

or commonly know as:

"a bit more transparent way to state
your research assumptions and questions"

Jose Rivera

May 5, 2022

What are we going to talk about? I

- 1 About research
 - A typical scientific lab
 - Research hypothesis production
- 2 DAGs and PP
- 3 Example cases
 - Experimental design: the panacea
 - Simulation conventions
 - Fork bias: spurious relationships
 - Fork bias: masked relationships (a)
 - Fork bias: masked relationships (b)
 - Fork bias: multicollinearity



What are we going to talk about? II

- No more fork bias: neutral control
- Pipe bias: precision parasite
- Pipe bias: post-treatment
- Pipe bias: masked relationships
- Pipe/Fork bias: bias amplification
- Collider bias: M-bias
- Descendant bias: case control
- 4 Concluding remarks
- 5 Do you wanna know more???



1. About research

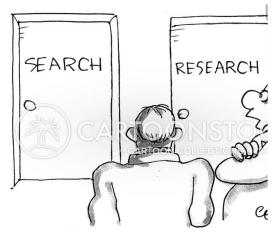
A typical scientific lab



A typical scientific lab¹

What is needed?

- 1. Quality of theory
- 2. Quality of data
- 3. Reliable procedures and code
- 4. Quality of data analysis
- 5. Documentation
- 6. Reporting



"DO WE NEED BOTH ?"

¹McElreath [12], lecture 20 and McElreath [13], chapter 17



A typical scientific lab

What we "normally" focus on?

- 1. Quality of theory
- 2. Quality of data
- 3. Reliable procedures and code
- 4. Quality of data analysis
- 5. Documentation
- 6. Reporting





A typical scientific lab

What can be improved? (with DAGs and PP)

- 1. Quality of theory
- 2. Quality of data
- 3. Reliable procedures and code
- 4. Quality of data analysis
- 5. Documentation
- 6. Reporting





1. About research

Research hypothesis production



Research hypothesis production

Well known challenges^a

- Insufficient data
- Wrong population
- Measurement error
- Selection bias
- Confounding



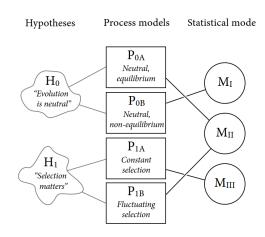


^aHernán [8], lesson 4

Research hypothesis production

but we should not forget^a

- No one-to-one relationship exists between our process models and statistical models,
- Nor between our hypothesis and a process models





^aFigure 1.2 reproduced from chapter 1 McElreath [13]

Research hypothesis production

and also

statistical models are just
 "machines to find association", not
 a reliable reflection of the theory
 (I can prove it!!).



Research hypothesis schematics²

- a. Estimand and process model
- b. Synthetic data generation
- c. Statistical model design and testing
- d. Apply statistical model to data



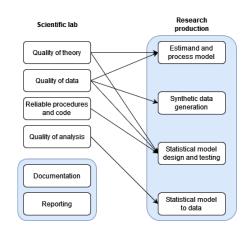
²McElreath [13], lecture 20, Pearl [16]. Follow Fogarty et al. [6] on item (c).



Research hypothesis schematic

Where does it match with the previous?

- a. Estimand and process model maps 1 (theory) and 2 (data) to a heuristic model.
- b. Synthetic data generation maps 2 (data) to an idealized data.
- c. Statistical model design and testing maps 1 (theory), 2 (data), and 3 (reliable code) to an statistical model.
- d. Apply statistical model to data maps 4 (analysis) onto a result.

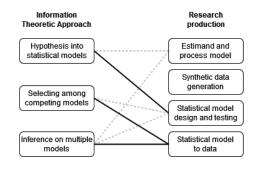




Where does the ITA fit?

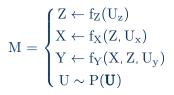
Information Theoretic Approach (ITA) is framework to select among competing models [1, 3]:

- 1. Hypothesis into statistical models, (how about a process model?)
- 2. Select among competing models, (do the code works as intended?)
- Make inferences based on one or multiple models. (do the code works as intended?, are there variables that can bias our results?)

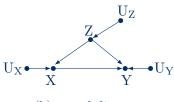




- Directed acyclic graphs (DAGs), are a type of structural causal model (SCM) [15, 4]
- DAGs can be represented by a structural model, and its associated causal diagram^a.
- we put distributional assumptions to the structural model through probabilistic programming (PP) [10]. (more in part 3)



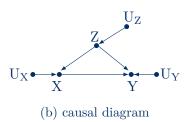
(a) structural model



^areproduced from Cinelli et al. [4].

- $V = \{Z, X, Y\}$ are called endogenous variables.
- **U** = {U_Z, U_X, U_Y} are called exogenous variables.
 (drawn when strictly required)
- $\mathbf{F} = \{f_Z, f_X, f_Y\}$ are called structural equations.

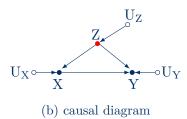
$$M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_X(Z, U_X) \\ Y \leftarrow f_Y(X, Z, U_Y) \\ U \sim P(\textbf{U}) \end{cases}$$



Causal diagram conventions [4],

- black nodes are observed variables.
- white nodes are unobserved variables.
- red nodes are variables for which we will decide its inclusion or not.

$$M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_X(Z, U_X) \\ Y \leftarrow f_Y(X, Z, U_Y) \\ U \sim P(\textbf{U}) \end{cases}$$

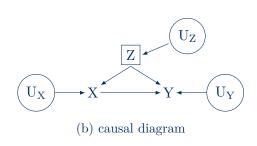




Other causal diagram conventions,

- no circle nodes are observed variables.
- circled nodes are unobserved variables.
- squared nodes are variables for which we will decide its inclusion or not.

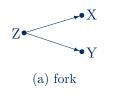
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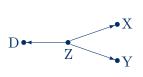




The benign case of DAG elementals

For everything can be depicted with them



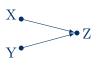


(d) descendant on fork

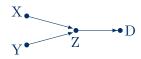




(e) descendant on pipe



(c) collider



(f) descendant on collider

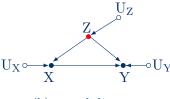
About D-separation

Causal graph theory [14, 15, 17, 18, 19],

- descendant (child, grandchild), parent (grandparent).
 (path specific)
- 2. paths (directional, non-directional).
- 3. paths are blocked or open according to the D-separation rules.
 (also path specific)
- 4. there are only four (4) D-separation rules.

$$M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_X(Z, U_X) \\ Y \leftarrow f_Y(X, Z, U_Y) \\ U \sim P(\textbf{U}) \end{cases}$$

(a) structural model



About D-separation

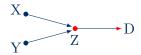
The D-separation (Directional) rules [8],

- If no variables being conditioned on, a path is blocked if and only if, two arrowheads on the path collide at some variable on the path.
- 2. Any path that contains a noncollider that has been conditioned on, is blocked (backdoor path)^a.
- 3. A collider that has been conditioned on does not block a path.
- 4. A collider that has a descendant that has been conditioned on does not block a path.











^athere is also a front-door path (if you wonder).

About D-separation

The D-separation rules implications, (independent of distributional assumptions)

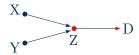
1.
$$X \perp \!\!\!\perp Y \Longrightarrow P(X, Y) = P(X) \cdot P(Y)$$

- 2. $X \perp \!\!\!\perp Y \mid Z \Longrightarrow$ $P(X, Y \mid Z) = P(X \mid Z) \cdot P(Y \mid Z)$ (same for fork or pipe)
- 3. $X \not\perp \!\!\! \perp Y | Z \Longrightarrow$ $P(X, Y|Z) \neq P(X|Z) \cdot P(Y|Z)$
- 4. $X \not\perp \!\!\! \perp Y \mid D \Longrightarrow P(X, Y \mid D) \neq P(X \mid D) \cdot P(Y \mid D)$



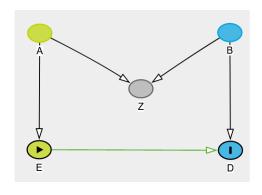






Oh DAGitty!! mijn vriendin

- browser (R package) environment for creating, editing, and analyzing causal diagrams [20].
- available online: http://dagitty.net
- But there are more fish in the sea: http://www.causalfusion.net [2] (b**** better have my \$\$\$)





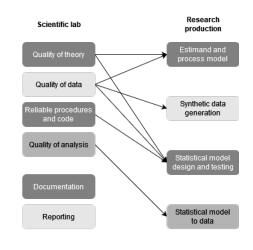
Where do DAGs and PP fit?

starts with:

- A clear definition of the estimand and process model (assumptions).
- An improved the reliability of your procedures.
- As a documentation procedure.

and leads to:

- A sound analysis, and result (even when we cannot have an answer to our question)
- An improved planning to get data.



