Methods for Causal Inference
Lecture 4

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Notations and conventions

- Variable to be manipulated: **treatment (T)**, e.g. drug

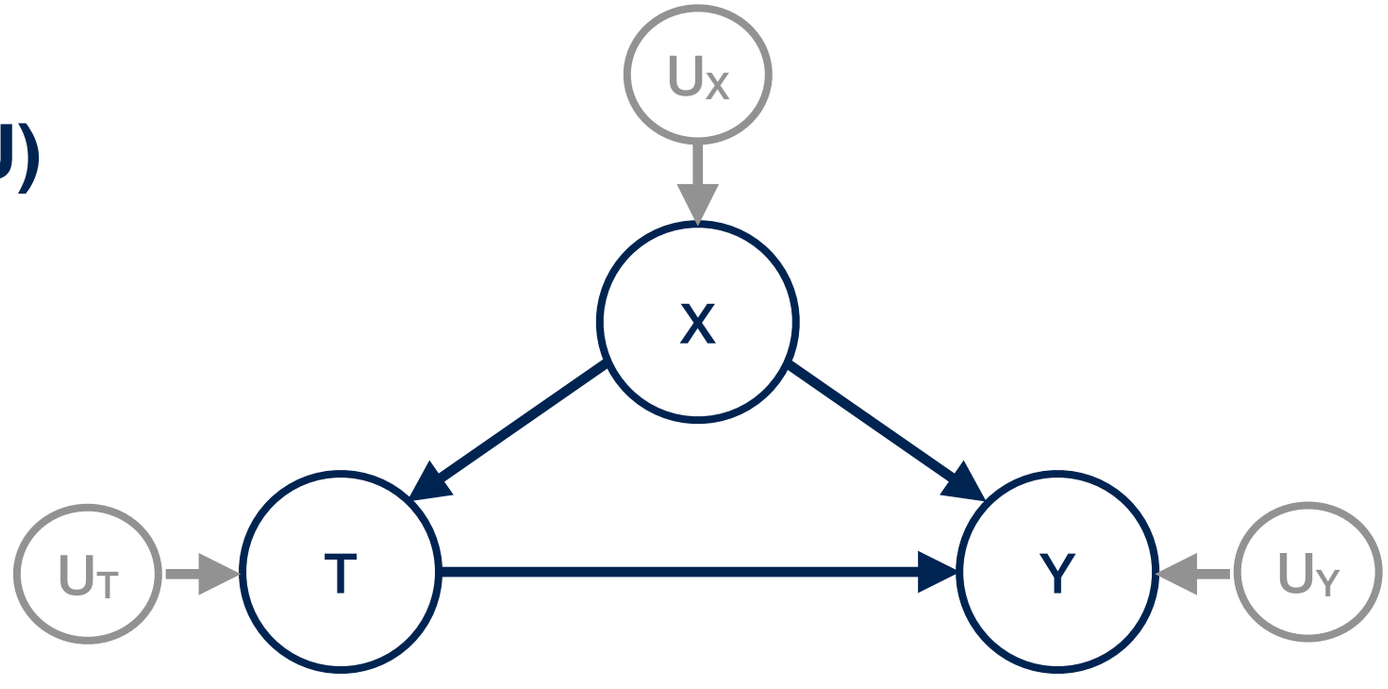
- Variable we observe as response: **outcome (Y)**, e.g. success/ failure of drug

- Other observable variables that can affect treatment and outcome causally and we wish to correct for: **confounders (X)**, e.g. age, gender, …

- Unobservable confounder **(U)**

For simplicity drop U_i's from graphs <u>if</u>:

$$U_T \perp\!\!\!\perp U_X \perp\!\!\!\perp U_Y$$



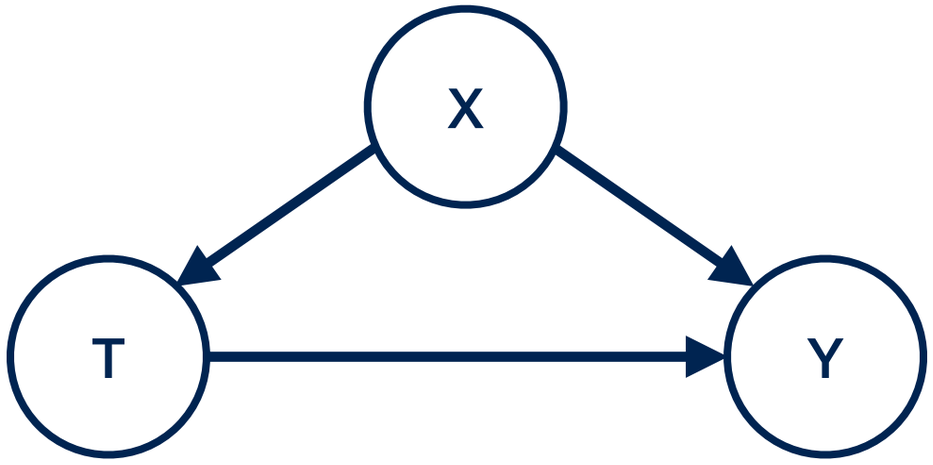
Two main Frameworks for causal estimation/discovery

- **Potential outcomes (Rubin):**

  - Requires a given treatment-outcome pair (known directionality)
  - Mainly applies to causal estimation (learning effects)
  - More familiar to biologists

- **Structural causal models (Pearl):**

  - Causal graph
  - Structural equations
  - Algorithmic: Causal Discovery



$$x = f_x(\epsilon_x),\ t = f_t(x, \epsilon_t),\ y = f_y(x, t, \epsilon_y)$$

Extend the language of probability theory: do-calculus

Assumption: Independent noise terms: $\epsilon_x \perp\!\!\!\perp \epsilon_t \perp\!\!\!\perp \epsilon_y$

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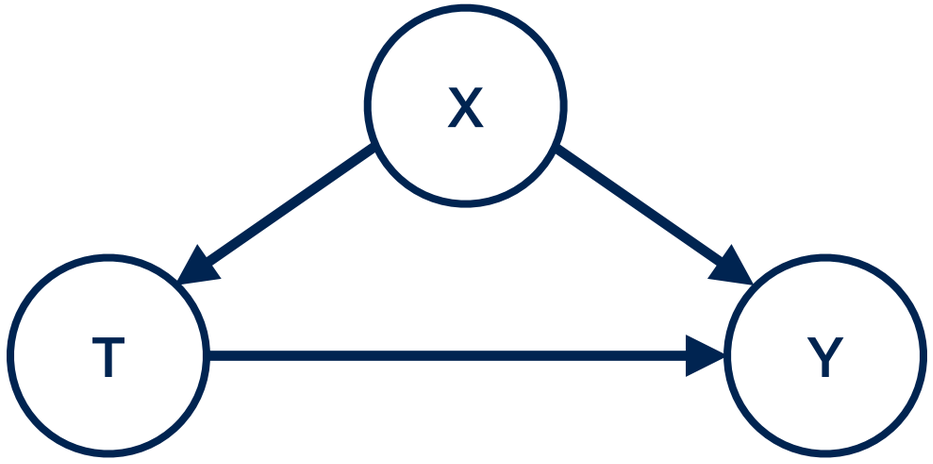

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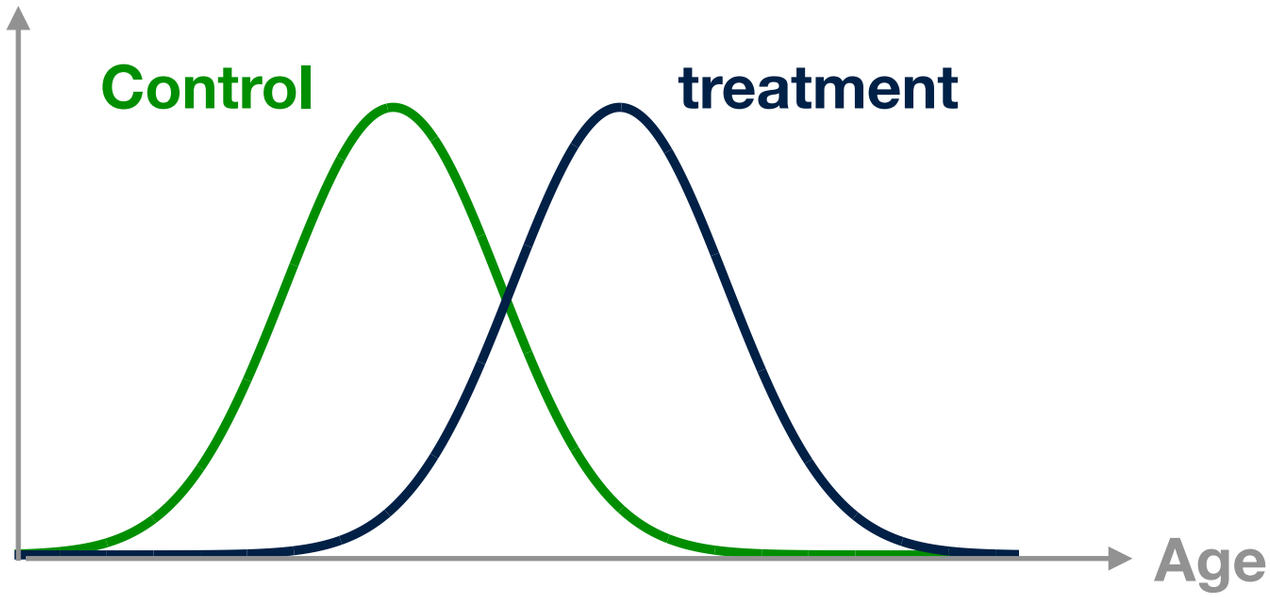
Recall: **Observational data,** what goes wrong?

