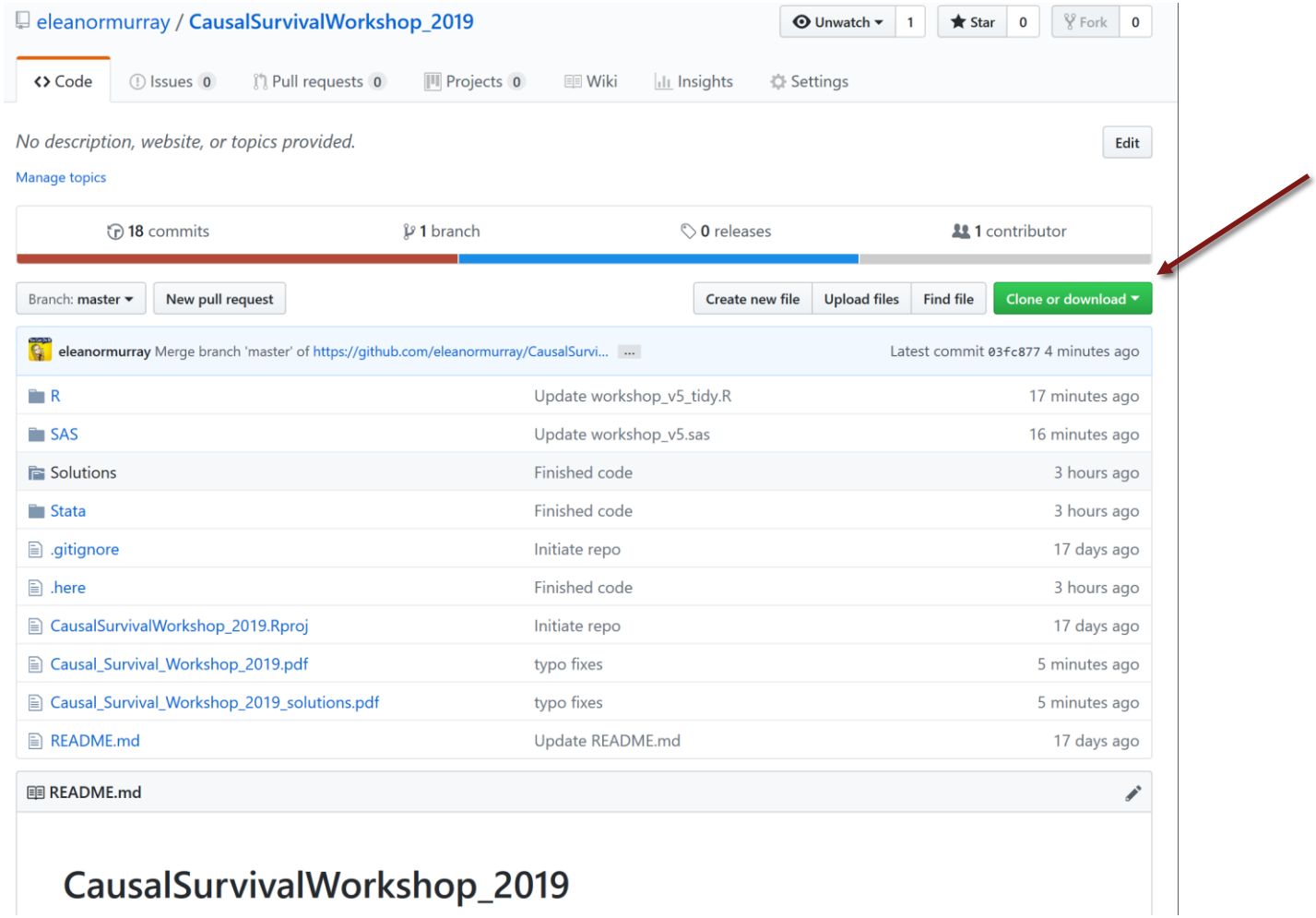
Download the workshop materials from:

https://github.com/eleanormurray/CausalSurvivalWorkshop_2019



Causal Survival Analysis in Follow-up Studies

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Workshop outline

Overview

Why are we here and what are we doing?

This workshop is about causal survival analysis for longitudinal or follow-up data

We'll learn how to estimate causal effects for point exposures and static sustained exposures on survival

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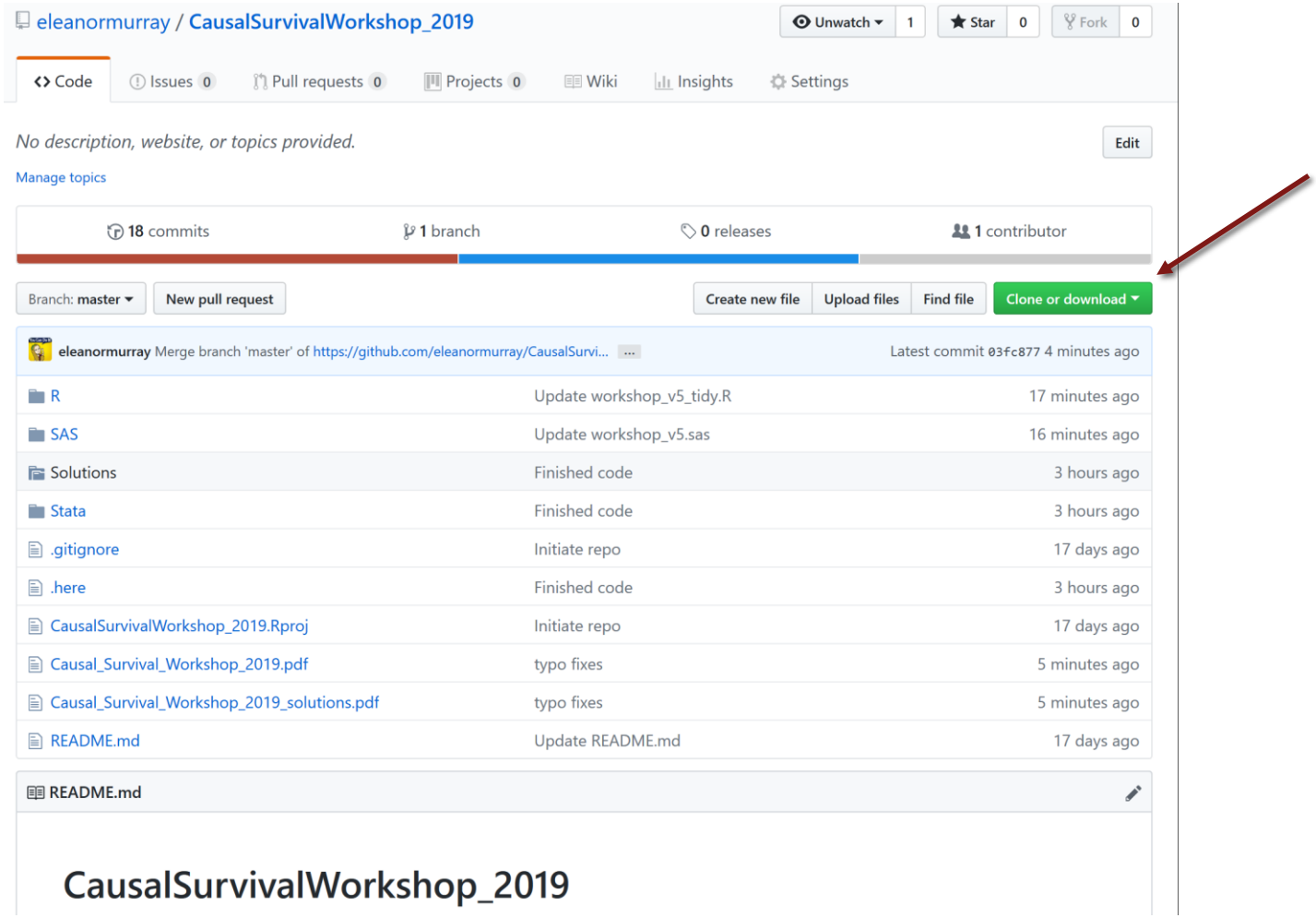


The case study: Coronary Drug Project (CDP)

NHLBI funded trial of lipid-lowering medications in men with a history of heart attacks

- Enrollment began in 1966, and follow-up ended 1975.
- 5 active treatments versus placebo

