# Comparative Effectiveness of Matching Methods for Causal Inference

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Harvard University

joint work with

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

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- Solution: The Space Graph helps us compare
- 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

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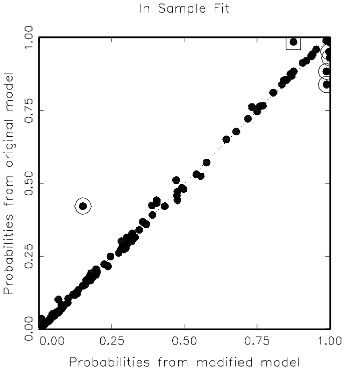
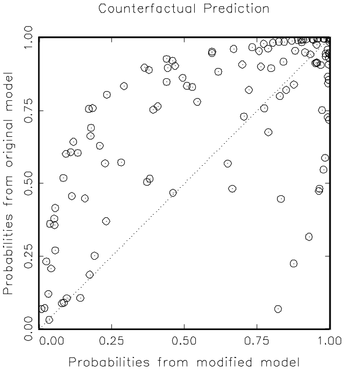
- Data analysis: Logit model
- The question: How *model dependent* are the results?

# 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 | — | — | — | .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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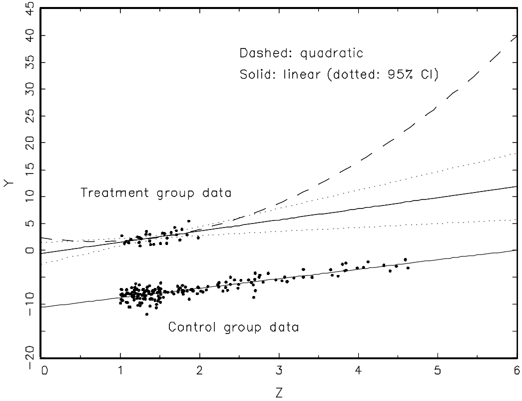

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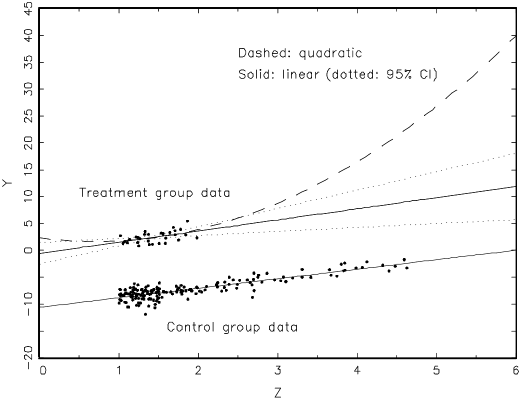

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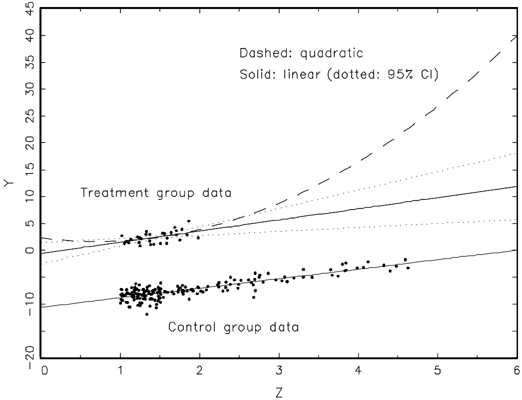

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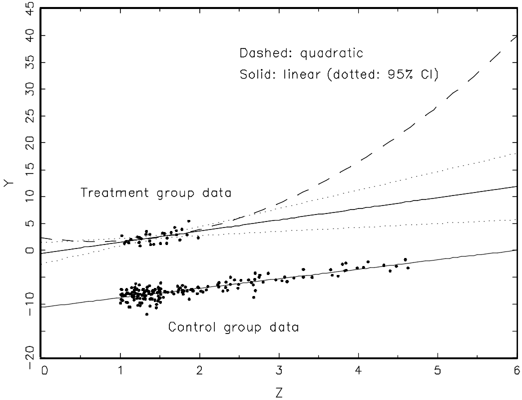

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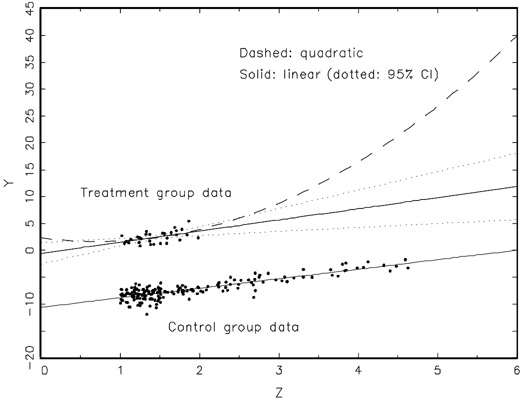

