Adaptive Hyper-box Matching for Interpretable Individualized Treatment Effect Estimation

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Adaptive Hyper-Box (AHB) Matching

Causal inference: $Y_i(1) - Y_i(0)$

Confounding in observational studies can bias results

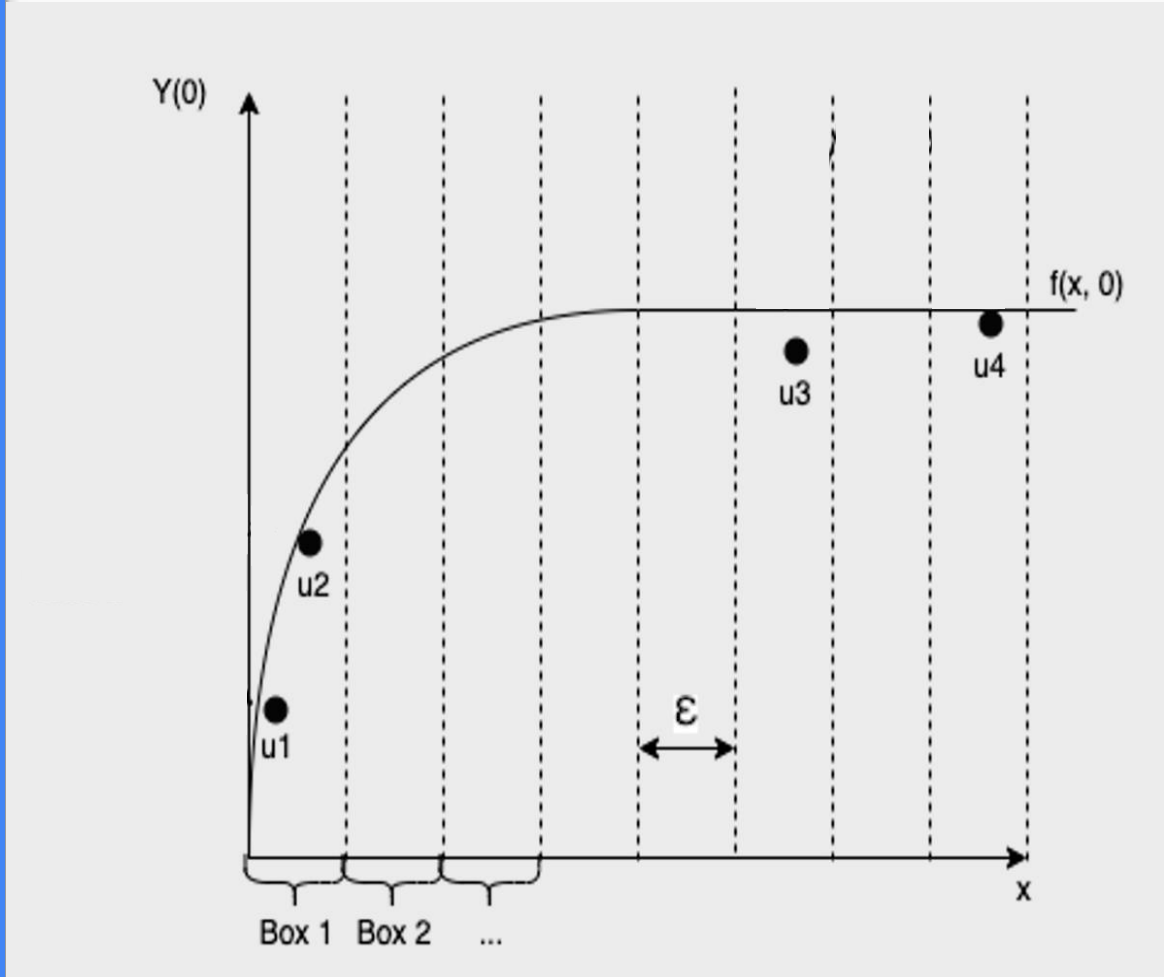
Matching similar units reduces bias

We match units to others falling within an axis-aligned hyper-box

The resulting matches are **case-based** and **interpretable**

Why Should Boxes Be Adaptive?

