

# Causality and biases

Rafał Urbaniak, Nikodem Lewandowski  
(LoPSE research group, University of Gdansk)

# Some hypotheses to consider

## Newsworthiness

“It seems the most newsworthy scientific studies the least trustworthy.”  
What could explain this?

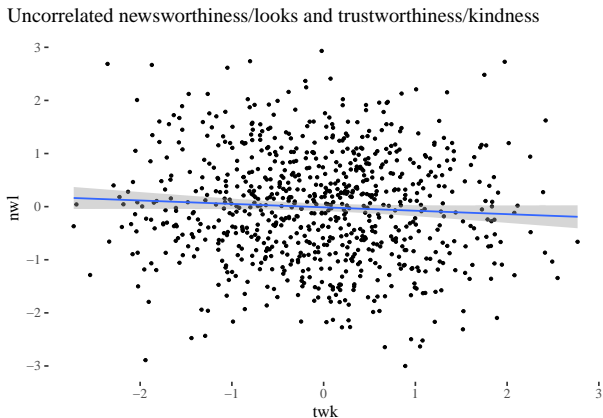
## Jerks

“It seems good-looking men are jerks.” What could explain this?

# Selection-distortion effect

```
N <- 800 #proposals/candidates
p <- .5  #proportion to select
# uncorrelated newsworthiness/looks and trustworthiness/kindness
nwl <- rnorm(N)
twk <- rnorm(N)
cor(nwl,twk)
```

```
## [1] -0.06152328
```



## Selection-distortion effect

```
s <- nwl + twk # total score  
q <- quantile( s , 1-p ) # top 10% threshold  
selected <- ifelse( s >= q , TRUE , FALSE )  
cor( twk[selected] , nwl[selected] )
```

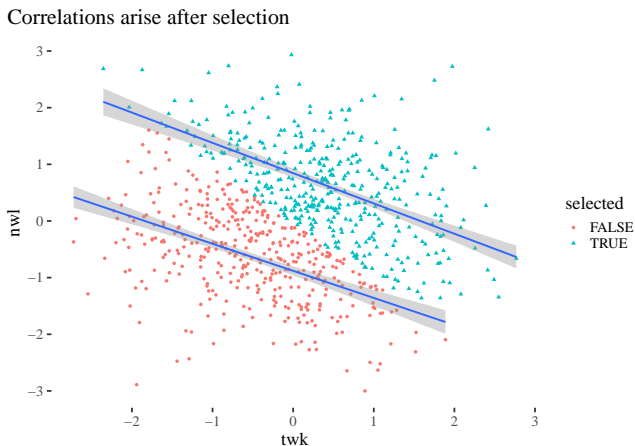
```
## [1] -0.5433415
```

```
cor( twk[!selected] , nwl[!selected] )
```

```
## [1] -0.5040041
```

# Selection-distortion effect

```
ggplot() + geom_point(aes(  
  x = twk, y = nwl, color = selected, shape = selected))+  
geom_smooth(aes(  
  x = twk, y = nwl, group = selected), method = "lm")+th+  
ggtitle("Correlations arise after selection")
```



## Multiple regression will not save you

```
news <- list(nwl = nwl, twk = twk,
            sel = as.integer(selected+1))

newsTWK <- quap(
  alist(
    nwl ~ dnorm( mu , sigma ) ,
    mu <- a + t * twk ,
    a ~ dnorm( 0 , 2 ) ,
    t ~ dnorm( 0 , .2 ) ,
    sigma ~ dexp( 1 )
  ) ,
  data= news )

precis(newsTWK)
```

##		mean	sd	5.5%	94.5%
## a		-0.01252908	0.03613758	-0.07028391	0.045225751
## t		-0.06223462	0.03627592	-0.12021054	-0.004258699
## sigma		1.02131620	0.02550846	0.98054875	1.062083648

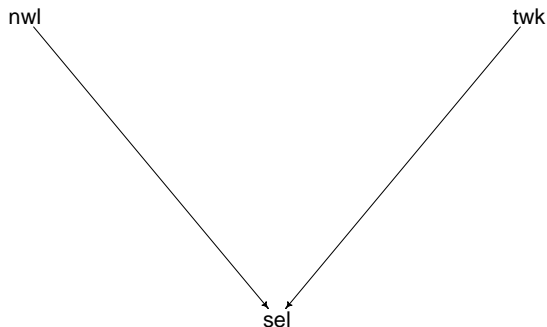
## Multiple regression will not save you

```
newsTWKselected <- quap(  
  alist(  
    nwl ~ dnorm( mu , sigma ) ,  
    mu <- a[sel] + t[sel] * twk ,  
    t[sel] ~ dnorm( 0 , .2 ) ,  
    a[sel] ~ dnorm(0, 2),  
    sigma ~ dexp( 1 )  
  ) ,  
  data= news )  
  
precis(newsTWKselected, depth = 2)
```

