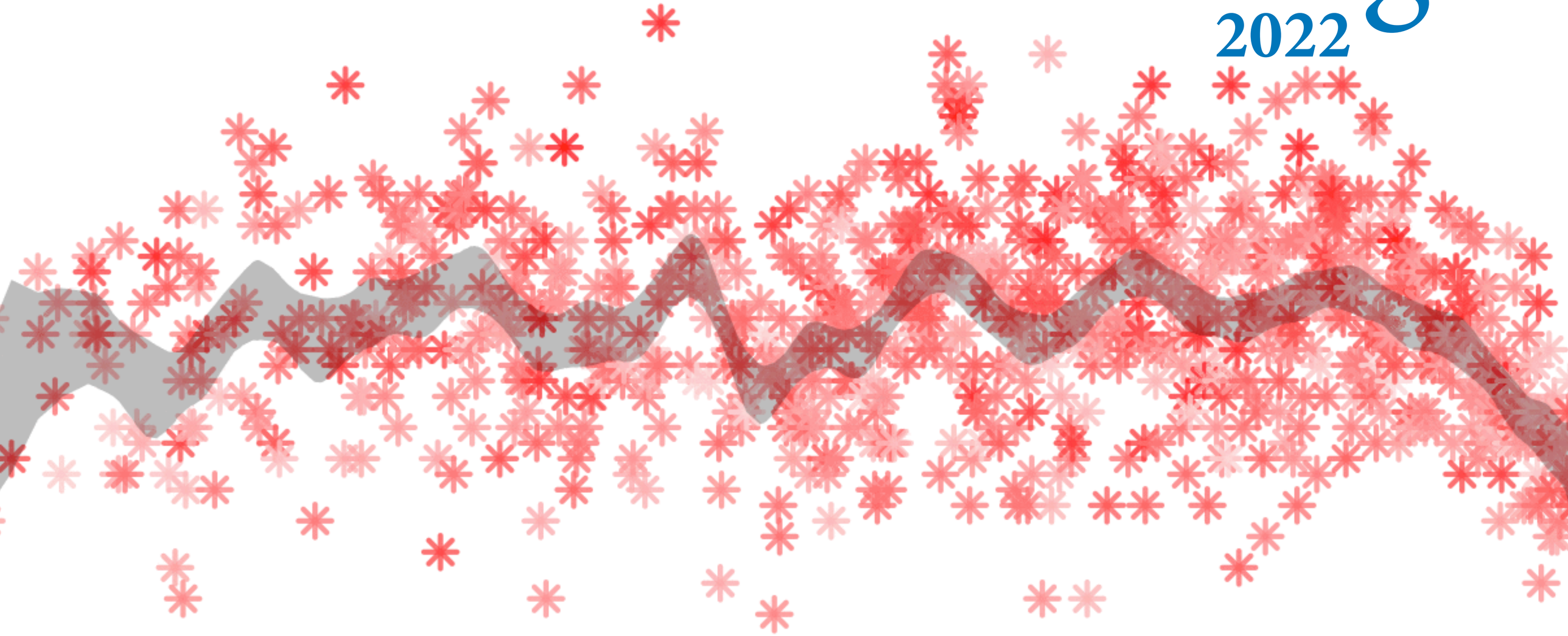
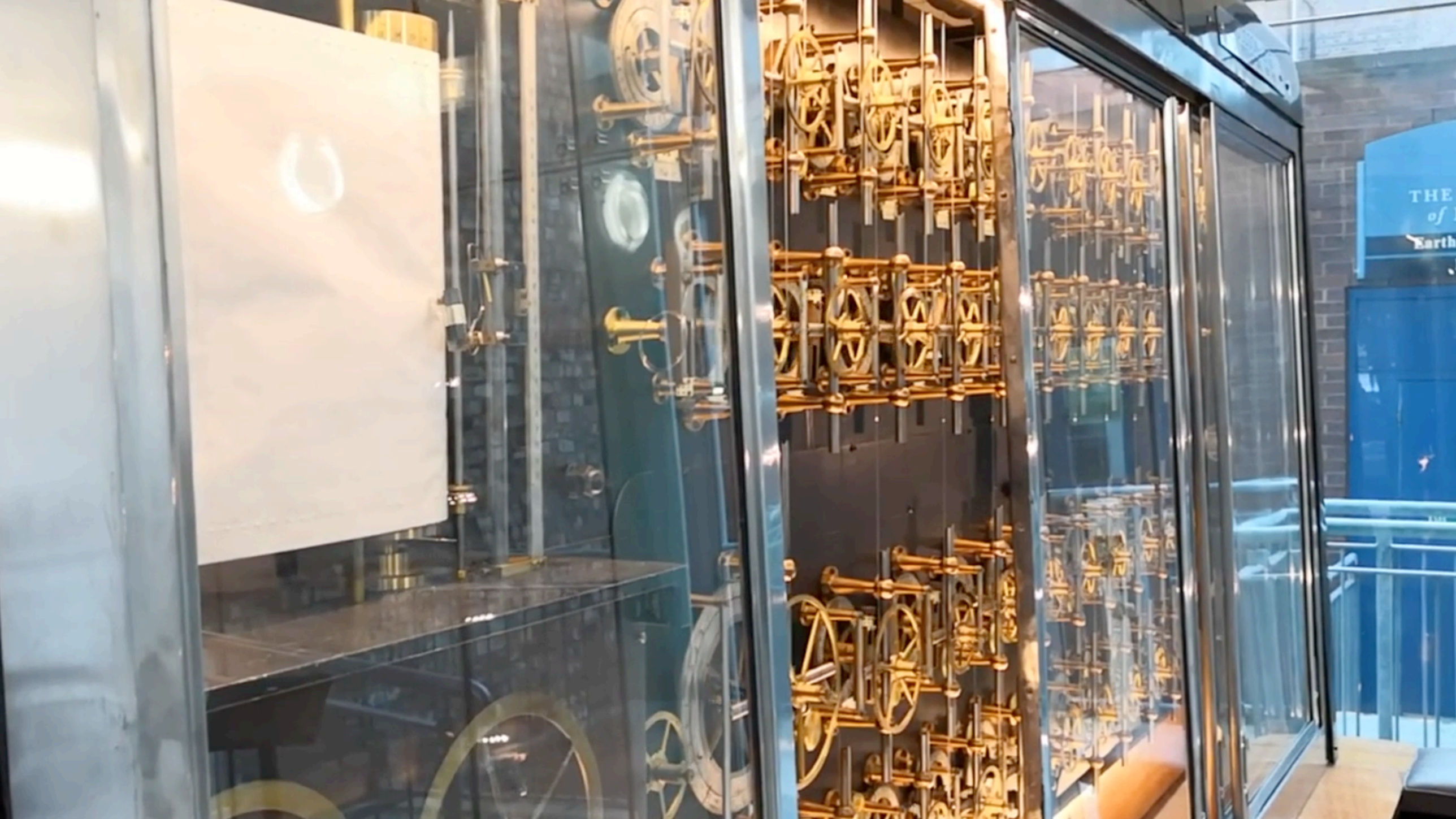
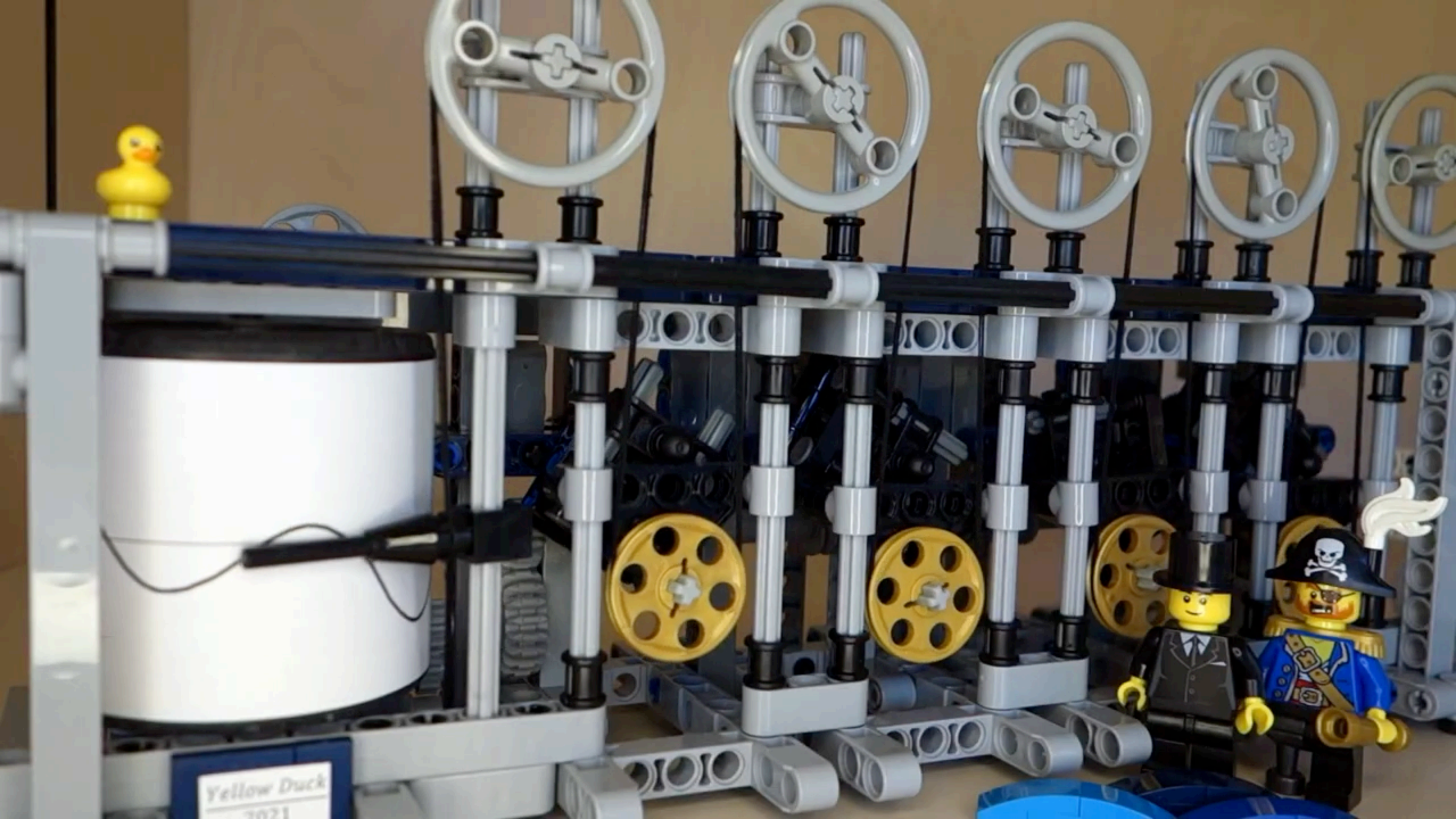
Statistical Rethinking

2022



10: Counts and Confounds




Yellow Duck
2021

Generalized Linear Models

Linear Models: Expected value is additive ("linear") combination of parameters

$$Y_i \sim \text{Normal}(\mu_i, \sigma)$$
$$\mu_i = \alpha + \beta_X X_i + \beta_Z Z_i$$

Generalized Linear Models: Expected value is some function of an additive combination of parameters

$$Y_i \sim \text{Bernoulli}(p_i)$$
$$f(p_i) = \alpha + \beta_X X_i + \beta_Z Z_i$$

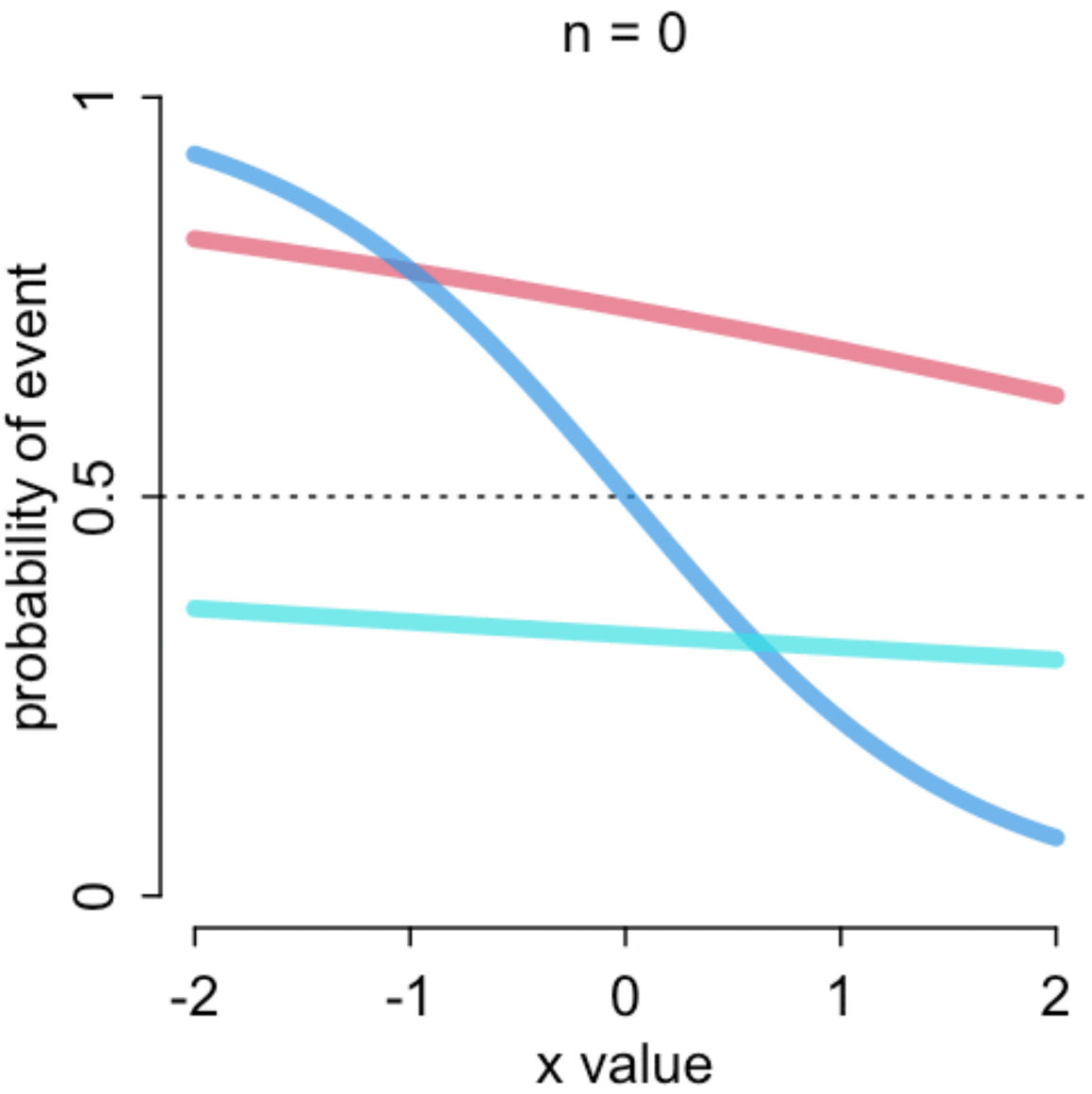
Generalized Linear Models:
Expected value is some function of an additive combination of parameters

Uniform changes in predictor not uniform changes in prediction

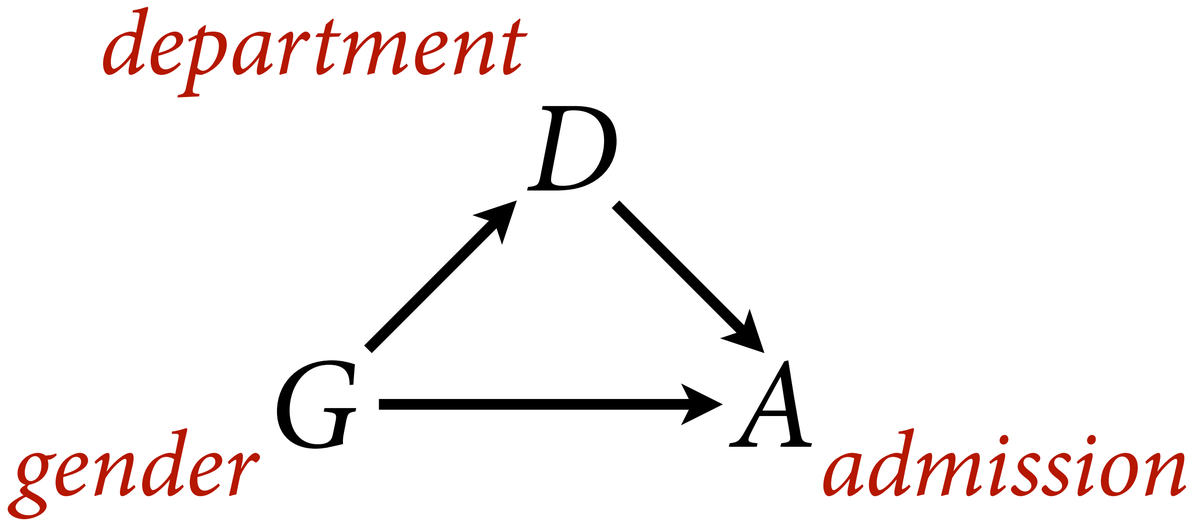
All predictor variables interact, moderate one another

Influences predictions & uncertainty of predictions

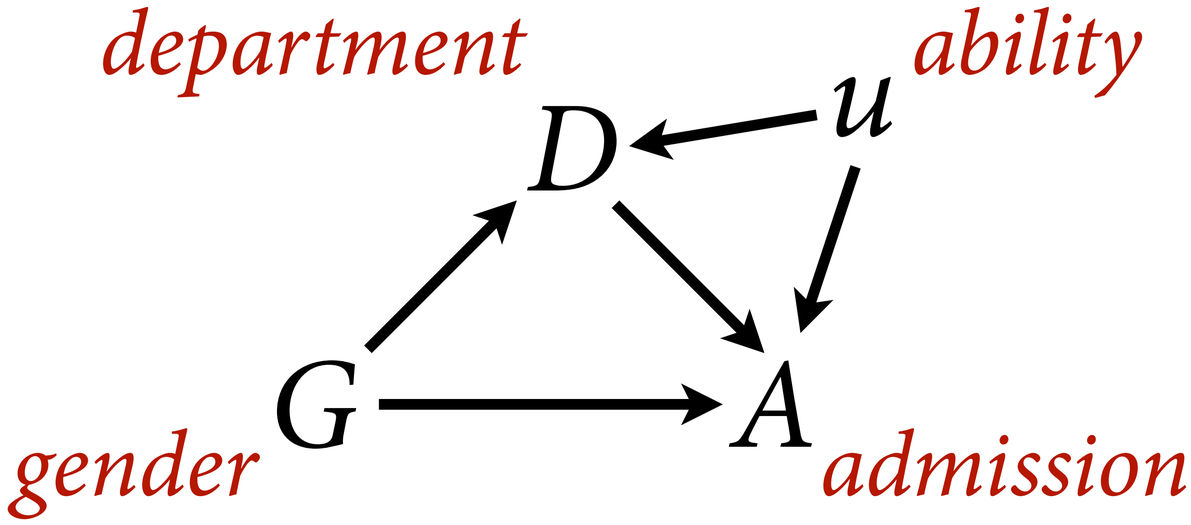
$$\text{logit}(p_i) = \alpha + \beta x_i$$