$$p(x|t=1) \neq p(x|t=0)$$



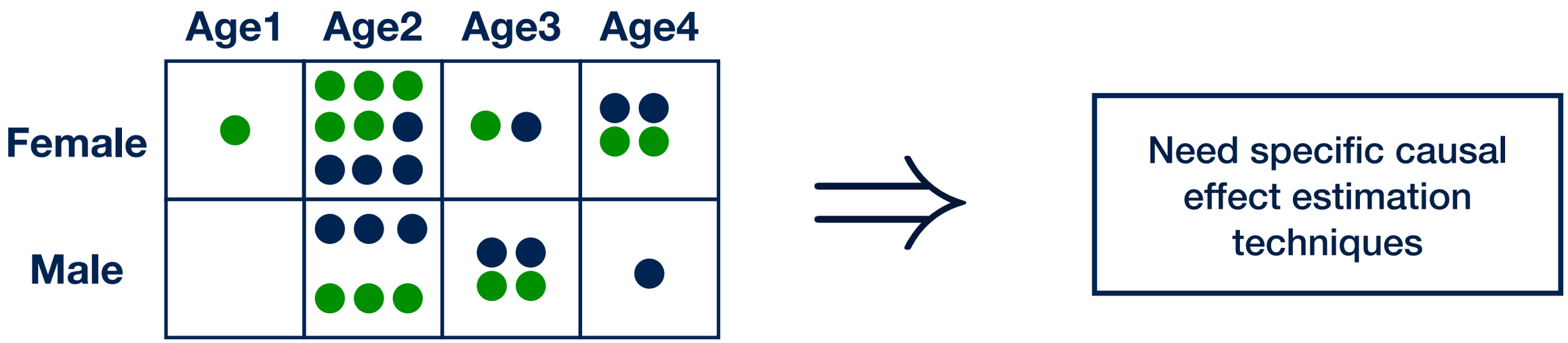
$$\left(\int y_1(x) p(x|t=1) dx \; - \int y_0(x) p(x|t=0) dx \right) \neq \int \big(y_1(x) - y_0(x) \big) p(x) dx$$

Observational data: Stratification

- Measure outcome (success/failure), **within** each of the young/old groups **separately**
- Take weighted average by the probability of being young/old

$$\mathbb{E}(\text{Healed}|t=1) = \mathbb{E}(\text{Healed}|t=1,\text{young})p(\text{young}) + \mathbb{E}(\text{Healed}|t=1,\text{old})p(\text{old})$$

- Disadvantages:
  - All possible confounders need to be observed
  - Assumes overlap between the two distributions (if there is no overlap, sample is not representative, e.g. performing the experiment only for old people)
  - Bad estimates as confounder dimensionality increases



Potential Outcomes Framework (Rubin-Neyman)

Definition: Given treatment, t, and outcome, y, the **potential outcome** of instance/individual (i) is denoted by $y_t^{(i)}$ is the value y *would have* taken if individual (i) had been under treatment t.

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$t^{(i)}$ is the observed treatment applied to individual (i), 0 or 1

Observed outcomes: $y_0^{(i)}$ **OR** $y_1^{(i)}$ depend on treatment (**fundamental problem of causal inference**):

$$y_{obs}^{(i)} = t^{(i)} y_1^{(i)} + (1 - t^{(i)}) y_0^{(i)} = \begin{cases} y_0^{(i)} & \text{if } t^{(i)} = 0 \\ y_1^{(i)} & \text{if } t^{(i)} = 1 \end{cases}$$

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Counterfactual (missing) outcome "what would have happened if …"

$$y_{CF}^{(i)} = (1 - t^{(i)}) y_1^{(i)} + t^{(i)} y_0^{(i)} = \begin{cases} y_1^{(i)} & \text{if } t^{(i)} = 0 \\ y_0^{(i)} & \text{if } t^{(i)} = 1 \end{cases}$$

Potential Outcomes Framework (Rubin-Neyman)

Inverting previous relations, equivalently:

$$y_0^{(i)} = \begin{cases} y_{CF}^{(i)} & \text{if } \; t^{(i)} = 1 \\ y_{obs}^{(i)} & \text{if } \; t^{(i)} = 0 \end{cases}$$

$$y_1^{(i)} = \begin{cases} y_{CF}^{(i)} & \text{if } \; t^{(i)} = 0 \\ y_{obs}^{(i)} & \text{if } \; t^{(i)} = 1 \end{cases}$$

Knowing the potential outcomes is equivalent to knowing the observed and counterfactual outcomes

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Individual treatment effect (causal): $\tau^{(i)} = y_1^{(i)} - y_0^{(i)}$

Average treatment effect (causal): $\tau = \hat{\mathbb{E}}[\tau^{(i)}] = \hat{\mathbb{E}}[y_1^{(i)} - y_0^{(i)}] = \frac{1}{N} \sum_{i=0}^{N} \left(y_1^{(i)} - y_0^{(i)} \right)$

Example (Missing data interpretation)

	treatment	outcome	Y_0	Y_1	Y_1-Y_0
0	0.0	-10.039205	-10.039205	?	?
1	0.0	-10.671335	-10.671335	?	?
2	1.0	-9.216676	?	-9.216676	?
3	0.0	-6.952074	-6.952074	?	?
4	1.0	-9.842891	?	-9.842891	?
...	...	...	...	...	...
995	0.0	-6.344171	-6.344171	?	?
996	1.0	-9.563686	?	-9.563686	?
997	1.0	-8.414478	?	-8.414478	?
998	0.0	-9.731127	-9.731127	?	?
999	1.0	-8.097447	?	-8.097447	?

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= -1.14

Example (counterfactuals)

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0	0.0	-10.039205	1.0	-8.807301
1	0.0	-10.671335	1.0	-8.687408
2	1.0	-9.216676	0.0	-10.466275
3	0.0	-6.952074	1.0	-6.769770
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Individual treatment effect:

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Estimated as:

$$\frac{1}{N}\sum_{i=0}^{N}\left(y_1^{(i)} - y_0^{(i)}\right)$$

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3	0.0	-6.952074	1.0	-6.769770	0.182305
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1.00 $\neq$ -1.14

Example (individual treatment effect)

	treatment	confounder	outcome	treatment_CF	outcome_CF	Y_1-Y_0
0	0.0	3.935767	-10.039205	1.0	-8.807301	1.231904
1	0.0	3.895803	-10.671335	1.0	-8.687408	1.983927
2	1.0	4.155425	-9.216676	0.0	-10.466275	1.249599
3	0.0	3.256590	-6.952074	1.0	-6.769770	0.182305
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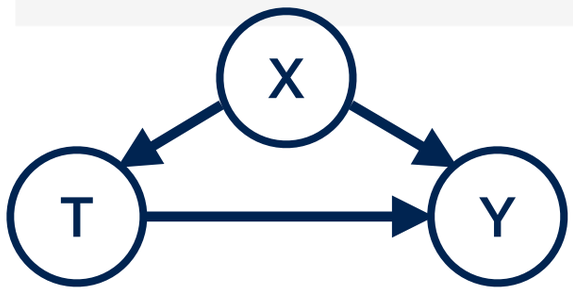

