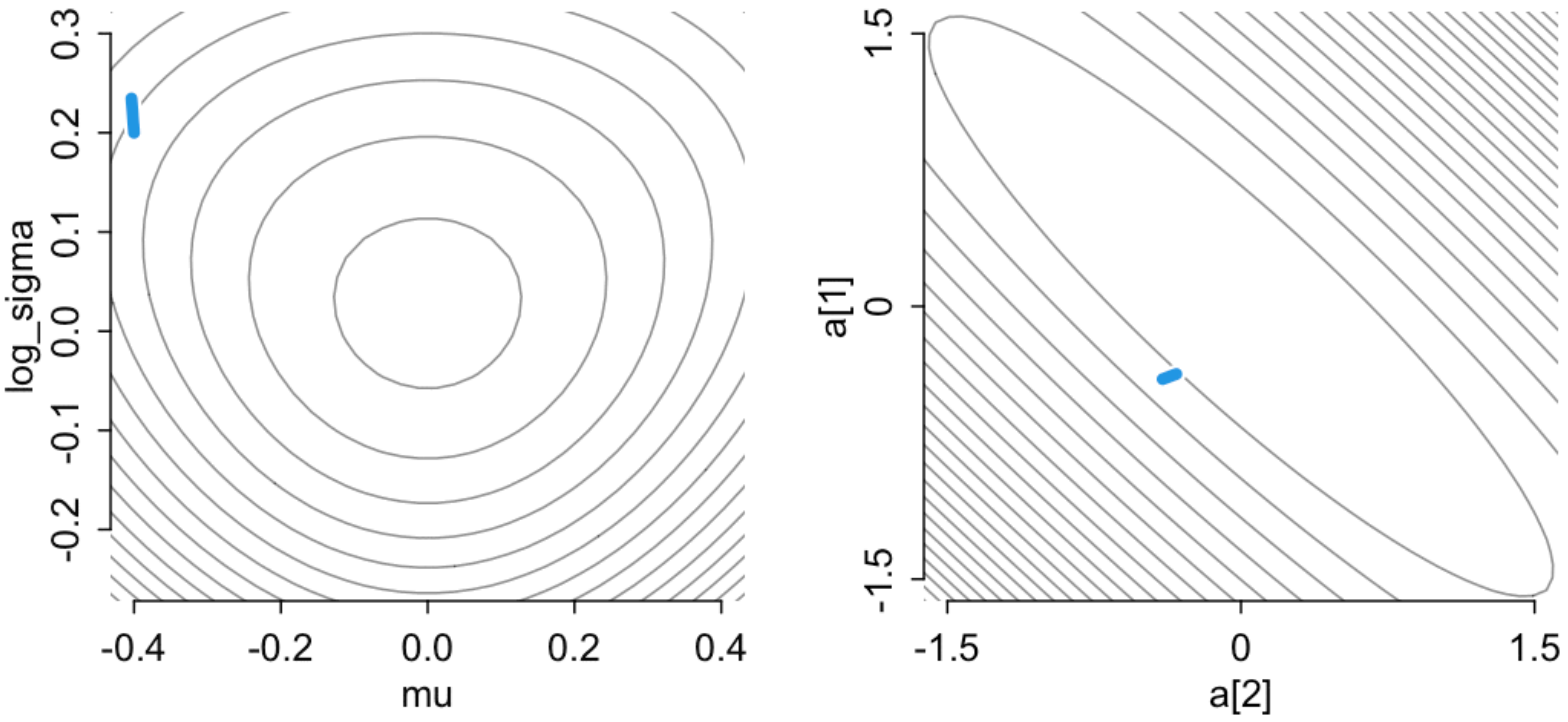
Statistical Rethinking
2023

9. Modeling Events

THE



Lecture 8


FLOW

Flow forward

Everything comes all at once:

Scientific modeling, research design, statistical modeling, coding, interpretation, communication, the price of eggs

Don’t have to understand it all at once

Nobody ever does

UC Berkeley Admissions

4526 graduate school applications for 1973 UC Berkeley

Stratified by department and gender of applicant

Gender discrimination by admission officers?

	dept	admit	reject	applications	gender
1	A	512	313	825	male
2	A	89	19	108	female
3	B	353	207	560	male
4	B	17	8	25	female
5	C	120	205	325	male
6	C	202	391	593	female
7	D	138	279	417	male
8	D	131	244	375	female
9	E	53	138	191	male
10	E	94	299	393	female
11	F	22	351	373	male
12	F	24	317	341	female

See ?UCBAdmissions for citation

Defining the range

How can gender equality monitoring look like in a diverse work and research culture?

The Max Planck Society's offers and programs for the support of Gender Equality are various and tailored to the special requirements of science and to the needs of various scientists. The design of the instruments that monitor and accompany the success and development of the measures has to be just as various and flexible. Within this framework, the Central Gender Equality Officer and her team provide counseling for all persons, levels, functions, groups, and committees. The objective is to guarantee a uniformly high level of Gender Equality work in the Institutes while preserving the professional and cultural

Gender Gaps at the Academies

David Card, Stefano DellaVigna, Patricia Funk & Nagore Iriberri

WORKING PAPER 30510 **DOI** 10.3386/w30510 **ISSUE DATE** September 2022

Historically, a large majority of the newly elected members of the National Academy of Science (NAS) and the American Academy of Arts and Science (AAAS) were men. Within the past two decades, however, that situation has changed, and in the last 3 years women made up about 40 percent of the new members in both academies. We build lists of active scholars from publications in the top journals in three fields – Psychology, Mathematics and Economics – and develop a series of models to compare changes in the probability of selection of women as members of the NAS and AAAS from the 1960s to today, controlling for publications and citations. In the early years of our sample, women were less likely to be selected as members than men with similar records. By the 1990s, the selection process at both academies was approximately gender-neutral, conditional on publications and citations. In the past 20 years, however, a positive preference for female members has emerged and strengthened in all three fields. Currently, women are 3-15 times more likely to be selected as members of the AAAS and NAS than men with similar publication and citation records.

PNAS BRIEF REPORT | SOCIAL SCIENCES COMPUTER SCIENCES

Gendered citation patterns among the scientific elite

Kristina Lerman[a,1], Yulin Yu[b], Fred Morstatter[a], and Jay Pujara[a]

Edited by Susan Fiske, Princeton University, Princeton, NJ; received April 8, 2022; accepted August 22, 2022

Diversity in science is necessary to improve innovation and increase the capacity of the scientific workforce. Despite decades-long efforts to increase gender diversity, however, women remain a small minority in many fields, especially in senior positions. The dearth of elite women scientists, in turn, leaves fewer women to serve as mentors and role models for young women scientists. To shed light on gender disparities in science, we study prominent scholars who were elected to the National Academy of Sciences. We construct author citation networks that capture the structure of recognition among scholars' peers. We identify gender disparities in the patterns of peer citations and show that these differences are strong enough to accurately predict the scholar's gender. In contrast, we do not observe disparities due to prestige, with few significant differences in the structure of citations of scholars affiliated with high-ranked and low-ranked institutions. These results provide further evidence that a scholar's gender plays a role in the mechanisms of success in science.

gender | bibliometrics | science of science | gender disparities

Gender disparities persist in many fields of science. Despite long-running efforts to increase women's representation in the scientific workforce, they continue to face barriers to advancement. Women are less likely than their male peers to be mentored by eminent faculty (1) and to be hired and promoted (2, 3). Women publish in less prestigious journals (4), have fewer collaborators (5), and are underrepresented among journal reviewers and editors (6), and their papers receive fewer citations (7, 8). The multifaceted gender disparities create a "glass ceiling," an invisible barrier that fundamentally limits professional recognition for even the best women scientists (9). As a result, the share of women in higher academic positions decreases steadily (3), with relatively few becoming full professors or receiving prestigious awards. For example, among physics faculty in 4-y colleges and universities, women represent 23% of assistant professors and 18% of associate professors

uniformly high level of Gender Equality work in the Institutes while preserving the professional and cultural

Causal foundations of bias, disparity and fairness

V.A. Traag[a] and L. Waltman

Centre for Science and Technology Studies (CWTS), Leiden University, the Netherlands

(Dated: July 27, 2022)

The study of biases, such as gender or racial biases, is an important topic in the social and behavioural sciences. However, the concept of bias is not always clearly defined in the literature. Definitions of bias are often ambiguous, or definitions are not provided at all. To study biases in a precise way, it is important to have a well-defined concept of bias. We propose to define bias as a direct causal effect that is unjustified. We propose to define the closely related concept of disparity as a direct or indirect causal effect that includes a bias. Our proposed definitions can be used to study biases and disparities in a more rigorous and systematic way. We compare our definitions of bias and disparity with various definitions of fairness introduced in the artificial intelligence literature. We also illustrate our definitions in two case studies, focusing on gender bias in science and racial bias in police shootings. Our proposed definitions aim to contribute to a better appreciation of the causal intricacies of studies of biases and disparities. This will hopefully also lead to an improved understanding of the policy implications of such studies.

Keywords: bias; disparity; fairness; causal model; gender bias; racial bias

https://arxiv.org/abs/2207.13665

Modeling events

Events: Discrete, unordered outcomes

Observations are counts

Unknowns are probabilities, odds

Everything interacts always everywhere

A beast known as “log-odds”

Admissions: Drawing the Owl

(1) Estimand(s)

(2) Scientific model(s)

(3) Statistical model(s)

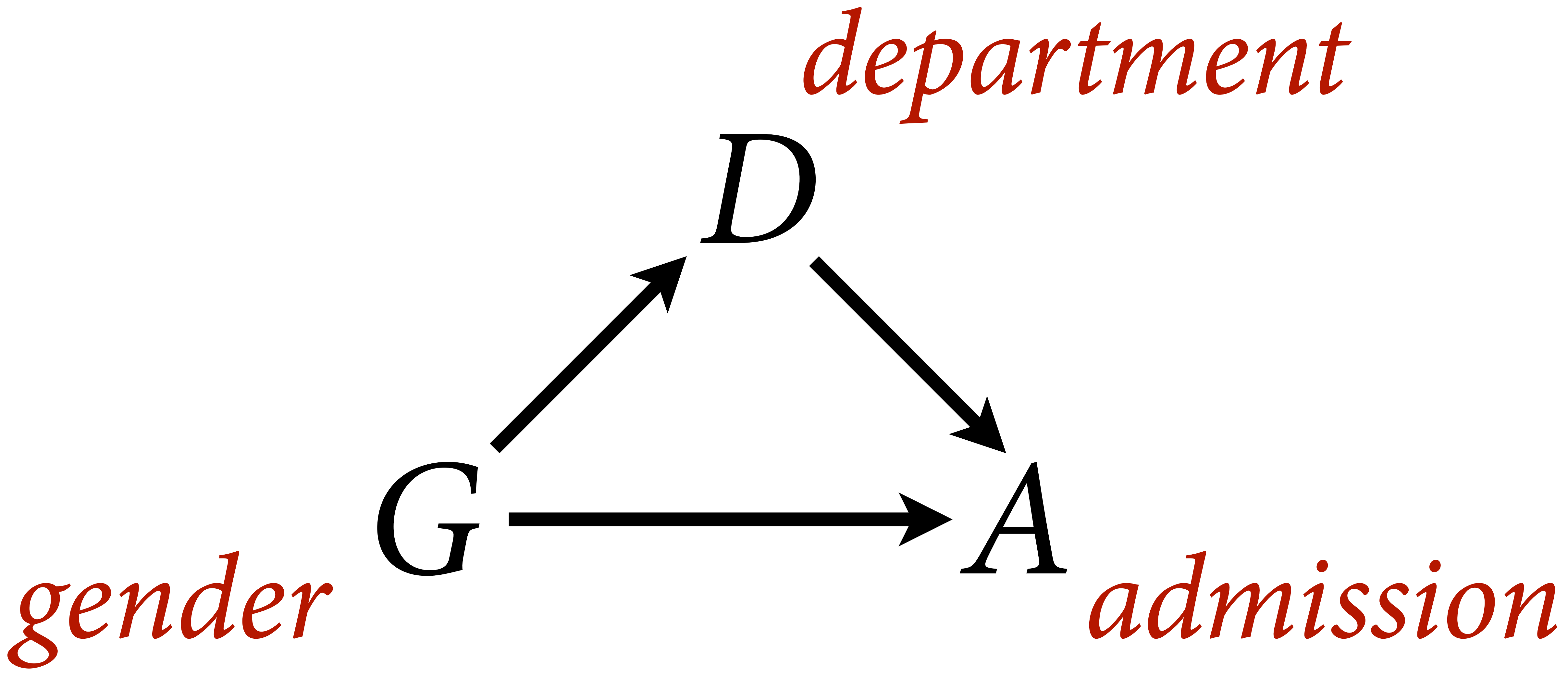
(4) Analyze

Admissions

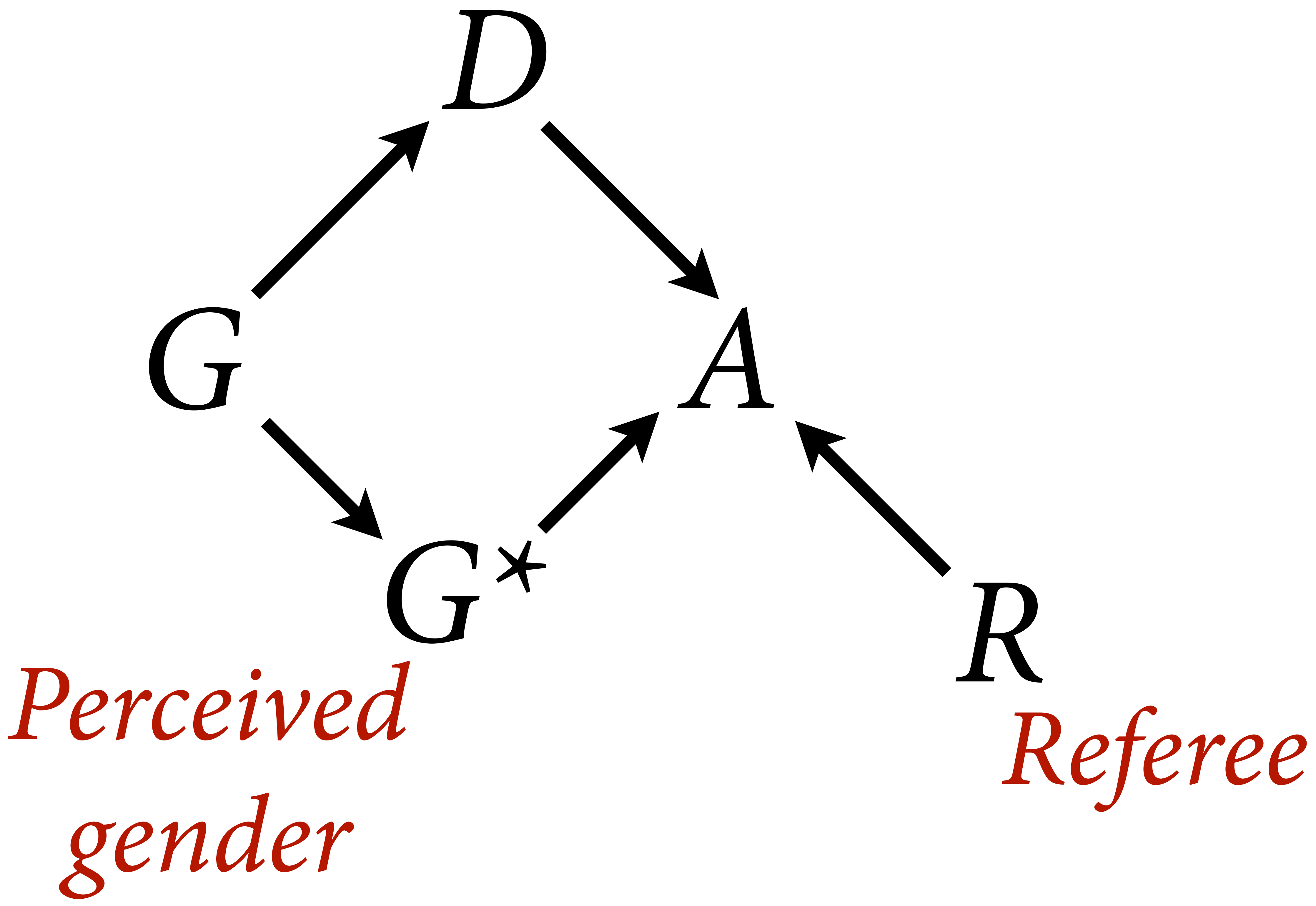
Was there gender discrimination in graduate admissions?

$$\text{gender}\; G \longrightarrow A \;\text{admission}$$

Admissions



What can the “causal effect of gender” mean?



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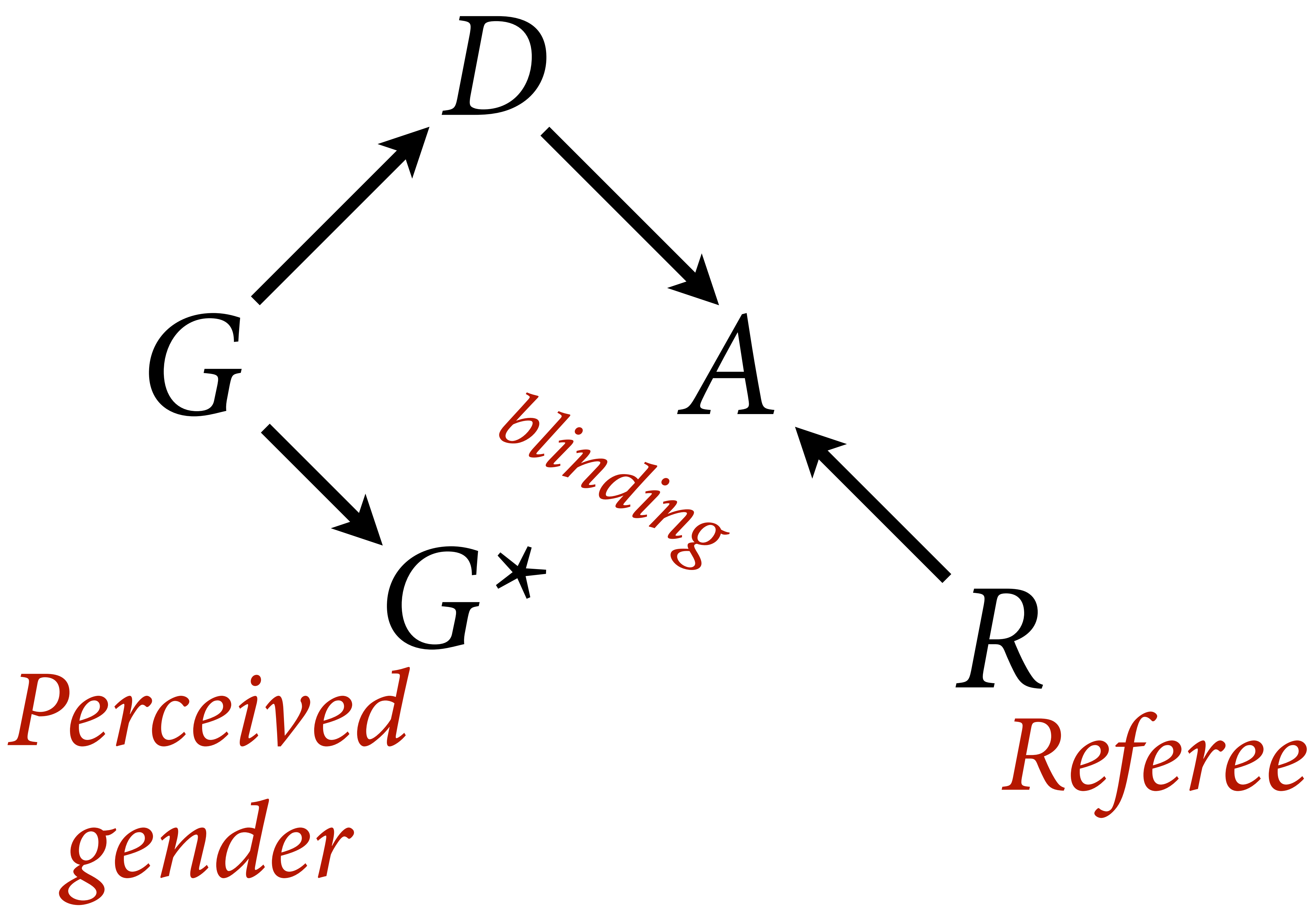

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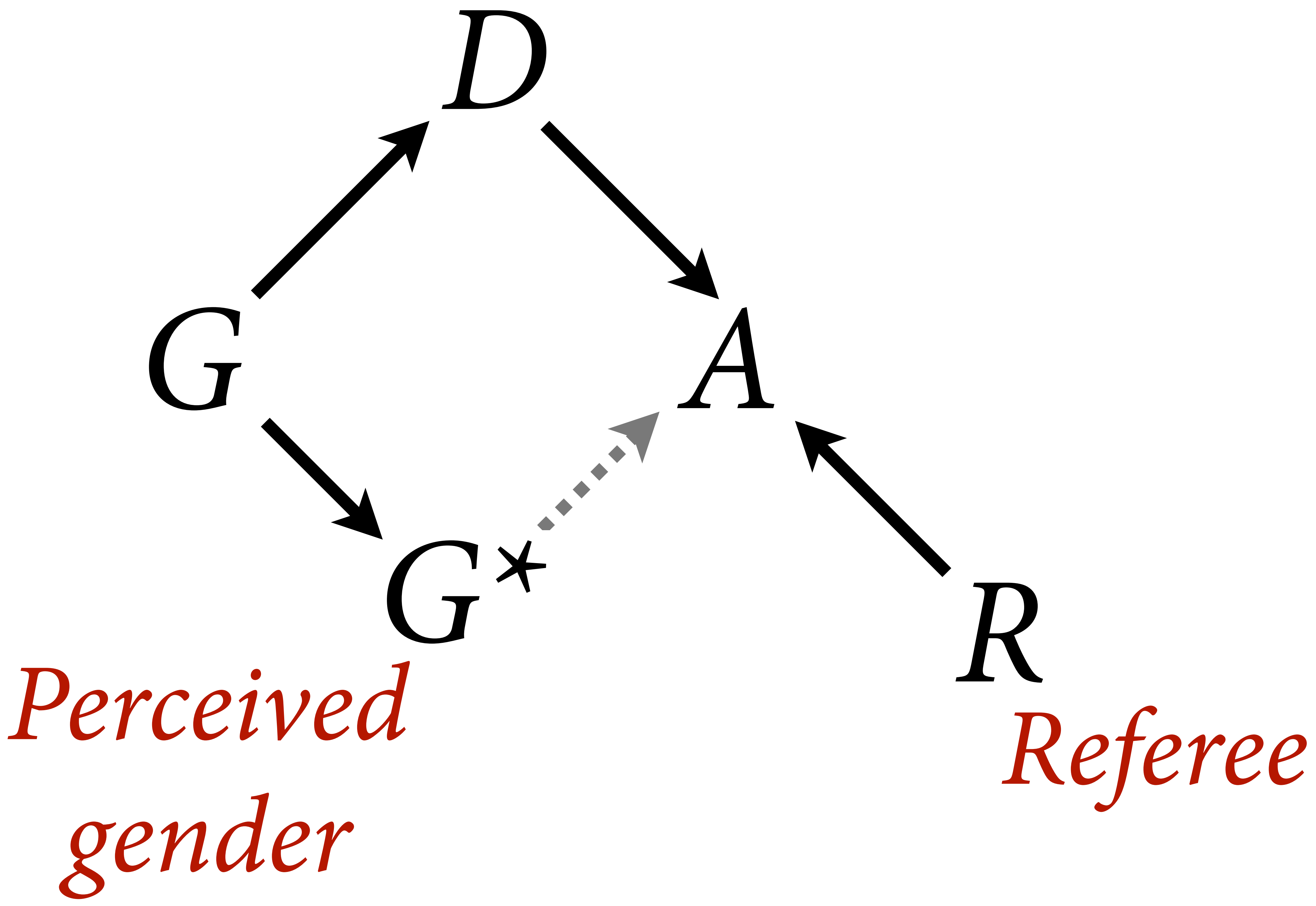
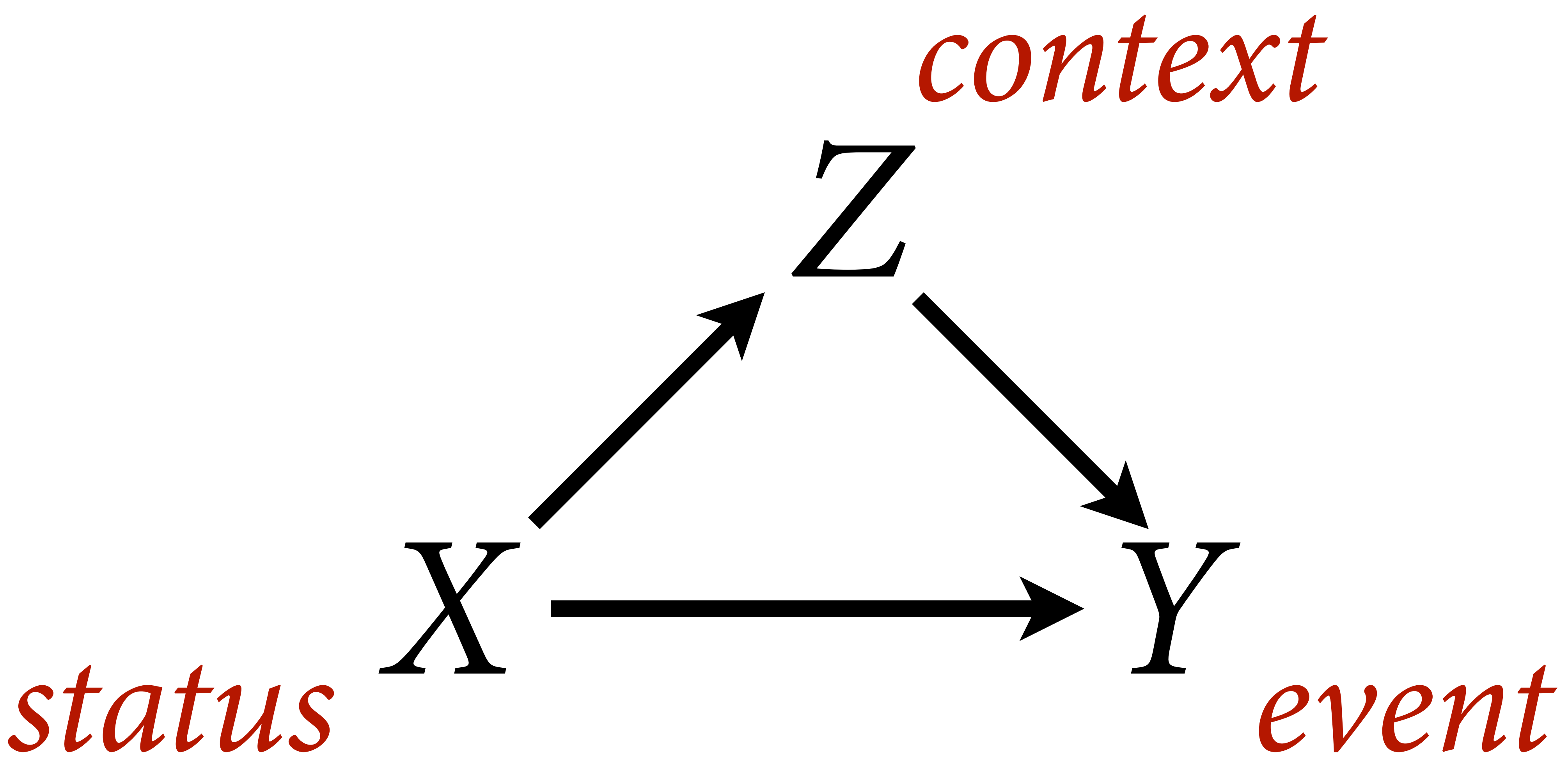
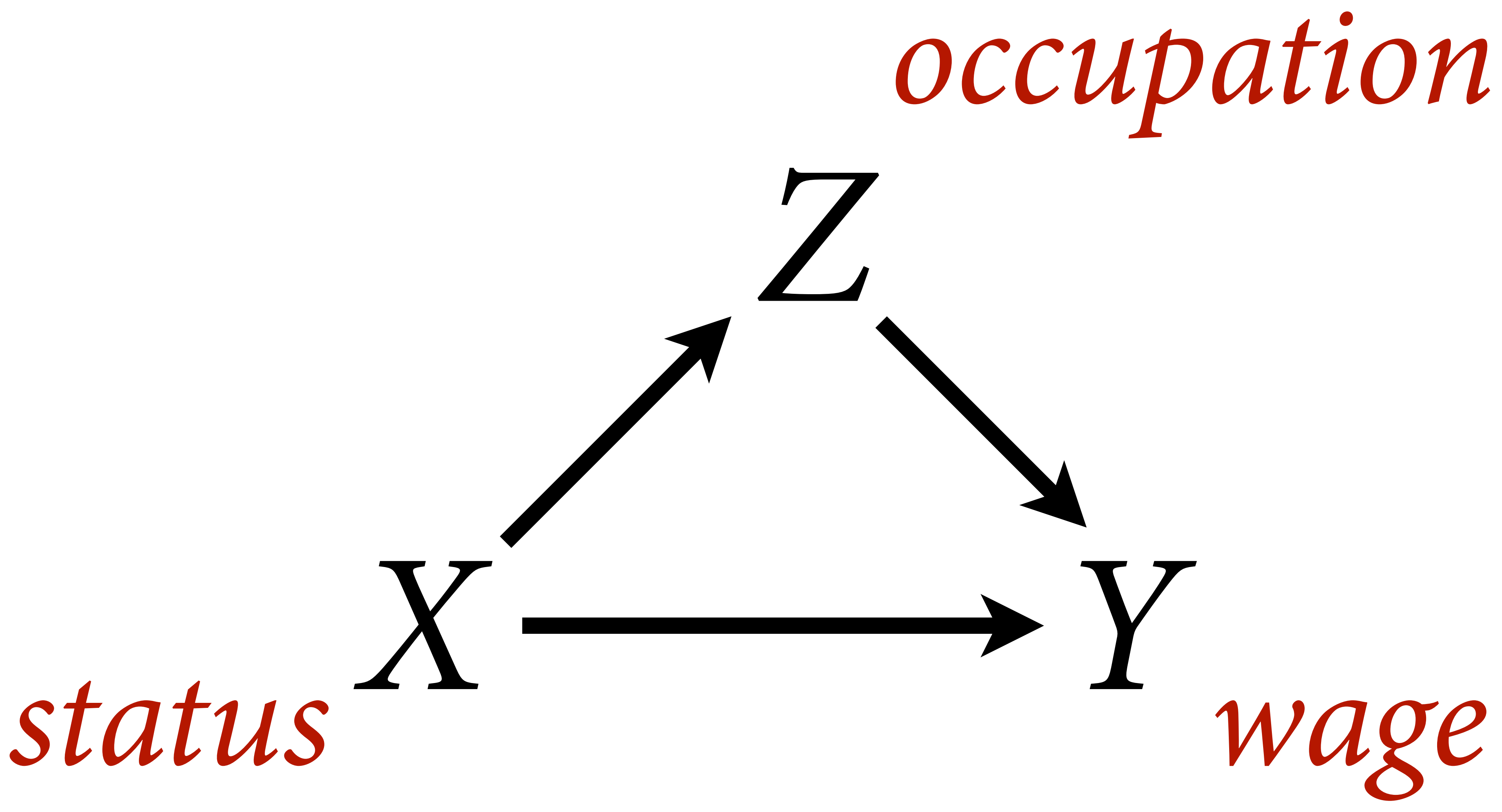