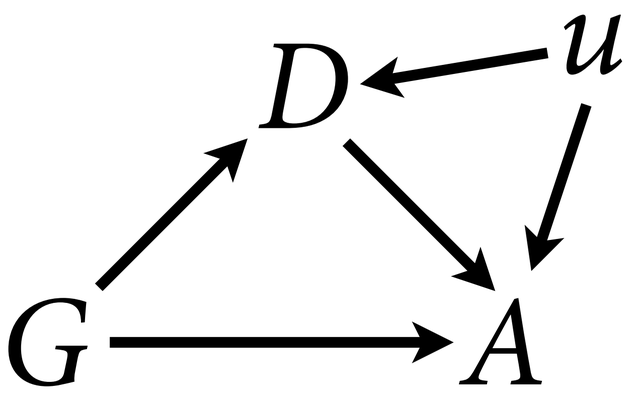
Confounded Admissions



Confounded Admissions



```
set.seed(17)
N <- 2000 # number of applicants
# even gender distribution
G <- sample( 1:2 , size=N , replace=TRUE )
# sample ability, high (1) to average (0)
u <- rbern(N,0.1)
# gender 1 tends to apply to department 1, 2 to 2
# and G=1 with greater ability tend to apply to 2 as well
D <- rbern( N , ifelse( G==1 , u*0.5 , 0.8 ) ) + 1
# matrix of acceptance rates [dept,gender]
accept_rate_u0 <- matrix( c(0.1,0.1,0.1,0.3) , nrow=2 )
accept_rate_u1 <- matrix( c(0.2,0.3,0.2,0.5) , nrow=2 )
# simulate acceptance
p <- sapply( 1:N , function(i)
    ifelse( u[i]==0 , accept_rate_u0[D[i],G[i]] ,
accept_rate_u1[D[i],G[i]] ) )
A <- rbern( N , p )
```



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N <- 2000 # number of applicants
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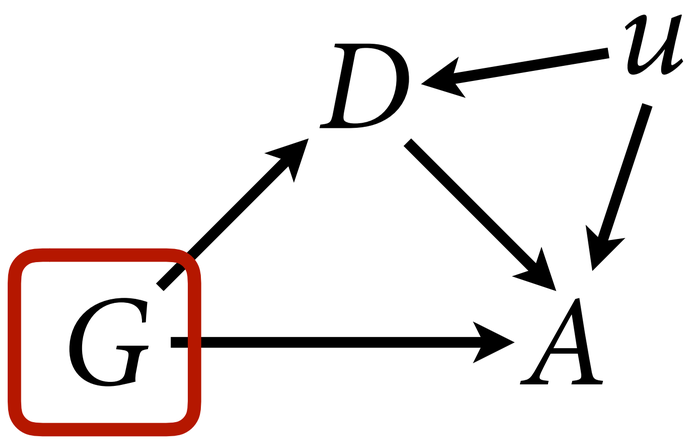

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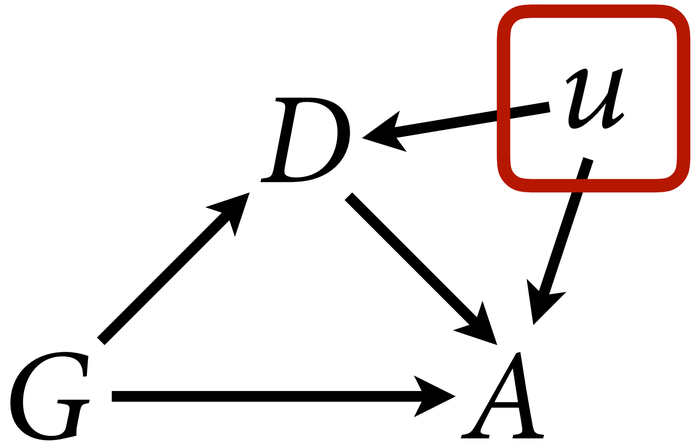

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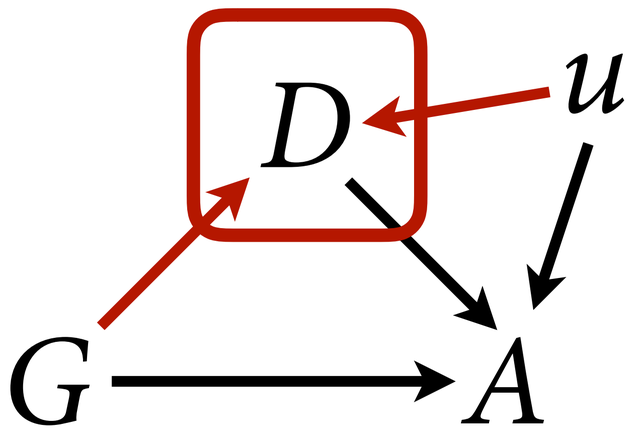

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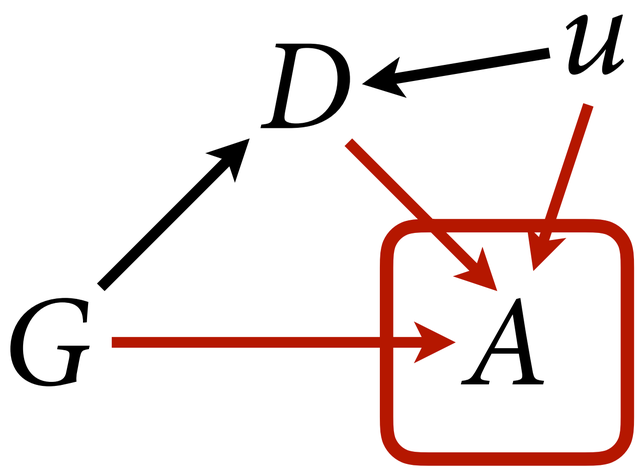



```
> accept_rate_u0
     [,1] [,2]
[1,]  0.1  0.1
[2,]  0.1  0.3
```

```
> accept_rate_u1
     [,1] [,2]
[1,]  0.2  0.2
[2,]  0.3  0.5
```

```
dat_sim <- list( A=A , D=D , G=G )

# total effect gender
m1 <- ulam(
    alist(
        A ~ bernoulli(p),
        logit(p) <- a[G],
        a[G] ~ normal(0,1)
    ), data=dat_sim , chains=4 , cores=4 )

# direct effects - now confounded!
m2 <- ulam(
    alist(
        A ~ bernoulli(p),
        logit(p) <- a[G,D],
        matrix[G,D]:a ~ normal(0,1)
    ), data=dat_sim , chains=4 , cores=4 )
```

total effect shows disadvantage

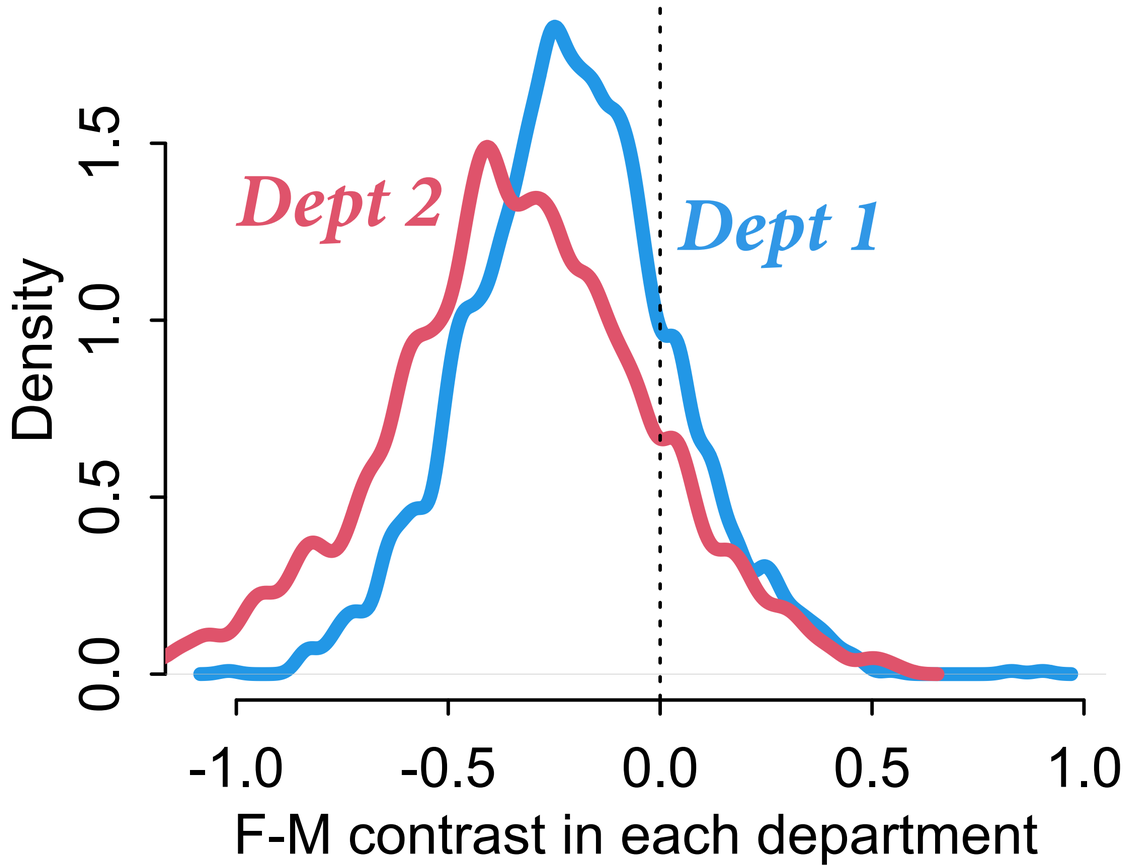
```
> precis(m1,depth=2)
      mean   sd  5.5% 94.5% n_eff Rhat4
a[1] -2.10 0.10 -2.26 -1.93  1297     1
a[2] -0.86 0.07 -0.97 -0.76  1008     1
```

direct effect confounded

```
> precis(m2,depth=3)
        mean   sd  5.5% 94.5% n_eff Rhat4
a[1,1] -2.18 0.11 -2.35 -2.01  2083     1
a[1,2] -0.99 0.30 -1.49 -0.51  2408     1
a[2,1] -1.97 0.21 -2.31 -1.65  2335     1
a[2,2] -0.65 0.07 -0.77 -0.53  2260     1
```

Let's look at the contrasts…

```r
post2 <- extract.samples(m2)

post2$fm_contrast_D1 <-
    post2$a[,1,1] - post2$a[,2,1]

post2$fm_contrast_D2 <-
    post2$a[,1,2] - post2$a[,2,2]
```



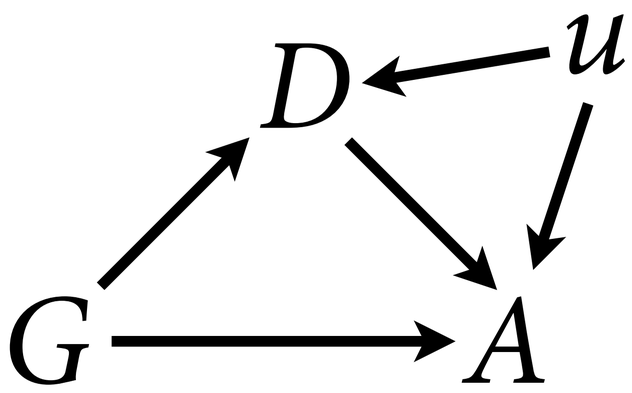
How can the confound hide discrimination?

You guessed it: Collider bias

Stratifying by D opens non-causal path through u

Can estimate total causal effect of G, but this isn't what we want

Cannot estimate direct effect of D or G



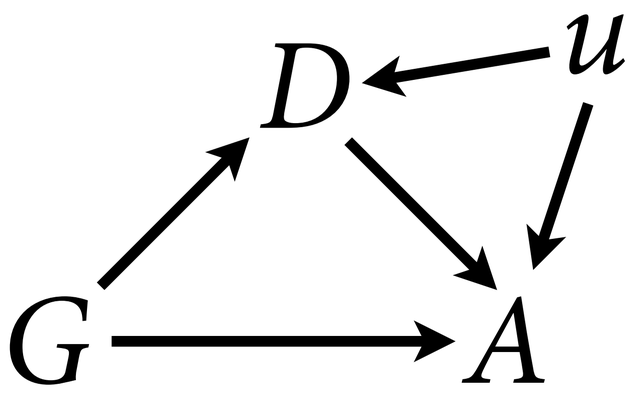
You guessed it: Collider bias

More intuitive explanation:

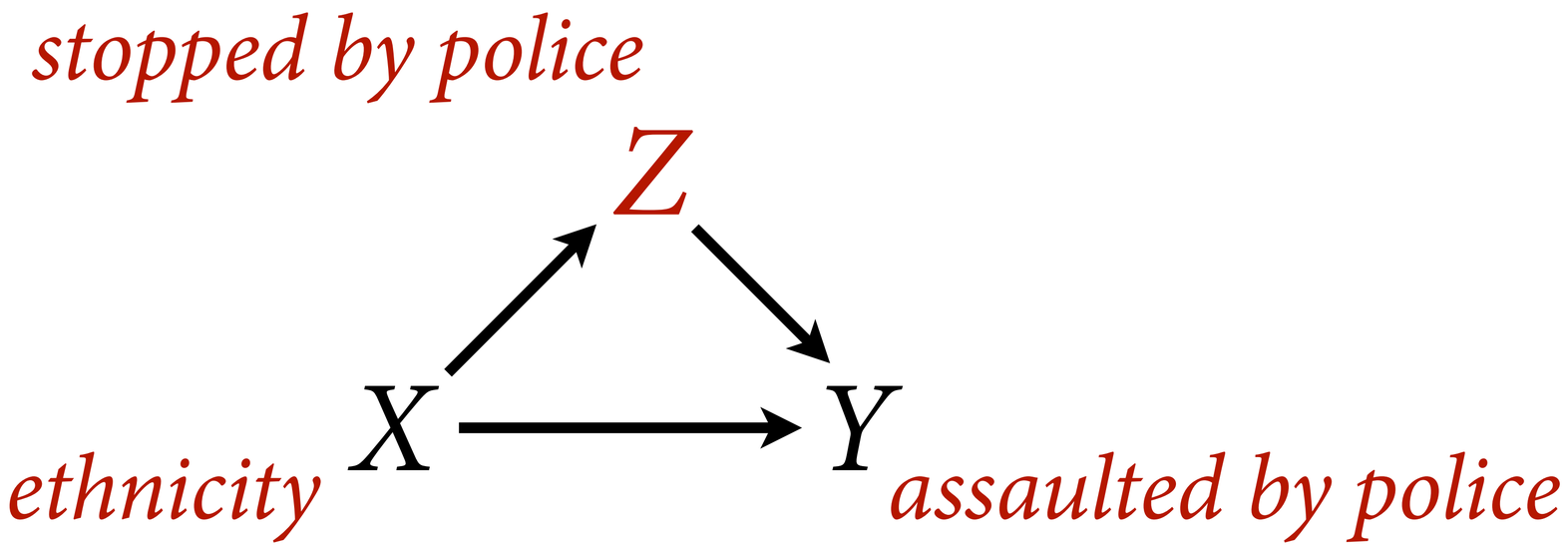
High ability G1s apply to discriminatory department anyway

G1s in that department are higher ability on average than G2s

High ability compensates for discrimination => masks evidence

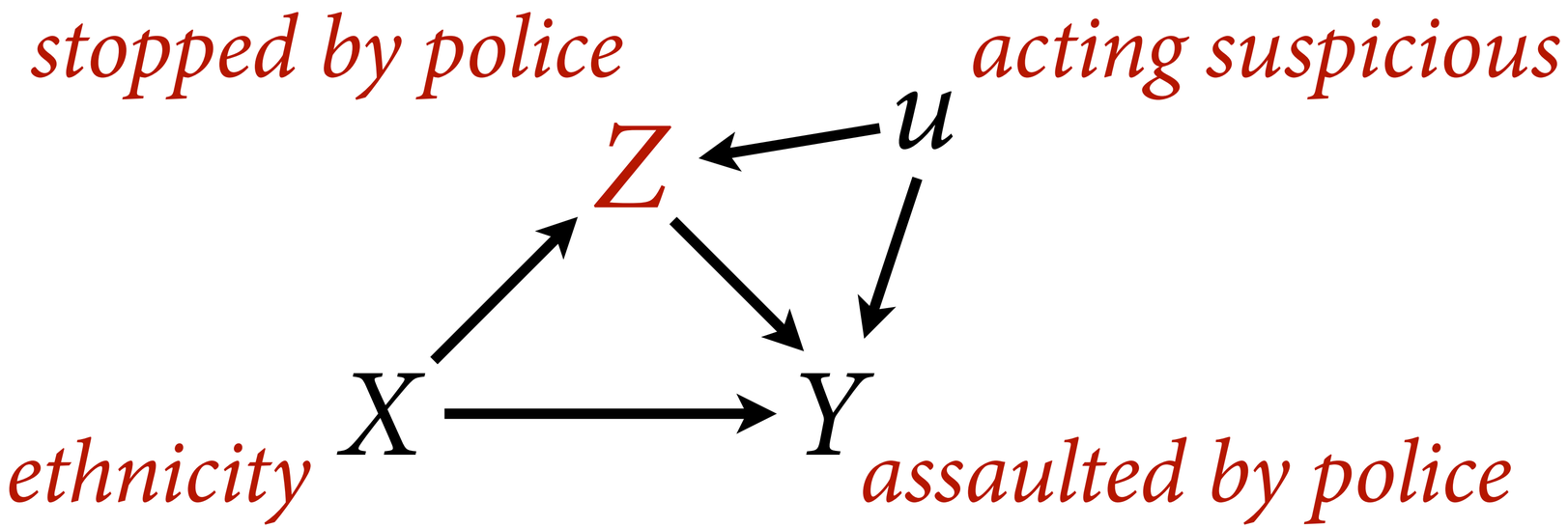


Policing confounds



Knox Lowe & Mummolo 2020 Administrative Records Mask Racially Biased Policing

Policing confounds

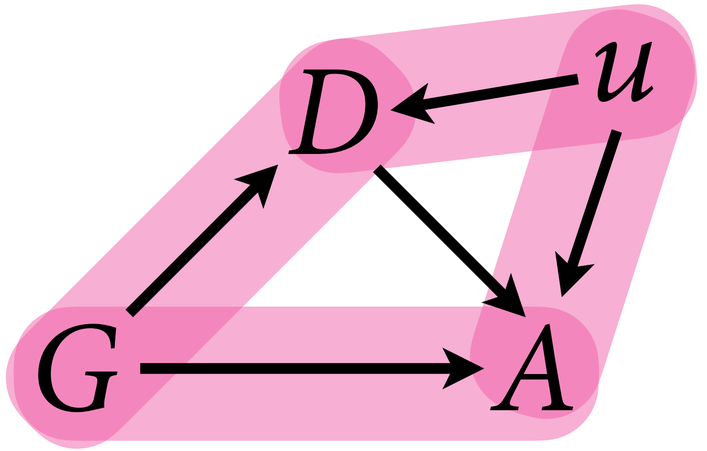


Data on police stops are confounded by lack of data on who wasn't stopped: forced conditioning on Z

