

Comparative Effectiveness of Matching Methods for Causal Inference

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joint work with

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Talk at Quantitative Issues in Cancer Research Working Seminar, Biostatistics, HSPH,
10/18/10

- Problem: Model dependence (review)

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- Solution: Matching to preprocess data (review)

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- Problem: Many matching methods & specifications
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- Problem: The most commonly used method can increase imbalance!
- Solution: Other methods do not share this problem
- \rightsquigarrow Lots of insights revealed in the process

Model Dependence Demonstration

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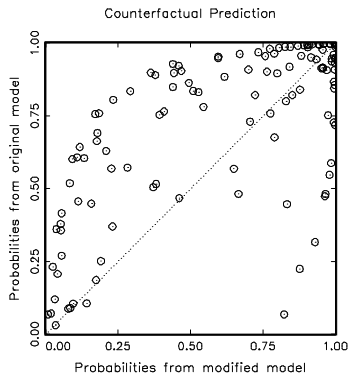
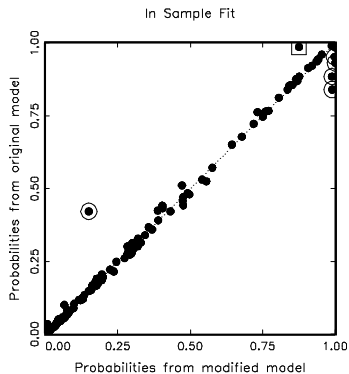
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- **Data analysis:** Logit model
- **The question:** How *model dependent* are the results?

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



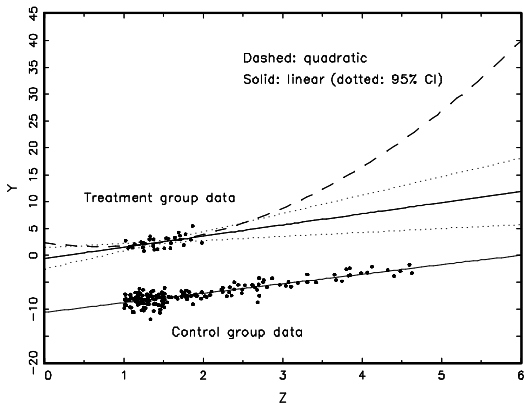
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(King and Zeng, 2006: fig.4 *Political Analysis*)

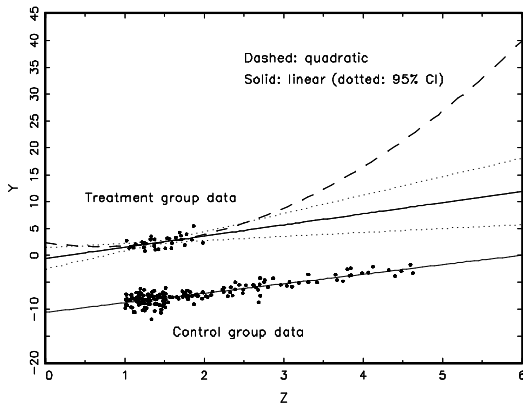
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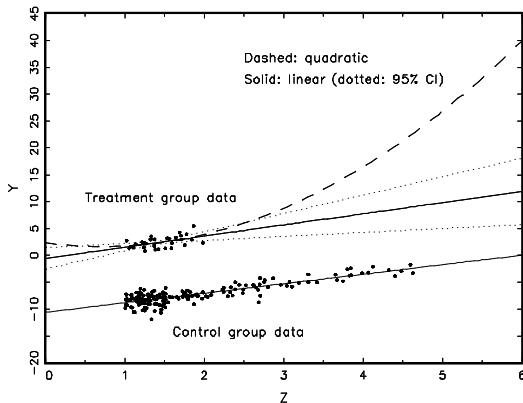
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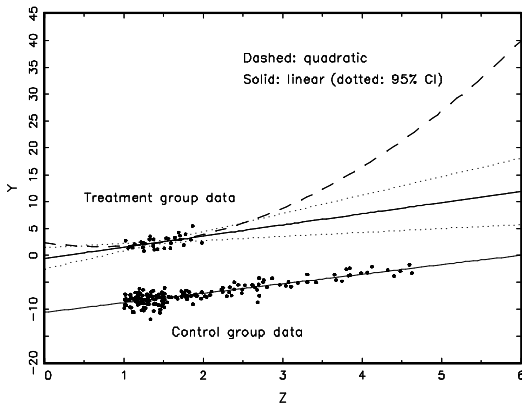


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- Preprocess I: Eliminate extrapolation region