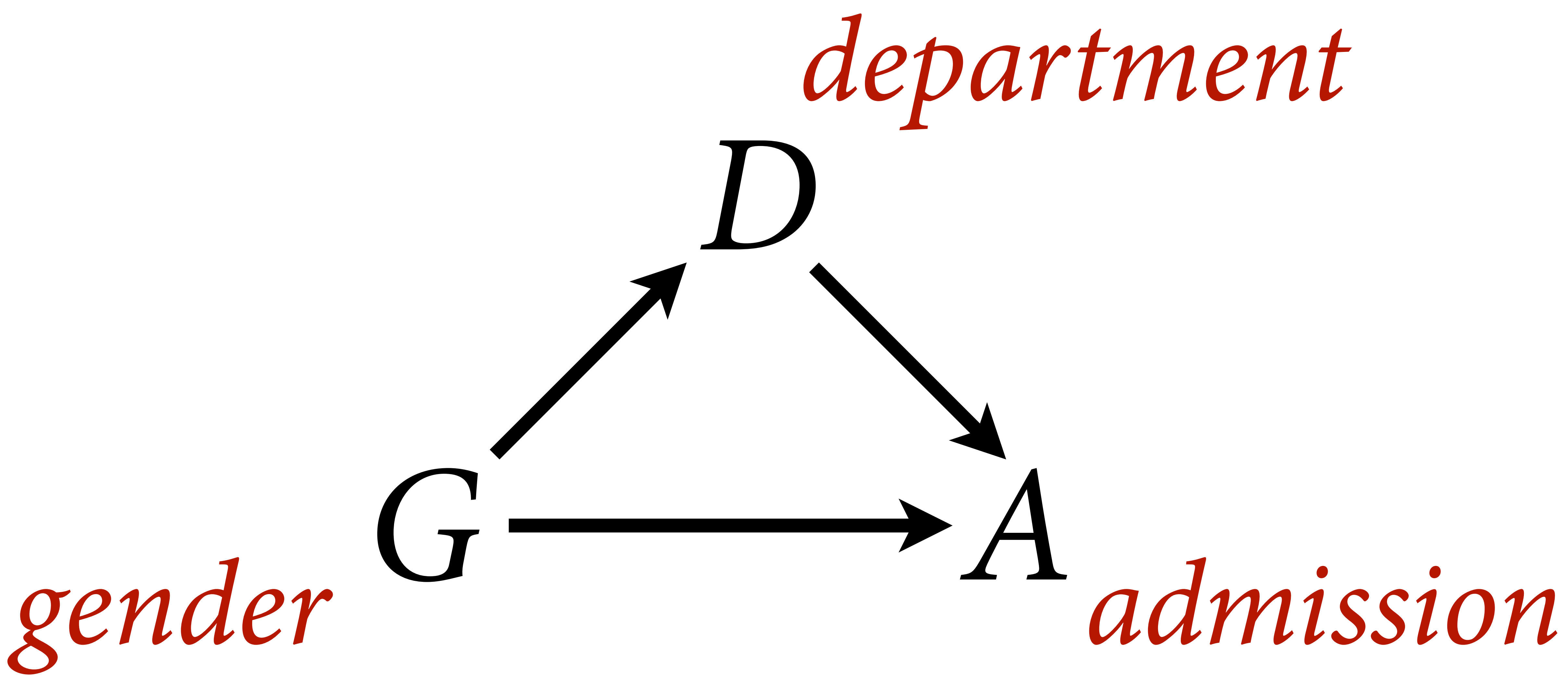
Context & discrimination



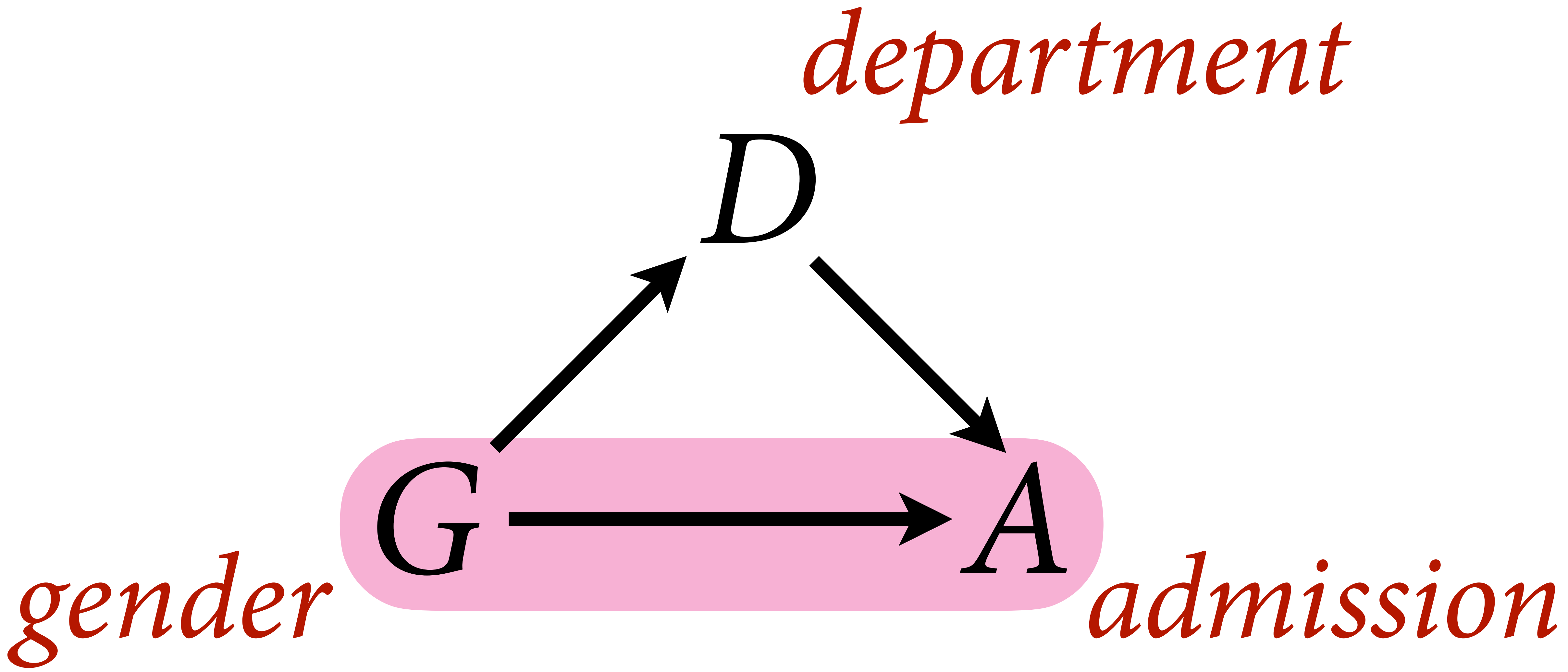
Wage discrimination



Which path is "discrimination"?



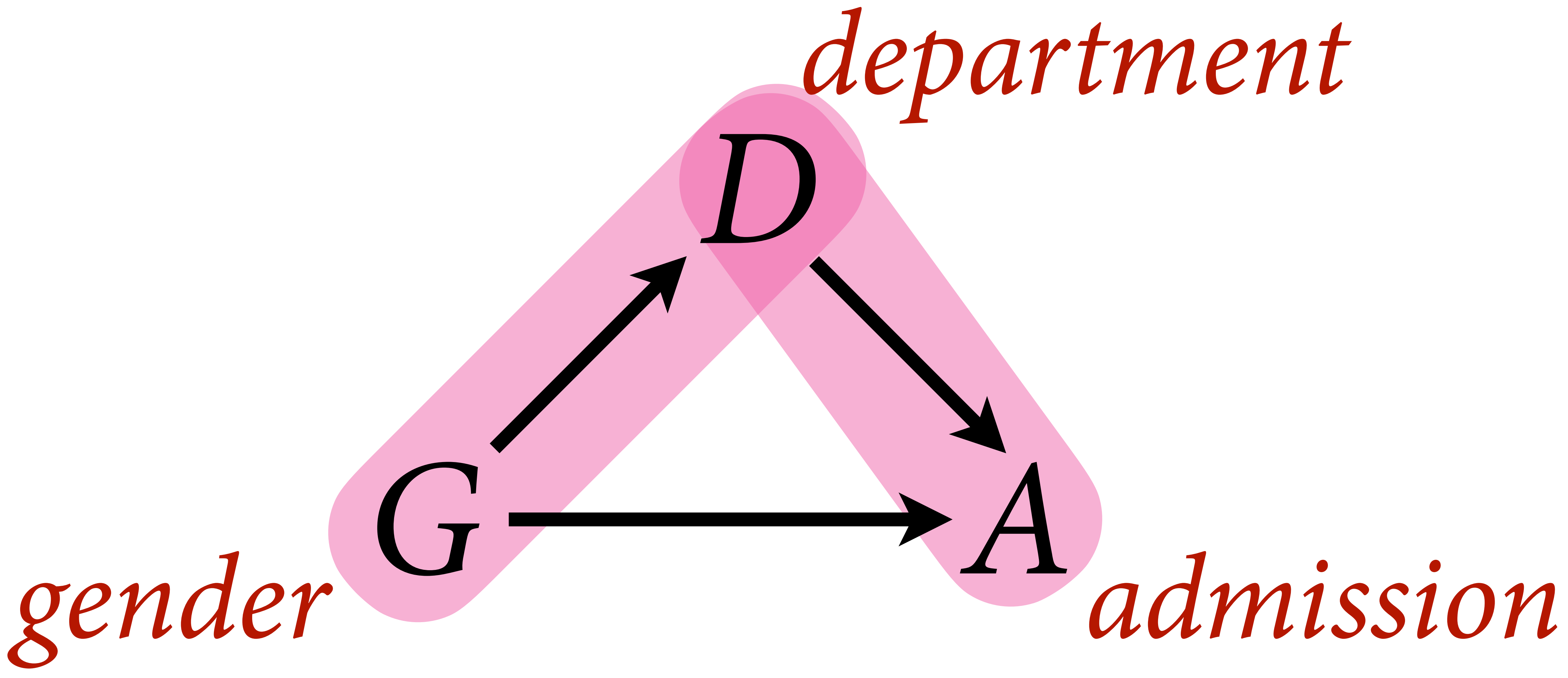
Which path is "discrimination"?



Direct discrimination

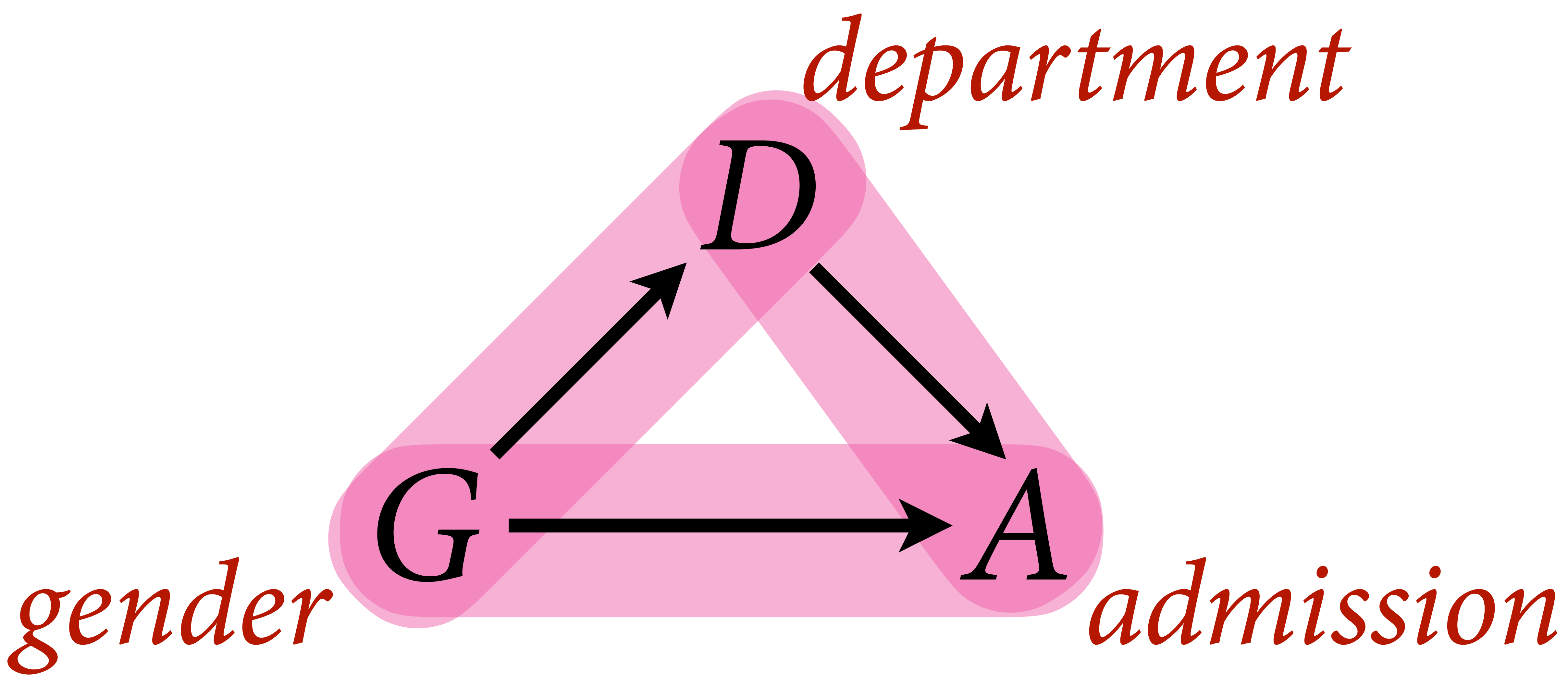
(status-based or taste-based discrimination)

Which path is "discrimination"?



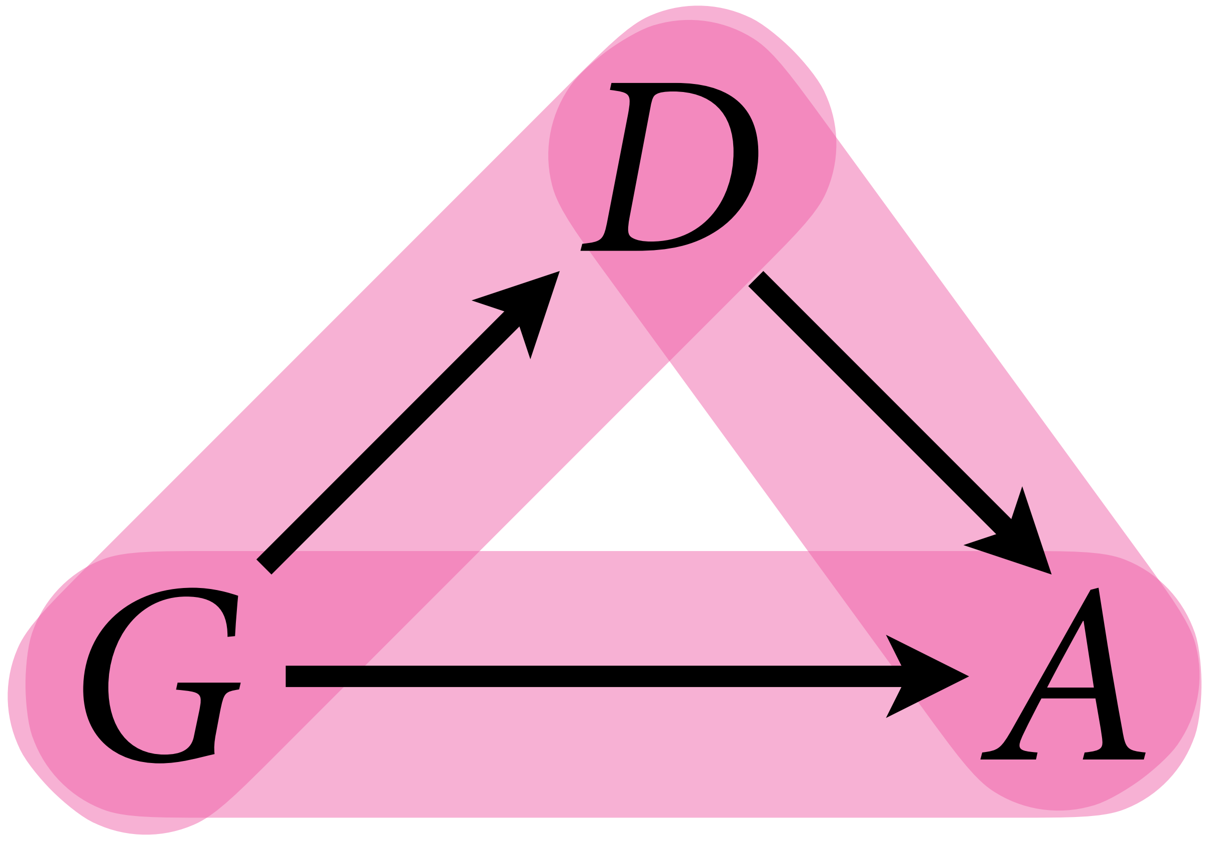
Indirect discrimination
(structural discrimination)

Which path is "discrimination"?



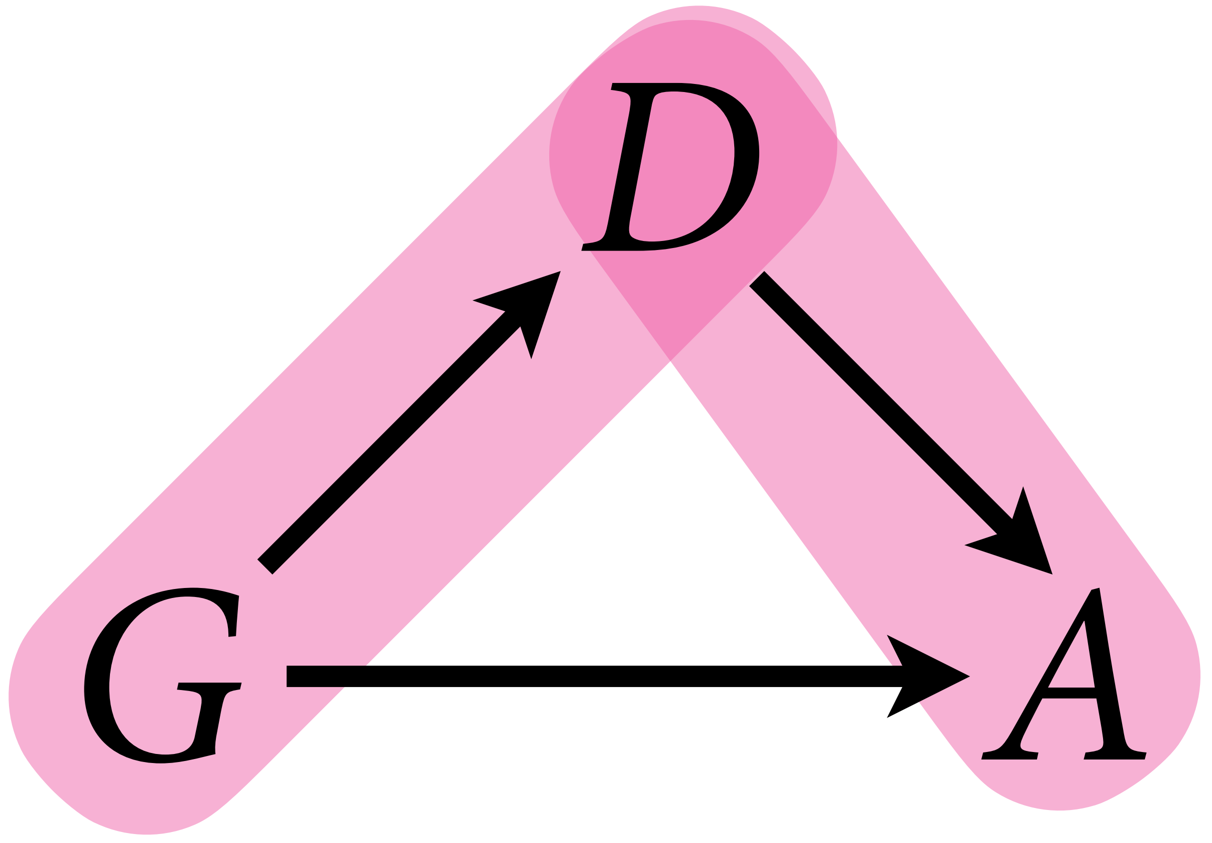
Total discrimination
(experienced discrimination)

Which path is "discrimination"?