##		mean	sd	5.5%	94.5%
##	t[1]	-0.4583950	0.04047583	-0.5230832	-0.3937068
##	t[2]	-0.5129769	0.04012847	-0.5771100	-0.4488439
##	a[1]	-0.8693598	0.04099812	-0.9348828	-0.8038369
##	a[2]	0.8342353	0.03918357	0.7716123	0.8968582
##	sigma	0.6967769	0.01741858	0.6689387	0.7246152

# Collider bias

```
newsDAG <- dagitty (  
  "dag{  
    nwl -> sel <- twk  
  }"  
)  
coordinates(newsDAG) <- list(  
  x=c(nwl=0,sel=1,twk=2) , y=c(nwl=0,sel=1,twk=0) )  
drawdag(newsDAG, cex = 2,  
  radius = 3, goodarrow = TRUE, xlim = c(-.2,2.2), ylim = c(-1.2,.2))
```





# Post-treatment bias

Blindly tossing in predictors is never a good idea

```
set.seed(21)
# number of subjects
N <- 100
# simulate initial aggression levels
aggression0 <- rnorm(N,1,.4)
#simulate vaccine
vaccine <- rep( 0:1 , each=N/2)
#simulate fungus
cordyceps <- rbinom( N , size=1 , prob=0.95 - vaccine * 0.5 )
# assign vaccines and simulate cordyceps and aggression
aggression1 <- aggression0 + rnorm(N, 1.2 + 2 *cordyceps, .4)
# compose a clean data frame
d <- data.frame( aggression0=aggression0 , aggression1=aggression1 ,
                vaccine=vaccine , cordyceps=cordyceps )
precis(d)[,-5]
```

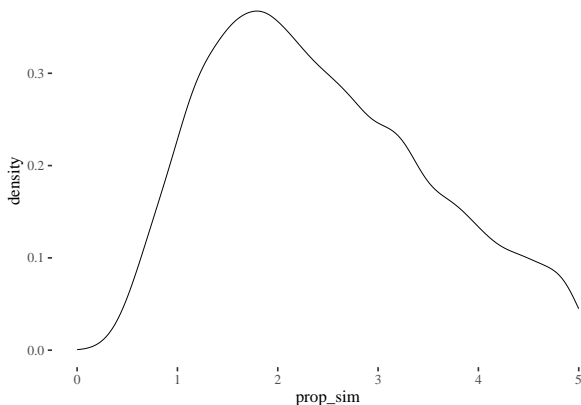
```
##           mean      sd      5.5%    94.5%
## aggression0 1.028994 0.4108600 0.3452403 1.702803
## aggression1 3.703373 1.0376606 1.8749605 5.038115
## vaccine      0.500000 0.5025189 0.0000000 1.000000
## cordyceps    0.740000 0.4408440 0.0000000 1.000000
```

# Choosing prior for proportional change

```
set.seed(23)
prop_sim <- rlnorm( 1e4 , .9 , .6 )
precis( data.frame(prop_sim) )[,5]
```

```
##           mean      sd      5.5%      94.5%
## prop_sim 2.942808 1.890235 0.9431349 6.351591
```

```
ggplot()+geom_density(aes(x = prop_sim))+xlim(0,5)+th
```



# Modeling aggression change

```
set.seed(12)
aggressionModel <- quap(
  alist(
    aggression1 ~ dnorm( mu , sigma ),
    mu <- aggression0*p,
    p ~ dlnorm( .9 , 0.6 ),
    sigma ~ dexp( 1 )
  ), data=d )

precis(aggressionModel)[,-5]
```

```
##           mean           sd      5.5%      94.5%
## p          3.230631 0.12417941 3.032169 3.429094
## sigma 1.375921 0.09630769 1.222003 1.529840
```

# Throwing in all predictors

```
aggressionModelAll <- quap(  
  alist(  
    aggression1 ~ dnorm( mu , sigma ),  
    mu <- aggression0 * p,  
    p <- a + bv*vaccine + bc*cordyceps,  
    a ~ dnorm(1,2),  
    bv ~ dnorm( 1 , 1 ),  
    bc ~ dlnorm( .9 , 0.6 ),  
    sigma ~ dexp( 1 )  
  ), data=d )
```

```
precis(aggressionModelAll)[,-5]
```

