

Causal inference in analyzing administrative healthcare data:

Can we integrate machine learning approaches within this framework?

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Outline

- ① Notations and Questions
 - Regression vs. Propensity score (PS)
- ② Health care databases
- ③ High-dimensional propensity score (hdPS)
 - The original mechanism
 - Machine learning-based hdPS
 - AI-based hdPS
 - Future directions
- ④ Examples in Canadian data

Reference Preview

Will be primarily discussing Schneeweiss (2018). Will also briefly mention Karim, Pang, and Platt (2018), Weeberpals et al. (2021), Zivich and Breskin (2021).

- Schneeweiss (2018) Clinical Epidemiology
- Karim et al. (2018) Epidemiology
- Weeberpals et al. (2021) Epidemiology
- Zivich and Breskin (2021) Epidemiology

Notations and Motivating Example

- Y = Outcome
 - Airway disease (among BC immigrants)
- A = Primary exposure
 - Respiratory tuberculosis
- $C = (C_1, \dots, C_7)$ are covariates measured at baseline
 - age, sex, income, education, comorbidity score, TB incidence in birth country, year of residency in BC



Research Paper

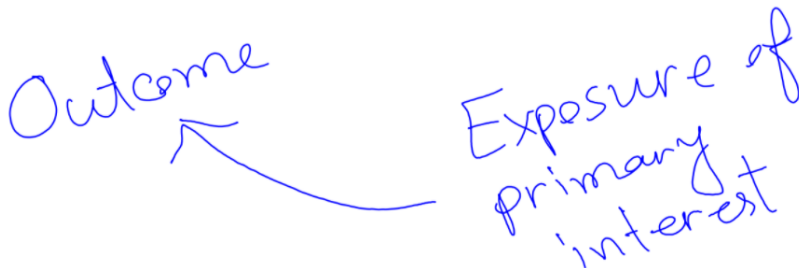
Post-tuberculosis airway disease: A population-based cohort study of people immigrating to British Columbia, Canada, 1985–2015

C. Andrew Basham^{a,b,*}, Mohammad E. Karim^{a,c}, Victoria J. Cook^{b,d}, David M. Patrick^{a,b,d}, James C. Johnston^{a,b,d}

Questions

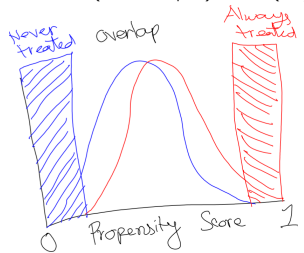
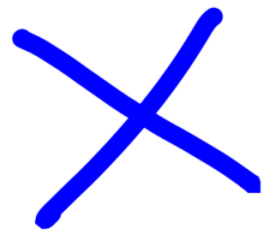
Inferential goals

- ➊ Prediction, developing risk scores (predict Y)
- ➋ Identifying important predictors (identify C_1 , C_2 that are important to predict Y)
- ➌ Descriptive, exploratory (is A and Y associated?)
- ➍ Evaluating a predictor of primary interest (does A cause Y ?)



Regression vs. Propensity score

- For RCT, adjustment may not be essential, as design takes care of bias sources.
- For RWE studies, more caution necessary. Adjustment of C is important (usually large #s).

Model / Method	Propensity score	Regression analysis
Exposure Modelling	$PS = P(A = 1 C) = f(C)$ 	No design stage analysis 
Outcome Modelling	$E(Y A, C) = g(A, C)$	$E(Y A, C) = g(A, C)$

Health care databases

Why use non-randomized data at all?

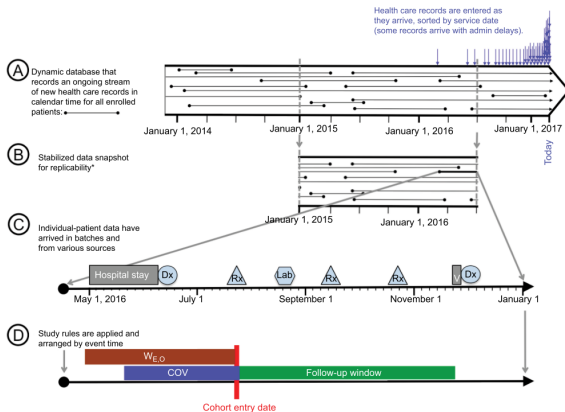
- clinical health records
 - medical facility
 - hospital
 - clinic and practice.
- administrative data
 - PharmaNet
 - Medical Services Plan
- clinical registries
 - TB registry
 - MS registry