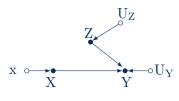




Experimental design³

- Purpose: to control all factors responsible for the outcome's variation.
 (understand the system)
- It is modeled by modifying the structural model (and causal diagram).

(a) structural model



³Cinelli et al. [4], appendix A (p. 15)



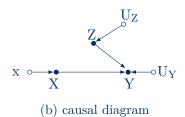
 $M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_X(x) \\ Y \leftarrow f_Y(X, Z, U_Y) \\ U \sim P(\boldsymbol{U}) \end{cases}$

Experimental design

- intervention on X can be written in do-calculus^a as: $P(\mathbf{V} \mid do(X = x))$.
- remember:

$$\begin{aligned} & \boldsymbol{V} = \{Z, X, Y\}, \\ & \boldsymbol{U} = \{U_Z, U_X, U_Y\}, \text{ and } \\ & \boldsymbol{F} = \{f_Z, f_X, f_Y\}. \end{aligned}$$

$$M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_X(x) \\ Y \leftarrow f_Y(X, Z, U_Y) \\ U \sim P(\textbf{U}) \end{cases}$$



^aan appropriate treatment can be found with the usual suspects [14, 15, 17, 18])

Effects of interest

two types of effects,

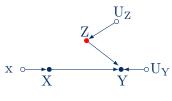
- 1. Average causal effect: ACE(x) = E[Y|do(x+1)] E[Y|do(x)]
- 2. Controlled direct effect: $CDE(x,z) = E[Y|do(x+1),do(z)] \\ E[Y|do(x),do(z)]$

points to consider:

- CDE takes a particular relevance with observational data.
- There is also a distinction between total effect and direct effect.

$$M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_x(x) \\ Y \leftarrow f_Y(X, Z, U_Y) \\ U \sim P(\textbf{U}) \end{cases}$$

(a) structural model



3. Example cases

Simulation conventions



Simulation conventions

one way to defined it,

$$Z = U_Z$$
 ; $U_Z \sim N(0, \sigma_Z)$

$$X = \beta_Z Z + U_X \hspace{1cm} ; U_X \sim N(0, \sigma_X)$$

$$Y = \beta_Z Z + \beta_X X + U_Y$$
; $U_Y \sim N(0, \sigma_Y)$

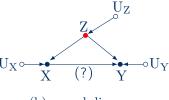
a more succinct way,

$$Z \sim N(0, \sigma_Z)$$

 $X \sim N(\beta_Z Z, \sigma_X)$
 $Y \sim N(\beta_Z Z + \beta_X X, \sigma_Y)$

$$M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_X(Z, U_X) \\ Y \leftarrow f_Y(Z, X, U_Y) \\ U \sim P(U) \end{cases}$$

(a) structural model





Spurious relationships⁴

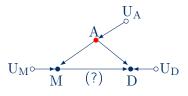
also known as,

- \blacksquare spurious association
- confounder
- \blacksquare an instance of fork bias

research question,

- Does M has a (direct) effect on D? variables,
 - A, median age at marriage
 - M, marriage rate
 - D, divorce rate

(a) structural model



⁴McElreath [12], chapter 05 (p. 125)



 $M = \begin{cases} A \leftarrow f_A(U_A) \\ M \leftarrow f_M(A, U_M) \\ D \leftarrow f_D(A, M, U_D) \\ U \sim P(\boldsymbol{U}) \end{cases}$

Simulation setting

```
# sim
A = rnorm( 100 )
M = rnorm( 100 , mean=-1*A )
D = rnorm( 100 , mean=-1*A + 0*M )
d = data.frame(A=A, M=M, D=D)
```

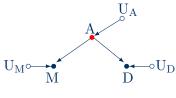
(c) R code

Implications,

- M #D
- M ⊥LD | A

$$M = \begin{cases} A \leftarrow f_A(U_A) \\ M \leftarrow f_M(A, U_M) \\ D \leftarrow f_D(A, U_D) \\ U \sim P(\textbf{U}) \end{cases}$$

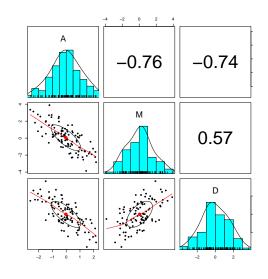
(a) structural model



"Eyeballing" analysis

based on correlation analysis,

- cor(A, D) < 0 and cor(M, D) > 0 goes in line of our "rudimentary" understanding of the data.
- why there is cor(M, D) > 0? (hint: univariate correlation)
- we include M as a covariate in our statistical model
 (is our research hypothesis)





Regression, regression!!

based on statistical analysis,

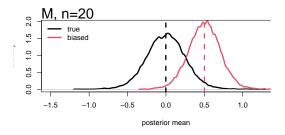
• we have two different stories, (which one is the "truth"?)

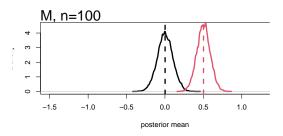
```
summary(lm(D ~ M, data=d)) # spurious relation
lm(formula = D \sim M, data = d)
Residuals:
               10 Median
-2.80012 -0.90447 -0.03866 0.80220 2.82970
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
                        0.12412 -1.877
                        0.08986 4.477 2.04e-05 ***
             0.40233
> summary(lm(D \sim A + M, data=d)) # controlled relation
lm(formula = D \sim A + M, data = d)
Residuals:
              10 Median
                                         Max
-2.27295 -0.68174 0.03781 0.78885 2.95320
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.18854
            -1.03121
            -0.06134
                        0.09362
                                -0.655
```

I'll get more data!!

imagine we can continue sampling,

- top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the incorrect model, the larger the sample size,
 - the more certain you are about your biased estimates (the winner's curse)







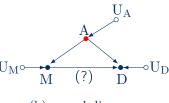
The dream team!!

based on DAG and statistical model,

- the 2nd D-separation rule requires you to control any noncollider to block the backdoor path,
 i.e. M ⊥LD | A
- conditioning on A we can find, E[D|do(m)] = E[E[D|M = m, A]] (law of total expectation)
- then we can find the ACE(m) = E[D|do(m+1)] E[D|do(m)] (Frisch-Waugh-Lovell theorem)

$$M = \begin{cases} A \leftarrow f_A(U_A) \\ M \leftarrow f_M(A, U_M) \\ D \leftarrow f_D(A, M, U_D) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

(a) structural model



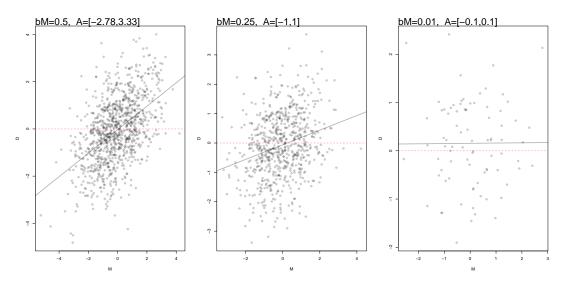
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based on DAG and statistical analysis,

■ the less biased model is the second, (assuming our DAG is true)



So, what is going on?