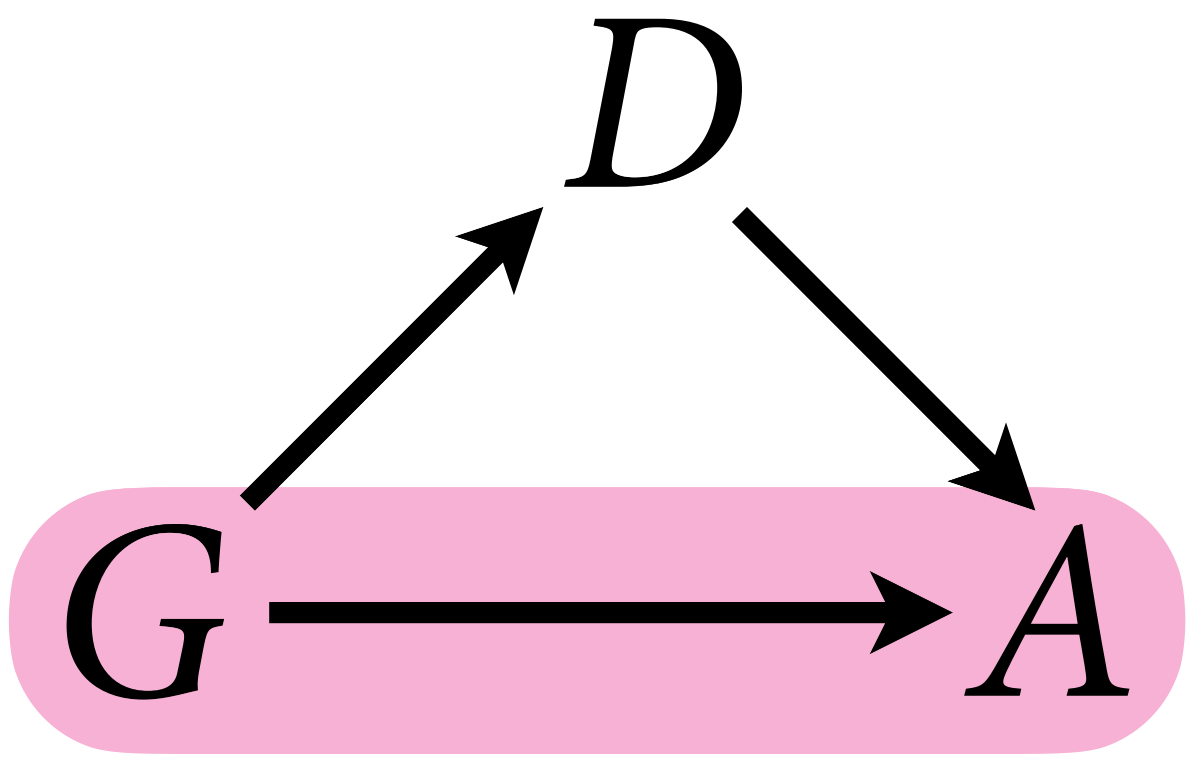
Total

Requires mild assumptions



Indirect

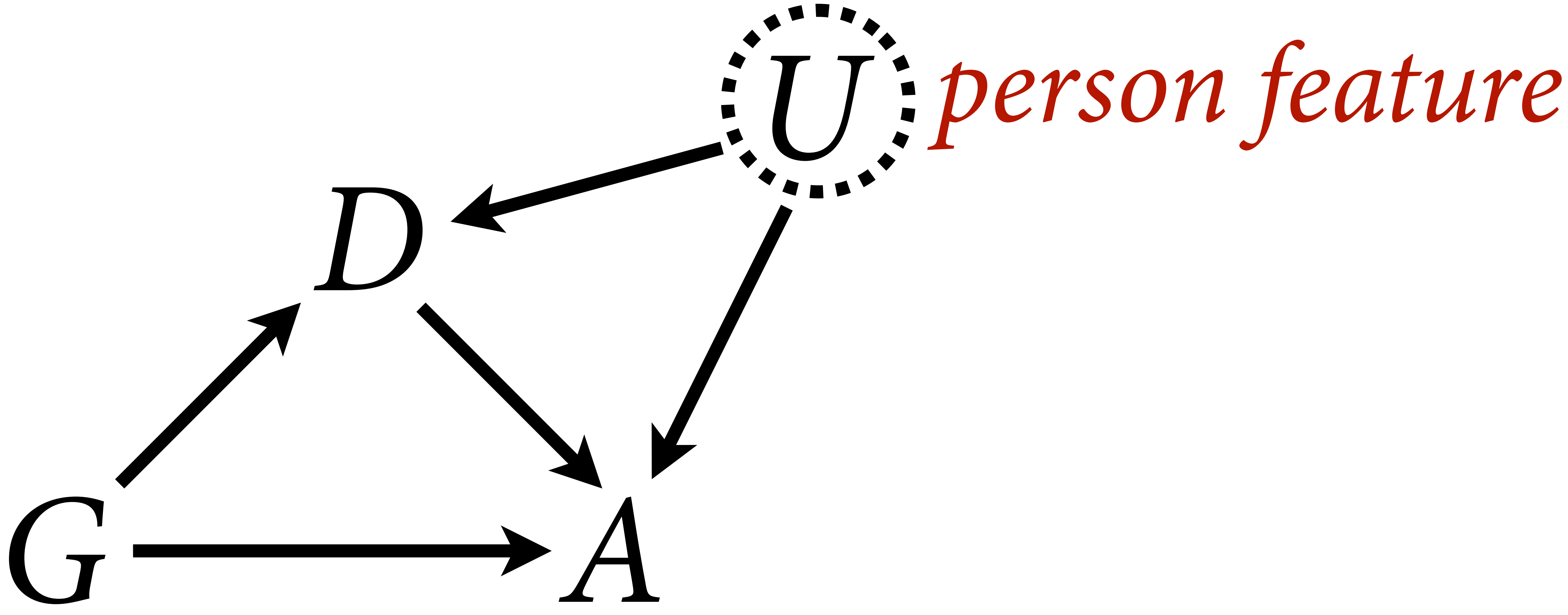
Requires strong assumptions



Direct

Requires strong assumptions

Confounds!



Will ignore for now, but confounds will return

Admissions: Drawing the Owl

(1) Estimand(s)

(2) Scientific model(s)

(3) Statistical model(s)

(4) Analyze

Generative model

How can choice of department create structural discrimination?

When departments vary in baseline admission rates.

```
# generative model, basic mediator scenario

N <- 1000 # number of applicants
# even gender distribution
G <- sample( 1:2 , size=N , replace=TRUE )
# gender 1 tends to apply to department 1, 2 to 2
D <- rbern( N , ifelse( G==1 , 0.3 , 0.8 ) ) + 1
# matrix of acceptance rates [dept,gender]
accept_rate <- matrix( c(0.1,0.3,0.1,0.3) , nrow=2 )
# simulate acceptance
A <- rbern( N , accept_rate[D,G] )
```

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

Generative model

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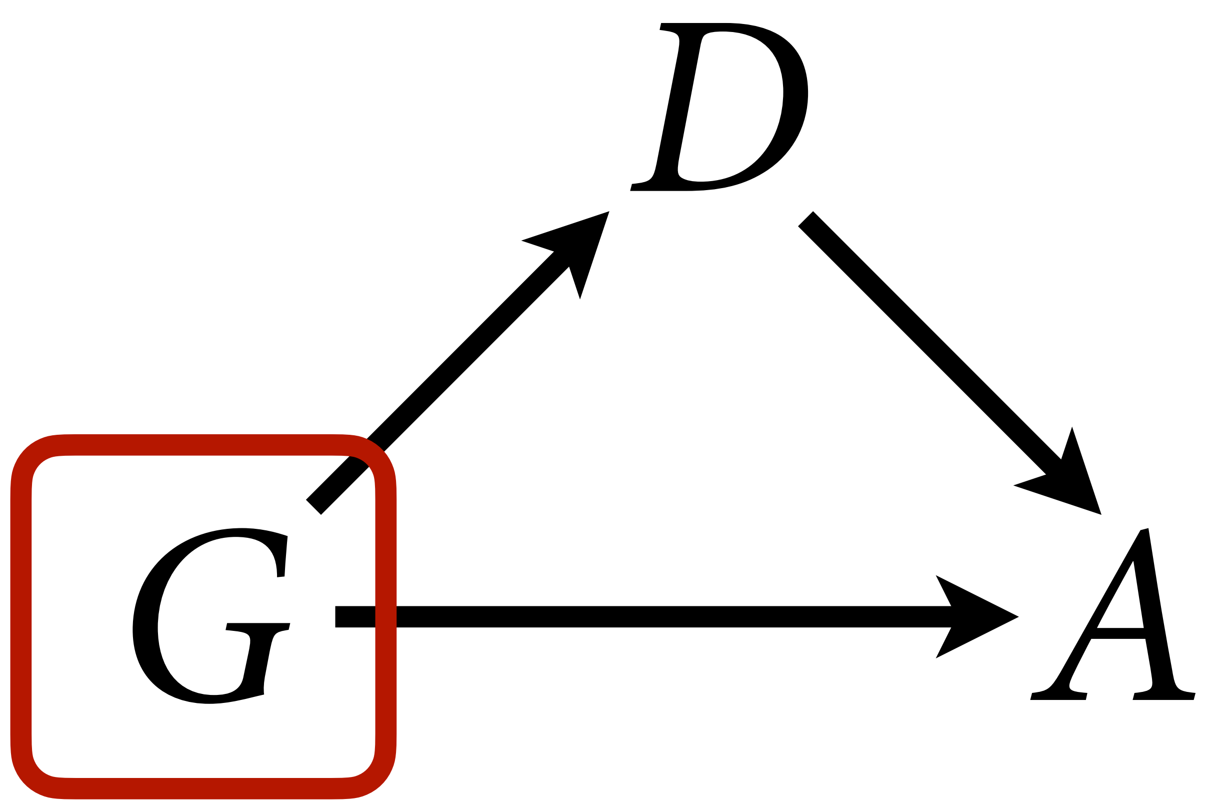

Generative model

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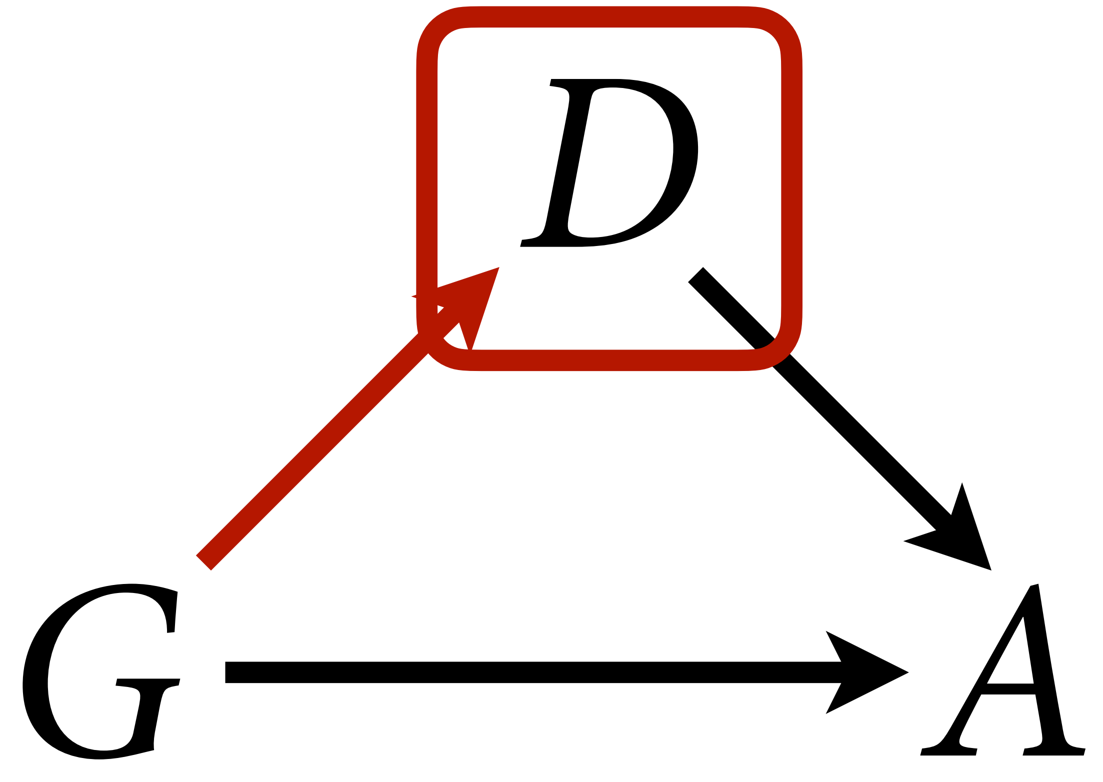
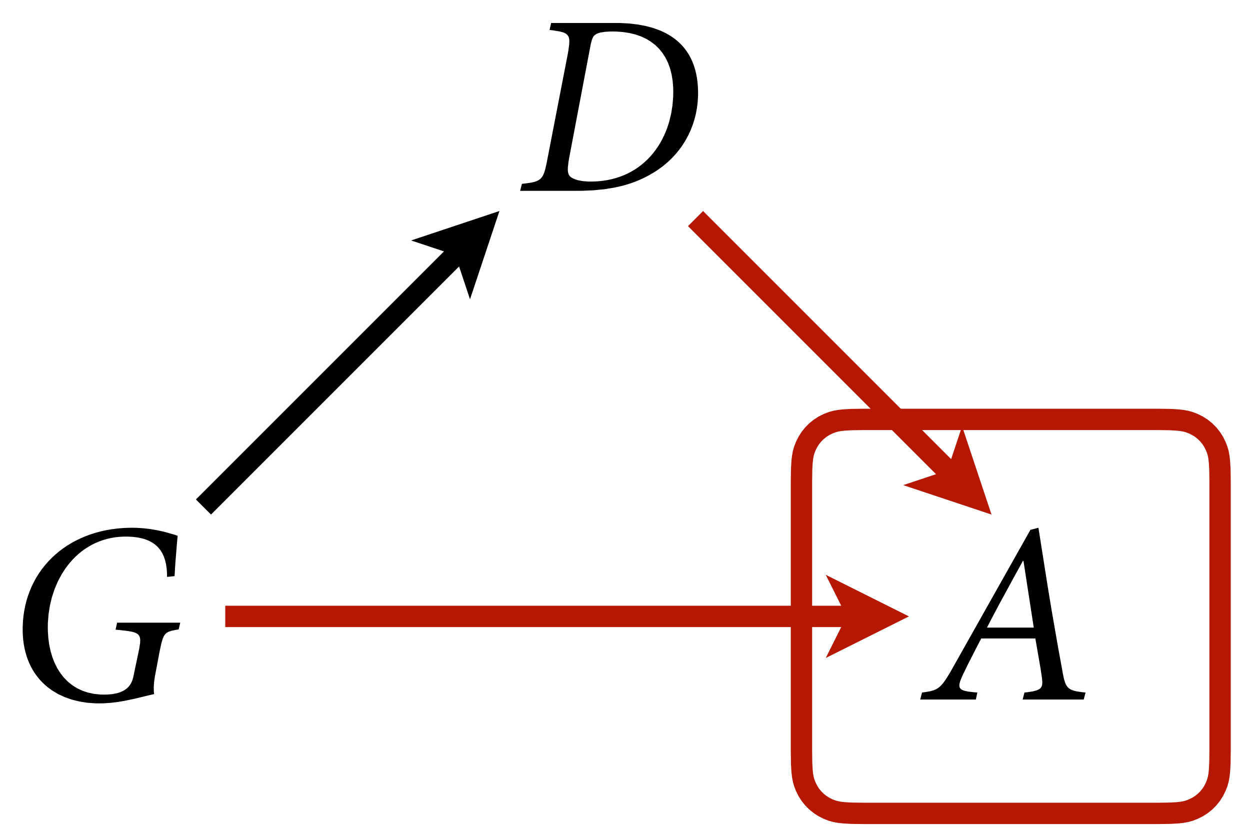


Generative model

```r
# generative model, basic mediator scenario

N <- 1000 # number of applicants
# even gender distribution
G <- sample( 1:2 , size=N , replace=TRUE )
# gender 1 tends to apply to department 1, 2 to 2
D <- rbern( N , ifelse( G==1 , 0.3 , 0.8 ) ) + 1
# matrix of acceptance rates [dept,gender]
accept_rate <- matrix( c(0.1,0.3,0.1,0.3) , nrow=2 )
# simulate acceptance
A <- rbern( N , accept_rate[D,G] )
```

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



Generative model

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# matrix of acceptance rates [dept,gender]
accept_rate <- matrix( c(0.1,0.3,0.1,0.3) , nrow=2 )
# simulate acceptance
A <- rbern( N , accept_rate[D,G] )
```

```
> table(G,D)
   D
G     1   2
  1 361 161
  2  99 379
```

```
> table(G,A)
   A
G     0   1
  1 421 101
  2 350 128
```

Accept rates
Gender 1: 19%
Gender 2: 27%

Generative model

```r
# generative model, basic mediator scenario

N <- 1000 # number of applicants
# even gender distribution
G <- sample( 1:2 , size=N , replace=TRUE )
# gender 1 tends to apply to department 1, 2 to 2
D <- rbern( N , ifelse( G==1 , 0.3 , 0.8 ) ) + 1
# matrix of acceptance rates [dept,gender]
accept_rate <- matrix( c(0.05,0.2,0.1,0.3) , nrow=2 )
# simulate acceptance
A <- rbern( N , accept_rate[D,G] )
```

```
> table(G,D)
   D
G     1   2
  1 355 164
  2  95 386
```

```
> table(G,A)
   A
G     0   1
  1 473  46
  2 404  77
```

Accept rates
Gender 1: 9%
Gender 2: 16%

```
> accept_rate
     [,1] [,2]
[1,] 0.05  0.1
[2,] 0.20  0.3
```

same pattern as absence of discrimination

Generative model

Could do a lot better

Admission rate depends upon size of applicant pool, distribution of qualifications

Should sample applicant pool and then sort to select admissions

Rates are conditional on structure of applicant pool