Health care databases: Advantages

- larger sample size
- diverse population
- longitudinal records over many years
- detailed
 - health encounters,
 - comorbidity history,
 - drug exposure history
- possibility to link other databases
 - Immigration
 - Vital Statistics

Health care databases: Study implementation

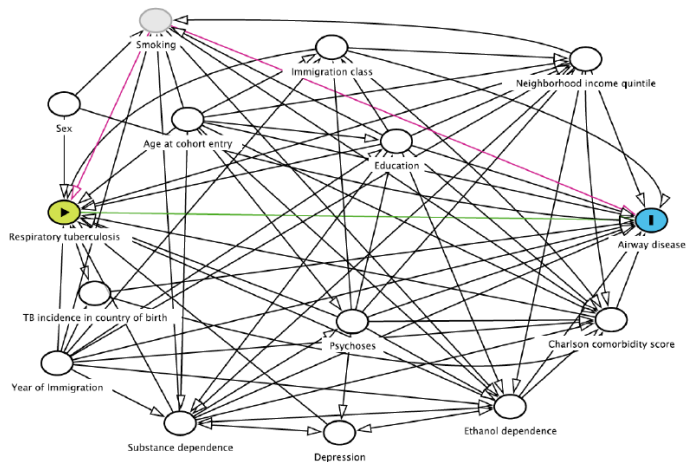
Schneeweiss (2018): freeze a data cut from dynamic data stream, encounters collected at covariate assessment period and follow-up, apply rules/algorithms to define variables.



Health care databases: Limitations

- Not specifically designed for answering a particular research question.
- Data sparsity:
 - no defined or routine interview dates
 - data collection relies on visits and encounters
- Investigators have no control over which factors were measured during the data collection stage.
 - smoking in TB
 - MRI data in MS

Health care databases: Limitations



Methods: Expectation vs. Reality (Part I: unmeasured confounder)

Exposure Model

$$P(A = 1|C) = f(C) \\ = \frac{1}{1 + \exp[\alpha_0 + \alpha_1 C_1 + \alpha_2 C_2 + \alpha_3 C_3 + \alpha_4 C_4 + \alpha_5 C_5 + \alpha_6 C_6 + \alpha_7 C_7]}$$

Outcome Model

$$E(Y|A, C) = g(A, C) \\ = \beta_0 + \psi A + \beta_1 C_1 + \beta_2 C_2 + \beta_3 C_3 + \beta_4 C_4 + \beta_5 C_5 + \beta_6 C_6 + \beta_7 C_7$$

Assumption

$$Y|A, C \sim N[E(Y|A, C), \sigma^2]$$

Methods: Expectation vs. Reality (Part 2: model misspecification)

Exposure Model

$$\begin{aligned} P(A = 1|C) &= f(C) \\ &= \frac{1}{1 + \exp[\alpha_0 + \alpha_1(C_2 \times C_3) + \alpha_2(C_4^2 \times \frac{\exp C_5}{5 \times C_7}) + \alpha_3 C_6]} \end{aligned}$$

Outcome Model

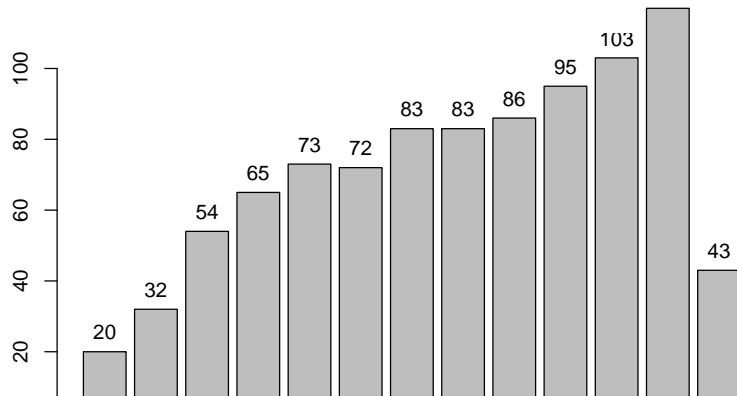
$$\begin{aligned} E(Y|A, C) &= g(A, C) \\ &= \beta_0 + \psi A + \beta_1 C_1^2 + \beta_2(C_2 \times C_3 \times C_7) + \beta_3 \frac{\exp C_4}{C_5 \times 2} \end{aligned}$$

