# Subpopulation Analysis in Causal Inference: A Healthcare Case Study

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# Background

- RCTs gold standard for treatment evaluation
- Problem arises in presence of heterogeneous treatment effects (HTE)
	- ATT becomes a combination of multiple effect levels
	- Biased treatment effect estimation



## Our Contribution

- Machine Learning based Causal Estimation Procedure
	- Applicable for contexts in which HTE is present in complex subpopulations
- End-to-end framework based on matching and unsupervised learning
	- Non-parametric approach



# Problem Setup

- A subject is a tuple  $s = (x,c,t,y)$ 
	- Sampled from distribution D
	- x is the d-dimensional feature vector
	- c is the effect-level subpopulation to which the subject belongs
	- t is binary treatment assignment
	- Y is the observed outcome
- S<sup>T</sup> and S<sup>C</sup> are all treated and control population with N<sup>T</sup> and N<sup>C</sup> number of subjects
- We want to identify
	- If there exist meaningful subpopulations with heterogenous treatment effects within a population
	- How this heterogeneity affects the population-level estimation of ATE

# Methodology



Fig. 1: Overview of workflow. (a) Stage 1: Matching to get counterfactuals. (b) Stage 2: PCM to recover effect-subpopulations.

#### Goals

- Let  $S<sup>T</sup>$  and  $S<sup>C</sup>$  be treated and untreated controls respectively
- Goal 1:
	- for each subject  $S<sup>T</sup>$  estimate the counterfactual  $\tilde{v}$
- Goal 2:
	- uncover the hidden effect levels  $C_1,.....,C_L$  where L denotes the number of hidden effect levels
	- Assign each treated subject  $s \in S<sup>T</sup>$  to its corresponding effect-level group c

# Stage 1: Counterfactual Estimation

- We use a hybrid matching technique described in [9]
	- To produce counterfactual outcomes ( $\tilde{v}$ ) for each treated subject (S<sup>T</sup>)
- Combines
	- K-nearest neighbors
	- Exact matching
	- Coarsened exact matching
- Reason:
	- some features in the health space should be exactly controlled for, like age and ER-visits, while others can be approximately matched, like blood pressure and weight.

#### Stage 2: Determine Effect-Levels

- Each treated  $s \in S^T$  is now a tuple  $s = (x, v, \tilde{v})$ 
	- x is the feature, v is the observed outcome,  $\tilde{v}$  is the estimated counterfactual outcome
- Determine subpopulation effect-levels L
- Assign each treated subject  $s \in S^T$  to a level  $c_1$  using a pre-cluster and merge (PCM) algorithm developed in [3]
	- Cluster using features x
	- Compute treatment effects within each cluster
	- Group clusters into effect levels using PCM
	- Assign subjects to subpopulations and estimate subpopulation effects

#### Case Study

- Effectiveness of health intervention (HI) program for pre-diabetics
	- Proprietary data from a local health insurance provider
	- 1604 patients enrolled between November 2017 and April 2021 treated group
	- 350k patients in the control group
	- Features included demographics, lab results, prior health conditions, and history of events (Acute Care, Inpatient Care, and Emergency Visits) within the last 2 and 6 months
- The goal was to evaluate this program
	- Measured by survival analysis on the time it takes after enrollment in HI for a patient to use acute care (in-patient or ER usage)

# Results and Discussion (Whole Treated Population)

- Compare Restricted Mean Survival Time (RMST) from Kaplan Meier **Curves** 
	- Between treated and matched controls
- Dotted vertical line is the start of the intervention
- Significant positive treatment effect with p-value 0.01
- Matching process produces near identical survival curves prior to HI, as it should



Fig: Kaplan Meier curves, on the outcome: "Time to Acute Care" for all treated population.

# Results and Discussion (ATE Clusters)

- PCM Algorithm with agglomerative clustering and 10 clusters
- Visual inspection suggests three effect levels of [0, 0.2], [0.3, 0.4], and 0.85
- Competing techniques for learning HTE based on decision trees were not able to recover this
- Merging clusters results in three final effect-levels
	- Sick (with zero effect)
	- Healthy (with positive effect)
	- Critical (with very positive effect)



Fig: Clusters of ATE (18 Month RMST) retrieved by PCM

# Results and Discussion (Effect-Level Subgroup Analysis)



Fig. 2: Kaplan Meier's, survival curves for "Time to Acute Care." (a) "Sick" subpopulation with no effect ( $p = 0.44$ ). (b) "Healthy" subpopulation with positive effect ( $p = 0.01$ ). (c) "Critical" subpopulation with large positive effect ( $p = 0.08$ ).

# Results and Discussion (Effect-Level Subgroup Analysis)

TABLE I: Feature breakdown of the subpopulations from PCM. The p-value quantifies how well matched the subpopulation is w.r.t. its controls, with respect to a given feature (high p-value means the controls match the subpopulation). The "\*" means that in both treated and matched controls the feature was always 0.



# Conclusion

- Our work extends the causal analysis to non-targeted health interventions and clinical trials -
	- treated population can consist of subpopulations exhibiting different effects to the treatment
- Novel PCM strategy finds three subpopulations with significantly different effects
- Strength of PCM was showcased on an appropriate case study
- Essential if one is to best understand the benefits and side-effects of a treatment