Comparative Effectiveness of Matching Methods for Causal Inference

Gary King Institute for Quantitative Social Science Harvard University

joint work with

Richard Nielsen (Harvard), Carter Coberley, James Pope, Aaron Wells (Healthways)

Harvard, IQSS

(for a talk at Princeton University, 10/15/10)

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- Problem: The most commonly used method can increase imbalance!
- Solution: Other methods do not share this problem
- → Lots of insights revealed in the process

Replication: Doyle and Sambanis, APSR 2000

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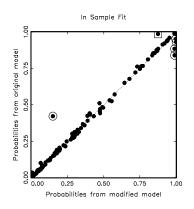
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- The question: How model dependent are the results?

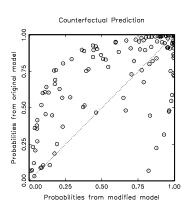
Two Logit Models, Apparently Similar Results

	Original "Interactive" Model			Modified Model		
Variables	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	<u> </u>	_	_	.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

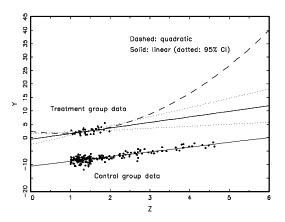
Doyle and Sambanis: Model Dependence



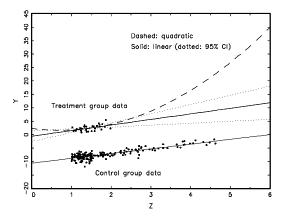


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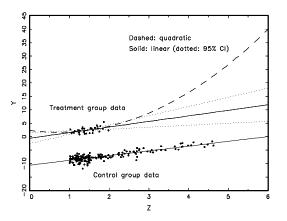


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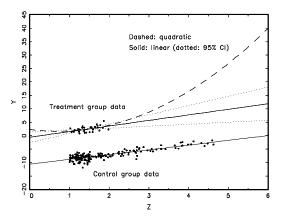
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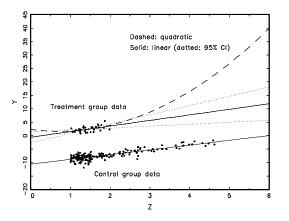
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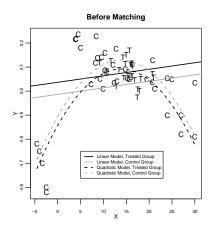


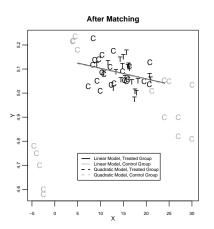
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- Preprocess II: Match (prune bad matches) within interpolation region
- Model remaining imbalance

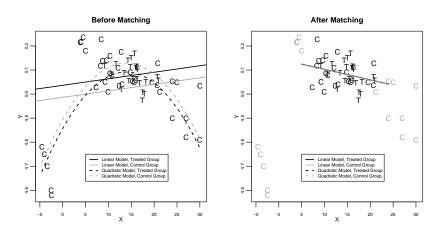
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Matching reduces model dependence, bias, and variance

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

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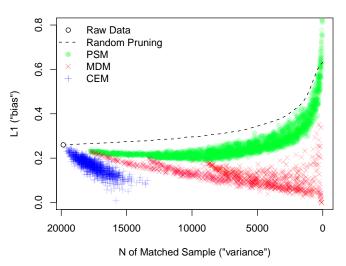
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- Better measure (difference of multivariate histograms):

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

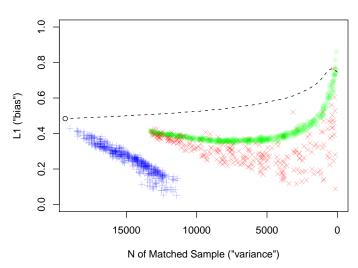
A Space Graph: Real Data

Healthways Data



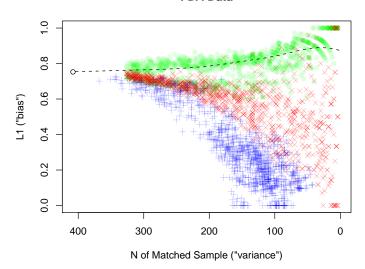
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Called/Not Called Data



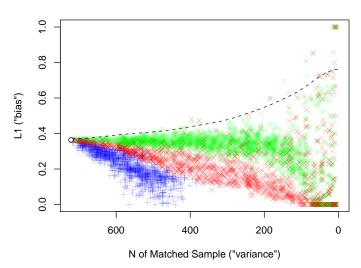
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FDA Data

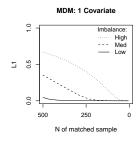


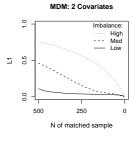
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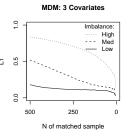
Lalonde Data Subset



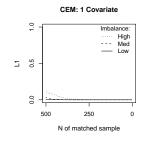
A Space Graph: Simulated Data — Mahalanobis

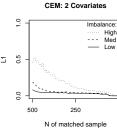


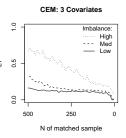




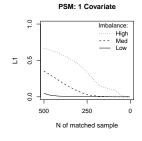
A Space Graph: Simulated Data — CEM

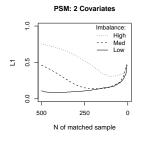


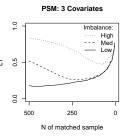




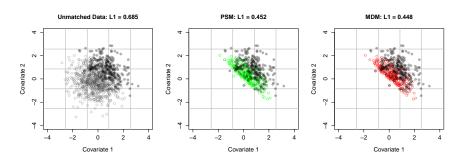
A Space Graph: Simulated Data — Propensity Score



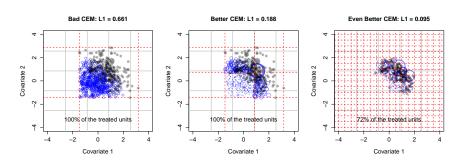




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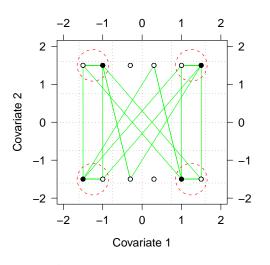


CEM Weights and Nonparametric Propensity Score

CEM Pscore:
$$\widehat{\Pr}(T_i = 1|X_i) = \frac{m_i^T}{m_i^T + m_i^C}$$

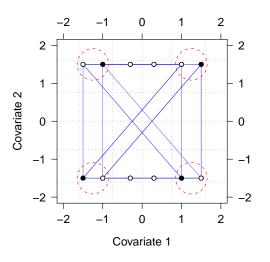
CEM Weight:
$$w_i = \frac{m_i^T}{m_i^C}$$
 (Unnormalized)

PSM Approximates Random Matching in Balanced Data



PSM MatchesCEM and MDM Matches

Destroying CEM by using PSM's Two Step Approach



CEM MatchesCEM-generated PSM Matches

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- You can easily check with the Space Graph

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

http://GKing.Harvard.edu/cem