Assumption

$$Y|A, C \sim N[E(Y|A, C), \sigma^2]$$

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Citation of Schneeweiss et al. (2009)



hdPS proxy collection

Schneeweiss (2018):

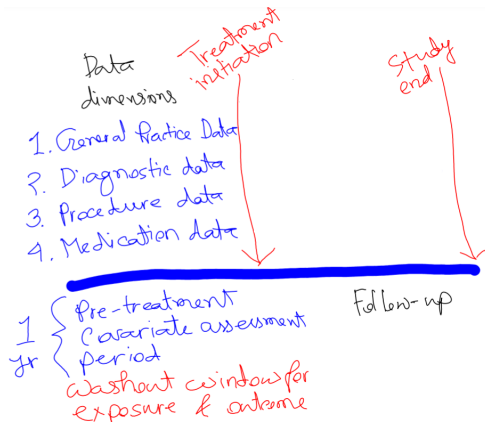
Unobserved confounder	Observable proxy measurement	Coding examples
Very frail health	Use of oxygen canister	CPT-4
Sick but not critical	Code for hypertension during a hospital stay	ICD-9, ICD-10
Health-seeking behavior	Regular check-up visit; regular screening examinations	ICD-9, CPT-4, #PCP visits
Fairly healthy senior	Receiving the first lipid-lowering medication at age 70 years	NDC, ATC, Read
Chronically sick	Regular visits with specialist; hospitalization; many prescription drugs	#specialist visits, NDC, ATC
Outcome surveillance intensity	General markers for health care utilization intensity	#visits, #different drugs

They were the first to propose adjusting for something that **may not be interpretable** directly with the context of the research question. Logic was two fold:

- 1 variables from same subject should be **correlated** = has relevant information
- 2 adjust items that are **predictive of outcome** (as established in PS literature)

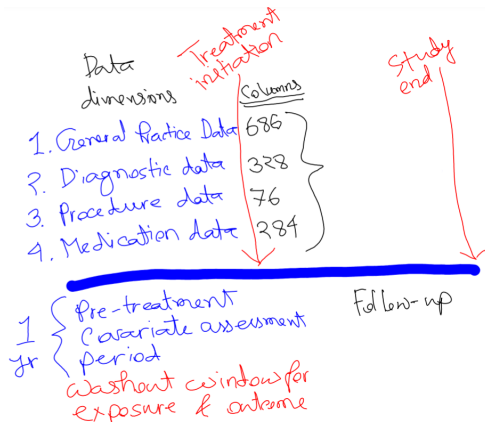
hdPS proxy collection from same subjects (1)

Collection of proxy data for the unmeasured + mis-measured variables (Karim, Pang, and Platt 2018)



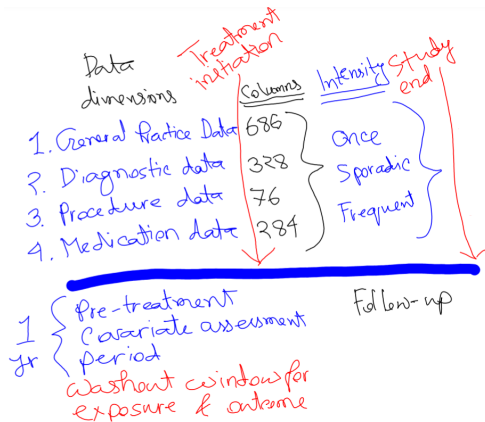
hdPS proxy collection from same subjects (1)

Collection of proxy data for the unmeasured + mis-measured variables (Karim, Pang, and Platt 2018)



