

Nordic Probabilistic AI School

Causal Machine Learning

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Healthy AI Lab www.healthyai.se

*Machine learning for improved data-driven decision-making
with applications in healthcare*

- Decision making & causality
- Generalization & transfer learning
- Healthcare applications



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Many who do ML ask

- We fit a supervised learning model—how can we **use** it?
- We have our results; how should we **interpret** them?
- If we act on our model's predictions, are our **decisions** better?

Let's help answer them!

Part I
Causal machine
learning

Part II
Coding example
(IncomeSim)

Part III
Reflections

IncomeSim

Simulator of causal effects of **studies** on **future income**

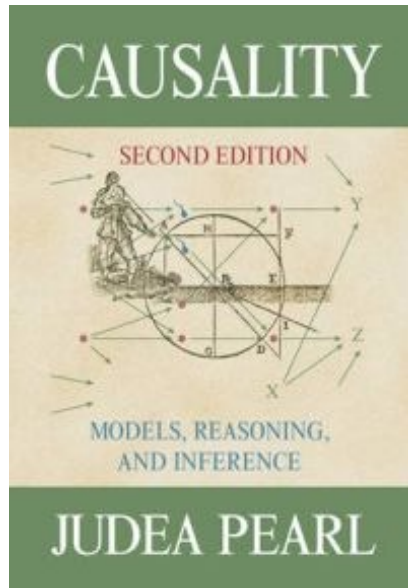
Based on the well-known Adult dataset from UCI

On the repository: <https://github.com/Healthy-AI/IncomeSim/>

You can find a link to a Colab notebook there!

We can't cover everything today!

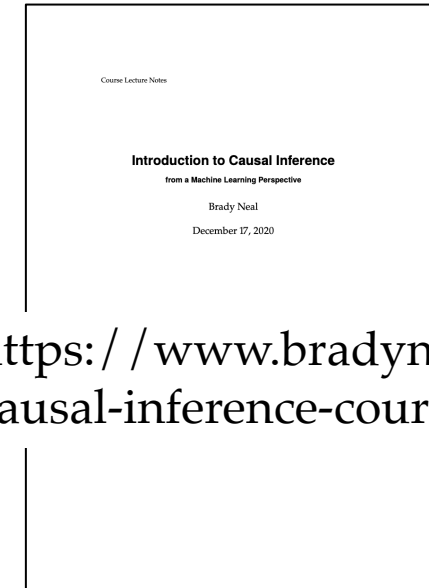
Causality
Pearl, 2009



Counterfactuals and
Causal Inference (2nd Ed)
Morgan & Winship, 2014



Brady Neal's
Causal inference course

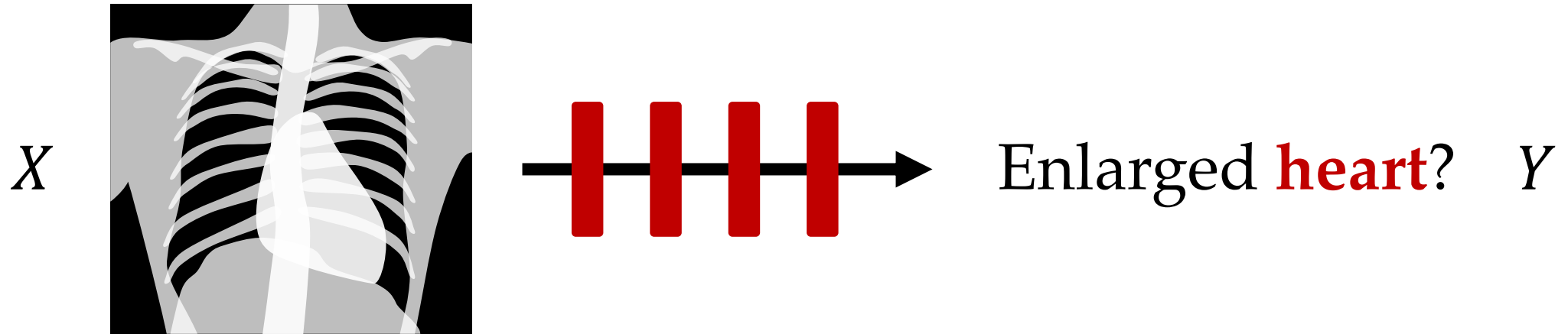


[https://www.bradyneal.com/
causal-inference-course](https://www.bradyneal.com/causal-inference-course)

Part I: Causal machine learning

Part I.a: Supervised learning recap

ML example: Chest X-ray classification



How do we learn?

One of the most common* learning principles for selecting hypotheses is **risk minimization**

$$\min_{h \in \mathcal{H}} R(h) \quad \text{where} \quad R(h) := \mathbb{E}_{X,Y \sim p}[L(h(X), Y)]$$

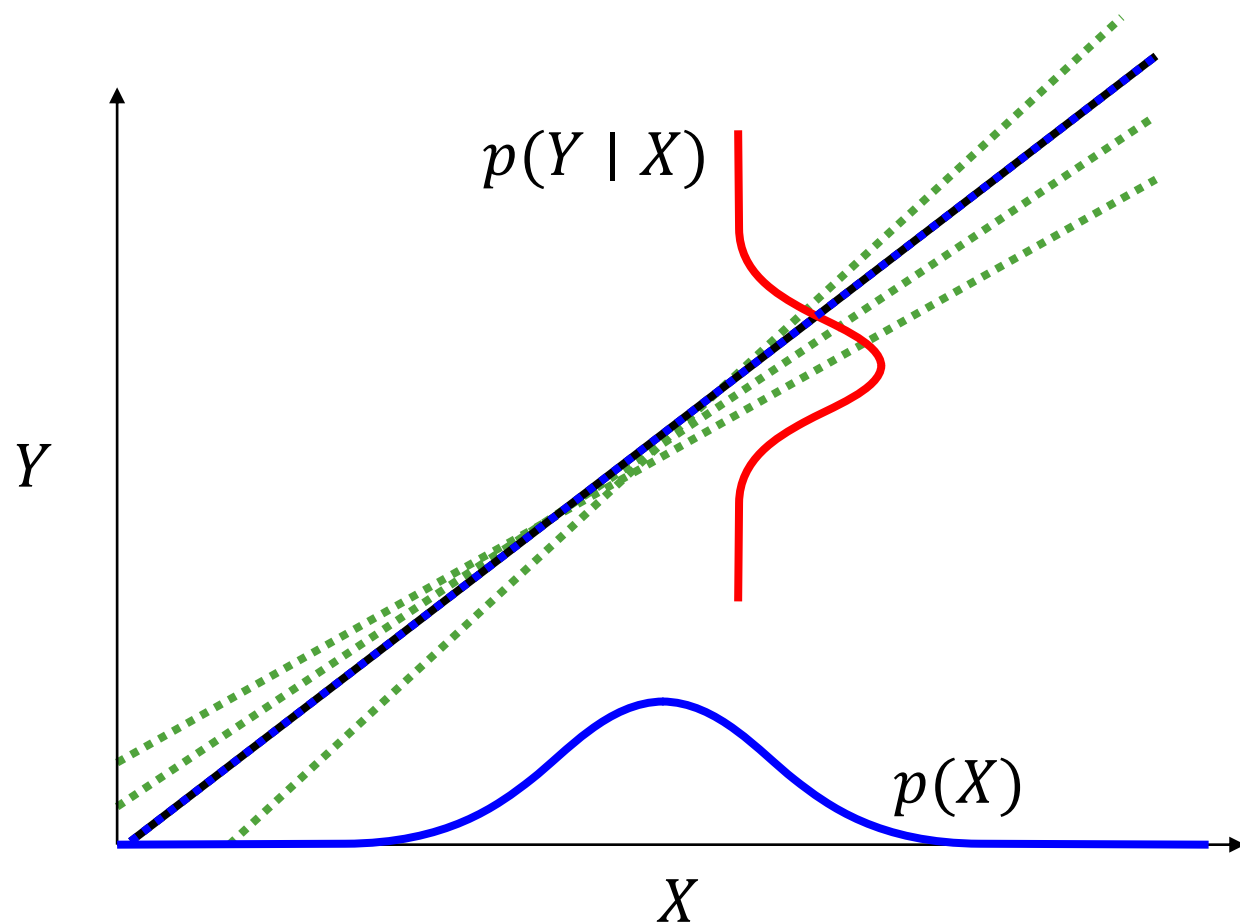
and $L : Y \times Y \rightarrow \mathbb{R}_+$ is a **loss function**

R is called “risk” or “generalization error”

For example, **mean squared error**: $R(h) := \mathbb{E}_{X,Y \sim p}[(h(X) - Y)^2]$

* Another example is maximum likelihood estimation. These are *sometimes* equivalent

Example: Least-squares linear regression



If $Y = kx + b + \epsilon$ with
 $\epsilon \sim \mathcal{N}(0, \sigma^2)$

and

$$h^*(x) = \arg \min_h \mathbb{E}_{X,Y}[(h(X) - Y)^2]$$

then

$$h^*(x) = \mathbb{E}[Y | X = x] = kx + b$$

The best possible model is the
conditional expectation $\mathbb{E}[Y | x]$

Empirical risk minimization (ERM)

Since the distribution of inputs and labels is unknown,
instead of minimizing R , we minimize the **empirical risk** $\hat{R}(h)$

The “training error”

$$\min_{h \in \mathcal{H}} \hat{R}(h) \quad \text{where} \quad \hat{R}(h) := \frac{1}{m} \sum_{i=1}^m L(h(x_i), y_i)$$

Find the hypothesis \hat{h} which fits **observed examples** the best

Sample splitting for evaluation

Almost any ML course will teach sample splitting for evaluation

Example: Fit data to 80% of your data, evaluate on unseen 20%

This allows to estimate the generalization error using a test set D_{te}

$$R(h) = \mathbb{E}_{D_{\text{te}}} \left[\frac{1}{n_{\text{te}}} \sum_{(x_i, y_i) \in D_{\text{te}}} L(h(x_i), y_i) \right] \approx \frac{1}{n_{\text{te}}} \sum_{(x_i, y_i) \in D_{\text{te}}} L(h(x_i), y_i) = \hat{R}(h)$$

The test error tells us **something** about our model's performance

Is this answering the right questions?

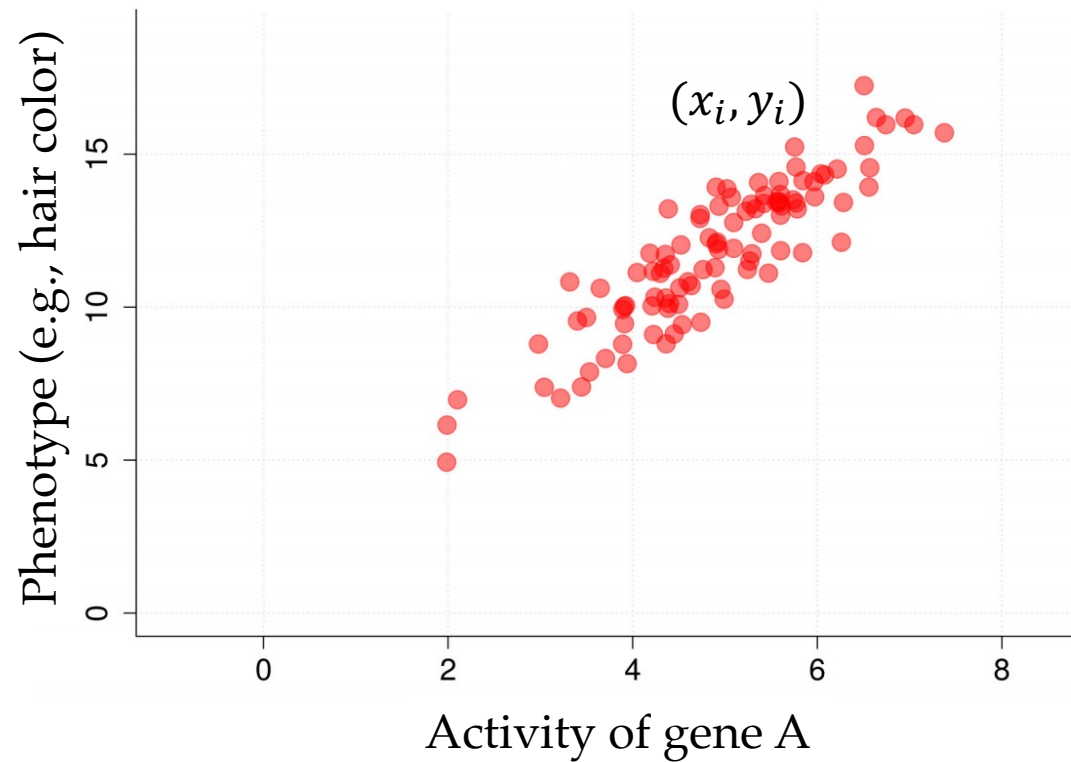
- We fit a supervised learning model—how can we **use** it?
- We have our results; how should we **interpret** them?
- If we act on our model's predictions, are our **decisions** better?

Are these answered by the test error?

Does smaller test error imply better decisions?

Part I.b: Machine learning & causality

Example: Gene knock out



Example from Jonas Peters.

Genetic data

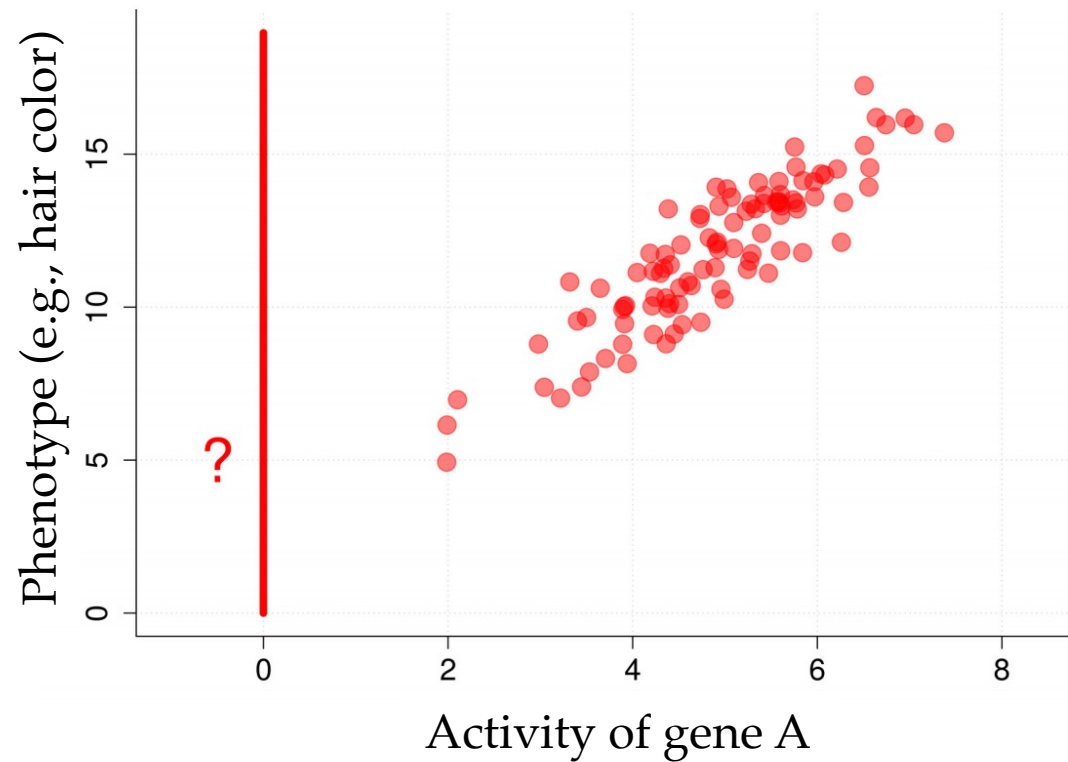
Assume we have sequenced the **genome** of 100 individuals drawn from a population p

We are interested in the relationship between Gene A (X) and the phenotype **hair color** (Y)

Can we influence hair color?

Example: Gene knock out

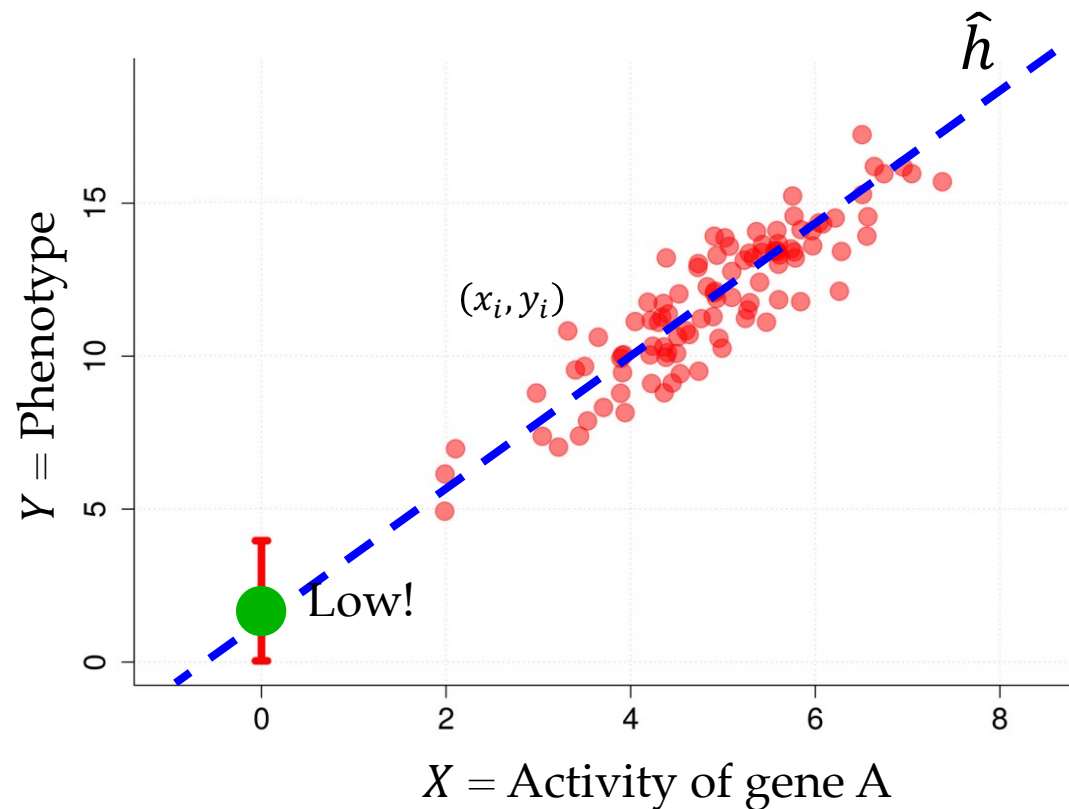
What if we “knock out” Gene A (**intervene** by setting its activity to 0)?