##	mean	sd	5.5%	94.5%
## a	1.7361277	0.2838563	1.2824704	2.1897849
## bv	0.2785707	0.2290837	-0.0875492	0.6446906
## bc	1.8454706	0.2607080	1.4288088	2.2621323
## sigma	1.1118171	0.0779973	0.9871624	1.2364719

# Throwing in all predictors

```
aggressionModelVaccine <- quap(  
  alist(  
    aggression1 ~ dnorm( mu , sigma ),  
    mu <- aggression0 * p,  
    p <- a + bv*vaccine,  
    a ~ dnorm(1,2),  
    bv ~ dnorm( 1 , 1 ),  
    sigma ~ dexp( 1 )  
  ), data=d )
```

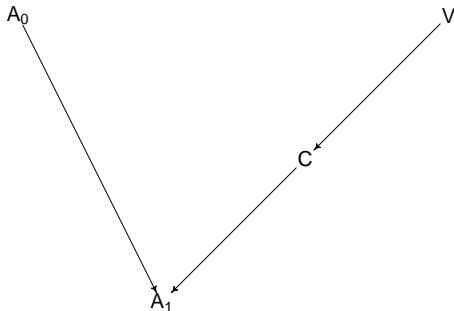
```
precis(aggressionModelVaccine)[,-5]
```

```
##           mean           sd      5.5%      94.5%  
## a           3.4774336 0.16402146  3.2152956  3.7395716  
## bv          -0.5186644 0.23454769 -0.8935169 -0.1438119  
## sigma       1.3340238 0.09356404  1.1844904  1.4835572
```

```
cordyceps <- rbinom( N , size=1 , prob=0.95 - vaccine * 0.5 )
```

## C d-separates V from A1

```
aggressionDAG <- dagitty( "dag {  
A_0 -> A_1  
C -> A_1  
V -> C  
}" )  
coordinates( aggressionDAG ) <- list( x=c(A_0=0,V=1.5,C=1,A_1=.5) ,  
                                       y=c(A_0=0,V=0,C=.5,A_1=1) )  
drawdag( aggressionDAG, cex = 2, radius = 3, goodarrow = TRUE,  
         xlim = c(-.3,1.7), ylim = c(-1.2,.2))
```



## C d-separates V from A1

```
impliedConditionalIndependencies(aggressionDAG)
```

```
## A_0 _||_ C
```

```
## A_0 _||_ V
```

```
## A_1 _||_ V | C
```

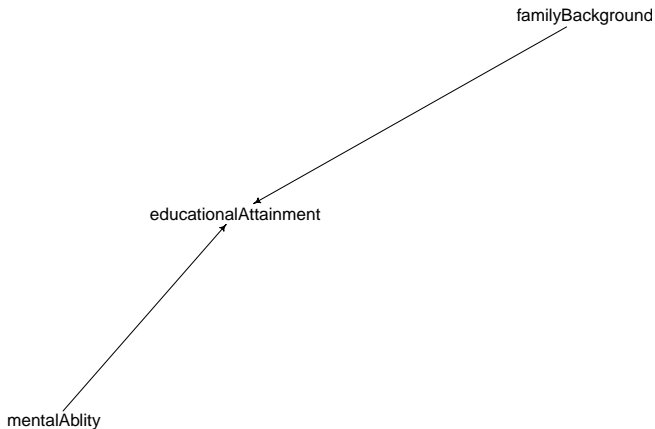
# The counterfactual model of data analysis

- individual:  $i$
- potential outcomes:  $Y_i^0, Y_i^1$  (only one observable)
- look at groups, with defensible assumptions estimate the **average effect**



# Causality creeps

Example: status attainment tradition



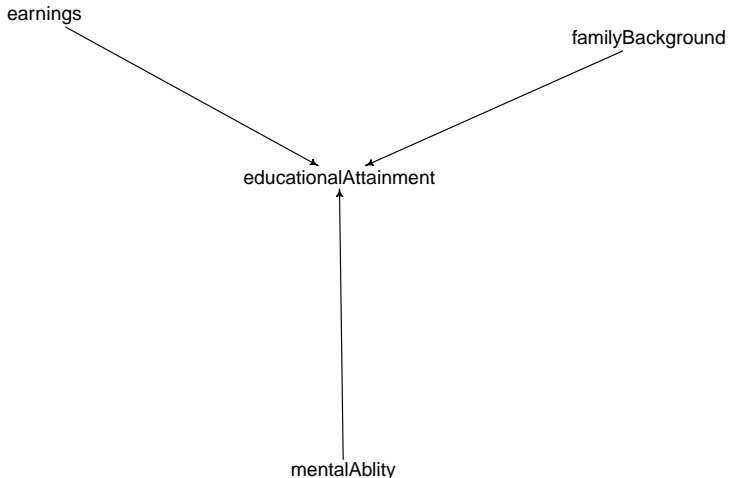
Implicit Wisconsin model

Students follow their own aspirations.

