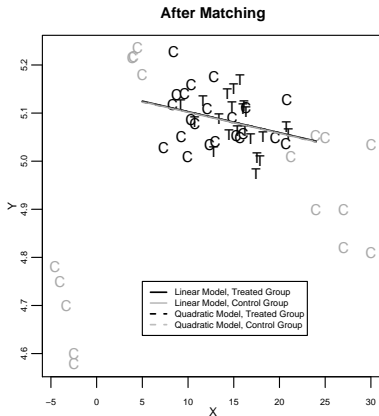
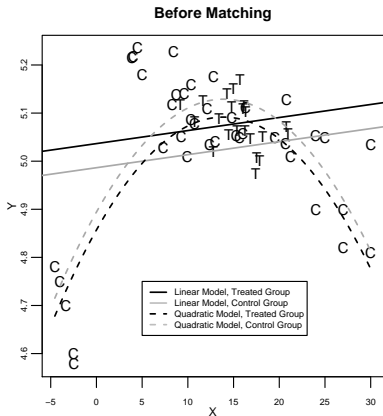
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Matching reduces model dependence, bias, and variance

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- Can apply other matching methods within CEM strata (inherit CEM's properties)

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 - Classic measure: Difference of means (for each variable)
 - Better measure (difference of multivariate histograms):

$$\mathcal{L}_1(f, g; H) = \frac{1}{2} \sum_{\ell_1 \dots \ell_k \in H(\mathbf{X})} |f_{\ell_1 \dots \ell_k} - g_{\ell_1 \dots \ell_k}|$$

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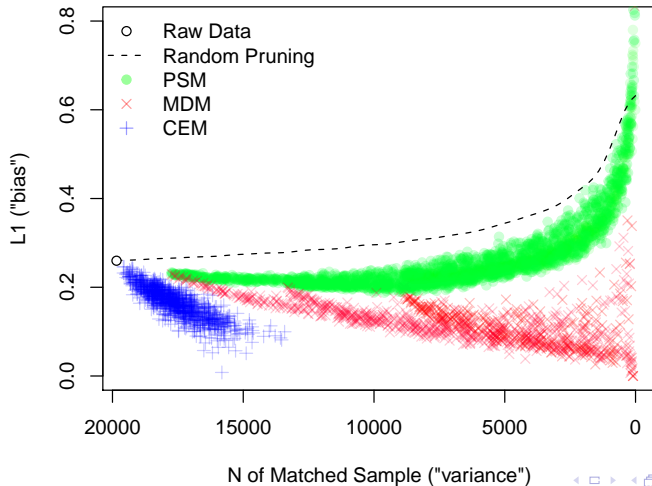
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- MDM & PSM: Choose matched n , match, check imbalance
- CEM: Choose imbalance, match, check matched n
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- Our idea: Compute lots of matching solutions, identify the frontier of lowest imbalance for each given n , and choose a matching solution

A Space Graph: Real Data

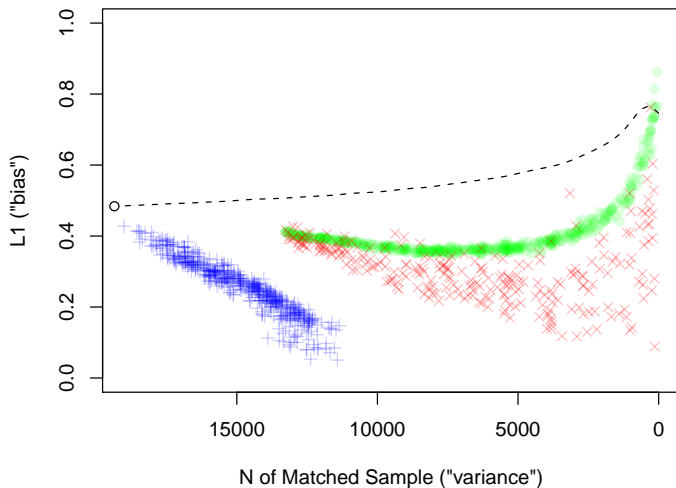
King, Nielsen, Coberley, Pope, and Wells (2011)