Masked relationships $(a)^5$

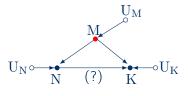
also known as,

- omitted variable bias
- an instance of fork bias

research question,

- Does N has a (direct) effect on K? variables.
 - M, mammal mass in kg.
 - N, ratio neocortex over total brain mass
 - K, Kcal. per gram of milk

(a) structural model



⁵McElreath [12], chapter 05 (p. 144)



 $M = \begin{cases} M \leftarrow f_M(U_M) \\ N \leftarrow f_N(M, U_N) \\ K \leftarrow f_K(M, N, U_K) \\ U \sim P(\textbf{U}) \end{cases}$

Simulation setting

```
# sim
M = rnorm( 100 )
N = rnorm( 100 , 1*M )
K = rnorm( 100 , 1*N + -1*M )
d = data.frame(N=N, M=M, K=K)
```

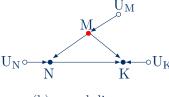
(c) R code

Implications,

- N #K
- N #K | M

$$M = \begin{cases} M \leftarrow f_M(U_M) \\ N \leftarrow f_N(M, U_N) \\ K \leftarrow f_K(M, N, U_K) \\ U \sim P(\textbf{U}) \end{cases}$$

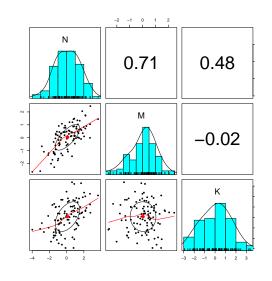
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"Eyeballing" analysis

based on correlation analysis,

- cor(N, K) > 0 goes in line of our "rudimentary" understanding of the data.
- but why there is $cor(M, k) \approx 0$? (hint: univariate correlation)
- we might not include M as a covariate in our statistical model





Regression, regression!!

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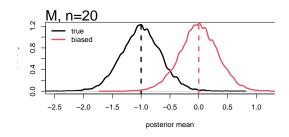
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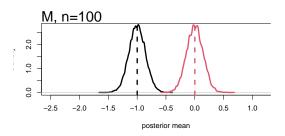
```
summarv(lm(K \sim N. data=d)) # biased estimate
Call:
lm(formula = K \sim N, data = d)
Residuals:
    Min
             10 Median
-2.8355 -0.8110 0.0188 0.7897 3.4276
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.01401
                        0.09332
                                 5.680 1.38e-07 ***
             0.53002
 summary(lm(K ~ N + M, data=d)) # less biased estima
Call:
lm(formula = K \sim N + M, data = d)
Residuals:
              10 Median
                                         Max
-2.50873 -0.72626 -0.01968 0.69016 2.93000
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.22096
                        0.09845
             0.95510
                        0.10089
                                  9.466 1.91e-15
            -1.06246
                        0.15462 -6.871 6.14e-10 ***
```

I'll get more data!!

imagine we can continue sampling,

- top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the incorrect model, the larger the sample size,
 - the more certain you are about your biased estimates







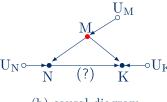
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(a) structural model



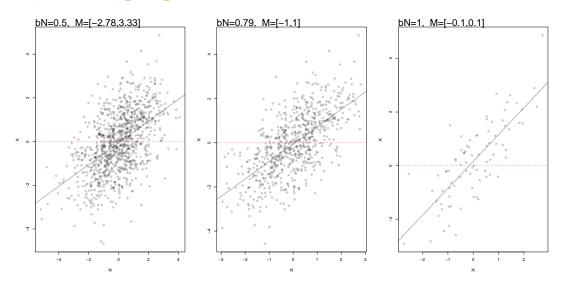
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based on DAG and statistical analysis,

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So, what is going on?





3. Example cases

Fork bias: masked relationships (b



Masked relationships $(b)^6$

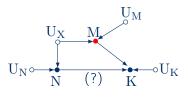
also known as,

- (unobserved) omitted variable bias
- an instance of fork bias

research question,

- Does N has a (direct) effect on K? variables.
 - U_X, unobservable (e.g. genetics)
 - M, mammal mass in kg.
 - N, neocortex over total brain mass
 - K, Kcal. per gram of milk

(a) structural model



⁶McElreath [12], chapter 05 (p. 144)



 $M = \begin{cases} N \leftarrow f_N(U_N, U_X) \\ M \leftarrow f_M(U_M, U_X) \\ K \leftarrow f_K(M, N, U_K) \\ U \sim P(\textbf{U}) \end{cases}$

Simulation setting

```
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N = rnorm( 100 , 1*U )
M = rnorm( 100 , 1*U )
K = rnorm( 100 , 1*N + -1*M )
d = data.frame(U=U,N=N,M=M,K=K)
```

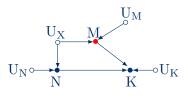
(c) R code

Implications,

- N #K
- N #K | M

$$M = \begin{cases} N \leftarrow f_N(U_N, U_X) \\ M \leftarrow f_M(U_M, U_X) \\ K \leftarrow f_K(M, N, U_K) \\ U \sim P(\textbf{U}) \end{cases}$$

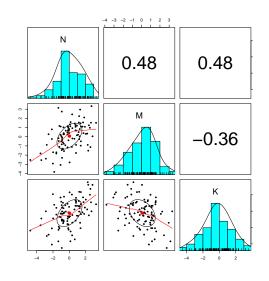
(a) structural model



"Eyeballing" analysis

based on correlation analysis,

- cor(N, K) > 0 goes in line of our "rudimentary" understanding of the data.
- cor(M, K) < 0 does NOT goes in line of our "rudimentary" understanding of the data. (hint: univariate correlation)
- we include M as a covariate in our statistical model (by chance?)



Regression, regression!!

based on statistical analysis,

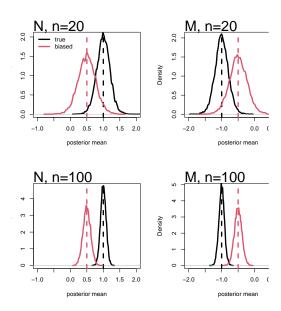
• we have two different stories, (which one is the "truth"?)

```
summarv(lm(K \sim N. data=d)) # unobserved path still
Call:
lm(formula = K \sim N. data = d)
Residuals:
             10 Median
 -3.7763 -0.8480 0.1497 0.9874 3.3530
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.24867
                        0.14573 -1.706 0.0911
                        0.09502 5.410 4.46e-07 ***
             0.51406
 summary(lm(K \sim N + M, data=d)) # unobserved path c
Call:
lm(formula = K \sim N + M, data = d)
Residuals:
     Min
               1Q Median
                                          Max
-2.58218 -0.58434 -0.00579 0.72016 1.78724
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.19978
             0.90893
                        0.06958 13.064
                                           <2e-16 ***
            -0.89676
                        0.07572 -11.843
                                           <2e-16 ***
```

I'll get more data!!

imagine we can continue sampling,

- top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the incorrect model, the larger the sample size,
 - the more certain you are about your biased estimates





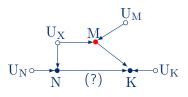
The dream team!!

based on DAG and statistical model,

- the 2nd D-separation rule requires control on any noncollider to block the backdoor path,
 i.e. N ⊥K | U_X
 (but it is unobservable)
- still we use the 2nd D-separation rule by controlling for M, i.e. N ⊥K | M
- conditioning on M we can still find, E[K|do(n)] = E[E[K|N = n, M]](law of total expectation)
- then we can find the ACE(n) = E[D|do(n+1)] E[D|do(n)] (Frisch-Waugh-Lovell theorem??)

$$M = \begin{cases} N \leftarrow f_N(U_N, U_X) \\ M \leftarrow f_M(U_M, U_X) \\ K \leftarrow f_K(M, N, U_K) \\ U \sim P(\textbf{U}) \end{cases}$$

(a) structural model

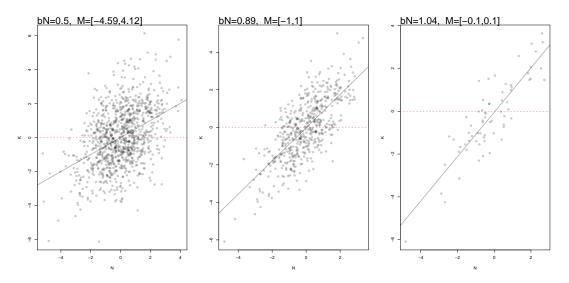


the dream team!!

based on DAG and statistical analysis,

■ the less biased model is the second, (assuming our DAG is true)

So, what is going on?