Question?
What do you think
would be the value of
the phenotype?

Example from Jonas Peters.

Out-of-the-box ML solution



Example from Jonas Peters.

Step 2.

Pick a learning principle

$$h^* = \arg \min_h \mathbb{E}_p[(h(X) - Y)^2]$$

Step 3.

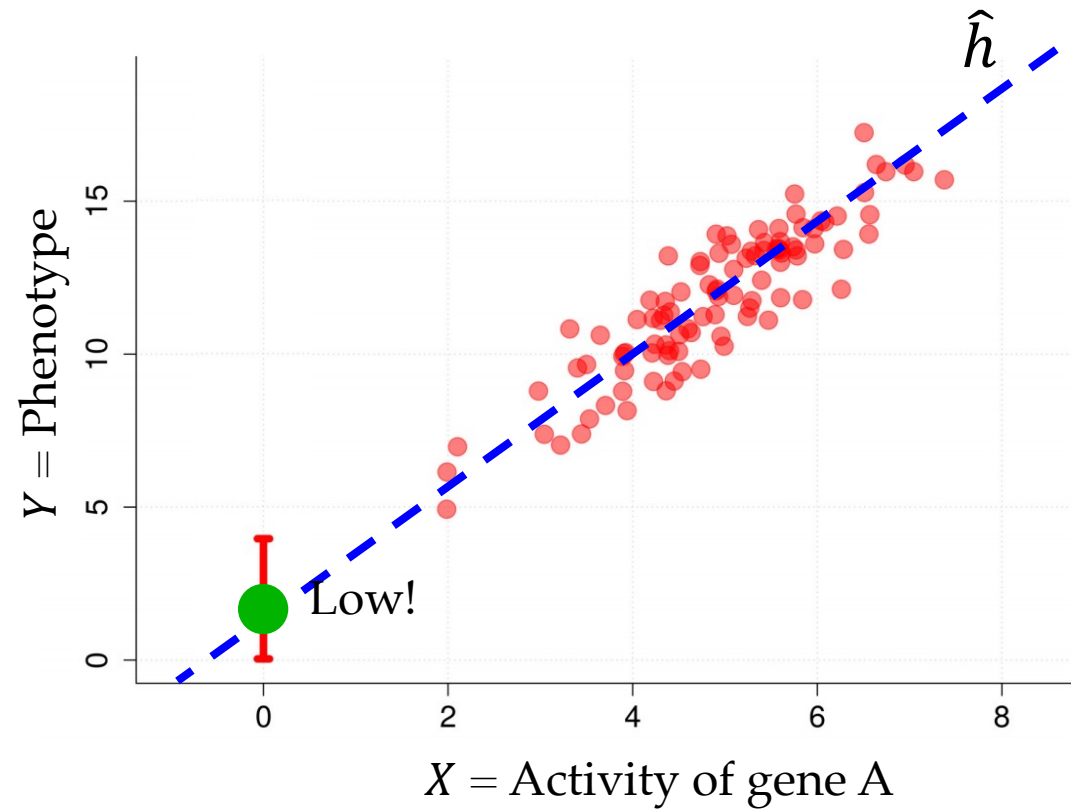
Learn a hypothesis from data

$$\hat{h} = \arg \min_h \frac{1}{m} \sum_{i=1}^m (h(x_i) - y_i)^2$$

Step 4.

Evaluate test error. **Good fit!**

ML which regresses Y on X would return something like this



Question:
Is this correct?
How do you know?

Example from Jonas Peters.

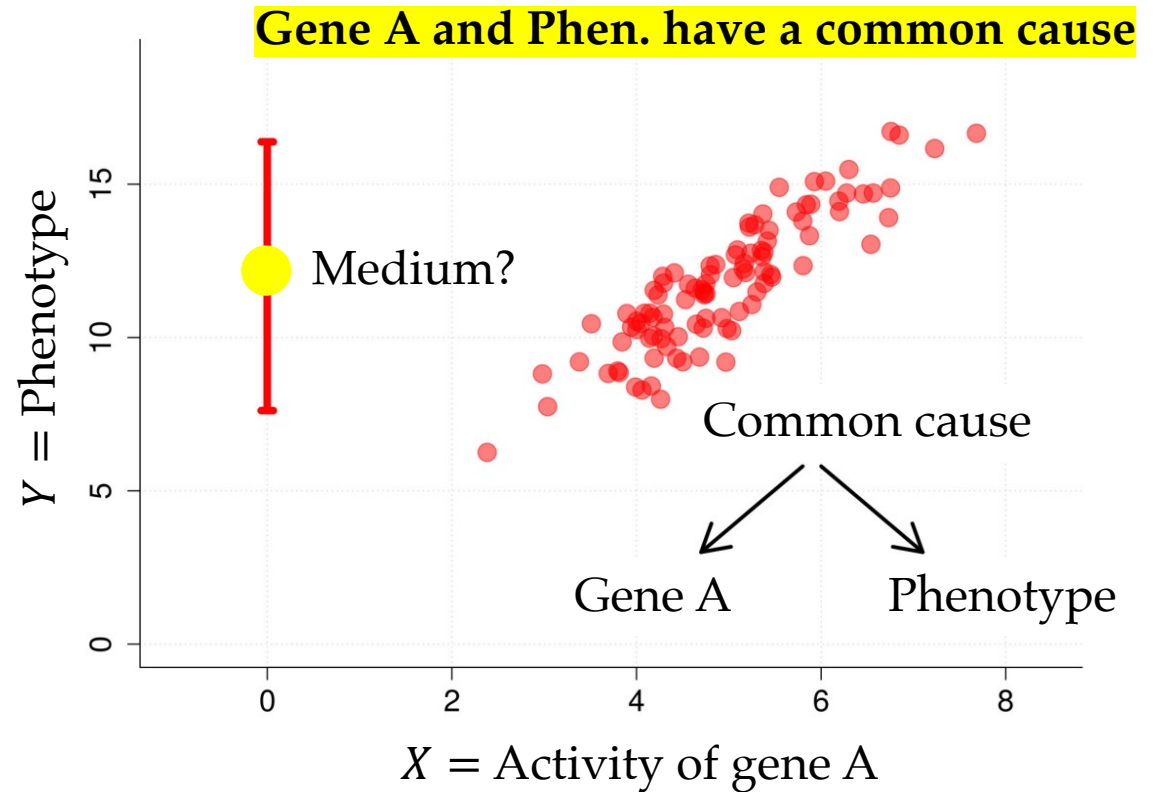
If there is a **common cause** which influences both gene activity X and phenotype Y

... the phenotype may not change when we knock out Gene A!

The association is **confounded!**

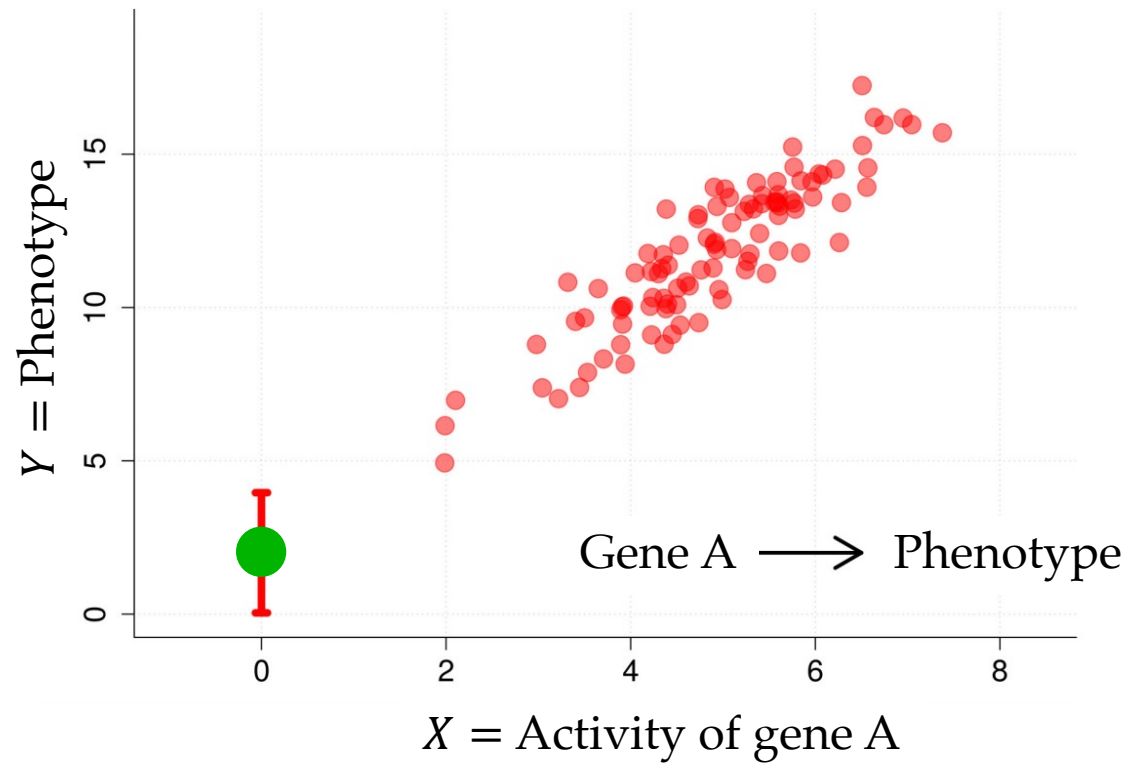
Example from Jonas Peters.