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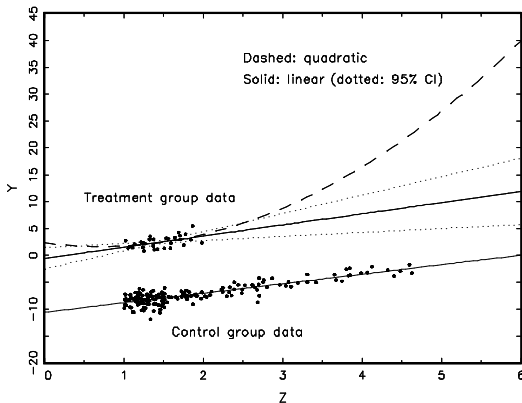


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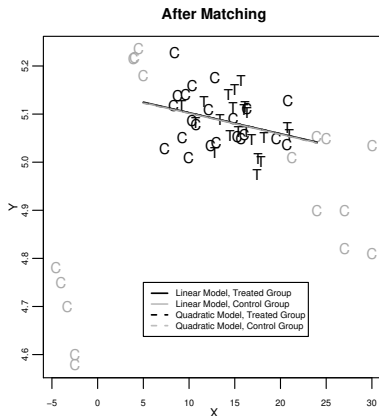
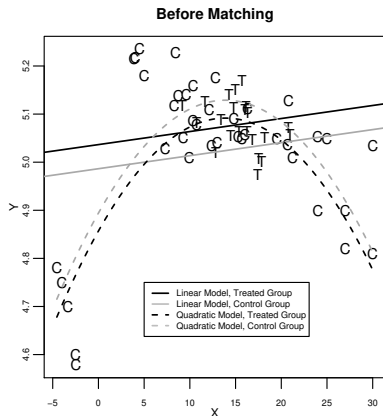
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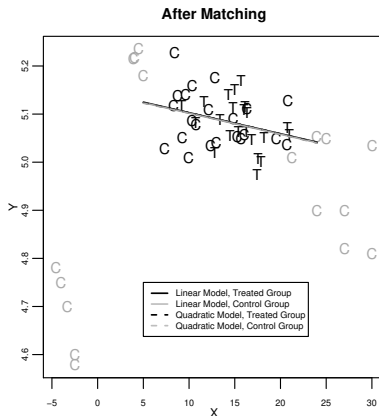
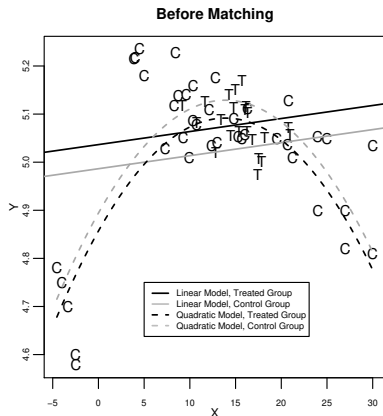
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Matching reduces model dependence, bias, and variance

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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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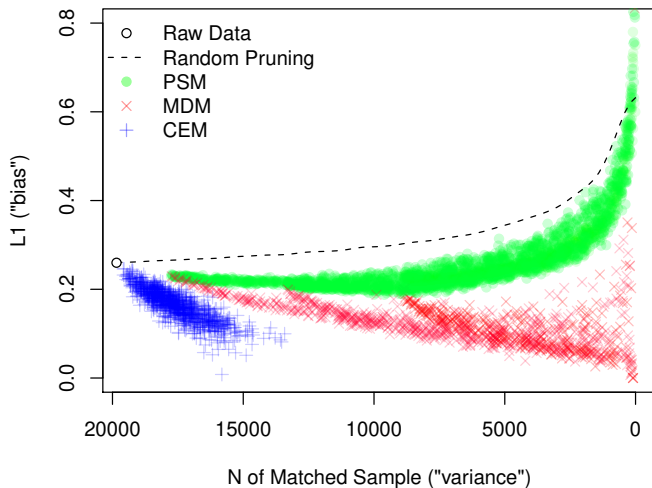
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- Best practice: iterate
- Choose matched solution & matching method becomes irrelevant
- Our idea: Compute lots of matching solutions, identify the frontier of lowest imbalance for each given n , and choose a matching solution