```
> table(G,D)
   D
G     1   2
  1 355 164
  2  95 386
```

```
> table(G,A)
   A
G     0   1
  1 473  46
  2 404  77
```

Accept rates
Gender 1: 9%
Gender 2: 16%

PAUSE

Admissions: Drawing the Owl

(1) Estimand(s)

(2) Scientific model(s)

(3) Statistical model(s)

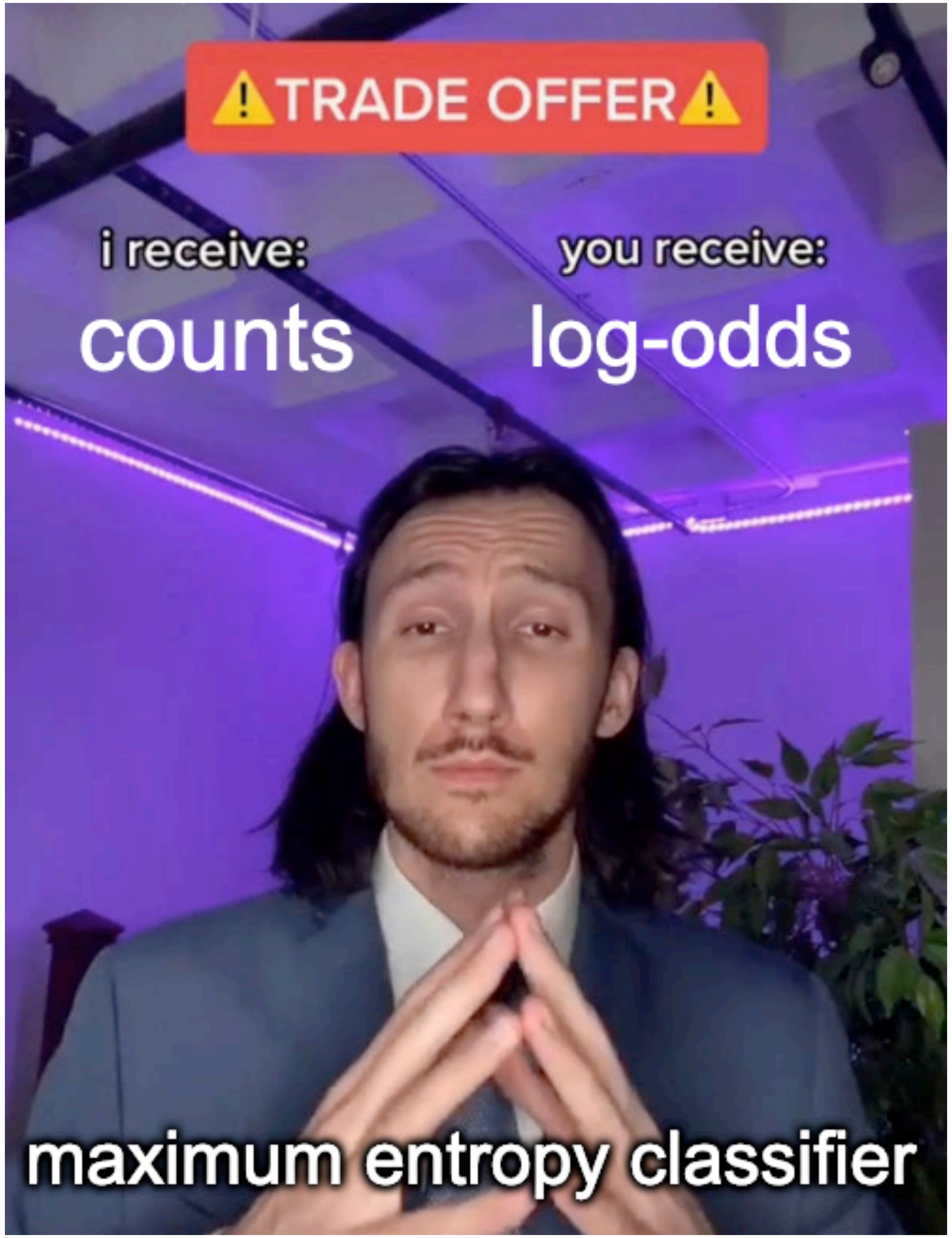
(4) Analyze

Modeling events

We observe: Counts of events

We estimate:
Probability (or log-odds) of events

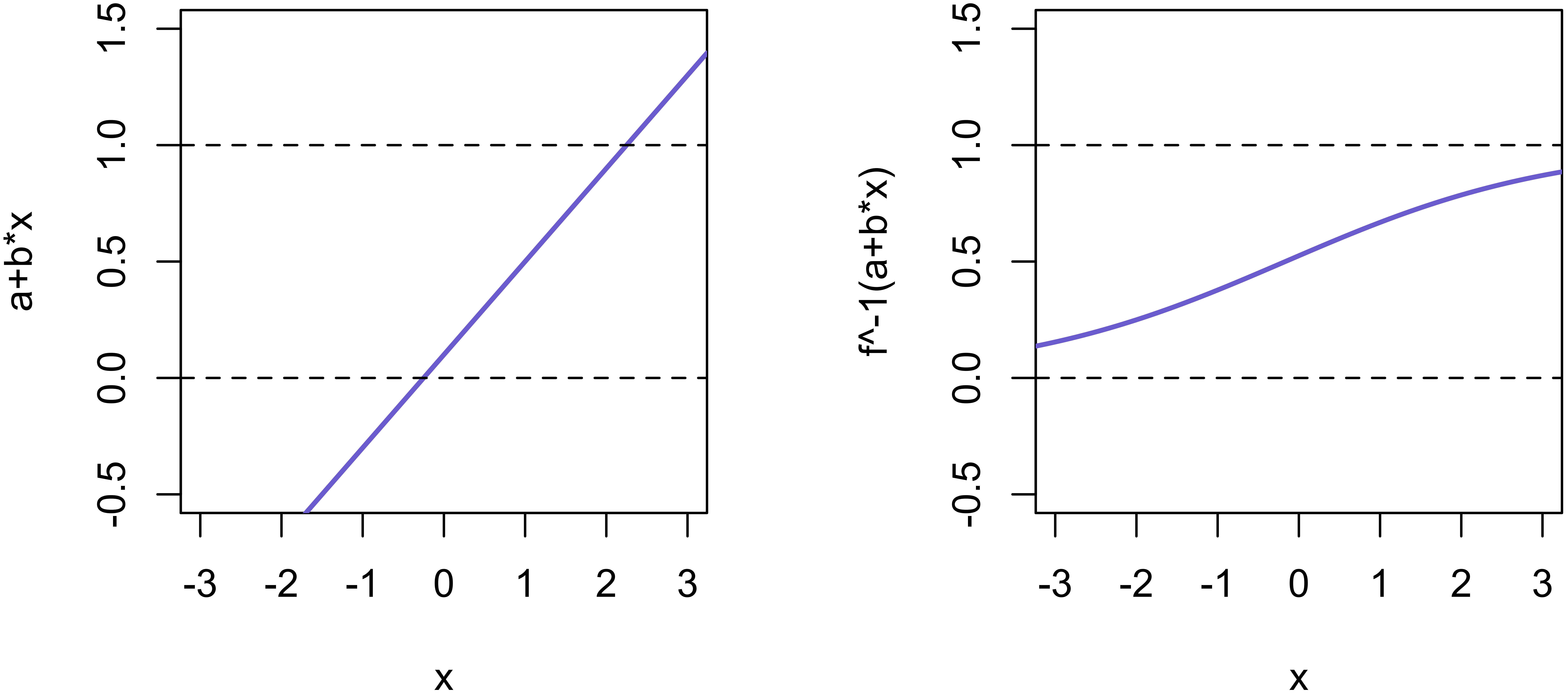
Like the globe tossing model, but need "proportion of water" stratified by other variables



Generalized Linear Models

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

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



a+b*x
f^-1(a+b*x)
1.5
1.0
0.5
0.0
-0.5
-3
-2
-1
0
1
2
3
x

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

0/1 outcome

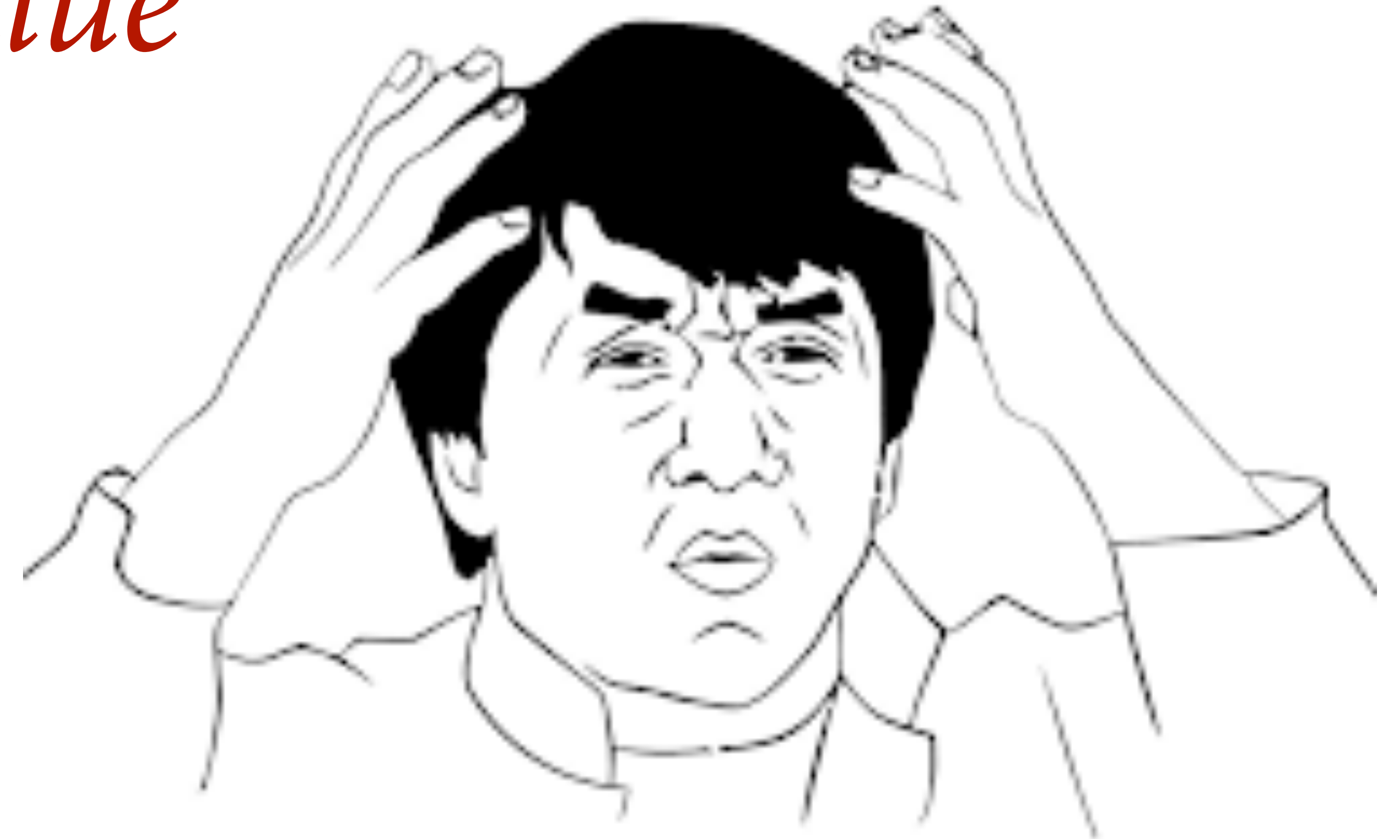
probability of event

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

$$f(p_i) = \underbrace{\alpha + \beta_X X_i + \beta_Z Z_i}$$

f() maps probability scale to linear model scale

can take any real value



Links and inverse links

f is the link function

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

Links parameters of distribution to linear model

f^{-1} is the inverse link function

$$p_i = f^{-1}(\alpha + \beta_X X_i + \beta_Z Z_i)$$

Example inverse function

$$f(a) = a^2$$

Example inverse function

$$f(a) = a^2$$

$$f^{-1}(a^2) = \sqrt{a^2} = a$$

Distributions and link functions

Distributions: Relative number of ways to observe data, given assumptions about rates, probabilities, slopes, etc.

Distributions are matched to constraints on observed variables

Link functions are matched to distributions

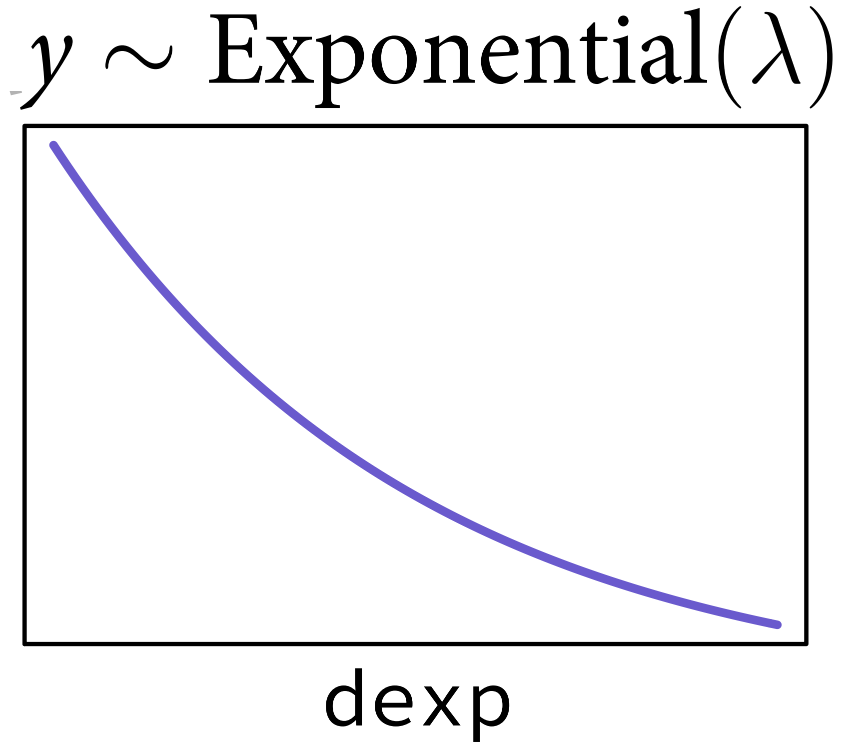


Figure 9.5

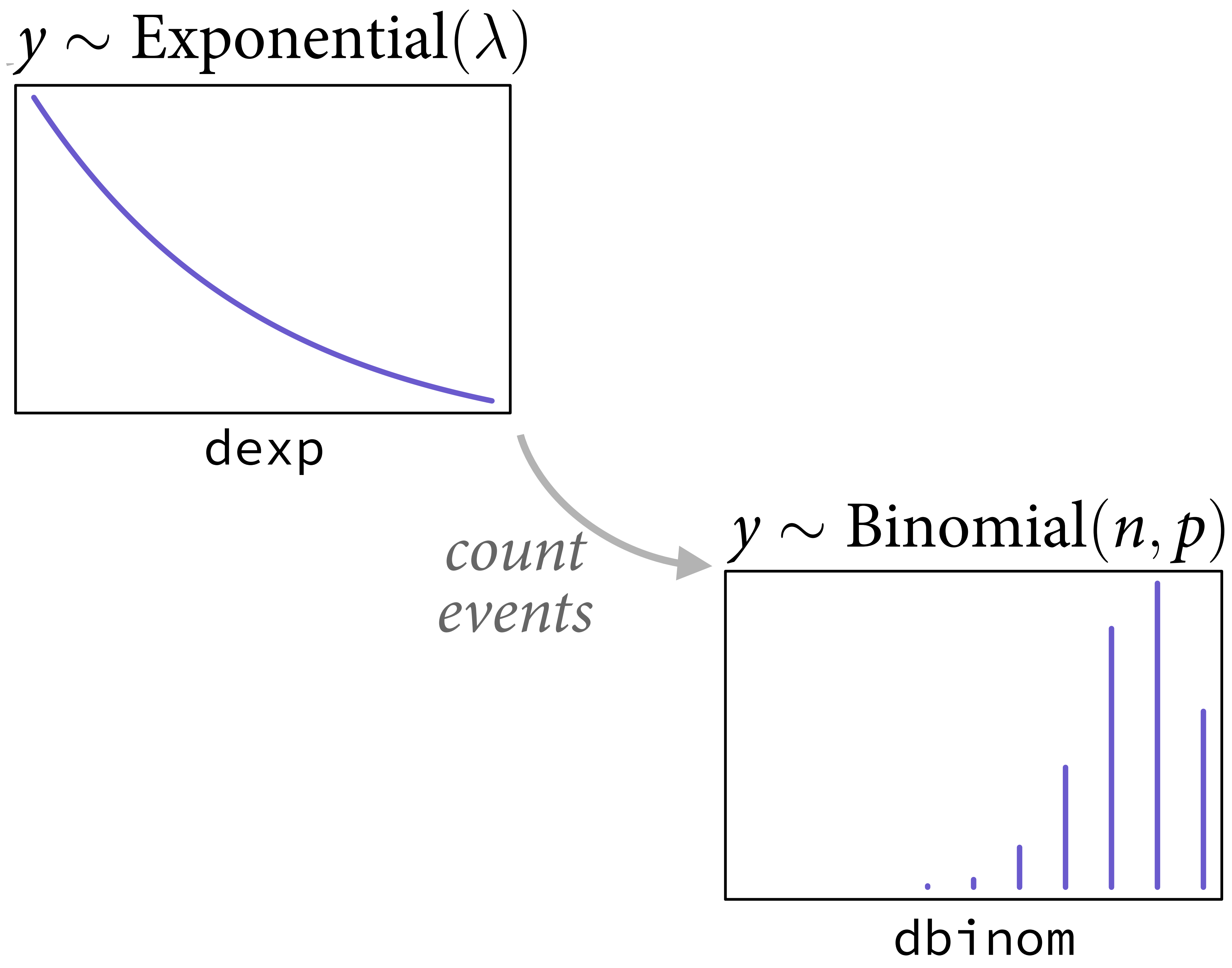

$y \sim \text{Exponential}(\lambda)$
dexp
count
events
$y \sim \text{Binomial}(n, p)$
dbinom

Figure 9.5

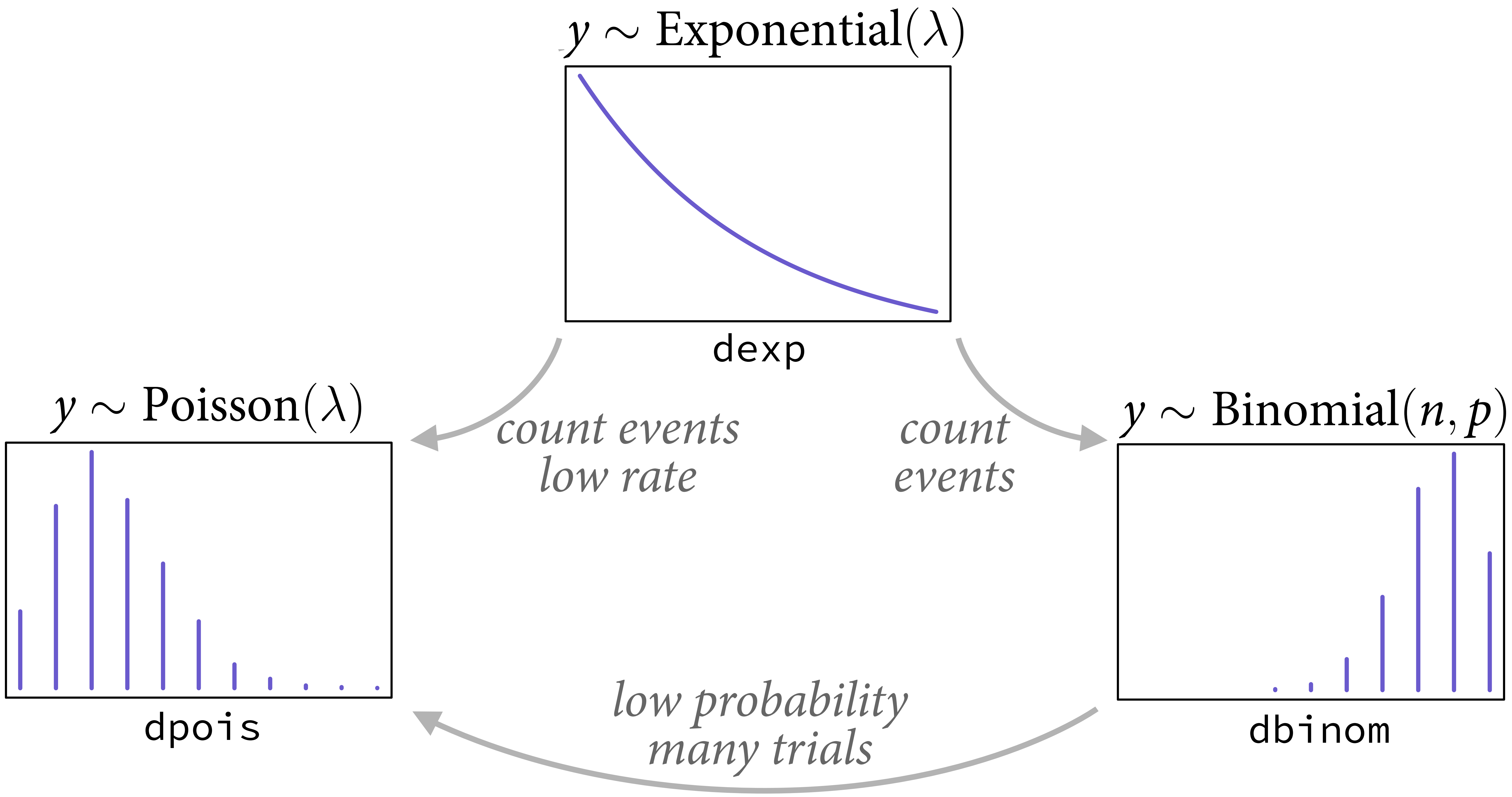
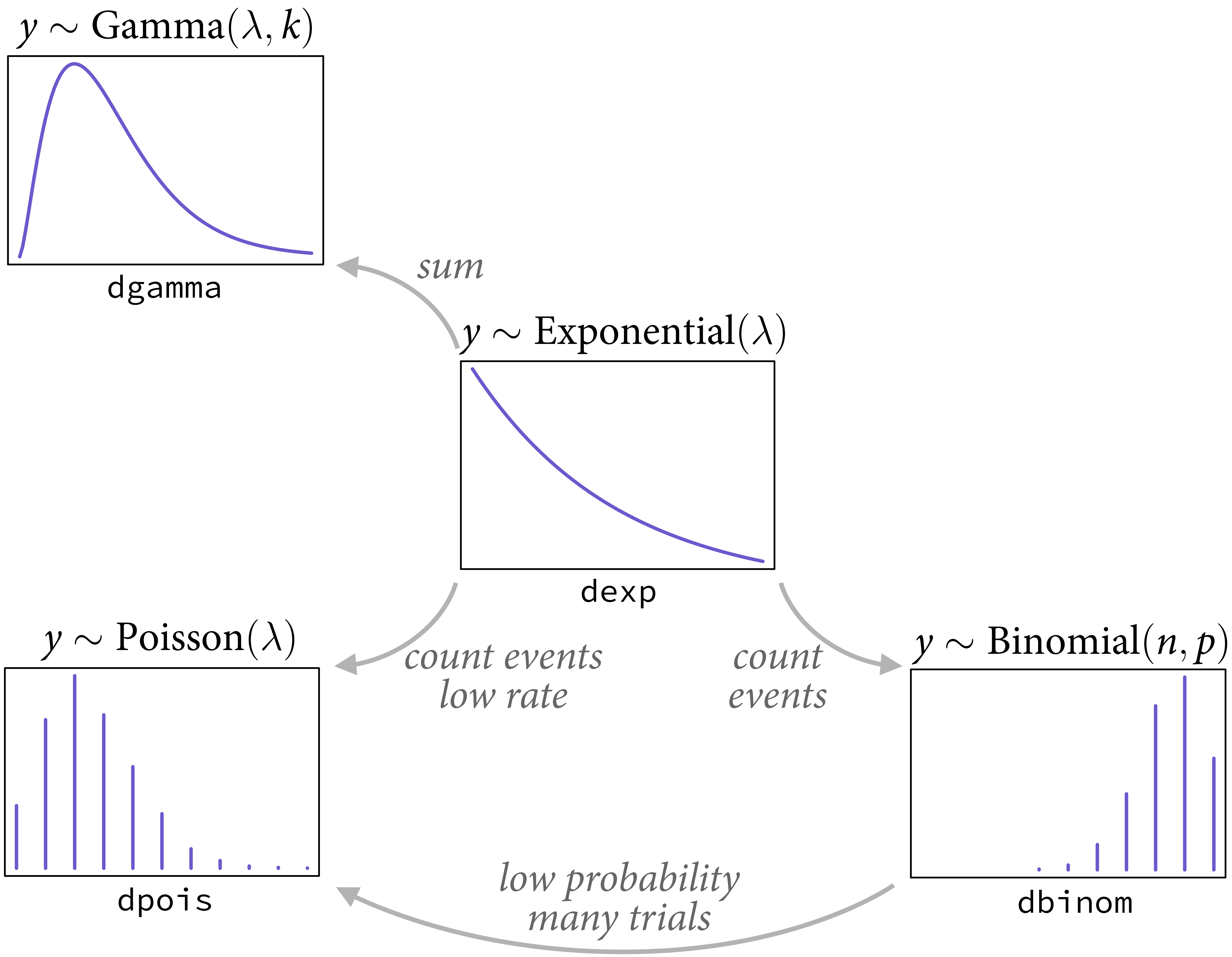
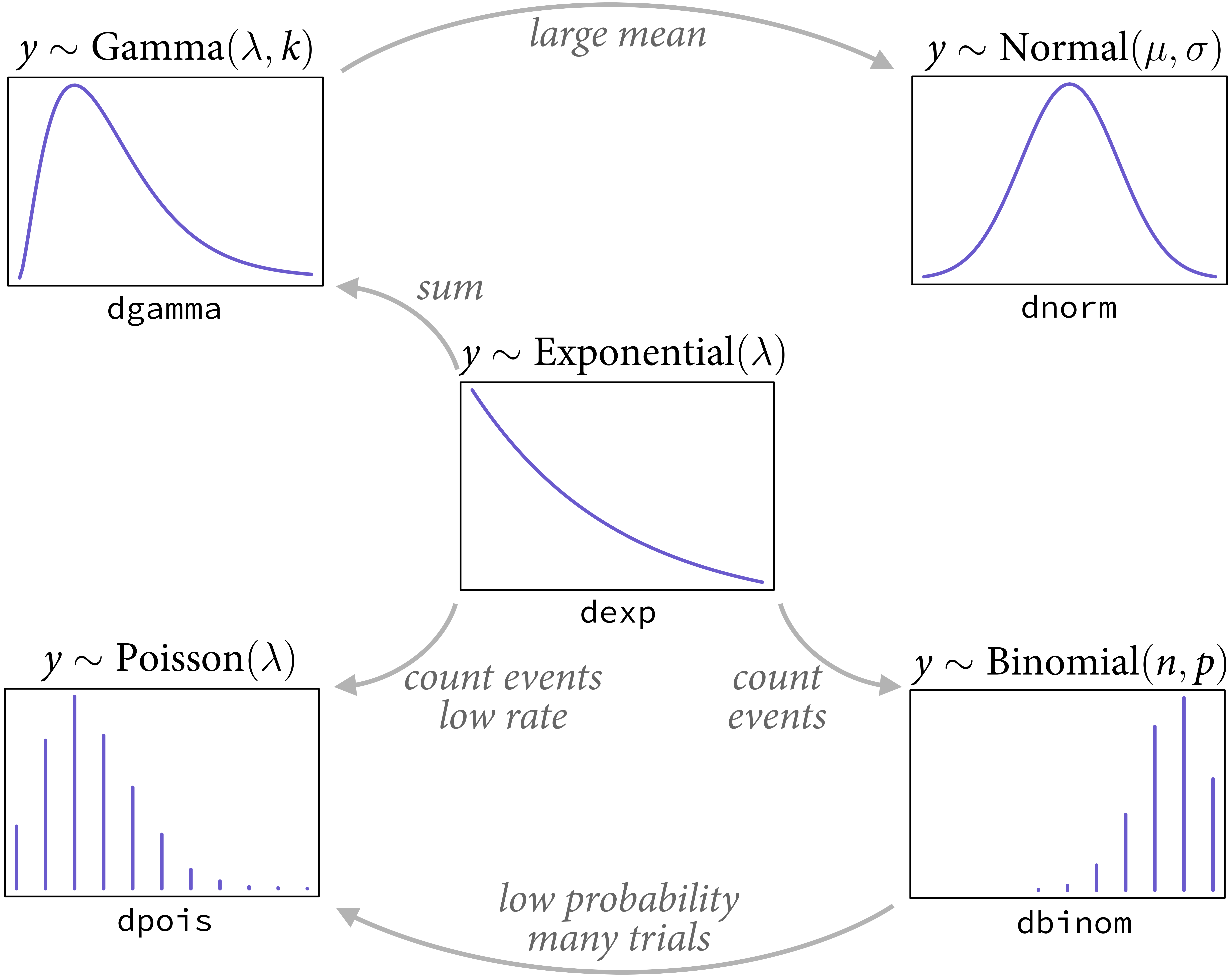

$y \sim \text{Exponential}(\lambda)$
dexp
$y \sim \text{Poisson}(\lambda)$
dpois
$y \sim \text{Binomial}(n, p)$
dbinom
count events
low rate
count
events
low probability
many trials

Figure 9.5



$y \sim \text{Gamma}(\lambda, k)$
dgamma
sum
$y \sim \text{Exponential}(\lambda)$
dexp
$y \sim \text{Poisson}(\lambda)$
count events low rate
count events
$y \sim \text{Binomial}(n, p)$
dpois
low probability many trials
dbinom

Figure 9.5


$y \sim \text{Gamma}(\lambda, k)$
dgamma
large mean
$y \sim \text{Normal}(\mu, \sigma)$
dnorm
sum
$y \sim \text{Exponential}(\lambda)$
dexp
$y \sim \text{Poisson}(\lambda)$
dpois
count events
low rate
count
events
$y \sim \text{Binomial}(n, p)$
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low probability
many trials

Figure 9.5

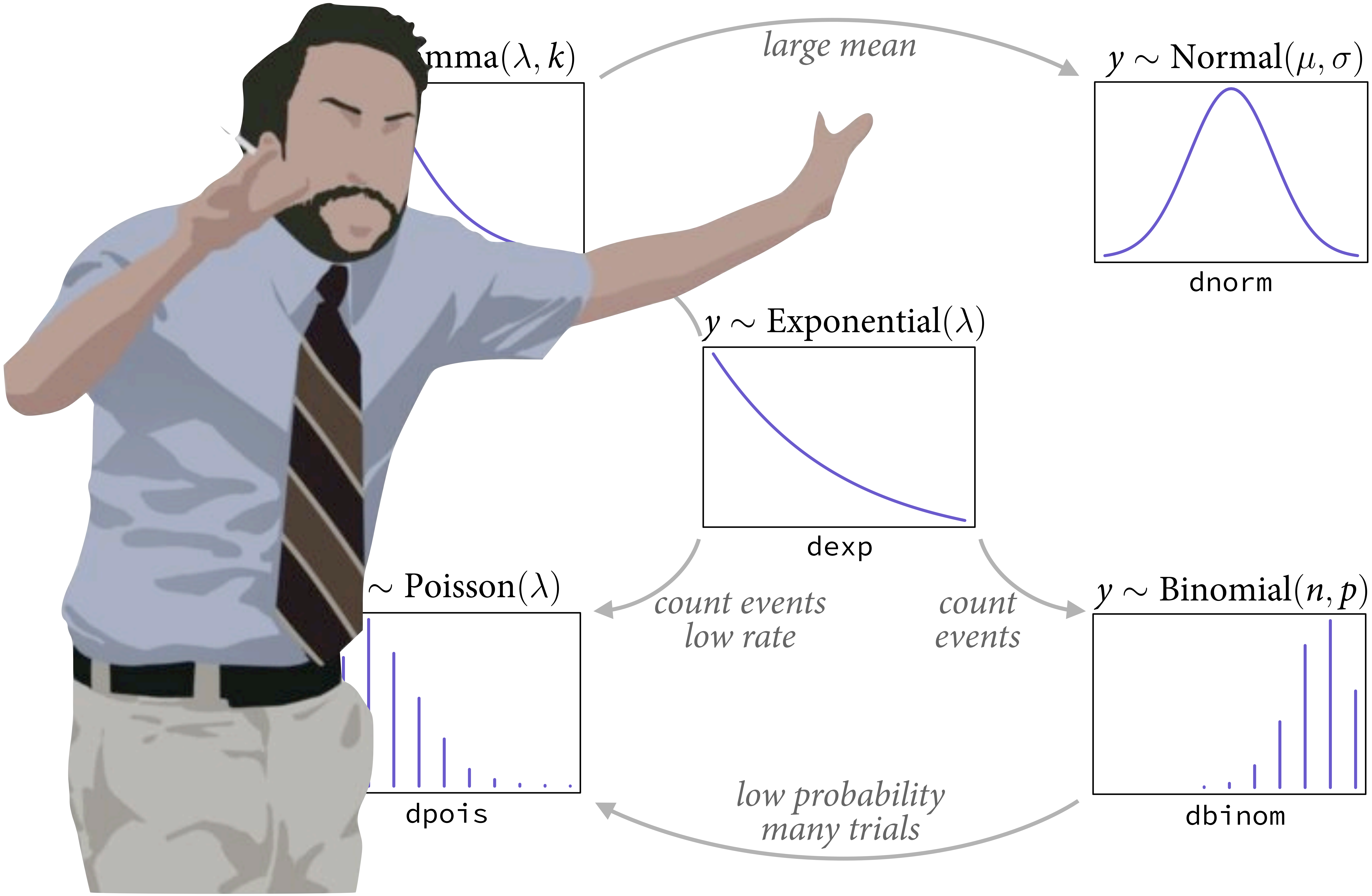

mma(λ, k)
large mean
$y \sim$ Normal(μ, σ)
dnorm
$y \sim$ Exponential(λ)
dexp
$\sim$ Poisson(λ)
count events
low rate
count
events
$y \sim$ Binomial(n, p)
dpois
low probability
many trials
dbinom

Figure 9.5

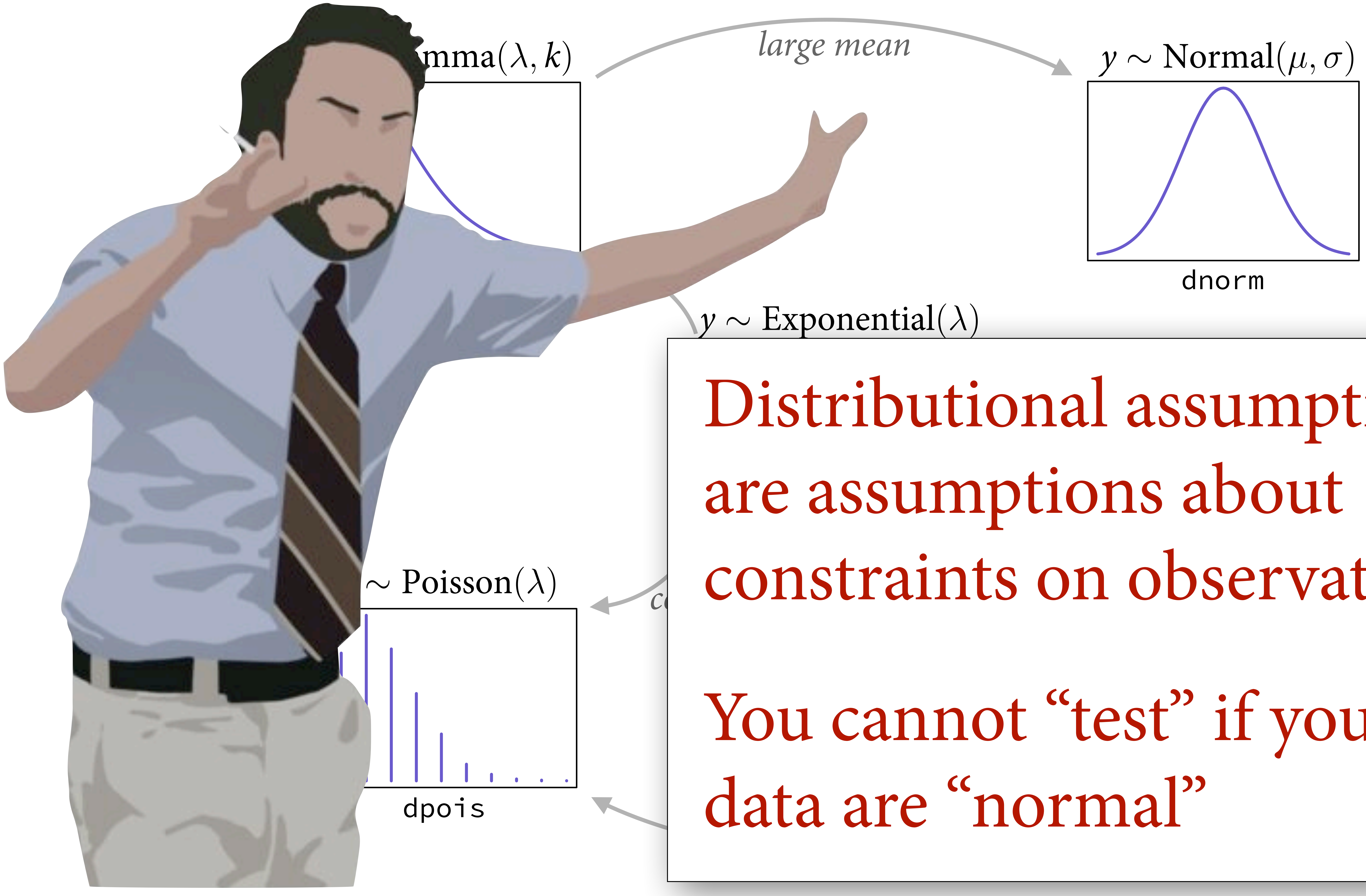


Figure 9.5

Distributional assumptions are assumptions about constraints on observations

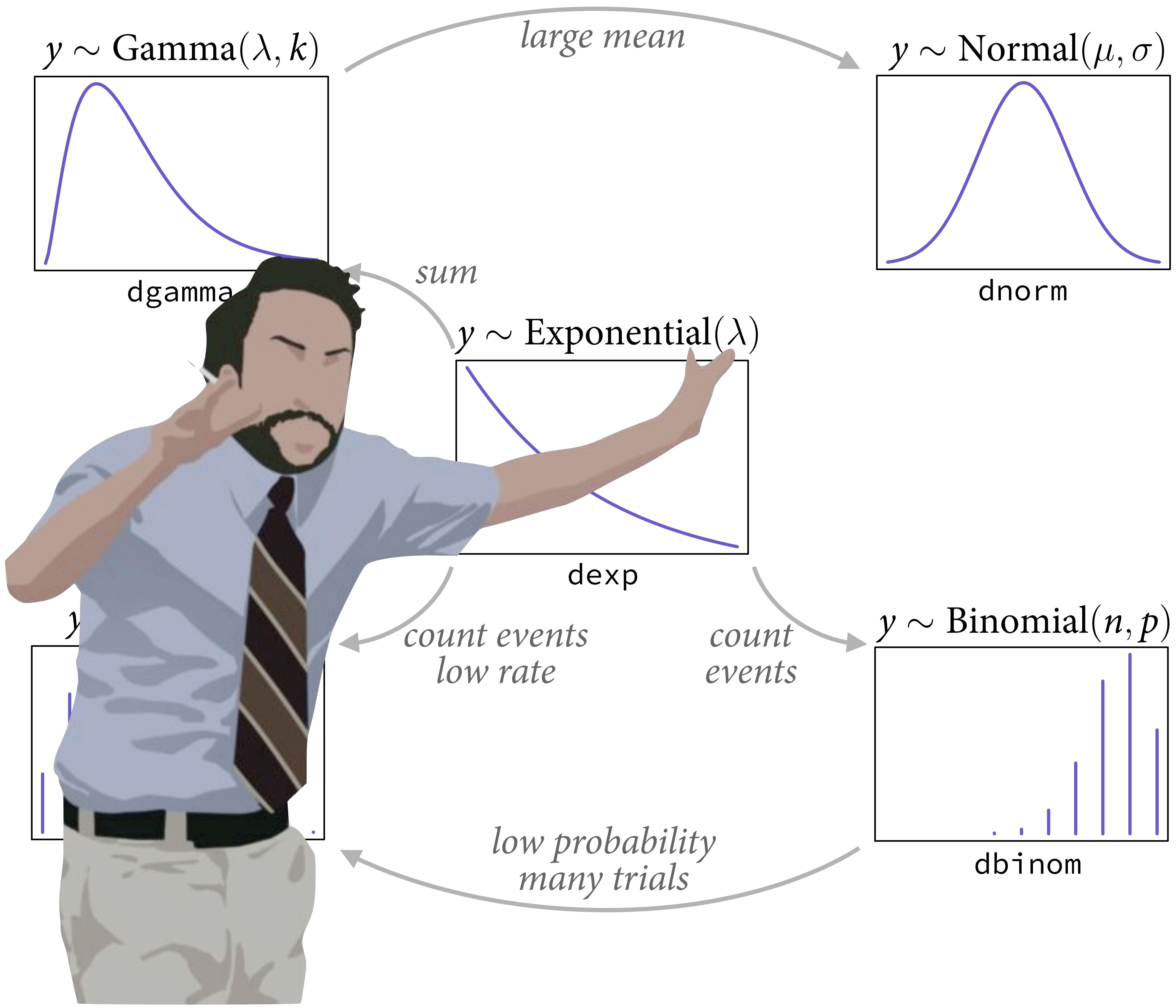
You cannot "test" if your data are "normal"

Distributions and link functions

Distributions: Relative number of ways to observe data, given assumptions

Distributions are matched to constraints on observed variables

Link functions are matched to distributions



Overthinking: Binomial maximum entropy. The usual way to derive a maximum entropy distribution is to state the constraints and then use a mathematical device called the *Lagrangian* to solve for the probability assignments that maximize entropy. But instead we'll extend the strategy used in the Overthinking box on page 306. As a bonus, this strategy will allow us to derive the constraints that are necessary for a distribution, in this case the binomial, to be a maximum entropy distribution.

Let p be the binomial distribution, and let p_i be the probability of a sequence of observations i with number of successes x_i and number of failures $n - x_i$. Let q be some other discrete distribution defined over the same set of observable sequences. As before, KL divergence tells us that:

$$-H(q, p) \geq H(q) \implies -\sum_i q_i \log p_i \geq -\sum_i q_i \log q_i$$