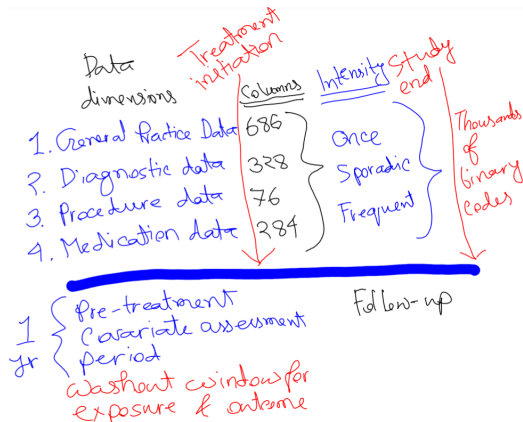
hdPS proxy collection from same subjects (1)

Collection of proxy data for the unmeasured + mis-measured variables (Karim, Pang, and Platt 2018)



hdPS proxy collection from same subjects (1)

Collection of proxy data for the unmeasured + mis-measured variables (Karim, Pang, and Platt 2018): but restricted to 2,400 empirical covariates EC (based on high prevalence)



hdPS proxy collection from same subjects (1)

List of additional proxy variables:

Dimension 1 Practice	Dimension 2 Diagnostic	Dimension 3 Procedure	Dimension 4 Medication
EC-dim1-1-once	EC-dim2-1-once	EC-dim3-1-once	EC-dim4-1-once
EC-dim1-1-sporadic	EC-dim2-1-sporadic	EC-dim3-1-sporadic	EC-dim4-1-sporadic
EC-dim1-1-frequent	EC-dim2-1-frequent	EC-dim3-1-frequent	EC-dim4-1-frequent
...	
EC-dim1-686-frequent	EC-dim2-328-frequent	EC-dim3-76-frequent	EC-dim4-284-frequent

4 dimension \times 3 intensity \times 200 most prevalent codes = 2,400 ECs

hdPS mechanism: find EC as $h(\text{outcome, exposure prevalence})$ (2)

Assumption:

- $p_{u=1,a=1}$ = prevalence of unmeasured confounder among treated ($A = 1$)
- $p_{u=1,a=0}$ = prevalence of unmeasured confounder among untreated ($A = 0$)
- $p_{u=1,y=1}$ = prevalence of unmeasured confounder among dead ($Y = 1$)
- $p_{u=1,y=0}$ = prevalence of unmeasured confounder among alive ($Y = 0$)

Bross (1966) formula says, the amount of bias due to u is

$$\text{Bias}_M = \frac{p_{u=1,a=1} \times \left(\frac{p_{u=1,y=1}}{p_{u=1,y=0}} - 1 \right) + 1}{p_{u=1,a=0} \times \left(\frac{p_{u=1,y=1}}{p_{u=1,y=0}} - 1 \right) + 1}$$

hdPS mechanism: find EC as h(outcome, exposure prevalence) (2)

Assumption Calculate:

- $p_{EC=1,a=1}$ = prevalence of ~~unmeasured confounder~~ EC among treated ($A = 1$)
- $p_{EC=1,a=0}$ = prevalence of ~~unmeasured confounder~~ EC among untreated ($A = 0$)
- $p_{EC=1,y=1}$ = prevalence of ~~unmeasured confounder~~ EC among dead ($Y = 1$)
- $p_{EC=1,y=0}$ = prevalence of ~~unmeasured confounder~~ EC among alive ($Y = 0$)

Bross (1966) formula says, the amount of bias due to EC is

$$\text{Bias}_M = \frac{p_{EC=1,a=1} \times \left(\frac{p_{EC=1,y=1}}{p_{EC=1,y=0}} - 1 \right) + 1}{p_{EC=1,a=0} \times \left(\frac{p_{EC=1,y=1}}{p_{EC=1,y=0}} - 1 \right) + 1}$$

hdPS: select hdPS variables from ECs

- 1 Rank (descending) each EC by the magnitude of log-bias: $|\log \text{Bias}_M|$

Rank by bias	$ \log \text{Bias}_M $	EC
1	0.42	EC-dim1-21-once
2	0.32	EC-dim2-95-once
3	0.25	EC-dim4-289-once
...
2,400	0.01	EC-dim4-64-frequent

- 2 Take top 500 of these ECs. These are hdPS variables.