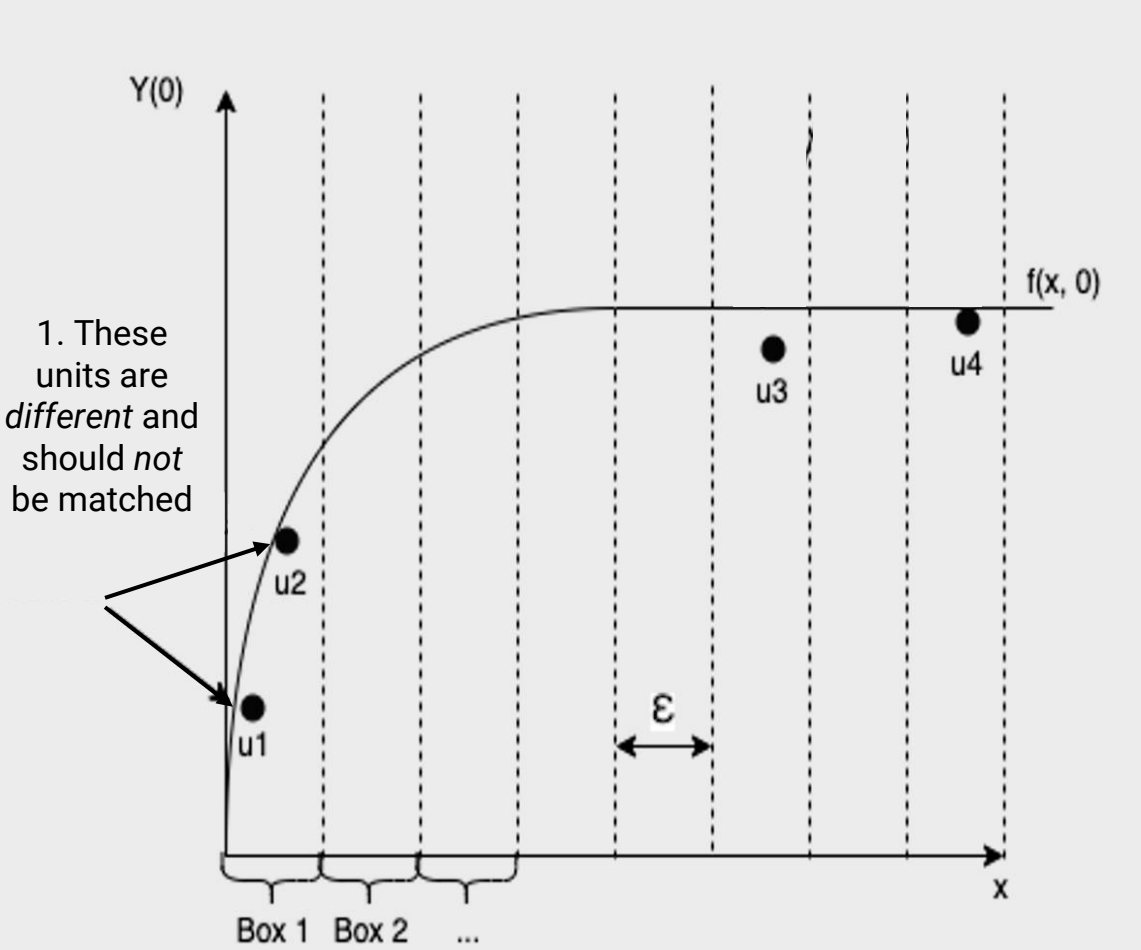
Two examples:



Why Should Boxes Be Adaptive?

Two examples:

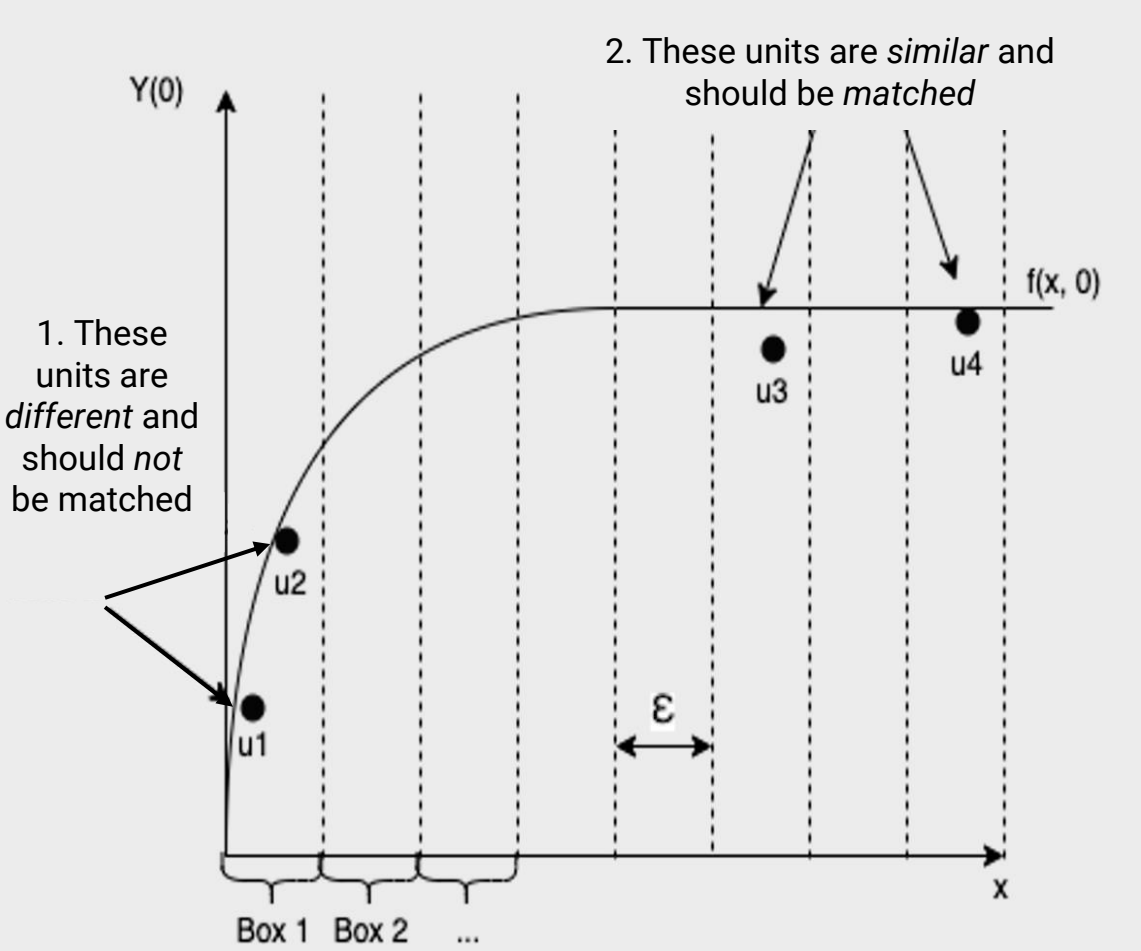
1. Should *not* be matched, but are → **biased** estimates.



Why Should Boxes Be Adaptive?

Two examples:

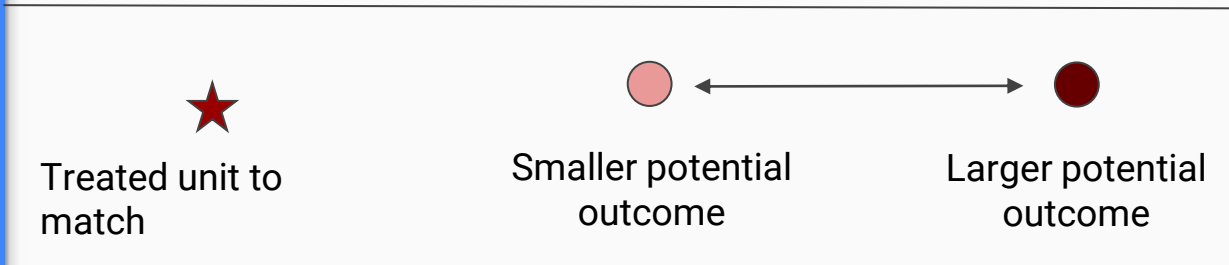
1. Should *not* be matched, but are → **biased** estimates.
2. *Should* be matched, but aren't → **variable** estimates.