Explanation B



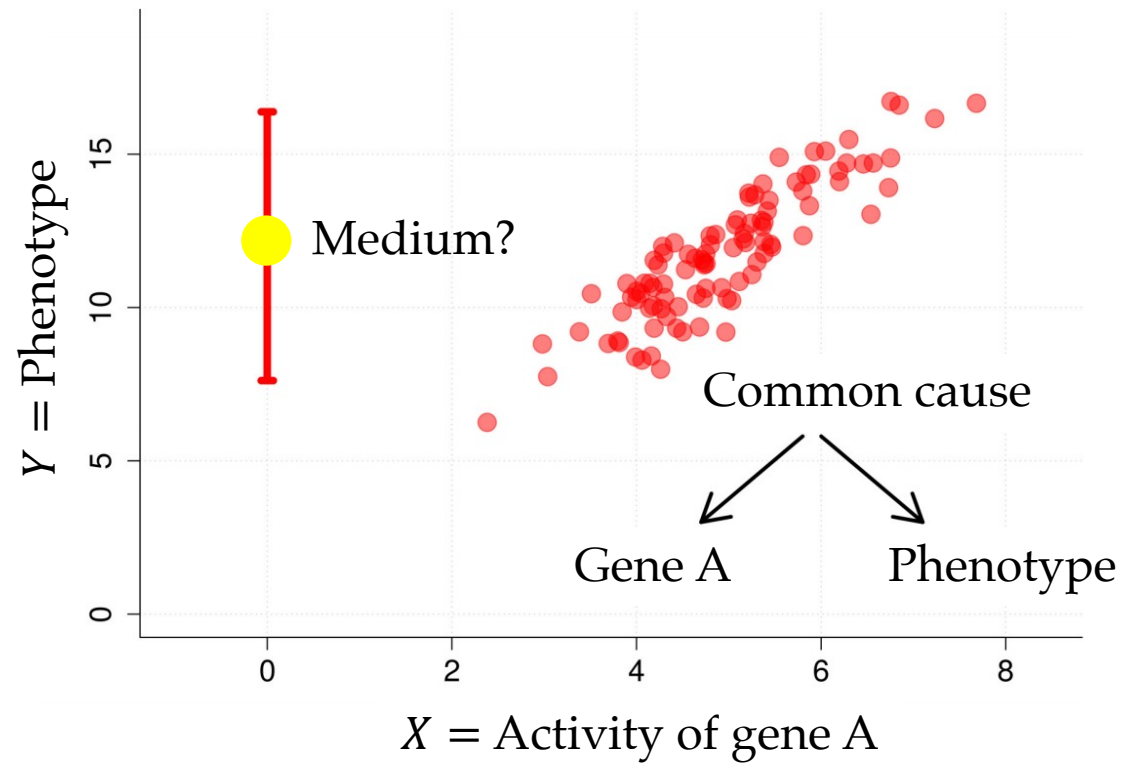
Explanation A

Gene A causes phenotype



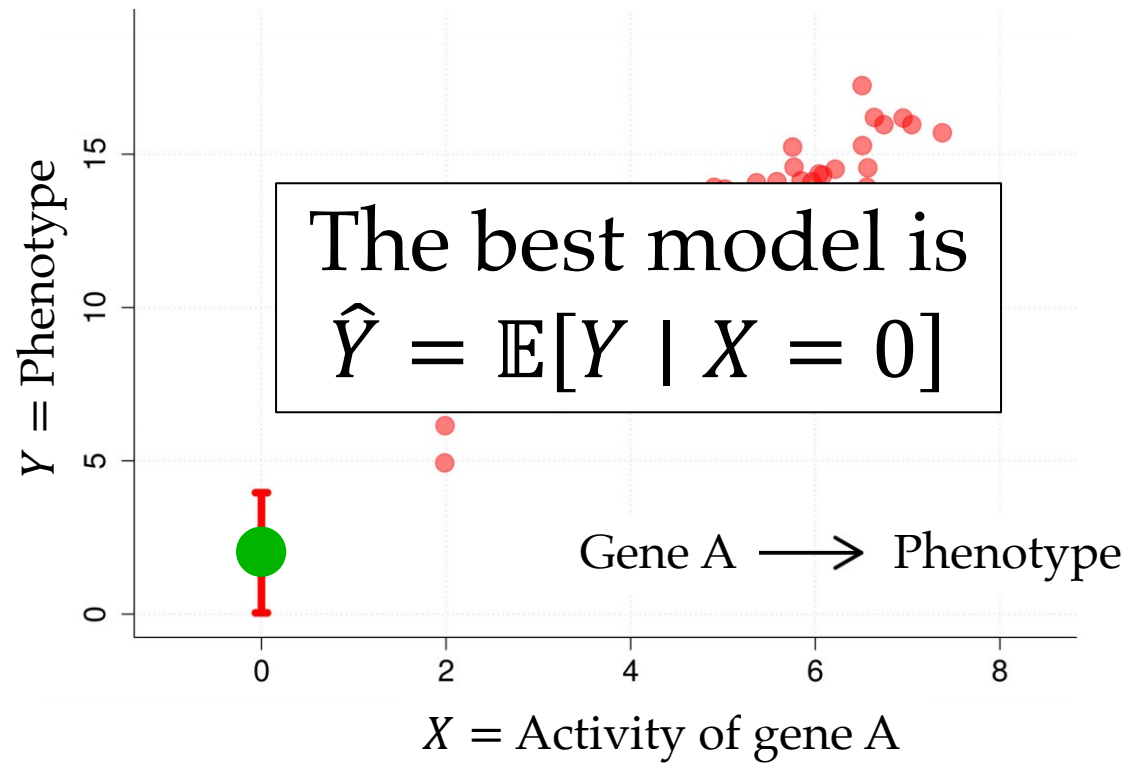
Explanation B

Gene A and Phen. have a common cause



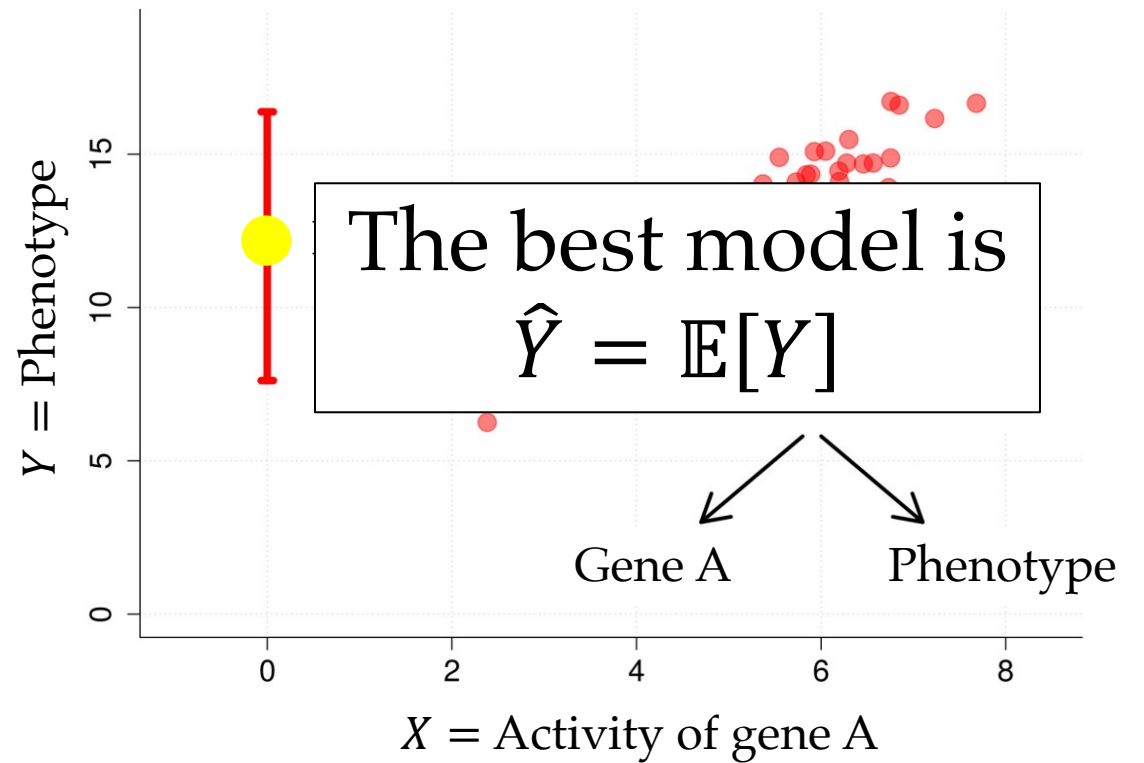
Explanation A

Gene A causes phenotype



Explanation B

Gene A and Phen. have a common cause



Causation \neq association

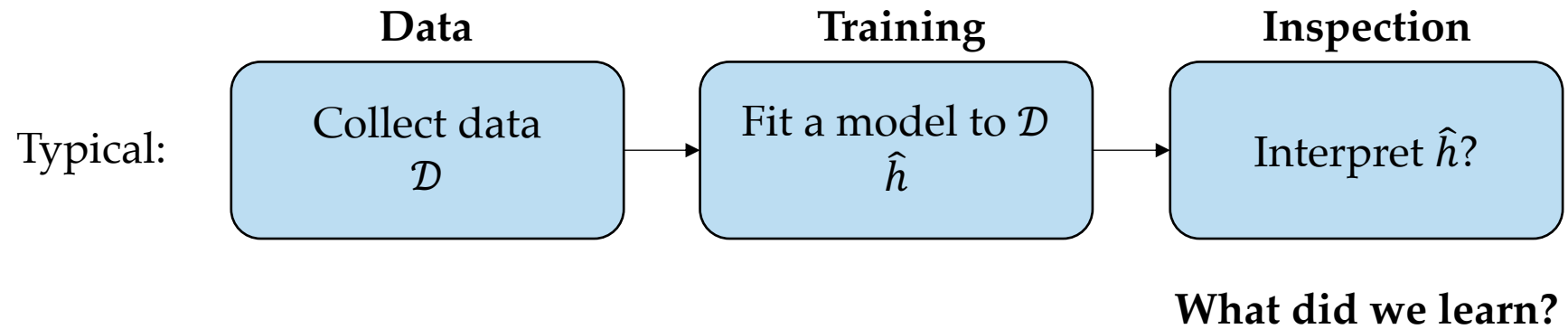
The two scenarios are equally plausible given *only* the data,
but *the right learning task* depends on causality

$$\mathbb{E}[Y \mid X = 0] \neq \mathbb{E}[Y \mid do(X = 0)] \neq \mathbb{E}[Y] \quad \text{in general}$$

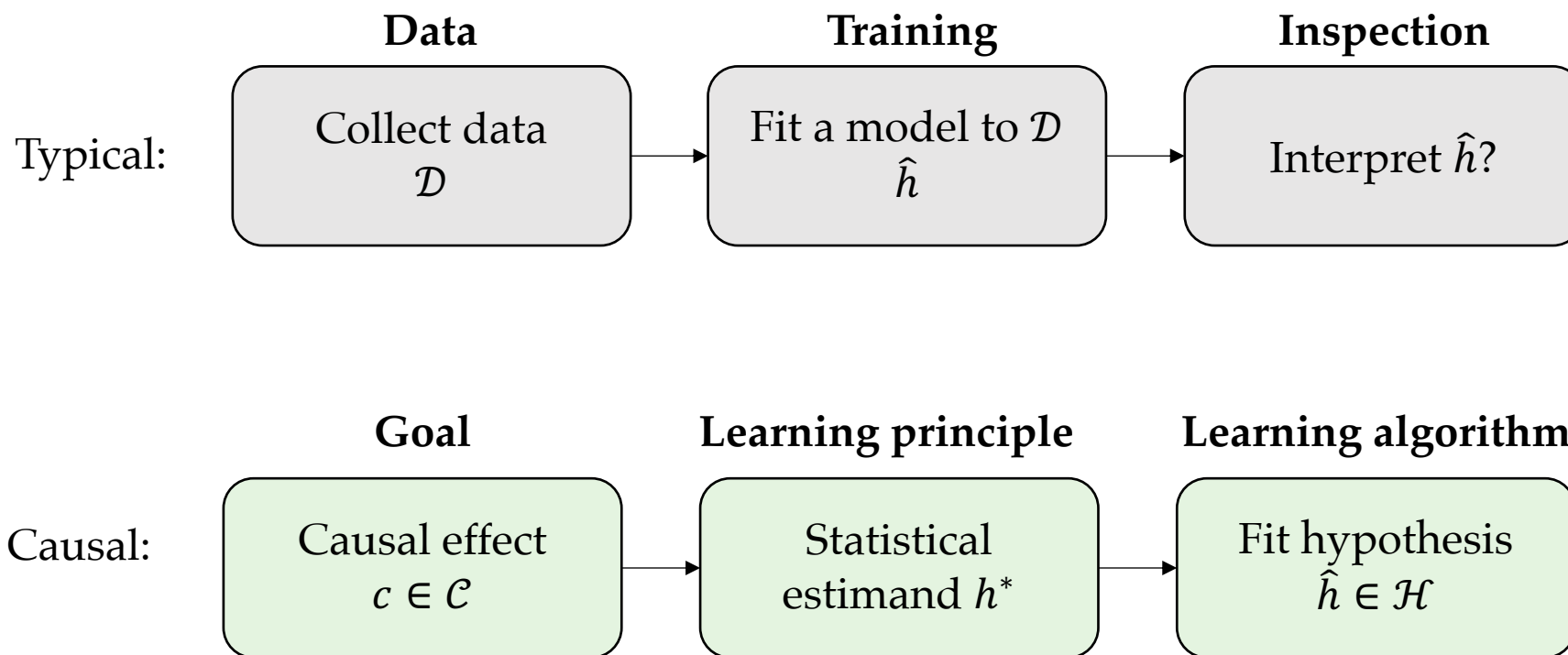
This is not a question of learning (or data)!

Even a perfect regression $f(x) \approx y$ will get the wrong answer
and the right model may have higher “test error”!

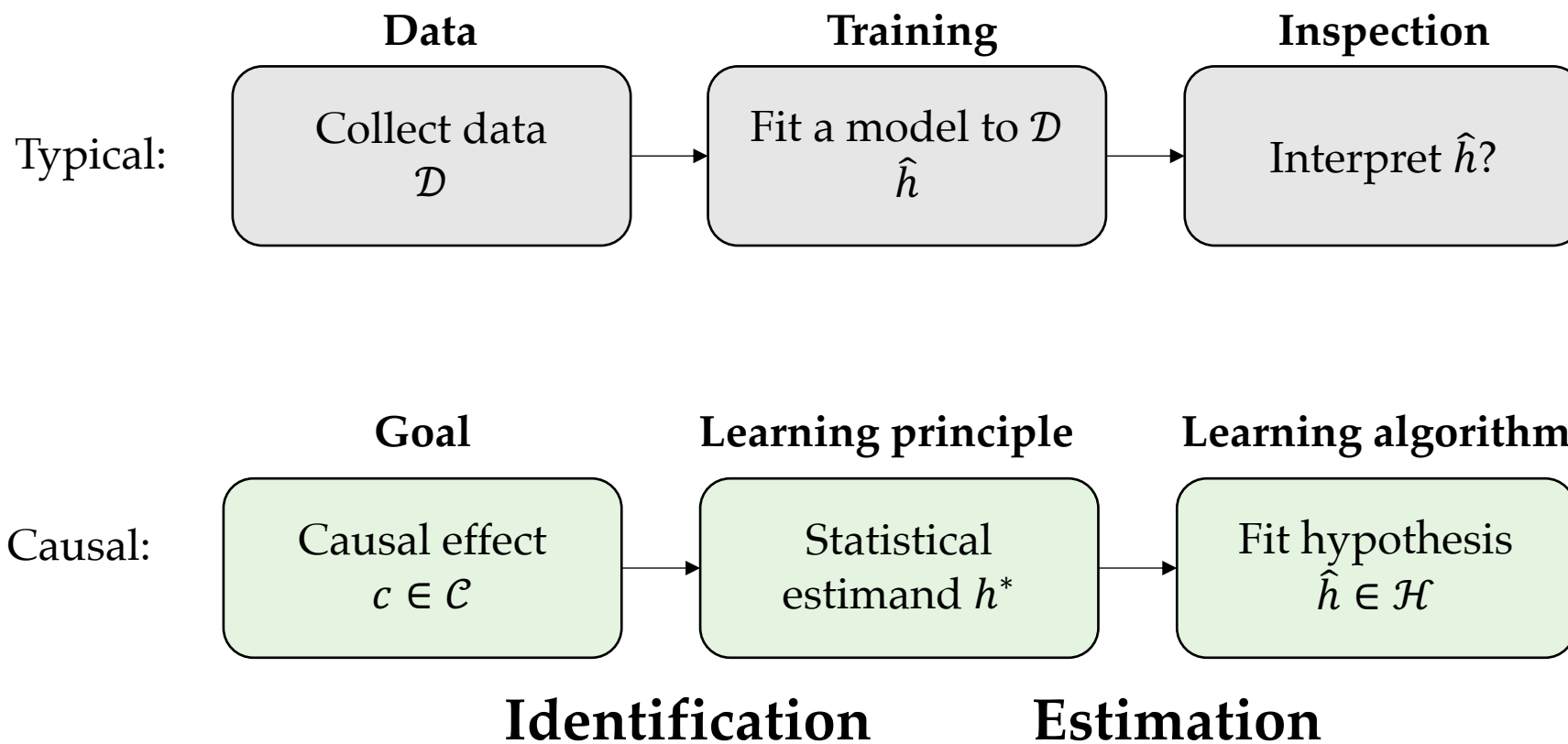
A common ML pattern...



Causal machine learning should be different!



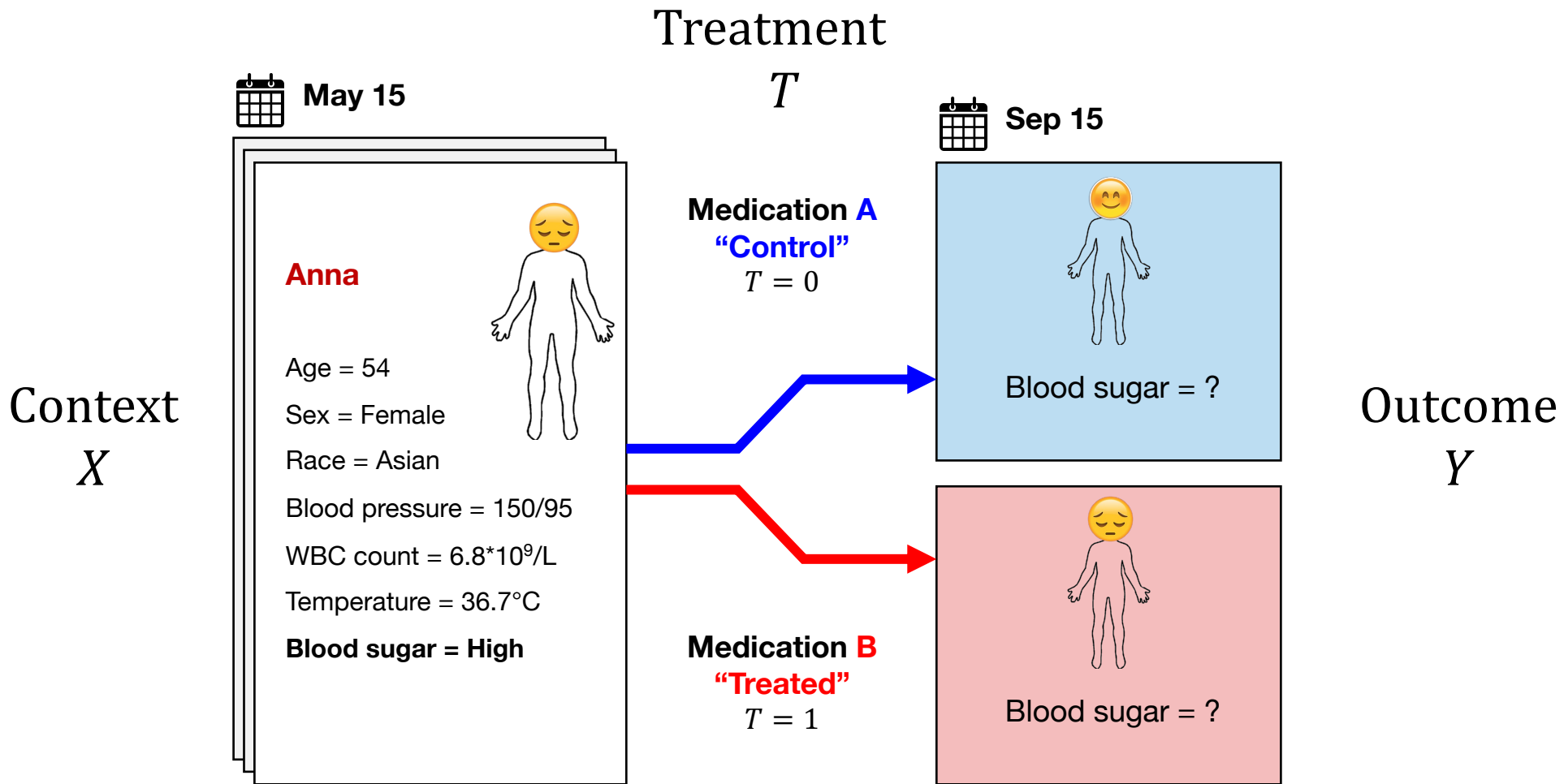
Causal machine learning should be different!

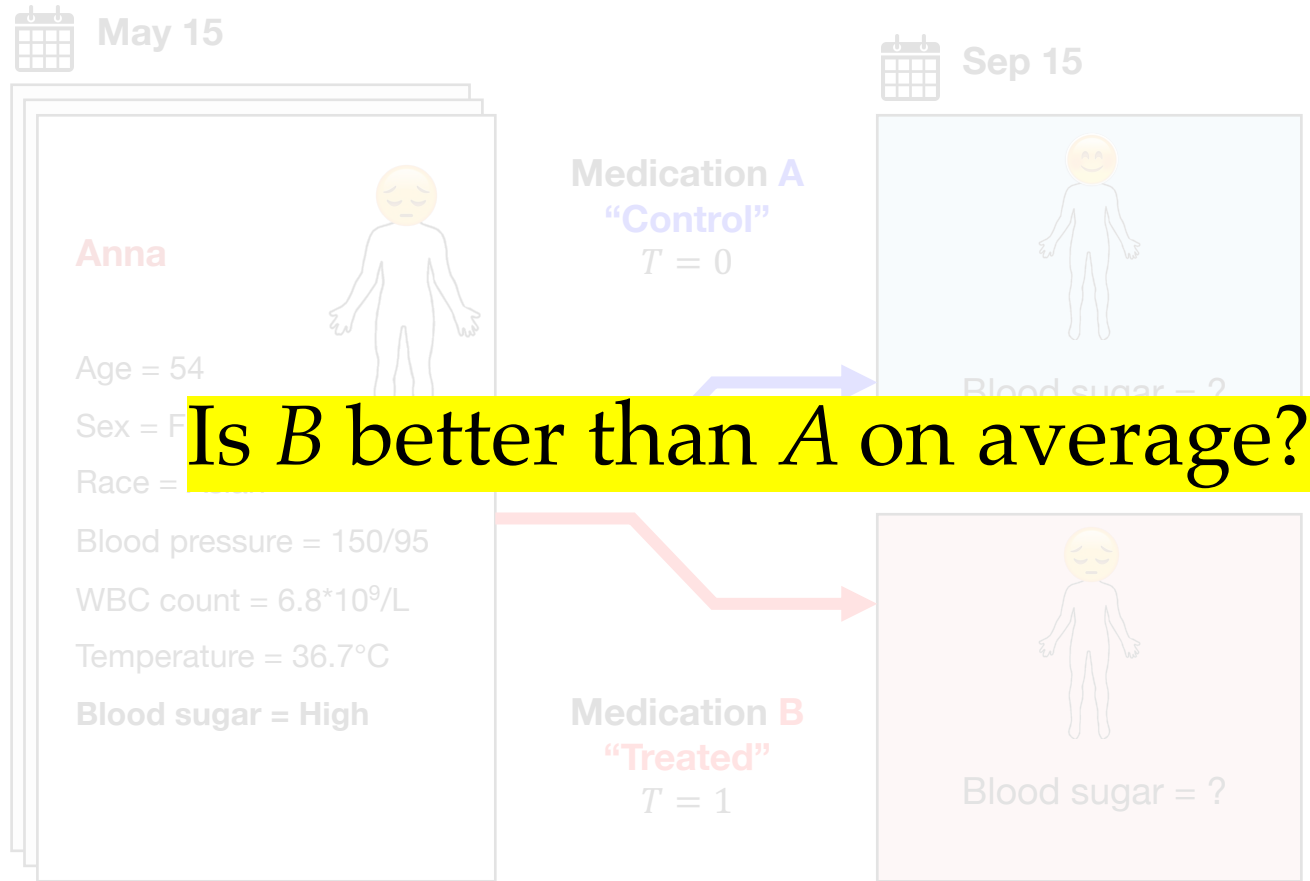


To make *decisions from data*,
we need a way to *specify causal questions*
to identify the *right goal* for machine learning

Part I.c: Potential outcomes of interventions

See e.g., Hernán & Robins, Chapter 1

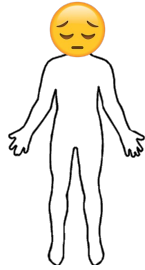




We can imagine two **potential** scenarios for our patients

 May 15

Anna



Age = 54

Sex = Female

Race = Asian

Blood pressure = 150/95

WBC count = $6.8 \times 10^9/L$

Temperature = $36.7^\circ C$

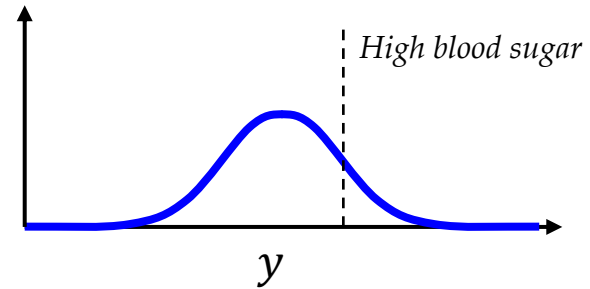
Blood sugar = High

Medication A

“Control”

$T = 0$

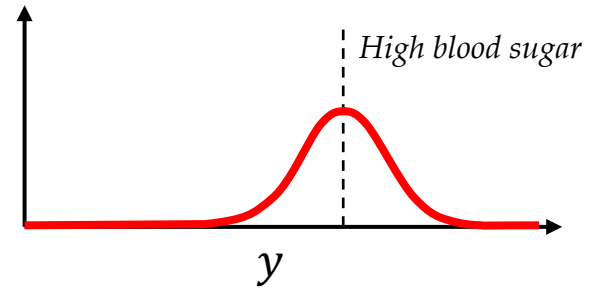
 Sep 15



Medication B

“Treated”

$T = 1$

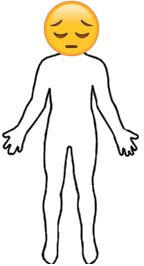


Which is better?