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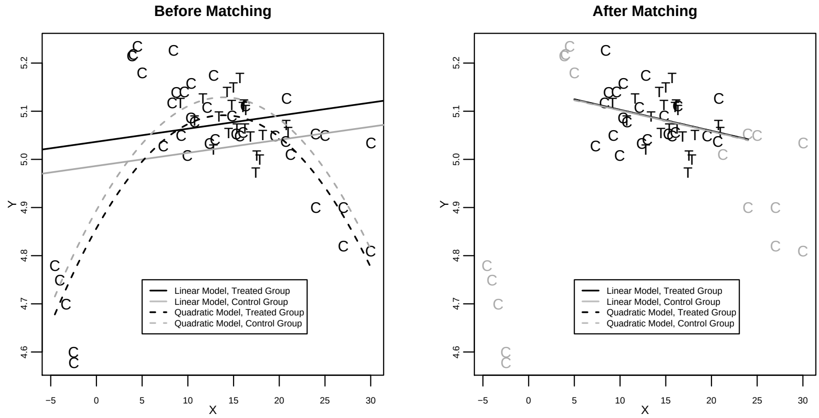

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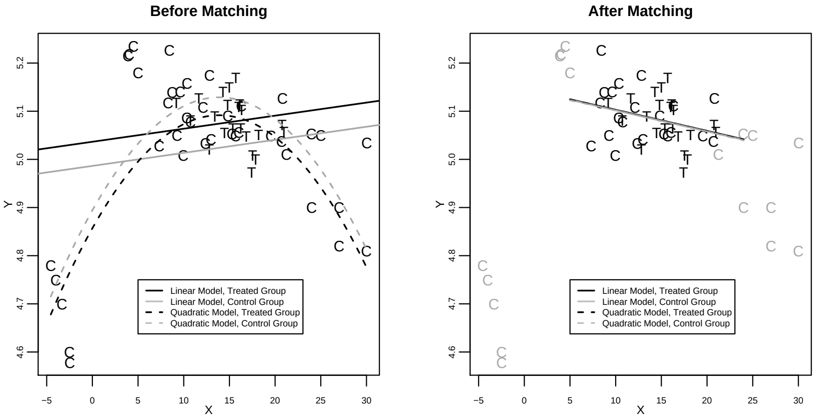

Matching reduces model dependence, bias, and variance

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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):

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

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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

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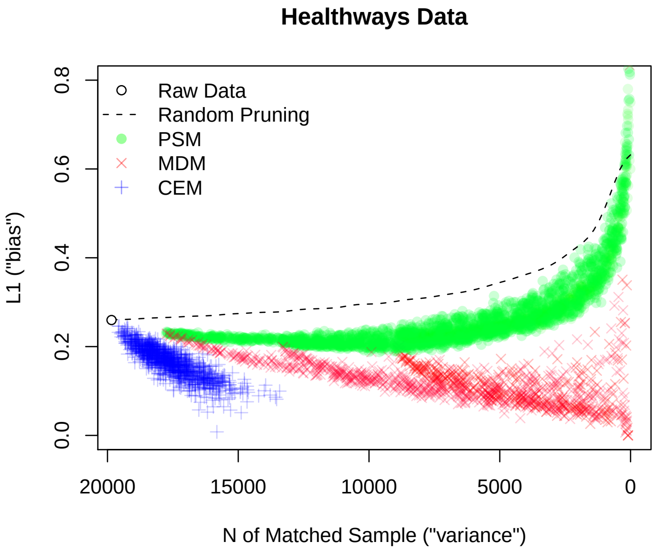

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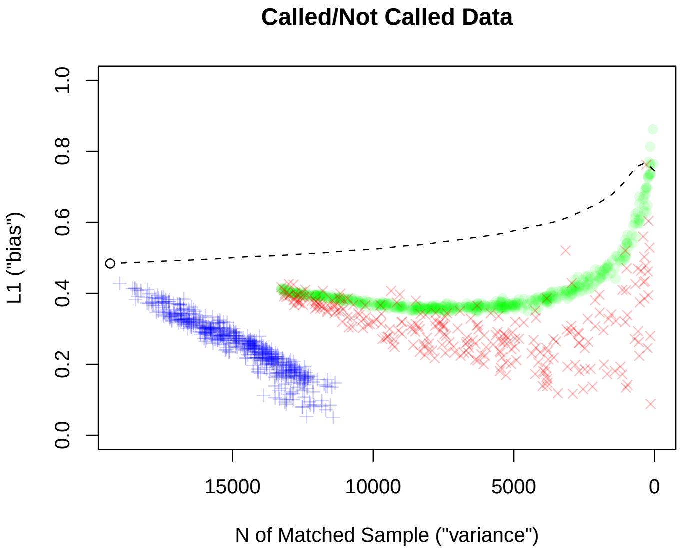

