

Coarsened Exact Matching

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- Stefano M. Iacus, Gary King, and Giuseppe Porro, "Causal Inference Without Balance Checking: Coarsened Exact Matching," 2010.

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- Stefano M. Iacus, Gary King, and Giuseppe Porro, "Multivariate Matching Methods That are Monotonic Imbalance Bounding," 2010.

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- Related Software: [cem](#), (also works within [MatchIt](#)), [Zelig](#)

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 - Least important (variance): matched n **chosen ex ante**
 - Most important (bias): imbalance reduction **checked ex post**
- Hard to use: Improving balance on 1 variable can reduce it on others
 - Best practice: choose n -match-check, tweak-match-check, tweak-match-check, . . .
 - Actual practice: choose n , match, publish, STOP.
(Is balance even improved?)

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If ϵ is reduced, $\gamma(\epsilon)$ decreases & $\gamma(\epsilon)$ is unchanged

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- Approximate invariance to measurement error:

	CEM	pscore	Mahalanobis	Genetic
% Common Units	96.5	70.2	80.9	80.0

Other CEM properties we prove

- Automatically eliminates extrapolation region (no separate step)
- Bounds model dependence
- Bounds causal effect estimation error
- Meets the congruence principle
 - The principle: data space = analysis space
 - Estimators that violate it are nonrobust and counterintuitive
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- Simple to teach: coarsen, then exact match

Imbalance Measures

Variable-by-Variable Difference in Global Means

$$I_1^{(j)} = \left| \bar{X}_{m_T}^{(j)} - \bar{X}_{m_C}^{(j)} \right|, \quad j = 1, \dots, k$$

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Local Imbalance by Variable (given strata fixed by matching method)

$$I_2^{(j)} = \frac{1}{S} \sum_{s=1}^S \left| \bar{X}_{m_T^s}^{(j)} - \bar{X}_{m_C^s}^{(j)} \right|, \quad j = 1, \dots, k$$

CEM in Practice: EPBR-Compliant Data

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X_1	X_2	X_3	X_4	X_5	Seconds
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⇒ **CEM dominates EPBR-methods in EPBR Data**

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Monte Carlo: Exact replication of Diamond and Sekhon (2005), using data from Dehejia and Wahba (1999). CEM coarsening automated.

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BIAS	SD	RMSE	Seconds	\mathcal{L}_1
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	BIAS	SD	RMSE	Seconds	\mathcal{L}_1
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GEN	78.3	499.5	505.6	27.38	1.12

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CEM in Practice: Non-EPBR Data

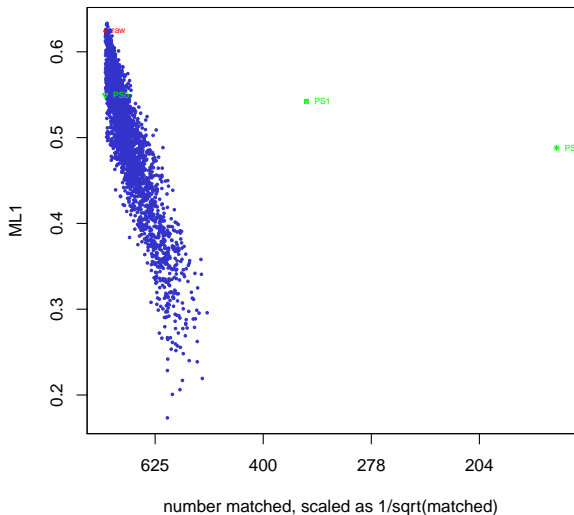
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⇒ **CEM works well in non-EPBR data too**