Coronary drug project research group *JAMA* 1975

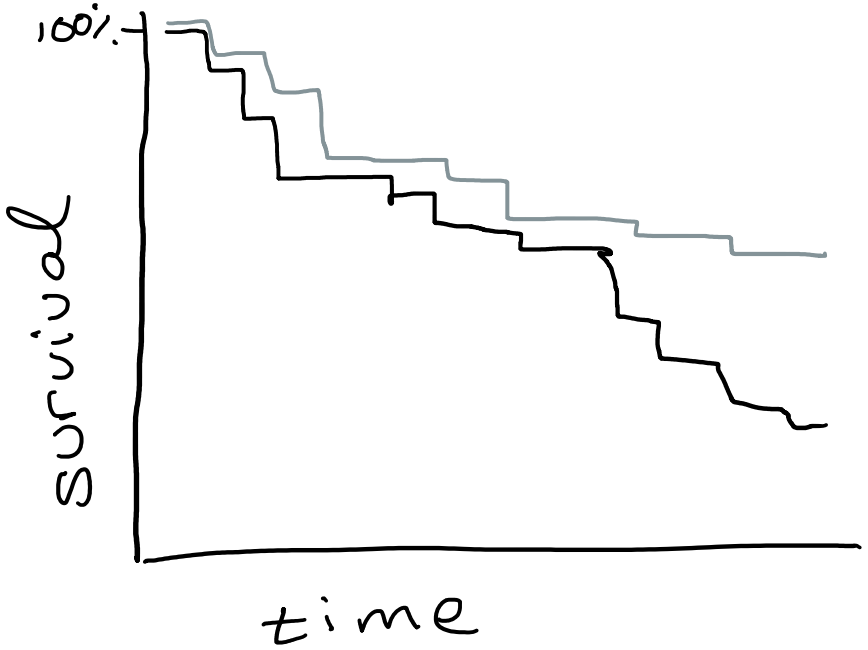
The case study: Coronary Drug Project (CDP)

Protocol	Description
Eligibility Criteria	Men with a history of a myocardial infarction in previous 3 months 30-64 years old
Treatment Arms	5 lipid-influencing drugs vs. placebo
Follow-up	Randomization until 5 years, LTFU, or death
Outcome	5-year mortality risk
Causal contrasts of interest	Intention-to-treat effect Effect of good adherence to trial protocol versus poor adherence, stratified by randomization arm

Coronary drug project research group *JAMA* 1975

Survival analysis basics

Survival analysis allows us to compare the **time-to-event** rather than just the number of events



Murray. 2019. Causal Survival Analysis

The first challenge: administrative censoring

Let's define T as the time to death

- T=1 for subjects who die in month 1
- T=2 for subjects who die in month 2, etc.
- T is unknown for subjects who are alive at end of follow-up

This is called administrative censoring: time of death T is unknown for subjects who have not died by end of follow-up

Administrative censoring is different from loss to follow-up

Some people will drop out of our study. For these

- T is unknown after some point during follow-up

This is called loss to follow-up. We often need to deal with this in our studies, but for the workshop we have data with no loss to follow-up.

Some survival analysis definitions

Survival probability: $\Pr[T>k]$

Risk (cumulative incidence): $\Pr[T\leq k]$

- All deaths between baseline and time *k*
- Compared to the number of individuals at baseline

Discrete hazard: $\Pr[T=k+1|T>k]$

- Recent deaths occurring during interval *k* to *k+1*
- Compared to the number individuals alive (and under follow-up) at *k*

Defining exposures strategies

Point exposures are exposures that happen at a single point in time, typically at baseline. Randomization is (usually) a point exposure.

Sustained exposures are exposures that happen repeatedly over time. Many randomized trials assign participants to sustained exposures.

Defining exposures strategies

Static sustained exposures are sustained exposures that don't change over time. An example is "always eat vegetables".

Dynamic sustained exposures are sustained exposures which change over time, especially if the change is dependent on time-varying individual characteristics. An example is "take treatment unless a contraindication develops"

Defining exposures strategies

One last definition that may be useful:

A grace period is a pre-specified time frame in which you are interested in exposure happening. This important for sustained exposures, especially in observational data.

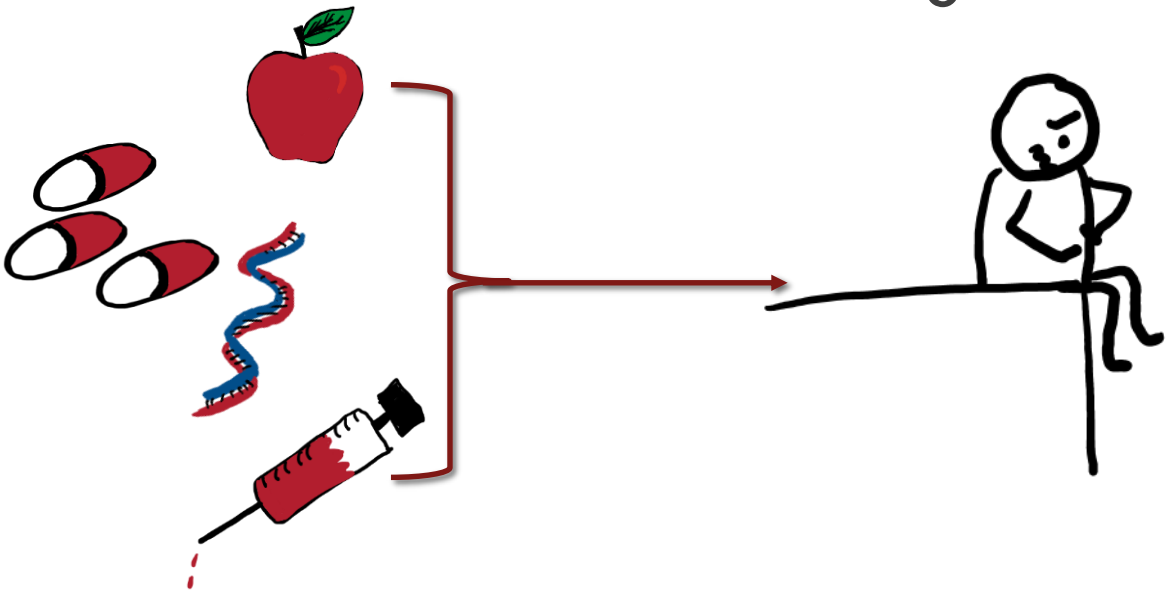
Causal inference for survival analysis is difficult because

- Time-varying confounding-exposure feedback
- Time zero & immortal time bias
- Exposures can be hard to define well

These problems are less likely with a randomized trial, but common in observational studies

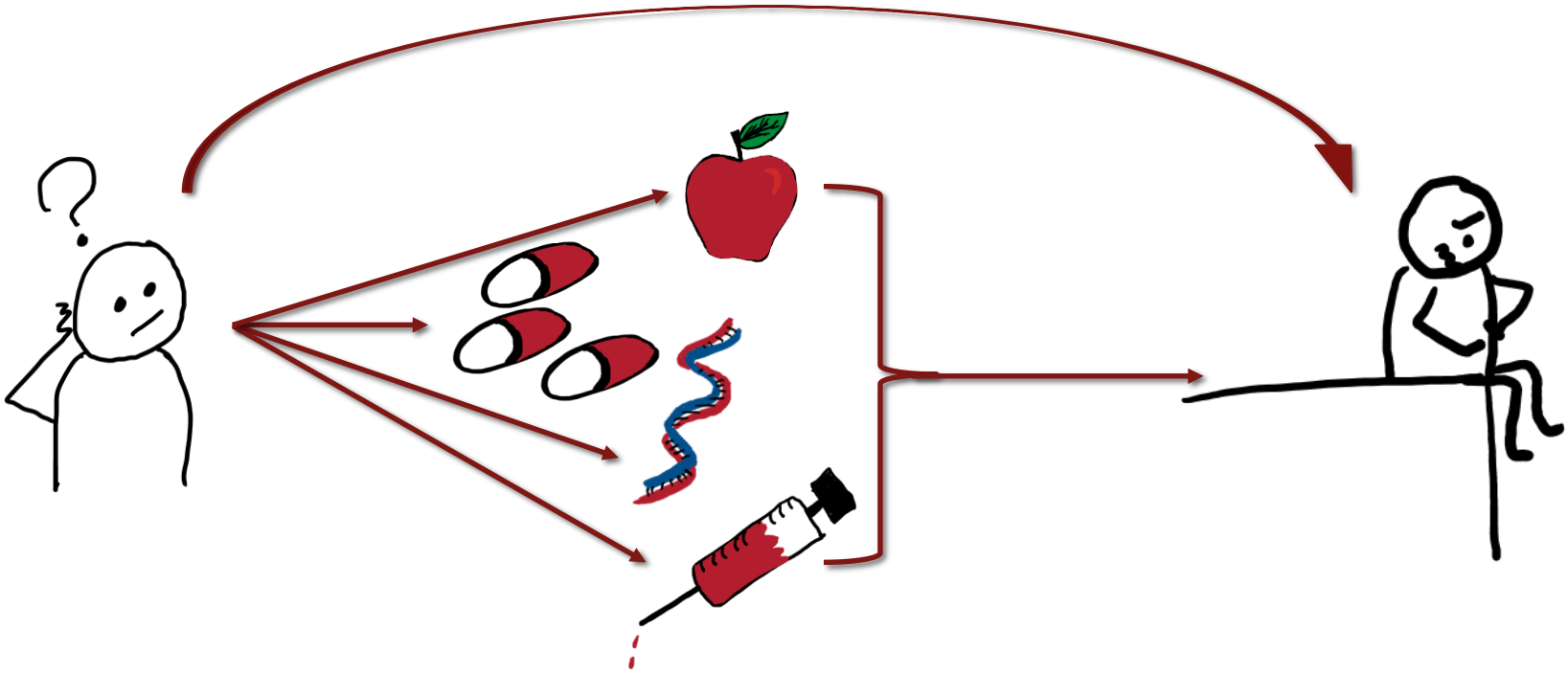
Why are well-defined exposures important?