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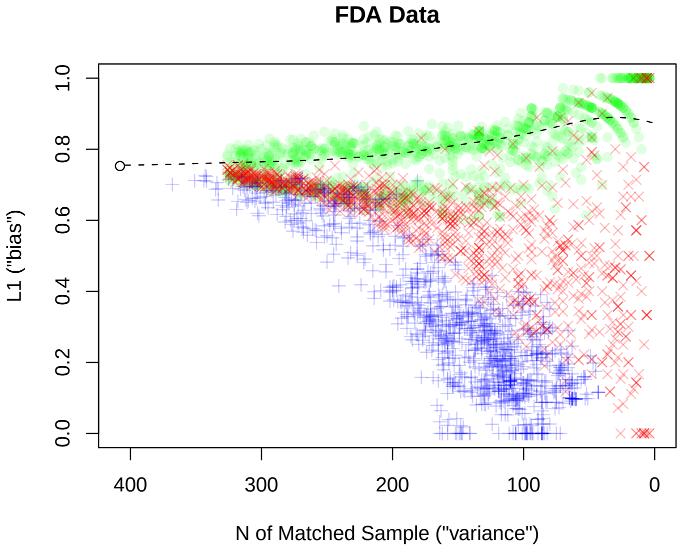

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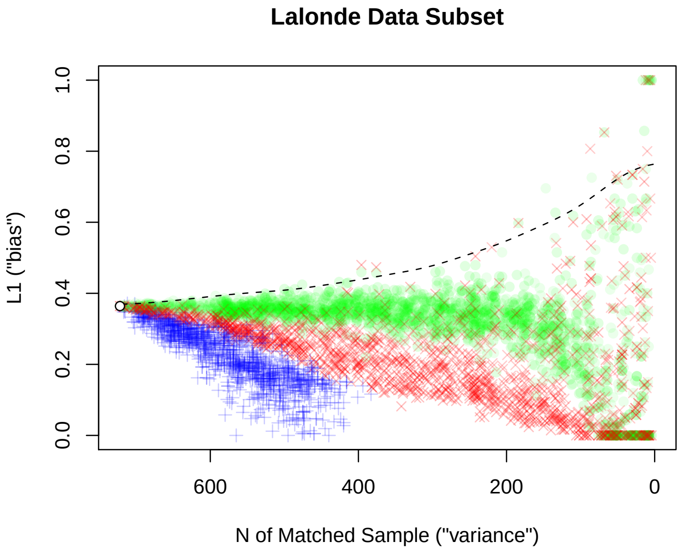
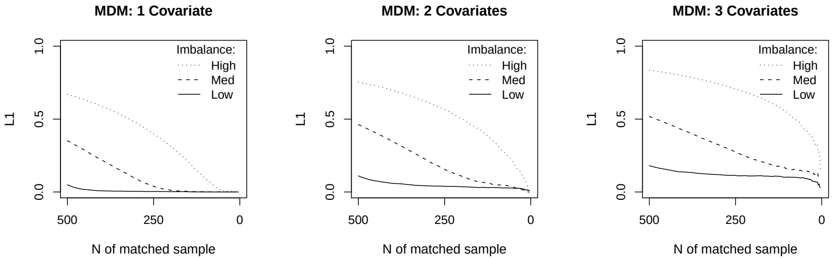
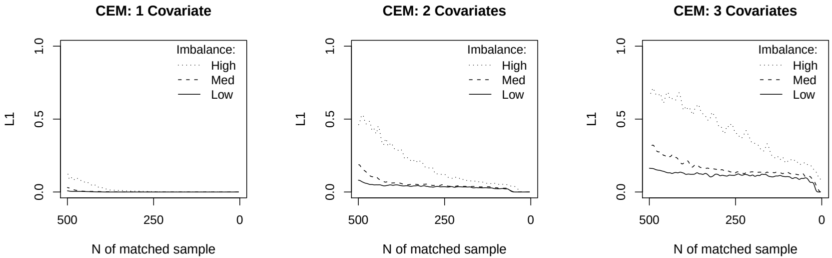