Knox Lowe & Mummolo 2020 Administrative Records Mask Racially Biased Policing

Imagine we could measure the confound

```
# if we could measure u
dat_sim$u <- u
m3 <- ulam(
    alist(
        A ~ bernoulli(p),
        logit(p) <- a[G,D] + buA*u,
        matrix[G,D]:a ~ normal(0,1),
        buA ~ normal(0,1)
    ), data=dat_sim ,
constraints=list(buA="lower=0") ,
    chains=4 , cores=4 )

post3 <- extract.samples(m3)
post3$fm_contrast_D1 <-
    post3$a[,1,1] - post3$a[,2,1]
post3$fm_contrast_D2 <-
    post3$a[,1,2] - post3$a[,2,2]
```



Need to block non-causal path through u

Imagine we could measure the confound

```
# if we could measure u
dat_sim$u <- u
m3 <- ulam(
    alist(
        A ~ bernoulli(p),
        logit(p) <- a[G,D] + buA*u,
        matrix[G,D]:a ~ normal(0,1),
        buA ~ normal(0,1)
    ), data=dat_sim ,
constraints=list(buA="lower=0") ,
    chains=4 , cores=4 )

post3 <- extract.samples(m3)
post3$fm_contrast_D1 <-
    post3$a[,1,1] - post3$a[,2,1]
post3$fm_contrast_D2 <-
    post3$a[,1,2] - post3$a[,2,2]
```

Add *u* to linear model

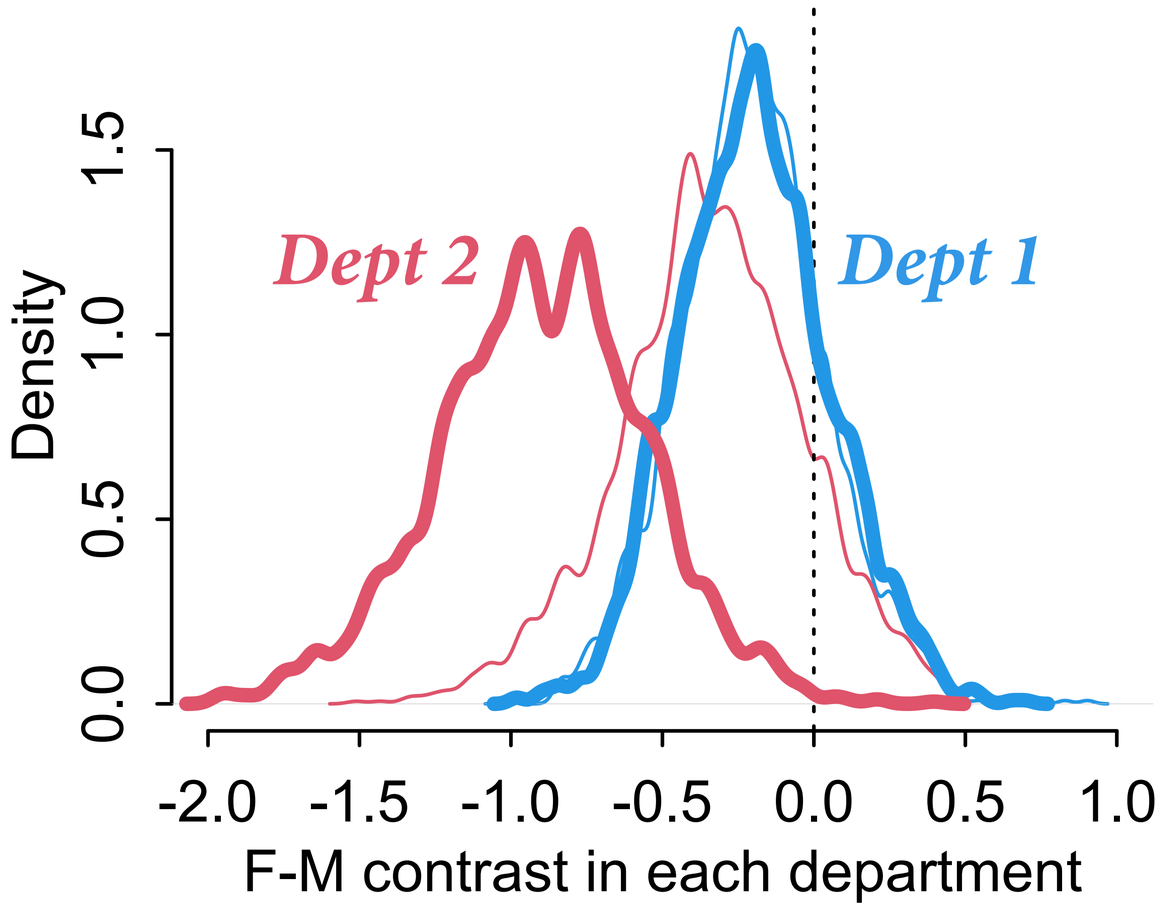
Imagine we could measure the confound

```
# if we could measure u
dat_sim$u <- u
m3 <- ulam(
    alist(
        A ~ bernoulli(p),
        logit(p) <- a[G,D] + buA*u,
        matrix[G,D]:a ~ normal(0,1),
        buA ~ normal(0,1)
    ), data=dat_sim ,
constraints=list(buA="lower=0") ,
    chains=4 , cores=4 )

post3 <- extract.samples(m3)
post3$fm_contrast_D1 <-
    post3$a[,1,1] - post3$a[,2,1]
post3$fm_contrast_D2 <-
    post3$a[,1,2] - post3$a[,2,2]
```

Constrain effect of u to +

Imagine we could measure the confound

```
# if we could measure u
dat_sim$u <- u
m3 <- ulam(
    alist(
        A ~ bernoulli(p),
        logit(p) <- a[G,D] + buA*u,
        matrix[G,D]:a ~ normal(0,1),
        buA ~ normal(0,1)
    ), data=dat_sim ,
constraints=list(buA="lower=0") ,
    chains=4 , cores=4 )

post3 <- extract.samples(m3)
post3$fm_contrast_D1 <-
    post3$a[,1,1] - post3$a[,2,1]
post3$fm_contrast_D2 <-
    post3$a[,1,2] - post3$a[,2,2]
```



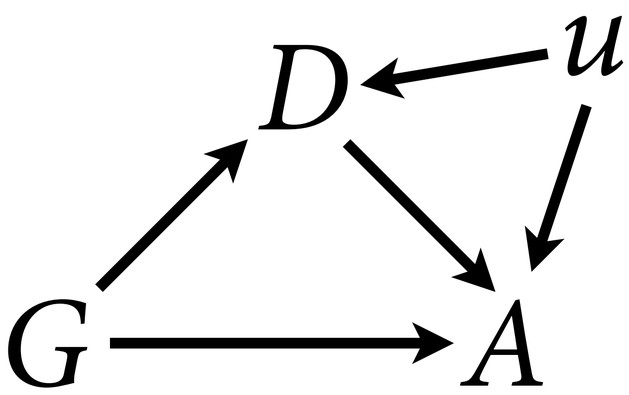
De-confounding

What can be done?

Experiments

Sensitivity analysis

Measure proxies of confound

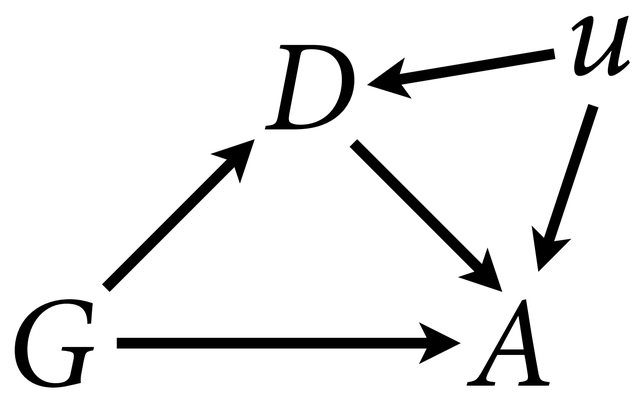


Sensitivity analysis

What are the implications of what we don't know?

Assume confound exists, model its consequences for different strengths/kinds of influence

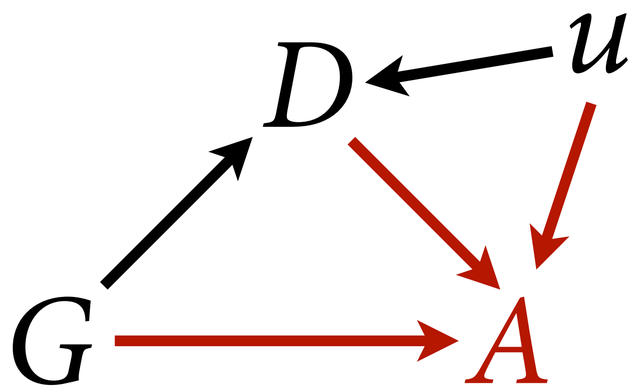
How strong must the confound be to change conclusions?



Sensitivity analysis

$$A_i \sim \text{Bernoulli}(p_i)$$

$$\text{logit}(p_i) = \alpha[G_i, D_i] + \beta_{G[i]} u_i$$



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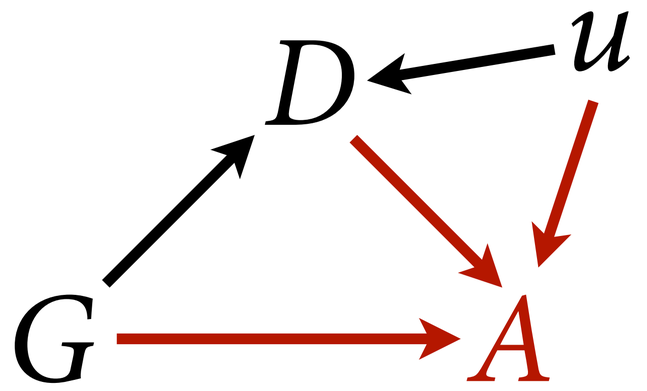
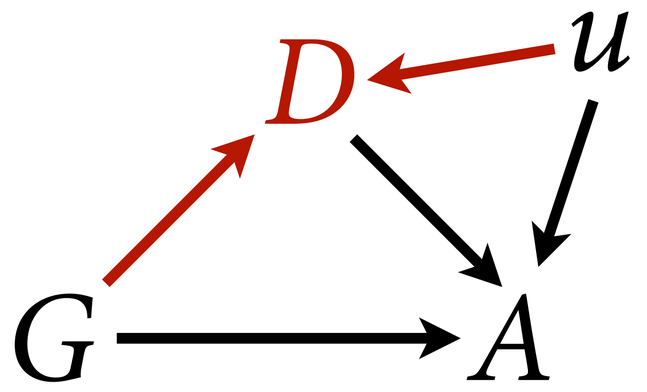


$$(D_i = 2) \sim \text{Bernoulli}(q_i)$$

$$\text{logit}(q_i) = \delta[G_i] + \gamma_{G[i]} u_i$$

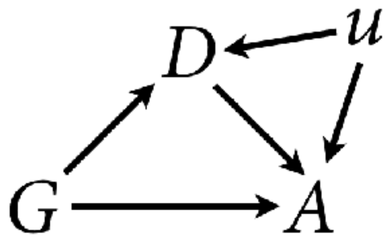


```
datl$D1 <- ifelse(datl$D==1,1,0)
datl$N <- length(datl$D)
datl$b <- c(1,1)
datl$g <- c(1,0)

mGDu <- ulam(
    alist(
        # A model
        A ~ bernoulli(p),
        logit(p) <- a[G,D] + b[G]*u[i],
        matrix[G,D]:a ~ normal(0,1),

        # D model
        D1 ~ bernoulli(q),
        logit(q) <- delta[G] + g[G]*u[i],
        delta[G] ~ normal(0,1),

        # declare unobserved u
        vector[N]:u ~ normal(0,1)
    ), data=datl , chains=4 , cores=4 )
```



$$A_i \sim \text{Bernoulli}(p_i)$$

$$\text{logit}(p_i) = \alpha[G_i, D_i] + \beta_{G[i]} u_i$$

$$(D_i = 2) \sim \text{Bernoulli}(q_i)$$

$$\text{logit}(q_i) = \delta[G_i] + \gamma_{G[i]} u_i$$

$$u_j \sim \text{Normal}(0,1)$$

```
datl$D1 <- ifelse(datl$D==1,1,0)
datl$N <- length(datl$D)
datl$b <- c(1,1)
datl$g <- c(1,0)

mGDu <- ulam(
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        A ~ bernoulli(p),
        logit(p) <- a[G,D] + b[G]*u[i],
        matrix[G,D]:a ~ normal(0,1),

        # D model
        D1 ~ bernoulli(q),
        logit(q) <- delta[G] + g[G]*u[i],
        delta[G] ~ normal(0,1),

        # declare unobserved u
        vector[N]:u ~ normal(0,1)
    ), data=datl , chains=4 , cores=4 )
```
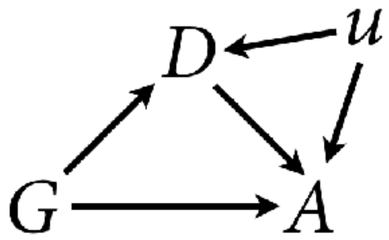
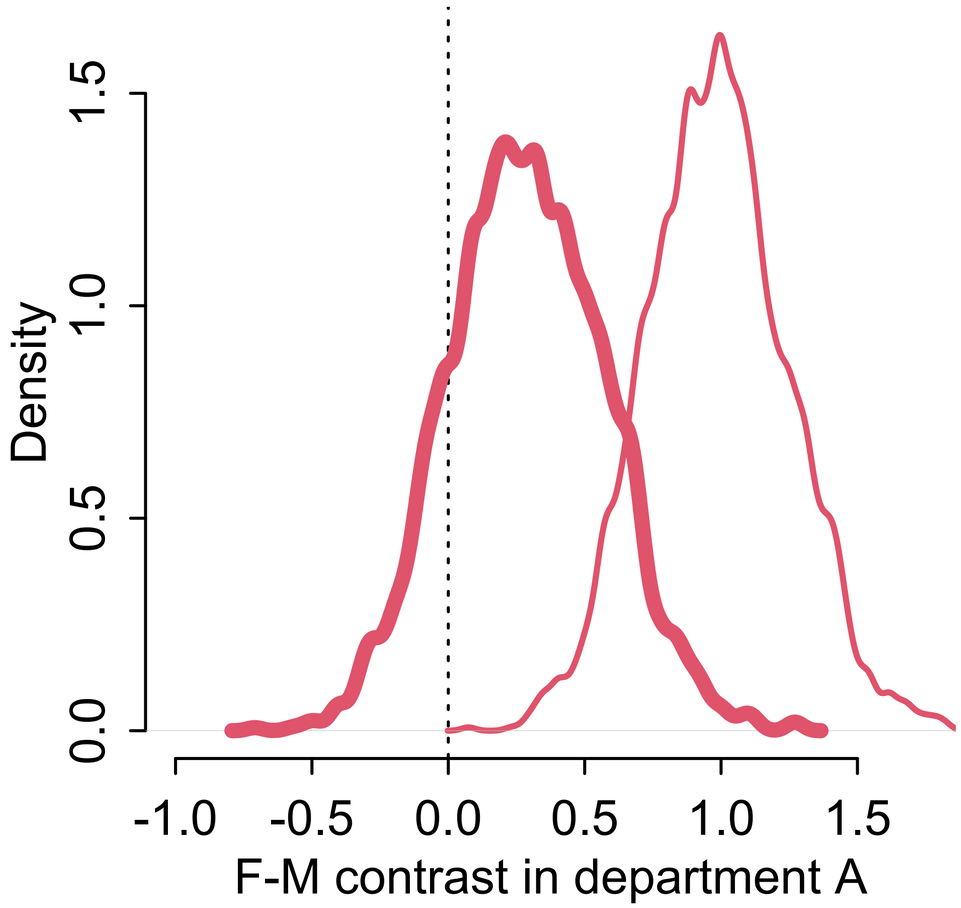
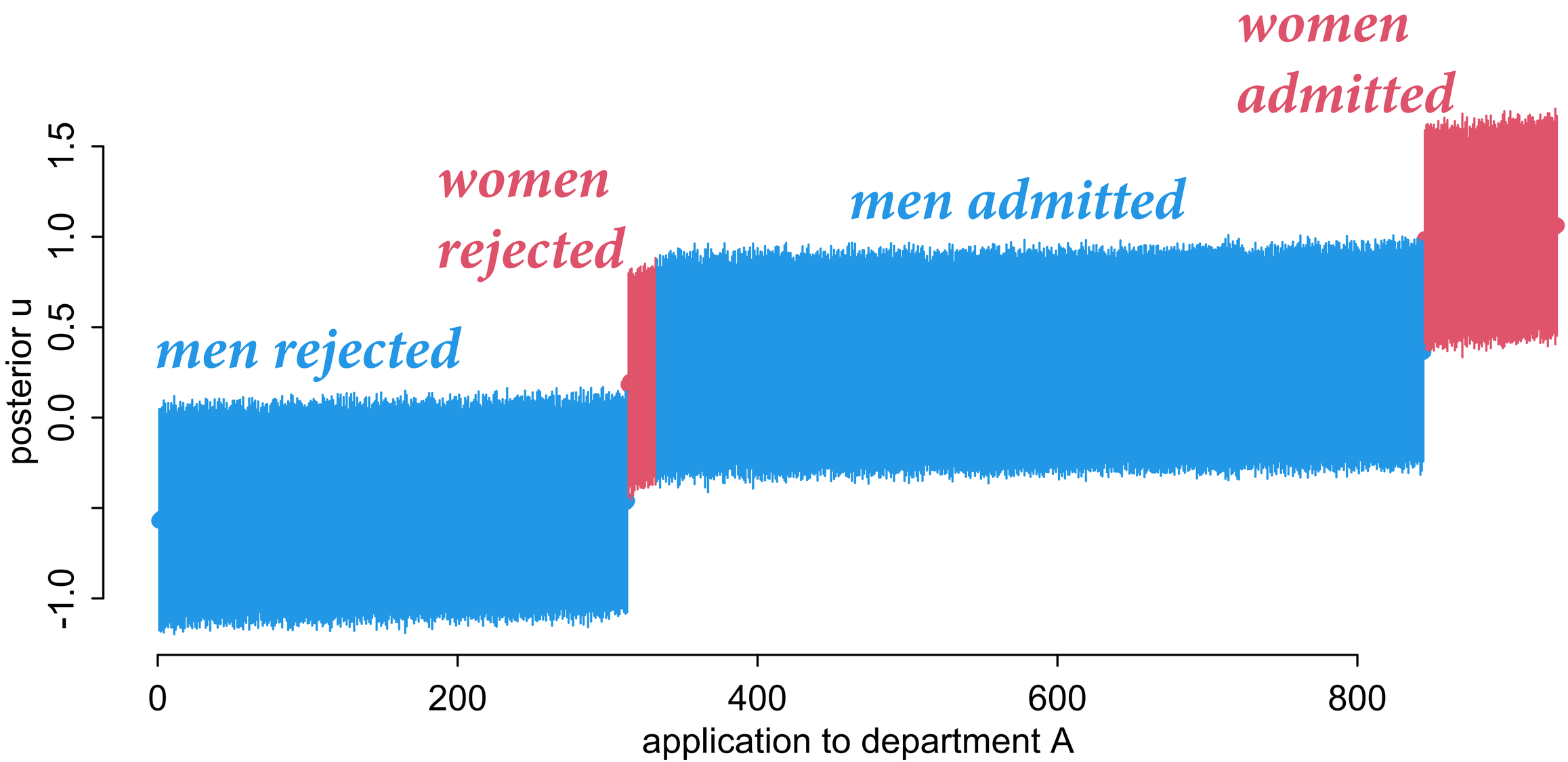
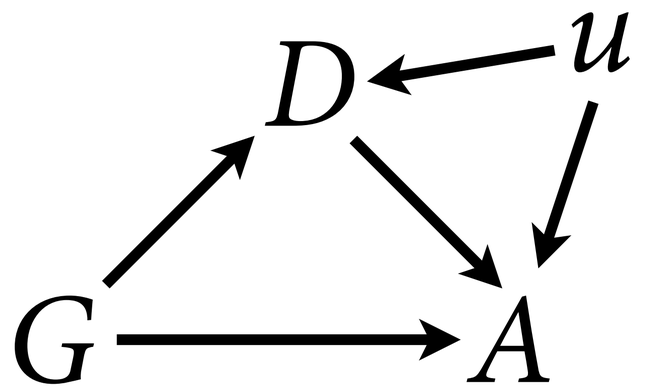





