When Standard Methods Succeed

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when correlation *is* causation

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When you have no *confounders* and there is a linear relationship between the exposure and the outcome, that correlation is a causal relationship

randomized controlled trials
A/B testing

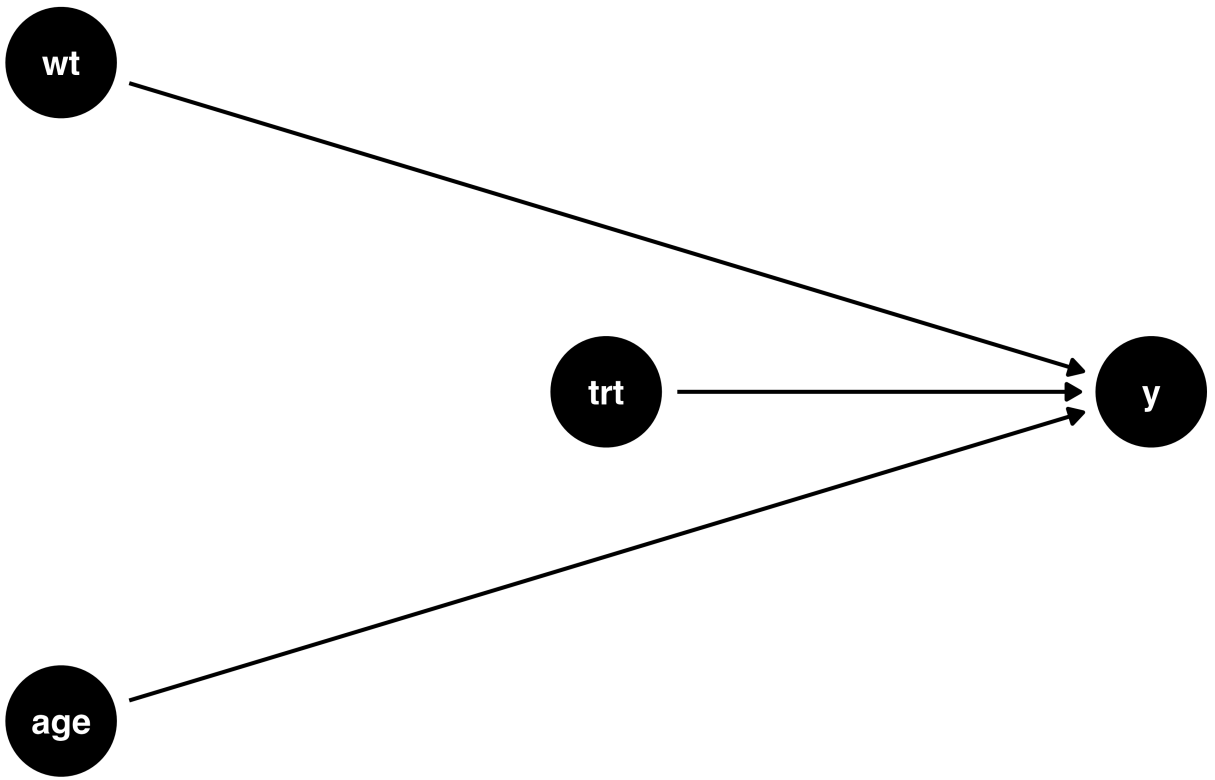
Even in these cases, using the methods you will learn here can help!

1. Adjusting for baseline covariates can make an estimate *more efficient*
2. Propensity score weighting is *more efficient* than direct adjustment
3. Sometimes we are *more comfortable with the functional form of the propensity score* (predicting exposure) than the outcome model

Example

- **simulated** data (100 observations)
- Treatment is **randomly** assigned
- There are **two baseline covariates**: `age` and `weight`

Example



- True average treatment effect: 1

Unadjusted model

```
lm(y ~ treatment, data = data)
```

Characteristic	Beta	SE[1]	95% CI[1]	p-value
treatment	0.93	0.803	-0.66, 2.5	0.2

[1] SE = Standard Error, CI = Confidence Interval

Adjusted model

```
lm(y ~ treatment + weight + ag
```

Characteristic	Beta	SE[1]	95% CI[1]	p-value
treatment	1.0	0.204	0.59, 1.4	<0.001
weight	0.34	0.106	0.13, 0.55	0.002
age	0.20	0.005	0.19, 0.22	<0.001

[1] SE = Standard Error, CI = Confidence Interval

Propensity score adjusted model

Characteristic	Beta	SE	95% CI	p-value
treatment	1	0.202	0.6, 1.4	<0.00

Example

- **simulated** data (10,000 observations)
- Treatment is **randomly** assigned
- There are **two baseline covariates**: `age` and `weight`

Unadjusted model

```
lm(y ~ treatment, data = data)
```

Characteristic	Beta	SE[1]	95% CI[1]	p-value
treatment	0.96	0.083	0.80, 1.1	<0.001