What we're going to do now is work with $H(q, p)$ and simplify it until we can isolate the constraint that defines the class of distributions for which p has maximum entropy. Let $\lambda = \sum_i p_i x_i$ be the expected value of p. Then from the definition of $H(q, p)$:

$$-H(q, p) = -\sum_i q_i \log \left[\left(\frac{\lambda}{n} \right)^{x_i} \left(1 - \frac{\lambda}{n} \right)^{n - x_i} \right] = -\sum_i q_i \left(x_i \log \left[\frac{\lambda}{n} \right] + (n - x_i) \log \left[1 - \frac{\lambda}{n} \right] \right)$$

After some algebra:

$$-H(q, p) = -\sum_i q_i \left(x_i \log \left[\frac{\lambda}{n - \lambda} \right] + n \log \left[\frac{n - \lambda}{n} \right] \right) = -n \log \left[\frac{n - \lambda}{n} \right] - \log \left[\frac{\lambda}{n - \lambda} \right] \underbrace{\sum_i q_i x_i}_{\bar{q}}$$

The term on the far right labeled $\bar{q}$ is the expected value of the distribution q. If we knew it, we could complete the calculation, because no other term depends upon q_i. This means that expected value is the constraint that defines the class of distributions for which the binomial p has maximum entropy. If we now set the expected value of q equal to λ, then $H(q) = H(p)$. For any other expected value of q, $H(p) > H(q)$.

Finally, notice the term $\log[\lambda/(n - \lambda)]$. This term is the log of the ratio of the expected number of successes to the expected number of failures. That ratio is the "odds" of a success, and its logarithm is called "log odds." This quantity will feature prominently in models we construct from the binomial distribution, in Chapter 11.

work with $H(q,p)$ and simplify it until we can isolate the constraint
utions for which p has maximum entropy. Let $\lambda = \sum_i p_i x_i$ be the
the definition of $H(q,p)$:

$$\Big)^{x_i} \left(1 - \frac{\lambda}{n}\right)^{n-x_i} \Bigg] = -\sum_i q_i \left(x_i \log\left[\frac{\lambda}{n}\right] + (n - x_i) \log\left[1 - \frac{\lambda}{n}\right] \right)$$

$$\frac{\lambda}{n-\lambda}\Bigg] + n \log\left[\frac{n-\lambda}{n}\right] \Bigg) \Bigg) = -n \log\left[\frac{n-\lambda}{n}\right] - \boxed{\log\left[\frac{\lambda}{n-\lambda}\right]} \underbrace{\sum_i q_i x_i}_{\bar{q}}$$

d $\bar{q}$ is the expected value of the distribution q. If we knew it, we could
use no other term depends upon q_i. This means that expected value is
class of distributions for which the binomial p has maximum entropy.

Logit link

Bernoulli/Binomial models most often use logit link

$$\text{logit}(p_i) = \log \frac{p_i}{1 - p_i}$$

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

$$\text{logit}(p_i) = \alpha + \beta_X X_i + \beta_Z Z_i$$

$$p_i = \text{logit}^{-1}(\alpha + \beta_X X_i + \beta_Z Z_i)$$

Logit link

Bernoulli/Binomial models most often use logit link

$$\text{logit}(p_i) = \log \underbrace{\boxed{\frac{p_i}{1-p_i}}}_{odds}$$

“log odds” *odds*

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

$$\text{logit}(p_i) = \alpha + \beta_X X_i + \beta_Z Z_i$$

$$p_i = \underbrace{\text{logit}^{-1}}_{\text{“logistic”}}(\alpha + \beta_X X_i + \beta_Z Z_i)$$

From link to inverse link

$$\operatorname{logit}(p_i) = \log \frac{p_i}{1 - p_i} = q_i$$

$$\operatorname{logit}^{-1}(q_i) = \,?$$

From link to inverse link

$$\operatorname{logit}(p_i) = \log \frac{p_i}{1 - p_i} = q_i$$

$$\operatorname{logit}^{-1}(q_i) = \ ? = p_i$$

From link to inverse link

$$\text{logit}(p_i) = \log \frac{p_i}{1 - p_i} = q_i$$

$$\text{logit}^{-1}(q_i) = ? = p_i$$

$$\log \frac{p_i}{1 - p_i} = q_i$$

$$\boxed{p_i = \frac{\exp(q_i)}{1 + \exp(q_i)}}$$

logit^{-1}

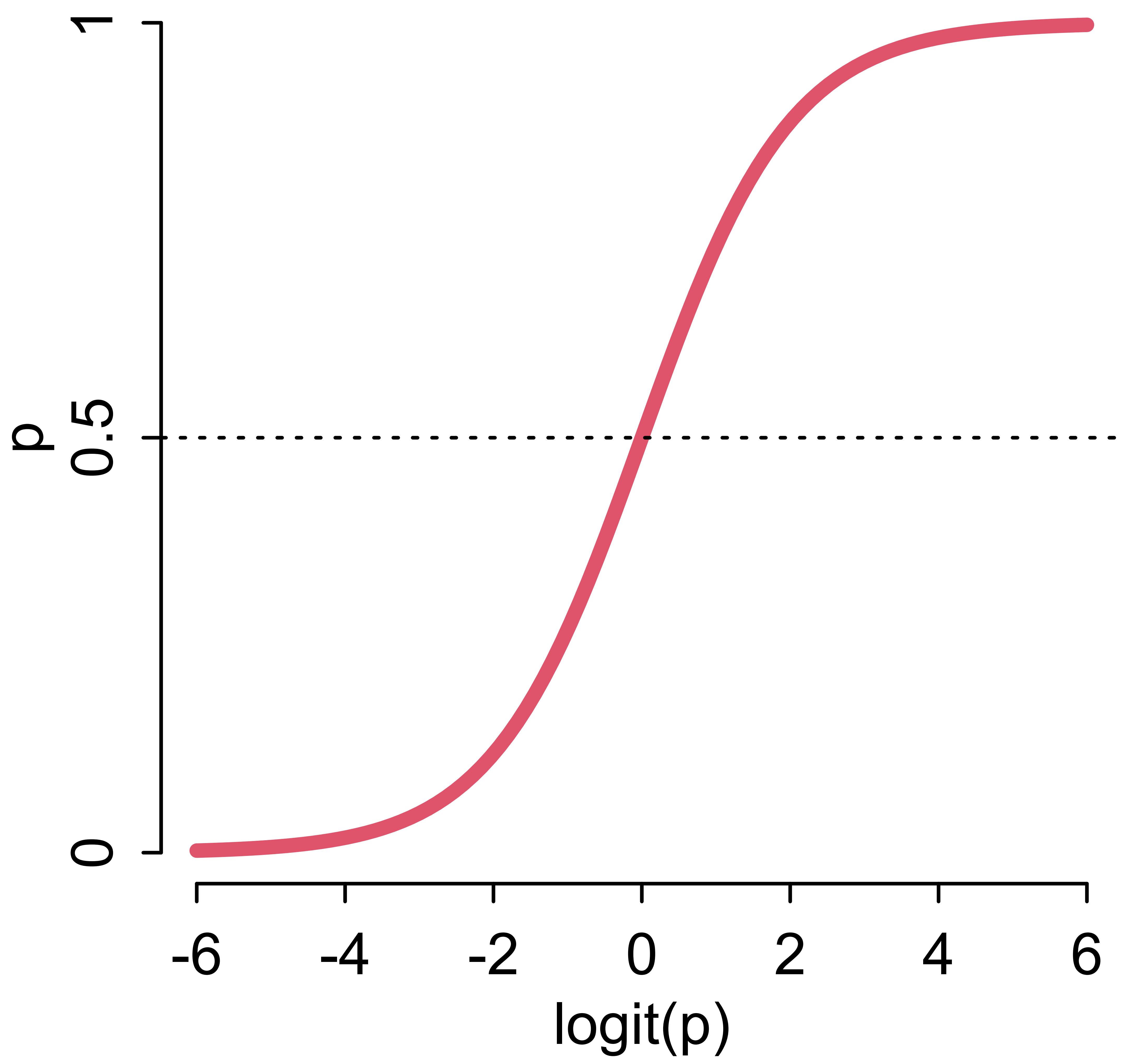
logit link is a harsh transform

"log-odds scale": The value of the linear model

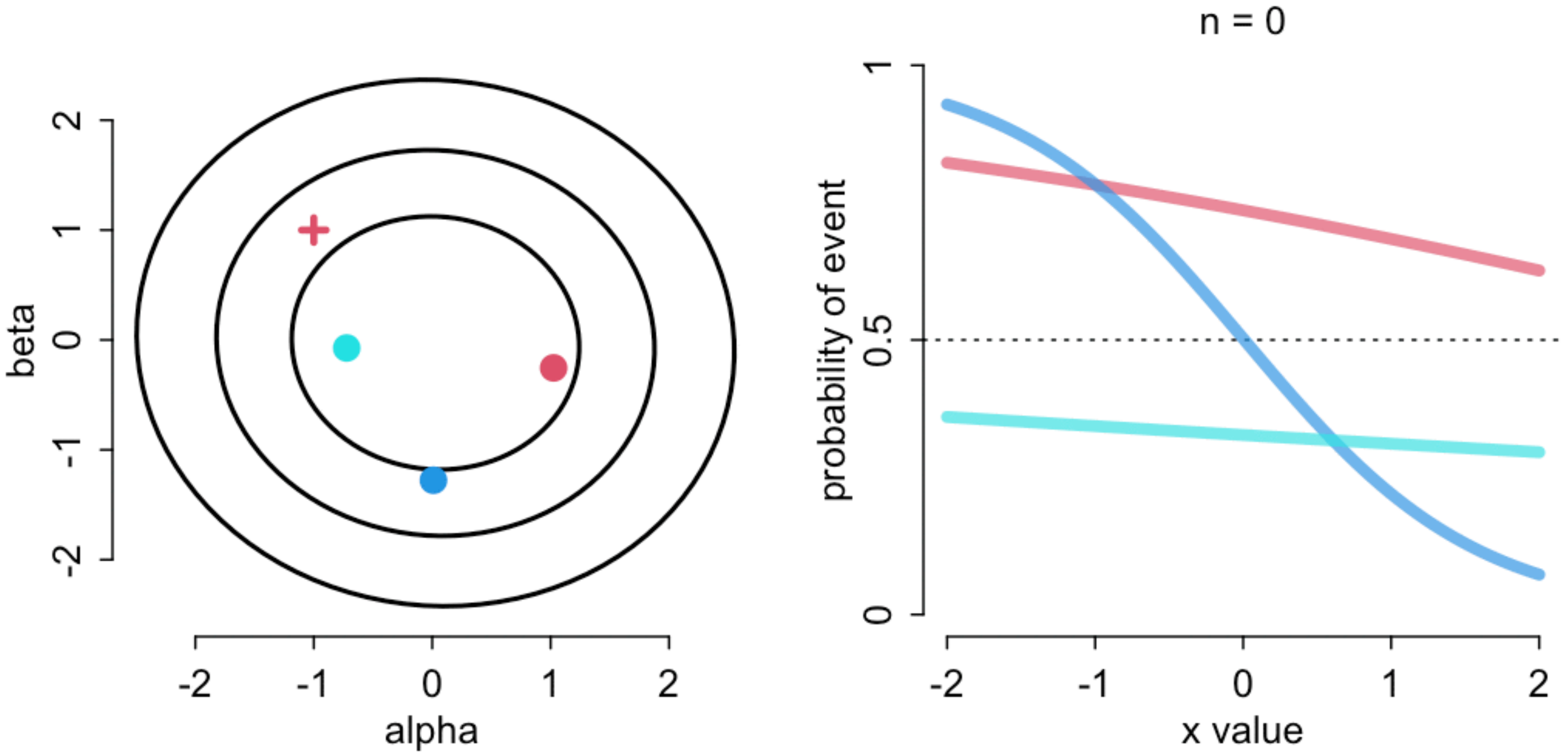
logit(p)=0, p=0.5

logit(p)=4, p=nearly always

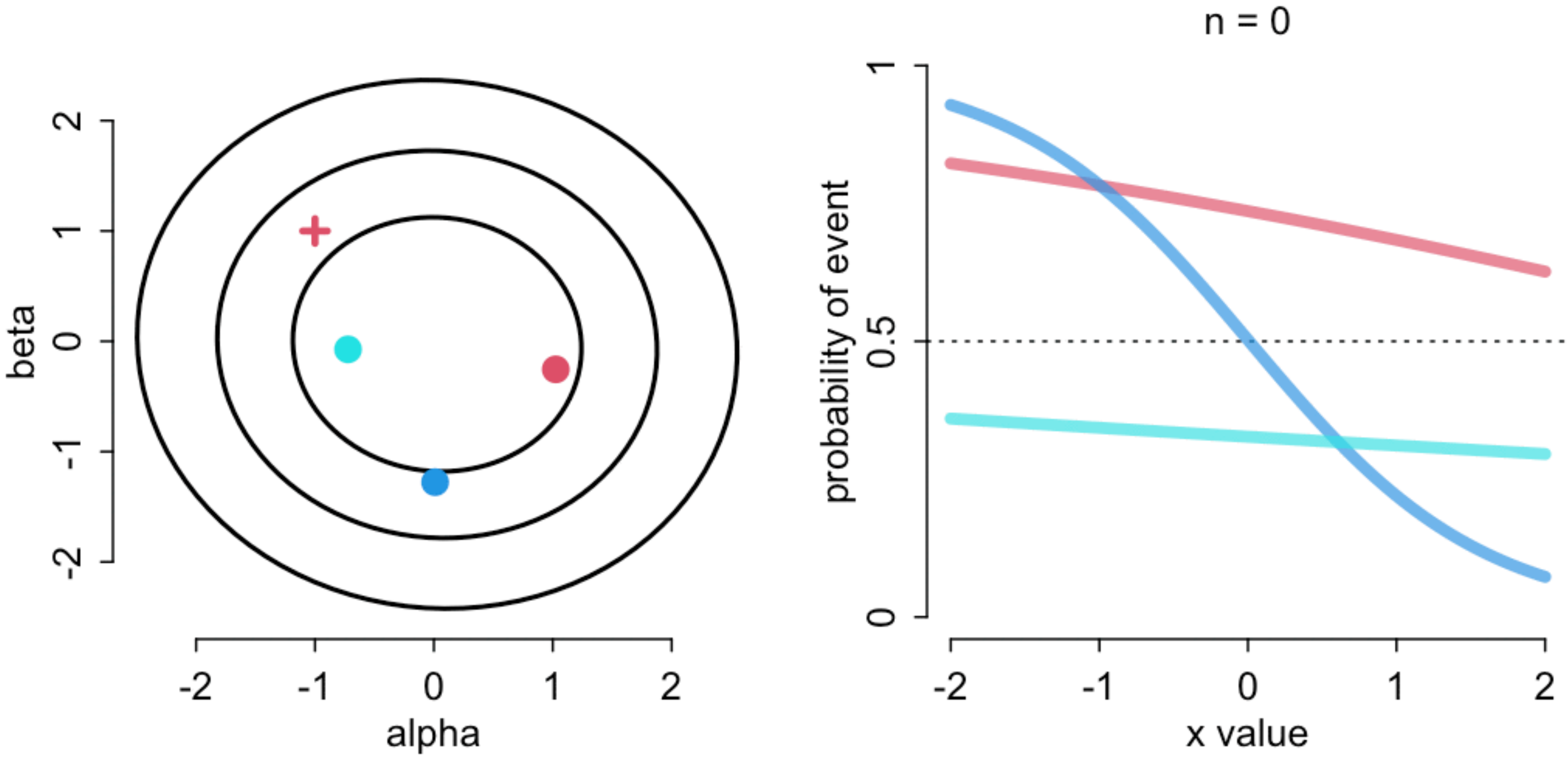
logit(p)=–4, p=hardly ever



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



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

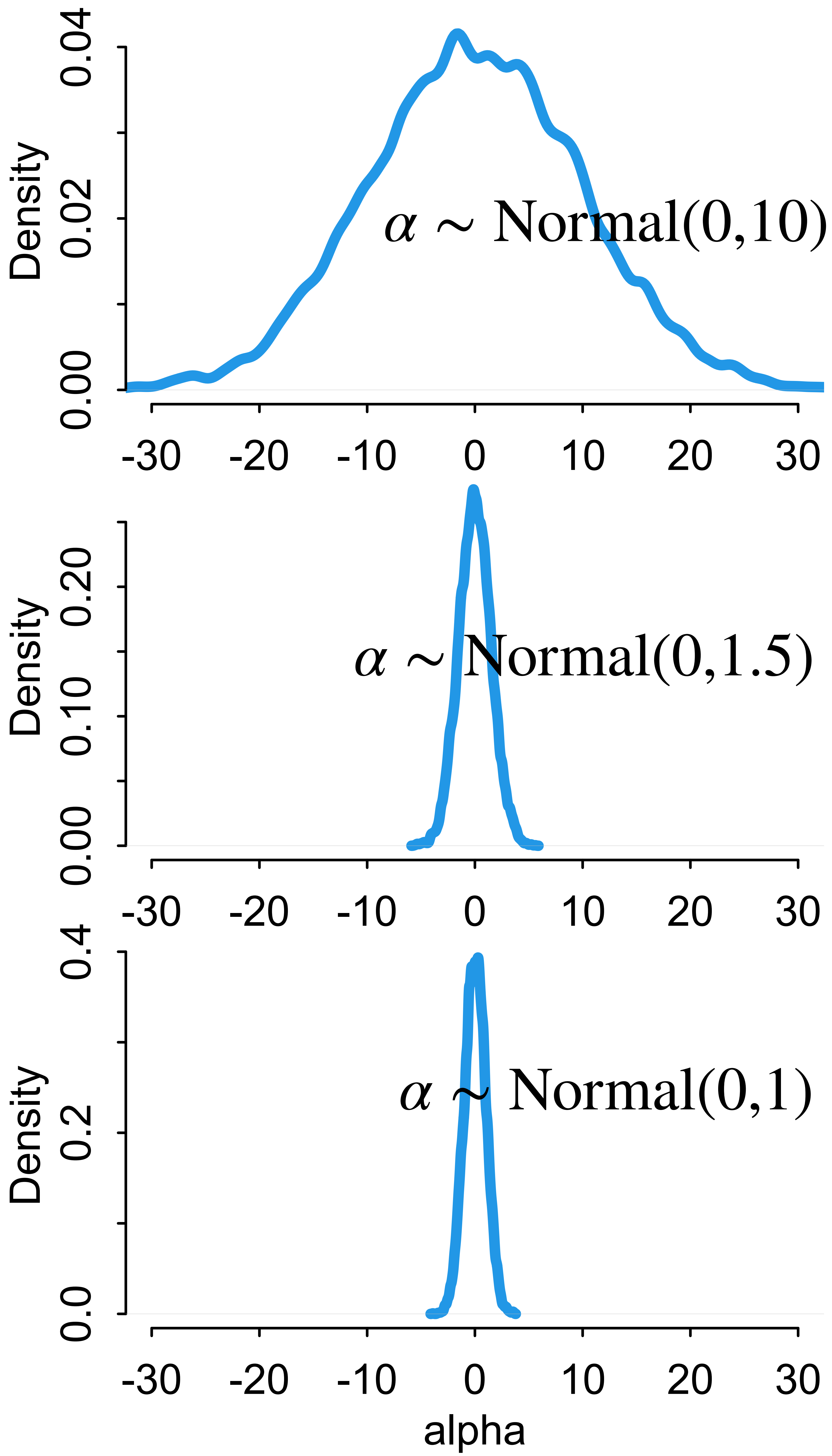


Logistic priors

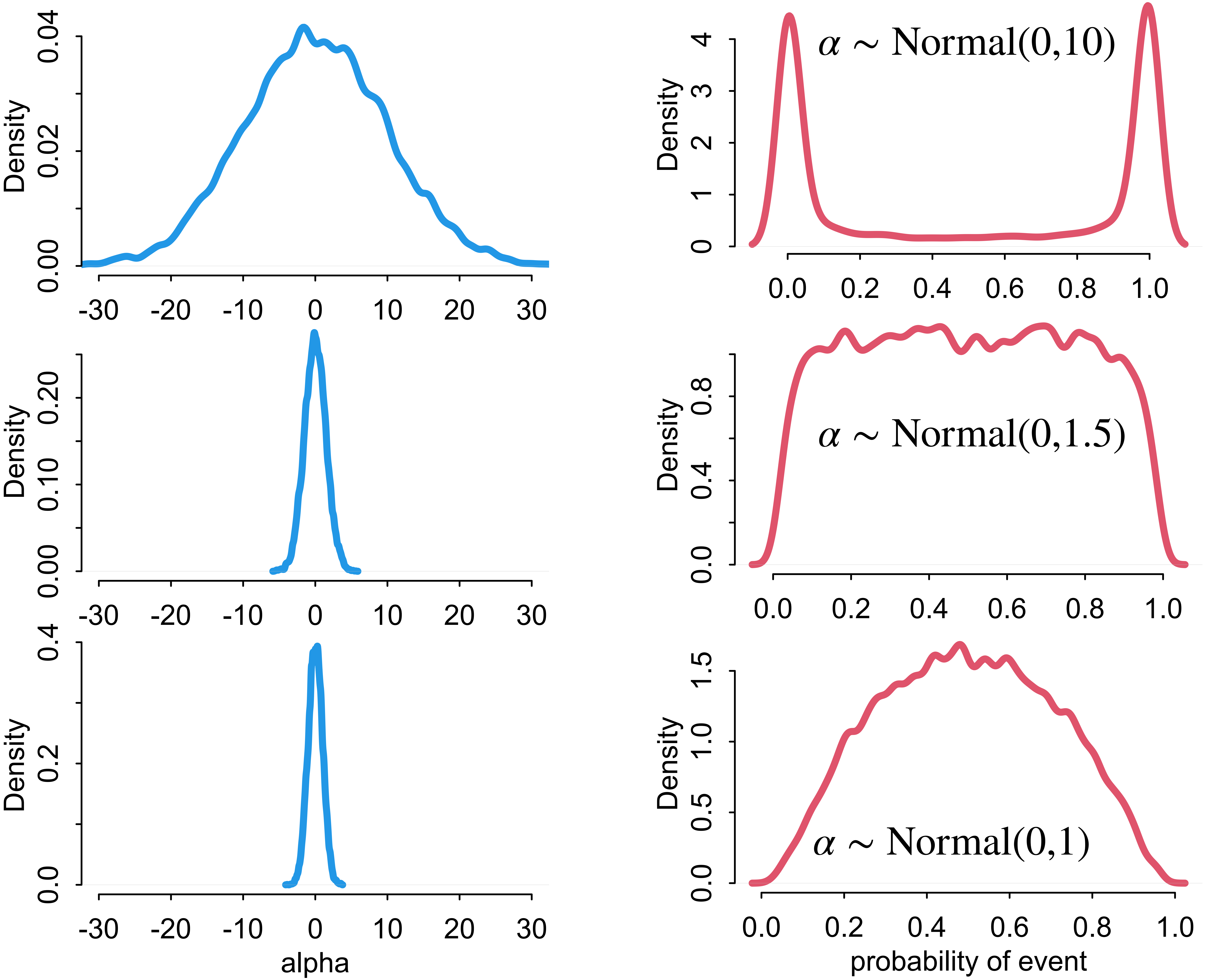
$$\text{logit}(p_i) = \alpha$$

The logit link compresses parameter distributions

Anything above +4 = almost always
Anything below –4 = almost never



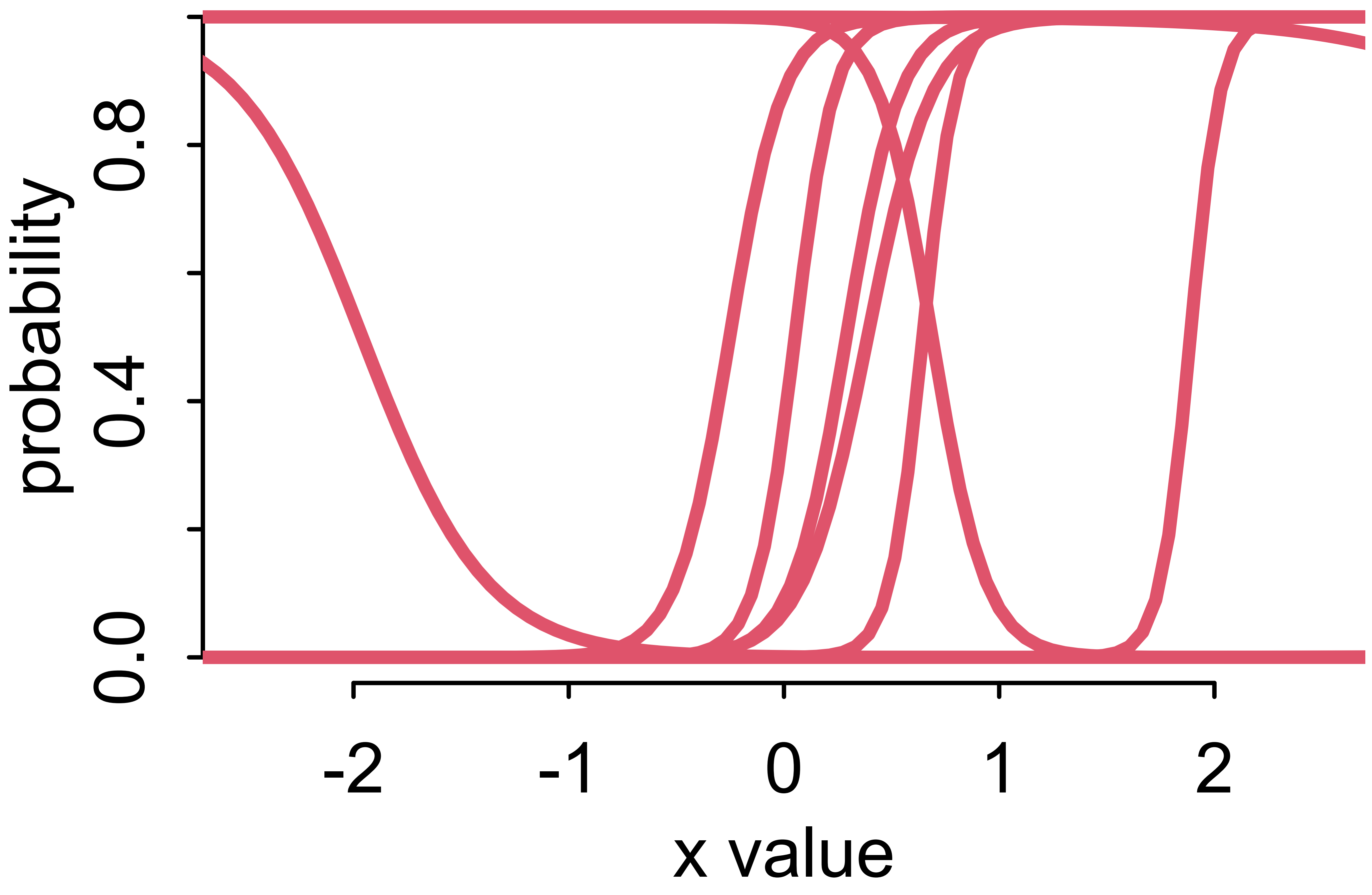
$$\text{logit}(p_i) = \alpha$$



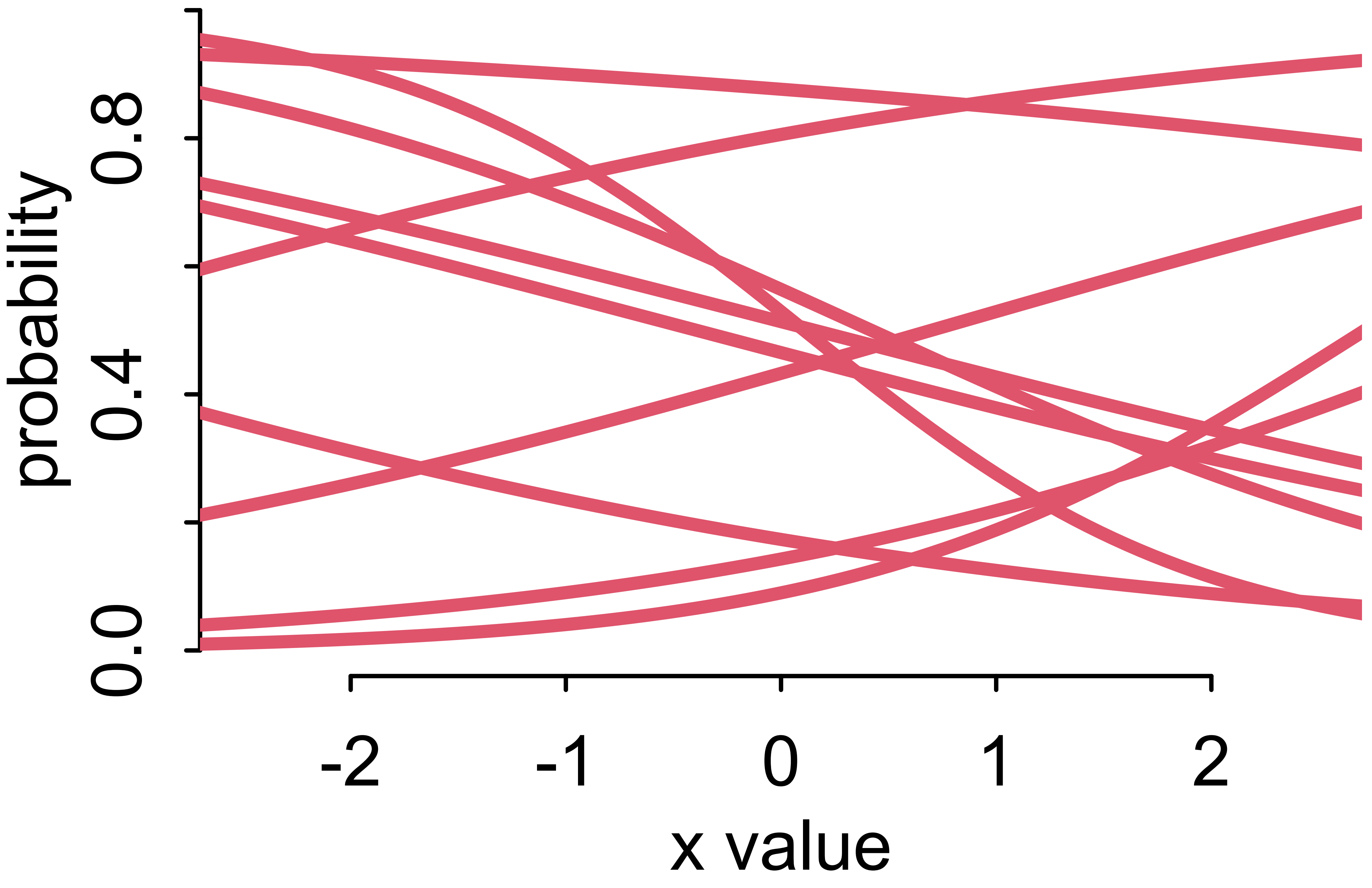
$$\text{logit}(p_i) = \alpha + \beta x_i$$

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

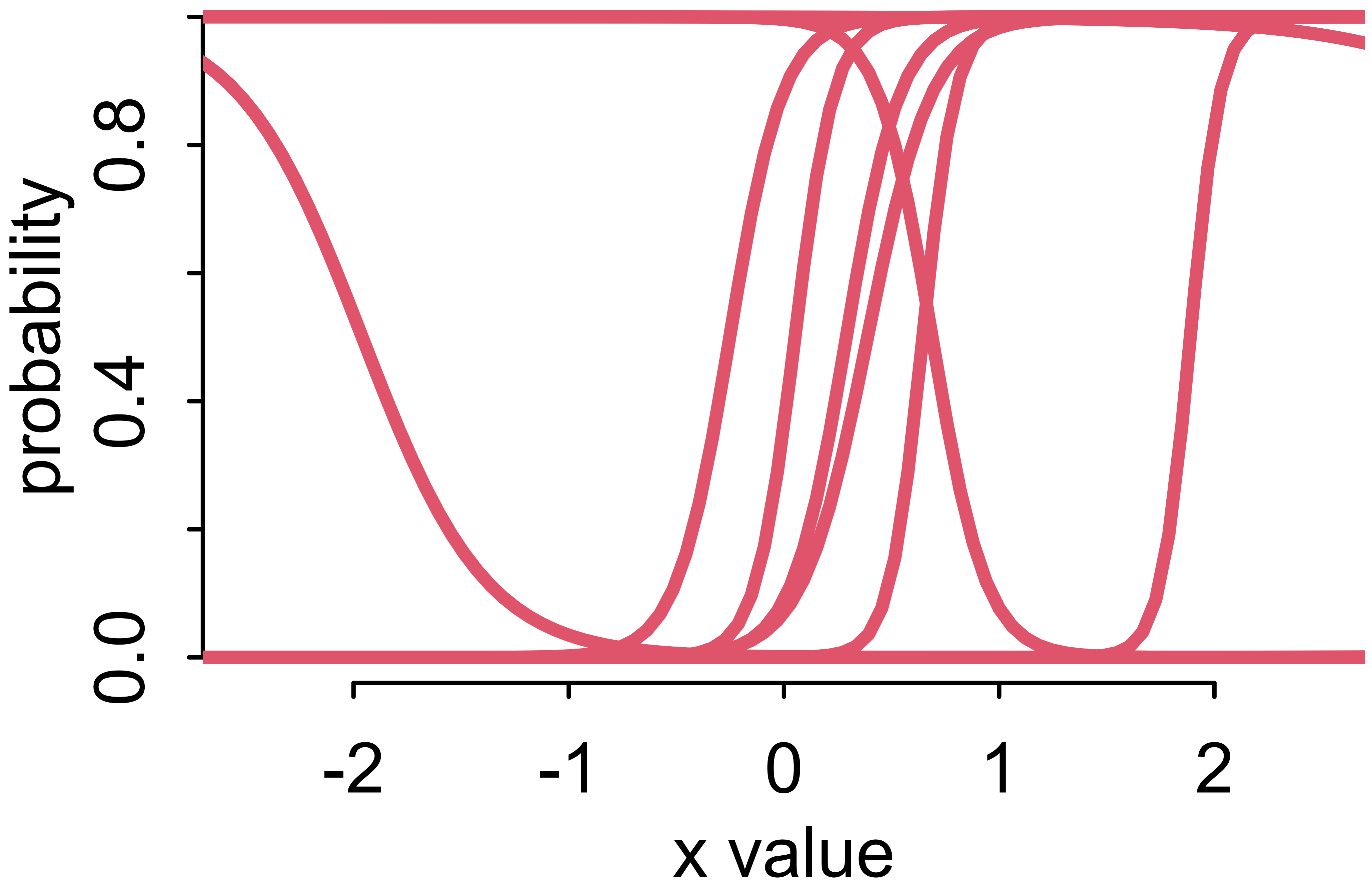
```r
a <- rnorm(1e4,0,10)
b <- rnorm(1e4,0,10)