Posterior *u* values, Department A



Sensitivity analysis

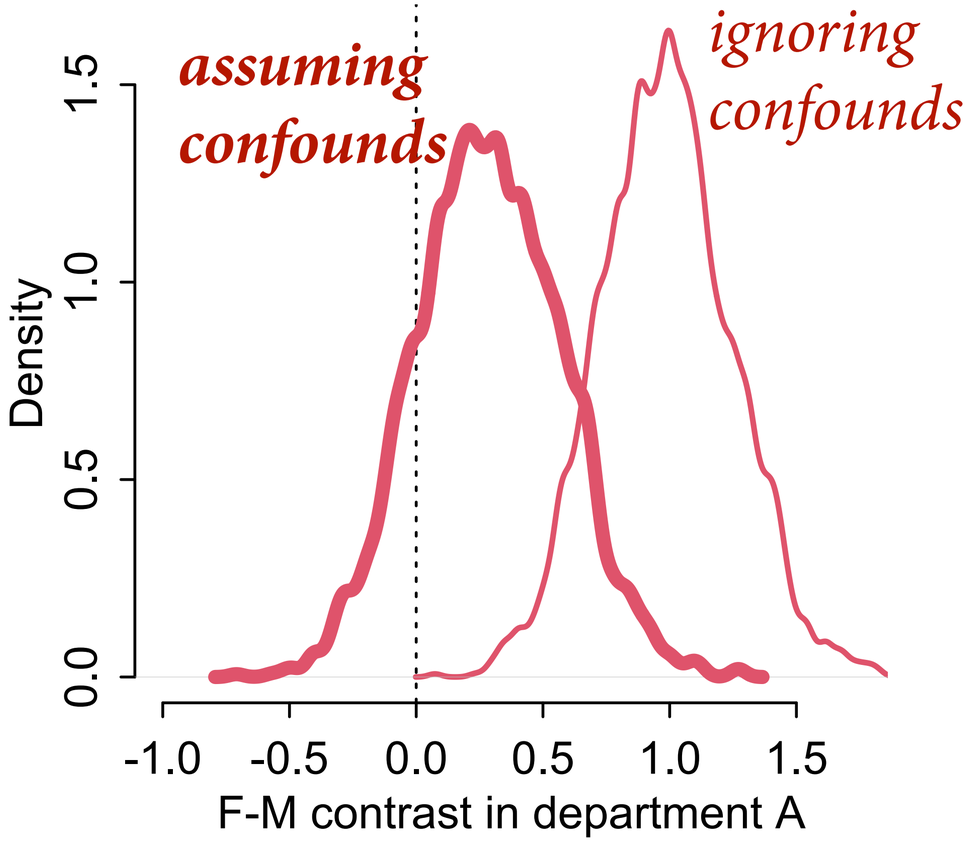


What are the implications of what we don't know?

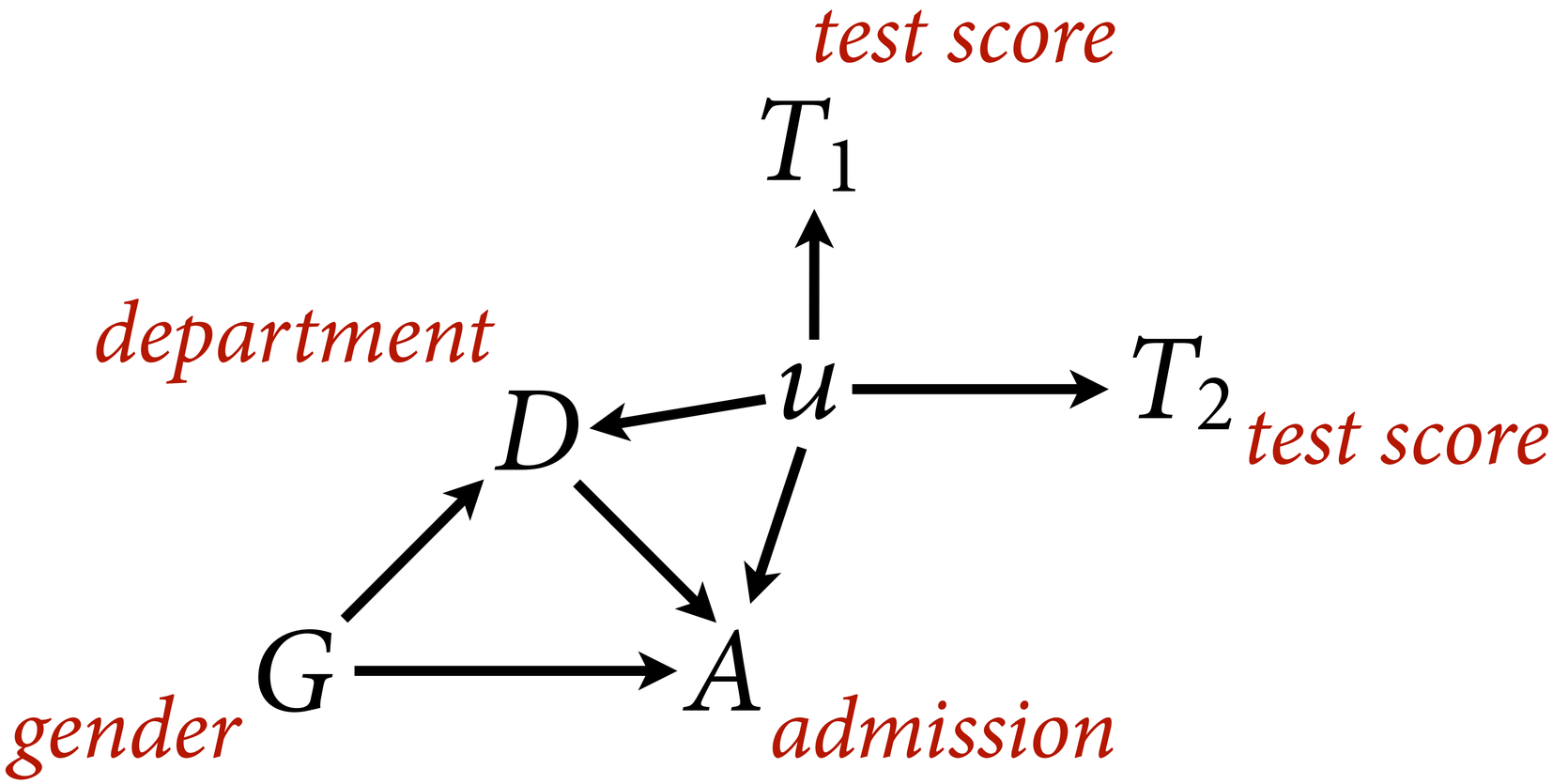
Somewhere between pure simulation and pure analysis

Vary confound strength over range and show how results change –or– vary other effects and estimate confound strength

Confounds often persist — don't pretend



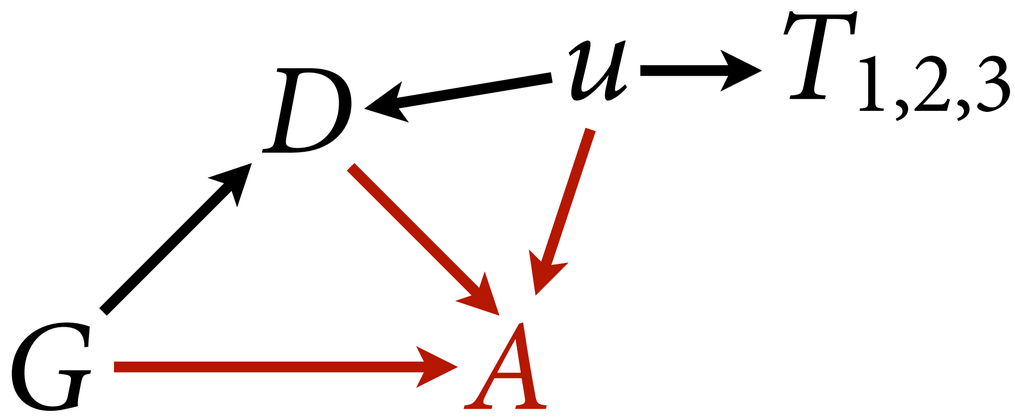
De-confounding



De-confounding

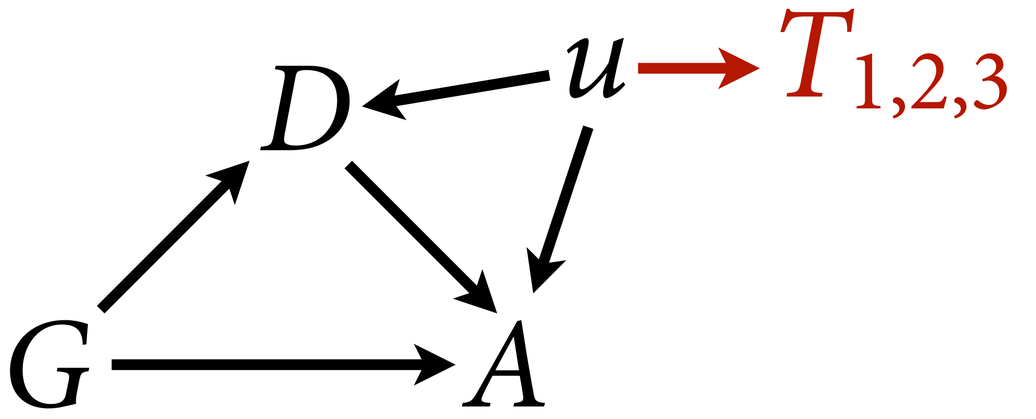
$$A_i \sim \text{Bernoulli}(p_i)$$

$$\text{logit}(p_i) = \alpha[G_i, D_i] + \beta_{G[i]} u_i$$

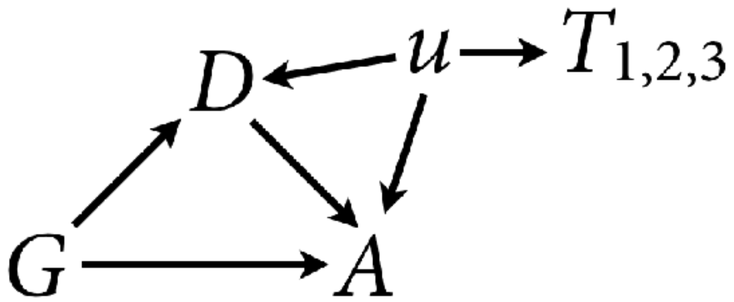


$$T_{i,j} \sim \text{Normal}(u_i, \tau_j)$$

$$u_k \sim \text{Normal}(0,1)$$



```
T1 <- rnorm(N,u,0.1)
T2 <- rnorm(N,u,0.5)
T3 <- rnorm(N,u,0.25)

m4 <- ulam(
    alist(

        # A model
        A ~ bernoulli(p),
        logit(p) <- a[G,D] + b*u[i],
        matrix[G,D]:a ~ normal(0,1),
        b ~ normal(0,1),

        # u and T model
        vector[N]:u ~ normal(0,1),
        T1 ~ normal(u,tau[1]),
        T2 ~ normal(u,tau[2]),
        T3 ~ normal(u,tau[3]),
        vector[3]:tau ~ exponential(1)

    ), data=dat_sim , chains=4 , cores=4 ,
constraints=list(b="lower=0") )
```



