A Short Introduction to Directed Acyclic Graphs (DAGs)

Joshua P. Entrop

Läkemedelsverket, Enhet för Effekt och Säkerhet, October 31st, 2024



Karolinska Institutet

Background - Counterfactuals

Counterfactuals

 Y_i^x denotes the potential outcome Y of individual i under treatment x.

E.g. my (i) sleep quality tonight (Y) if I at pasta (x = 1) instead of oats (x = 0) for dinner.

Problem

- We are interest in $\mathbb{E}[Y^{x=0}] \mathbb{E}[Y^{x=1}]$
- We know $\mathbb{E}[Y|x=0] \mathbb{E}[Y|x=1]$

Hence, we need a method for translating our contrafactual outcomes of interest into observable quantities.

Solution: Pearl's *do*-calculus, which requires 3 assumptions.

1. Consistency ($Y_i^x = Y_i$, if $X_i = x$)

The counterfactual outcome Y_i^x corresponds to the observed outcome Y_i if individual i received treatment x in the real world.

1. Consistency ($Y_i^x = Y_i$, if $X_i = x$)

2. Conditional Exchangeability ($Y^{X} \perp X | L$)

The counterfactual outcome is independent of the observed treatment given some adjustment set ${\ensuremath{\mathbb L}}.$

- 1. Consistency ($Y_i^x = Y_i$, if $X_i = x$)
- 2. Conditional Exchangeability ($Y^{x} \perp X | L$)
 - 3. Positivity ($\mathbb{P}[X = x, L = l] > 0$)

It should in theory be possible to identify both treated and untreated individuals for each possible combination of the variables included in the adjustment set L.

- 1. Consistency ($Y_i^x = Y_i$, if $X_i = x$)
- 2. Conditional Exchangeability ($Y^{x} \perp X | L$)
- 3. Positivity ($\mathbb{P}[X = x, L = l] > 0$)

Idetifiability Assumptions and DAGs

- 1. Consistency ($Y_i^x = Y_i$, if $X_i = x$)
- 2. Conditional Exchangeability ($Y^x \perp X | L$)
- 3. Positivity ($\mathbb{P}[X = x, L = l] > 0$)



Mathematically speaking, a DAG is a visual representation of a joint distribution of variables defined by:

- ▶ Nodes: Variables in our causal network
- Arrows: Direction of causation
- Note that the absence of an arrow is a stronger assumption than the presence of it, i.e., complete independence.

Mathematically speaking, a DAG is a visual representation of a joint distribution of variables defined by:

- Nodes: Variables in our causal network
- Arrows: Direction of causation
- Note that the absence of an arrow is a stronger assumption than the presence of it, i.e., complete independence.

X Y
S
Figure 1. Some nodes

Mathematically speaking, a DAG is a visual representation of a joint distribution of variables defined by:

- ▶ Nodes: Variables in our causal network
- Arrows: Direction of causation
- Note that the absence of an arrow is a stronger assumption than the presence of it, i.e., complete independence.



Figure 1. A direct effect

Mathematically speaking, a DAG is a visual representation of a joint distribution of variables defined by:

- Nodes: Variables in our causal network
- Arrows: Direction of causation
- Note that the absence of an arrow is a stronger assumption than the presence of it, i.e., complete independence.



Figure 1. An indirect effect

Mathematically speaking, a DAG is a visual representation of a joint distribution of variables defined by:

- ▶ Nodes: Variables in our causal network
- ► Arrows: Direction of causation
- Note that the absence of an arrow is a stronger assumption than the presence of it, i.e., complete independence.





Mathematically speaking, a DAG is a visual representation of a joint distribution of variables defined by:

- ▶ Nodes: Variables in our causal network
- ► Arrows: Direction of causation
- Note that the absence of an arrow is a stronger assumption than the presence of it, i.e., complete independence.



Figure 1. A collider

Mathematically speaking, a DAG is a visual representation of a joint distribution of variables defined by:

- Nodes: Variables in our causal network
- ► Arrows: Direction of causation
- Note that the absence of an arrow is a stronger assumption than the presence of it, i.e., complete independence.



