Causal Inference in The Age of Big Data: Linearithmic Algorithm for Blocking/Matching/Clustering

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What's the Big Deal about Big Data?

- One view: We just have to handle the data
 - Build a bigger computer system
 - It is a database problem
- Another view:
 - we need an integration between inferential and algorithmic thinking
- Measuring human activity has generated massive datasets with granular information that can be used for personalization of treatments, creating markets, modeling behavior
- Many inferential issues: e.g., unknown sampling frames, heterogeneity, targeting optimal treatments, compound loss functions

Massive Experiments

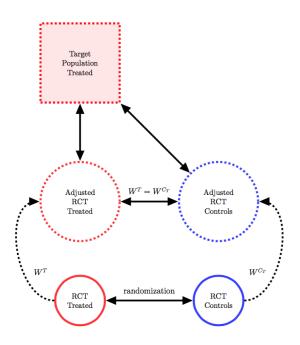
- Rising interest in fine-grained inference: e.g., subgroups
- Some traditional experimental design methods have become computationally infeasible—e.g., blocking
- Blocking: create strata and then randomize within strata
- Polynomial time solution not quick enough. Linearithmic is survivable.
 Sublinear needed in some cases.
- Algorithm can also be used for matching and clustering

The Problem

- Randomized Controlled Trials (RCTs) are rare and often small, especially a problem with medical experiments
- RCTs usually not conducted on the population of interest
- Combine information from both RCTs and population data to estimate treatment effects in the population
- Precise targeting of treatments, e.g., precision medicine

The Sample Selection Problem

- We want to make inferences for the full population of interest:
 - RCTs raise issues of Randomization Bias (Heckman and Smith 1995): poor external validity
 - NRSs raise issues of Selection Bias, or non random assignment to treatment
- How to combine information from RCTs and NRSs?



A New Blocking Method

The method minimizes the pair-wise Maximum Within-Block Distance: λ

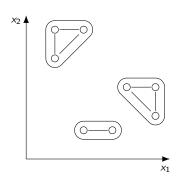
- Any valid distance metric (must satisfy the triangle inequality)
- Ensures good covariate balance by design
- Works for any number of treatments and any minimum number of observations per block
- It is fast: $O(n \log n)$ expected time
- It is memory efficient: O(n) storage
- Approximately optimal: $\leq 4 \times \lambda$
- Special cases
 - ① with one covariate: λ
 - 2 with two covariates: $\leq 2 \times \lambda$

Some Current blocking approaches

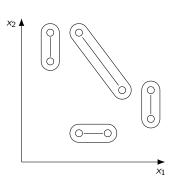
- Optimal Multivariate Matching Before Randomization
 - No efficient way to extend approach to more than two treatment categories
 - Even for two treatment categories, doesn't scale well
- Matched-pairs blocking: Pair "most-similar" units together. For each pair, randomly assign one unit to treatment, one to control
 - Natural clustering in the data ignored
 - Cannot estimate conditional variances
 - Difficulty with treatment effect heterogeneity

Threshold blocking: relaxing the block structure

Threshold blocking



Fixed-sized blocking

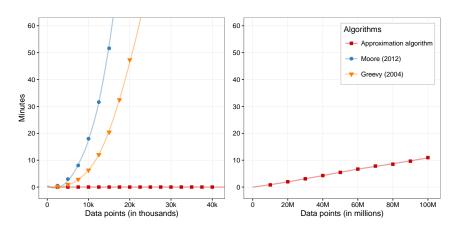


An Advantage

Theorem

For all samples, all objective functions and all desired block sizes, the optimal threshold blocking is always weakly better than the optimal fixed-sized blocking.

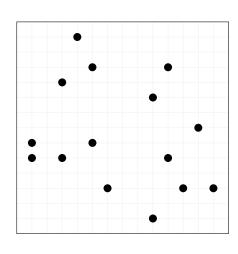
- Proof: interpret blocking as an non-linear integer programming problem.
 - The search set of threshold blocking is a superset of fixed-sized blocking



Input:

- Units' covariates
- Distance metric
- Minimum block size: k = 2

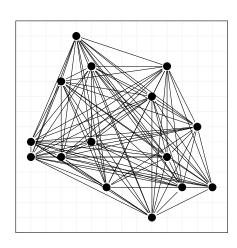
- A undirected complete graph with distances as edge weights
- ② Find (k-1)-nearest neighbor graph
- 3 Construct the second power of NNG
- Find a maximal independent set (seeds)
- Form blocks with the seeds and their neighbors in NNG
- Assign remaining units to a block containing any neighbor



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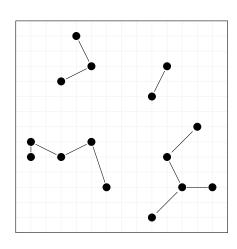
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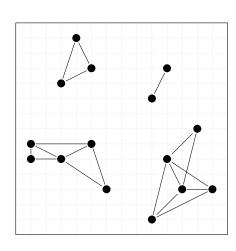
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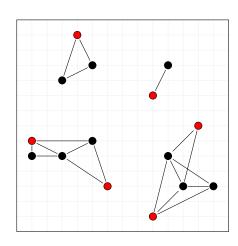
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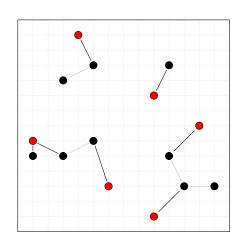
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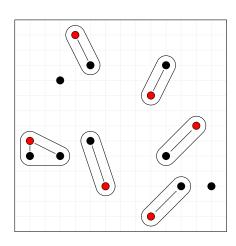
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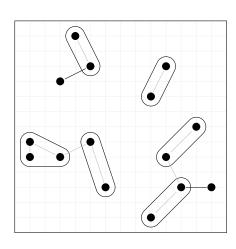
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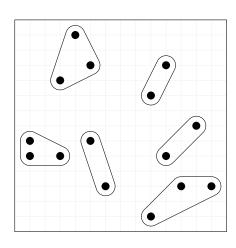
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Conclusion

- Closer to clustering than traditional blocking/matching methods
- Fast algorithm:
 - NNG plus $O(d^0kn)$ time and $O(d^0kn)$ space
 - K-d trees NN: $O(2^d kn \log n)$ expected time, $O(2^d kn^2)$ worst time, and O(kn) storage
 - Compare with bipartite, network flow methods:
 - e.g., Derigs: $O(n^3 \log n + dn^2)$ worst time and $O(d^0 n^2)$ space

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