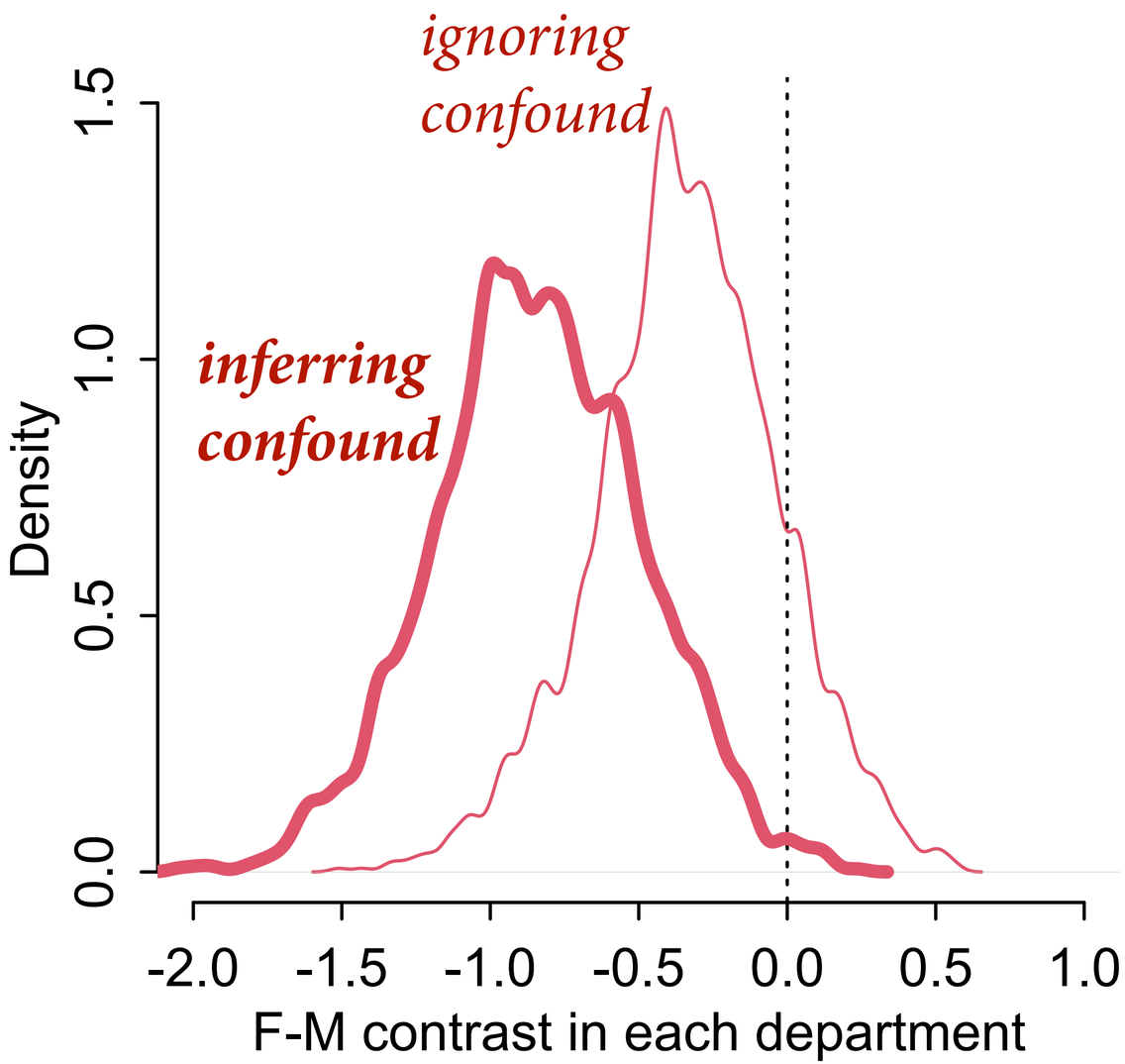
$$A_i \sim \text{Bernoulli}(p_i)$$

$$\text{logit}(p_i) = \alpha[G_i, D_i] + \beta_{G[i]} u_i$$

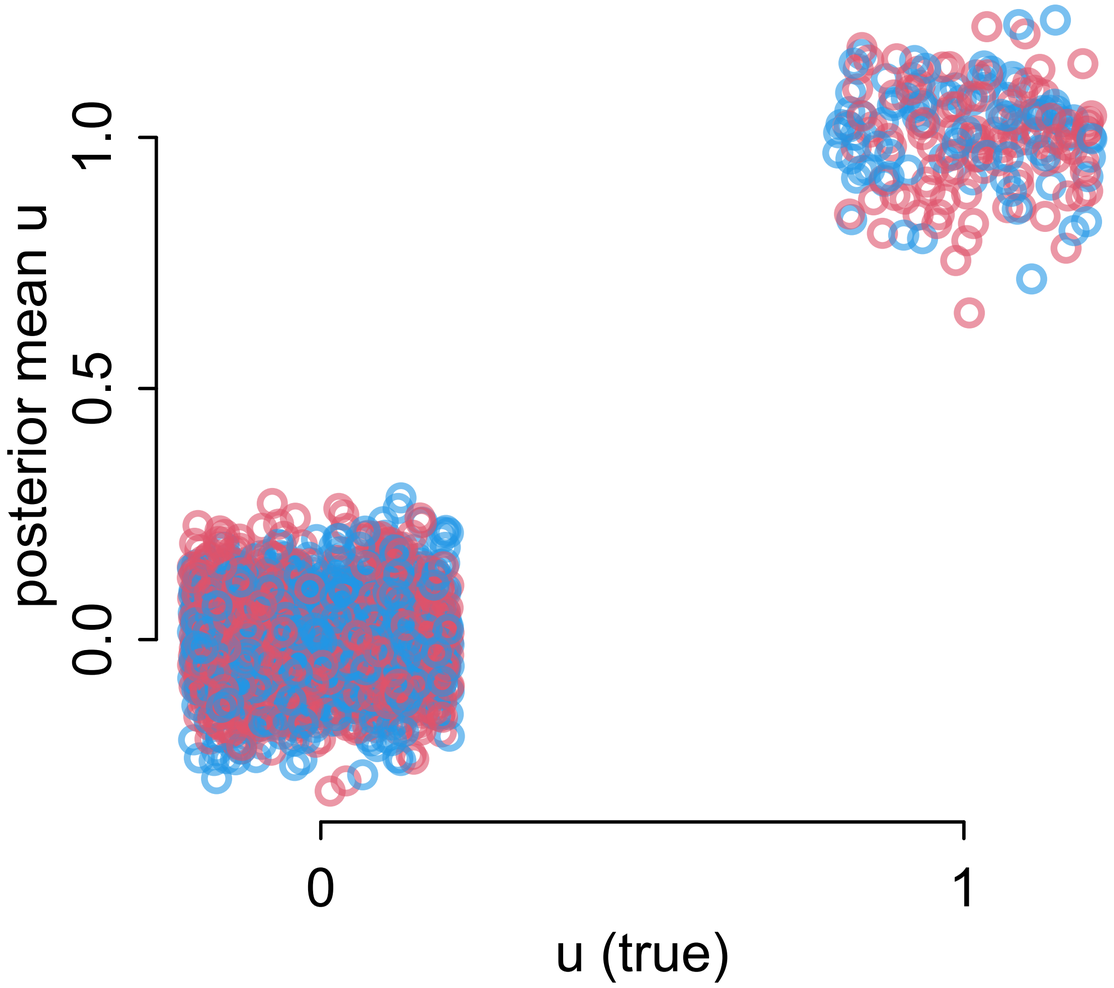
$$u_k \sim \text{Normal}(0,1)$$

$$T_{i,j} \sim \text{Normal}(u_i, \tau_j)$$

**This model samples inefficiently; learn to fix later in course*

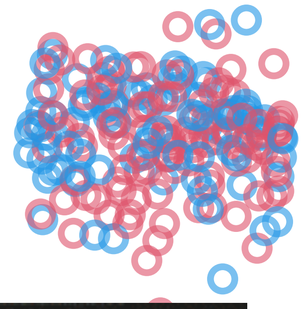


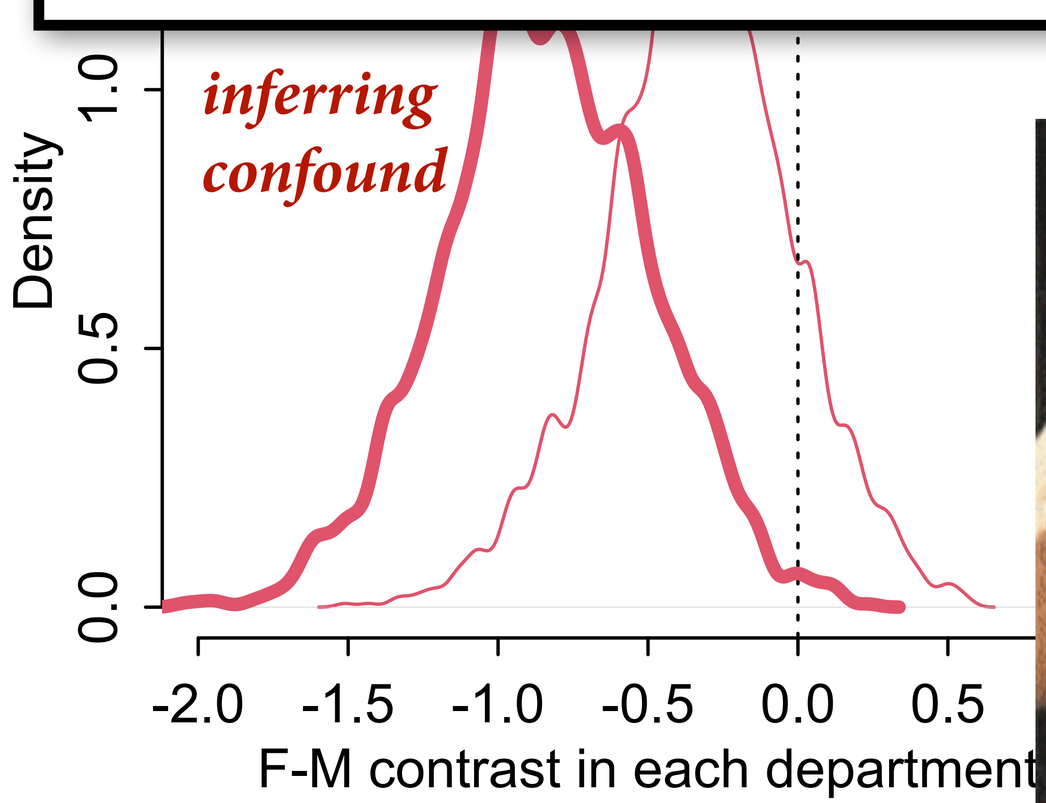
$$u_k \sim \text{Normal}(0,1)$$



More parameters (2008) than observations (2000)!

Normal(0,1)





Charlie Chaplin, Modern Times (1936)

PAUSE

Oceanic tool complexity

How is technological complexity related to population size?

To social structure?

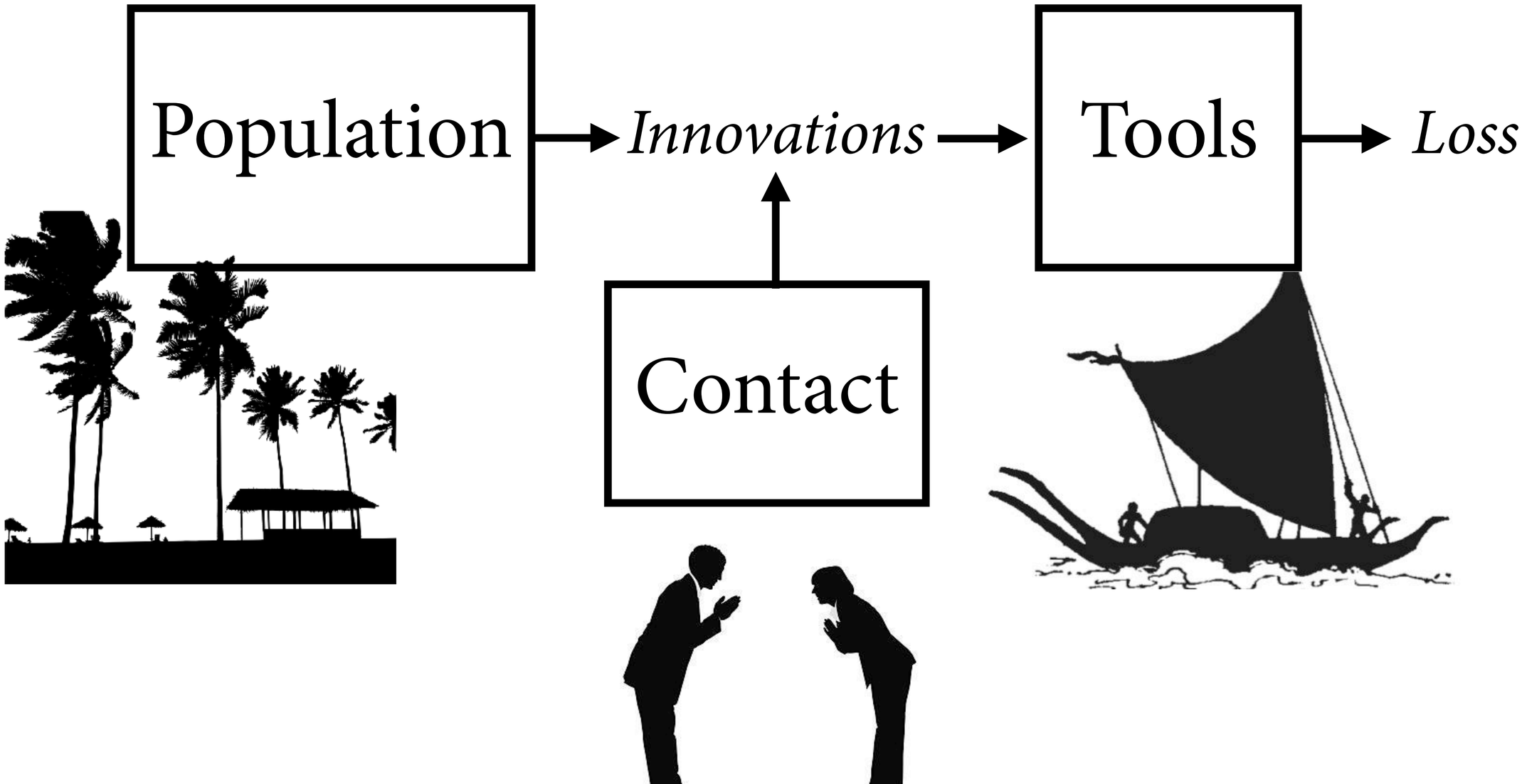
data(Kline)

	culture	population	contact	total_tools	mean_TU
1	Malekula	1100	low	13	3.2
2	Tikopia	1500	low	22	4.7
3	Santa Cruz	3600	low	24	4.0
4	Yap	4791	high	43	5.0
5	Lau Fiji	7400	high	33	5.0
6	Trobriand	8000	high	19	4.0
7	Chuuk	9200	high	40	3.8
8	Manus	13000	low	28	6.6
9	Tonga	17500	high	55	5.4
10	Hawaii	275000	low	71	6.6

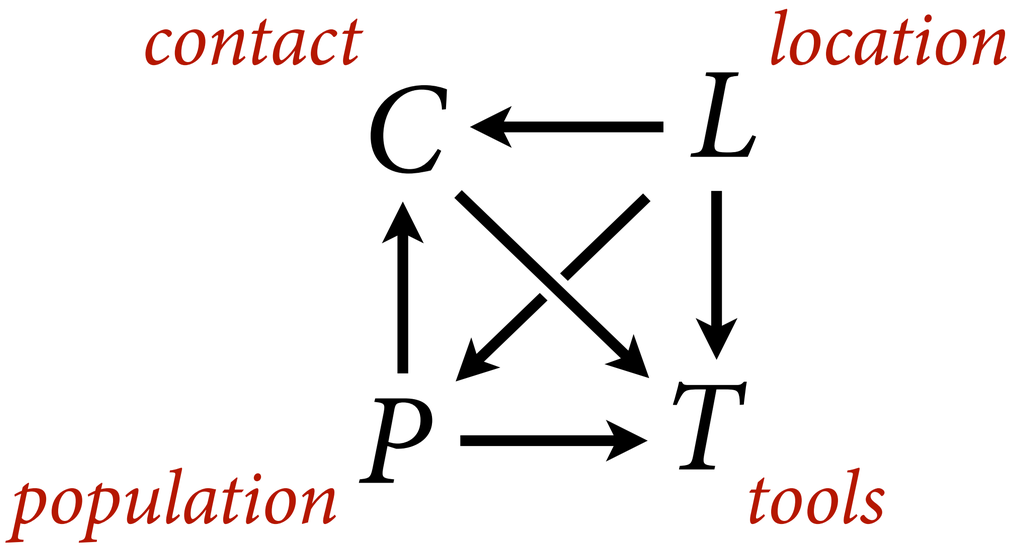
Estimand: Causal influence of **population size** and **contact** on **total tools**

Kline & Boyd 2010 Population size predicts technological complexity in Oceania

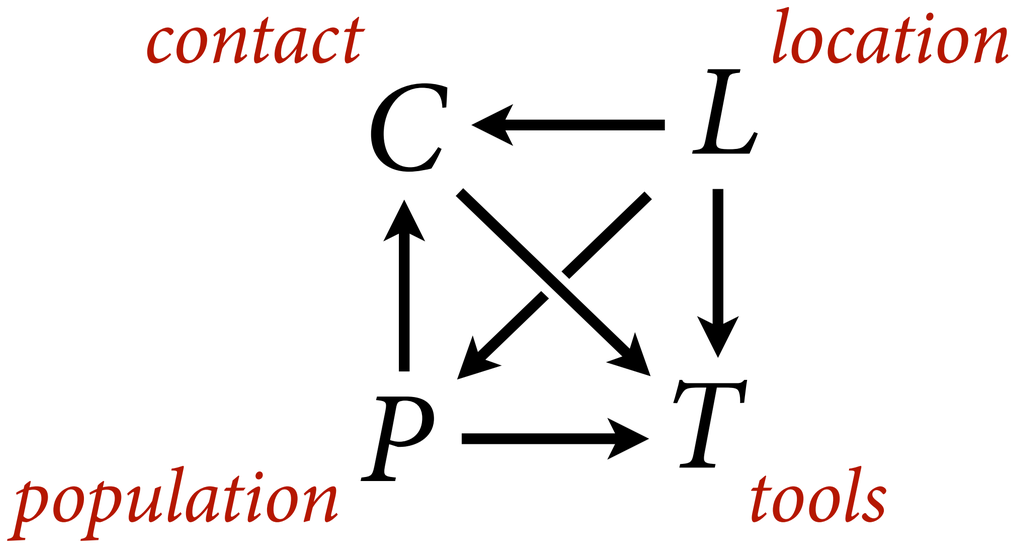
Technological complexity



Technological complexity



Technological complexity



Adjustment set for *P*: *L*

Also want to stratify by *C*, to study interaction

Modeling tools

Tool count is not binomial: No maximum

Poisson distribution: Very high maximum and very low probability of each success

Here: Many many possible technologies, very few realized in any one place

Poisson link is log

Poisson distribution takes shape from expected value

Must be positive

Exponential scaling can be surprising!