Potential Outcomes: Assumptions

- **SUTVA:** Stable Unit Treatment Value Assumption
  - **Consistency:** Well-defined treatment (no different versions) observed outcome is independent of how the treatment is assigned
  - **No interference**: Different individuals (units) within a population do not influence each other (e.g. does not work in social behavioural studies, care must be taken for time series data when defining the units)

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- **Unconfoundedness (ignorability/exchangeability):** Treatment assignment is random, given confounding features X

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- e.g., restricting to the old group, person A has the same probability of receiving the treatment as person B
- There may be difference in sample size between case and control:
  $p(t = 1|x)$ not necessarily = $p(t = 0|x)$
- However, if we do not restrict to the old group, there is a clear preference: older individuals are more likely to receive the drug
- **No unobserved confounders**
  (see later: unverifiable in observational data)

Unconfoundedness: A graphical representation

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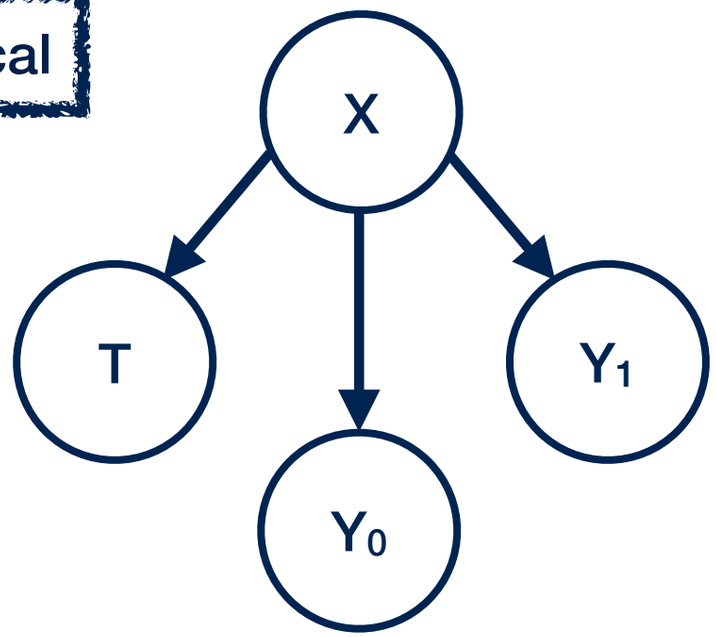
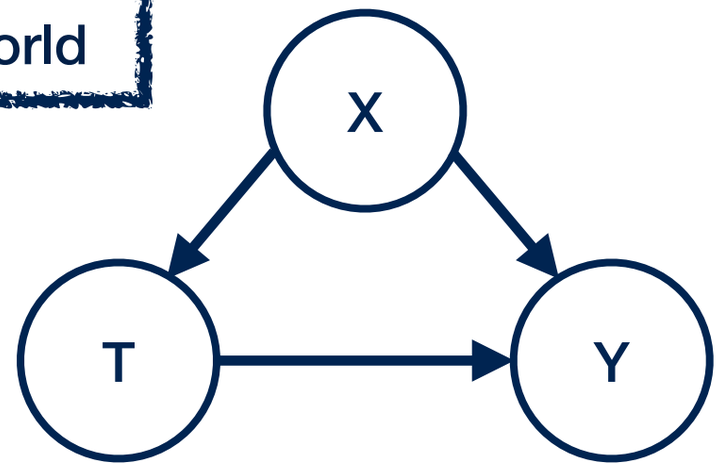
Hypothetical



Real world



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If everyone is prevented from receiving the treatment: Y_0

Then the hypothetical outcomes are entirely determined by the set of features X of the individuals.

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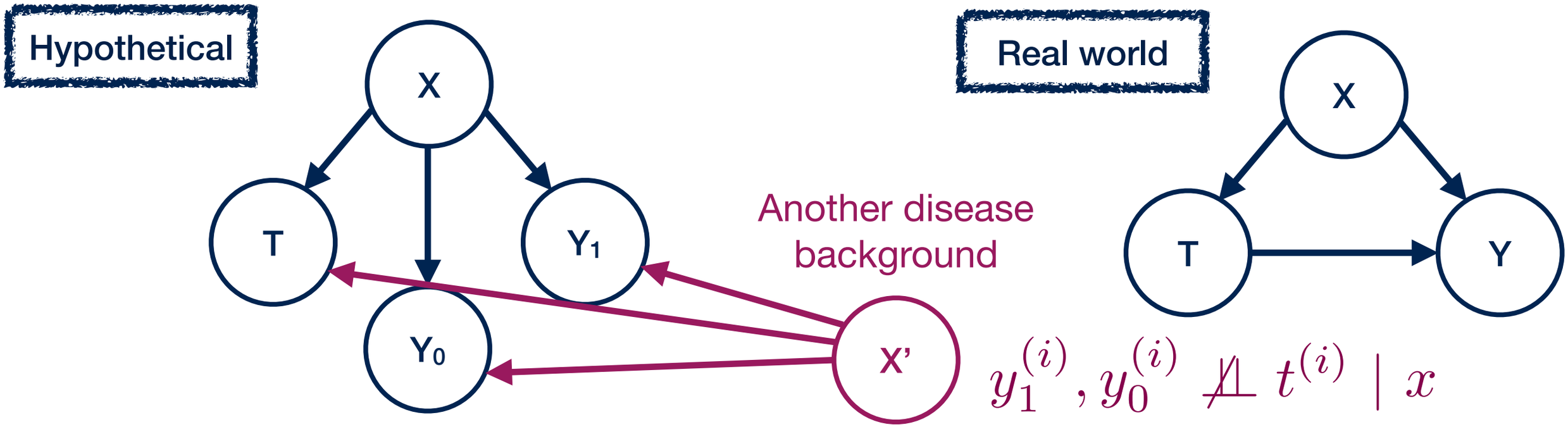

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Positivity

For existing values of covariates in the population, i.e., $P(X = x) > 0$ (binary T)

$$0 < P(T = 1|X = x) < 1$$

Intuitively: If everyone was given the treatment, i.e., there is not control group, we have no idea if/how the outcomes observed are due to the treatment itself (because we have no background to compare it to!)

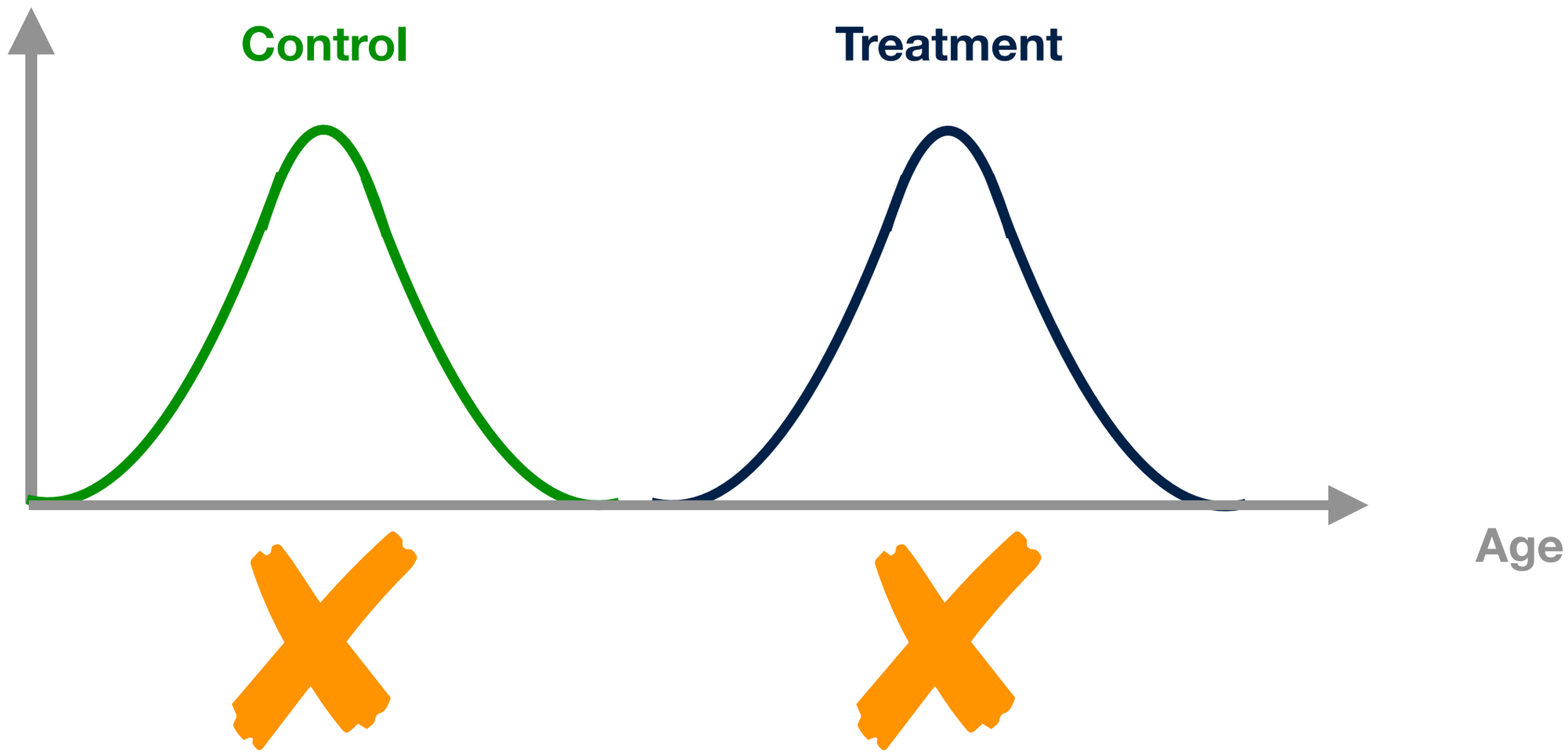
Similarly, when everyone is in the control group: Then we will not have tested the treatment.