Two “potential” random variables

May 15

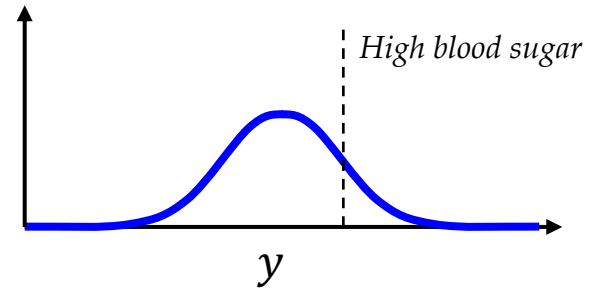
Anna



Age = 54
Sex = Female
Race = Asian
Blood pressure = 150/95
WBC count = $6.8 \times 10^9/L$
Temperature = $36.7^\circ C$
Blood sugar = High

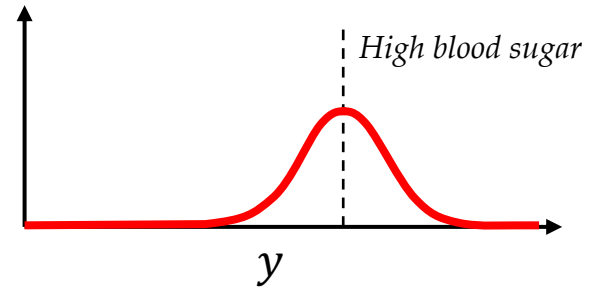
Medication A
“Control”
 $T = 0$

Sep 15



$$Y(0) \sim p_0(Y)$$

Medication B
“Treated”
 $T = 1$



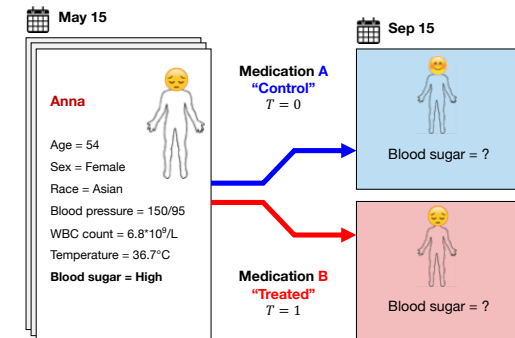
$$Y(1) \sim p_1(Y)$$

Potential outcomes¹ (Neyman-Rubin model)

$Y(0)$: What *would* happen under treatment 0 (“control”)

$Y(1)$: What *would* happen under treatment 1 (“treatment”)

We call $Y(0)$, $Y(1)$ “potential outcomes”.



¹See e.g., Hernan & Robins, Chapter 1

Causal effects of interventions

Potential outcomes let us define the **causal effect*** Δ of a binary intervention $T \in \{0,1\}$ as

$$\Delta = Y(1) - Y(0)$$

Δ is a *random variable*, just like $Y(0), Y(1)$

Compare with $\mathbb{E}[Y \mid do(X = x)] - \mathbb{E}[Y \mid do(X = x')]$ from earlier!

*Causal effects are also called “treatment effects”

Interpreting causal effects

We should understand Δ as the **increase in the outcome** as we intervene with $T \leftarrow 1$ compared to $T \leftarrow 0$

If $\Delta > 0$, and higher outcome is better, treatment 1 is preferred

If $\Delta < 0$, and higher outcome is better, treatment 0 is preferred

The causal effect can tell us which *action*, which *decision*, is best

How can we learn Δ from data?

SCMs vs potential outcomes

SCMs which you learned about in the morning is a more general model than potential outcomes

Potential outcomes is a convenient tool for many problems where only a certain intervention is of interest

Observational studies: Using historical data

Example:

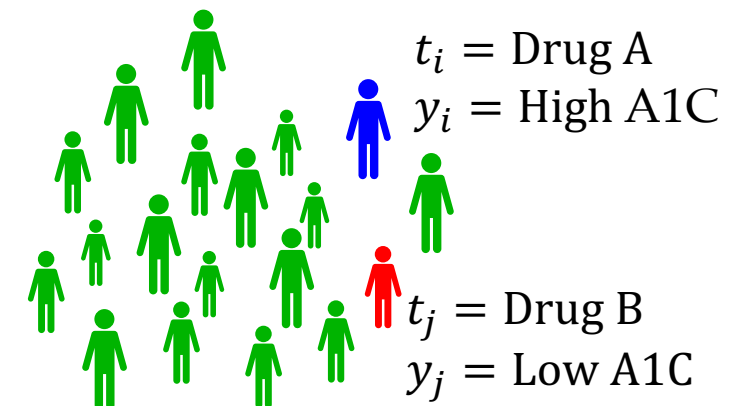
We have been treating pre-diabetic patients for 10 years

We know **which drugs** T were given to which patients and we know what **their blood sugar** Y was 6 months later, as well as some **context** X

We have data $D = \{(x_i, t_i, y_i)\}_{i=1}^m$

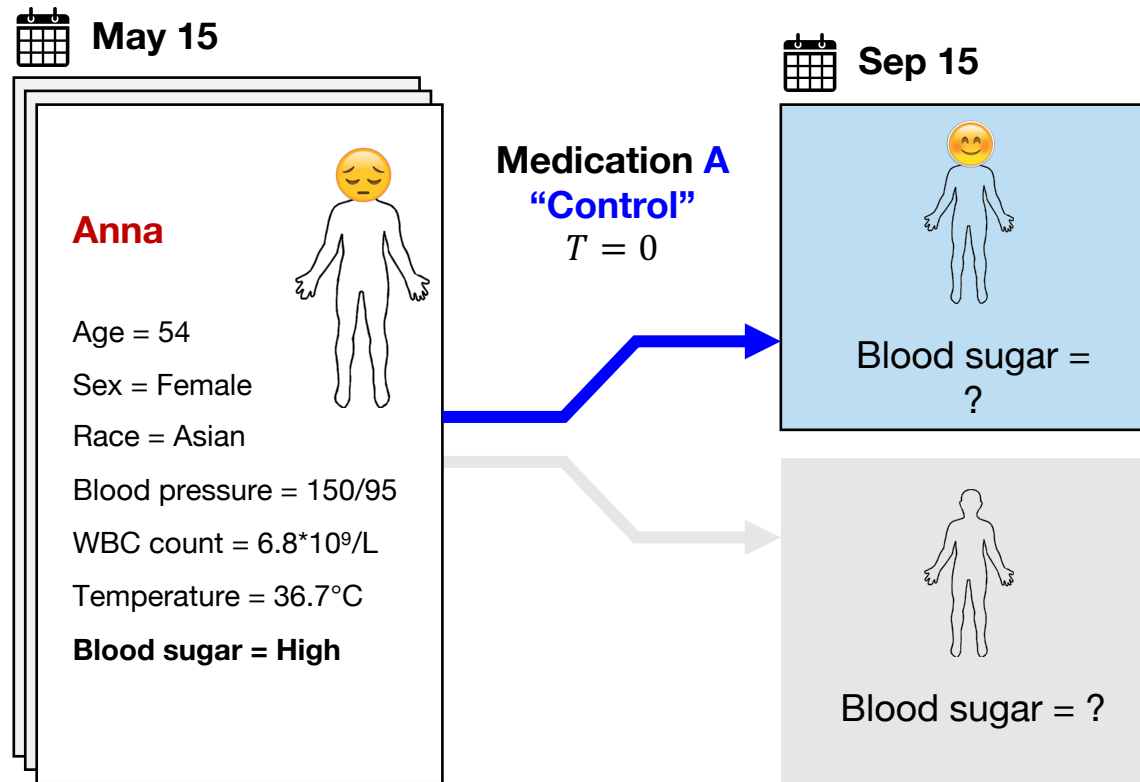
Dataset D

Context X	Treatment T	Outcome Y
Older male	Drug A	High A1C
Young female	Drug B	Low A1C
Young male	Drug B	Low A1C
...



Fundamental problem of causal inference

We can only observe the outcome of **one intervention**



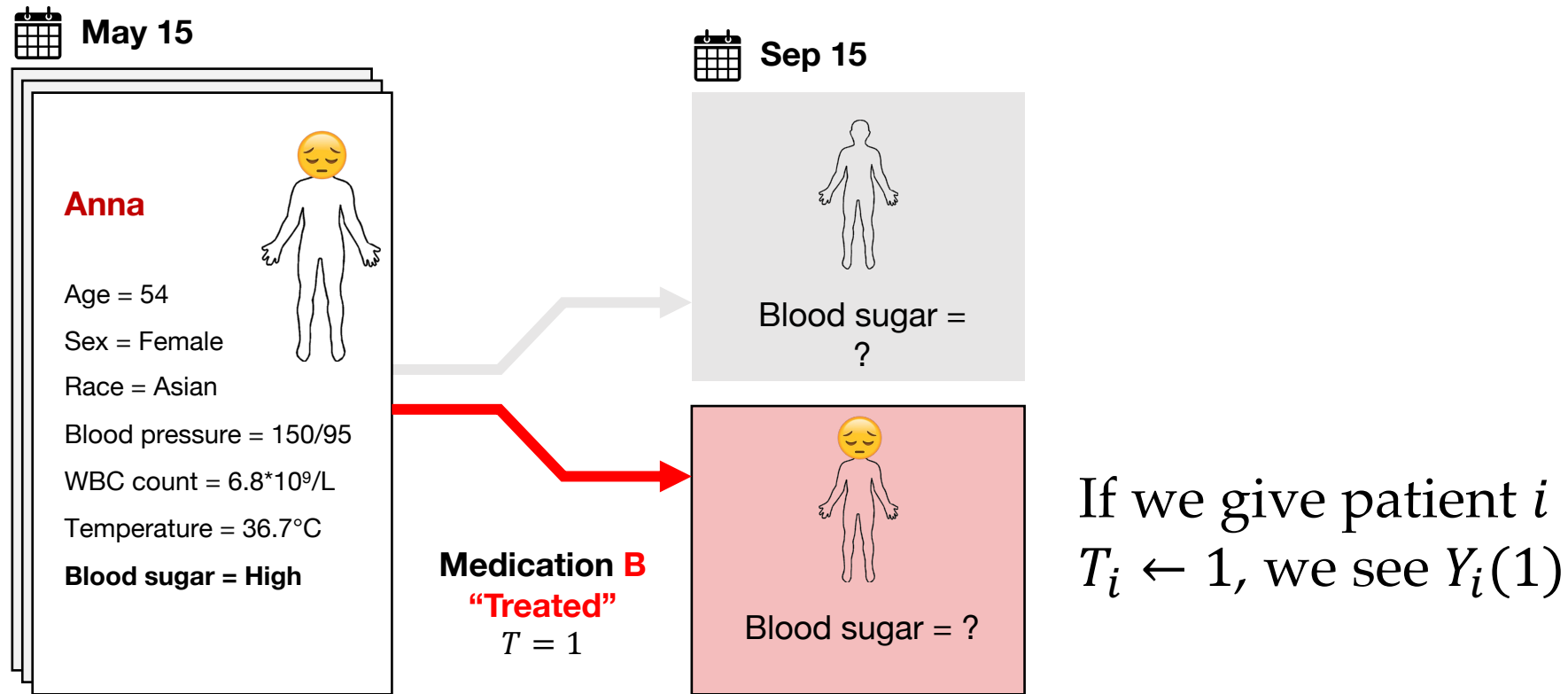
*If we give subject i
 $T_i \leftarrow 0$, we see $Y_i(0)$

Context X	Outcome $Y(0)$	Outcome $Y(1)$
Older male	High A1C	?
Young female	?	Low A1C
Young male	?	Low A1C
...

* This is an implicit assumption called "Consistency". $Y = Y(T)$

Fundamental problem of causal inference

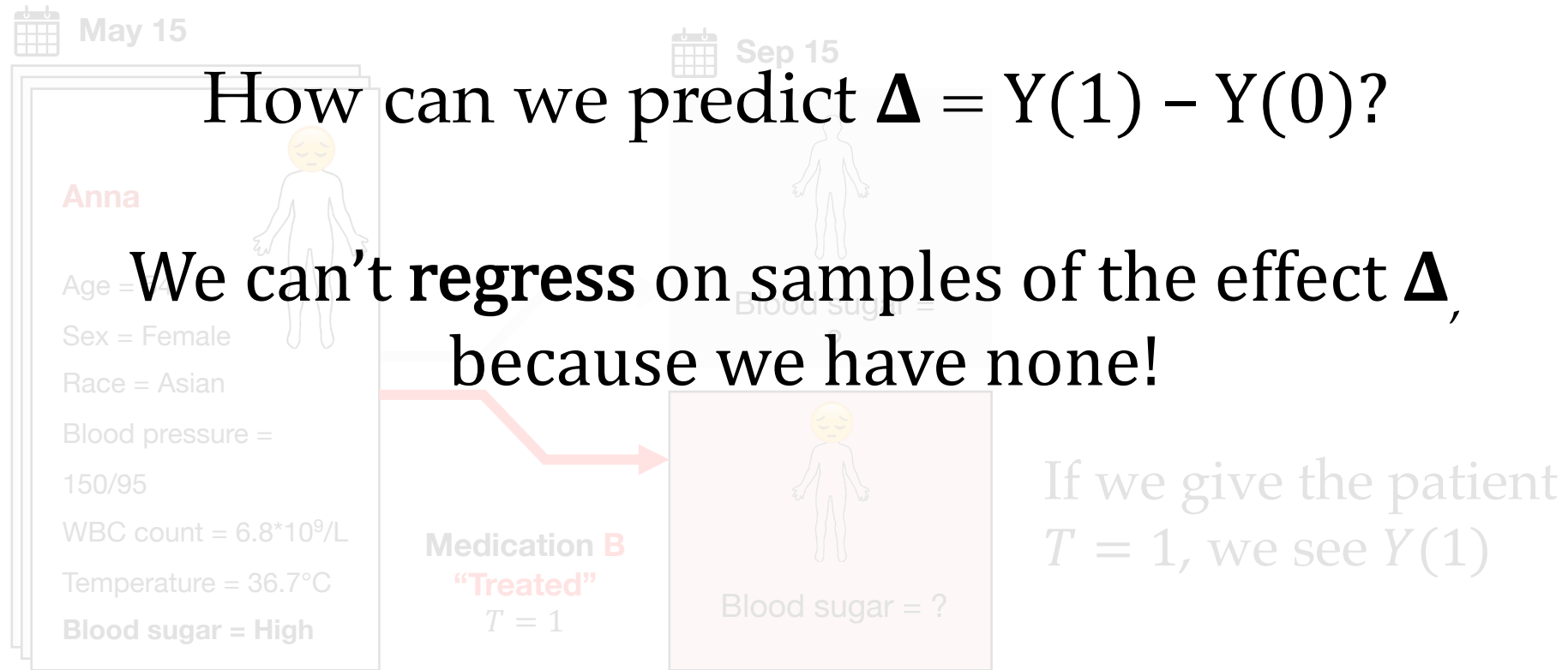
We can only observe the outcome of **one intervention**



* This is an implicit assumption called "Consistency". $Y = Y(T)$

Fundamental problem of causal inference

We can only observe the outcome of **one** intervention



Average treatment effect

First, let's consider the **population average effect** instead

Definition.