xseq <- seq(from=-3,to=3,len=100)
p <- sapply( xseq , function(x)
inv_logit(a+b*x) )

plot( NULL , xlim=c(-2.5,2.5) , ylim=c(0,1) ,
xlab="x value" , ylab="probability" )
for ( i in 1:10 ) lines( xseq , p[i,] , lwd=3 ,
col=2 )
```



$$\alpha \sim \text{Normal}(0,1.5)$$
$$\beta \sim \text{Normal}(0,0.5)$$

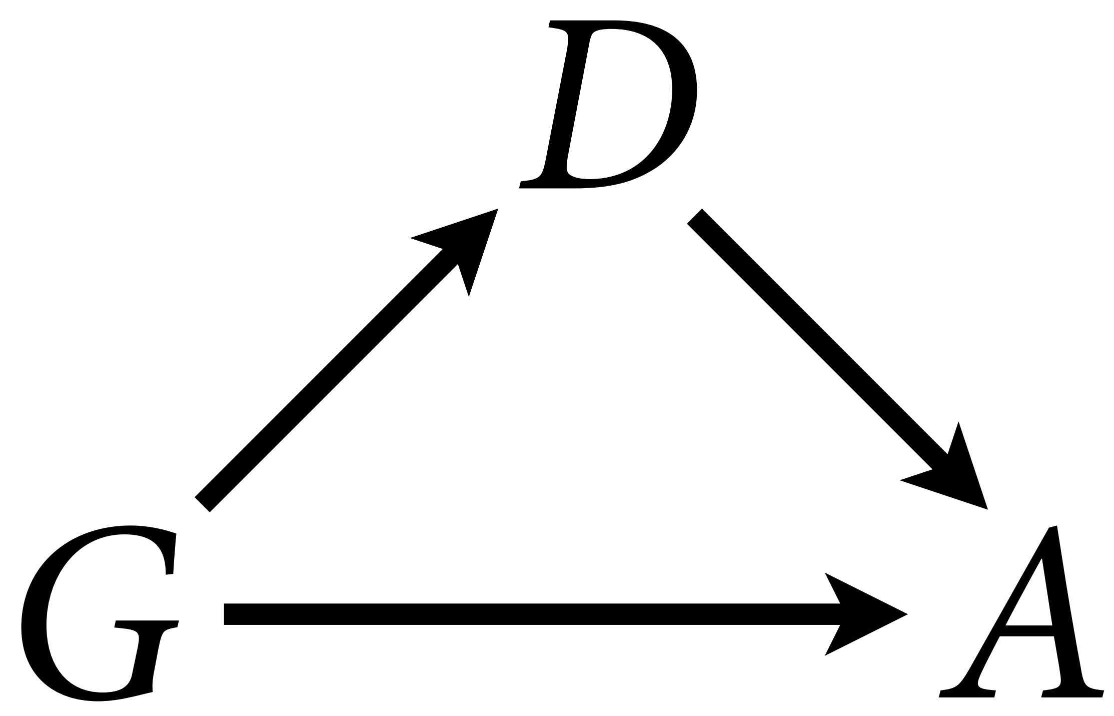


$$\alpha \sim \text{Normal}(0,10)$$
$$\beta \sim \text{Normal}(0,10)$$



A statistical model

```r
# generative model, basic mediator scenario

N <- 1000 # number of applicants
# even gender distribution
G <- sample( 1:2 , size=N , replace=TRUE )
# gender 1 tends to apply to department 1, 2 to 2
D <- rbern( N , ifelse( G==1 , 0.3 , 0.8 ) ) + 1
# matrix of acceptance rates [dept,gender]
accept_rate <- matrix( c(0.05,0.2,0.1,0.3) , nrow=2 )
# simulate acceptance
A <- rbern( N , accept_rate[D,G] )
```



Estimand: Total effect of G

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

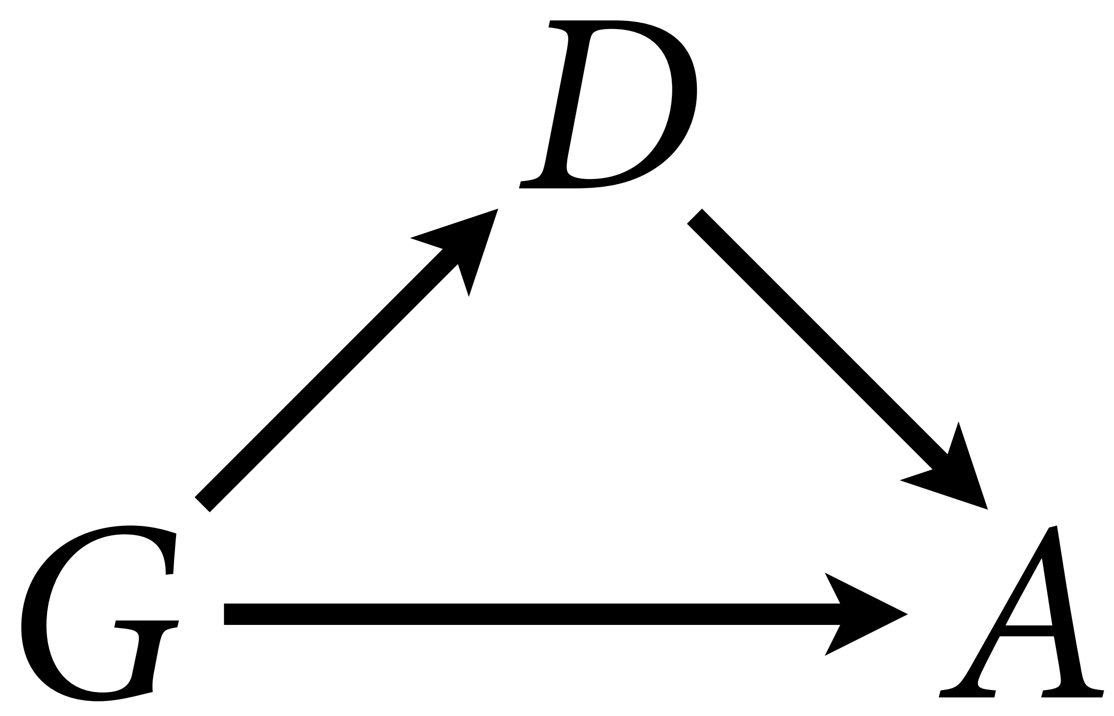
$$\text{logit}(p_i) = \alpha[G_i]$$

Genders

$$\alpha = [\alpha_1, \alpha_2]$$

$$\Pr(A_i = 1) = p_i$$

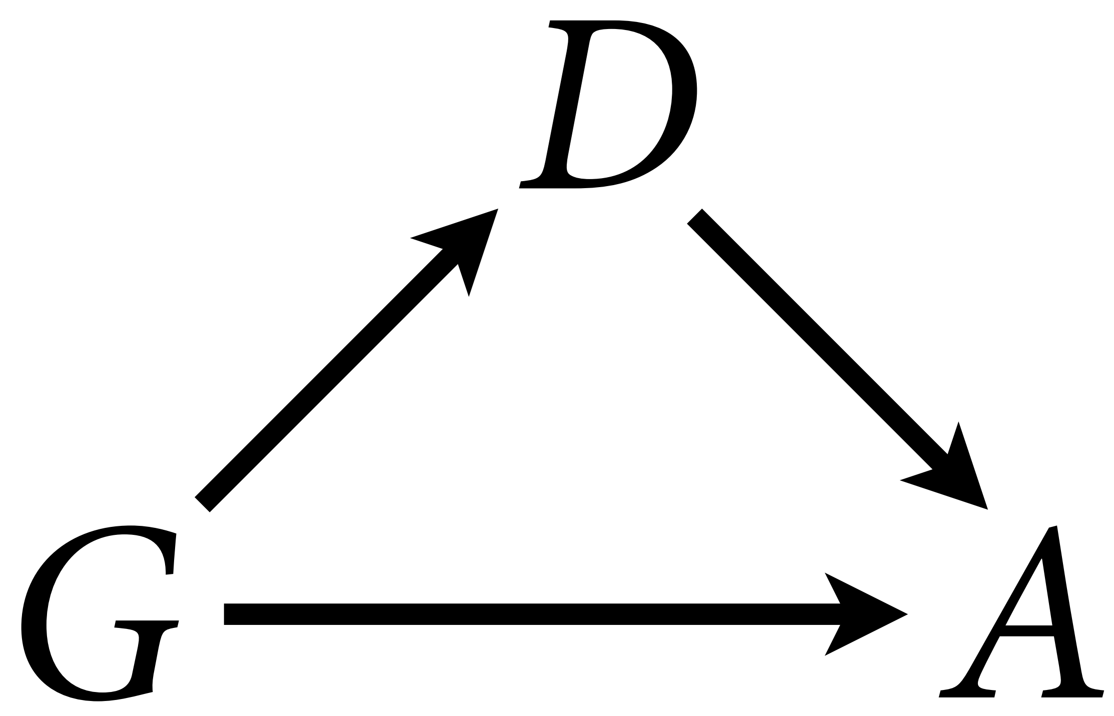
$$p_i = \frac{\exp(\alpha[G_i])}{1 + \exp(\alpha[G_i])}$$



Estimand: Direct effect of G

$$A_i \sim \text{Bernoulli}(p_i)$$
$$\text{logit}(p_i) = \alpha[G_i, D_i]$$

$$\begin{array}{cc} & \textit{Departments} \\ \alpha = & \begin{bmatrix} \alpha_{1,1} & \alpha_{1,2} \\ \alpha_{2,1} & \alpha_{2,2} \end{bmatrix} \textit{Genders} \end{array}$$



Total effect

$$
\begin{aligned}
A_i &\sim \text{Bernoulli}(p_i) \\
\text{logit}(p_i) &= \alpha[G_i] \\
\alpha_j &\sim \text{Normal}(0,1)
\end{aligned}
$$

Direct effect(s)

$$
\begin{aligned}
A_i &\sim \text{Bernoulli}(p_i) \\
\text{logit}(p_i) &= \alpha[G_i, D_i] \\
\alpha_{j,k} &\sim \text{Normal}(0,1)
\end{aligned}
$$

Total effect

$$A_i \sim \text{Bernoulli}(p_i)$$
$$\text{logit}(p_i) = \alpha[G_i]$$
$$\alpha_j \sim \text{Normal}(0,1)$$

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

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

Direct effect(s)

$$A_i \sim \text{Bernoulli}(p_i)$$
$$\text{logit}(p_i) = \alpha[G_i, D_i]$$
$$\alpha_{j,k} \sim \text{Normal}(0,1)$$

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

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

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

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

```
precis(m1,depth=2)
```

```
      mean   sd  5.5% 94.5% n_eff Rhat4
a[1] -1.80 0.13 -2.01 -1.60  1549     1
a[2] -1.09 0.10 -1.25 -0.93  1159     1
```

Direct effect(s)

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

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

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

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

```
precis(m1,depth=2)
```

```
      mean   sd  5.5% 94.5% n_eff Rhat4
a[1] -1.80 0.13 -2.01 -1.60  1549     1
a[2] -1.09 0.10 -1.25 -0.93  1159     1
```

Direct effect(s)

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

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 )
```

```
precis(m2,depth=3)
```

```
        mean   sd  5.5% 94.5% n_eff Rhat4
a[1,1] -2.31 0.18 -2.60 -2.04  2529     1
a[1,2] -0.92 0.19 -1.23 -0.62  2216     1
a[2,1] -1.93 0.31 -2.45 -1.44  2214     1
a[2,2] -0.93 0.11 -1.11 -0.75  2055     1
```

Total effect

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

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

```
precis(m1,depth=2)
```

	mean	sd	5.5%	94.5%	n_eff	Rhat4
a[1]	-1.80	0.13	-2.01	-1.60	1549	1
a[2]	-1.09	0.10	-1.25	-0.93	1159	1

Direct effect(s)