hdPS: estimate treatment effect

Exposure Model (investigator-specified covariates)

$$P(A = 1|C) = f(C)$$
$$= \frac{1}{1 + \exp[\alpha_0 + \alpha_1 C_1 + \alpha_2 C_2 + \alpha_3 C_3 + \alpha_4 C_4 + \alpha_5 C_5 + \alpha_6 C_6 + \alpha_7 C_7]}$$

Outcome Model (in the PS matched or weighted data)

$$E(Y|A, C) = g(A, C)$$
$$= \beta_0 + \psi A$$

hdPS: estimate treatment effect

Exposure Model (investigator-specified covariates + hdPS variables [EC])

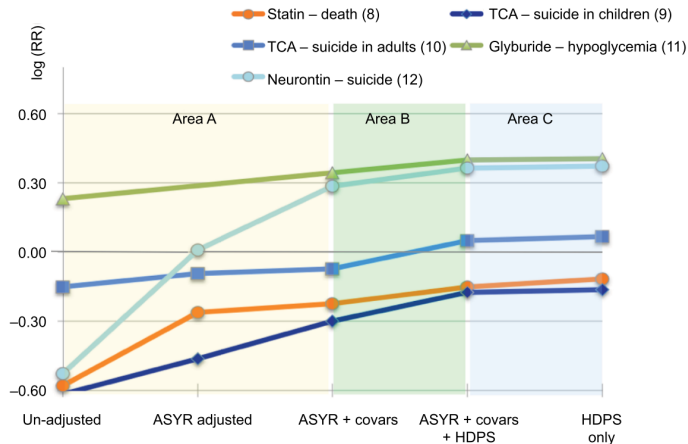
$$P(A = 1|C) = f(C)$$
$$= \frac{1}{1 + \exp[\alpha_0 + \alpha_1 C_1 + \alpha_2 C_2 + \alpha_3 C_3 + \alpha_4 C_4 + \alpha_5 C_5 + \alpha_6 C_6 + \sum_{i=1}^{500} \alpha'_i \text{EC}_i]}$$

Outcome Model (in the PS matched or weighted data)

$$E(Y|A, C) = g(A, C)$$
$$= \beta_0 + \psi A$$

hdPS: estimate treatment effect

Performance of hdPS. Schneeweiss (2018):



ML-hdPS: deal with collinearity

Kitchen SSink Exposure Model ($A \sim C + EC$)

$$P(A = 1|C, EC) = \frac{1}{1 + \exp[\alpha_0 + \alpha_1 C_{\text{important}} + \alpha_2 C_{\text{potential confounder}} + \sum_{i=1}^{2,400} \alpha'_i EC_i]}$$

Outcome Model for EC selection ($Y \sim C + \text{top-500 ECs}$)

$$f(Y|C, EC) = \alpha_0 + \alpha_1 C_{\text{important}} + \alpha_2 C_{\text{potential confounder}} + \sum_{i=1}^{500} \alpha'_i EC_i$$

ML-hdPS: deal with collinearity

hdPS Exposure Model ($A \sim C + \text{top-ranked EC}$)

$$P(A = 1|C, EC) = \frac{1}{1 + \exp[\alpha_0 + \alpha_1 C_{\text{important}} + \alpha_2 C_{\text{potential confounder}} + \sum_{i=1}^{\text{top } 500} \alpha'_i \text{EC}_i]}$$

Outcome Model for EC selection ($Y \sim C + \text{ECs}$)

$$f(Y|C, EC) = \alpha_0 + \alpha_1 C_{\text{important}} + \alpha_2 C_{\text{potential confounder}} + \sum_{i=1}^{2,400} \alpha'_i \text{EC}_i$$

ML-hdPS: deal with collinearity

Exposure Model (investigator-specified covariates + hdPS variables [EC])

$$P(A = 1|C) = \frac{1}{1 + \exp[\alpha_0 + \alpha_1 C_1 + \alpha_2 C_2 + \alpha_3 C_3 + \alpha_4 C_4 + \alpha_5 C_5 + \alpha_6 C_6 + \sum_{i=1}^{500} \alpha'_i \text{EC}_i]}$$

ML extensions: exposure model vs. outcome model

- ECs selected separately
 - are usually highly correlated, and
 - has inflated variance.
- Karim, Pang, and Platt (2018) used elastic net and LASSO to reduce the number of selected hdPS variables (EC variables).
 - found that the hybrid method (elastic net of hdPS) performs better than ML or hdPS.
 - quality of proxy information matters.