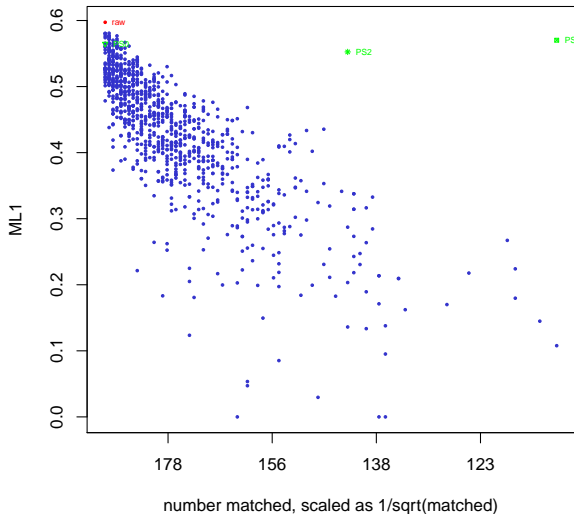
Bias v Efficiency in Matching Methods: I

The space of matching solutions



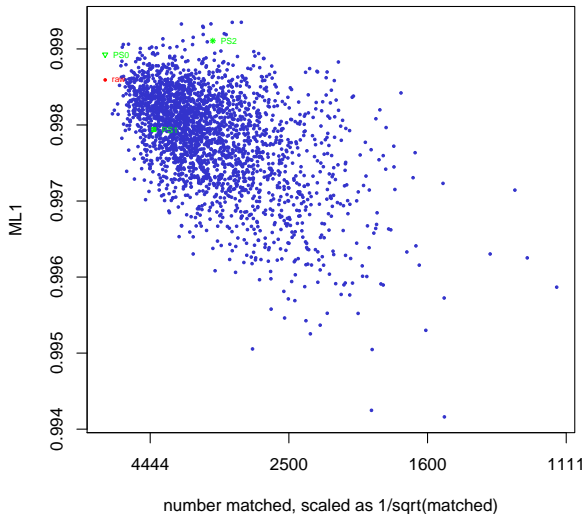
Bias v Efficiency in Matching Methods: II

The space of matching solutions



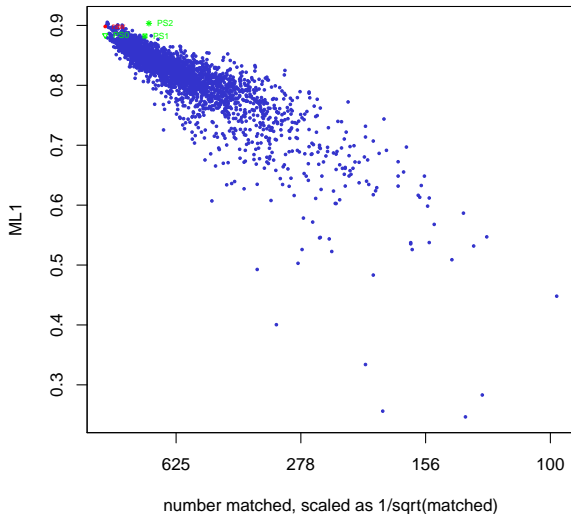
Bias v Efficiency in Matching Methods: III

The space of matching solutions



Bias v Efficiency in Matching Methods: IV

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CEM Extensions I

- CEM and **Multiple Imputation for Missing Data**

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- **Detecting Extreme Counterfactuals**

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CEM Extensions II: Improving Existing Matching Methods

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 - cannot be used to eliminate extrapolation region
 - don't possess most other CEM properties
 - but inherent CEM properties if applied within CEM strata
- 2 **Propensity Score matching:**
 - requires correct specification or balance can drop (the usual specification tests are irrelevant; must check balance)
 - CEM strata can bound bias in pscore matching
 - may be good for applications with many covariates we know little about (so we're willing to take balance on any subset)
- 3 **Mahalanobis distance:** can apply within CEM strata
- 4 **Genetic Matching:** can constrain results to CEM strata
- 5 **Synthetic Matching, or Robins' weights:** CEM can identify region to apply weights, increasing efficiency/robustness

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- 7 **↪ & whatever else you all come up with**

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

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