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

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 )
```

```
precis(m2,depth=3)
```

	mean	sd	5.5%	94.5%	n_eff	Rhat4
a[1,1]	-2.31	0.18	-2.60	-2.04	2529	1
a[1,2]	-0.92	0.19	-1.23	-0.62	2216	1
a[2,1]	-1.93	0.31	-2.45	-1.44	2214	1
a[2,2]	-0.93	0.11	-1.11	-0.75	2055	1

```
> inv_logit(coef(m2))
    a[1,1]     a[1,2]     a[2,1]     a[2,2]
0.06296434 0.21109945 0.08253890 0.20003819
```

PAUSE


Yellow Duck

Admissions: Drawing the Owl

(1) Estimand(s)

(2) Scientific model(s)

(3) Statistical model(s)

(4) Analyze

UC Berkeley Admissions

4526 graduate school applications for 1973 UC Berkeley

Stratified by department and gender of applicant

Evidence of gender discrimination?

	dept	admit	reject	applications	gender
1	A	512	313	825	male
2	A	89	19	108	female
3	B	353	207	560	male
4	B	17	8	25	female
5	C	120	205	325	male
6	C	202	391	593	female
7	D	138	279	417	male
8	D	131	244	375	female
9	E	53	138	191	male
10	E	94	299	393	female
11	F	22	351	373	male
12	F	24	317	341	female

See ?UCBAdmissions for citation

Logistic & Binomial Regression

Logistic regression:
Binary [0,1] outcome and logit link

$$A_i \sim \text{Bernoulli}(p_i)$$
$$\text{logit}(p_i) = \alpha[G_i, D_i]$$

Binomial regression:
Count [0,N] outcome and logit link

$$A_i \sim \text{Binomial}(N_i, p_i)$$
$$\text{logit}(p_i) = \alpha[G_i, D_i]$$

Completely equivalent for inference

LOOOOOOONG

	A	G	D
1	0	2	1
2	0	1	1
3	1	2	2
4	1	2	2
5	0	2	2
6	0	1	1
7	0	2	2
8	0	2	2
9	0	2	2
10	0	2	2
11	0	2	2
12	1	2	2
13	0	2	2
14	0	1	1
15	0	2	2
16	0	1	2
17	0	1	1
18	0	1	1
19	0	1	1
20	0	1	1

```
dat_sim2 <- aggregate( A ~ G + D , dat_sim , sum )
dat_sim2$N <- aggregate( A ~ G + D , dat_sim , length )$A
```

	G	D	A	N
1	1	1	30	355
2	2	1	10	92
3	1	2	38	135
4	2	2	117	418

Aggregated

Logistic & Binomial Regression

```
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 )
```

$$A_i \sim \text{Bernoulli}(p_i)$$
$$\text{logit}(p_i) = \alpha[G_i, D_i]$$

```
m2_bin <- ulam(
    alist(
        A ~ binomial(N,p),
        logit(p) <- a[G,D],
        matrix[G,D]:a ~ normal(0,1)
    ), data=dat_sim2 , chains=4 , cores=4 )
```

$$A_i \sim \text{Binomial}(N_i, p_i)$$
$$\text{logit}(p_i) = \alpha[G_i, D_i]$$

Completely equivalent for inference

Logistic & Binomial Regression

```
m2 <- ulam(
    alist(
        A ~ binomial(1,p),
        logit(p) <- a[G,D],
        matrix[G,D]:a ~ normal(0,1)
    ), data=dat_sim , chains=4 , cores=4 )
```

$$A_i \sim \text{Binomial}(1, p_i)$$
$$\text{logit}(p_i) = \alpha[G_i, D_i]$$

```
m2_bin <- ulam(
    alist(
        A ~ binomial(N,p),
        logit(p) <- a[G,D],
        matrix[G,D]:a ~ normal(0,1)
    ), data=dat_sim2 , chains=4 , cores=4 )
```

$$A_i \sim \text{Binomial}(N_i, p_i)$$
$$\text{logit}(p_i) = \alpha[G_i, D_i]$$

Completely equivalent for inference

Total effect

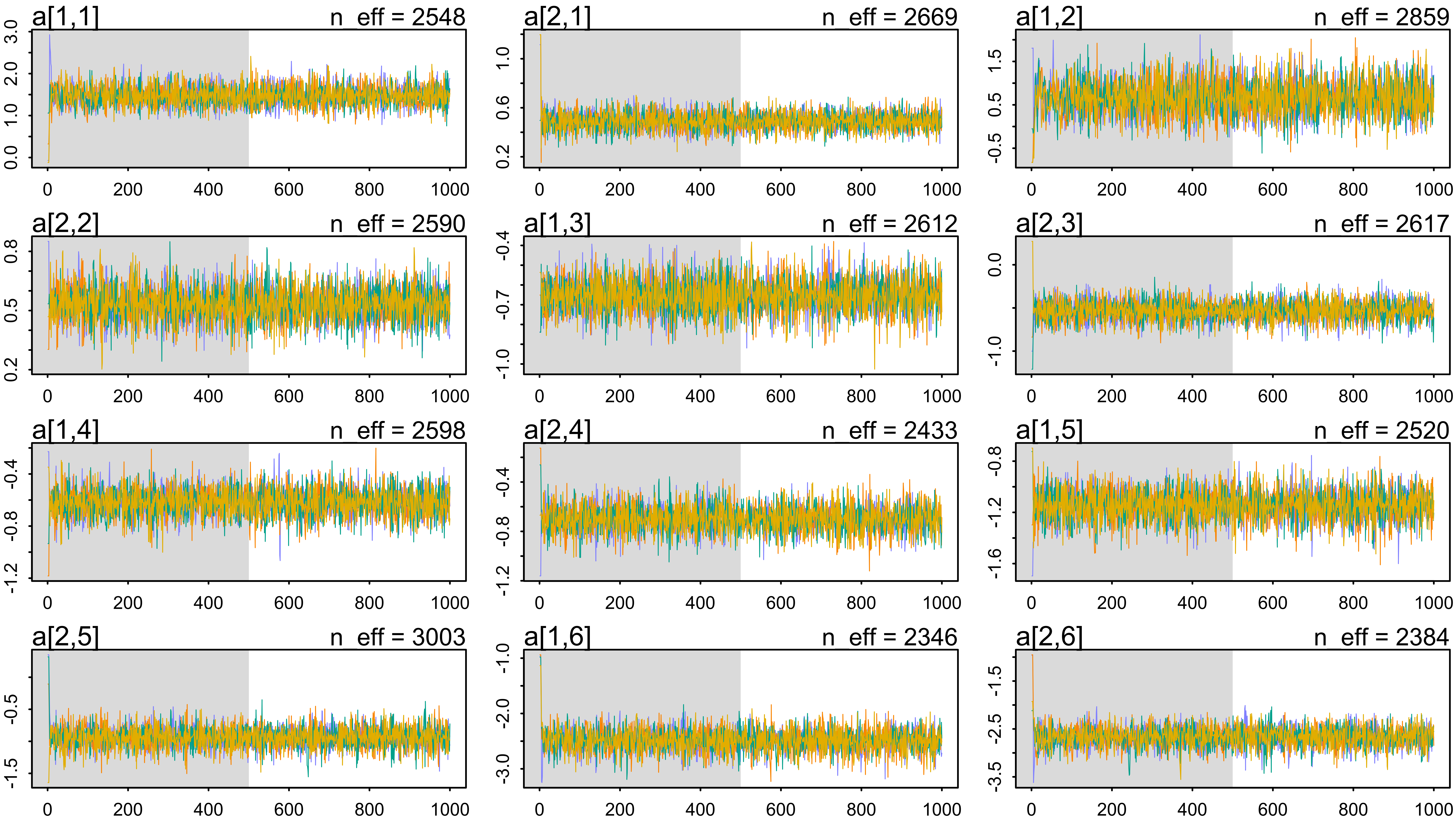
```r
data(UCBadmit)
d <- UCBadmit

dat <- list(
    A = d$admit,
    N = d$applications,
    G = ifelse(d$applicant.gender=="female",1,2),
    D = as.integer(d$dept)
)

# total effect gender
mG <- ulam(
    alist(
        A ~ binomial(N,p),
        logit(p) <- a[G],
        a[G] ~ normal(0,1)
    ), data=dat , chains=4 , cores=4 )
```

Total effect

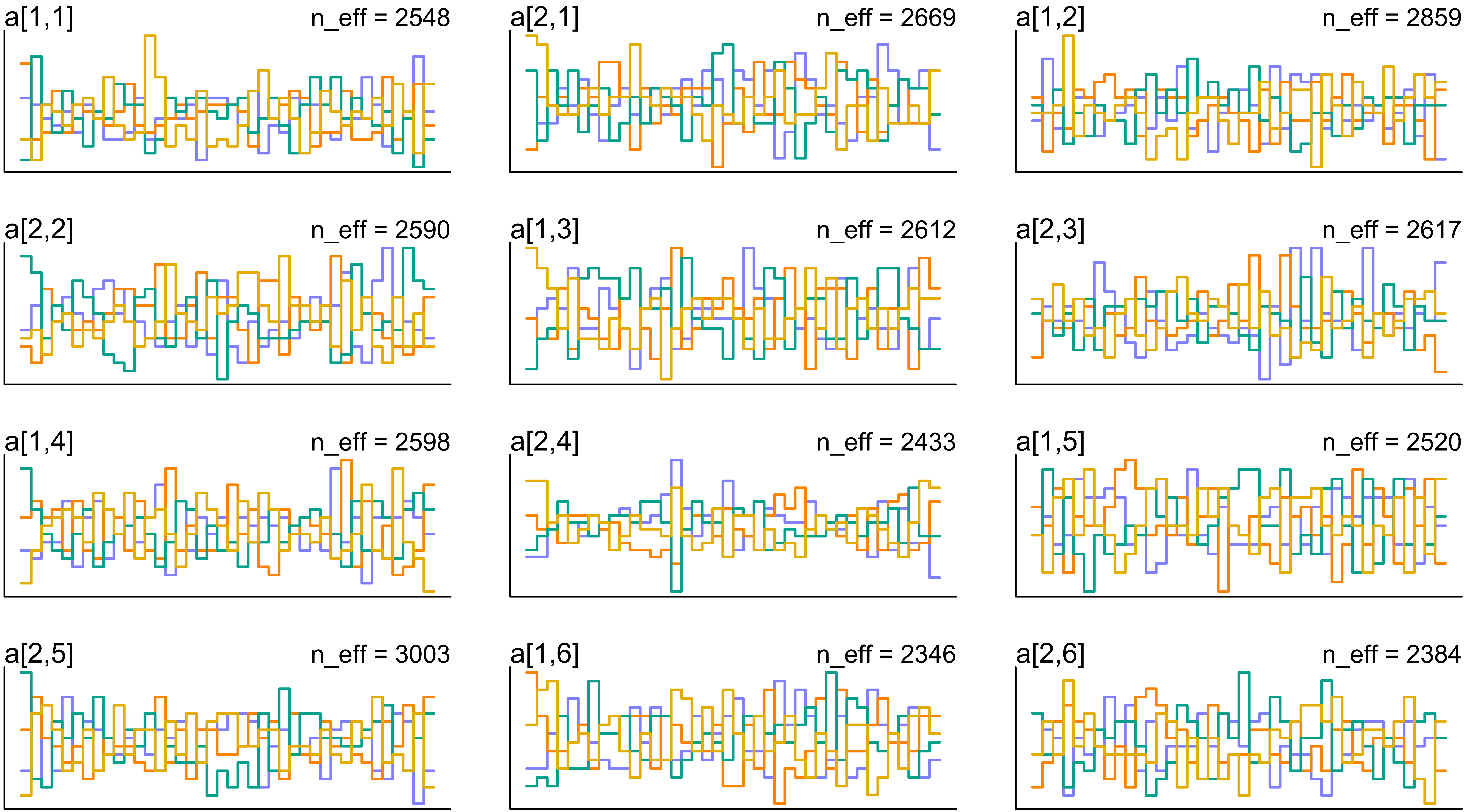
```
data(UCBadmit)
d <- UCBadmit

dat <- list(
    A = d$admit,
    N = d$applications,
    G = ifelse(d$applicant.gender=="female",1,2),
    D = as.integer(d$dept)
)

# total effect gender
mG <- ulam(
    alist(
        A ~ binomial(N,p),
        logit(p) <- a[G],
        a[G] ~ normal(0,1)
    ), data=dat , chains=4 , cores=4 )
```

Direct effect(s)

```
# direct effects
mGD <- ulam(
    alist(
        A ~ binomial(N,p),
        logit(p) <- a[G,D],
        matrix[G,D]:a ~ normal(0,1)
    ), data=dat , chains=4 , cores=4 )
```



a[1,1]
n_eff = 2548
a[2,1]
n_eff = 2669
a[1,2]
n_eff = 2859
a[2,2]
n_eff = 2590
a[1,3]
n_eff = 2612
a[2,3]
n_eff = 2617
a[1,4]
n_eff = 2598
a[2,4]
n_eff = 2433
a[1,5]
n_eff = 2520
a[2,5]
n_eff = 3003
a[1,6]
n_eff = 2346
a[2,6]
n_eff = 2384


a[1,1]
n_eff = 2548
a[2,1]
n_eff = 2669
a[1,2]
n_eff = 2859
a[2,2]
n_eff = 2590
a[1,3]
n_eff = 2612
a[2,3]
n_eff = 2617
a[1,4]
n_eff = 2598
a[2,4]
n_eff = 2433
a[1,5]
n_eff = 2520
a[2,5]
n_eff = 3003
a[1,6]
n_eff = 2346
a[2,6]
n_eff = 2384

```r
# total effect gender
mG <- ulam(
    alist(
        A ~ binomial(N,p),
        logit(p) <- a[G],
        a[G] ~ normal(0,1)
    ), data=dat , chains=4 , cores=4 )
```

	mean	sd	5.5%	94.5%	n_eff	Rhat4
a[1]	-0.83	0.05	-0.91	-0.75	1487	1
a[2]	-0.22	0.04	-0.28	-0.16	1499	1

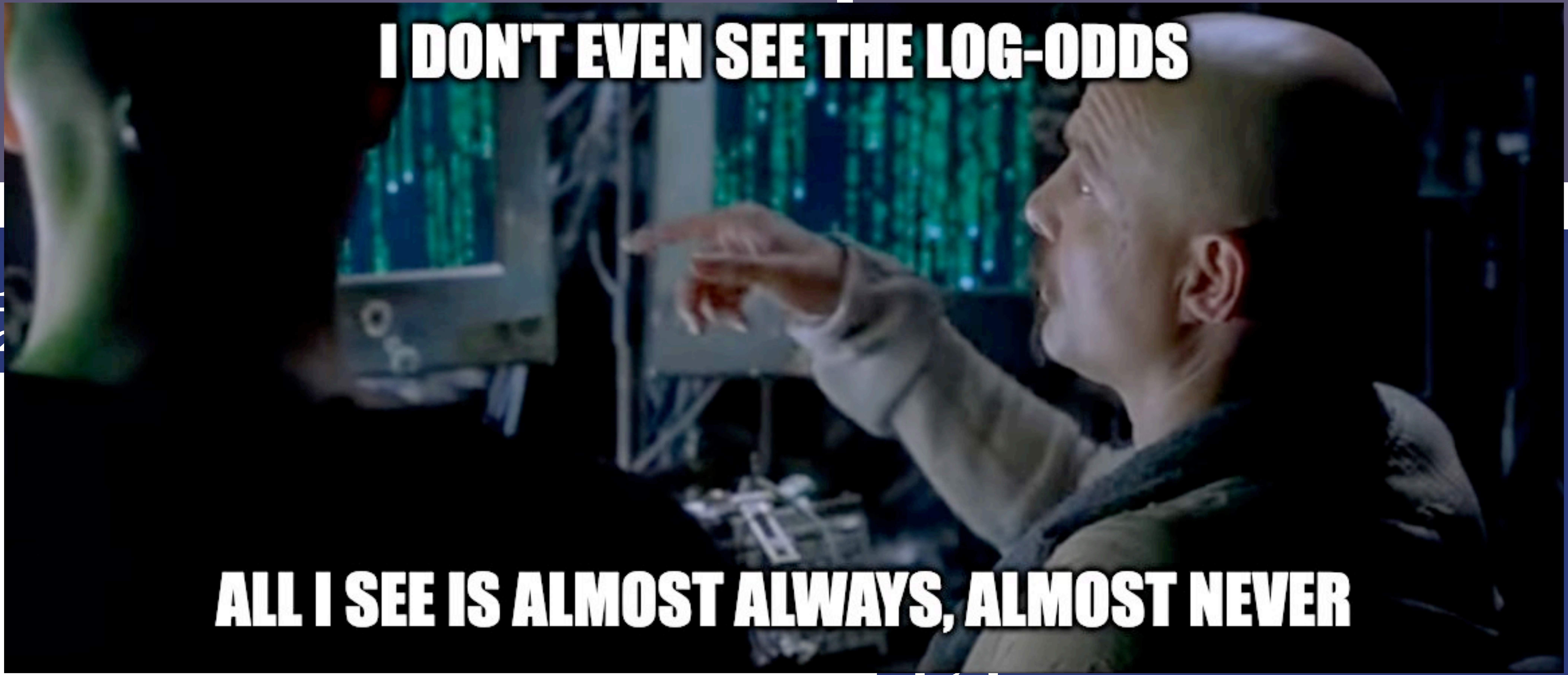
```r
# direct effects
mGD <- ulam(
    alist(
        A ~ binomial(N,p),
        logit(p) <- a[G,D],
        matrix[G,D]:a ~ normal(0,1)
    ), data=dat , chains=4 , cores=4 )
```

	mean	sd	5.5%	94.5%	n_eff	Rhat4
a[1,1]	1.48	0.24	1.11	1.87	2548	1
a[1,2]	0.66	0.40	0.03	1.32	2859	1
a[1,3]	-0.65	0.08	-0.79	-0.52	2612	1
a[1,4]	-0.62	0.11	-0.79	-0.45	2598	1
a[1,5]	-1.15	0.12	-1.34	-0.96	2520	1
a[1,6]	-2.50	0.20	-2.81	-2.18	2346	1
a[2,1]	0.49	0.07	0.38	0.60	2669	1
a[2,2]	0.53	0.08	0.40	0.67	2590	1
a[2,3]	-0.53	0.11	-0.72	-0.35	2617	1
a[2,4]	-0.70	0.10	-0.87	-0.54	2433	1
a[2,5]	-0.94	0.16	-1.20	-0.69	3003	1
a[2,6]	-2.67	0.21	-3.00	-2.34	2384	1

```
# total effect gender
mG <- ulam(
    alist(

    ),
```

```
# direct effects
mGD <- ulam(
    alist(

    )
```

```
a[1
a[2
```

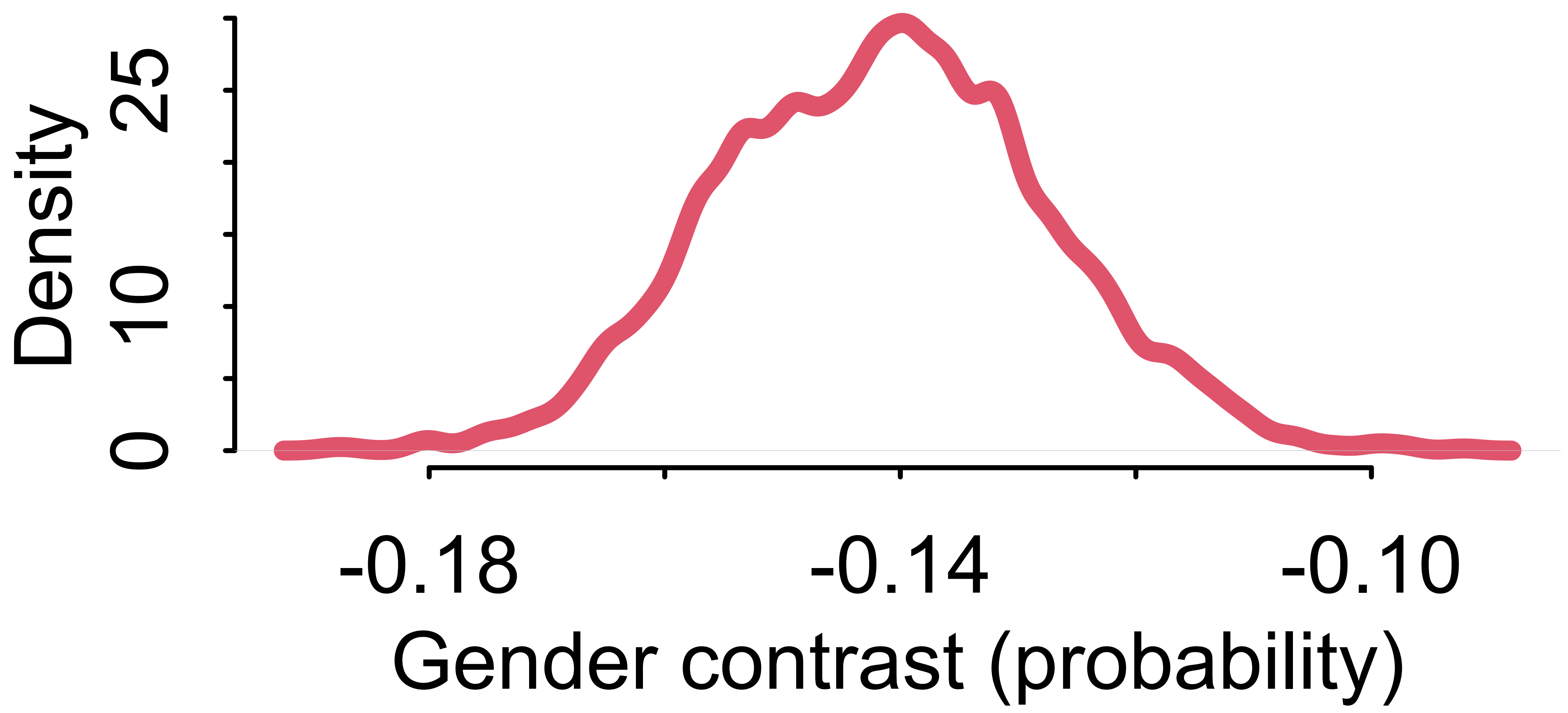



```
                                           Rhat4
                                               1
                                               1
                                               1
                                               1
                                               1
                                               1
                                               1
                                               1
                                               1
                                               1
a[2,5] -0.94 0.16 -1.20 -0.69   3003       1
a[2,6] -2.67 0.21 -3.00 -2.34   2384       1
```

Total effect

```
post1 <- extract.samples(mG)
PrA_G1 <- inv_logit( post1$a[,1] )
PrA_G2 <- inv_logit( post1$a[,2] )
diff_prob <- PrA_G1 - PrA_G2
dens(diff_prob,lwd=4,col=2,xlab="Gender
contrast (probability)")
```

men advantaged



Total effect

```
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```
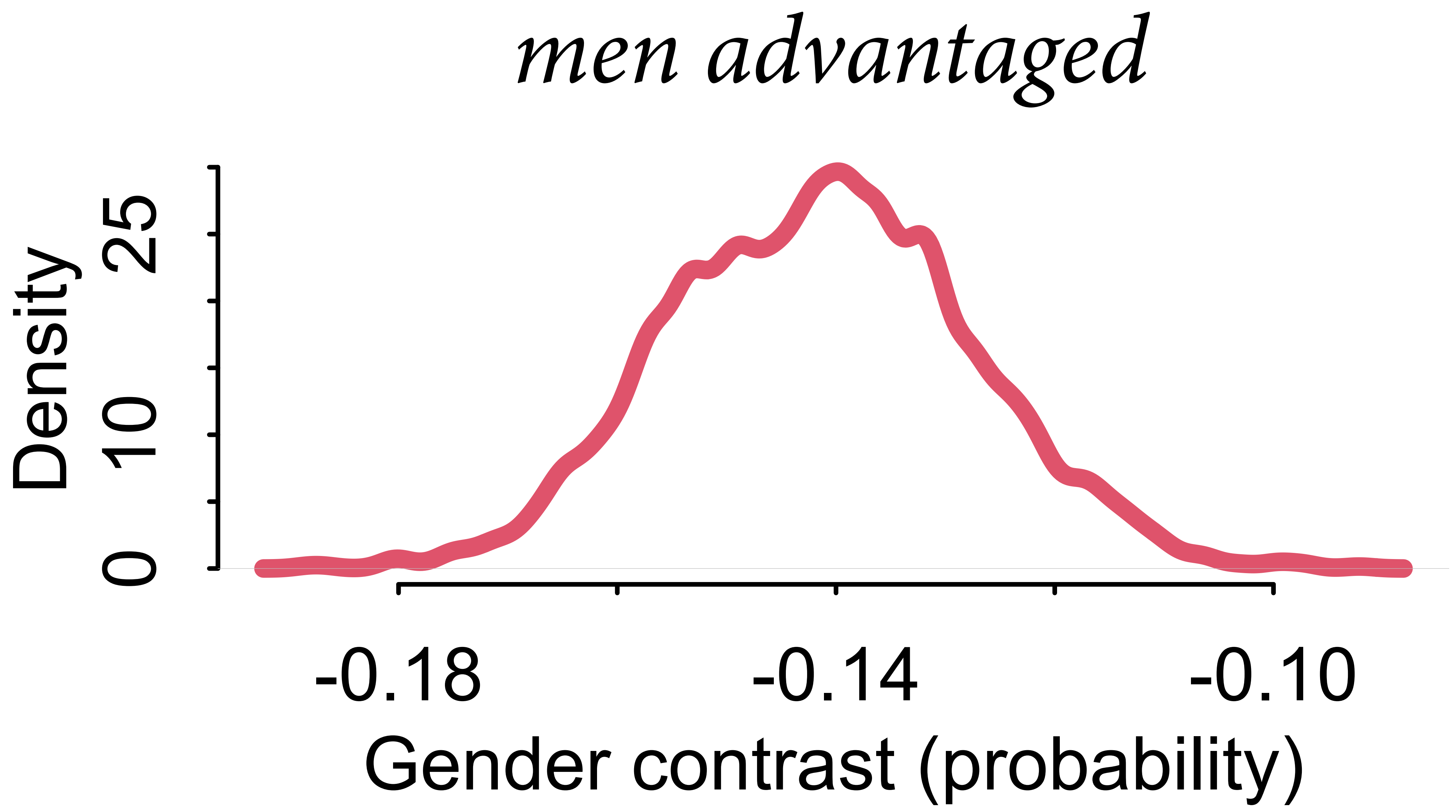
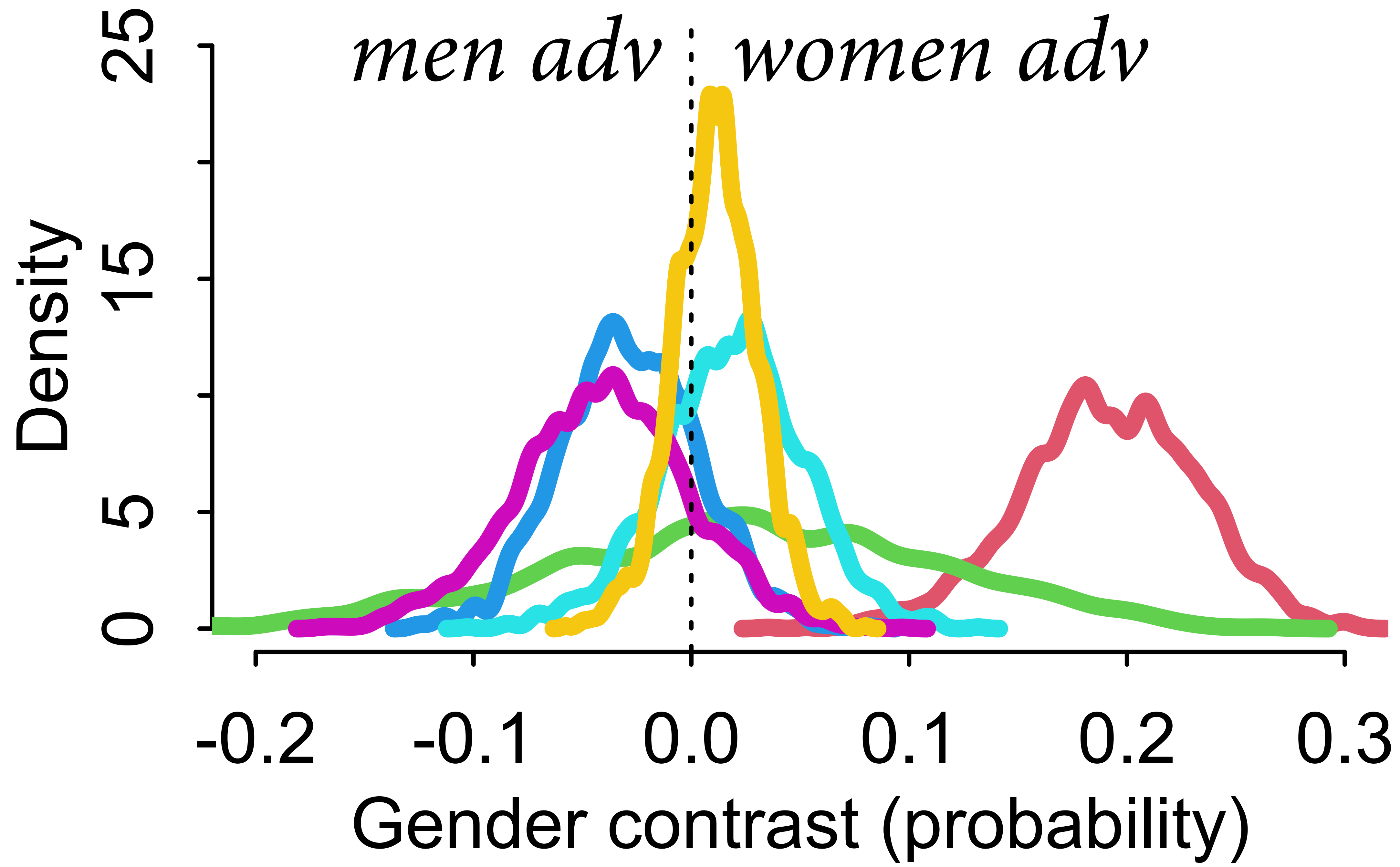