Similar scenario⁷

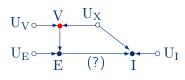
research question,

- Does E has a (direct) effect on I? variables,
 - U_X, unobservable (e.g. family context)
 - V, personal values
 - E, education
 - I, income

then,

■ we need to control by V to get an unbiased estimate of $E \to I$

(a) structural model



⁷Cinelli et al. [4] (p. 3), McElreath [13], lecture 6



 $M = \begin{cases} V \leftarrow f_M(U_V, U_X) \\ E \leftarrow f_E(V, U_E) \\ I \leftarrow f_I(E, U_X, U_I) \\ U \sim P(\textbf{U}) \end{cases}$

3. Example cases

Fork bias: multicollinearity



Multicollinearity⁸

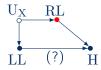
also known as,

- extreme case of masked relationships
- an instance of fork bias

research question,

- Should we include RL in our model? variables,
 - U_X, unobservable (e.g. genetics and context)
 - LL, individual's left leg
 - RL, individual's right leg
 - H, individual's height

(a) structural model



⁸McElreath [12], chapter 06 (p. 163)



 $M = \begin{cases} LL \leftarrow f_L(U_X) \\ RL \leftarrow f_L(U_X) \\ H \leftarrow f_K(RL, LL) \\ U \sim P(\textbf{U}) \end{cases}$

Simulation setting

```
# backward simulation
H = round( rnorm( 100 , 170, 2), 1)
Lp = runif( 100 , 0.5-0.05, 0.5+0.05)
LL = round( Lp*H + rnorm( 100 , 0, 1 ), 1)
RL = round( Lp*H + rnorm( 100 , 0, 1 ), 1)
d = data.frame(LL,RL,H)
```

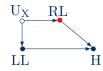
(c) R code

Implications,

■ LL #RL

$$M = \begin{cases} LL \leftarrow f_L(U_X) \\ RL \leftarrow f_L(U_X) \\ H \leftarrow f_K(RL, LL) \\ U \sim P(\textbf{U}) \end{cases}$$

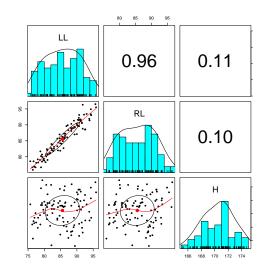
(a) structural model



"Eyeballing" analysis

based on correlation analysis,

- cor(LL, H) > 0, cor(RL, H) > 0 and cor(LL, RL) > 0 goes in line of our "understanding" of the data.
- we might not include RL as a covariate in our statistical model (based on univariate correlation)





Regression, regression!!

based on statistical analysis,

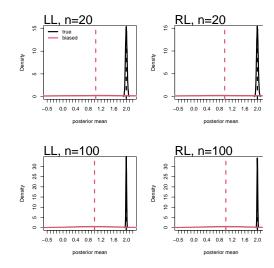
- the second regression show a smaller effect of LL,
- the second regression show way larger SE values (not rejecting the null)

```
> summarv(lm(H \sim -1 + LL. data=d)) # unbiased.
Call:
lm(formula = H \sim -1 + LL, data = d)
Residuals:
               10 Median
     Min
-17.9704 -8.3662 0.7494 10.5256 21.1464
Coefficients:
   Estimate Std. Error t value Pr(>|t|)
11 1.98486
               0.01229 161.6 <2e-16 ***
> summary(lm(H \sim -1 + LL + RL, data=d)) # ine
Call:
lm(formula = H \sim -1 + LL + RL. data = d)
Residuals:
    Min
             10 Median
                              30
                                     Max
-16.780 -8.592 0.532 10.253 18.299
Coefficients:
   Estimate Std. Error t value Pr(>|t|)
LL 1.0094
                0.6969
                         1.448
                                  0.151
     0.9757
                0.6970
                         1.400
                                  0.165
```

I'm sure data won't help

imagine we can continue sampling,

- \bullet top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the incorrect model, the larger the sample size,
 - the less certain are your biased estimates





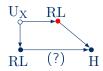
Not so great now??

based on DAG and statistical model,

- the 2nd D-separation rule requires control on any noncollider to block the backdoor path,
 i.e. LL ⊥H | U_X
 (but it is unobservable)
- we still use the 2nd D-separation rule by controlling for RL, but still we have LL 业H | RL
- issue goes beyond the backdoor path the issue is that RL and LL provide the same information, i.e. they form a singular matrix, (is like having a causal model like b)

$$M = \begin{cases} LL = RL \\ RL \leftarrow f_L(U_X) \\ H \leftarrow f_K(RL) \\ U \sim P(\textbf{U}) \end{cases}$$

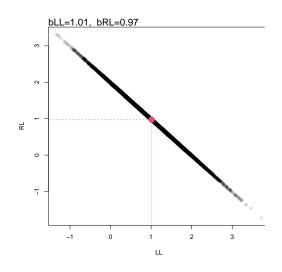
(a) structural model



So, what is going on then??

the parameters under the second regression,

- are in a thin ridge $Cor(bLL, bRL) \approx -1$
- statistical model does not find only one solution (red dot), the thin ridge implies there are infinite solutions for the model, (related to the singular matrix thing)





Not so great now??

based on DAG and statistical analysis,

■ the less biased and more precise model is the first,
(assuming our DAG is true)

3. Example cases

No more fork bias: neutral contro



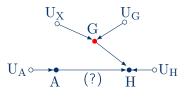
Neutral control⁹

also known as,

- precision "booster"
- similar to experimental design research question,
- Should we include G on our model? variables,
 - A, "hearing" age
 - G, gender
 - \blacksquare U_X, unobservable (e.g. no idea yet)
 - H, inverse logit of entropy (approximate of speech intelligibility)

$$M = \begin{cases} G \leftarrow f_G(U_G, U_X) \\ A \leftarrow f_A(U_A) \\ H \leftarrow f_H(A, G, U_H) \\ U \sim P(\textbf{U}) \end{cases}$$

(a) structural model





⁹Cinelli et al. [4] (p. 4)

Simulation setting

```
# sim
G = sample( 0:1, 100 , replace=T )
A = rnorm( 100 )
H = rnorm( 100 , -1*A + -1*G )
d = data.frame(G=G,A=A,SI=SI)
```

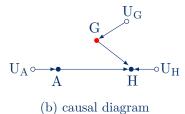
(c) R code

Implications,

- A ⊥LG
- A #H
- G #H

$$M = \begin{cases} G \leftarrow f_G(U_G) \\ A \leftarrow f_A(U_A) \\ H \leftarrow f_H(A, G, U_H) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

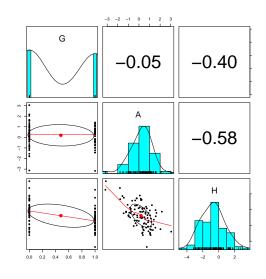
(a) structural model



"Eyeballing" analysis

based on correlation analysis,

- cor(G, H) < 0, $cor(G, A) \approx 0$ and cor(A, H) < 0 goes in line of our "rudimentary" understanding of the data.
- we include both as a covariate in our statistical model





Regression, regression!!

based on statistical analysis,

- almost no change on our estimates,
- lower standard errors for A when
 G is included
 (because we have explained variability

in H)

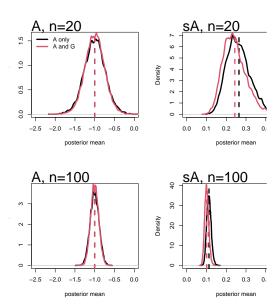
```
summary(lm(H \sim A, data=d)) # correct estimate
Call:
lm(formula = H \sim A, data = d)
Residuals:
    Min
             10 Median
-3.4714 -0.8797 -0.0633 0.8963 2.4346
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.5770
                         0.1216 -4.746 7.07e-06 ***
             -0 8410
                         0.1183 -7.108 1.92e-10 ***
 summary(lm(H ~ A + G, data=d)) # correct estimate,
Call:
lm(formula = H \sim A + G, data = d)
Residuals:
    Min
             10 Median
-2.7994 -0.6914 0.0579 0.7796 1.8274
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
            -0.87360
                        0.10090 -8.658 1.05e-13
            -1.25786
                        0.20371 -6.175 1.55e-08
```



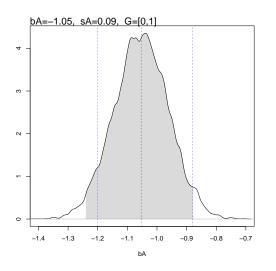
I'll get more data!!