Finding Boxes

Good boxes should have:

1. Low variability



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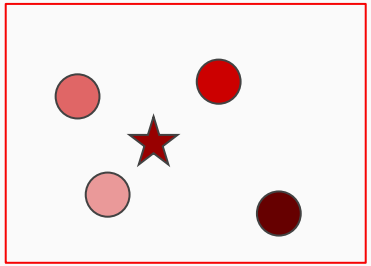

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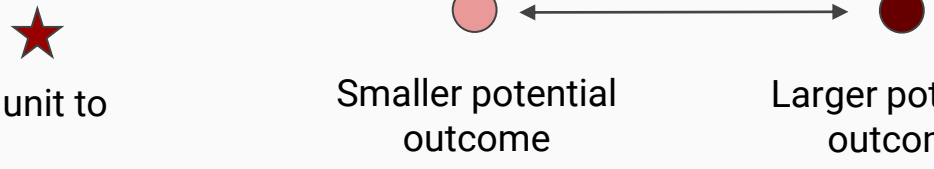

Finding Boxes

Good boxes should have:

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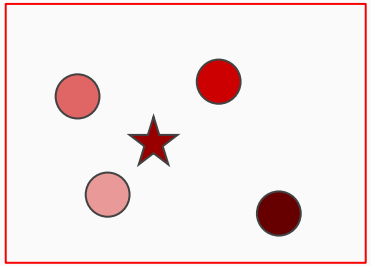
2. Low error



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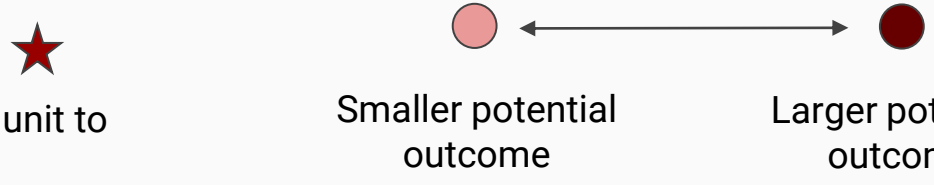

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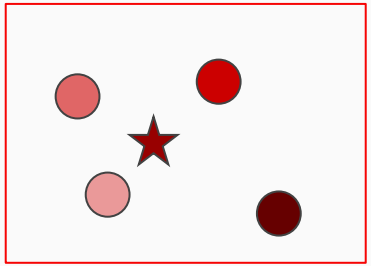

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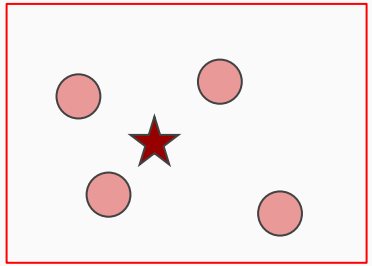

Bad Box

Treated unit to match

Smaller potential outcome

Larger potential outcome

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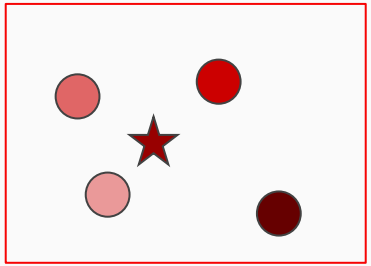

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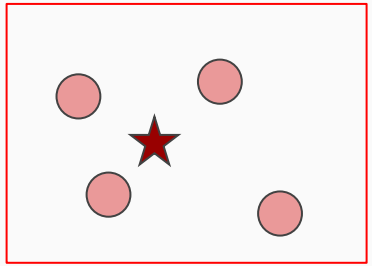

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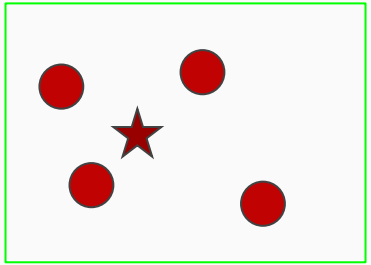

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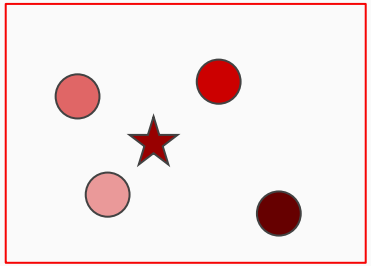
Black Box + Separate Training Set → **Honest** learning about outcome variability