Tutorial question: See why this condition is essential (**mathematically**)

Positivity (common support/overlap)

Control: T = 0

Treatment T=1



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Complete violation of positivity

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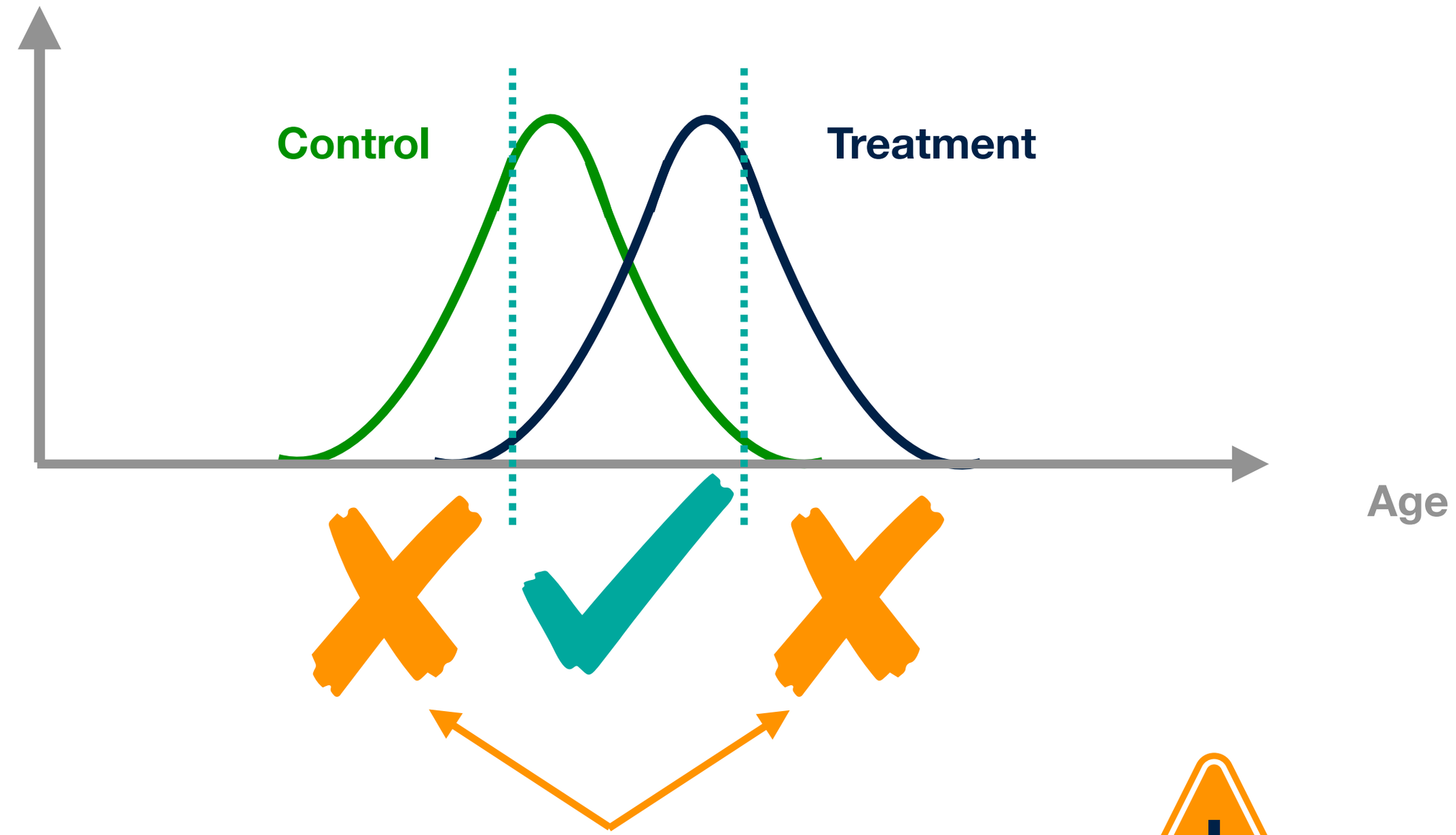

Some violation of positivity

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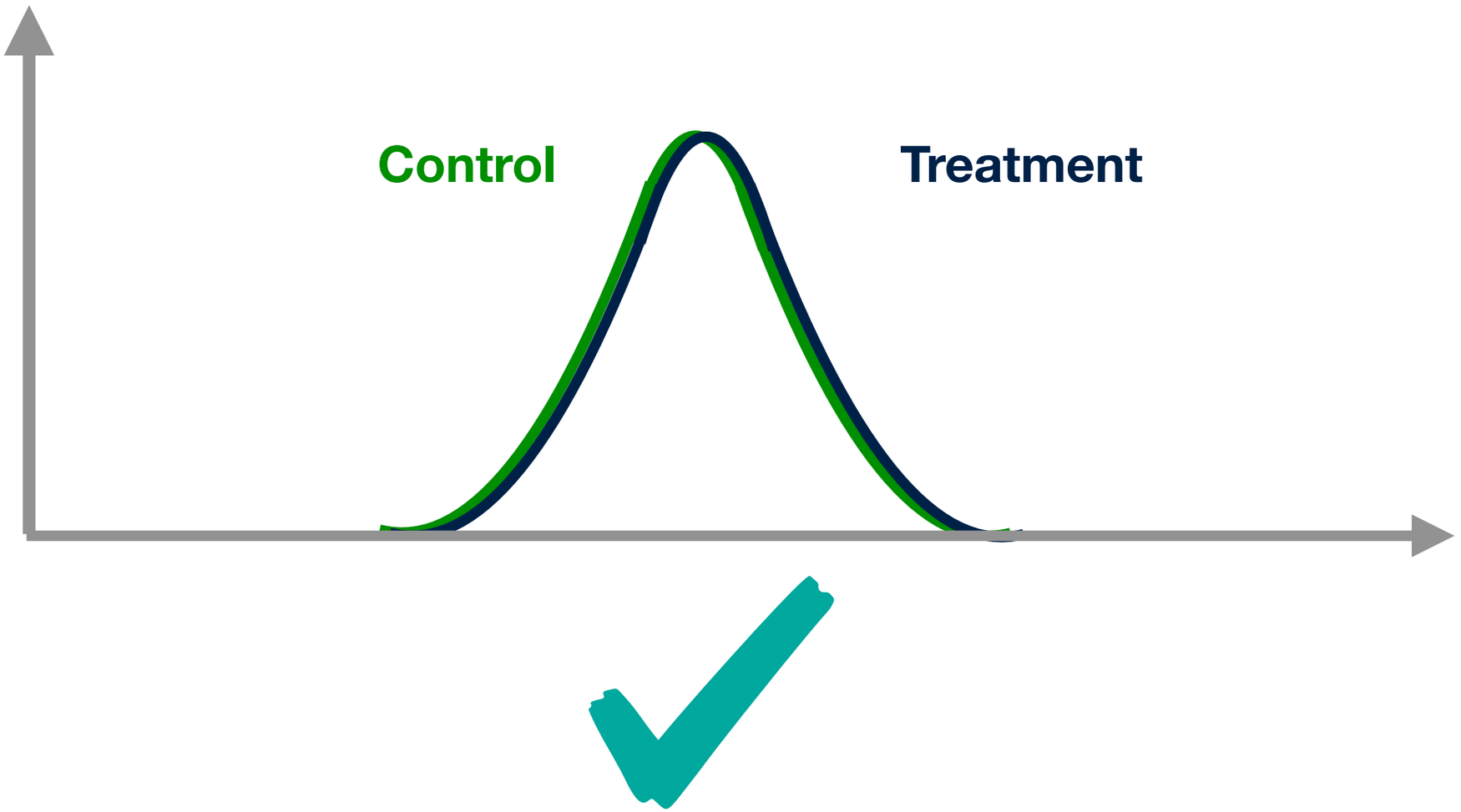