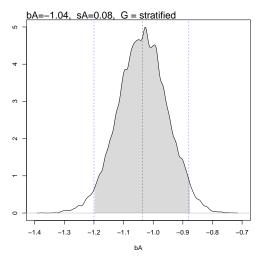
imagine we can continue sampling,

- top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the second model, the larger the sample size,
 - the more certain you are about your non-biased estimates (under the any model)



So, what is going on?







3. Example cases

Pipe bias: precision parasite



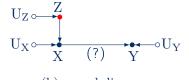
Precision parasite¹⁰

research question,

- Should we include Z in the model?
- variables,
 - **■** Z,
 - X,
 - Y,

$$M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_X(Z, U_X) \\ Y \leftarrow f_Y(X, U_Y) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

(a) structural model



¹⁰McElreath [13], lecture 6, Cinelli et al. [4] (p. 5)



Simulation setting

```
# Sim
Z = rnorm( 100 )
X = rnorm( 100 , 1*Z )
Y = rnorm( 100 , 1*X )
d = data.frame(Z,X,Y)
```

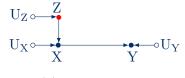
(c) R code

Implications,

- X #Y
- Z #Y | X

$$M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_X(Z, U_X) \\ Y \leftarrow f_Y(X, U_Y) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

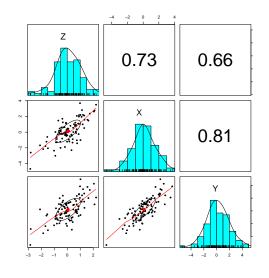
(a) structural model



"Eyeballing" analysis

based on correlation analysis,

- cor(Z, X) > 0 is not large enough to discard it as multicollinearity.
- cor(Z, Y) > 0 and cor(X, Y) > 0 indicate both should be in our model
 (it might be our research hypothesis)





Regression, regression!!

based on statistical analysis,

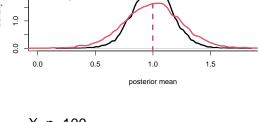
- no bias in parameter if Z is in,
- but we loose precision on X

```
> summary(lm(Y ~ X, data=d)) # unbiased effect, more
lm(formula = Y \sim X, data = d)
Residuals:
     Min
               10 Median
                                          Max
-2.41746 -0.73659 -0.09384 0.63812 2.10338
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.03433
             1 16908
                        0.06717 17.405
                                           <2e-16 ***
 summary(lm(Y \sim X + Z, data=d)) # unbiased effects,
Call:
lm(formula = Y \sim X + Z, data = d)
Residuals:
               10 Median
                                          Max
-2.27019 -0.74072 -0.06355 0.66643 2.20770
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.04722
                                            0.649
             1.08881
                                 10.512
                                           <2e-16 ***
             0.15431
                        0.15159
                                  1.018
                                            0.311
```

With more data??

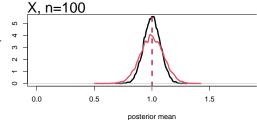
imagine we can continue sampling,

- top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the second model, the larger the sample size,
 - still less precise estimates
 - more difficult to test hypothesis



X, n=20

less precise





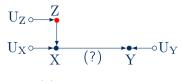
Now, what is going on here??

based on DAG and statistical model,

conditioning on Z reduces variation on X

$$M = \begin{cases} Z \leftarrow f_Z(U_Z) \\ X \leftarrow f_X(Z, U_X) \\ Y \leftarrow f_Y(X, U_Y) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

(a) structural model



Now, what is going on here??

based on DAG and statistical analysis,

■ the more appropriate model (for inference) is the first,
(assuming our DAG is true)

So, what is going on? $pipe1_triptych.pdf$

3. Example cases

Pipe bias: post-treatment



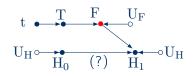
Post-treatment bias¹¹

case of,

- full mediation
- research question,
- Does the treatment T works? variables,
 - H_0 , height of plant at t=0
 - T, antifungal treatment
 - F, presence of fungus
 - H_1 , height of plant at t = 1

$$\mathbf{M} = \begin{cases} \mathbf{H}_0 \leftarrow \mathbf{f}_{H}(\mathbf{U}_{H}) \\ \mathbf{T} \leftarrow \mathbf{f}_{T}(\mathbf{t}) \\ \mathbf{F} \leftarrow \mathbf{f}_{F}(\mathbf{T}, \mathbf{U}_{F}) \\ \mathbf{H}_1 \leftarrow \mathbf{f}_{H}(\mathbf{F}, \mathbf{H}_0, \mathbf{U}_{H}) \\ \mathbf{U} \sim \mathbf{P}(\mathbf{U}) \end{cases}$$

(a) structural model



¹¹McElreath [12], chapter 6 (p. 170)



Simulation setting

```
# sim
h0 = rnorm( 100 , 10, 2)
Tr = rep( 0:1 , each=100/2 )
Fu = rbinom( n , size=1 , prob=0.5 + -0.4*Tr )
h1 = h0 + rnorm( n , 5 + -3*Fu)
d = data.frame( h0=h0, h1=h1, Tr=Tr, Fu=Fu )
```

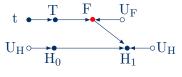
(c) R code

Implications,

- T ⊥⊥H₀
- \blacksquare T $\not\perp H_1$
- \blacksquare T $\not\perp$ H₁ | F

$$M = \begin{cases} H_0 \leftarrow f_H(U_H) \\ T \leftarrow f_T(t) \\ F \leftarrow f_F(T, U_F) \\ H_1 \leftarrow f_H(F, H_0, U_H) \\ U \sim P(\textbf{U}) \end{cases}$$

(a) structural model



Descriptive analysis

based on descriptive analysis,

- positive change in height with treatment.
- negative change in height with fungus.
- diluted relationship for T when both are in the model (hint: blocking path of information)

```
mean
                sd
                              se
                       50 0.248
                       50 0.205
Fu
       mean
       4.93 0.953
                      62 0.121
       1.81 0.902
      Fu
              mean
                                   se
                             19 0.186
              1.76 0.861
                             31 0.155
              4.93 1.02
                             43 0.155
              2.011.12
                              7 0.423
```



Again regression!!

based on statistical analysis we have two different stories (but not quite),

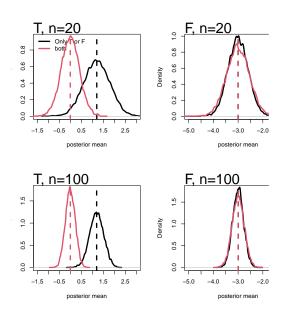
- treatment has a significant effect,
- but gets completely diluted when fungus is considered in the model

```
summary(lm(h1-h0 \sim Tr, data=d)) # only treatment
lm(formula = h1 - h0 \sim Tr, data = d)
Residuals:
             10 Median
-4.1166 -1.0929 0.1755 1.2621 3.3990
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)
              1 5656
                         0.3215
> summary(lm(h1-h0 ~ Tr + Fu, data=d)) # only fungus
lm(formula = h1 - h0 \sim Tr + Fu. data = d)
Residuals:
    Min
             10 Median
                                     Max
-2.1691 -0.4823 0.0963 0.5315 2.0357
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 4.86397
                                           <2e-16 ***
             0.09138
                        0.21579 0.423
                                            0.673
            -3.07122
                        0.22229 -13.816
                                           <2e-16 ***
```

I can guess what happens with more data!!

imagine we can continue sampling,

- top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the "incorrect" model, the larger the sample size,
 - the more certain you are about your biased T estimates (not F) (this result is not wrong!)