ML-hdPS: deal with model misspecification

Exposure Model

$$P(A = 1|C) = \frac{1}{1 + \exp[\alpha_0 + \alpha_1(C_2 \times C_3) + \alpha_2(C_4^2 \times \frac{\exp C_5}{5 \times C_7}) + \alpha_3 C_6]}$$

Outcome Model

$$E(Y|A, C) = \beta_0 + \psi A + \beta_1 C_1^2 + \beta_2(C_2 \times C_3 \times C_7) + \beta_3 \frac{\exp C_4}{C_5 \times 2}$$

More ML extensions

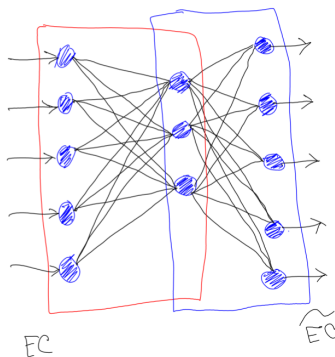
- Tree-based models: automatically detect function form
 - Karim, Pang, and Platt (2018) used random forest, and chose top important ECs
- Superlearner (ensemble learner) with tree-based + parametric models
- Double robust methods with Superlearner

AI-hdPS: towards dimension reduction

- Principal component (PC) analysis
 - compute linear transformation of all covariates to PCs, and top few PCs are selected to reduce dimension.
 - extract components of each variable responsible for most variance
 - incapable of learning non-linear feature representations

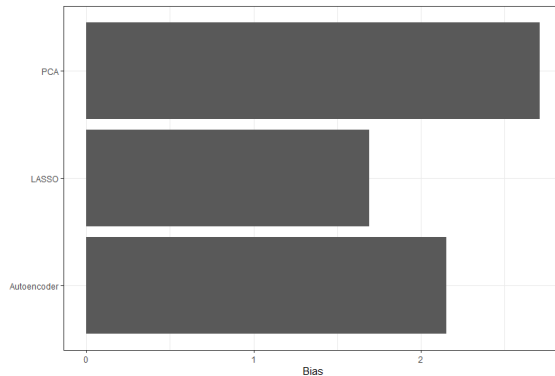
AI-hdPS: towards dimension reduction

- Weberpals et al. (2021) proposed to use **autoencoders** (3, 5, 7 layers) to reduce **EC** dimensions:



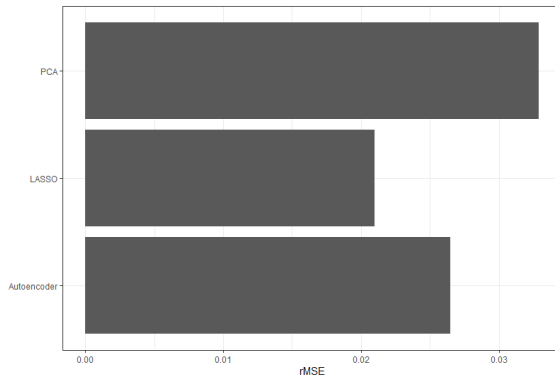
AI-hdPS: towards dimension reduction

% Bias



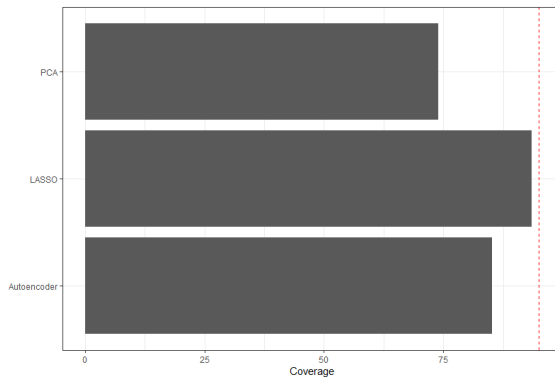
AI-hdPS: towards dimension reduction

rMSE



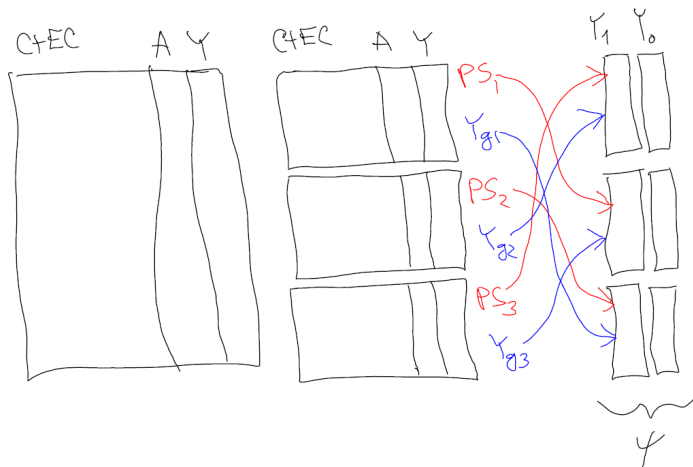
AI-hdPS: towards dimension reduction

Coverage: slower rate of convergence for non-parametric methods



Future directions

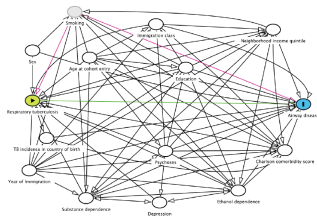
Zivich and Breskin (2021): Cross-fitting + together with double-robust approaches



A purist view

- Bias-based hdPS is not really PS!
 - design stage vs. analysis stage
 - hdPS uses $\text{corr}(\text{EC}, \text{outcome})$.
- Motivation of PS and hdPS are different to begin with
 - PS requires no unmeasured confounding
- I prefer to use hdPS as a sensitivity analysis.

Examples of hdPS (1)



Airway example: analysis approaches that were compared: hdPS as **sensitivity analyses**:

- PS decile-adjusted (investigator-specified covariates)
- hdPS decile-adjusted (investigator-specified + **EC**)
- LASSO-hdPS decile-adjusted (investigator-specified + LASSO-reduce **EC**)
- Others: E-value, other proxy variable adjustment

Conclusions were similar.

Examples of hdPS (2)

A 2017 JAMA paper

JAMA | Original Investigation

Association Between Serotonergic Antidepressant Use During Pregnancy and Autism Spectrum Disorder in Children

Hilary K. Brown, PhD; Joel G. Ray, MD, MSc, FRCPC; Andrew S. Wilton, MSc; Yona Lunsky, PhD, CPsych;
Tara Gomes, MHSc; Simone N. Vigod, MD, MSc, FRCPC

Method	HR	CI 95%
Unadjusted	2.16	1.64-2.86
Multivariable adjusted	1.59	1.17-2.17
IPTW hdPS	1.61	0.997-2.59
1-1 hdPS matching	1.64	1.07-2.53
Pre-pregnancy data	1.85	1.37-2.51

Conclusion: **not associated!**

Reference

- Karim, Mohammad Ehsanul, Menglan Pang, and Robert W Platt. 2018. "Can We Train Machine Learning Methods to Outperform the High-Dimensional Propensity Score Algorithm?" *Epidemiology* 29 (2): 191–98.
- Schneeweiss, Sebastian. 2018. "Automated Data-Adaptive Analytics for Electronic Healthcare Data to Study Causal Treatment Effects." *Clinical Epidemiology* 10: 771–78.
- Weberpals, Janick, Tim Becker, Jessica Davies, Fabian Schmich, Dominik Rüttinger, Fabian J Theis, and Anna Bauer-Mehren. 2021. "Deep Learning-Based Propensity Scores for Confounding Control in Comparative Effectiveness Research: A Large-Scale, Real-World Data Study." *Epidemiology*, *Doi: 10.1097/EDE.0000000000001338*.
- Zivich, Paul N, and Alexander Breskin. 2021. "Machine Learning for Causal Inference: On the Use of Cross-Fit Estimators." *Epidemiology*, *Doi: 10.1097/EDE.0000000000001332*.

Thank you!