$$Y_i \sim \text{Poisson}(\lambda_i)$$

$$\log(\lambda_i) = \alpha + \beta x_i$$

$$\lambda_i = \exp(\alpha + \beta x_i)$$

Poisson (poison) priors

Exponential scaling can be surprising

$$\log(\lambda_i) = \alpha$$

$$\alpha \sim \text{Normal}(0,10)$$

Poisson (poison) priors

Exponential scaling can be surprising

$$\log(\lambda_i) = \alpha$$

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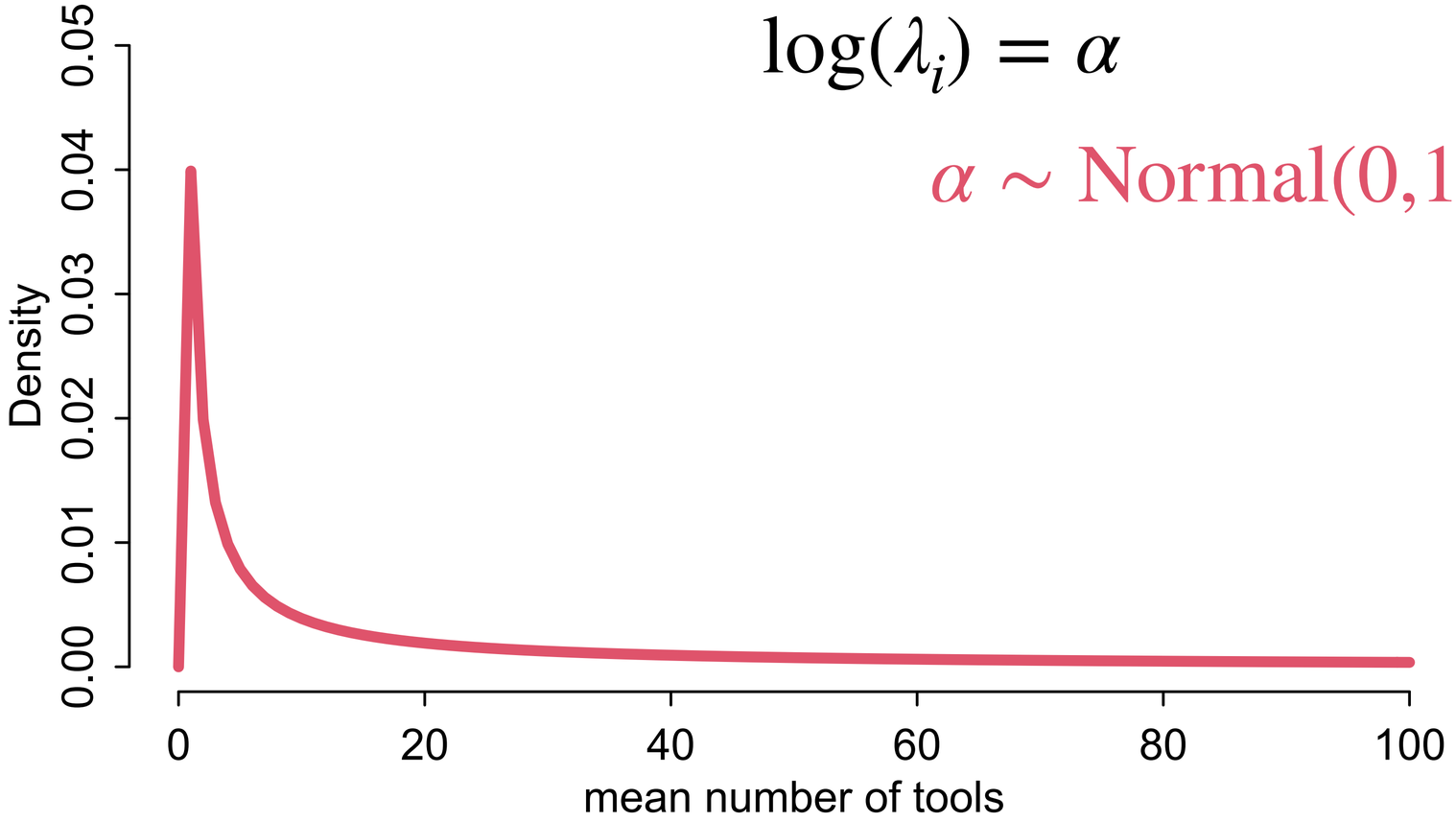
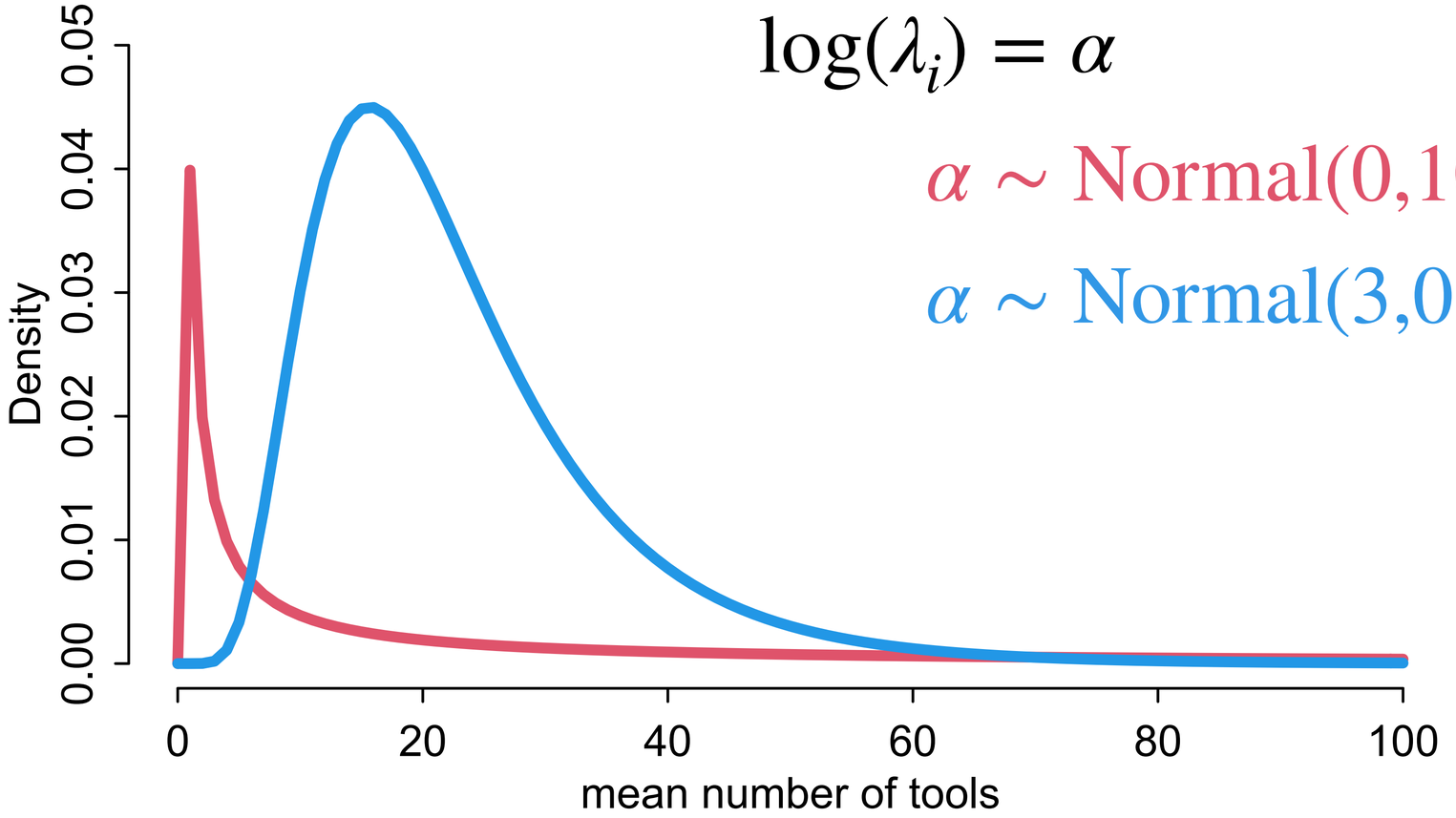


Poisson (poison) priors

Exponential scaling can be surprising



$$\log(\lambda_i) = \alpha$$

$$\alpha \sim \text{Normal}(0,10)$$

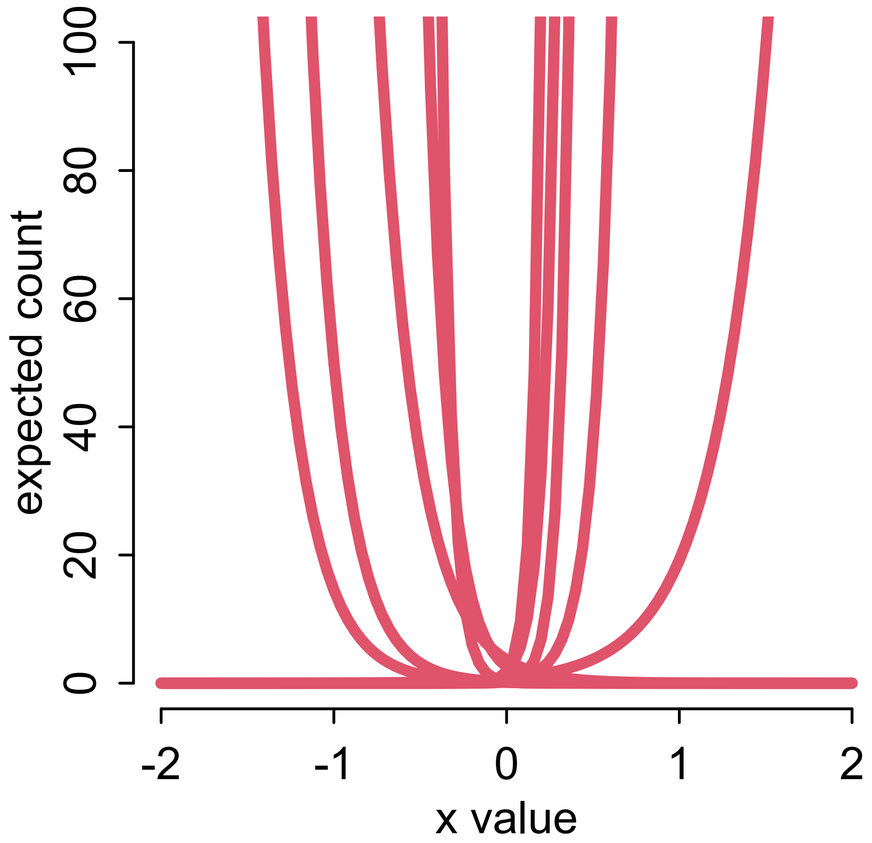
$$\alpha \sim \text{Normal}(3,0.5)$$

Poisson priors

$$\log(\lambda_i) = \alpha + \beta x_i$$

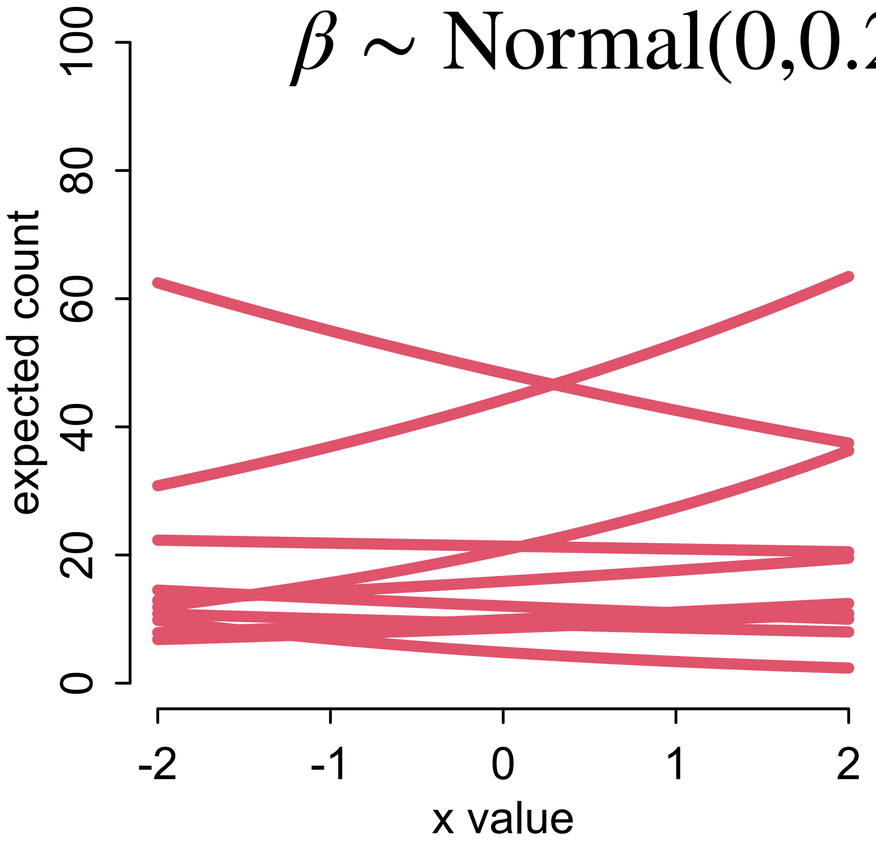
$\alpha \sim \text{Normal}(0,1)$

$\beta \sim \text{Normal}(0,10)$



$\alpha \sim \text{Normal}(3,0.5)$

$\beta \sim \text{Normal}(0,0.2)$



```r
data(Kline)
d <- Kline
d$P <- scale( log(d$population) )
d$contact_id <- ifelse( d$contact=="high" , 2 , 1 )
dat <- list(
    T = d$total_tools ,
    P = d$P ,
    C = d$contact_id )

# intercept only
m11.9 <- ulam(
    alist(
        T ~ dpois( lambda ),
        log(lambda) <- a,
        a ~ dnorm( 3 , 0.5 )
    ), data=dat , chains=4 , log_lik=TRUE )
# interaction model
m11.10 <- ulam(
    alist(
        T ~ dpois( lambda ),
        log(lambda) <- a[C] + b[C]*P,
        a[C] ~ dnorm( 3 , 0.5 ),
        b[C] ~ dnorm( 0 , 0.2 )
    ), data=dat , chains=4 , log_lik=TRUE )

compare( m11.9 , m11.10 , func=PSIS )
```

$$Y_i \sim \text{Poisson}(\lambda_i)$$

$$\log(\lambda_i) = \alpha_{C[i]} + \beta_{C[i]} \log(P_i)$$

$$\alpha_j \sim \text{Normal}(3,0.5)$$

$$\beta_j \sim \text{Normal}(0,0.2)$$

```r
data(Kline)
d <- Kline
d$P <- scale( log(d$population) )
d$contact_id <- ifelse( d$contact=="high" , 2 , 1 )
dat <- list(
    T = d$total_tools ,
    P = d$P ,
    C = d$contact_id )

# intercept only
m11.9 <- ulam(
    alist(
        T ~ dpois( lambda ),
        log(lambda) <- a,
        a ~ dnorm( 3 , 0.5 )
    ), data=dat , chains=4 , log_lik=TRUE )
# interaction model
m11.
    ), data=dat , chains=4 , log_lik=TRUE )

compare( m11.9 , m11.10 , func=PSIS )
```

```
> compare( m11.9 , m11.10 , func=PSIS )
Some Pareto k values are high (>0.5). Set pointwise=TRUE to inspect individual points.
Some Pareto k values are high (>0.5). Set pointwise=TRUE to inspect individual points.
          PSIS    SE dPSIS   dSE pPSIS weight
m11.10   85.9 13.50   0.0    NA   7.3      1
m11.9   141.3 33.69  55.4 33.13   8.0      0
```

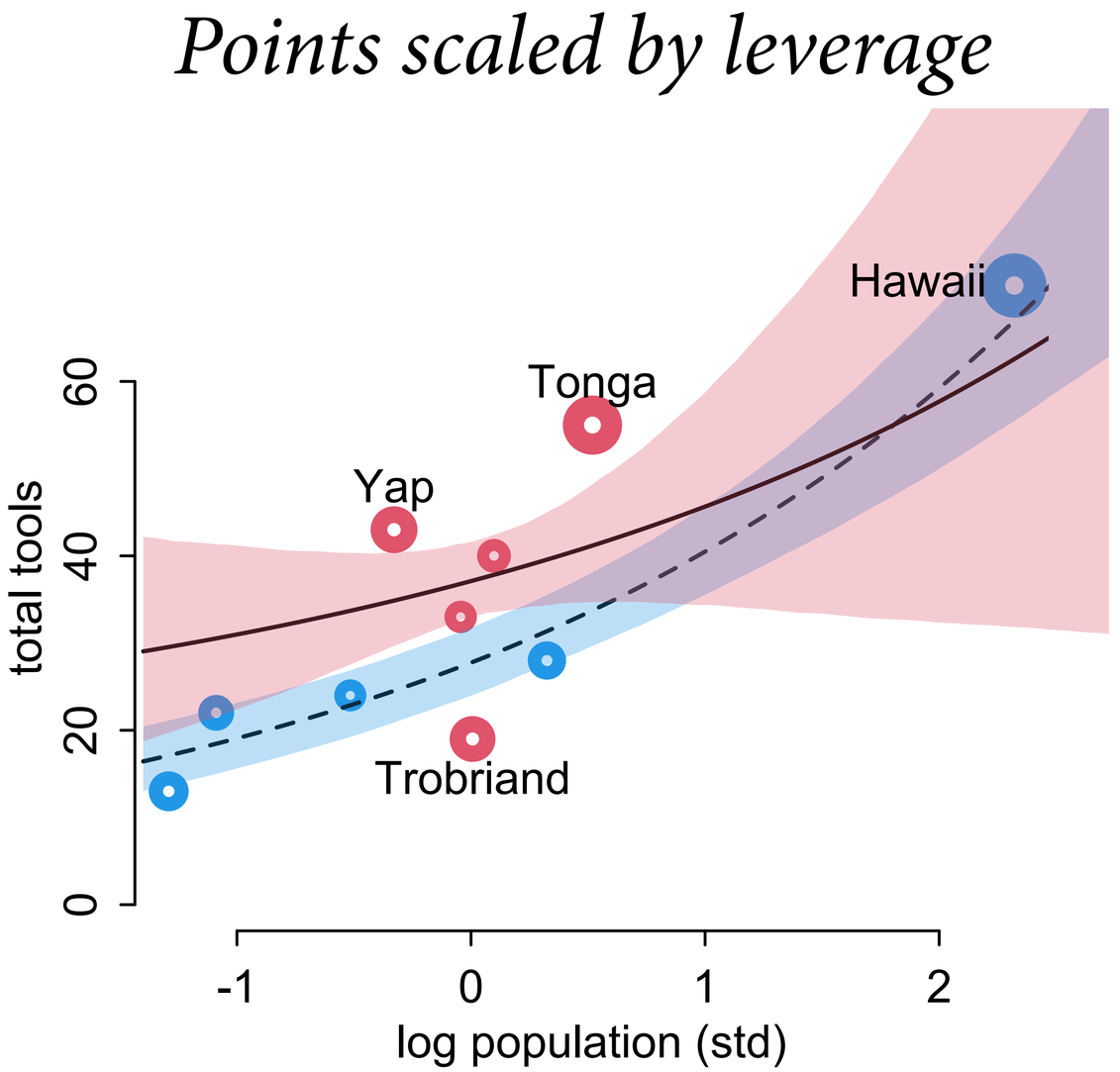
$$Y_i \sim \text{Poisson}(\lambda_i)$$

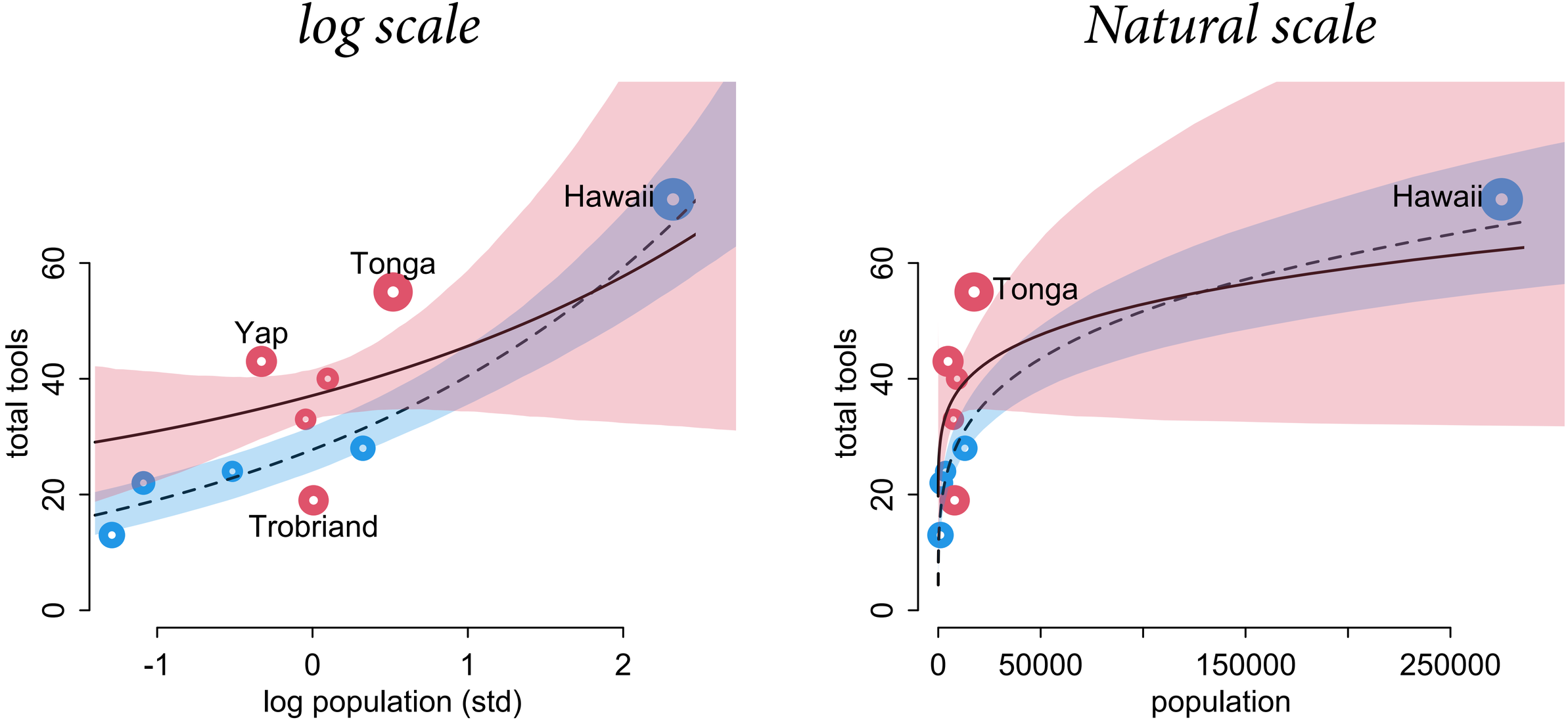
$$\log(\lambda_i) = \alpha_{C[i]} + \beta_{C[i]} \log(P_i)$$