The *average causal effect* (ATE) of a binary treatment $t \in \{0,1\}$ is

$$\tau := \mathbb{E}[\Delta] = \mathbb{E}[Y(1) - Y(0)]$$

The ATE averages over individual variation

The “average treatment effect” (ATE) is also called the “average causal effect” (ACE)

Example: LaLonde's study (1986)

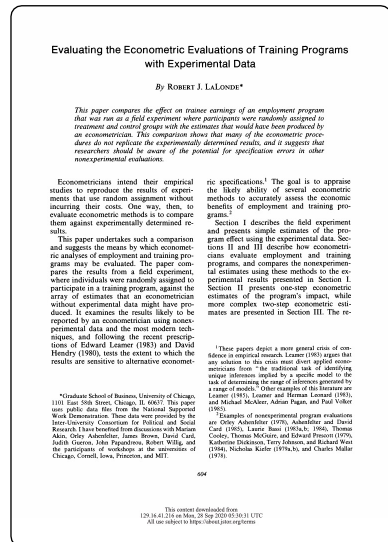
The LaLonde study looked at the effectiveness of a job training program, T , on the future real earnings of an individual, Y

Subjects were randomized into job training or not

The **average yearly real earnings** of subjects following job training was \$851 (\$886) **higher** for females (males) than without training*

$$\widehat{ATE}_{\text{female}} = \$851, \quad \widehat{ATE}_{\text{male}} = \$886$$

*The job training program cost \$6800–\$9100



Conditional average treatment effect

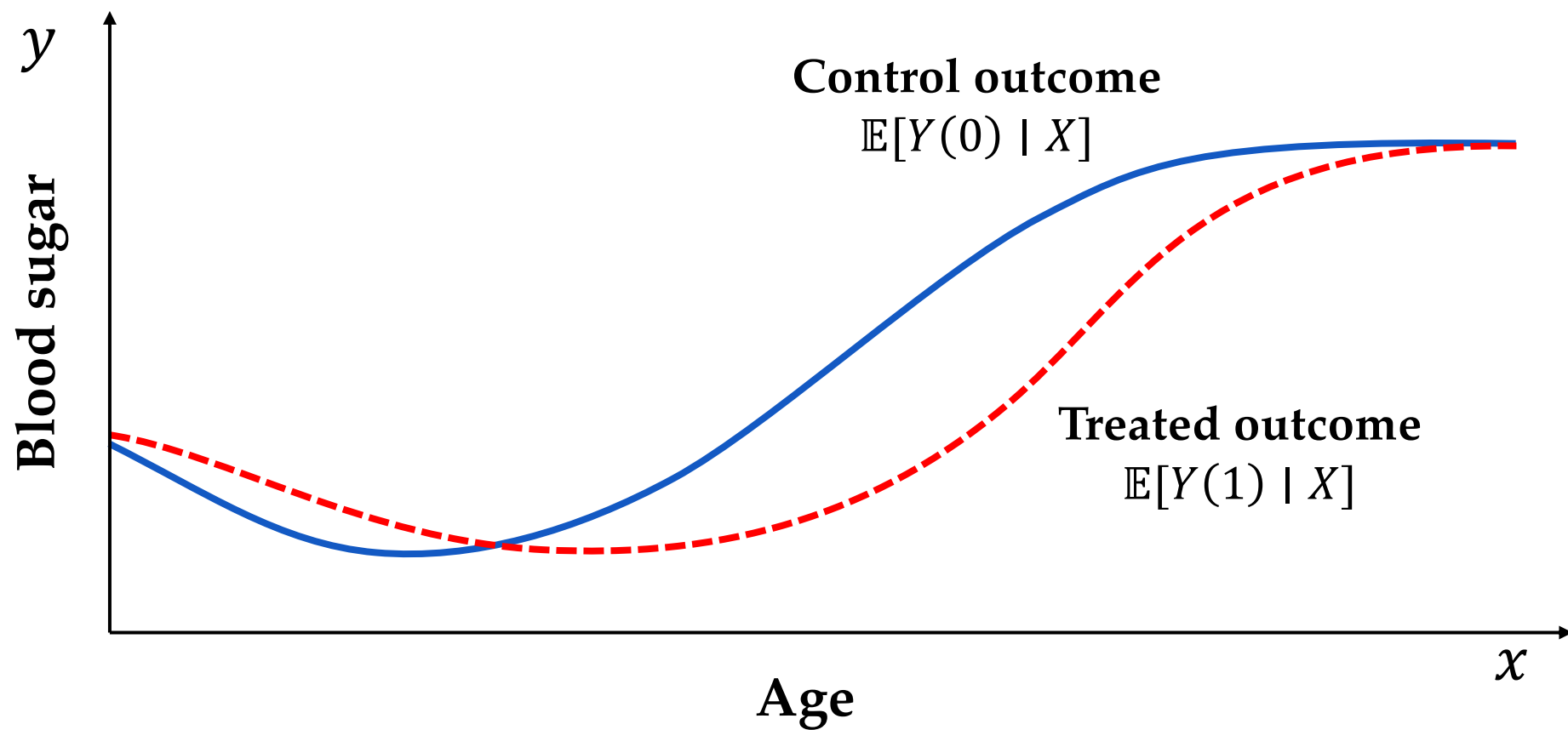
Let X represent a **context variable**, such as age, medical history, etc

Conditional average treatment effect (CATE) w.r.t. X :

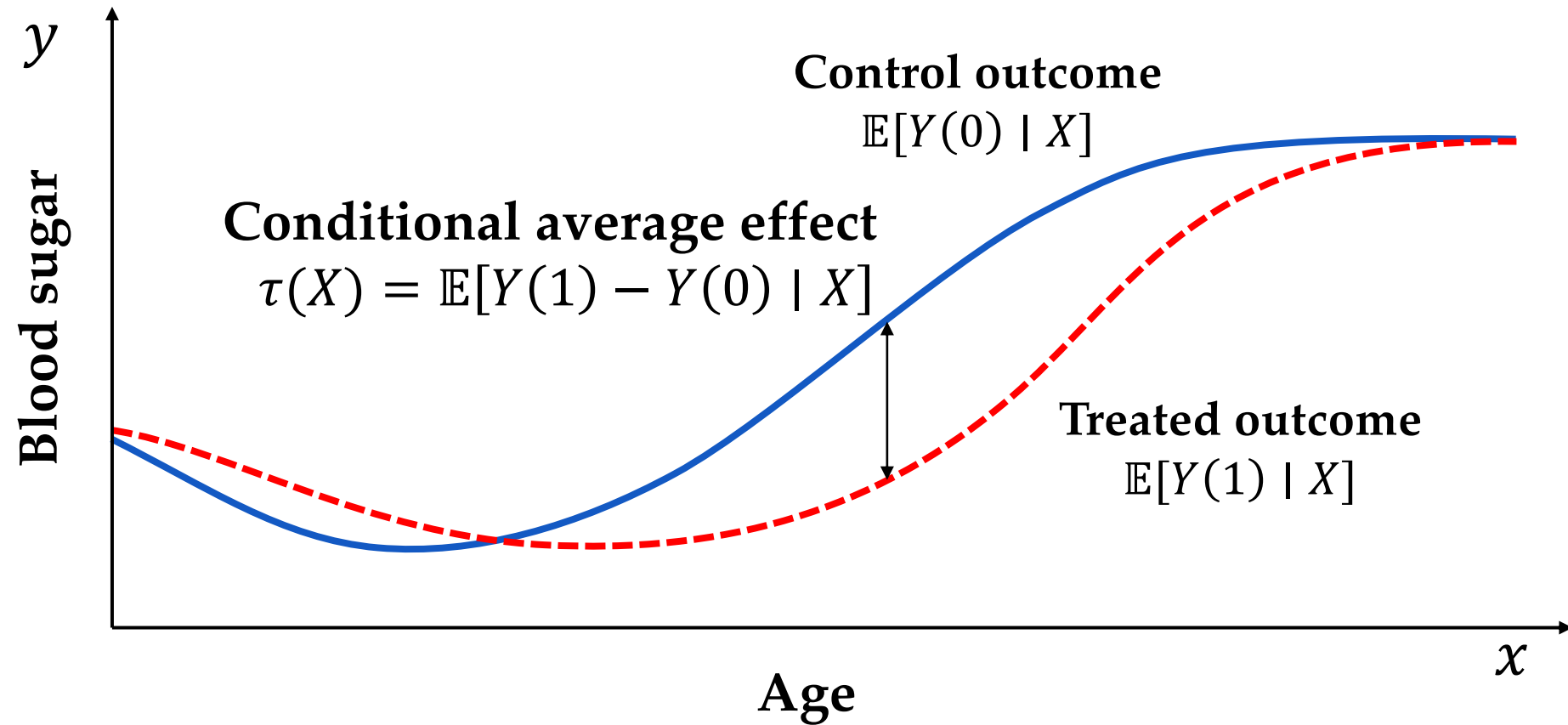
$$\tau(x) := \mathbb{E}_Y[\Delta \mid X = x] = \mathbb{E}_Y[Y(1) - Y(0) \mid X = x]$$

The ATE is the expected CATE, i.e., $\tau = \mathbb{E}_X[\tau(X)]$

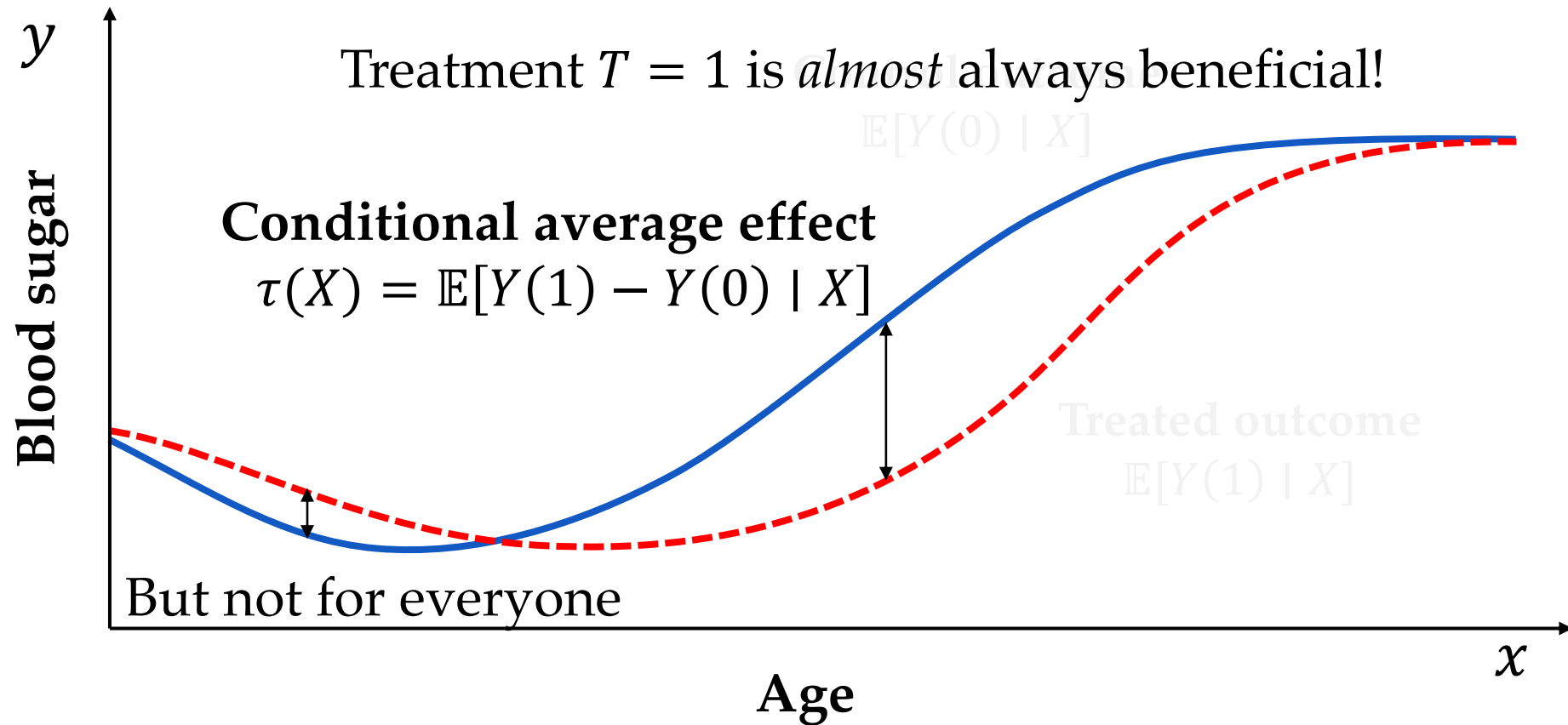
Potential outcomes and CATE



Potential outcomes and CATE



Potential outcomes and CATE

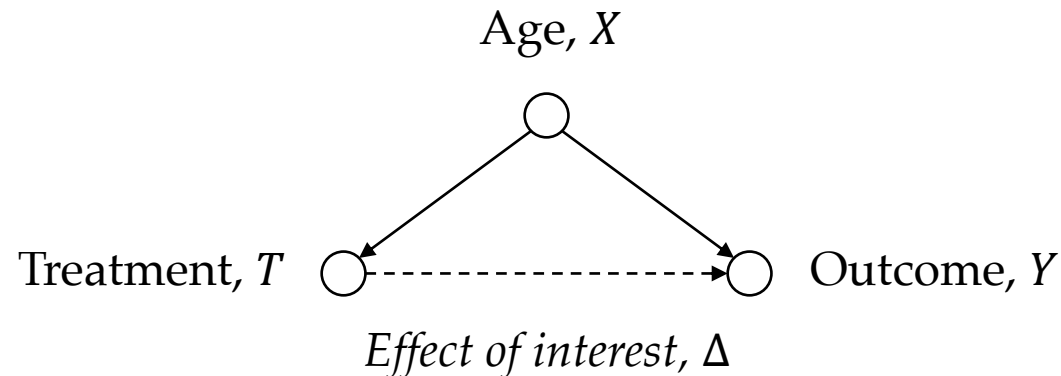


Part I.d: Partial observability & confounding

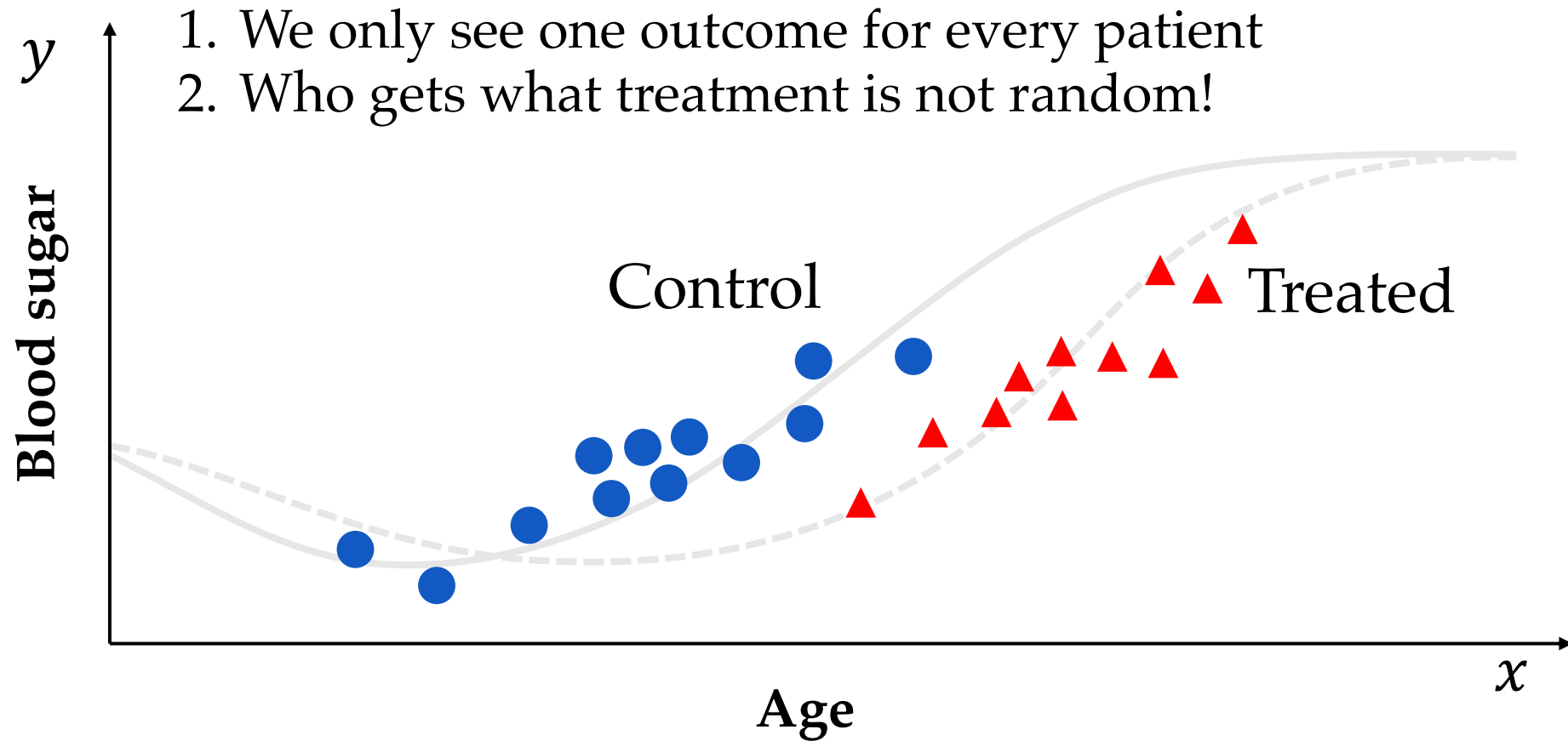
Confounding

Confounding biases are differences in the outcome between treatment groups which are not related to the treatment's effect