- A well-defined exposure is one for which we can specify an 'intervention' that creates that exposure
- When there are multiple possible interventions, our answer is a weighted average of all 'interventions' but we don't know the weights



Why are well-defined exposures important?

- Worse, if the 'intervention' is ill-defined, the confounding is probably also ill-defined!



Solution: the target trial framework

First, specify in detail a randomized trial you would like to conduct

Second, design your observational study so that it closely mimics this target trial

But, to design a good target trial, we need to understand randomized trials!

A little about our data

The datasets on the workshop github are simulated versions of the Coronary Drug Project trial

The data are in long format, which means we have 1 observation per person per visit

Long-format data

ID	time	Z	L_0	L_t	C_t	Y_t
1	0	1	0	0	0	0
1	1	1	0	1	0	0
1	2	1	0	1	0	1
2	0	0	1	1	0	0
2	1	0	1	0	0	0
2	2	0	1	0	1	.
3	0	1	1	1	0	0
3	1	1	1	0	0	0
3	2	1	1	0	0	0

We have 15 time-varying covariates, and 1 baseline-only variable

Table 2: Data Description

Variable	Notation	Definition	Values
simID	id	ID variable	Range: 0 to 4042
rand	Z	Randomization group	0: placebo; 1: clofibrate
visit	t	Visit number: visits occur quarterly	Range: 0 to 14
death	Y_t	Death recorded at visit t	0: alive; 1: died $T \in [t, t+1)$
adhpre0bin	A_{-1}	Adherence to placebo during pre-randomization run-in period	0: adherence $\geq$ 80%; 1: adherence $<$ 80%
adhr_b	A_0	Adherence to placebo at baseline (recorded at a special visit 2 weeks after randomization)	0: adherence $\geq$ 80%; 1: adherence $<$ 80%
adhr	A_t	Adherence to assigned treatment at visit t	0: adherence $\geq$ 80%; 1: adherence $<$ 80%
mi_bin	L	Myocardial infarction at baseline	0: 1 or 2; 1: $\geq$2
AntiHyp	L	Antihypotensive medication use at visit t	0: no; 1: yes
AnyQQS	L	ECG findings: Q/QS pattern at visit t	0: no; 1: yes
AnySTDep	L	ECG findings: ST depression at visit t	0: no; 1: yes
AP	L	Angina pectoris at visit t	0: no; 1: yes
CardioM	L	Cardiomegaly at visit t	0: no; 1: yes
CHF	L	Coronary heart failure at visit t	0: no; 1: yes
DIUR	L	Diuretic use at visit t	0: no; 1: yes
FVEB	L	ECG finding: Frequent ventricular beats at visit t	0: no; 1: yes
HiHeart	L	High heart rate at visit t	0: $<$70 bpm; 1: $\geq$ 70 bpm
HiSerChol	L	High serum cholesterol at visit t	0: $<$250; 1: $\geq$ 250
HiSerTrigly	L	High serum triglyesterol at visit t	0: $<$5.0; 1: $\geq$ 5.0
IC	L	Intermittent claudication at visit t	0: no; 1: yes
NIHA	L	New York Heart Association class at visit t	0: no limitations; 1: any limitation
OralHyp	L	Oral hypoglycemic agents use at visit t	0: no; 1: yes
VCD	L	ECG finding: Ventricular conduction defect at visit t	0: no; 1: yes

Exercise 1: Directed acyclic graphs

First, we need to choose an estimand

Directed acyclic graphs (DAGs) are a tool for summarizing the information we know about a research question we want to answer

Each DAG should be targeted to a specific question, so we first need to decide what we want to estimate

What options are there for causal estimands?

In randomized trials we can estimate:

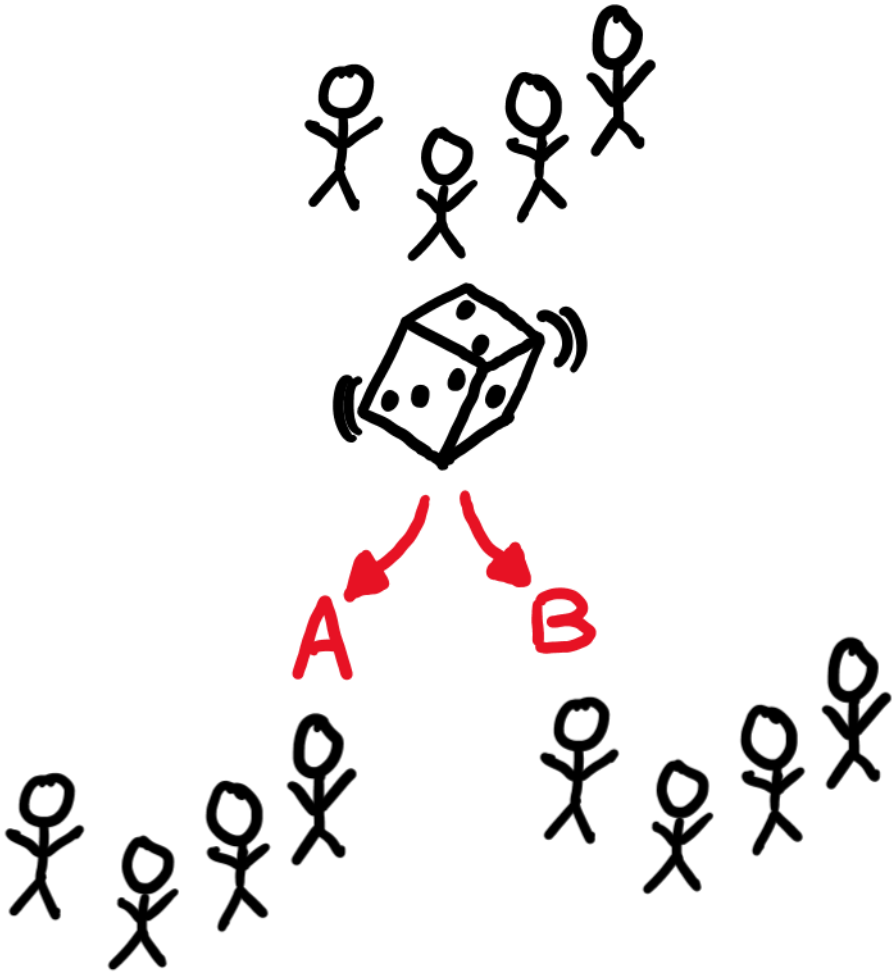
- Intention-to-treat effect
- Per-protocol effect

In an observational study we can generally only estimate:

- Per-protocol effect

Per-protocol analyses have a bad reputation!

But per-protocol effects are what we actually want to know!



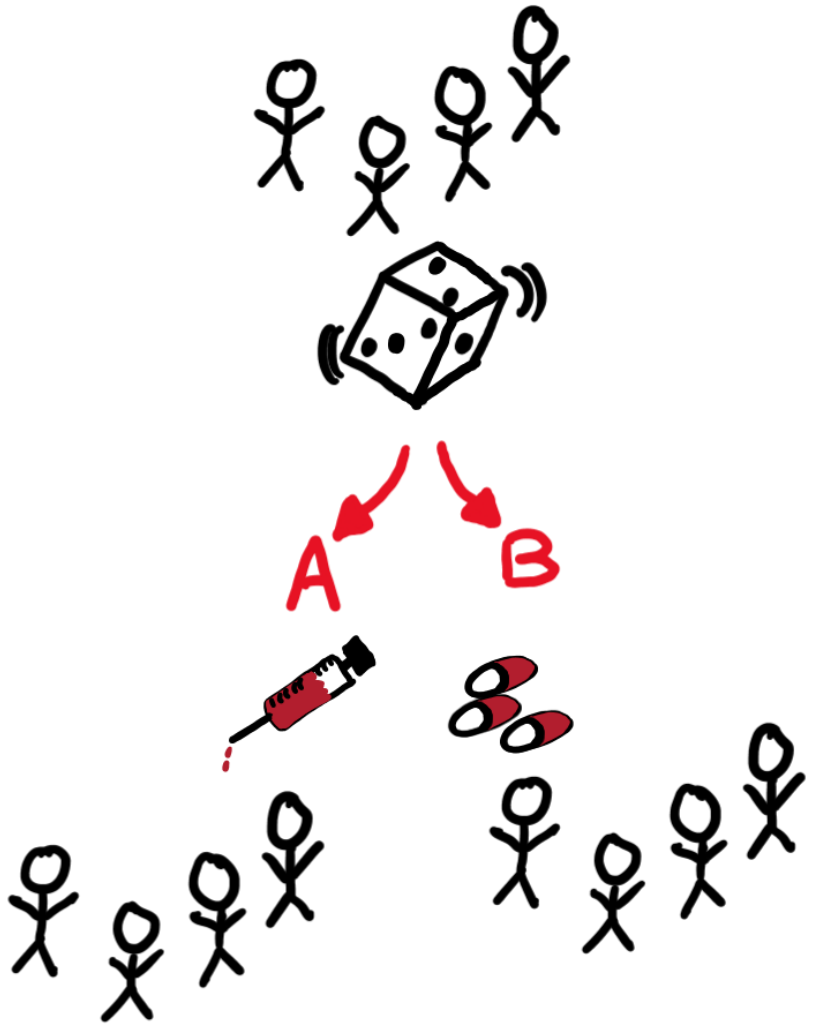
The intention-to-treat effect is the effect of **randomization**

If everyone initiates treatment, it can also be interpreted as the effect of initiating assigned treatment

But per-protocol effects are what we actually want to know!