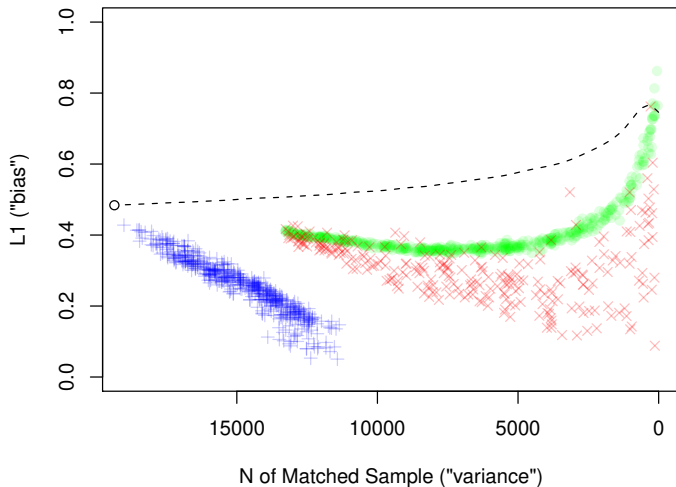
A Space Graph: Real Data

Healthways Data

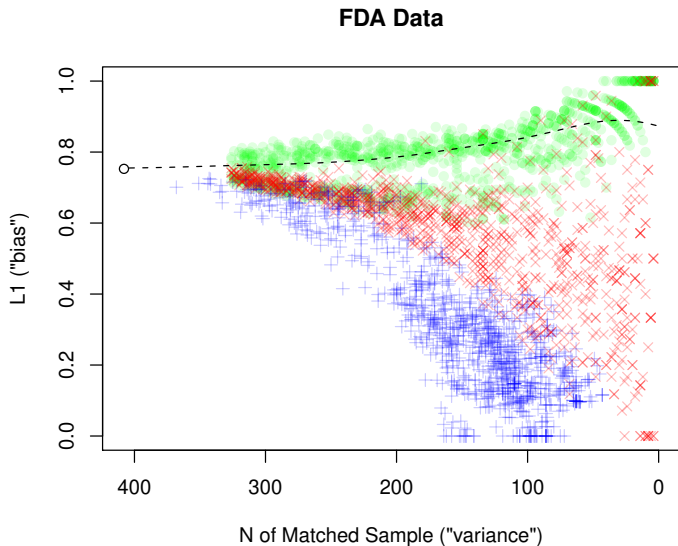


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Called/Not Called Data

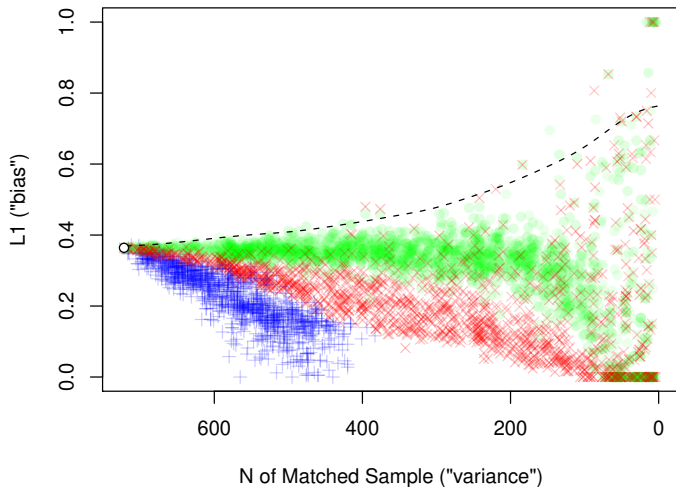


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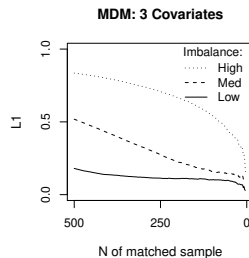
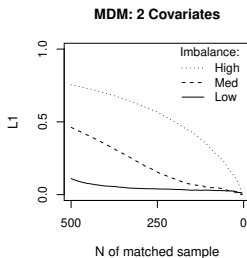
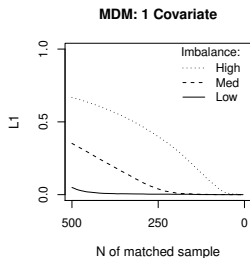


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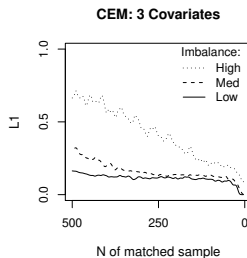
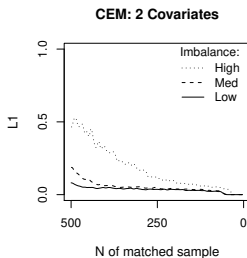
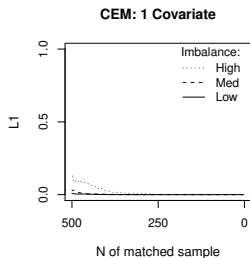
Lalonde Data Subset