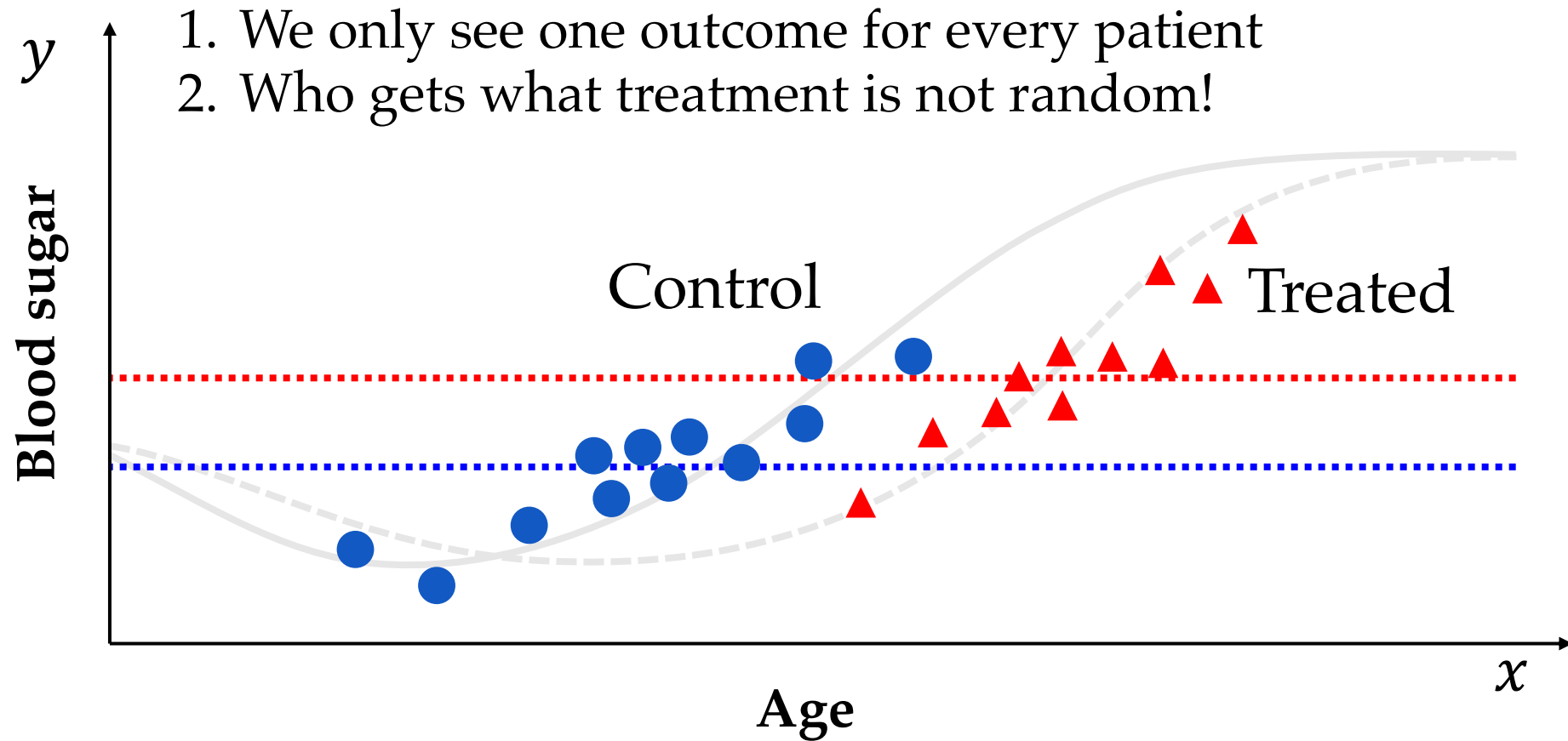
Example: Drug $T = 1$ is given to older patients than Drug B and older patients are at higher risk \Rightarrow Drug $T = 0$ looks worse!

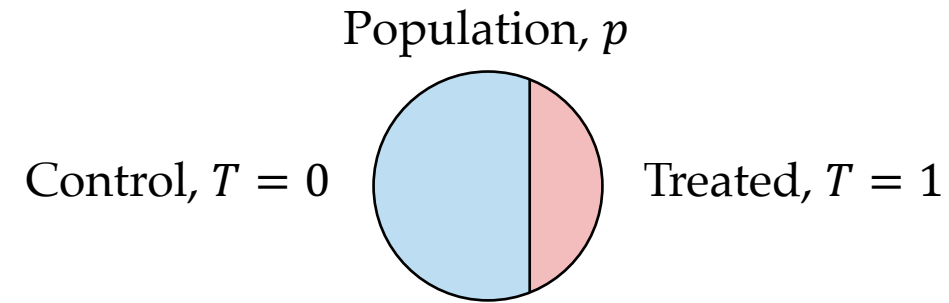


Observational studies

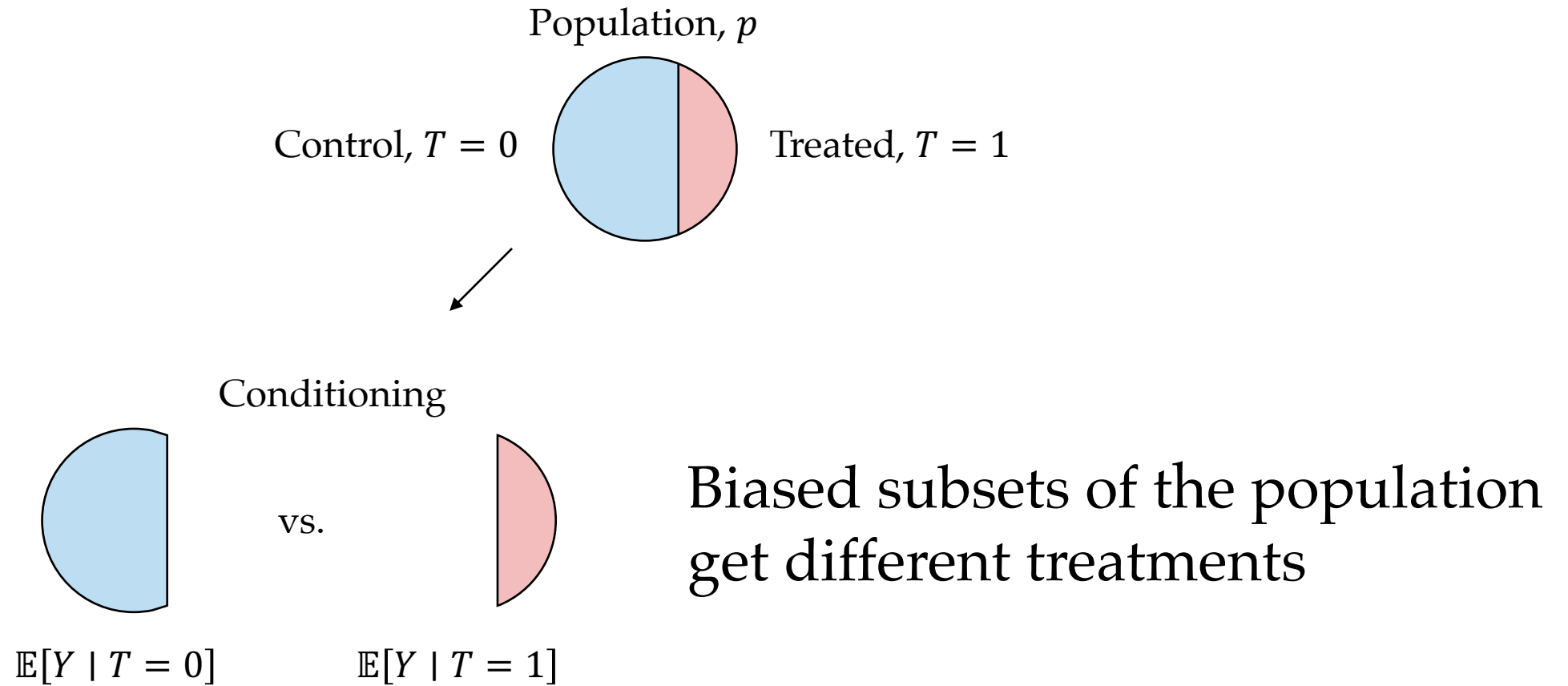


Observational studies

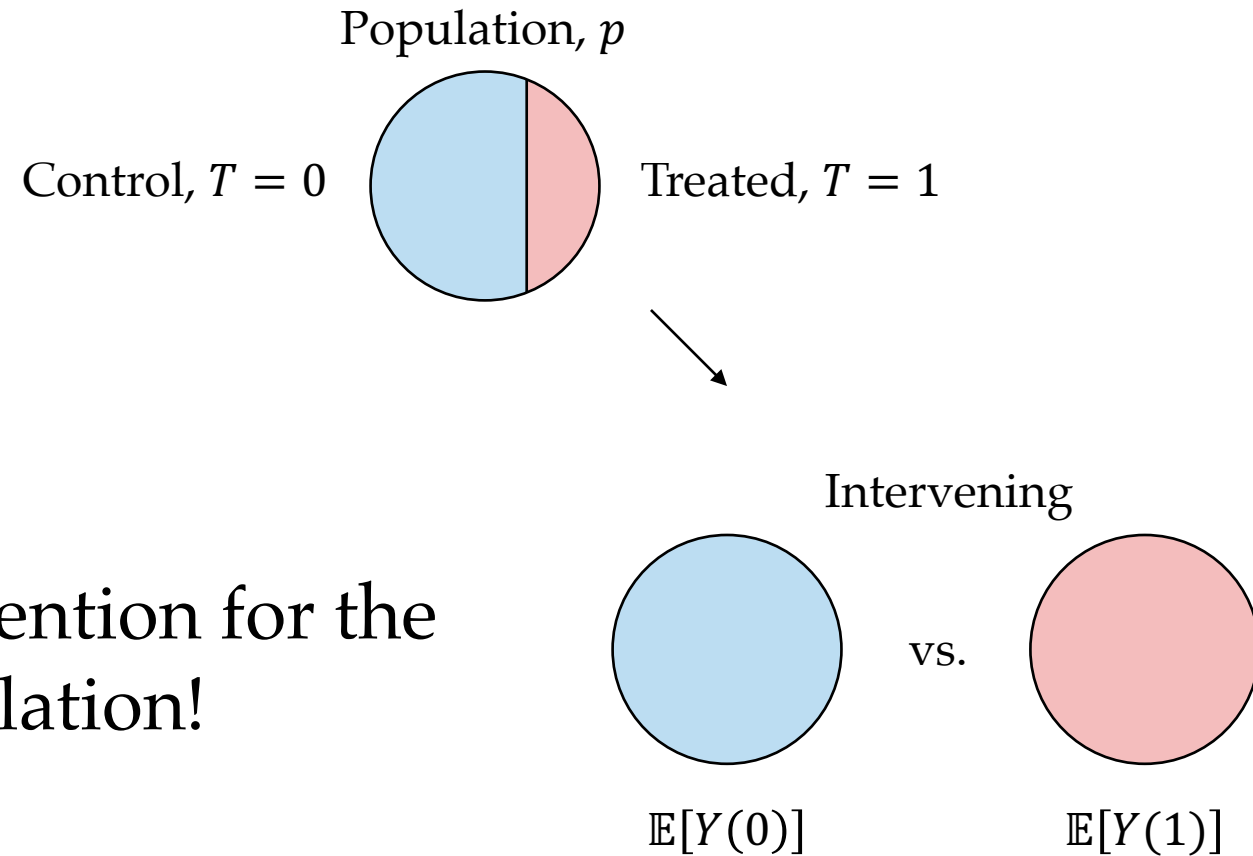




The discs represent
types of individuals,
the color their
treatment
status



Same intervention for the whole population!



Exchangeability

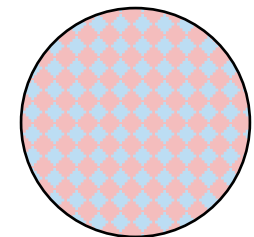
The best-case scenario is if there is *no pattern* in how treatments are assigned in the data-generating process related to the outcome,

$Y(t) \perp T$ ——— Treatment groups are
“exchangeable”!

In this case, $\mathbb{E}[Y(t)] = \mathbb{E}[Y \mid T = t]$

We have identified $\mathbb{E}[Y(t)]$ as a function of $p(X, T, Y)$

Population, p



Randomized experiments & identifiability

Experiments ensure exchangeability through **randomization**

Example: $T \sim \text{Bernoulli}(0.5) \Rightarrow T \perp Y(t)$

In observational studies, **can we still have exchangeability?**

Adjustment sets

Our strategy will be to *remove as much of the pattern* in treatment assignment as possible by *adjusting* for confounders

If we can find a group of subjects with context variables X that *would respond the same* if given the same treatment, we have

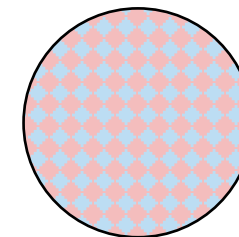
$$Y(t) \perp T \mid X$$

*Conditional exchangeability** given X

Subpopulation, $p(\cdot \mid x)$

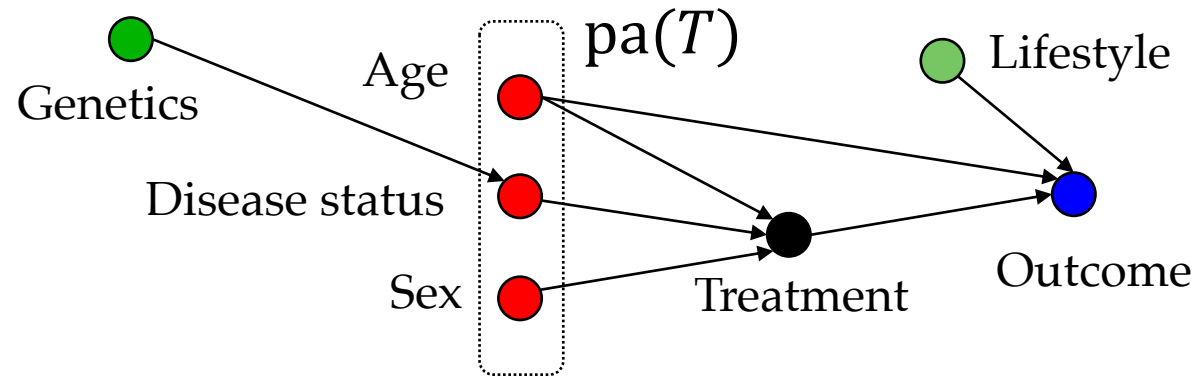
Such a variable X is called an **adjustment set**

* Sometimes called “ignorability”



Parent adjustment

A special case is when we know all direct causes of treatment — all parents in the *causal graph*. (Recall from this morning)



The full set of parents $pa(T)$ satisfies conditional exchangeability*!

It covers all patterns in treatment which may or may not be related to the outcome

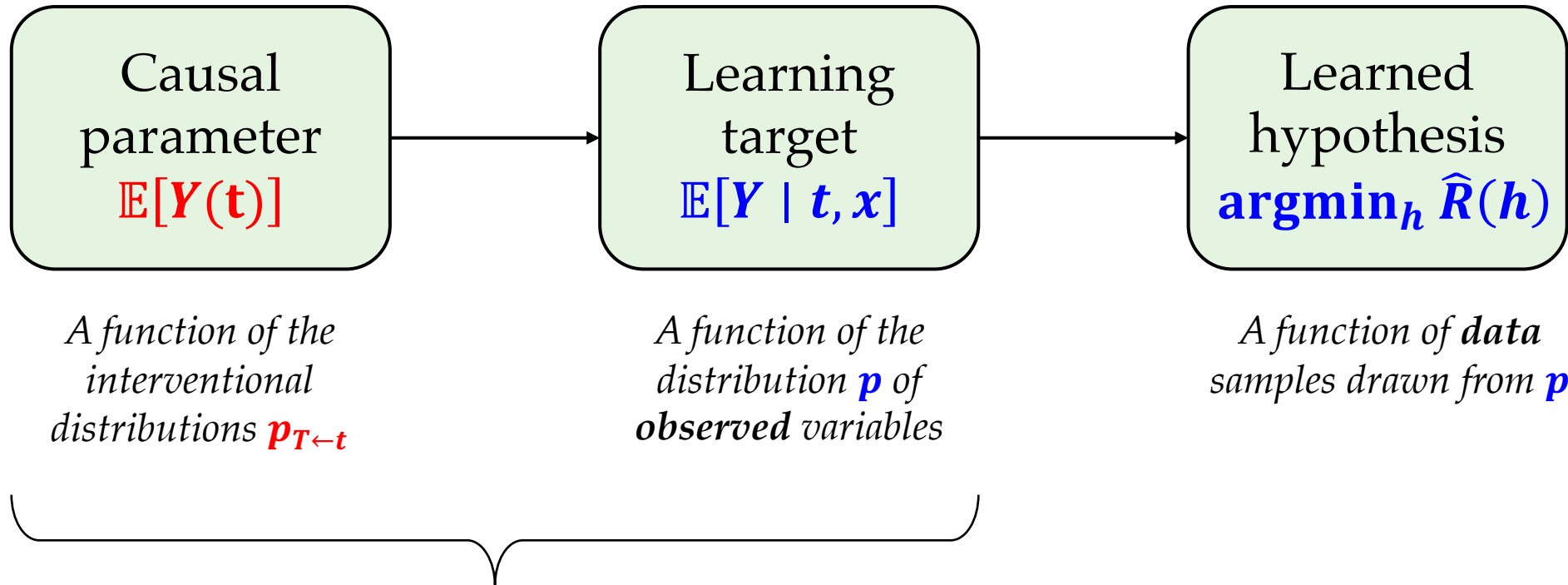
* See much more on this in Pearl, *Causality*, 2009, including more general criteria such as the backdoor criterion

Part II: Causal effect estimation

Regression & propensity adjustment

Identification

Estimation



What assumptions can we use here?

Identifying assumptions

We will make the following **identifying assumptions**

A set of variables X is known which satisfies, for all t and x :

1. **Conditional exchangeability:** $Y(t) \perp T \mid X = x$
2. **Treatment group overlap:** $p(T = t \mid X = x) > 0$
3. **Consistency:** $Y = Y(T)$

With these we can prove identifiability of ATE and derive methods!