The per-protocol effect is the effect of **receiving assigned treatment**

This doesn't have to be continuous, it can be according to some treatment *protocol*



Why do we bother with intention-to-treat effects?

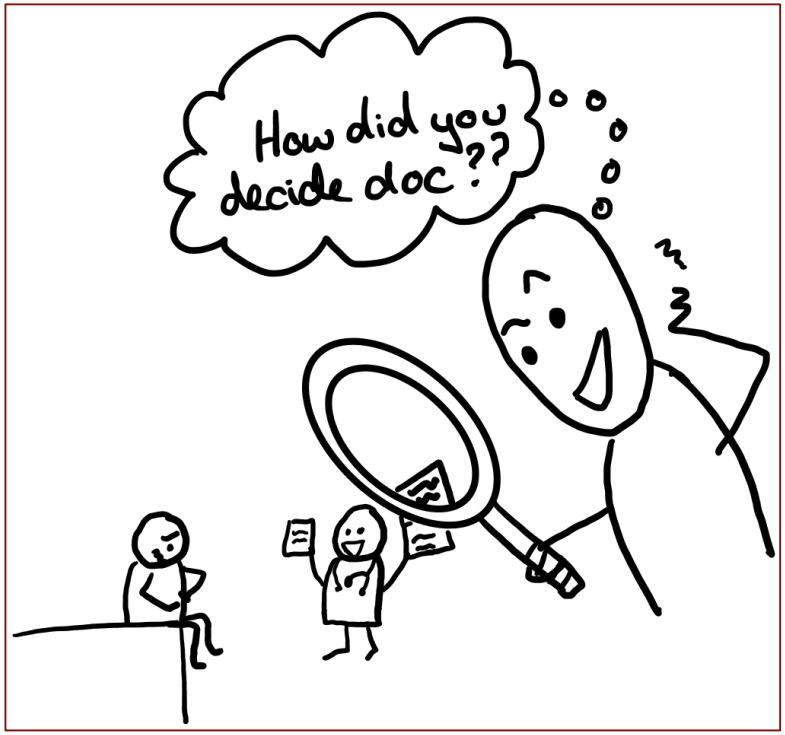
Causal inference relies on three main assumptions:

- Exchangeability
- Positivity
- Consistency

What is exchangeability?

- No unmeasured confounding: all common causes of the treatment and outcome are known and measured in the data

- No selection bias: we haven't conditioned or restricted on a variable that is a common effect of exposure and the outcome (or outcome cause)

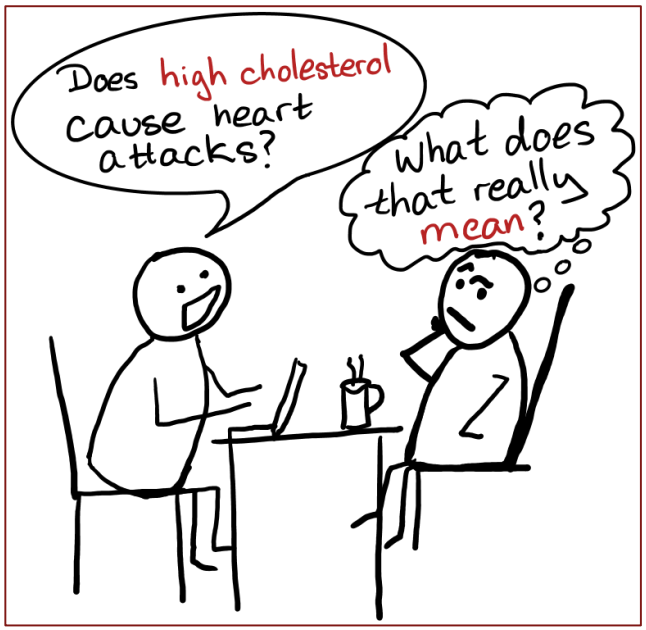


What is positivity?

- Positivity: there is a non-zero probability of all levels of treatment for all types of individuals in our population

What is consistency?

- Consistency: our treatment levels are clearly specified, aka:
  - Well-defined interventions
  - Well-defined causal questions



Ok, but why do we bother with intention-to-treat effects?

Randomization ensures no confounding at baseline for treatment assignment

Randomization also ensures positivity for treatment assignment

Randomization is a well-defined intervention

So, intention-to-treat analyses often give unbiased estimates of intention-to-treat effects

But not so fast!

Randomization ensures no confounding at baseline for treatment assignment

- Treatment happens after randomization
- Loss to follow-up happens after randomization

Post-randomization events are not guaranteed to be unconfounded!

Also the effect of randomization is not very interesting

- Often a lower bound on the effect of treatment compared to placebo
- Lower bound is insufficient for adverse events or safety
- When comparing active treatments, ITT can vary towards or away from the null
- No real world, clinical, equivalent of randomization
- Depends on the distribution of adherence in the trial & this can affect external validity

Per-protocol effects we could estimate:

- Effect of initiating treatment
- Effect of adhering to treatment protocol
- Effect of receiving point intervention, among the compliers (note, not adherers!)

Effect of treatment is an interesting effect

- Relevant for real world, clinical, decision making
- Allows better risk assessment for adverse events or safety
- Interpretable for both placebo and active / usual care comparators
- Doesn't depend on adherence patterns!

Per-protocol effect is the effect we really want!

Plus, per-protocol effects are patient-centered causal effects

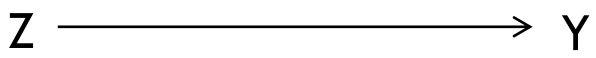
- Per-protocol effects are most relevant for people who can determine their own exposure, and have a high level of concern
- Discuss how/ why exposure occurred for maximum patient relevance

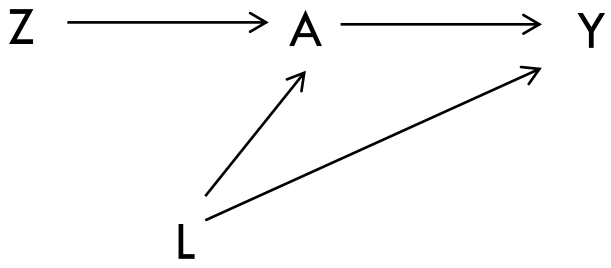
Murray EJ, et al. *Journal of Clinical Epidemiology*. 2018; 103: 10-21.

But, since we have a trial why not both?!