Complete overlap: No positivity violation

Positivity vs unconfoundedness

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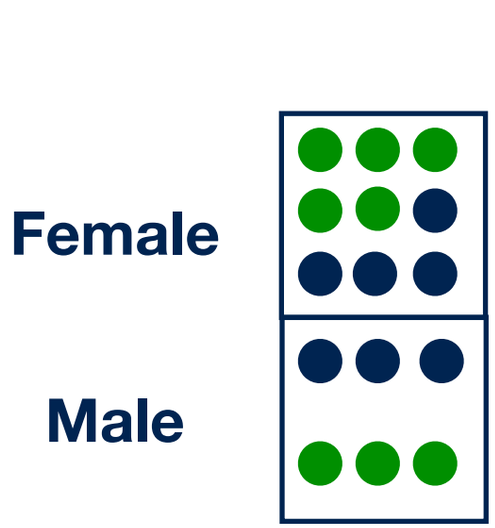
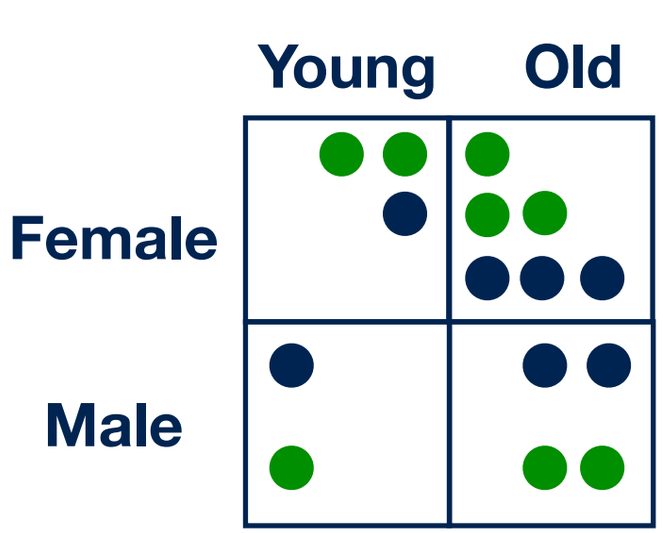
Example:





Easy to check for binary/categorical variable X:

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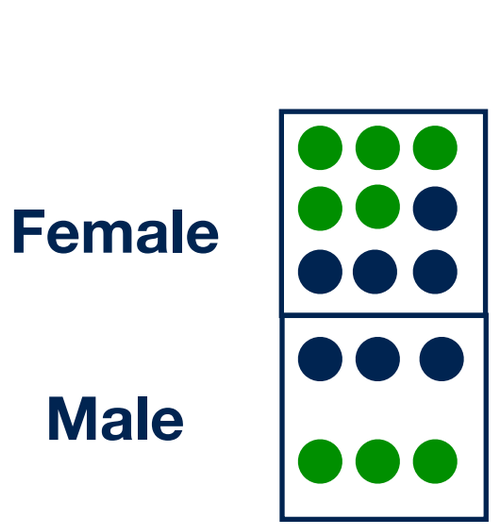
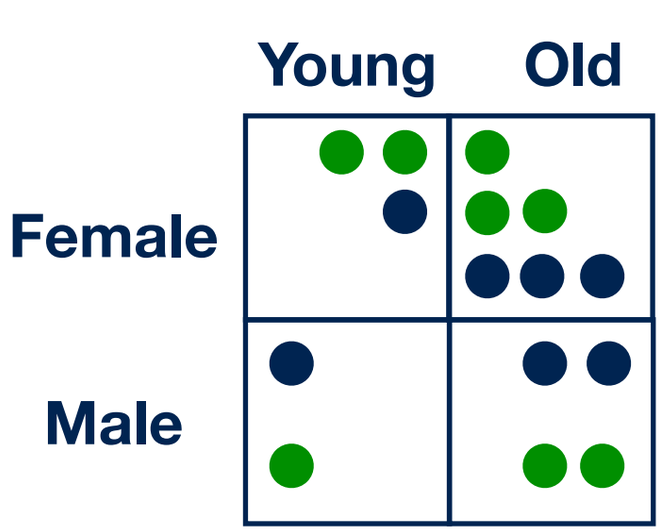
But the more we condition on, the harder it is to satisfy positivity

Example:

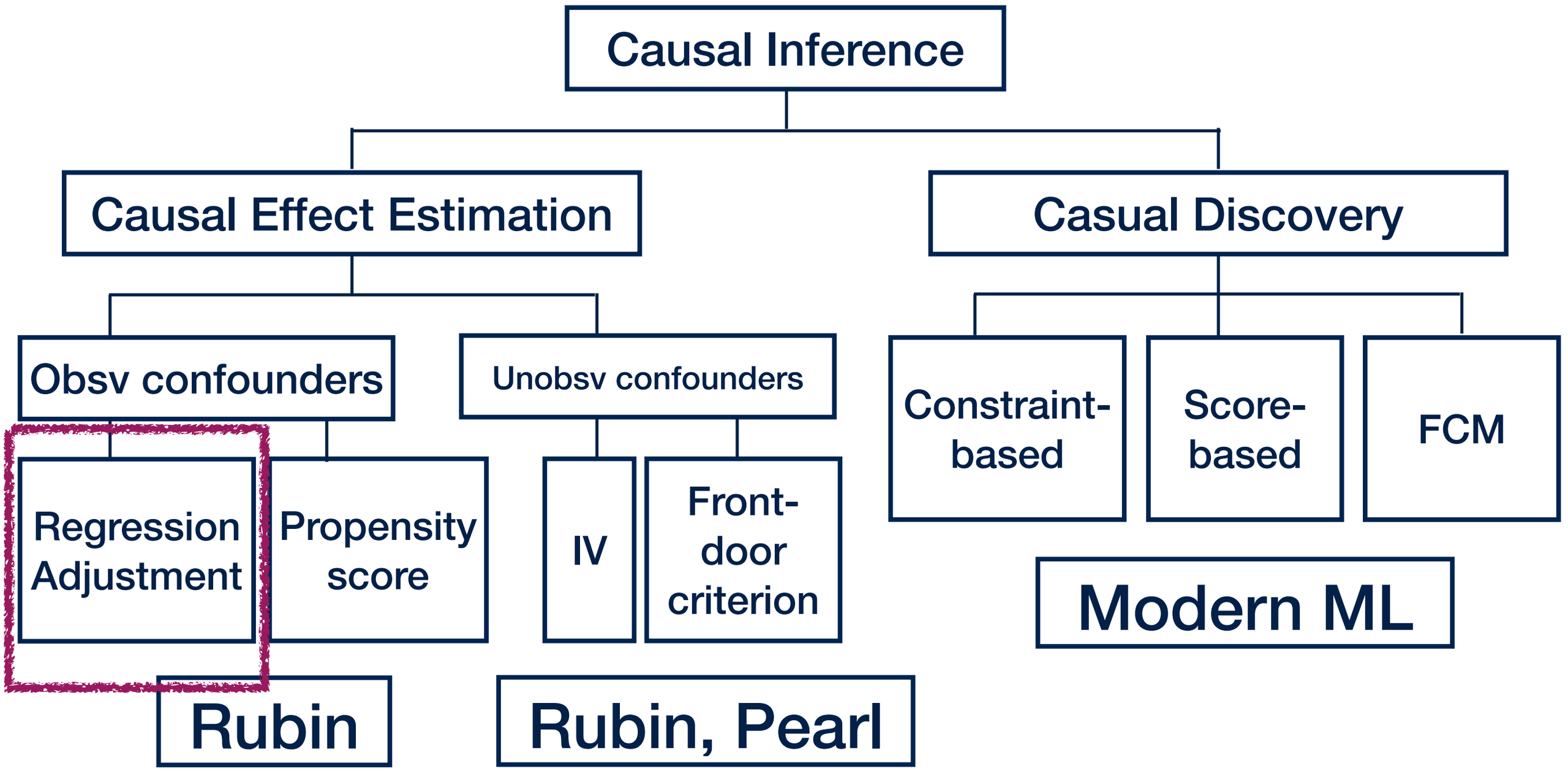




Tutorial question: Discuss the problem of no support, extrapolation and model-misspecification