Healthways Data

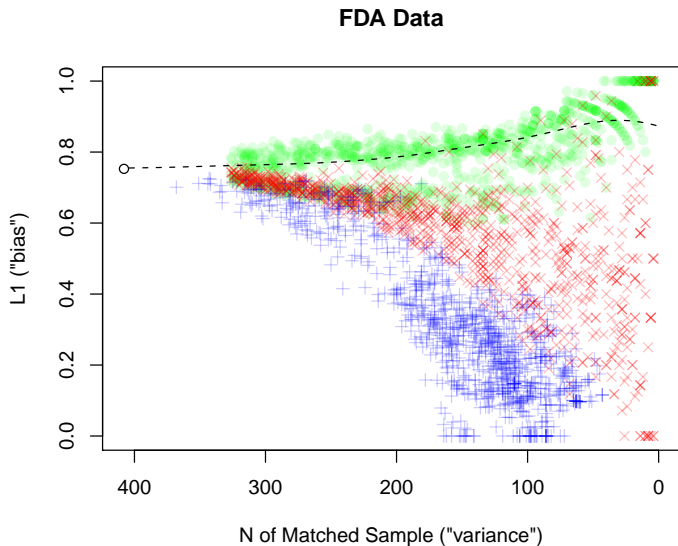


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Called/Not Called Data

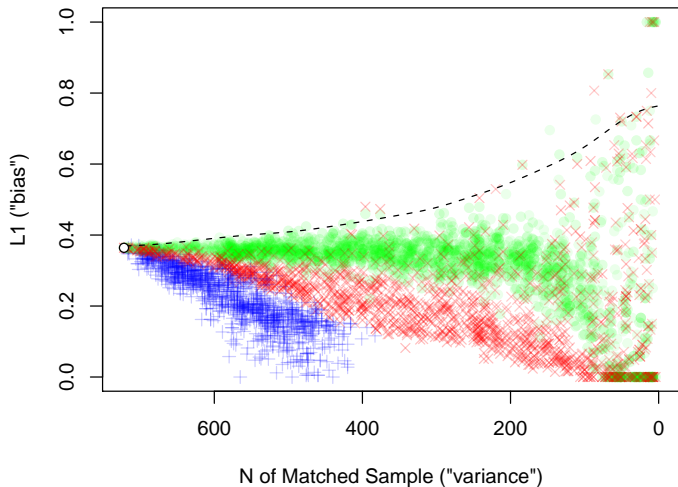


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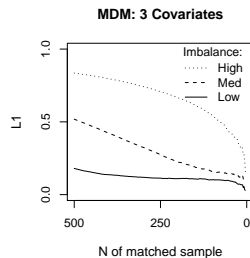
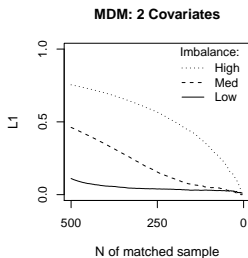
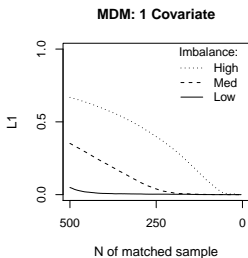


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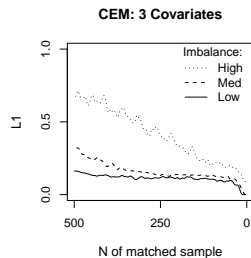
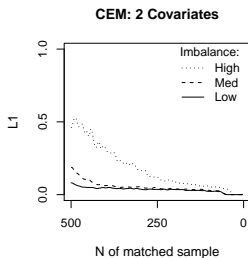
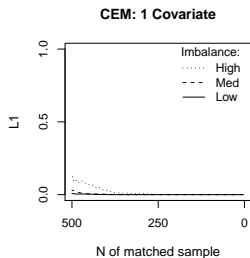
Lalonde Data Subset



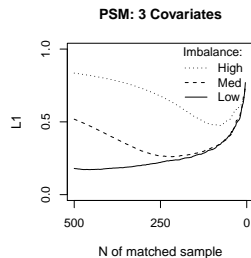
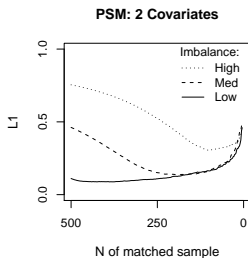
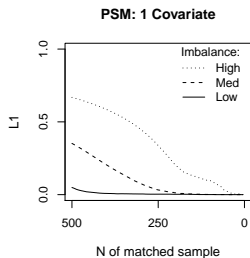
A Space Graph: Simulated Data — Mahalanobis