So, let's draw an intention-to-treat DAG

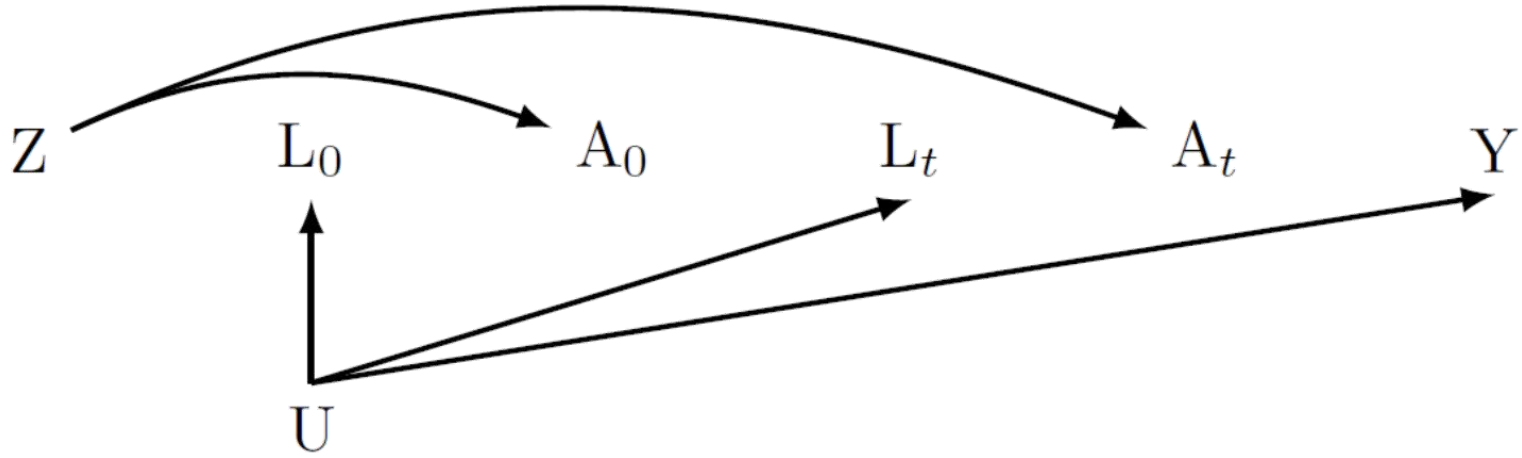
2 ways to draw an intention-to-treat DAGs (assuming no loss to follow-up)





Next, let's draw a per-protocol effect DAG

Different assumptions lead to different DAGs, and different analyses

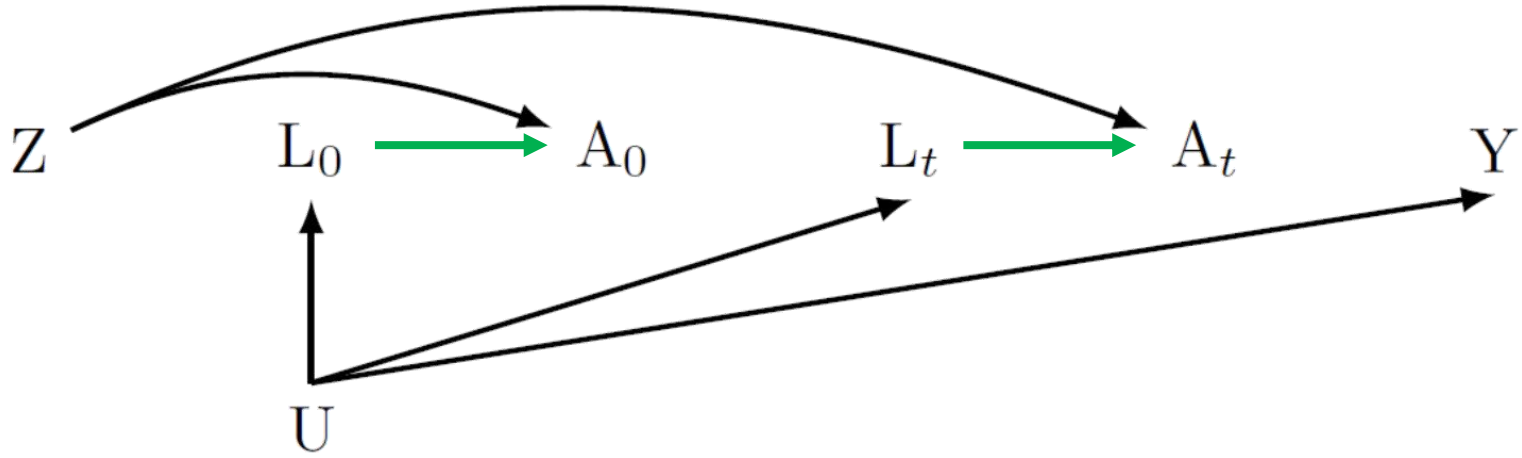


Random non-adherence

- No confounding adjustment needed

Hernan & Robins. 2017, NEJM 377:14

Different assumptions lead to different DAGs, and different analyses

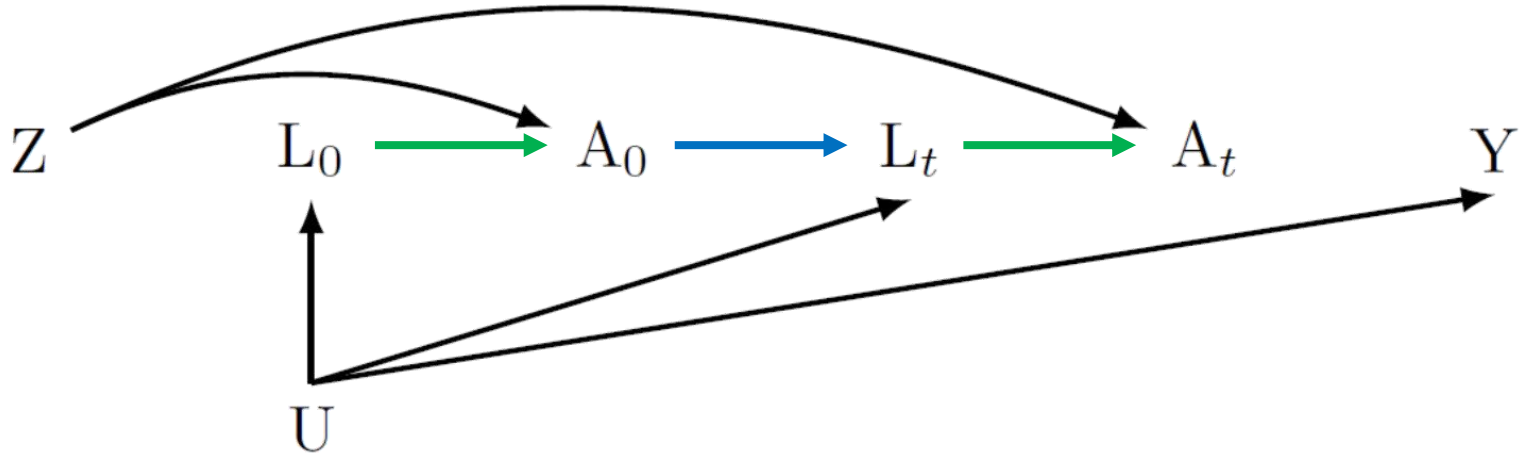


Adherence confounding by measured covariates

- Adjustment required using any method

Hernan & Robins. 2017, NEJM 377:14

Different assumptions lead to different DAGs, and different analyses

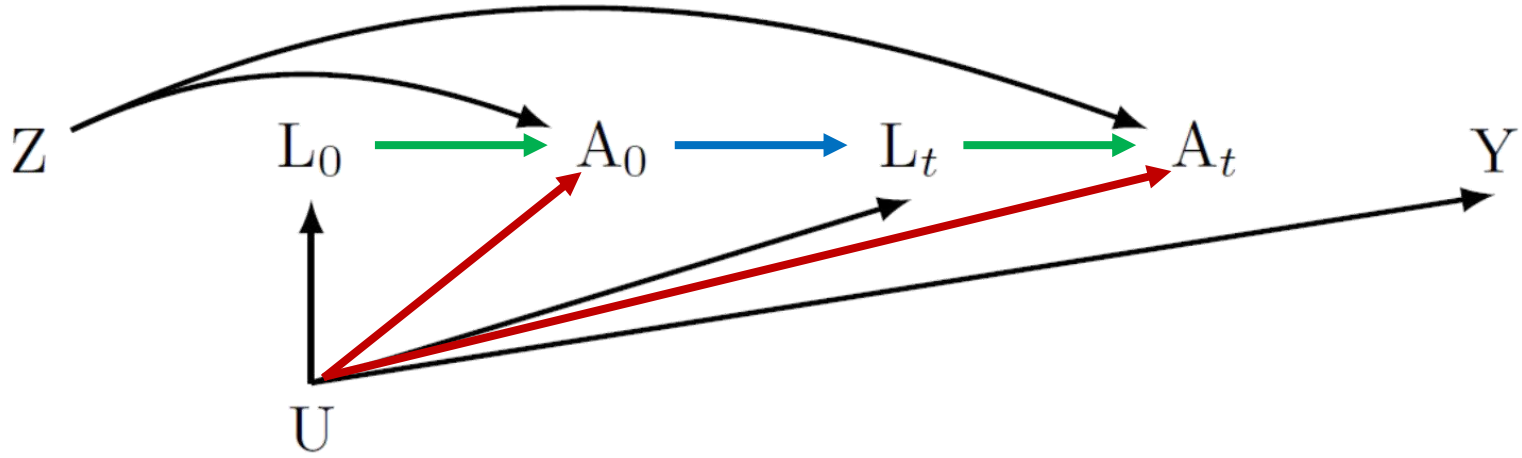


Adherence confounding by measured covariates and prior adherence

- G-methods required

Hernan & Robins. 2017, NEJM 377:14

Different assumptions lead to different DAGs, and different analyses



A dherence confounding by measured covariates, prior adherence, and unmeasured covariates