Two common methods

Regression adjustment

identifies the effects of treatment by accounting for the effect of confounding variables on the **outcome**

Use machine learning to model Y !

Propensity adjustment

identifies the effects of treatment by accounting for the effect of confounding variables on the **treatment**

Use machine learning to model T !

Part II.a: Regression adjustment

Proof of identifiability w. regression adjustment

Under **conditional exchangeability**, consistency

$$Y(t) \perp T \mid X \quad \text{and} \quad Y = Y(T)$$

we have

$$p(Y(t) \mid X) = p(Y(t) \mid T = t, X)$$

Cond. exchangeability
 $Y(t) \perp T \mid X$

Proof of identifiability w. regression adjustment

Under **conditional exchangeability**, **consistency**

$$Y(t) \perp T \mid X \quad \text{and} \quad Y = Y(T)$$

we have

$$p(Y(t) \mid X) = p(\textcolor{red}{Y}(t) \mid T = t, X) = p(\textcolor{red}{Y} \mid T = t, X)$$

Cond. exchangeability

Consistency
 $Y = Y(T)$

Proof of identifiability w. regression adjustment

Under **conditional exchangeability, consistency**

$$Y(t) \perp T \mid X \quad \text{and} \quad Y = Y(T)$$

we have

$$p(Y(t) \mid X) = p(Y(t) \mid T = t, X) = p(Y \mid T = t, X)$$

It follows that

$$\begin{aligned} \text{Interventional} \quad \mathbb{E}[Y(t) \mid X = x] &= \sum_y y p(Y(t) = y \mid X = x) \\ &= \sum_y y p(Y \mid X = x, T = t) = \mathbb{E}[Y \mid X = x, T = t] \quad \text{Observational} \end{aligned}$$

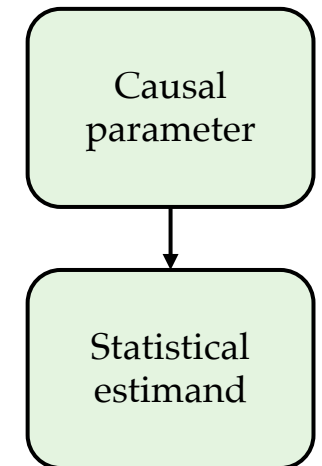
Final steps of identification

On the last slide, we proved $\mathbb{E}[Y(t) \mid X = x] = \mathbb{E}[Y \mid X = x, T = t]$ under conditional exchangeability and consistency

To get the ATE, we can average these conditionals

$$\begin{aligned} \text{ATE} &= \mathbb{E}[Y(1) - Y(0)] \\ &= \mathbb{E}_X[\mathbb{E}[Y \mid X = x, T = 1] - \mathbb{E}[Y \mid X = x, T = 0]] \end{aligned}$$

Can estimate with regression (need overlap to get right!)



Regression adjustment with “T-learner”*

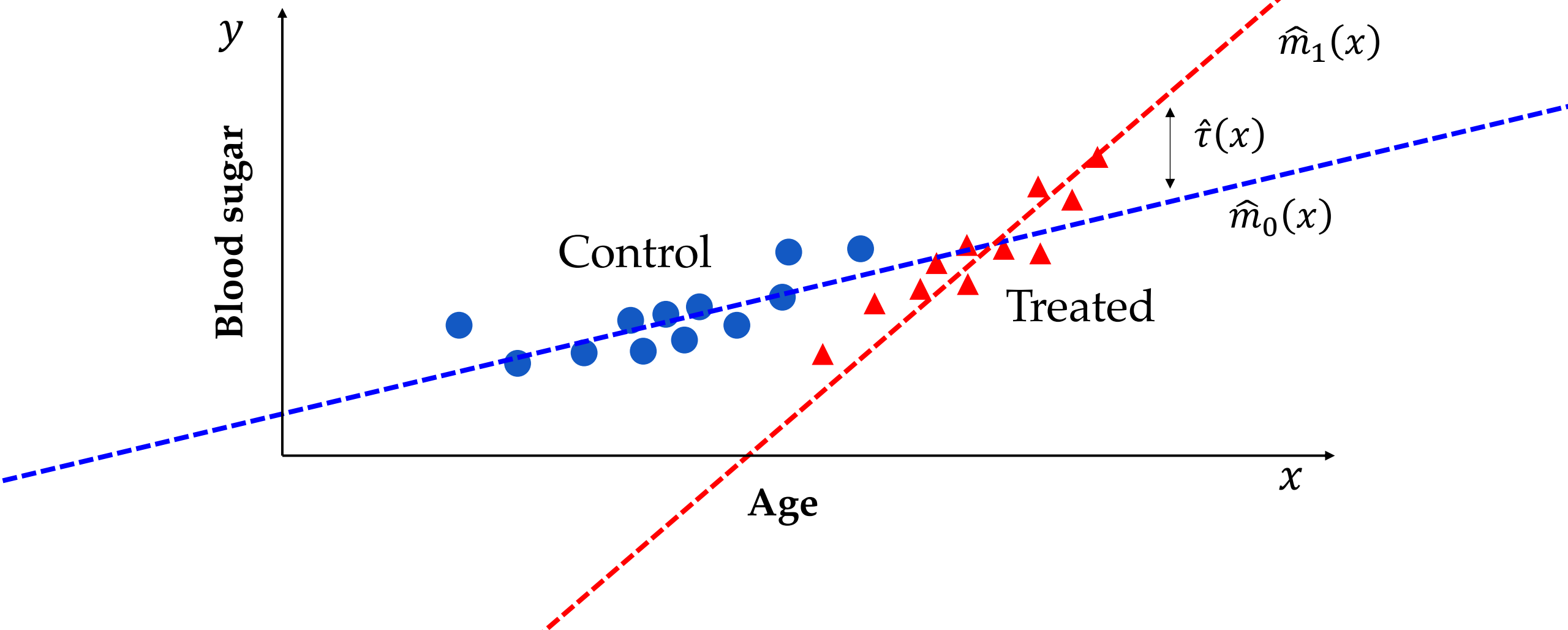
1. Identify a valid adjustment set X
2. Collect data $(x_1, t_1, y_1), \dots, (x_n, t_n, y_n)$
3. Fit regression models $\hat{m}_t(x) \approx \mathbb{E}[Y \mid X = x, T = t]$
e.g., using empirical risk minimization (ERM)*:

$$\hat{m}_t(x) = \arg \min_f \frac{1}{n_t} \sum_{i:t_i=t} (f(x_i) - y_i)^2$$

4. Return $\widehat{ATE} = \frac{1}{n} \sum_{i=1}^n (\hat{m}_1(x) - \hat{m}_0(x))$

*Künzel et al., *PNAS*, 2019

Regression adjustment, adjusting for Age



Part II.b: Inverse-propensity weighting

Propensity score

The propensity score $e(x) = p(T = 1 \mid X = x)$ is the probability that a subject with covariates x receives treatment¹

It is a summary of the adjustment set with an interesting property:

Assuming that X is an adjustment set, $e(X)$ is also one

¹Rosenbaum & Rubin, *The central role of the propensity score in observational studies of causal effects*, 1983

Inverse propensity score weighting (IPW)

Proof of identifiability. By definition, we have that

$$\mathbb{E}[Y(t)] = \sum_{x,y} p(X = x)p(Y(t) = y \mid X = x)y = (*)$$

|
Overall population

Inverse propensity score weighting (IPW)

Proof of identifiability. By definition, we have that

$$\mathbb{E}[Y(t)] = \sum_{x,y} p(X = x)p(Y(t) = y | X = x)y = (*)$$

Multiplying and dividing by $p(X = x | T = t)$, we get

$$(*) = \sum_{x,y} \underbrace{p(X = x | T = t)}_{\text{Treatment group } t} \frac{p(X = x)}{p(X = x | T = t)} \underbrace{p(Y(t) = y | X = x)}_{\text{Potential outcome}} y$$

Inverse propensity score weighting (IPW)

By **consistency, overlap, conditional exchangeability, Bayes rule,**

$$\begin{aligned}
 (*) &= \sum_{x,y} p(X = x \mid T = t) \frac{p(X = x)}{p(X = x \mid T = t)} \underbrace{p(Y = y \mid X = x, T = t)}_{\text{Observational outcome}} y \\
 &= \mathbb{E}_{X,Y} \left[\underbrace{\frac{p(T = t)}{p(T = t \mid X = x)}}_{> 0 \text{ due to overlap}} Y \mid T = t \right] \quad \square \quad \text{Weighted average}
 \end{aligned}$$

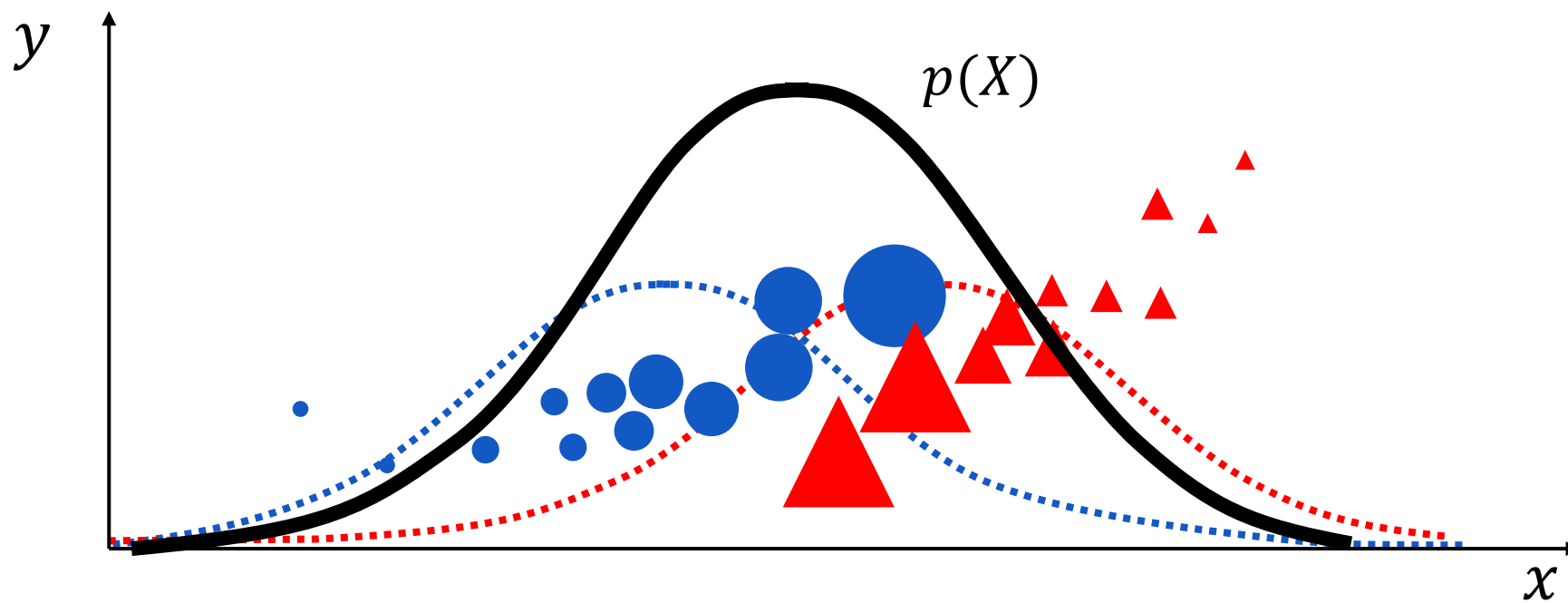
$\Rightarrow \mathbb{E}[Y(t)]$ can be identified by Inverse Propensity Weighting (IPW)

Inverse-Propensity Weighting Adjustment

1. Identify a valid adjustment set X
2. Collect data $(x_1, t_1, y_1), \dots, (x_n, t_n, y_n)$
3. Fit model $\hat{e}(x) \approx p(T = 1 \mid X = x)$ of the propensity score
4. Estimate $\hat{\tau} = \frac{1}{n} \sum_{i:t_i=1} \frac{y_i}{\hat{e}(x_i)} - \frac{1}{n} \sum_{i:t_i=0} \frac{y_i}{1-\hat{e}(x_i)}$
5. Return $\hat{\tau}$

IPW example

IPW emphasizes points to look like they came from $p(X)$



Demo: Causal effects of studies

IncomeSim

Simulator of causal effects of **studies** on **future income**

Based on the well-known Adult dataset from UCI

On the repository: <https://github.com/Healthy-AI/IncomeSim/>

You can find a link to a colab notebook there!

Today's task

We will work with the question

“What is the causal effect of starting a year of **studies** at on **income** after 10 years?”

We will work with samples generated by the simulator

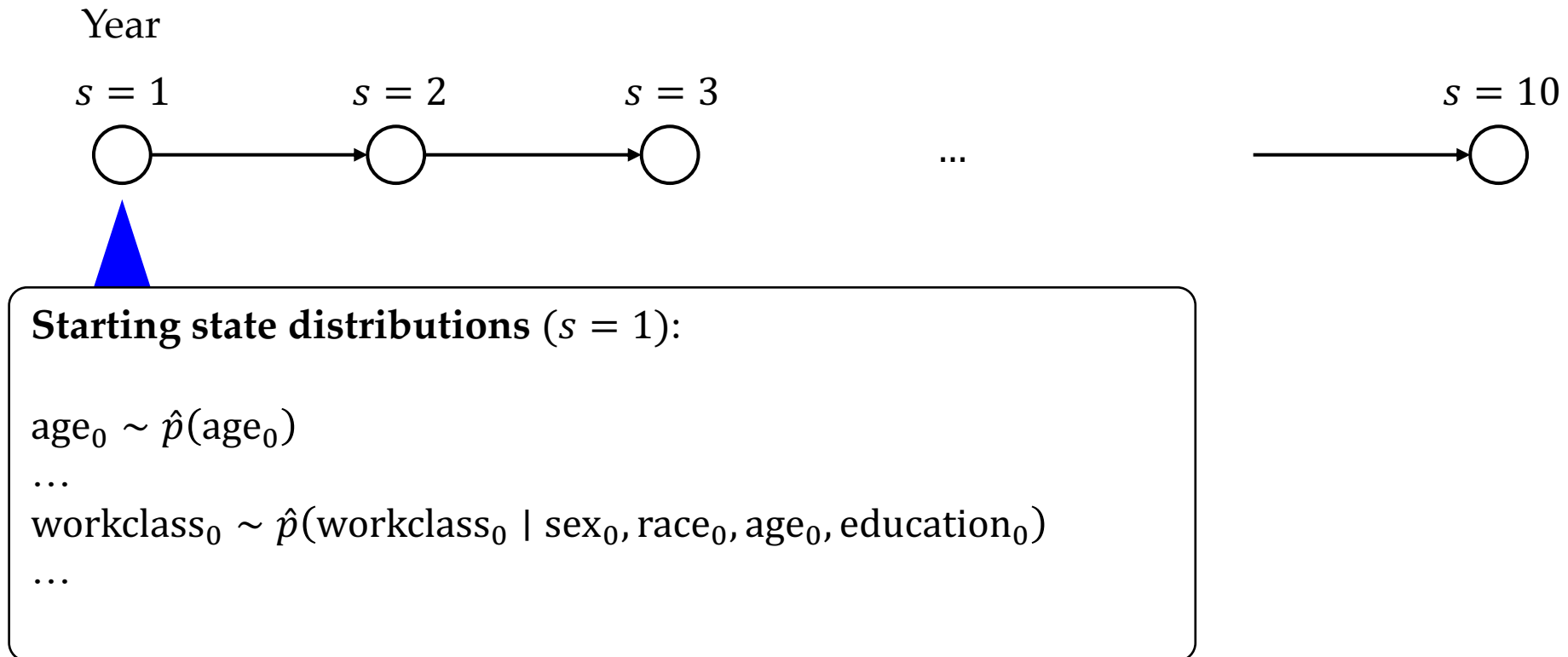
[Let's have a look at the data]

The simulator takes the variables from Adult and fits an autoregressive model of its variables in a particular order

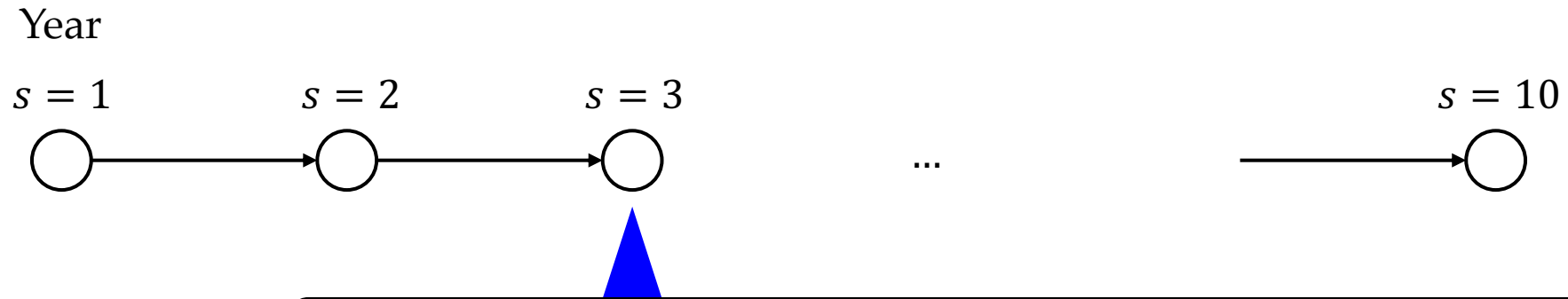
Example: 'workclass' a function of 'age', 'education', 'race', 'sex'

A variable 'training' is added by hand to capture the effects of studies on the other variables (through the 'education' marker)

Markov model



Markov model



Transition distributions ($s > 0$):

$$\text{age}_s \sim p(\text{age}_s \mid \text{age}_{s-1})$$

...

$$\text{workclass}_s \sim p(\text{workclass}_s \mid \text{workclass}_{s-1}, \text{sex}_s, \text{race}_s, \text{age}_s, \text{education}_s)$$

...