Overview of the course

- Estimating causal effects
- Randomised trial vs observational data

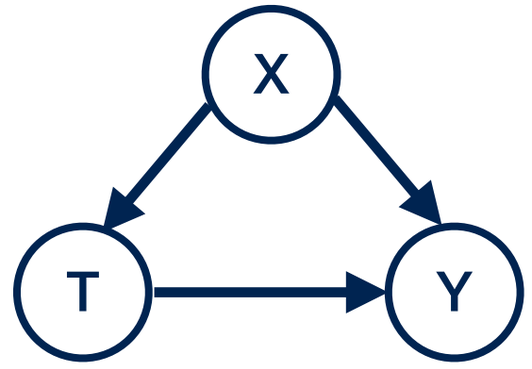


Regression Adjustment

- X is a sufficient set of confounders if conditioning on X, there would be no confounding bias

- For individual (i) there is only one **observed** outcome: $y^{(i)}_{\underline{t}_i}$
- Would like to estimate (infer) **counterfactual**: $\hat{y}^{(i)}_{1-t_i} = \hat{\mathbb{E}}\left[y^{(i)}|1-t_i, x^{(i)}\right]$

- Using a design matrix, fit: $Y = \beta_X X + \beta_T T + \epsilon$



$$T = \begin{pmatrix} \textbf{Ctrl} & \textbf{Drug} \\ 1 & 0 \\ 1 & 0 \\ .. & .. \\ 0 & 1 \\ 0 & 1 \end{pmatrix} \qquad X = \begin{pmatrix} \textbf{Young} & \textbf{Old} \\ 1 & 0 \\ 0 & 1 \\ .. & .. \\ 1 & 0 \\ 0 & 1 \end{pmatrix} \qquad \Rightarrow \qquad \begin{pmatrix} y^{(1)} \\ y^{(2)} \\ .. \\ y^{(N-1)} \\ y^{(N)} \end{pmatrix} = \begin{pmatrix} \beta_{t=0} + \beta_{x=\text{young}} \\ \beta_{t=0} + \beta_{x=\text{old}} \\ .. \\ \beta_{t=1} + \beta_{x=\text{young}} \\ \beta_{t=1} + \beta_{x=\text{old}} \end{pmatrix}$$

- Assumptions: Overlap and additivity

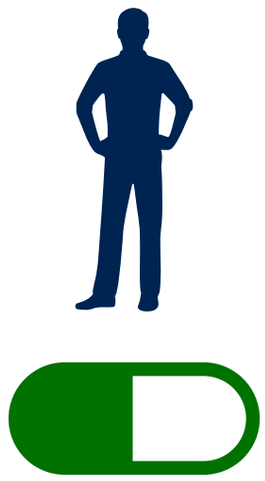
$$\tau = \hat{\mathbb{E}}[\tau^{(i)}] = \hat{\mathbb{E}}[y_1^{(i)} - y_0^{(i)}] = \frac{1}{N}\sum_{i=0}^{N}\left(y_1^{(i)} - y_0^{(i)}\right)$$

Matching

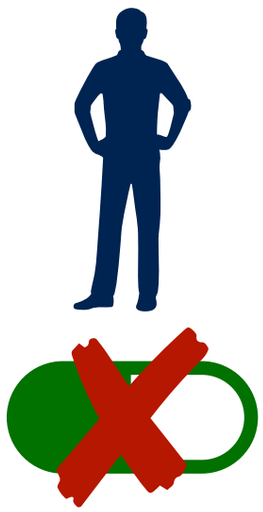
Idea: Create a ‘clone/twin’ for each individual (in terms of X)
i.e. if individual 1 has t = 1, then their ‘clone/twin’ has t = 0.

Blind ourselves to the outcomes, try to get as similar to a randomised experiment as possible (‘correct for confounding’)

Example:



Real world



Hypothetical
(counterfactual)

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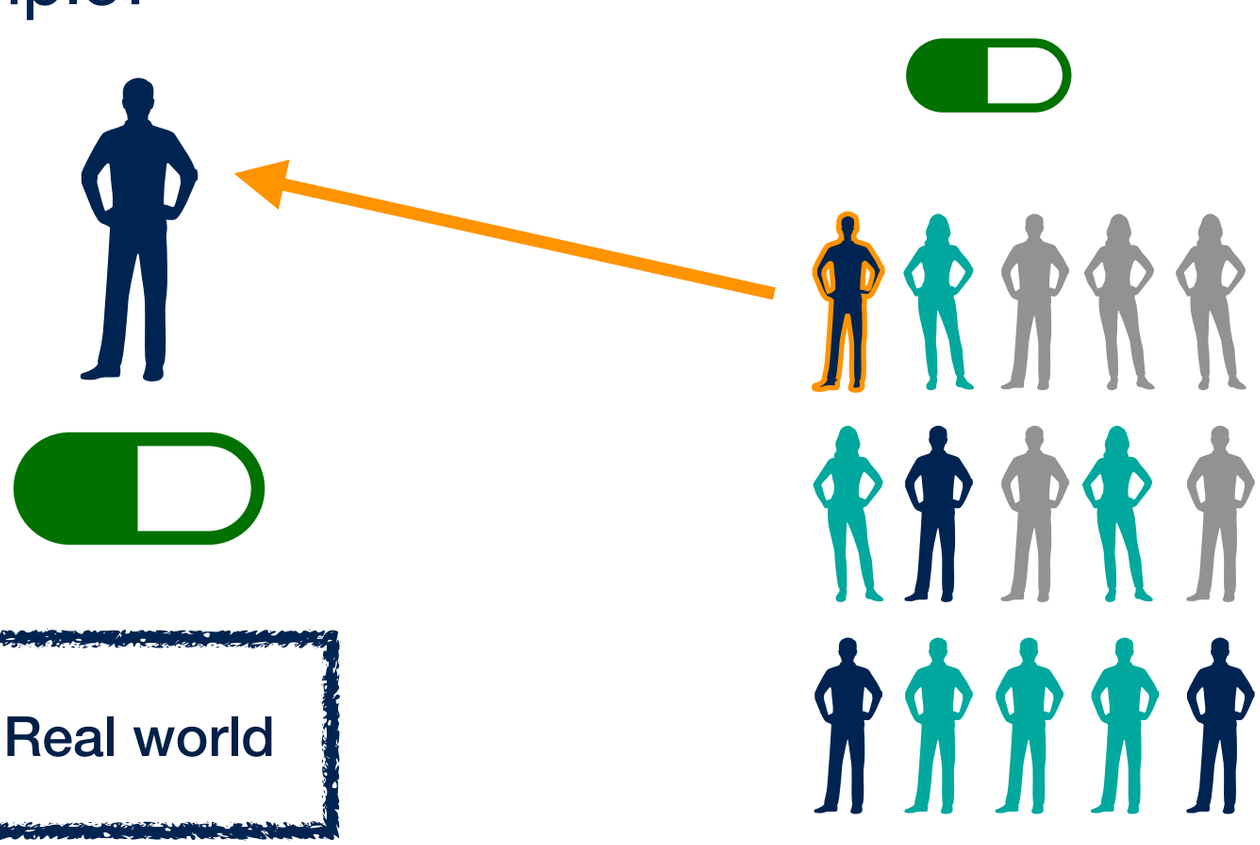