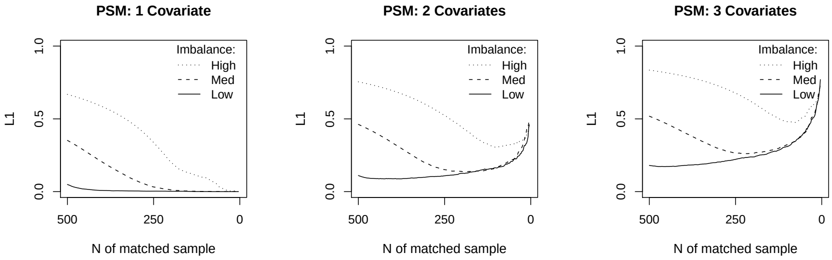
# A Space Graph: Simulated Data — Mahalanobis



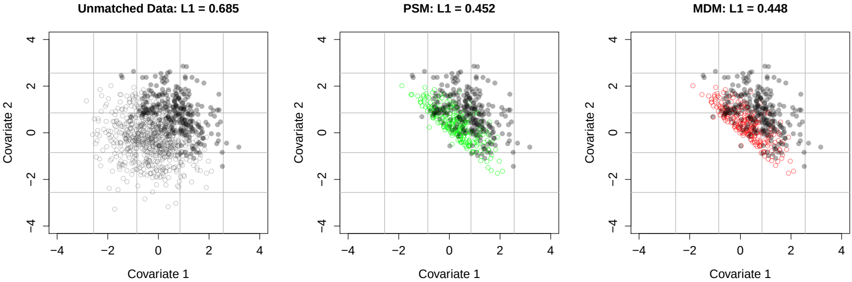
# A Space Graph: Simulated Data — CEM



# A Space Graph: Simulated Data — Propensity Score



# Data where PSM Works Reasonably Well — PSM & MDM



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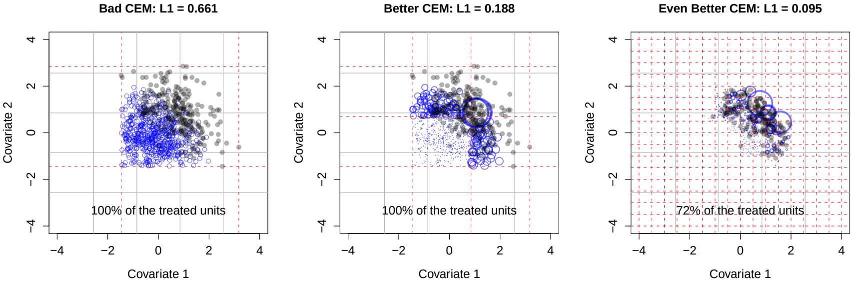

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CEM Weight: $$w_i = \frac{m_i^T}{m_i^C} \quad \text{(Unnormalized)}$$

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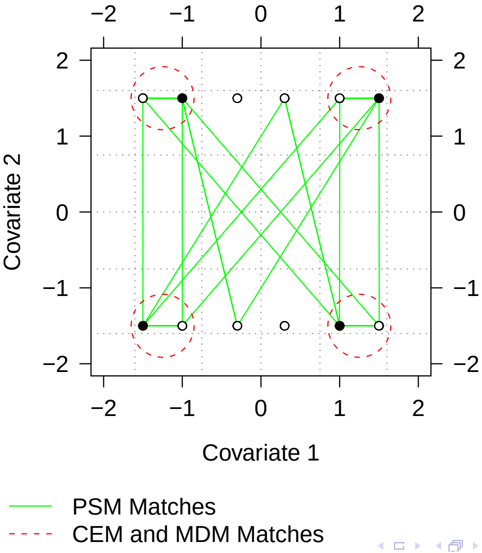
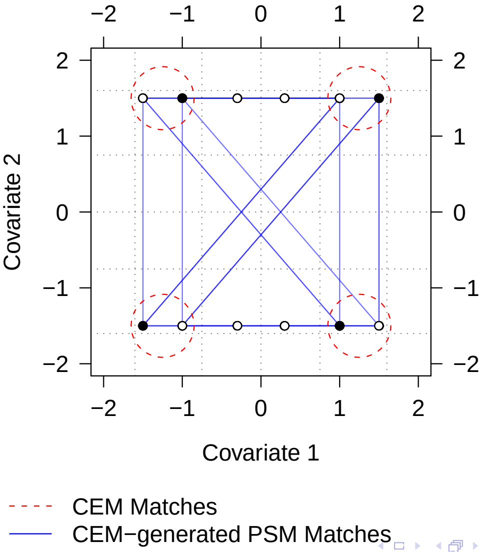
# PSM Approximates Random Matching in Balanced Data



# Destroying CEM with PSM's Two Step Approach



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

http://GKing.Harvard.edu/cem