- Strong assumptions + structural nested models

Hernan & Robins. 2017, NEJM 377:14

Exercise 2: Estimating intention-to-treat effects

Make sure you have the data downloaded

Go to Section 3.1 of the workshop handout and try to explore the data

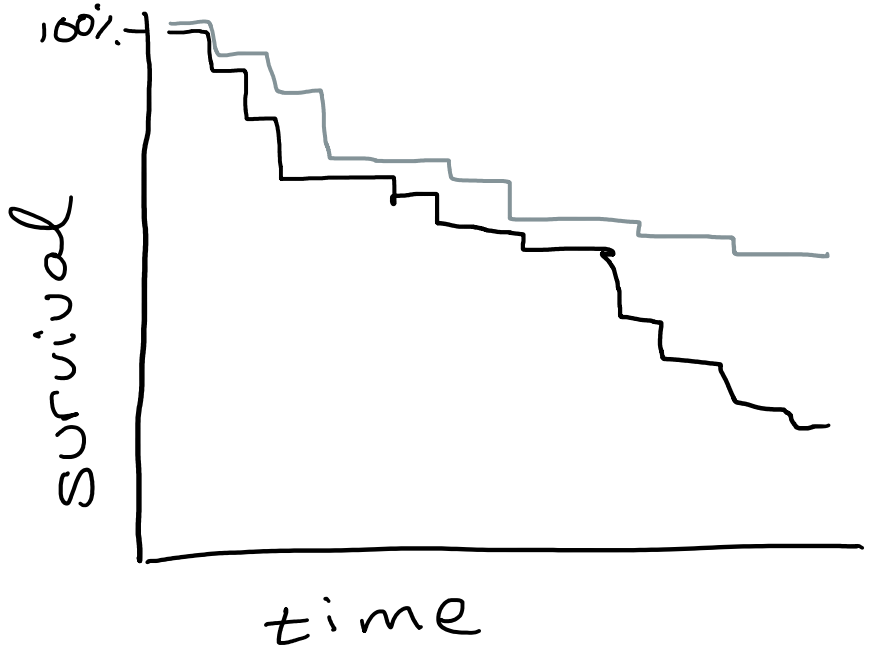
Non-parametric survival estimates

Since we have no loss to follow-up, we can estimate the causal effect of randomization on survival without making any additional assumptions

We can do this by comparing the Kaplan-Meier survival curves

Reminder: Survival curves

Kaplan-Meier curves look like staircases



Reminder: some definitions

Let's define T as the time to death

- T=1 for subjects who die in month 1
- T=2 for subjects who die in month 2, etc.
- T is unknown for subjects who are alive at end of follow-up

Reminder: survival analysis definitions

Survival probability: $\Pr[T>k]$

Risk (cumulative incidence): $\Pr[T\leq k]$

- All deaths between baseline and time *k*
- Compared to the number of individuals at baseline

Discrete hazard: $\Pr[T=k+1|T>k]$

- Recent deaths occurring during interval *k* to *k+1*
- Compared to the number individuals alive (and under follow-up) at *k*

Kaplan-Meier survival

Kaplan-Meier estimates survival at *k* as the product of conditional probabilities of having survived each interval between 0 and *k*

The conditional probability at each time is one minus the discrete hazard

For example, for $k=2$

$$\Pr[D_2=0] = \Pr[D_1=0]\Pr[D_2=0|D_1=0]$$

Kaplan-Meier survival

Semi-parametric ITT estimate

We can easily estimate the intention-to-treat effect on the hazard ratio scale if we're willing to make one additional assumption:

- The hazard ratio is constant over follow-up

Now we can use Cox proportional hazards regression

Cox proportional hazards regression

Parametric ITT estimate

If we're willing to make one more assumption, we can estimate the hazard ratio and the survival, plus the risk difference and risk ratio

- The baseline hazard has a specified functional form
- (here we assume quadratic)

Now we can use pooled logistic regression

Pooled logistic regression

Baseline covariate adjustment

Both semi-parametric and parametric survival methods allow adjustment for baseline covariates to estimate conditional hazard ratios

Maintaining interpretability

Conditional hazard ratios are hard to interpret

We would prefer to know the average hazard ratio, or even better the average survival and risks

We can estimate these from our pooled logistic regression model using standardization

id	rand	sex	age	race	death
1	0	0	65	1	0
2	1	0	58	1	1
3	0	1	67	1	1
4	1	0	54	0	0
5	0	1	48	0	0

id	rand	sex	age	race	death	Interv
1	0	0	65	1	0	0
2	1	0	58	1	1	0
3	0	1	67	1	1	0
4	1	0	54	0	0	0
5	0	1	48	0	0	0
1	0	0	65	1	0	1
2	1	0	58	1	1	1
3	0	1	67	1	1	1
4	1	0	54	0	0	1
5	0	1	48	0	0	1

```
expand 2, gen(interv)
```

id	rand	sex	age	race	death	Interv	Interv2
1	0	0	65	1	0	0	0
2	1	0	58	1	1	0	0
3	0	1	67	1	1	0	0
4	0	0	54	0	0	0	0
5	0	1	48	0	0	0	0
1	0	0	65	1	0	1	0
2	1	0	58	1	1	1	0
3	0	1	67	1	1	1	0
4	1	0	54	0	0	1	0
5	0	1	48	0	0	1	0
1	0	0	65	1	0	.	1
2	1	0	58	1	1	.	1
3	0	1	67	1	1	.	1
4	1	0	54	0	0	.	1
5	0	1	48	0	0	.	1

```
expand 2 if interv == 0, gen(interv
```

id	rand	sex	age	race	death	Interv	Interv2
1	0	0	65	1	0	0	0
2	1	0	58	1	1	0	0
3	0	1	67	1	1	0	0
4	0	0	54	0	0	0	0
5	0	1	48	0	0	0	0
1	0	0	65	1	0	1	0
2	1	0	58	1	1	1	0
3	0	1	67	1	1	1	0
4	1	0	54	0	0	1	0
5	0	1	48	0	0	1	0
1	0	0	65	1	0	-1	1
2	1	0	58	1	1	-1	1
3	0	1	67	1	1	-1	1
4	1	0	54	0	0	-1	1
5	0	1	48	0	0	-1	1

```
replace interv = -1 if interv2 == 1
```

id	rand	sex	age	race	death	Interv
1	0	0	65	1	0	0
2	1	0	58	1	1	0
3	0	1	67	1	1	0
4	0	0	54	0	0	0
5	0	1	48	0	0	0
1	0	0	65	1	0	1
2	1	0	58	1	1	1
3	0	1	67	1	1	1
4	0	0	54	0	0	1
5	0	1	48	0	0	1
1	0	0	65	1	0	-1
2	1	0	58	1	1	-1
3	0	1	67	1	1	-1
4	0	0	54	0	0	-1
5	0	1	48	0	0	-1

```
Drop interv2
```

id	rand	sex	age	race	death	Interv
1	0	0	65	1	.	0
2	1	0	58	1	.	0
3	0	1	67	1	.	0
4	1	0	54	0	.	0
5	0	1	48	0	.	0
1	0	0	65	1	.	1
2	1	0	58	1	.	1
3	0	1	67	1	.	1
4	1	0	54	0	.	1
5	0	1	48	0	.	1
1	0	0	65	1	0	-1
2	1	0	58	1	1	-1
3	0	1	67	1	1	-1
4	1	0	54	0	0	-1
5	0	1	48	0	0	-1

```
Replace death = . If interv != -1
```

id	rand	sex	age	race	death	Interv
1	0	0	65	1	.	0
2	0	0	58	1	.	0
3	0	1	67	1	.	0
4	0	0	54	0	.	0
5	0	1	48	0	.	0
1	0	0	65	1	.	1
2	1	0	58	1	.	1
3	0	1	67	1	.	1
4	1	0	54	0	.	1
5	0	1	48	0	.	1
1	0	0	65	1	0	-1
2	1	0	58	1	1	-1
3	0	1	67	1	1	-1
4	1	0	54	0	0	-1
5	0	1	48	0	0	-1

```
Replace death = . If interv != -1
Replace qsmk = 0 if interv == 0
```

id	rand	sex	age	race	death	Interv
1	0	0	65	1	.	0
2	0	0	58	1	.	0
3	0	1	67	1	.	0
4	0	0	54	0	.	0
5	0	1	48	0	.	0
1	1	0	65	1	.	1
2	1	0	58	1	.	1
3	1	1	67	1	.	1
4	1	0	54	0	.	1
5	1	1	48	0	.	1
1	0	0	65	1	0	-1
2	1	0	58	1	1	-1
3	0	1	67	1	1	-1
4	1	0	54	0	0	-1
5	0	1	48	0	0	-1

```
Replace death = . If interv != -1
Replace qsmk = 0 if interv == 0
Replace qsmk = 1 if interv == 1
```

id	rand	sex	age	race	death	Interv
1	0	0	65	1	.	0
2	0	0	58	1	.	0
3	0	1	67	1	.	0
4	0	0	54	0	.	0
5	0	1	48	0	.	0
1	1	0	65	1	.	1
2	1	0	58	1	.	1
3	1	1	67	1	.	1
4	1	0	54	0	.	1
5	1	1	48	0	.	1
1	0	0	65	1	0	-1
2	1	0	58	1	1	-1
3	0	1	67	1	1	-1
4	1	0	54	0	0	-1
5	0	1	48	0	0	-1