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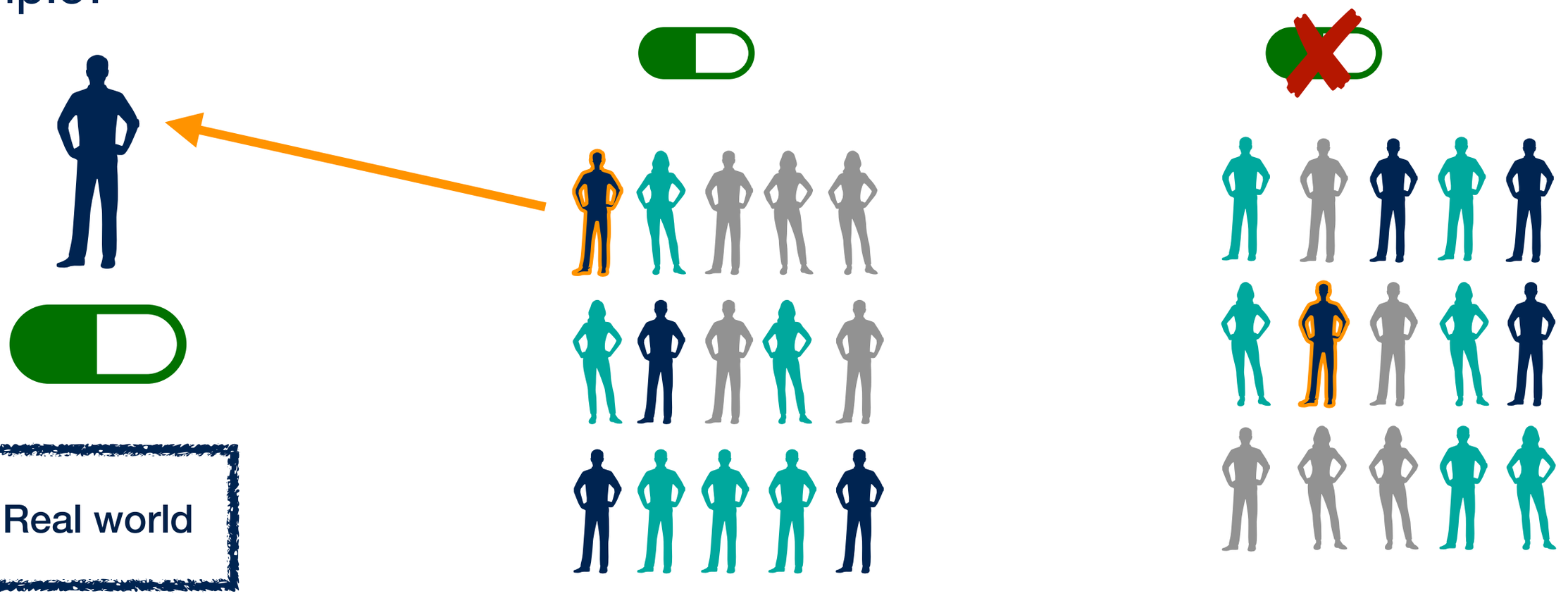

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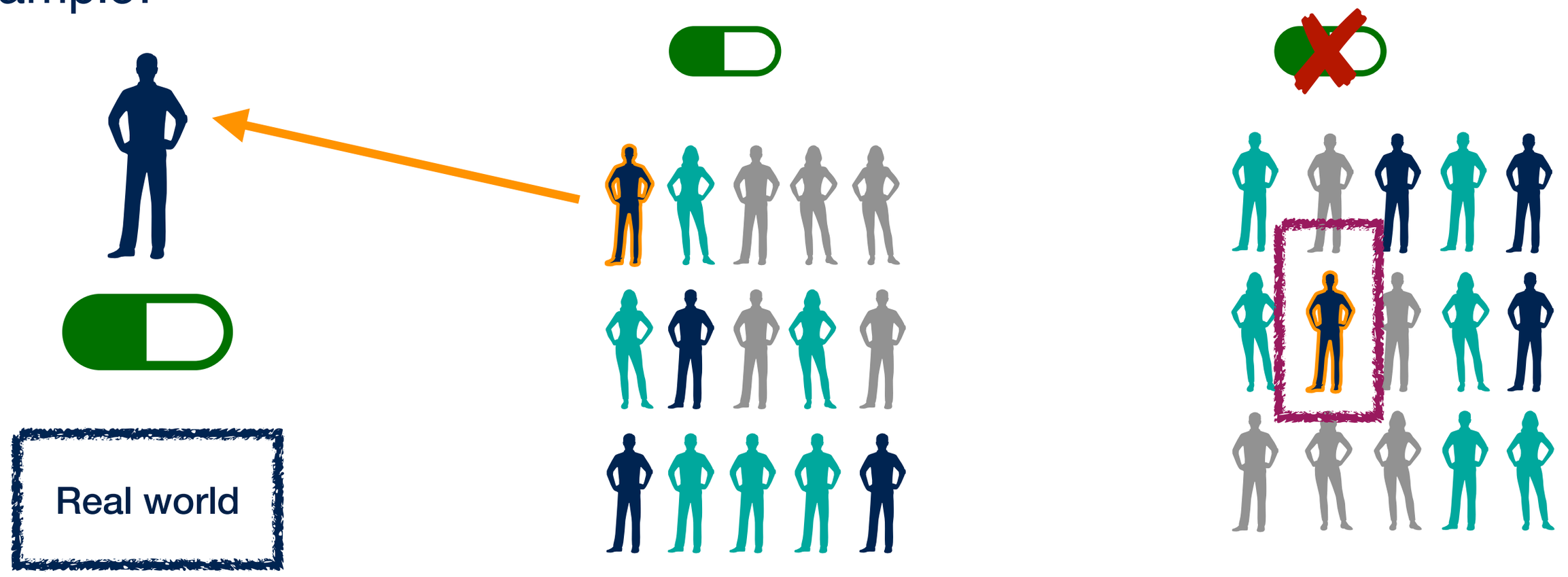


Matching

- Reveals **lack of overlap** in treatment vs control distributions: individuals in the treatment group that have no chance of having an '**equivalent**' in control group, ie, parts of the distribution with: $p(t=1|x)=0,\ p(t=0|x)=0$

- **Mahalanobis distance**: Difference scaled by variance

$$D(x^{(i)}, x^{(j)}) = \sqrt{\left(x^{(i)} - x^{(j)}\right)^T S^{-1} \left(x^{(i)} - x^{(j)}\right)},\ S = \mathrm{Cov}(X)$$

- Issues: Outliers. Use a calliper: maximum acceptable distance, to avoid violating the positivity assumption. But the populations becomes harder to define.

Propensity Score

- In a perfect **randomised** trial: p(t=1|x)=p(t=1)=0.5

- In an **observational study**, p(t=1|x) can be **estimated**, since it involves **observational data** at a t and x (hence identifiable).

- A **balancing score** is any function b(x) such that:

$$x \perp\!\!\!\perp t | b(x)$$

i.e., distribution of confounders is independent of treatment given b(x):

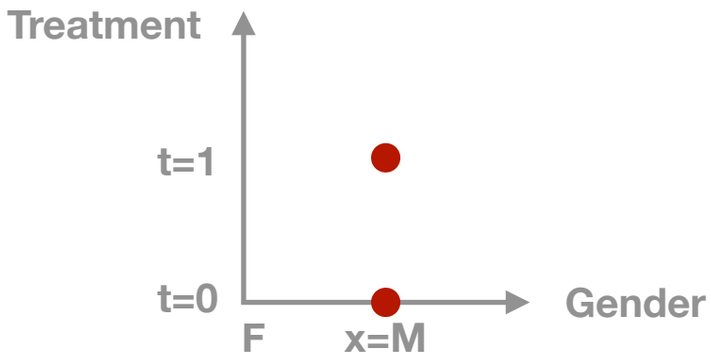
$$\boxed{p(X = x|b(x), t = 1) = p(X = x|b(x), t = 0)}$$

Rosenbaum, Rubin 1983

Propensity Score

- Candidate b(x) = x, trivially satisfies:

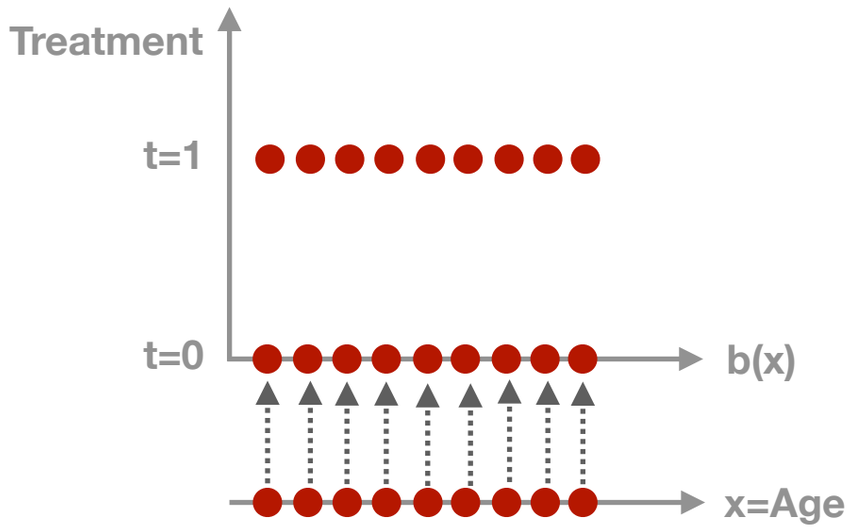
$$p(X = x|x, t = 1) = p(X = x|x, t = 0) = 1$$