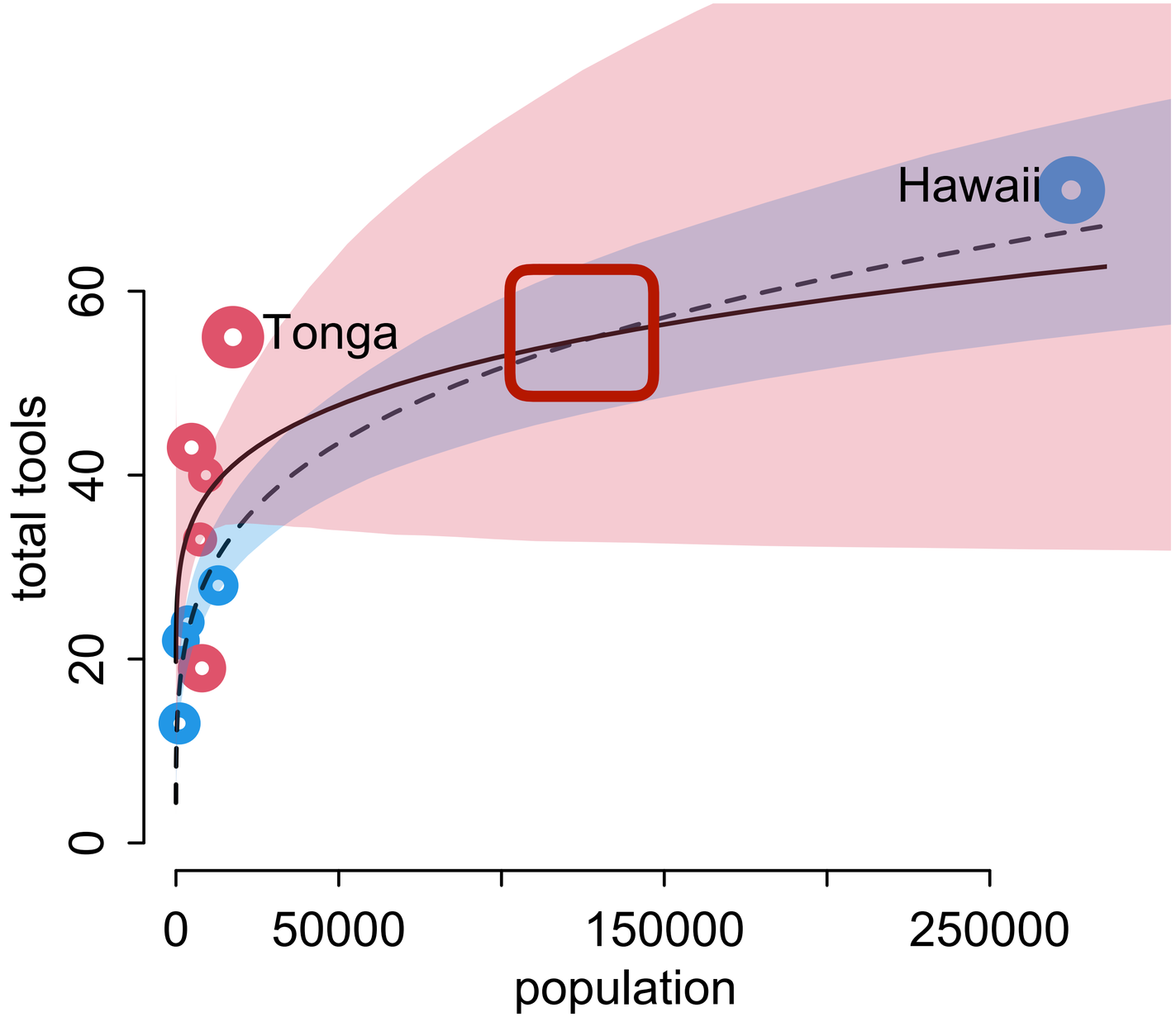
$$\alpha_j \sim \text{Normal}(3,0.5)$$

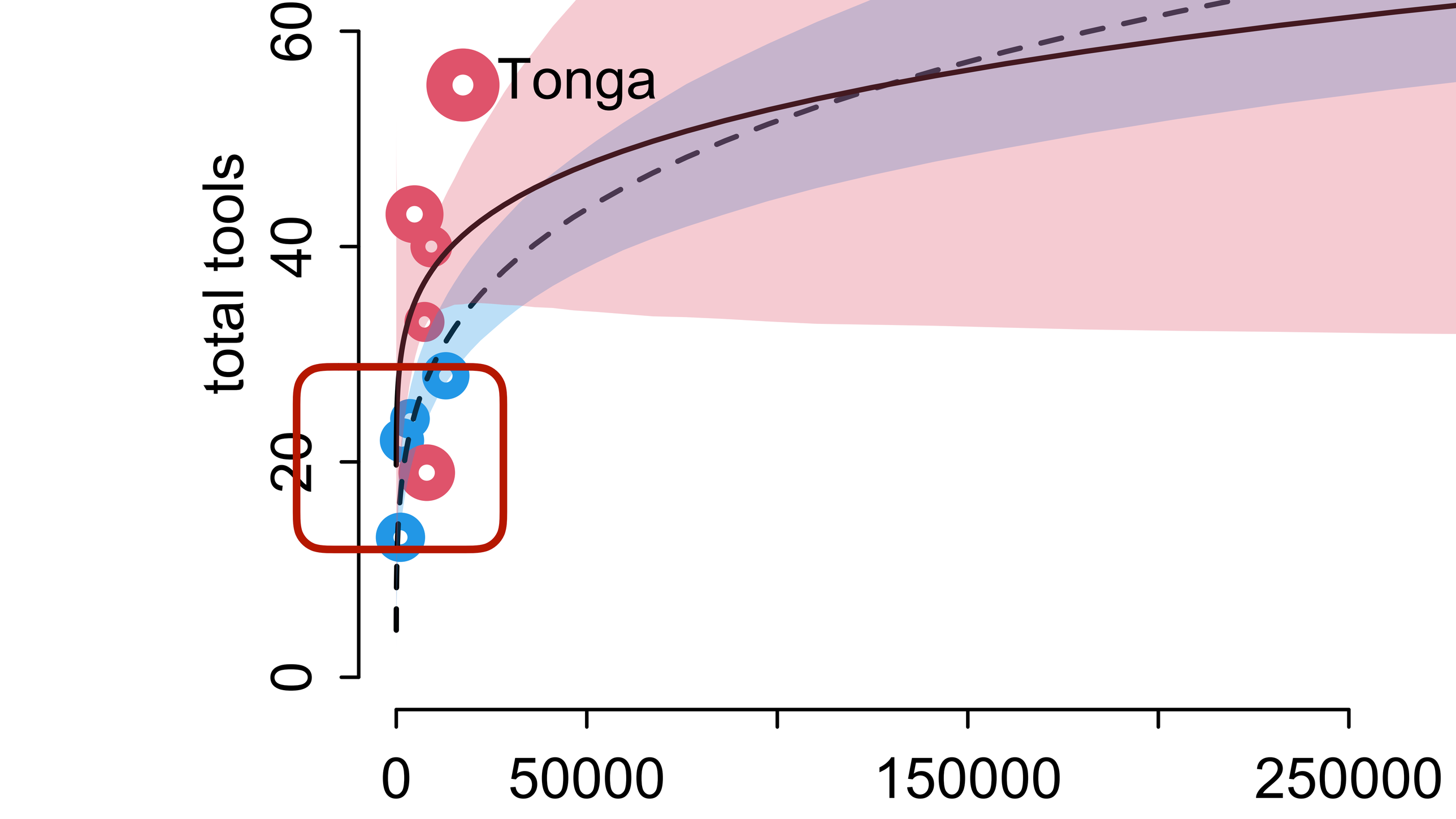
$$\beta_j \sim \text{Normal}(0,0.2)$$

```
k <- PSIS( m11.10 , pointwise=TRUE )$k
plot( dat$P , dat$T , xlab="log population (std)" ,
ylab="total tools" ,
    col=ifelse( dat$C==1 , 4 , 2 ) , lwd=4+4*normalize(k) ,
    ylim=c(0,75) , cex=1+normalize(k) )

# set up the horizontal axis values to compute predictions
at
P_seq <- seq( from=-1.4 , to=3 , len=100 )

# predictions for C=1 (low contact)
lambda <- link( m11.10 , data=data.frame( P=P_seq , C=1 ) )
lmu <- apply( lambda , 2 , mean )
lci <- apply( lambda , 2 , PI )
lines( P_seq , lmu , lty=2 , lwd=1.5 )
shade( lci , P_seq , xpd=TRUE , col=col.alpha(4,0.3) )

# predictions for C=2 (high contact)
lambda <- link( m11.10 , data=data.frame( P=P_seq , C=2 ) )
lmu <- apply( lambda , 2 , mean )
lci <- apply( lambda , 2 , PI )
lines( P_seq , lmu , lty=1 , lwd=1.5 )
shade( lci , P_seq , xpd=TRUE , col=col.alpha(2,0.3))
```




log scale
Natural scale
Hawaii
Tonga
Yap
Trobriand
total tools
0
20
40
60
-1
0
1
2
log population (std)
0
50000
150000
250000
population


Hawaii
Tonga
total tools
0
20
40
60
0
50000
150000
250000
population

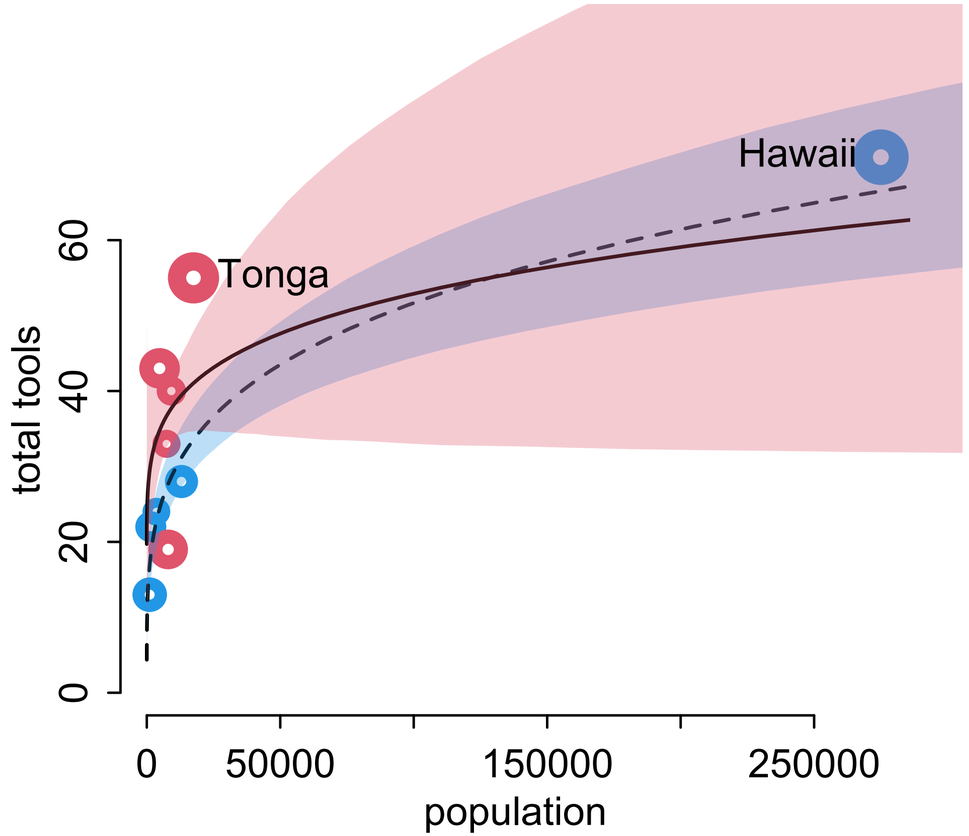

Tonga
total tools
0
20
40
60
0
50000
150000
250000

Oceanic tools

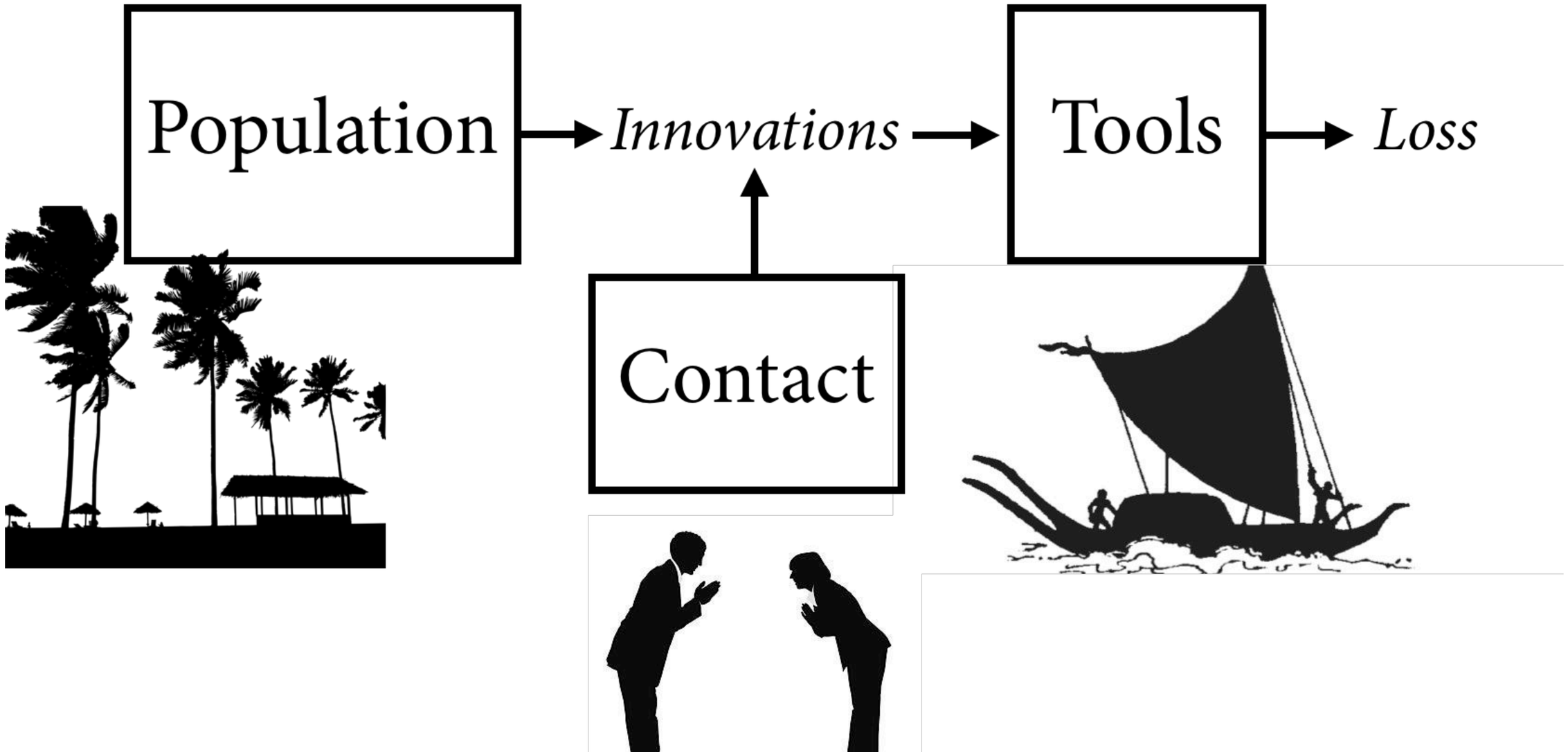
Two immediate ways to improve the model

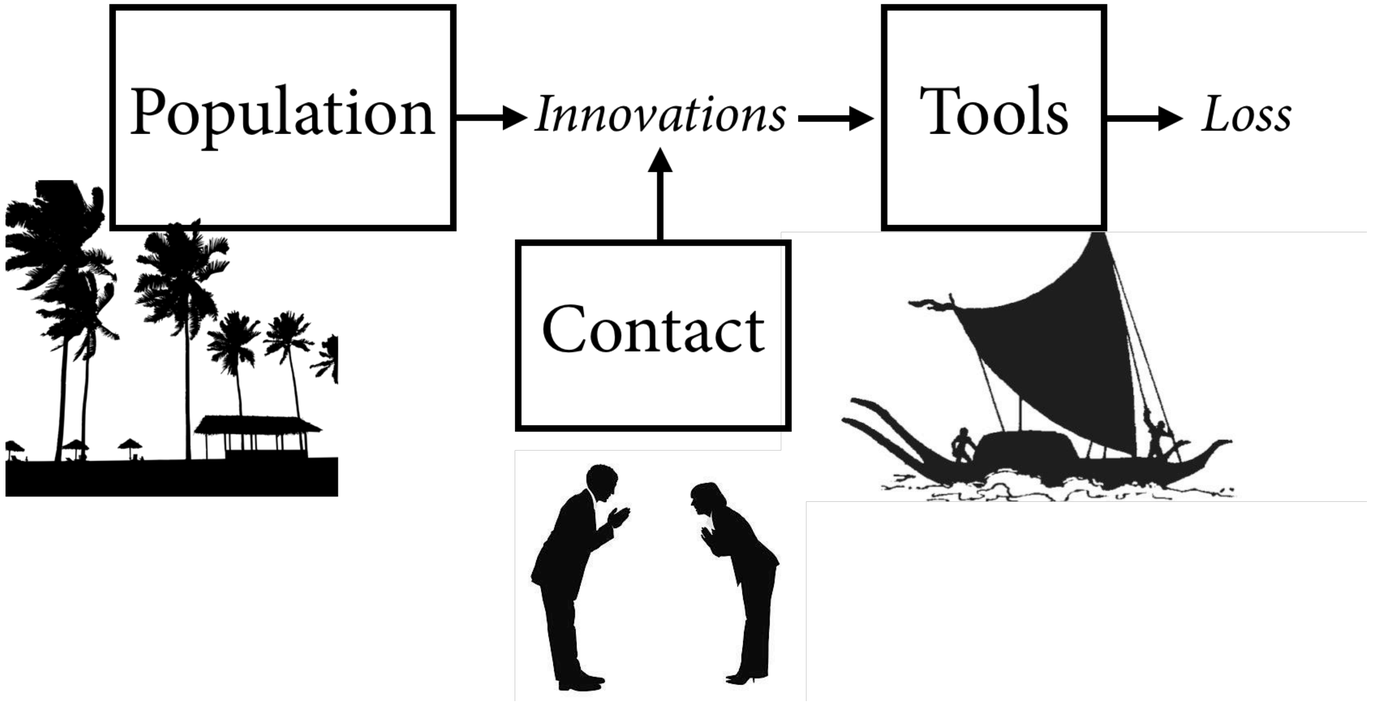
(1) Use a robust model: gamma-Poisson (neg-binomial)