Model will be fitted in this data, since it doesn't have missing values

id	rand	sex	age	race	death	Interv	pr_d
1	0	0	65	1	.	0	#
2	0	0	58	1	.	0	#
3	0	1	67	1	.	0	#
4	0	0	54	0	.	0	#
5	0	1	48	0	.	0	#
1	1	0	65	1	.	1	#
2	1	0	58	1	.	1	#
3	1	1	67	1	.	1	#
4	1	0	54	0	.	1	#
5	1	1	48	0	.	1	#
1	0	0	65	1	0	-1	#
2	1	0	58	1	1	-1	#
3	0	1	67	1	1	-1	#
4	1	0	54	0	0	-1	#
5	0	1	48	0	0	-1	#

```
Predict pr_d, pr
```

id	rand	sex	age	race	death	Interv	pr_d
1	0	0	65	1	.	0	#
2	0	0	58	1	.	0	#
3	0	1	67	1	.	0	#
4	0	0	54	0	.	0	#
5	0	1	48	0	.	0	#
1	1	0	65	1	.	1	#
2	1	0	58	1	.	1	#
3	1	1	67	1	.	1	#
4	1	0	54	0	.	1	#
5	1	1	48	0	.	1	#
1	0	0	65	1	0	-1	#
2	1	0	58	1	1	-1	#
3	0	1	67	1	1	-1	#
4	1	0	54	0	0	-1	#
5	0	1	48	0	0	-1	#

$E[Ya = 0]$

$E[Ya = 1]$

Kaplan-Meier survival

Kaplan-Meier estimates survival at *k* as the product of conditional probabilities of having survived each interval between 0 and *k*

The conditional probability at each time is one minus the discrete hazard

For example, for $k=2$

$$\Pr[D_2=0] = \Pr[D_1=0]\Pr[D_2=0|D_1=0]$$

Baseline standardization

Exercise 3: Per-protocol effects

Reminder: Per-protocol analyses have a bad reputation!

Isn't adherence *intractably* confounded?

INFLUENCE OF ADHERENCE TO TREATMENT AND RESPONSE OF CHOLESTEROL ON MORTALITY IN THE CORONARY DRUG PROJECT

THE CORONARY DRUG PROJECT RESEARCH GROUP

In 1980, the Coronary Drug Project (CDP) compared good and bad adherers in the placebo arm

- 9.4 percentage point reduction in 5-year mortality

Coronary Drug Project. 1980, NEJM; 303: 1038-41.

What is a per-protocol analysis?

Common approaches

- censor when non-adherent, don't adjust for confounding
- add adherence to regression model, adjust only for baseline confounders

Common ≠ correct!

Per-protocol analyses tell us

how did trial outcomes differ between those who did adhere to, or recieved, assignment A and those who did adhere to, or receive, assignment B?

Per-protocol analyses in the literature

Approach	Description

Per-protocol analyses in the literature

Approach	Description
1. “Modified ITT”	▪ censor never initiators

Per-protocol analyses in the literature

Approach	Description
1. "Modified ITT"	▪ censor never initiators
2. "Per-protocol population"	▪ censor if never initiate, cross-over, or discontinuation

Per-protocol analyses in the literature

Approach	Description
1. "Modified ITT"	▪ censor never initiators
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3. "As-treated"	▪ allow cross-over ▪ censor non-initiators or discontinuers

Methods 1 to 3:
Censor without adjustment

Per-protocol analyses in the literature

Approach	Description
1. "Modified ITT"	▪ censor never initiators
2. "Per-protocol population"	▪ censor if never initiate, cross-over, or discontinuation
3. "As-treated"	▪ allow cross-over ▪ censor non-initiators or discontinuers
4. Adherence adjustment	▪ include adherence in model for outcome model

Methods 1 to 3:
Censor without adjustment

Method 4:
Adjustment for baseline confounding only

Potential per-protocol analyses

Approach	Description
1. "Modified ITT"	▪ censor never initiators
2. "Per-protocol population"	▪ censor if never initiate, cross-over, or discontinuation
3. "As-treated"	▪ allow cross-over ▪ censor non-initiators or discontinuers
4. Adherence adjustment	▪ include adherence in model for outcome model
5. Instrumental variables, aka "contamination-adjusted ITT"	▪ compare outcome by trial arm, and correct using adherence by trial arm

Methods 1 to 3:
Censor without adjustment

Method 4:
Adjustment for baseline confounding only

Effects are different from analyses

Per-protocol effect tells us

> "how would trial outcomes differ if everyone adhered to assignment A versus if everyone adhered to assignment B"

Better per-protocol analyses

Approach	Description
Per-protocol effect estimation	▪ censor if deviate from protocol or include adherence in outcome model ▪ adjust for censoring or time-varying confounding
5. Instrumental variables, ~~aka "contamination-adjusted ITT"~~	▪ compare outcome by trial arm, and correct using adherence by trial arm

Re-visiting the Coronary Drug Project

Code & technical appendix available online

Table 2. Comparison of original and updated estimates for the placebo arm, Coronary Drug Project.

	Five-year mortality risk difference, % (95% CI)
	Unadjusted
Replication of 1980 analysis (N = 2630)	14.3 (10.8–17.8)
Updated 2015 analysis (N = 2401)	11.0 (6.5–15.6)

CI: confidence interval; ECG: electrocardiogram; MI: myocardial infarction.

Murray & Hernan. 2016, Clin Trials 13(4): 372-8.

Application to survival analysis

Code & technical appendix available online

Table 1 Estimated difference in 5-year mortality risk (95% confidence interval) when comparing 0% vs. 100% of follow-up being at least 80% adherent, Coronary Drug Project

Method	Unadjusted	Standardized by baseline covariates	+ IP weighting for post-randomization covariates
Censoring when binary adherence level deviates from baseline	9.6 (– 7.0, 28.9)	1.5 (– 11.0, 16.4)	0.01 (– 12.2, 13.2)
Dose-response hazards models			
Quadratic cumulative adherence	6.7 (– 3.2, 16.5)	2.6 (– 5.8, 11.1)	0.2 (– 8.2, 8.6)
Quadratic cumulative adherence, with time interaction	6.0 (– 5.8, 18.0)	1.6 (– 8.4, 11.6)	– 0.7 (– 12.2, 10.7)
Binary current adherence, plus quadratic cumulative adherence up to previous visit	11.6 (– 1.0, 24.2)	6.4 (– 3.9, 16.8)	4.5 (– 6.3, 15.3)
Binary current adherence, plus quadratic cumulative adherence up to previous visit, with time interaction	10.3 (– 2.3, 22.9)	4.0 (– 6.0, 14.1)	2.4 (– 9.3, 14.1)

Murray & Hernan. 2018, Trials 19: 158.