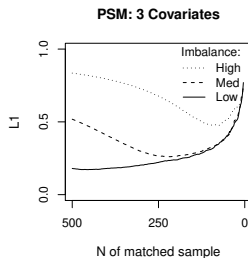
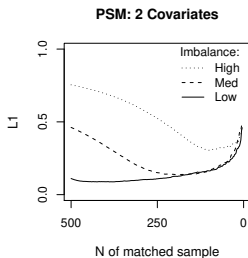
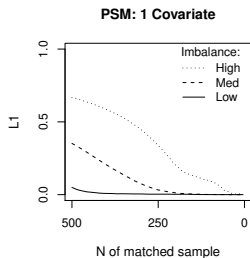
A Space Graph: Simulated Data — Mahalanobis



A Space Graph: Simulated Data — CEM

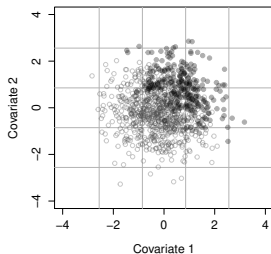


A Space Graph: Simulated Data — Propensity Score

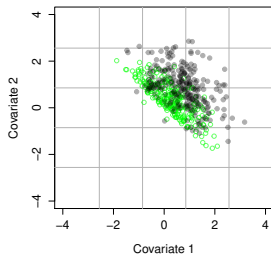


Data where PSM Works Reasonably Well — PSM & MDM

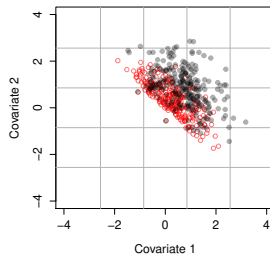
Unmatched Data: $L1 = 0.685$



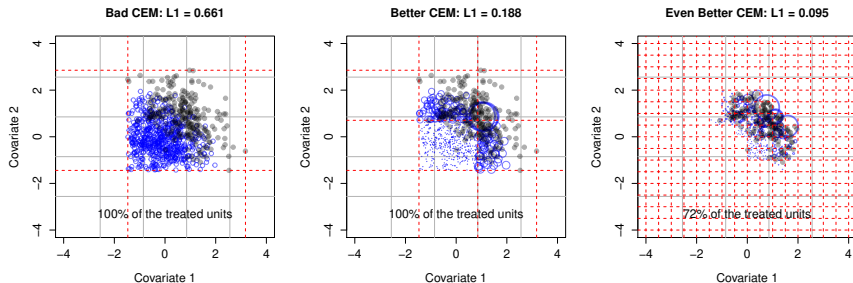
PSM: $L1 = 0.452$



MDM: $L1 = 0.448$



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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- Gives a better pscore than PSM

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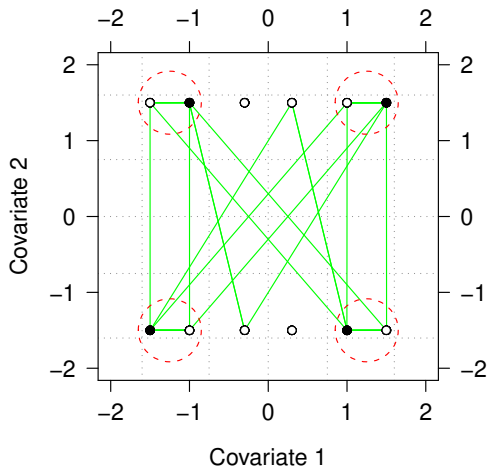
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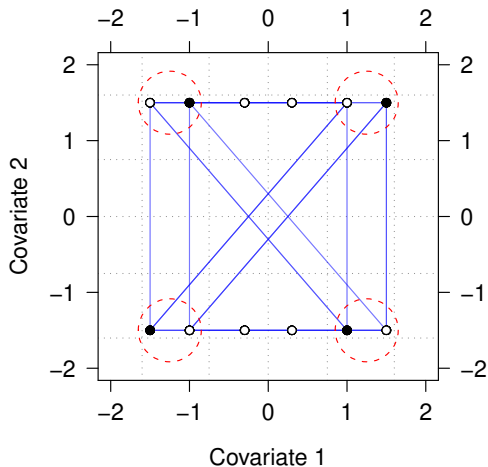
- Gives a better pscore than PSM
- Doesn't match based on crippled information

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>