Causal effect of studies

The data is a typical cross-sectional dataset:

- Some context variables X
 - A treatment variable T
 - An outcome variable Y
- } Values from simulator at $s = 1$
- } Value from simulator at $s = 10$

We could attempt to estimate the average treatment effect

$$\text{ATE} = \mathbb{E}[Y(1) - Y(0)]$$

The meaning of ATE?

In our case, the meaning of the ATE is

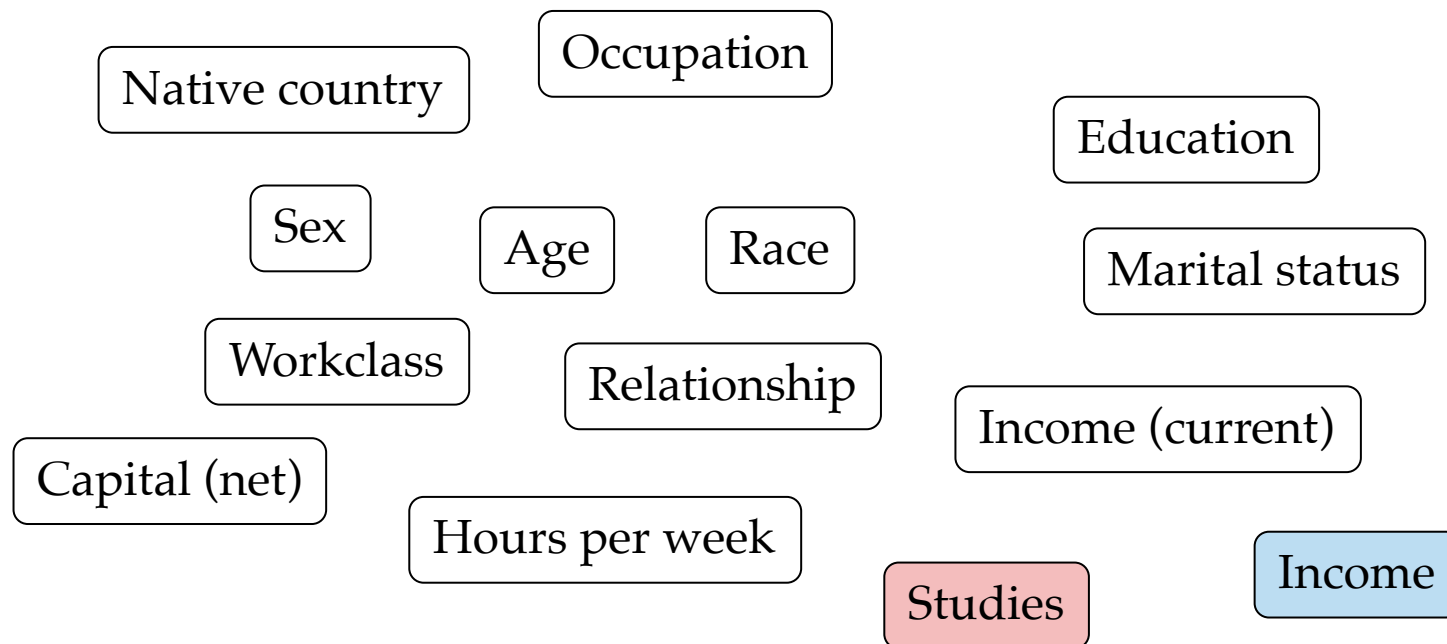
“If we made the population study according to $T = 1$ for a year and then did what they wanted for 9 years, how much higher/lower would their yearly income be compared to if we made them study according to $T = 0$?”

So what does $T = 1$ and $T = 0$ mean?

Recap: Steps to estimate ATE

1. Identify causal parameter *Average treatment effect*
2. Pick an identification strategy *Backdoor adjustment*
3. Identify a statistical estimand *e.g., conditional expectation*
4. Execute an estimation strategy *e.g., random forest regression*

What is the causal graph, the SCM?

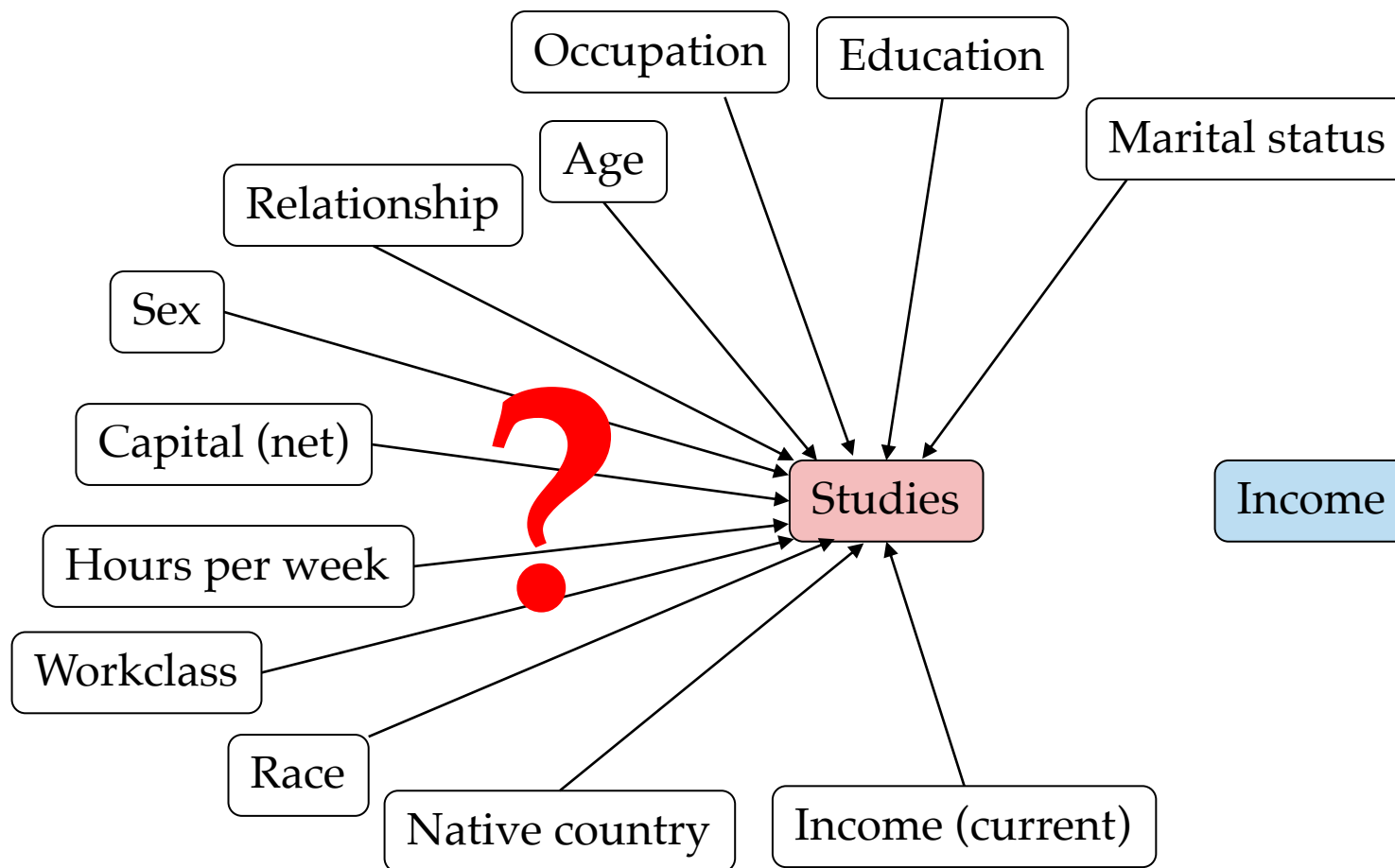


Recall: Parent adjustment

If we know **all direct causes** of the treatment (studies), these satisfy the backdoor criterion

⇒ They are an adjustment set

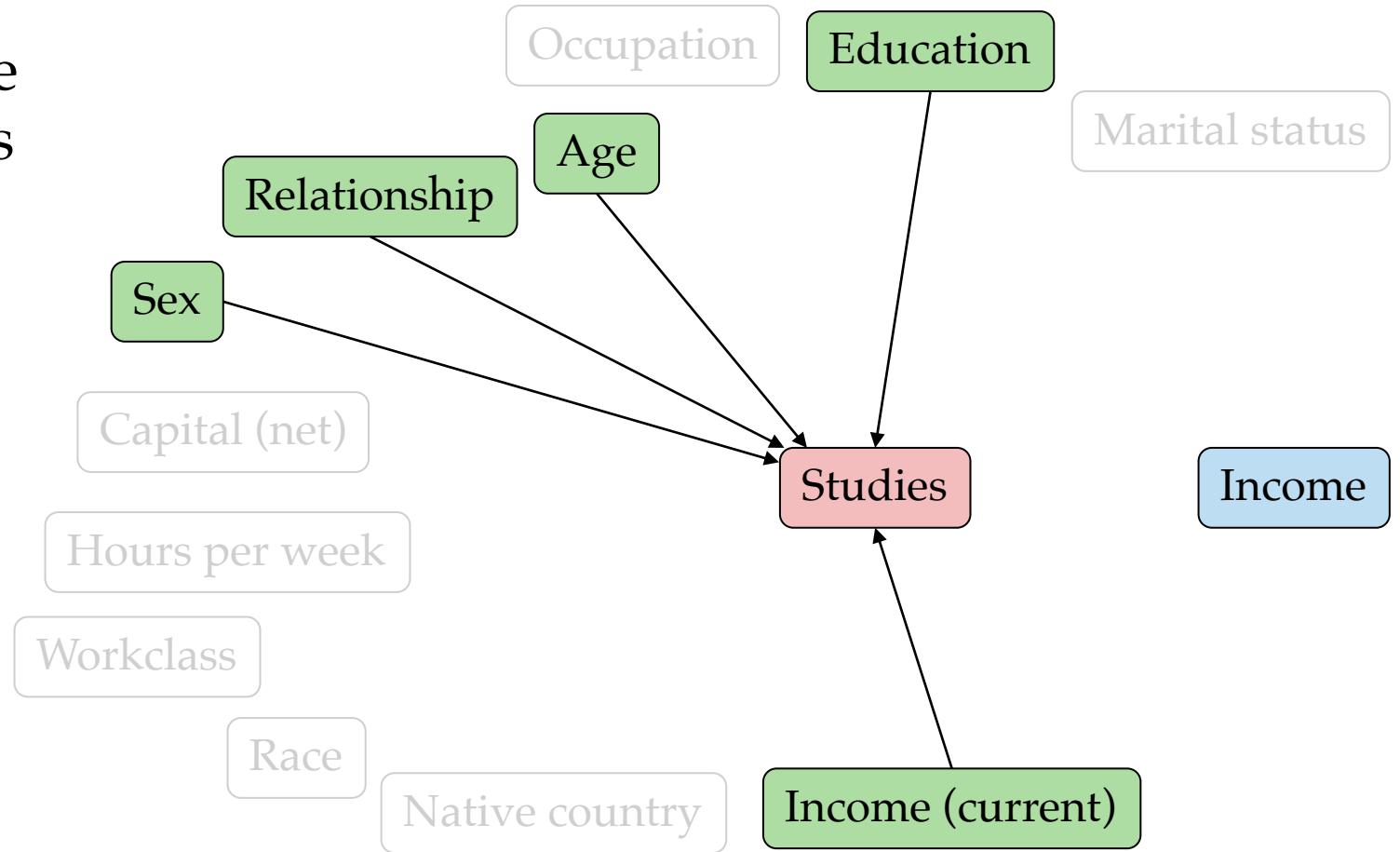
We don't need the whole graph!



Parent adjustment

Let's assume that these are *all* the direct causes

- 'Age',
 - 'Sex',
 - 'Relationship'
 - 'Education'
 - 'Income (current)'
- = adjustment set A



[OK, let's do it!]

Reflections

Where are we now?

We have derived and tested two techniques for causal estimation

- Regression adjustment
- Propensity adjustment

by identifying adjustment sets which satisfy assumptions:
conditional exchangeability, overlap and consistency

Advanced methods

There are **many** more methods for estimating ATE / CATE!

Many of these combine propensity / regression approaches and are “doubly robust”. This can also improve sample efficiency¹

Many neural network architectures^{2,3}! [This is where I started...]

¹See e.g., Nie & Wager, *Biometrika*, 2021 who introduced the “R-learner”, ²Johansson et al., *ICML*, 2016,

³<https://github.com/AliciaCurth/CATENets>

Many stones left unturned

Knowing *all* the direct causes of treatment *and* being able to measure them is often infeasible

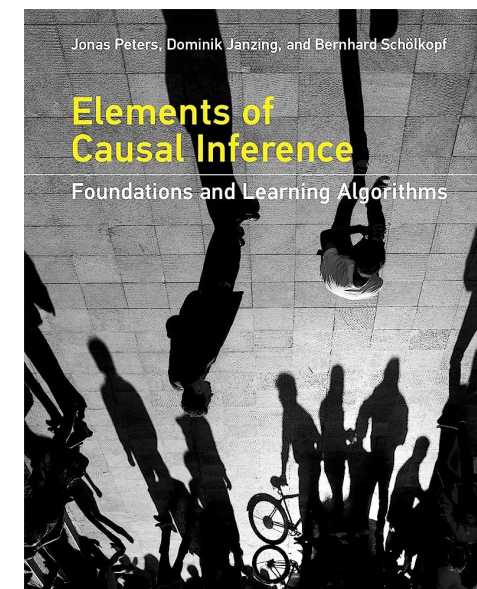
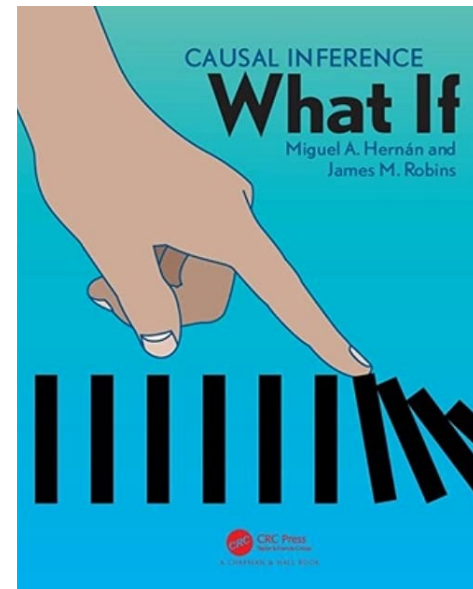
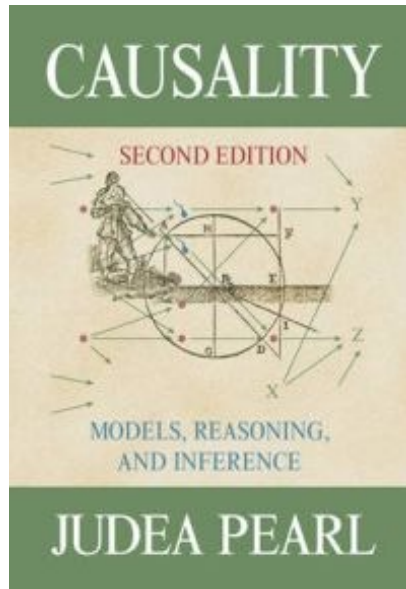
If we leave out some, there may be **unobserved confounders**

Our primary options are:

1. Look for other criteria for identifiability (e.g., backdoor criterion)
2. Aim only for partial identifiability (e.g., using sensitivity analysis)

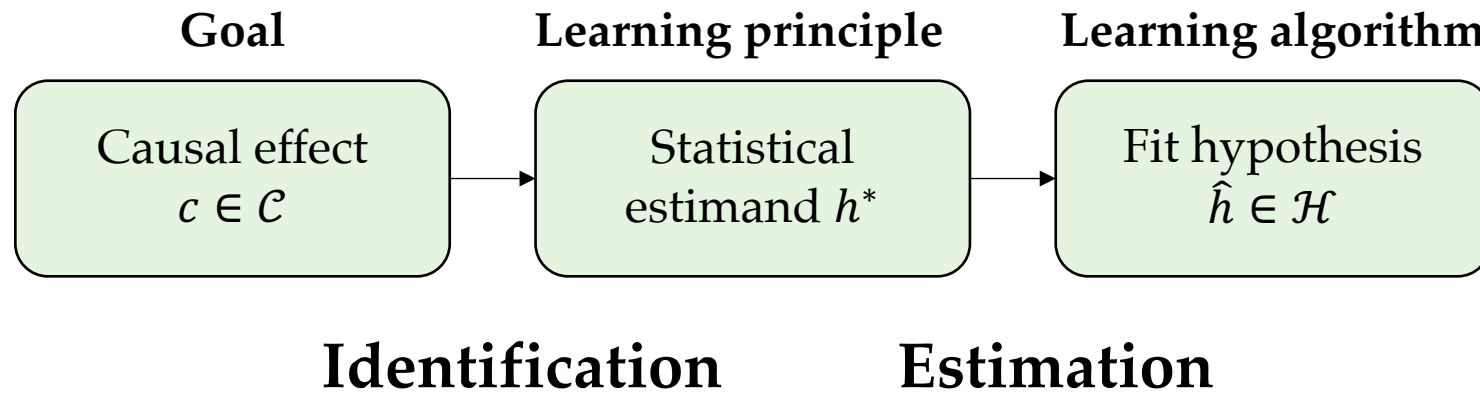
Going further

Causal machine learning is relatively young, but there is already a rich related literature—most of which was not covered today!



If you know that you will use your ML model to make decisions, make use of this fact!

Causal analysis is used to pick the right learning goal



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