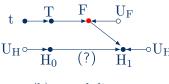
The dream team!!

based on DAG and statistical model,

- the 2nd D-separation states that if you to control any noncollider you block the backdoor path,
 i.e. T ⊥⊥H₁ | F
- therefore if we want to find if T = 1 works, we should not stratify by F

$$M = \begin{cases} H_0 \leftarrow f_H(U_H) \\ T \leftarrow f_T(t) \\ F \leftarrow f_F(T, U_F) \\ H_1 \leftarrow f_H(F, H_0, U_H) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

(a) structural model





the dream team!!

based on DAG and statistical analysis,

■ the model that answers our research question is the first one, (assuming our DAG is true)

So, what is going on? pipe2_triptych.pdf

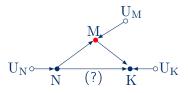


Masked relationships¹²

also known as,

- mediation
- Simpson's paradox
- an instance of pipe bias research question,
- Does N has a (direct) effect on K? variables,
 - M, mammal mass in kg.
 - N, neocortex over total brain mass
 - K, Kcal. per gram of milk

(a) structural model



¹²McElreath [12], chapter 05 (p. 144)



 $M = \begin{cases} N \leftarrow f_N(U_N) \\ M \leftarrow f_M(N, U_M) \\ K \leftarrow f_K(M, N, U_K) \\ U \sim P(\textbf{U}) \end{cases}$

Simulation setting

```
# sim
N = rnorm( 100 )
M = rnorm( 100 , 1*N )
K = rnorm( 100 , 1*N + -1*M )
d = data.frame(N=N,M=M,K=K)
```

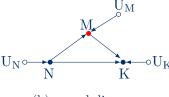
(c) R code

Implications,

- N #K
- N #K | M

$$M = \begin{cases} N \leftarrow f_N(U_N) \\ M \leftarrow f_M(M, U_M) \\ K \leftarrow f_K(M, N, U_K) \\ U \sim P(\textbf{U}) \end{cases}$$

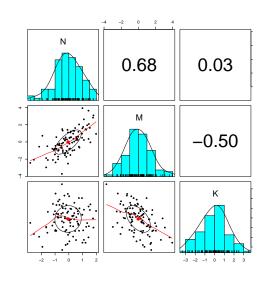
(a) structural model



"Eyeballing" analysis

based on correlation analysis,

- cor(M, K) < 0 does NOT goes in line of our "rudimentary" understanding of the data.
- and why there is $cor(N, K) \approx 0$? (hint: univariate correlation)
- we include N as a covariate in our statistical model
 (is our research hypothesis)





Regression, regression!!

based on statistical analysis,

■ two regressions with two different results, which model is the "true"?

```
summary(lm(K \sim N, data=d)) # biased estimate
Call:
lm(formula = K \sim N, data = d)
Residuals:
             10 Median
                                     Max
-3.1751 -0.9009 0.1519 0.8574 3.6041
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.10412
                         0.13808
             0.05005
                        0.14487 0.345
                                            0.730
> summary(lm(K ~ N + M, data=d)) # less biased estimate
Call:
lm(formula = K \sim N + M, data = d)
Residuals:
              1Q Median
-2.58484 -0.59175 0.04378 0.61175 2.43360
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.06181
                        0.09825
            0.98297
                        0.13994
                                7.024 2.98e-10 ***
            -0.93107
                        0.09457 -9.846 2.89e-16 ***
```

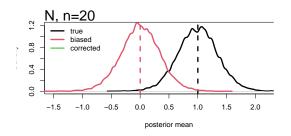
I'll get more data!!

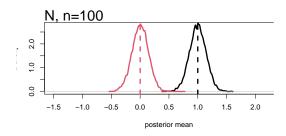
imagine we can continue sampling,

- \blacksquare top: 10,000 samples n = 20
- \blacksquare bottom: 10,000 samples n = 100

the larger the sample size,

- the more certain you are about your estimates
- the more mistaken you are about your research question (under the "incorrect" model)







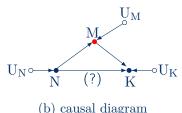
The dream team!!

based on DAG and statistical model,

- the 2nd D-separation rule requires you to control any noncollider to block the backdoor path,
 i.e. N ⊥K | M
- conditioning on M we can find, E[K|do(n)] = E[E[K|N = n, M]] (law of total expectation)
- then we can find the ACE(n) = E[D|do(n+1)] E[D|do(n)] (Frisch-Waugh-Lovell theorem)

$$M = \begin{cases} N \leftarrow f_N(U_N) \\ M \leftarrow f_M(M, U_M) \\ K \leftarrow f_K(M, N, U_K) \\ U \sim P(\textbf{U}) \end{cases}$$

(a) structural model





the dream team!!

based on DAG and statistical analysis,

■ the less biased model is the second, (assuming our DAG is true)

So, what is going on? $pipe3_triptych.pdf$

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Bias amplification¹³

also known as,

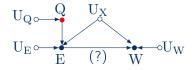
- (unobserved) omitted variable bias
- related to instrumental variables
- an instance of fork bias

research question,

- Do E has a (direct) effect on W? variables,
 - Q, instrumental variable (e.g. quarter of the year)
 - E, educational level
 - \blacksquare U_X, unobservables (e.g. ability)
 - W, future wages

$$M = \begin{cases} Q \leftarrow f_Q(U_Q) \\ E \leftarrow f_E(Q, U_X, U_E) \\ W \leftarrow f_W(E, U_X, U_W) \\ U \sim P(\textbf{U}) \end{cases}$$

(a) structural model



¹³McElreath [12], chapter 14 (p. 455), Cinelli et al. [4] (p. 5)



Simulation setting

```
# sim
U = rnorm( 100 )
Q = sample( 1:4, 100, replace=T )
E = rnorm( 100 , 1*Q + 1*U )
W = rnorm( 100 , 0*E + 1*U )
d = data.frame(U=U,Q=Q,E=E,W=W)
```

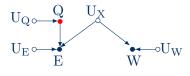
(c) R code

Implications,

- **■** E #W
- \blacksquare E $\bot\!\!\!\bot W \mid U_X \text{ (impossible)}$
- \blacksquare Q $\bot\!\!\!\bot U_X$ (cannot be tested)
- Q ⊭E
- Q ⊥LW | E (cannot be tested) (exclusion restriction)

$$M = \begin{cases} Q \leftarrow f_Q(U_Q) \\ E \leftarrow f_E(Q, U_X, U_E) \\ W \leftarrow f_W(U_X, U_W) \\ U \sim P(\textbf{U}) \end{cases}$$

(a) structural model

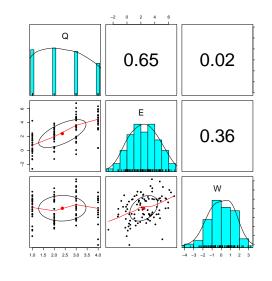


"Eyeballing" analysis

based on correlation analysis,

- cor(Q, E) > 0 and cor(E, W) > 0 goes in line of our "rudimentary" understanding of the data.
- cor(Q, W) > 0 tells you about the exclusion restriction?

 (hint: No)
- we might NOT include Q as a covariate in our statistical model (but is the instrumental variable!!!)