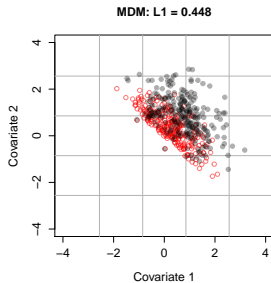
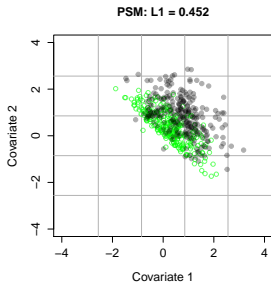
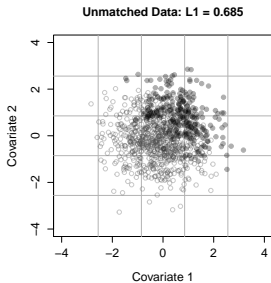
A Space Graph: Simulated Data — CEM



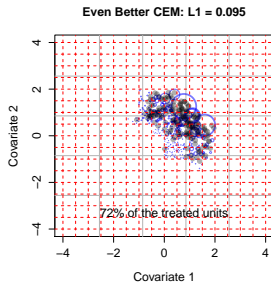
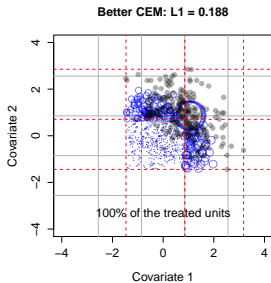
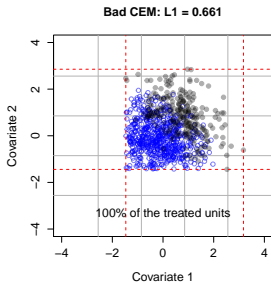
A Space Graph: Simulated Data — Propensity Score



Data where PSM Works Reasonably Well — PSM & MDM



Data where PSM Works Reasonably Well — CEM



CEM Weights and Nonparametric Propensity Score

CEM Weight: $w_i = \frac{m_i^T}{m_i^C}$ (Unnormalized)

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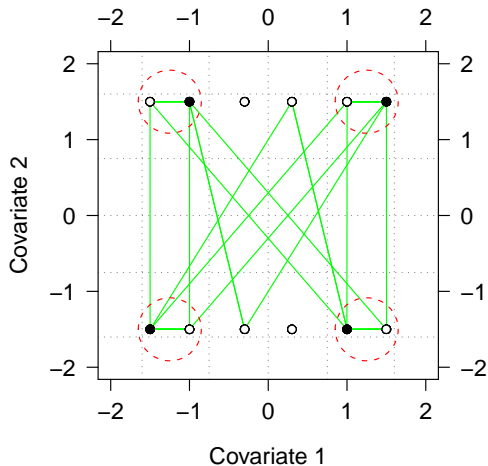
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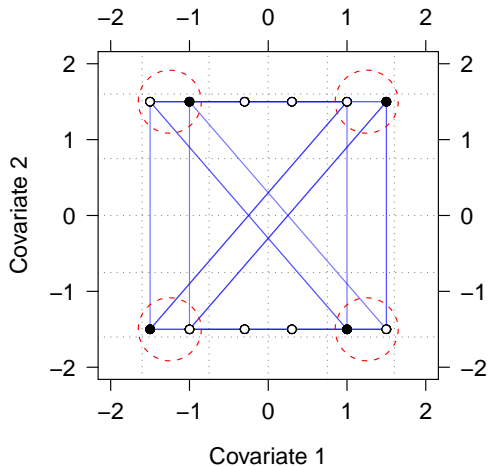
- Gives a better pscore than PSM
- Doesn't match based on crippled information

PSM Approximates Random Matching in Balanced Data



- PSM Matches
- - - CEM and MDM Matches

Destroying CEM with PSM's Two Step Approach



- CEM Matches
- CEM-generated PSM Matches

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For papers, software (for R and Stata), tutorials, etc.

<http://GKing.Harvard.edu/cem>