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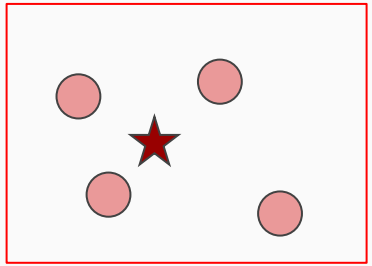

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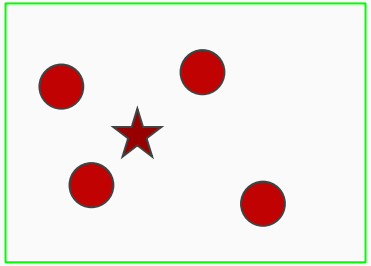

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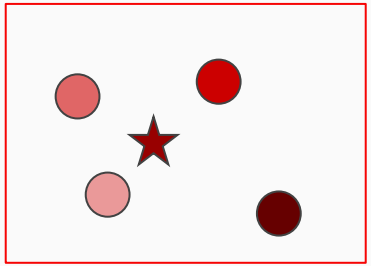
Optimization solved by MIP solver or fast approximation



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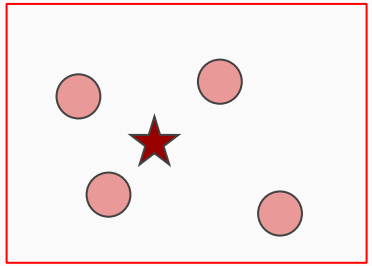

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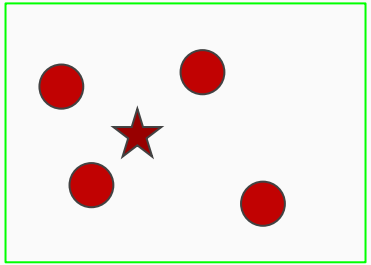

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Simulations

Y = confounder + (TE modifier) * treatment + error

Various forms of confounder, treatment effect modifier:

- Constant
- Linear
- Quadratic
- Constant within Box

Goal: estimate ITE of treated units

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Compare to:

- BART
- Propensity Score Matching
- Prognostic Score Matching
- Genetic Matching
- Coarsened Exact Matching
- Full Matching
- Prognostic Score Matching w/ True Counterfactuals
- Mahalanobis Distance Matching

Results

Estimation of ITE of treated units: mean absolute error normalized by ATT

p	Method / g / h	AHB		Black Box	Benchmark	Matching					
		MIP	Fast	BART	Best CF	CEM	Full Matching	GenMatch	Mahal	Nearest Neighbor	Prognostic
(0, 0, 2)	None / Const	0.09	0.05	**0.04**	0.25	1.01	0.32	0.36	0.34	0.37	0.25
(2, 0, 0)	Box / Const	**0.11**	0.16	0.24	0.24	0.24	3.03	0.66	0.62	3.05	0.29
(2, 0, 0)	Linear / Const	0.17	0.22	**0.14**	0.26	0.23	0.82	0.38	0.36	0.91	0.28
(2, 0, 0)	Quad / Const	0.10	**0.04**	0.08	0.25	0.22	0.42	0.38	0.37	0.45	0.27
(2, 0, 4)	Quad / Const	**0.02**	**0.02**	**0.02**	0.16	NA	0.21	0.12	0.11	0.24	0.04
(1, 1, 0)	Box / Box	**0.30**	0.45	0.65	0.73	0.58	2.59	2.37	1.02	2.30	0.94
(1, 0, 1)	Binary / Const	**0.02**	**0.02**	**0.02**	0.09	**0.02**	0.12	0.49	0.10	0.10	0.09
(1, 1, 6)	Binary / Binary	**0.06**	**0.06**	0.09	0.17	0.20	0.71	0.97	0.27	0.61	0.18
(2, 0, 0)	Mixed / Const	0.07	0.12	**0.06**	0.09	0.12	0.48	0.15	0.15	0.55	0.10

Summary

AHB constructs boxes to match units that are:

1. *Large* where the treatment effect is **near-constant**
2. *Small* where the treatment effect is **highly variable**

The resulting matches are **case-based** and **interpretable**

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Thank You!

almostmatchingexactly.github.io

Marco, Vittorio, Sudeepa, Cynthia, Alex