Regression, regression!!

based on statistical analysis,

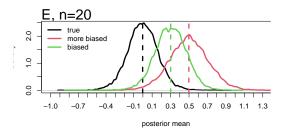
- two different stories (which model is the "truth"?)
- one is "worse"/"better" than the other?
- are both wrong?

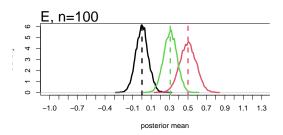
```
summary(lm(W ~ E, data=d)) # biased
lm(formula = W \sim E, data = d)
Residuals:
    Min
             10 Median
-4.0726 -0.9674 0.1771 0.9234 2.8787
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.60816
                       0.20506 -2.966 0.003793 **
             0.25408
                       0.06559 3.873 0.000194 ***
> summary(lm(W ~ E + O, data=d)) # more biased
call.
lm(formula = W \sim E + 0. data = d)
Residuals:
             10 Median
-3.7405 -0.9774 0.0879 0.9162 2.9825
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.12229
                        0.30650
             0.42054
                        0.08262
                                 5.090 1.75e-06 ***
            -0.47716
                        0.15361 -3.106 0.00249 **
```

I'll get more data!!

imagine we can continue sampling,

- top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the incorrect model, the larger the sample size,
 - the more certain you are about your biased estimates (under the any model!!)







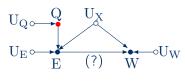
Yo, what is going on??

based on DAG and statistical model,

- the 2nd D-separation rule requires control on any noncollider to block the backdoor path,
 i.e. E ⊥⊥W | U_X
 (but U_X is unobservable)
- if we use Q in the model, the 3rd D-separation rule kicks in:
 "A collider that has been conditioned on does not block a path."
 i.e. Q ⊥ U_X | E
 (e.g. switch, electricity, and light bulb)

$$M = \begin{cases} Q \leftarrow f_Q(U_Q) \\ E \leftarrow f_E(Q, U_X, U_E) \\ W \leftarrow f_W(E, U_X, U_W) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

(a) structural model



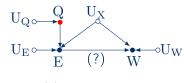
Yo, what is going on??

open paths?:

- \blacksquare E \rightarrow W
- \blacksquare E \rightarrow U_x \rightarrow W
- $\blacksquare \ E \to U_x \to Q \to E \to W$
- \blacksquare E \to U_x \to Q \to E \to U_X \to W

$$M = \begin{cases} Q \leftarrow f_Q(U_Q) \\ E \leftarrow f_E(Q, U_X, U_E) \\ W \leftarrow f_W(E, U_X, U_W) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

(a) structural model



What should I do then??

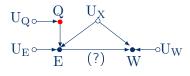
$$egin{aligned} \begin{pmatrix} \mathbf{W} \\ \mathbf{E} \end{pmatrix} &\sim \mathbf{MVN} \left[\begin{pmatrix} \mu_{\mathbf{W}} \\ \mu_{\mathbf{E}} \end{pmatrix}, \mathbf{\Sigma} \right] \\ \mu_{\mathbf{W}} &= \alpha_{\mathbf{W}} + \beta_{\mathbf{EW}} \mathbf{E} \\ \mu_{\mathbf{E}} &= \alpha_{\mathbf{E}} + \beta_{\mathbf{QE}} \mathbf{Q} \end{aligned}$$
(c) probabilistic model

based on DAG and statistical model, use the knowledge of the system

- \blacksquare one model for $Q \to E$
- \blacksquare one model for $E \to W$
- use the knowledge that cov(E, W) > 0 due to unobserved confounder U_X, (i.e. cov(E, W) = Σ = SRS)

$$M = \begin{cases} Q \leftarrow f_Q(U_Q) \\ E \leftarrow f_E(Q, U_X, U_E) \\ W \leftarrow f_W(E, U_X, U_W) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

(a) structural model



did it worked???

based on DAG and bayesian statistical analysis,

- appropriate value estimated, (assuming our DAG is true)
- it picks up some of the unobserved correlation R[1, 2]

```
mean
        0.02 \ 0.18 \ -0.26
       -0.14 0.16 -0.40
        1.00 0.07
boe
bEW
        0.05 0.07 -0.06
R[1,1]
                   1.00
R[1,2]
                    0.15
                          0.50
R[2,1]
                    0.15
                          0.50
        1.25 0.10
                    1.11
        1.39 0.10
                   1.24
```



did it worked???

frequentists guys apply Two Stage Least Squares (2SLS)^a:

- \blacksquare regress $E \leftarrow Q$,
- predict Ê,
- \blacksquare regress W \leftarrow \hat{E}

```
s1 = lm( E ~ Q, data=d)
Ehat = s1$fitted.values
s2 = lm( W ~ Ehat, data=d)
# se not corrected
require(AER)
tsls = ivreg( W ~ E | Q, data=d)
# se corrected
```

```
summary(s2)
lm(formula = W \sim Ehat. data = d)
Residuals:
             10 Median
-4.1911 -1.0670 -0.0643 1.3802 4.6813
Coefficients:
           Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.5992
              0.2093
                        0.1263 1.658
Fhat
                                           0.101
> summary(tsls)
ivreg(formula = W \sim E \mid Q, data = d)
Residuals:
             10 Median
-3.6571 -1.1852 -0.1819 1.0945 4.5328
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
                         0.3325 -1.802
(Intercept) -0.5992
              0.2093
                         0.1145
                                 1.829
                                          0.0705
```

^aHanck et al. [7], section 12.1, See McElreath [12] chapter 14 (p. 460) for a discussion on the method.

So, what is going on? pipefork1_triptych.pdf

Similar case, contextual confounds¹⁴ research question,

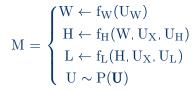
- Does W has an effect on L?
- should we include H in our model?

variables,

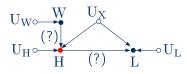
- W, win the lottery
- H, happiness
- U_X, contextual confound
- L, lifespan

Short answer;

- for total effects: No (two question marks together)
- for direct effect of $H \to L$: will be always counfounded



(a) structural model





¹⁴McElreath [13], lecture 6

3. Example cases

Collider bias: M-bias



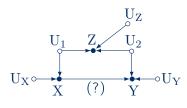
M-bias¹⁵

case of,

- bias on pre-treatment variable research question,
- Should we include Z in our model? variables,
 - Z, "health" quality of friends (defined as a continuum)
 - X, health of individual 1
 - \blacksquare U₁, hobbies of individual 1
 - Y, health of individual 2
 - \blacksquare U₂, hobbies of individual 2

$$M = \begin{cases} X \leftarrow f_X(U_1, U_X) \\ Z \leftarrow f_Z(U_1, U_2, U_Z) \\ Y \leftarrow f_Y(X, U_2, U_Y) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

(a) structural model



¹⁵McElreath [13], lecture 6; Cinelli et al. [4] (p. 4)



Simulation setting

```
# sim
U1 = sample(1:5, 100 , replace=T)
U2 = sample(1:5, 100 , replace=T)
Z = rnorm( 100 , 0.5*U1 + 0.5*U2)
X = rnorm( 100 , 1*U1 + 0*Z)
Y = rnorm( 100 , 1*U2 + 0*X + 0*Z)
d = data.frame(U1,U2,Z,X,Y)
```

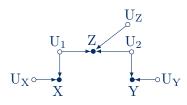
(c) R code

Implications,

- X ⊥1Y
- X #Y | Z

$$M = \begin{cases} X \leftarrow f_X(U_1, U_X) \\ Z \leftarrow f_Z(U_1, U_2, U_Z) \\ Y \leftarrow f_Y(X, U_2, U_Y) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

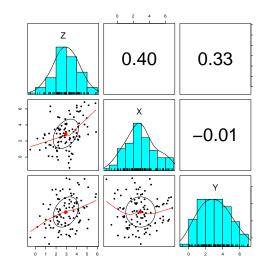
(a) structural model



Descriptive analysis

based on descriptive analysis,

- \blacksquare Cor(X, Y) \approx 0, quite low
- larger Cor(Z, Y), while Cor(Z, X) is not high enough to discard it as a cause of multicollinearity,
- we might include Z rather than X (but the effect of X is our interest!!)
- then we include Z and X





Again regression!!

based on statistical analysis,

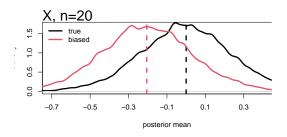
- X does not have an effect of Y, (in the first nor the second model)
- but X has an (non-negligible)
 effect when Z is in the model
 (but we do not reject the null)
- The increase of the X effect might lead you to think that with more data, we can reject the null (and you would be right!!)
- But is it correct to include Z?