# Causality creeps

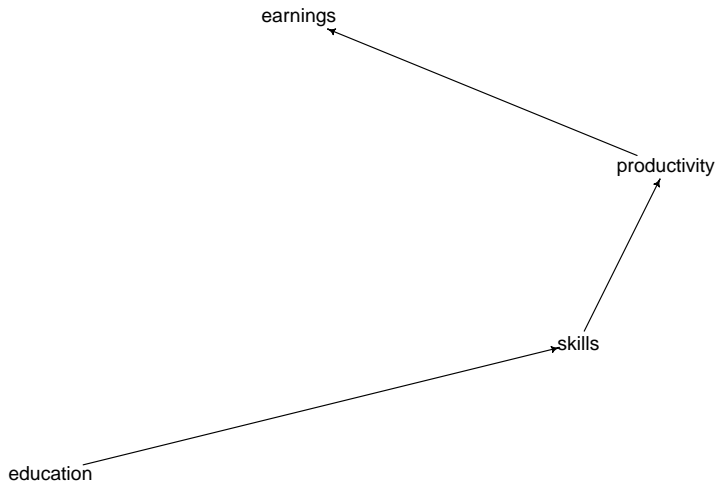
## Critics

You can have all aspirations you want, resources will limit you



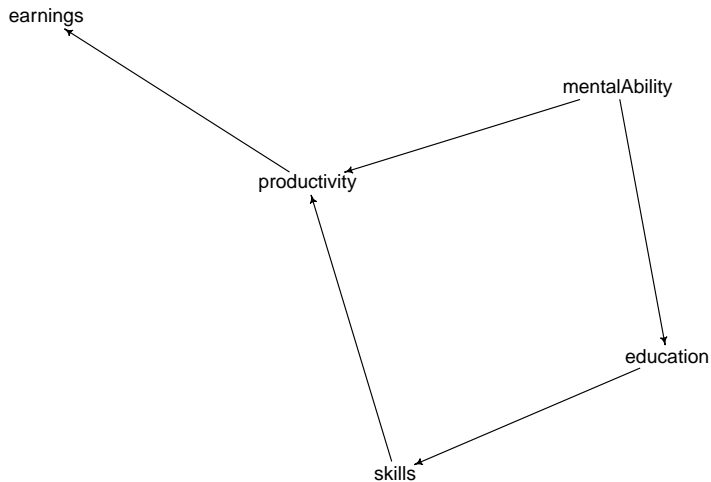
# Causality creeps

Example: economic theory of human capital



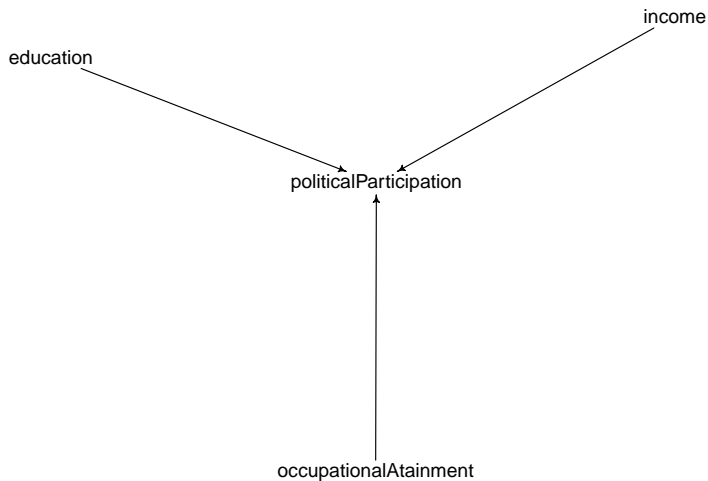
# Causality creeps

Example: economic theory of human capital



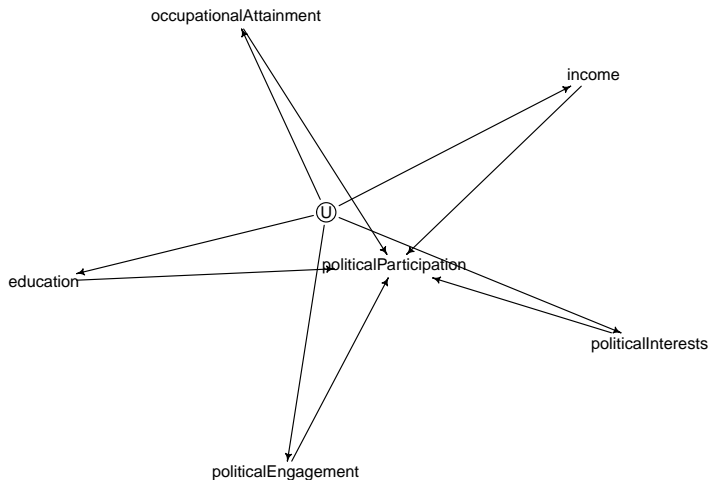
# Causality creeps

Example: political participation



# Causality creeps

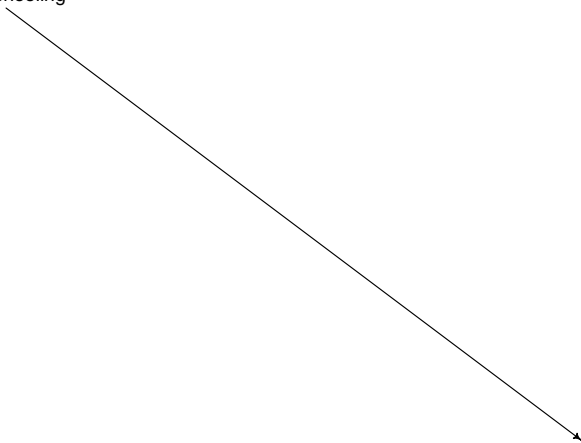
## Example: political participation



# Causality creeps

Example: Catholic schooling