Figure 1. Conditioned on a collider

Back-door criteria

Back-door criteria



Figure 2. The closed back door

Back-door criteria



Figure 2. The closed back door

Back-door criteria



Figure 2. The closed back door



Figure 3. The open back door

Back-door criteria



Figure 2. The closed back door



Figure 3. The open back door

Back-door criteria



Figure 2. The closed back door



Figure 3. The open back door



- R: Randomisation
- T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



- R: Randomisation
- T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- S: Collider (fatigue)
- M: Mediator (physical activity)
- U: Confounder (SES)
- C: Drop out



- R: Randomisation
 - T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- ► S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



- R: Randomisation
 - T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- ► S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



Figure 4. DAG of a randomised experiment

- R: Randomisation
 - T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- ► S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



- R: Randomisation
 - T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



- R: Randomisation
 - T: Treatment
- Y: Outcome (weight loss)
- ▶ P: Prognostic factors (baseline BMI)
- ► S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



- R: Randomisation
- T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- ► S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



- R: Randomisation
 - T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- ► S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



- R: Randomisation
- T: Treatment
- Y: Outcome (weight loss)
- ▶ P: Prognostic factors (baseline BMI)
- ► S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



- R: Randomisation
 - T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- ► S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out

A Blinded Randomised Experiment



- R: Randomisation
 - T: Treatment
- Y: Outcome (weight loss)
- P: Prognostic factors (baseline BMI)
- ► S: Collider (fatigue)
- M: Mediator (physical activity)
- ► U: Confounder (SES)
- C: Drop out



Figure 5. DAG of an ICE mechanism

- R: Randomisation
- T: Treatment
- ► C: ICE (treatment discontinuation)
- Yt: Outcome at time t
- U: Confounder (behavioural trait)
- M_{y2}: A mechanism for assigning a value to Y.



Figure 5. DAG of an ICE mechanism

- R: Randomisation
- T: Treatment
- C: ICE (treatment discontinuation)
- Yt: Outcome at time t
- U: Confounder (behavioural trait)
- M_{y2}: A mechanism for assigning a value to Y.



Figure 5. DAG of an ICE mechanism

- R: Randomisation
- T: Treatment
- C: ICE (treatment discontinuation)
- Yt: Outcome at time t
- U: Confounder (behavioural trait)
- M_{y2}: A mechanism for assigning a value to Y.



Figure 5. DAG of an ICE mechanism

- R: Randomisation
- T: Treatment
- ► C: ICE (treatment discontinuation)
- Yt: Outcome at time t
- U: Confounder (behavioural trait)
- M_{y2}: A mechanism for assigning a value to Y.



Figure 5. DAG of an ICE mechanism

- R: Randomisation
- T: Treatment
- ► C: ICE (treatment discontinuation)
- Yt: Outcome at time t
- U: Confounder (behavioural trait)
- M_{y2}: A mechanism for assigning a value to Y.



Figure 5. DAG of an ICE mechanism

- R: Randomisation
- ► T: Treatment
- C: ICE (treatment discontinuation)
- Yt: Outcome at time t
- U: Confounder (behavioural trait)
- M_{y2}: A mechanism for assigning a value to Y.



Figure 5. DAG of an ICE mechanism

- R: Randomisation
- ► T: Treatment
- C: ICE (treatment discontinuation)
- Yt: Outcome at time t
- U: Confounder (behavioural trait)
- M_{y2}: A mechanism for assigning a value to Y.



- R: Randomisation
- T: Treatment
- Yt: Outcome at time t (survival)
- U: Confounder (patient global health)



- R: Randomisation
- T: Treatment
- Yt: Outcome at time t (survival)
- U: Confounder (patient global health)



- R: Randomisation
- T: Treatment
- Yt: Outcome at time t (survival)
- U: Confounder (patient global health)



- R: Randomisation
- ► T: Treatment
- Yt: Outcome at time t (survival)
- U: Confounder (patient global health)



Contact Information

joshua.entrop@ki.se

joshua-entrop.com



Link to the slides and materials