(2) Use a more principled scientific model

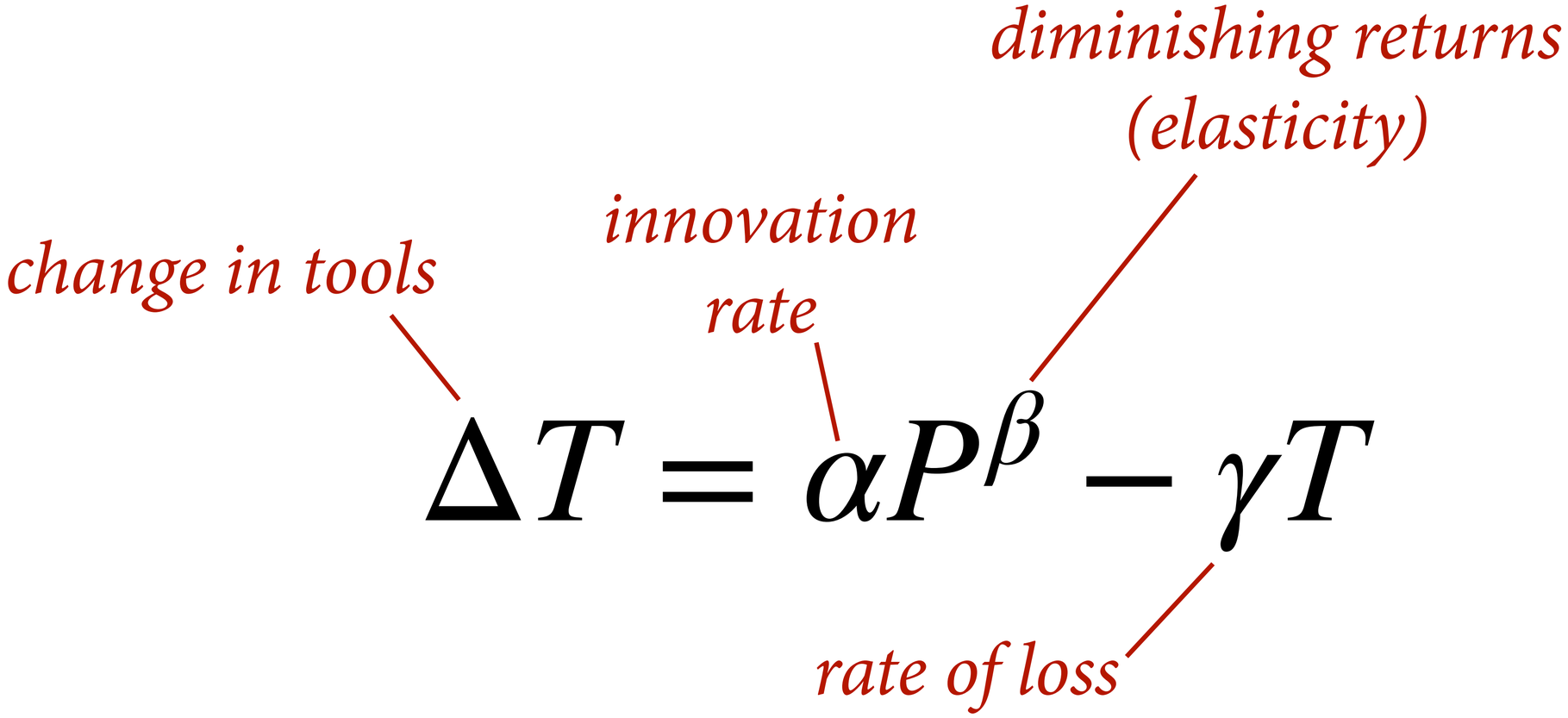


Technological complexity





$$\Delta T = \alpha P^{\beta} - \gamma T$$


diminishing returns
(elasticity)
innovation
rate
change in tools
$\Delta T = \alpha P^{\beta} - \gamma T$
rate of loss

diminishing returns depend upon contact

$$\Delta T = \alpha_C P^{\beta_C} - \gamma T$$

innovation depends upon contact

$$\Delta T = \alpha_C P^{\beta_C} - \gamma T = 0$$

Solve for T

$$\Delta T = \alpha_C P^{\beta_C} - \gamma T = 0$$

Solve for T

$$\hat{T} = \frac{\alpha_C P^{\beta_C}}{\gamma}$$

$$\hat{T} = \frac{\alpha_C P^{\beta_C}}{\gamma}$$

$$T_i \sim \text{Poisson}(\lambda_i)$$

$$\lambda_i = \hat{T}$$

```
# innovation/loss model

dat2 <- list( T=d$total_tools, P=d$population,
C=d$contact_id )

m11.11 <- ulam(
    alist(
        T ~ dpois( lambda ),
        lambda <- exp(a[C])*P^b[C]/g,
        a[C] ~ dnorm(1,1),
        b[C] ~ dexp(1),
        g ~ dexp(1)
    ), data=dat2 , chains=4 , cores=4 )
```

All parameters must be positive

Two ways to do this

(1) use exp()

(2) use appropriate prior

```
# innovation/loss model

dat2 <- list( T=d$total_tools, P=d$population,
C=d$contact_id )

m11.11 <- ulam(
    alist(
        T ~ dpois( lambda ),
        lambda <- exp(a[C])*P^b[C]/g,
        a[C] ~ dnorm(1,1),
        b[C] ~ dexp(1),
        g ~ dexp(1)
    ), data=dat2 , chains=4
```

```
> precis(m11.11,2)
      mean   sd  5.5% 94.5% n_eff Rhat4
a[1] 0.85 0.68 -0.26  1.90   698     1
a[2] 0.93 0.83 -0.39  2.31   902     1
b[1] 0.26 0.03  0.21  0.32  1149     1
b[2] 0.29 0.10  0.12  0.45   711     1
g    1.11 0.70  0.32  2.43   862     1
```

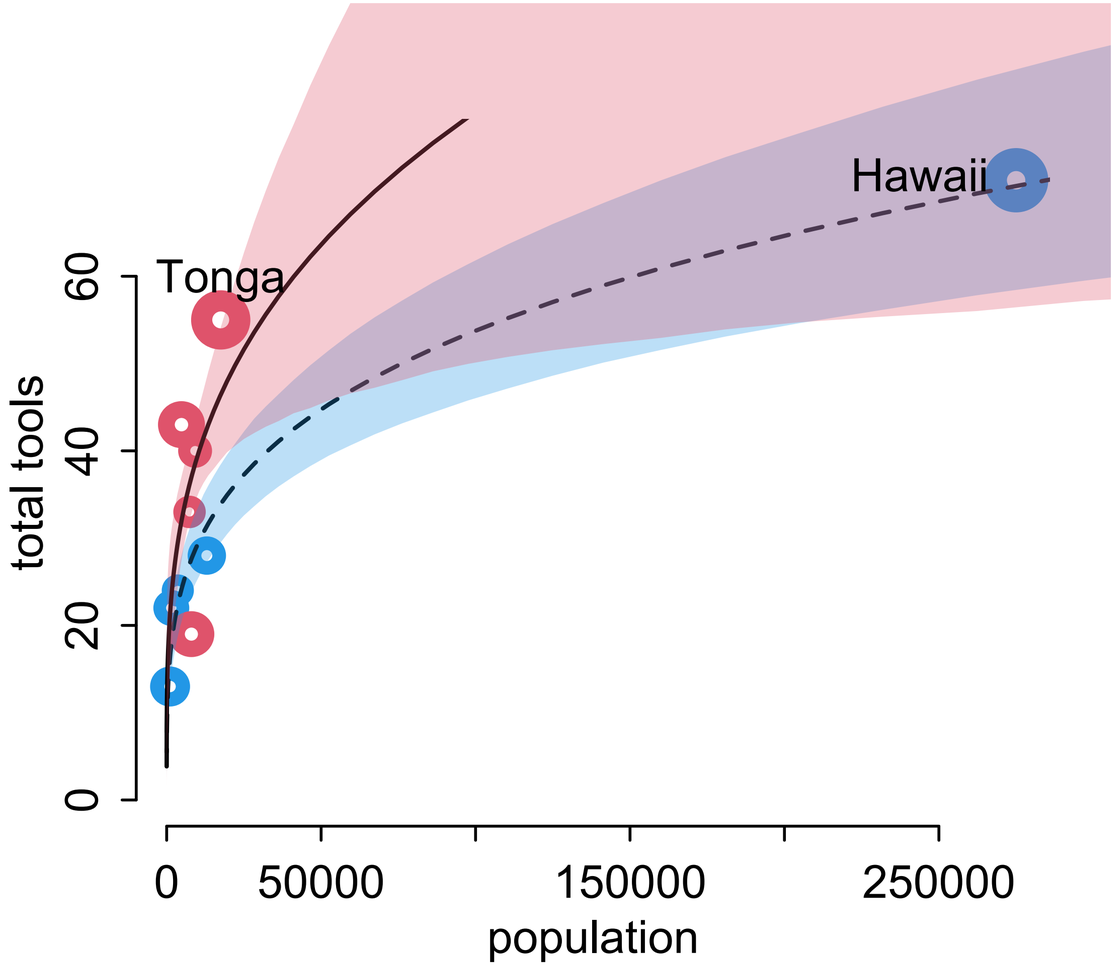
All parameters must be positive

Two ways to do this

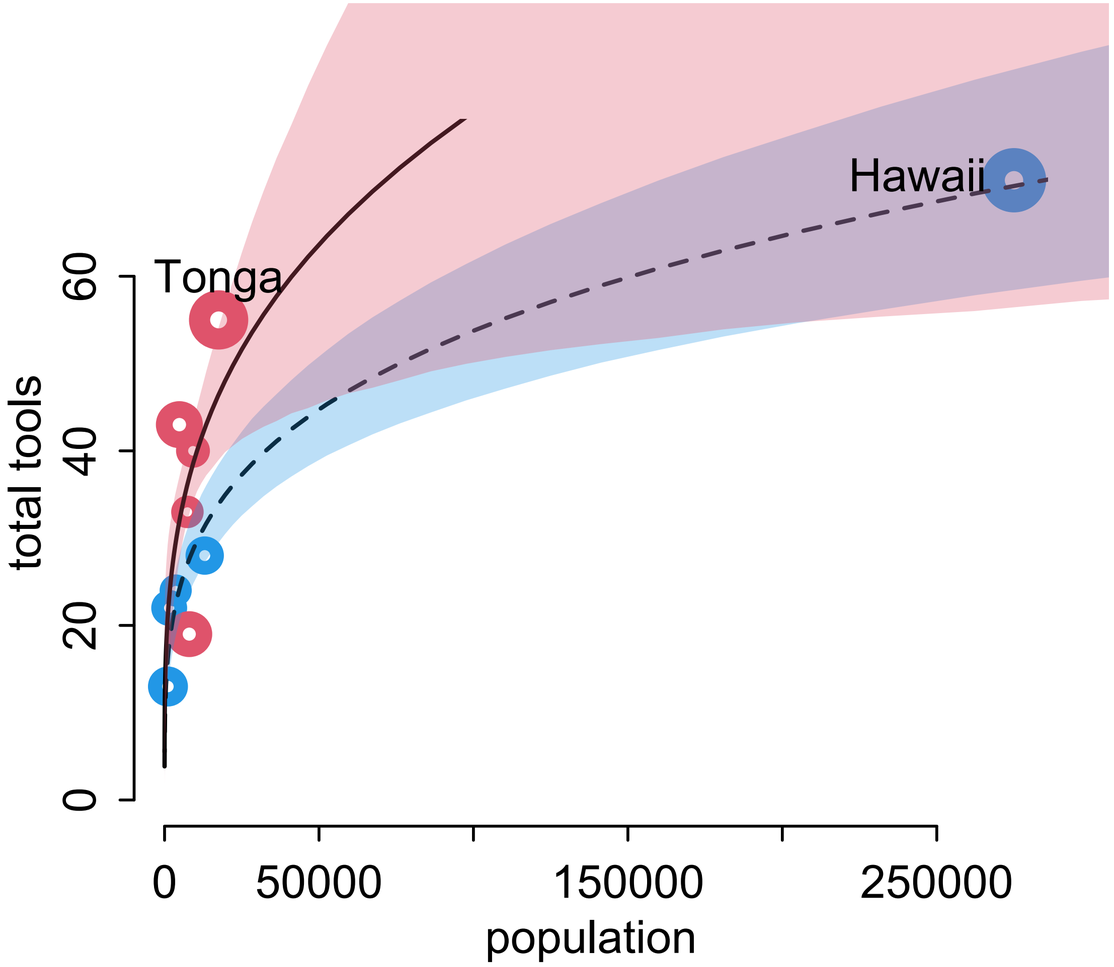
(1) use exp()

propriate prior

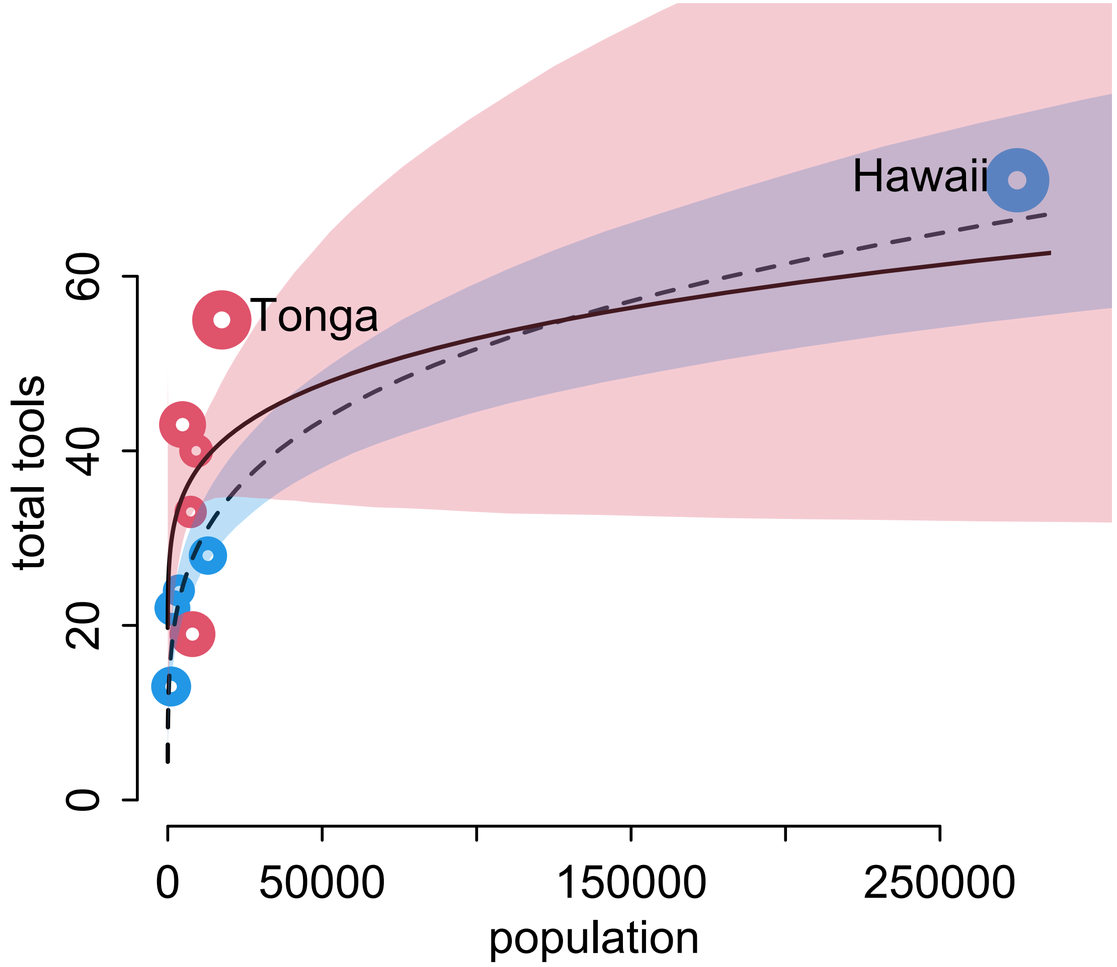
```
# innovation/loss model

dat2 <- list( T=d$total_tools, P=d$population,
C=d$contact_id )

m11.11 <- ulam(
    alist(
        T ~ dpois( lambda ),
        lambda <- exp(a[C])*P^b[C]/g,
        a[C] ~ dnorm(1,1),
        b[C] ~ dexp(1),
        g ~ dexp(1)
    ), data=dat2 , chains=4 , cores=4 )
```



Innovation/loss model



Generalized linear model



Still have to deal with location as confound

Count GLMs

Before you see the values, you know a count is zero or positive

Maximum entropy priors: Binomial, Poisson, and extensions

More event types: Multinomial and categorical

Robust regressions:
Beta-binomial, gamma-Poisson (neg-binomial)

Examples to come

Course Schedule

Week 1	Bayesian inference	Chapters 1, 2, 3
Week 2	Linear models & Causal Inference	Chapter 4
Week 3	Causes, Confounds & Colliders	Chapters 5 & 6
Week 4	Overfitting / MCMC	Chapters 7, 8, 9
Week 5	Generalized Linear Models	Chapters 10, 11
Week 6	Mixtures & ordered categories	Chapters 11 & 12
Week 7	Multilevel models I	Chapter 13
Week 8	Multilevel models II	Chapter 14
Week 9	Measurement & Missingness	Chapter 15
Week 10	Generalized Linear Madness	Chapter 16

https://github.com/rmcelreath/stat_rethinking_2022