Let's look at adherence in the placebo arm of our simulated data

Inverse probability weighting

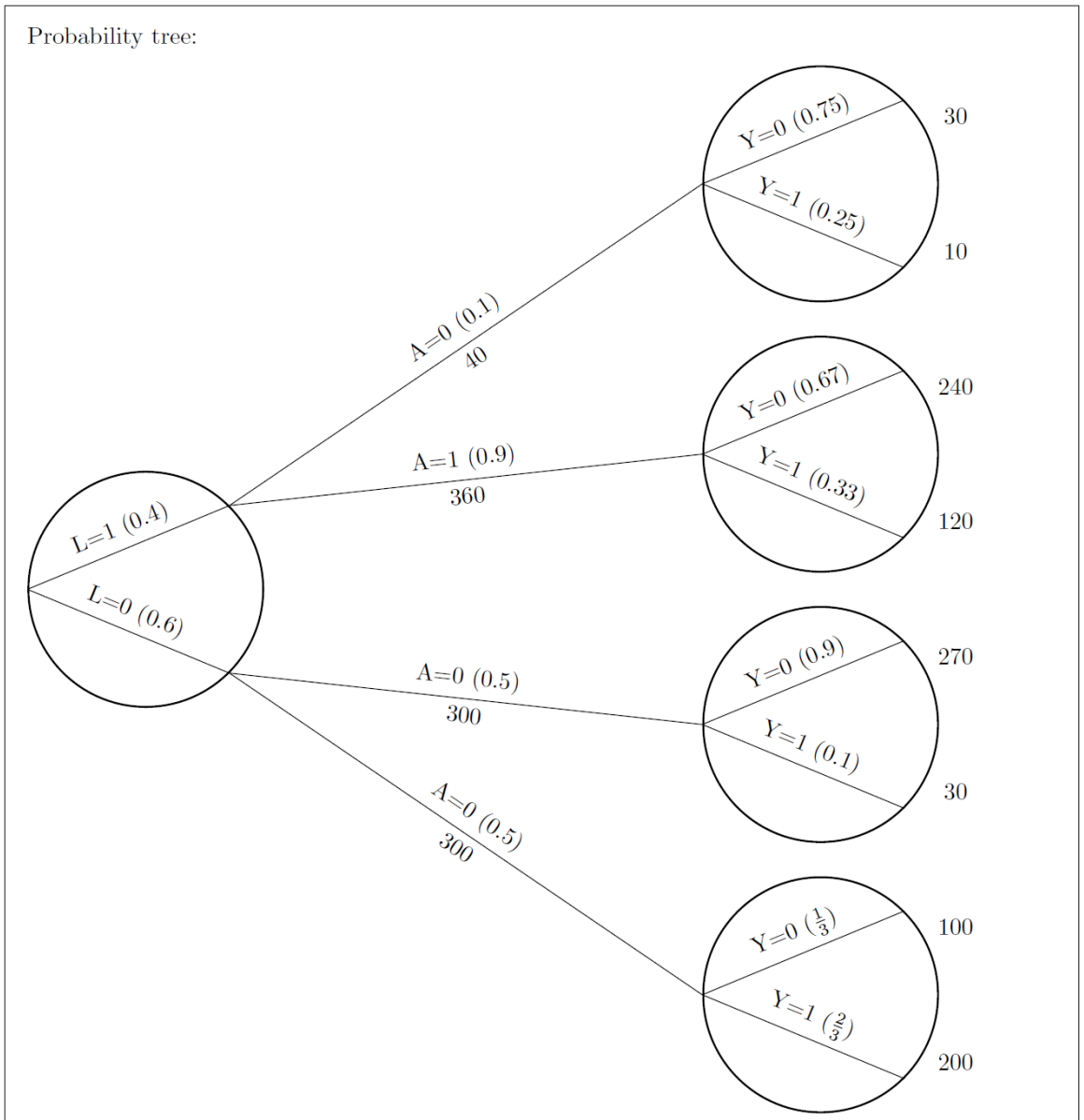
Step 1: identify adherent person-time

Step 2: build inverse probability weights for adherence and fit separately in each trial arm

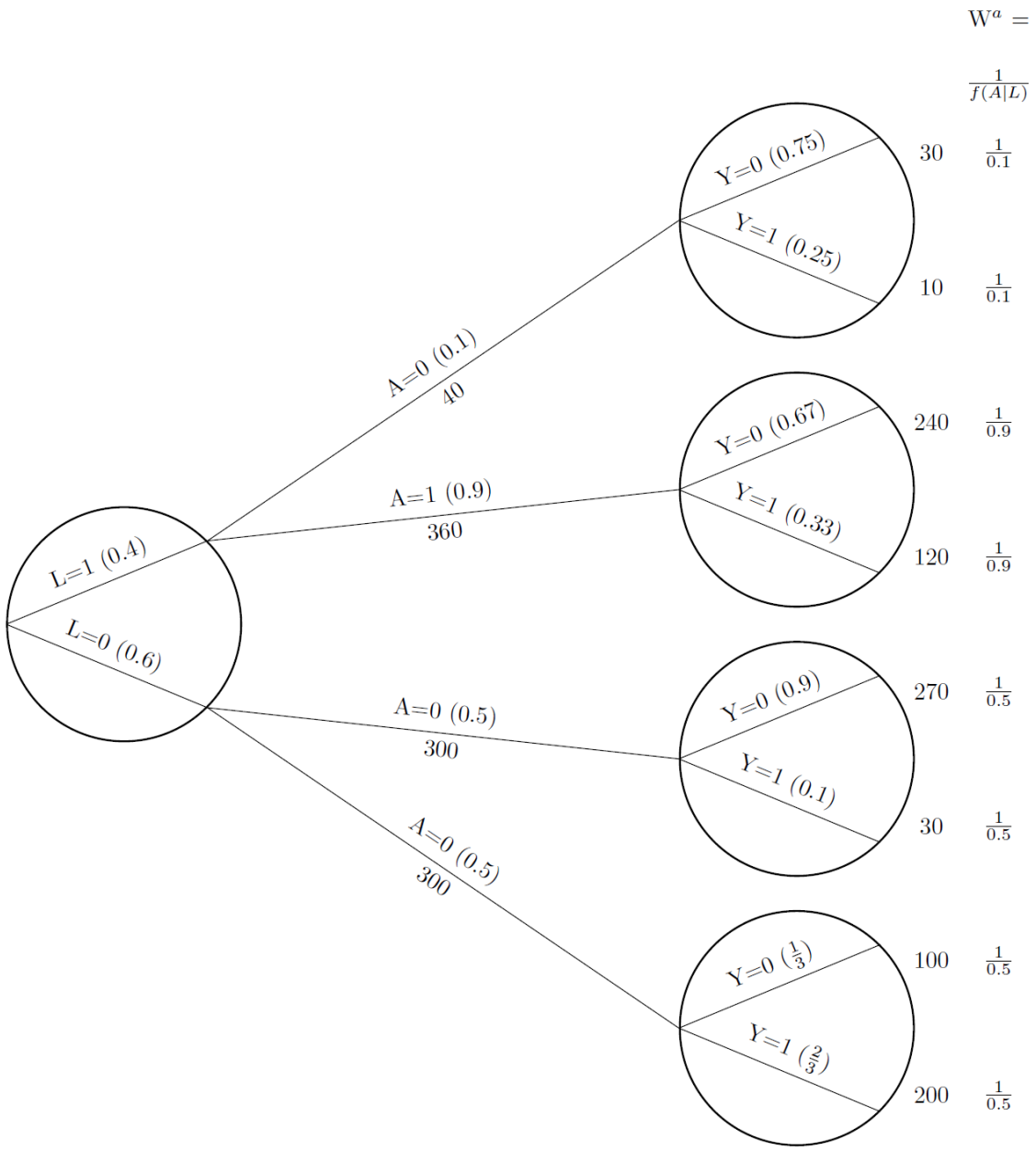
Step 3: censor when non-adherent

Step 4: fit an IP-weighted model for the outcome given trial arm, baseline covariates

Step 5: generate estimated survival & risks standardized over baseline covariates


Probability tree:
L=1 (0.4)
L=0 (0.6)
A=0 (0.1)
40
A=1 (0.9)
360
A=0 (0.5)
300
A=0 (0.5)
300
Y=0 (0.75)
Y=1 (0.25)
30
10
Y=0 (0.67)
Y=1 (0.33)
240
120
Y=0 (0.9)
Y=1 (0.1)
270
30
Y=0 (1/3)
Y=1 (2/3)
100
200

Probability tree:



Estimating the placebo arm effect with IPW

Estimating the per-protocol effect

You've already learned the basics of everything you need to know to estimate the per-protocol effect

Changes:

- Our adherence definition has changed
- We fit the IP weights separately in each arm
- Our strategies for standardization have changed

Estimate the per-protocol effect

Wrap-up

What we learned

For point exposures:

- Non-parametric survival curves
- Unadjusted hazard ratios from semi-parametric and parametric models
- Conditional hazard ratios from semi-parametric and parametric models
- Average hazard ratios, survival curves, risk differences, and cumulative incidence ratios from parametric survival models

What we learned

For static sustained exposures:

- Non-parametric survival curves
- Unadjusted hazard ratios from semi-parametric and parametric models
- Conditional hazard ratios from semi-parametric and parametric models
- Average hazard ratios, survival curves, risk differences, and cumulative incidence ratios from parametric survival models

What about observational studies?

Our observational studies have confounding

If we have a point exposure, we need to worry about baseline confounding

If we have a sustained exposure, we need to worry about baseline and time-varying confounding

We've learned how to handle both of these already!

Extensions

Some more complicated scenarios you may encounter:

- Loss to follow-up – address this with additional inverse probability weights
- Dynamic sustained strategies – these typically require unstabilized weights
- Grace periods – whenever someone is following multiple strategies, clone them, and when you know which strategy they're following censor them & adjust for censoring with IPW.

Where to get more information?

Some references:

- Choosing a causal effect: Hernan & Scharfstein. 2018, Ann Intern Med; 168(7):515-6.
- Review of per-protocol effect estimation: Hernan & Robins. 2017, NEJM 377:14
- Placebo arm adherence analyses: Murray & Hernan. 2018, Trials 19:158; Murray & Hernan. 2016, Clin Trials 13(4): 372-8.
- Per-protocol effect estimation: Lodi et al, 2016. AIDS; 30(17):2659-63.
- G-methods: Causal Inference, Hernan & Robins. (Chapter 17 is survival analysis for point exposures) Available online at: https://www.hsph.harvard.edu/miguel-hernan/causal-inference-book/

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THANK YOU