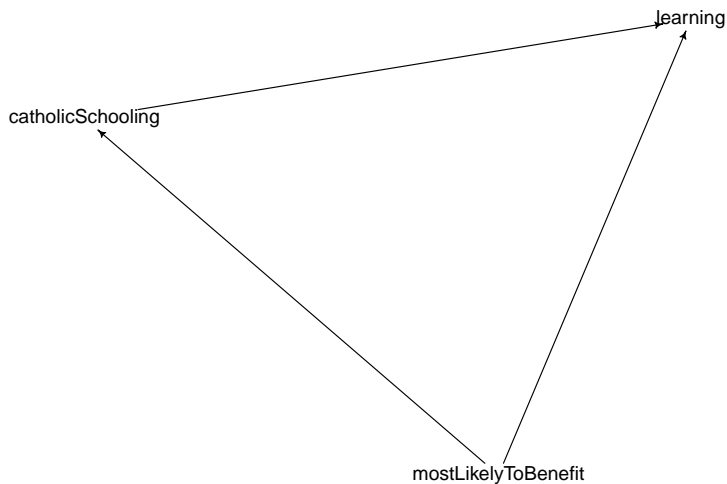
catholicSchooling



learning

# Causality creeps

## Catholic schooling (self selection)





# Causality creeps

Example: manpower training

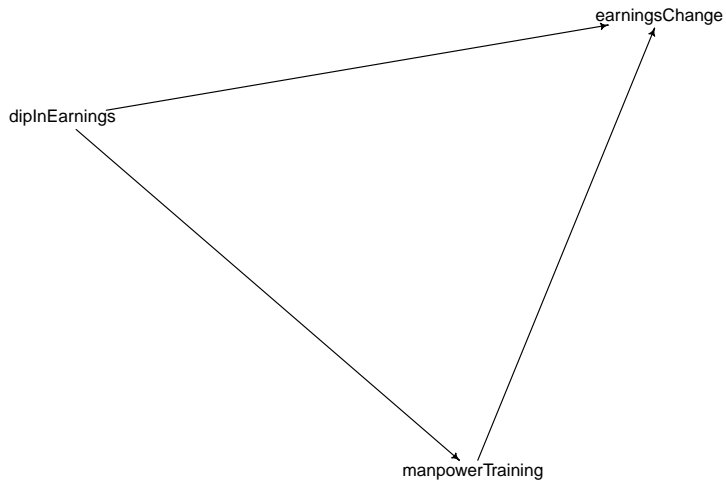
earningsChange



manpowerTraining

# Causality creeps

## Manpower training (Ashenfelter's dip)



# The straightforward solution

## Randomize

Cut the arrows coming into the predictors.

# The straightforward solution

## Randomize

Cut the arrows coming into the predictors.

## The problem

- most data are observational
- randomization is often impossible, impractical, or unethical