[1] SE = Standard Error, CI = Confidence Interval

Adjusted model

```
lm(y ~ treatment + weight + ag
```

Characteristic	Beta	SE[1]	95% CI[1]	p-value
treatment	1.0	0.020	0.98, 1.1	<0.001
weight	0.20	0.010	0.18, 0.22	<0.001
age	0.20	0.000	0.20, 0.20	<0.001

[1] SE = Standard Error, CI = Confidence Interval

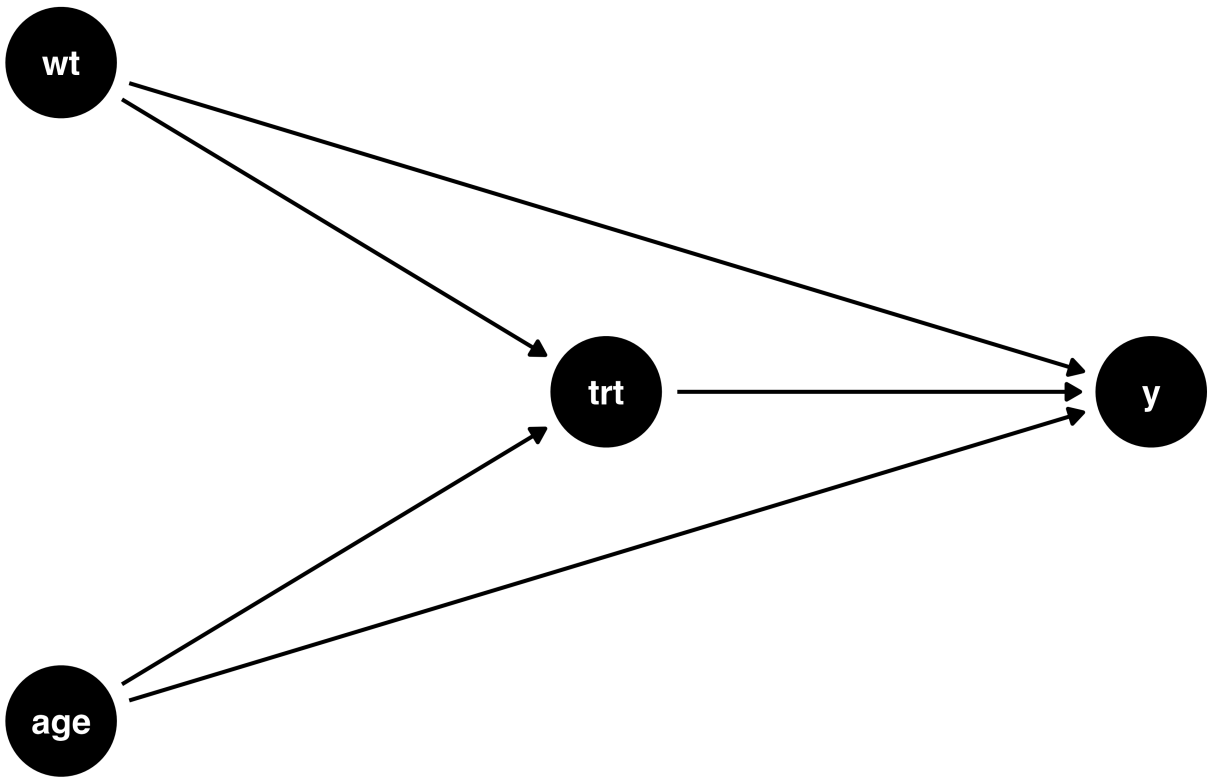
Propensity score adjusted model

Characteristic	Beta	SE	95% CI	p-value
treatment	1	0.02	1, 1.1	<0.001

Example

- **simulated** data (10,000 observations)
- Treatment is **not** randomly assigned
- There are **two baseline confounders**: `age` and `weight`
- The treatment effect is **homogeneous**

Example



- True average treatment effect: 1

Unadjusted model

```
lm(y ~ treatment, data = data)
```

Characteristic	Beta	SE[1]	95% CI[1]	p-value
treatment	1.8	0.085	1.7, 2.0	<0.001

[1] SE = Standard Error, CI = Confidence Interval

Adjusted model

```
lm(y ~ treatment + weight + ag
```

Characteristic	Beta	SE[1]	95% CI[1]	p-value
treatment	0.98	0.021	0.94, 1.0	<0.001
weight	0.20	0.010	0.18, 0.22	<0.001
age	0.20	0.000	0.20, 0.20	<0.001

[1] SE = Standard Error, CI = Confidence Interval

Propensity score adjusted model

Characteristic	Beta	SE	95% CI	p-value
treatment	1	0.022	0.9, 1	<0.00

time-varying confounding