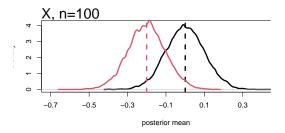
```
summary(lm(Y ~ X, data=d)) # unbiased effects (effi
lm(formula = Y \sim X. data = d)
Residuals:
             10 Median
-3.7452 -1.3300 -0.0253 1.2414 3.9479
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 3.067474
> summary(lm(Y \sim X + Z, data=d)) # biased effects (e
lm(formula = Y \sim X + Z, data = d)
Residuals:
    Min
             10 Median
                                      Max
 -3.3756 -1.0898 0.0351 1.0540
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.83324
             -0.15765
             0.56590
                         0.14974
                                    3 779 0 000272
```

Ok, I get it!!, more data, more wrong!!

imagine we can continue sampling,

- top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the "incorrect" model, the larger the sample size,
 - the more certain you are about your biased estimates (with enough you could reject the null)







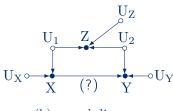
The dream team strikes back!!

based on DAG and statistical model,

- the 3rd D-separation states that a collider that has been conditioned on does not block a path, in this case: $X \to U_1 \to Z \to U_2 \to Y$ i.e. $X \not\perp \!\!\! \perp \!\!\! \perp Y \mid Z$
- therefore if we want to find the direct effect of $X \to Y$, we should not stratify by Z

$$\mathbf{M} = \begin{cases} \mathbf{X} \leftarrow f_{\mathbf{X}}(\mathbf{U}_1, \mathbf{U}_{\mathbf{X}}) \\ \mathbf{Z} \leftarrow f_{\mathbf{Z}}(\mathbf{U}_1, \mathbf{U}_2, \mathbf{U}_{\mathbf{Z}}) \\ \mathbf{Y} \leftarrow f_{\mathbf{Y}}(\mathbf{X}, \mathbf{U}_2, \mathbf{U}_{\mathbf{Y}}) \\ \mathbf{U} \sim P(\mathbf{U}) \end{cases}$$

(a) structural model





The dream team strikes back!!

based on DAG and statistical analysis,

■ the model that answers our research question is the first one, (assuming our DAG is true)

So, what is going on? $\operatorname{collider4_triptych.pdf}$

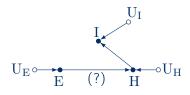


Case control¹⁶

also,

- an instance of descendant bias research question,
 - Does E has a (direct) effect on H?
- Should we include I on our model? variables,
- E, education
 - H, hours in occupation (standardized)
 - I, income

(a) structural model



¹⁶McElreath [13], lecture 06; Cinelli et al. [4] (p. 8)



 $M = \begin{cases} E \leftarrow f_E(U_E) \\ H \leftarrow f_H(E, U_H) \\ I \leftarrow f_I(H, U_I) \\ U \sim P(\textbf{U}) \end{cases}$

Simulation setting

```
# sim
E = rnorm( 100 )
H = rnorm( 100 , -1*E )
I = rnorm( 100 , -1*H )
d = data.frame(E,H,I)
```

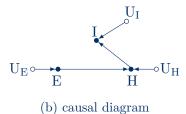
(c) R code

Implications,

- E #H
- E #I | H

$$M = \begin{cases} E \leftarrow f_E(U_E) \\ H \leftarrow f_H(E, U_H) \\ I \leftarrow f_I(H, U_I) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

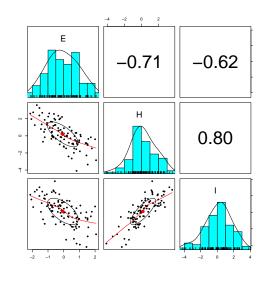
(a) structural model



"Eyeballing" analysis

based on correlation analysis,

- cor(E, I) < 0 does NOT goes in line of our "rudimentary" understanding of the data.
- while cor(H, I) > 0 indicate the more you work the more you gain (but is it the only way?)
- since cor(H, I) is high we might include it as a covariate in our statistical model (to improve the precision?)





Regression, regression!!

based on statistical analysis,

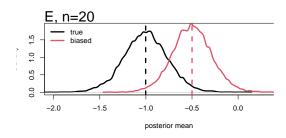
- we now have two models with two different "levels" of effects
- which one is the "truth"?

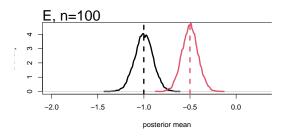
```
summarv(lm(H \sim E. data=d)) # unbiased effects
Call:
lm(formula = H \sim E. data = d)
Residuals:
               10 Median
 -2.19319 -0.60621 -0.06694 0.55674 2.77776
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.04689
                        0.09534 0.492
            -0.90223
                        0.08930 -10.104
 summary(lm(H ~ E + I. data=d)) # biased effects
Call.
lm(formula = H \sim E + I, data = d)
Residuals:
                    Median
                                         Max
-1 22991 -0 54882
                   0.01153 0.46886 1.79879
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.05036
            -0.45847
                        0.07915
                                 -5.793 8.57e-08
             0.55017
                        0.05728
                                  9.604 9.61e-16
```

The data tell-tell story!!

imagine we can continue sampling,

- top: 10,000 samples n = 20
- bottom: 10,000 samples n = 100 under the incorrect model, the larger the sample size,
 - the more certain you are about your biased estimates







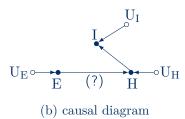
The dream team!!

based on DAG and statistical model,

- stratifying (controlling) on I, we are already explaining variability in H
 (I is a descendant of H)
- the remaining is explained by E (big chunk is already explained)

$$M = \begin{cases} E \leftarrow f_E(U_E) \\ H \leftarrow f_H(E, U_H) \\ I \leftarrow f_I(H, U_I) \\ U \sim P(\boldsymbol{U}) \end{cases}$$

(a) structural model





the dream team!!

based on DAG and statistical analysis,

■ the less biased model is the first, (assuming our DAG is true)



So, what is going on? $descendant 1_trip tych.pdf$

4. Concluding remarks



Concluding remarks

- Research is filled with challenges (you: duh!!)
- Statistical models are not theory (you: so obvious again!!)
- Don't trust your statistical model when no DAG is involved (me: how about that?!)
- For explanation, without a DAG the (sample) size does not matter (me: sorry?!)
- For prediction, sometimes a DAG can help (me: did you expect this one?!)



Concluding remarks

Additionally, simulation can serve,

- a reflection of a hypothesis, and its research complexities (me: DAGs baby!!)
- a place where you can reflect the status of a population (test what happens if??, post-stratification??)
- as a data where you can test your statistical model on various purposes
 (parameter recovery, power?)

think2.jpg



5. Do you wanna know more???



5. Do you wanna know more????



- [1] Anderson, D. [2008]. Model Based Inference in the Life Sciences: A Primer on Evidence, Springer.
- [2] Bareinboim, E. and Pearl, J. [2016]. Causal inference and the data-fusion problem, Proceedings of the National Academy of Sciences 113(27): 7345–7352. doi: https://doi.org/10.1073/pnas.1510507113.
- [3] Chamberlain, T. [1965]. The method of multiple working hypotheses, Science 148(3671): 754–759. url: https://www.jstor.org/stable/1716334.
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