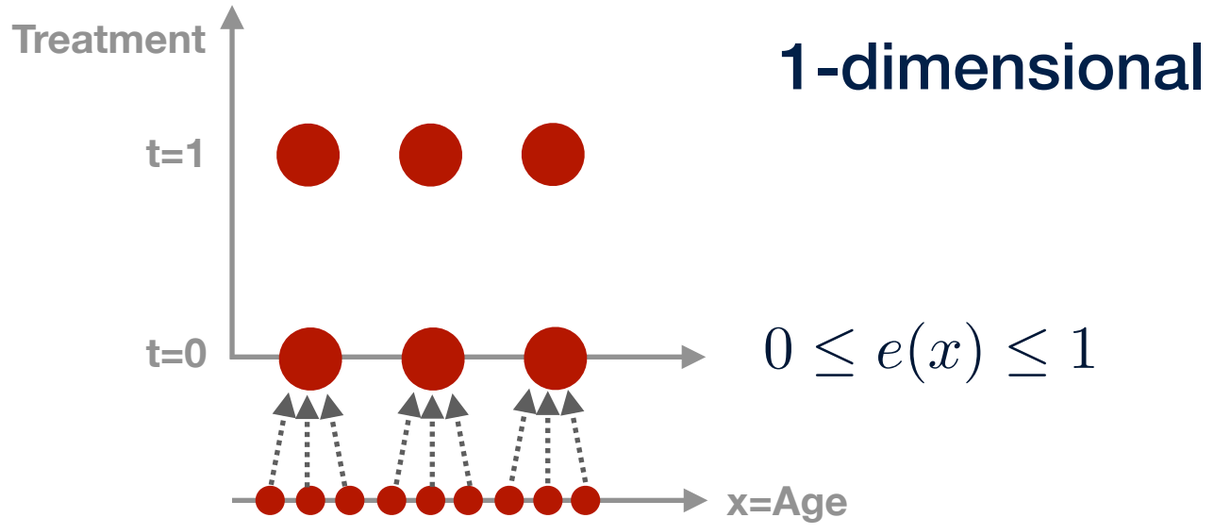


- b(x) = x is the **finest** such function: OK for e.g. binary confounders, but only gives point estimates for (almost) continuous confounders!

- **Propensity score** is the **coarsest** such function (i.e. more data points, leading to better estimates):

$$e(x) = p(t = 1|x)$$





Propensity Score Matching

- Let the distribution of covariates follow an exponential family of distributions ($P_{t^*}(x)$ polynomial of degree k):

$$p(x|t = t^*) = h(X) \exp(P_{t^*}(x)) \ , \ \text{for } t = 0 \text{ or } 1$$

- Estimate propensity score e(x)=p(t=1|x):

$$\log\left(\frac{e(x)}{1-e(x)}\right) = \log\left(\frac{p(t=1|x)}{p(t=0|x)}\right) = \log\left(\frac{p(x|t=1)p(t=1)}{p(x|t=0)p(t=0)}\right) = \log\left(\frac{p(t=1)}{p(t=0)}\right) + P_1(x) - P_0(x)$$

- If we consider k=1, linear exponential family (e.g. Bernoulli),

$$\log\left(\frac{e(x)}{1-e(x)}\right) = wx + w_0 \ \Rightarrow \ e(x) = \frac{1}{1+e^{-wx-w_0}}$$

- Fit parameters by maximising log-likelihood: $LL = \frac{1}{N}\sum_{i=0}^{N} \log p(t^{(i)}|x^{(i)})$

Rosenbaum, Rubin 1983

Propensity Score Matching Algorithms

- Match control and treatment individuals based on their propensity score
- Greedy matching:
  - Randomly order list of control and treated.
  - Start with the first individual from e.g. treated and match to control with the smallest distance (i.e. obtains the **local** minimum)
  - Remove individuals from control and matched treated
  - Move to the next treated subject

Treatment	Control
40	50
65	25

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Total diff: 50

Total diff: 30

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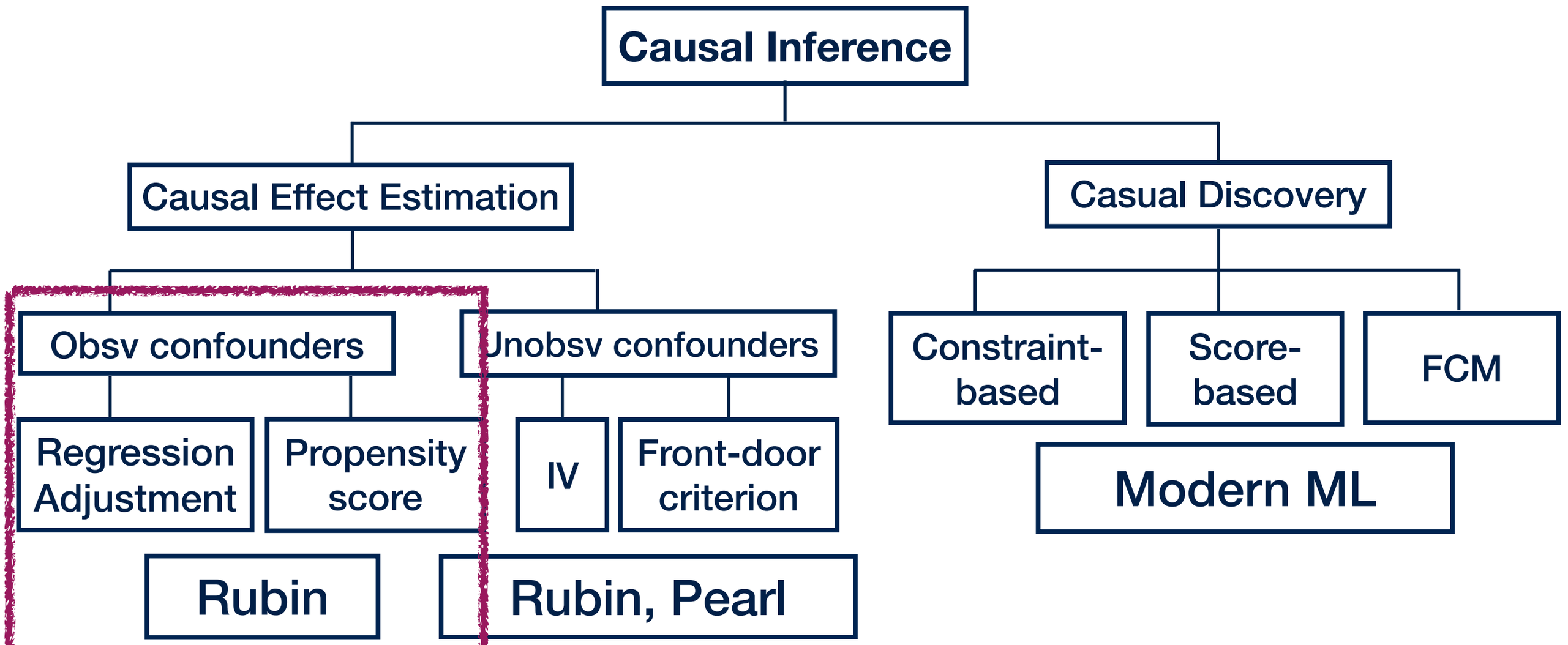
- Optimal matching: Minimises the **global** distance, computationally demanding

- **ATE**: $\tau = \hat{\mathbb{E}}[\tau^{(i)}] = \hat{\mathbb{E}}[y_1^{(i)} - y_0^{(i)}] = \frac{1}{N}\sum_{i=0}^{N}\left(y_1^{(i)} - y_0^{(i)}\right)$

Overview of the course

- **Lecture 1**: Introduction & motivation, why do we care about causality?
- **Lecture 2**: Recap of probability theory, e.g., variables, events, conditional probabilities, independence, law of total probability, Bayes' rule
- **Lecture 3**: Recap of regression, multiple regression, graphs, SCM
- **Lectures 4-20**:



Methods for Causal Inference
Lecture 4

Ava Khamseh
School of Informatics

2021-2022