Direct effect(s)

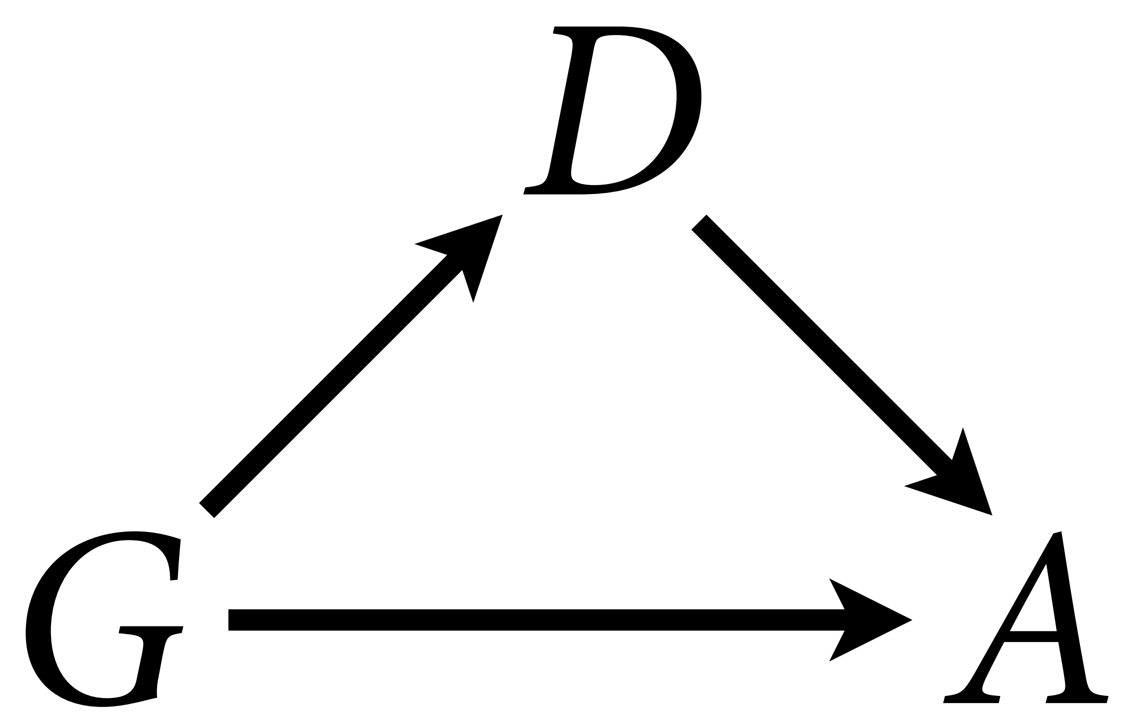
```
post2 <- extract.samples(mGD)
PrA <- inv_logit( post2$a )
diff_prob_D_ <- sapply( 1:6 , function(i)
PrA[,1,i] - PrA[,2,i] )

plot(NULL,xlim=c(-0.2,0.3),ylim=c(0,25),xlab="G
ender contrast (probability)",ylab="Density")
for ( i in 1:6 ) dens( diff_prob_D_[,i] , lwd=4
, col=1+i , add=TRUE )
```



What is the **average direct effect** of gender across departments?

Depends upon distribution of applications, probability woman/man applies to each department

What is the intervention actually?



What is the average **direct** effect of gender across departments?

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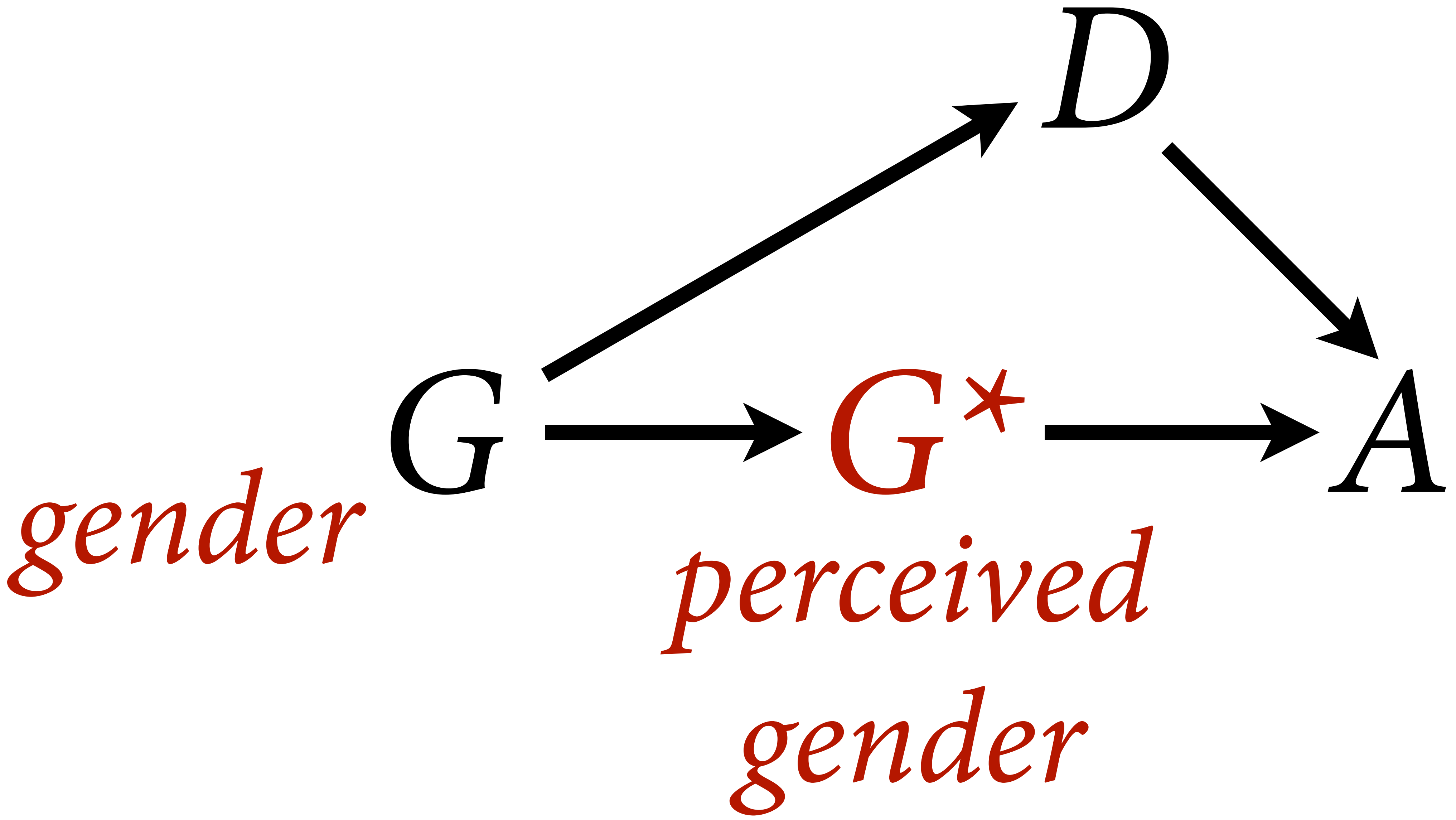
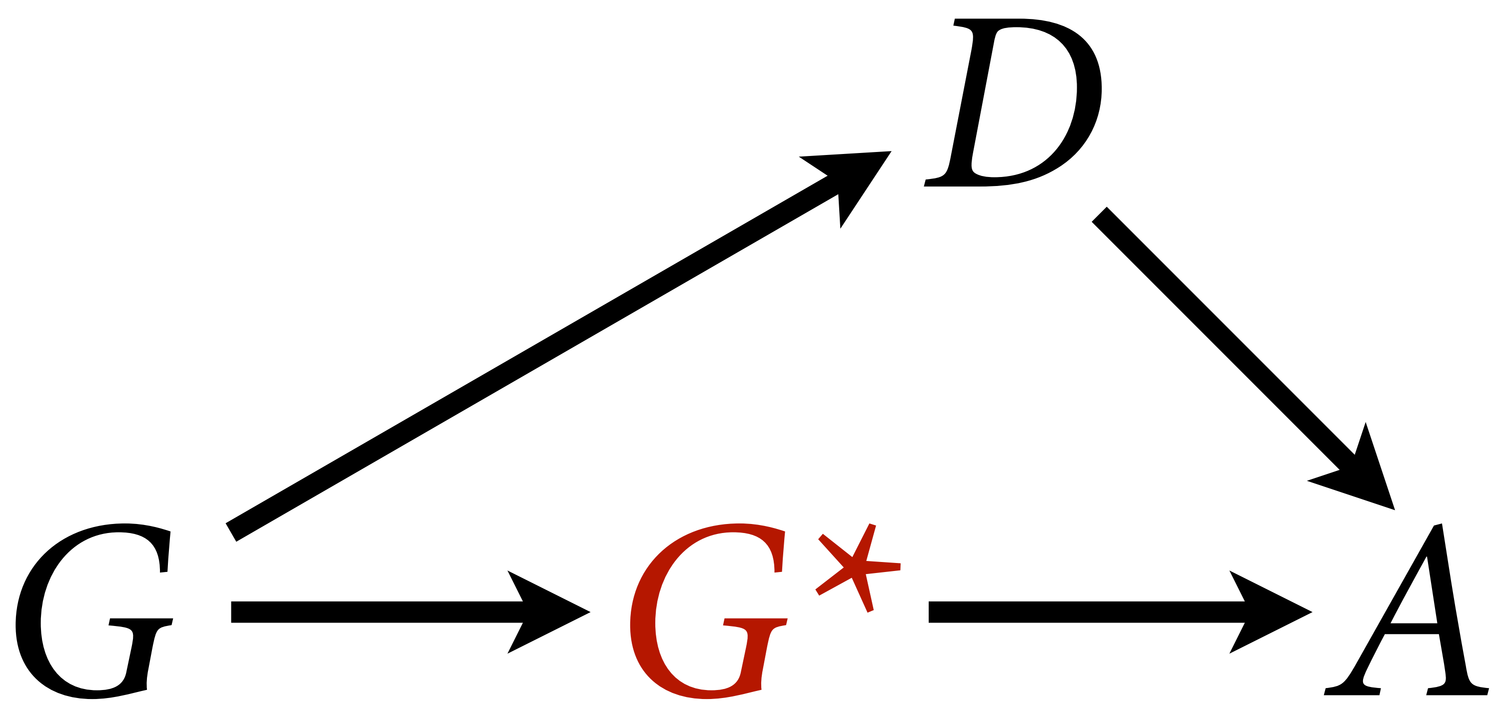
What is the intervention actually?



What is the intervention actually?



To calculate causal effect of G^*, must average (marginalize) over departments

Easy to do it as a simulation

NB: We are still assuming no confounds!

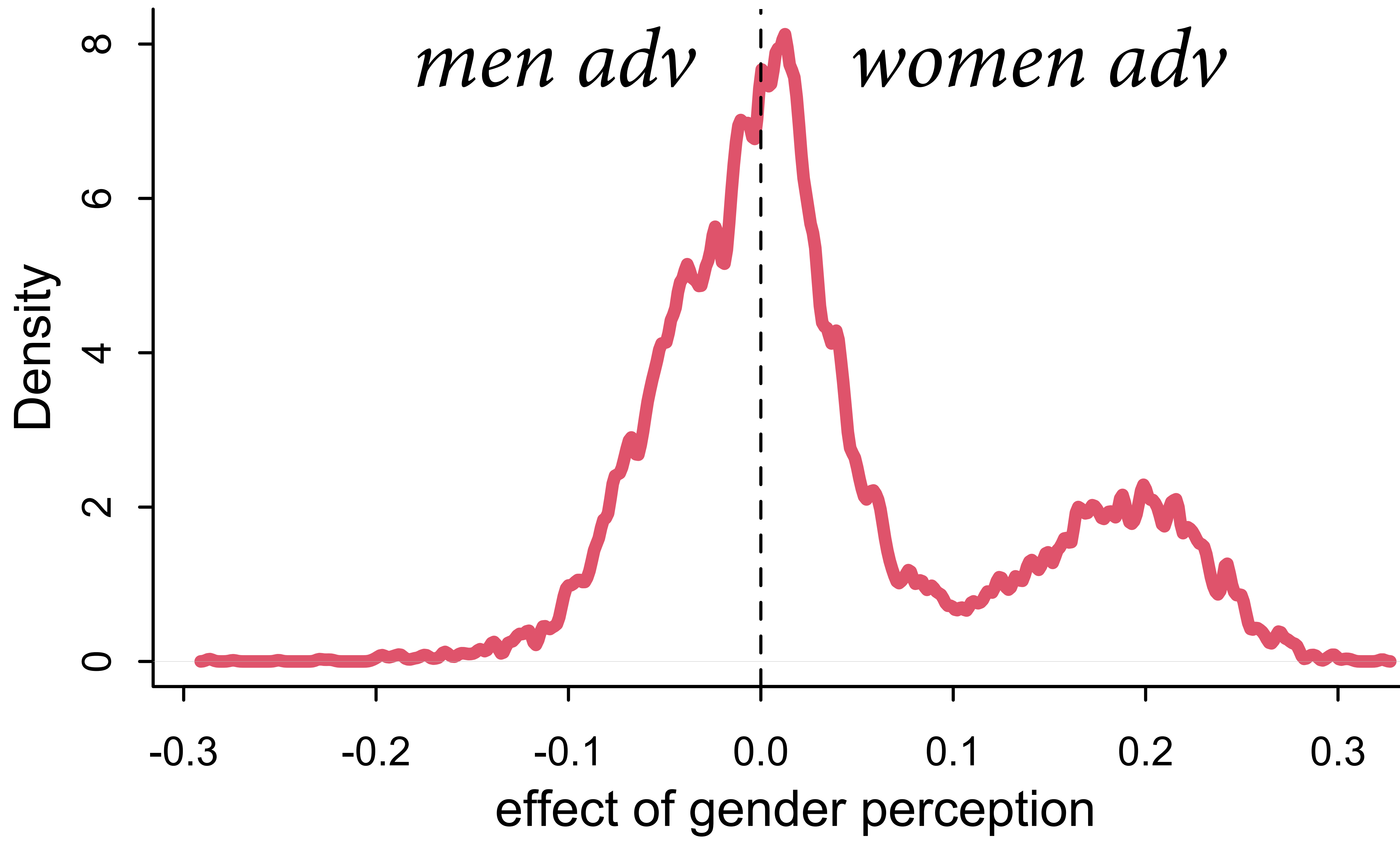
```r
# number of applicatons to simulate
total_apps <- sum(dat$N)

# number of applications per department
apps_per_dept <- sapply( 1:6 , function(i)
sum(dat$N[dat$D==i]) )

# simulate as if all apps from women
p_G1 <- link(mGD,data=list(
    D=rep(1:6,times=apps_per_dept),
    N=rep(1,total_apps),
    G=rep(1,total_apps)))

# simulate as if all apps from men
p_G2 <- link(mGD,data=list(
    D=rep(1:6,times=apps_per_dept),
    N=rep(1,total_apps),
    G=rep(2,total_apps)))

# summarize
dens( p_G1 - p_G2 , lwd=4 , col=2 ,
xlab="effect of gender perception" )
```



```
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p_G1 <- link(mGD,data=list(
    D=rep(1:6,times=apps_per_dept),
    N=rep(1,total_apps),
    G=rep(1,total_apps)))

# simulate as if all apps from men
p_G2 <- link(mGD,data=list(
    D=rep(1:6,times=apps_per_dept),
    N=rep(1,total_apps),
    G=rep(2,total_apps)))
```
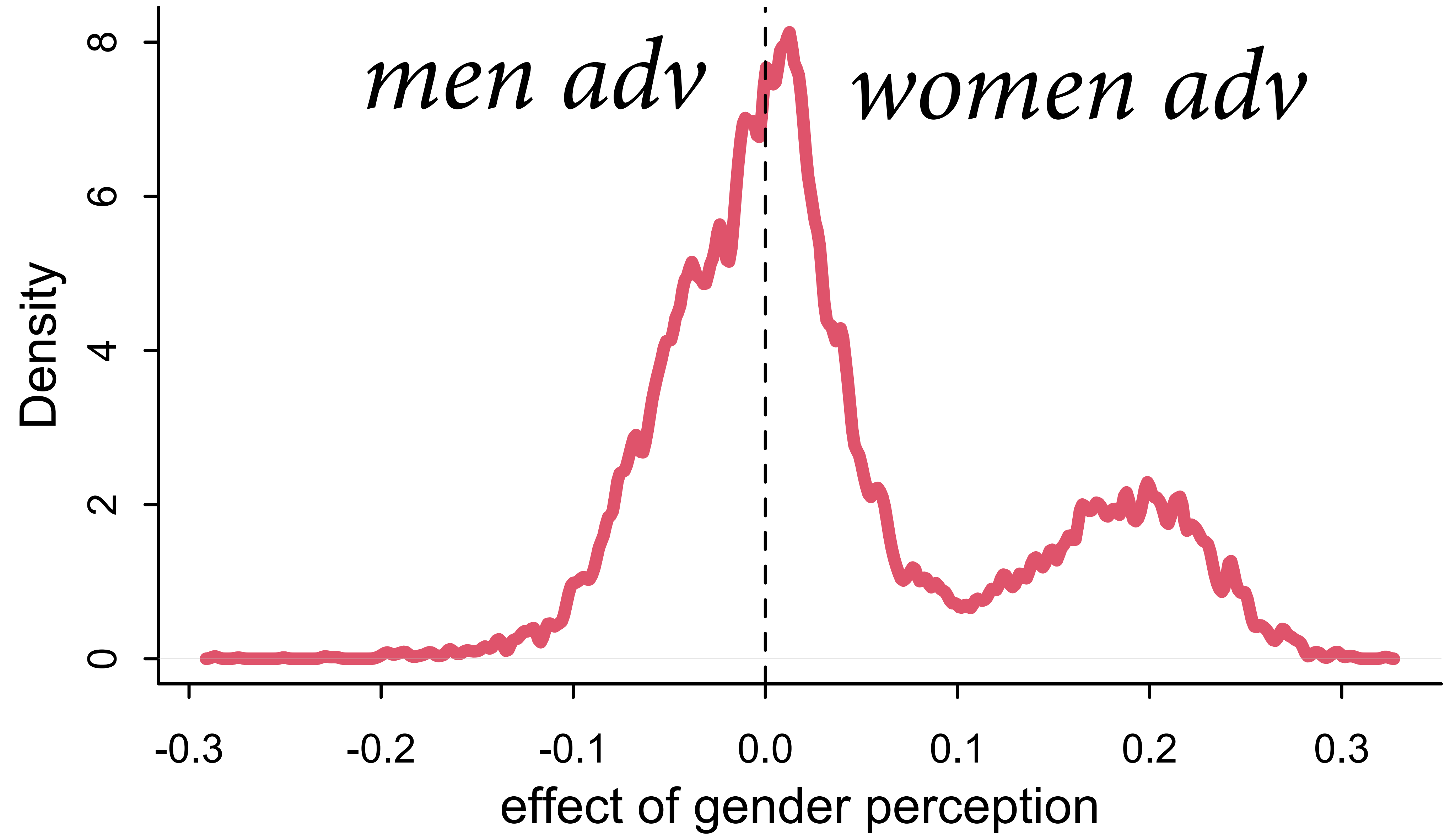
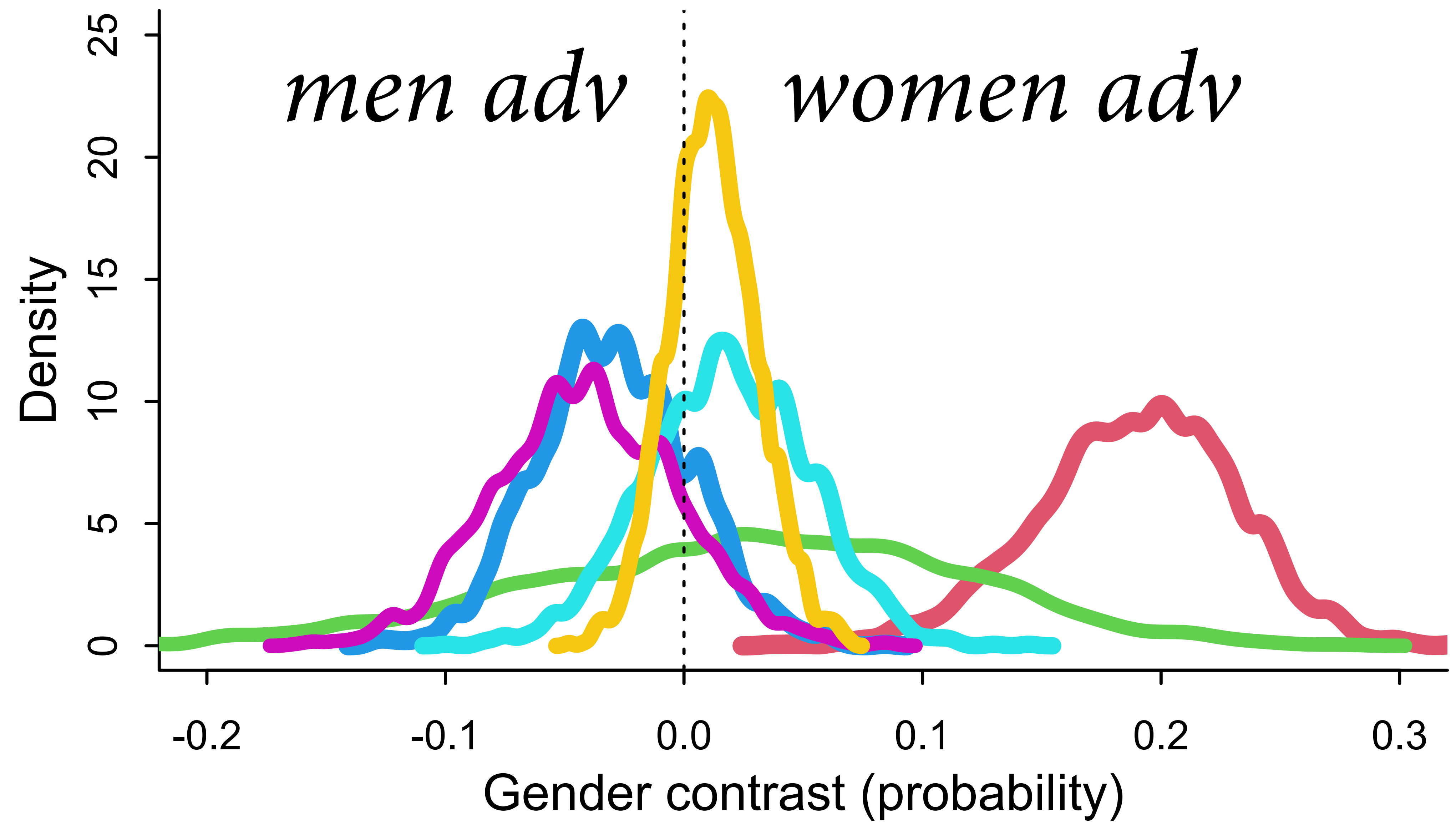




```
# show each dept density with weight as in
population
w <- xtabs( dat$N ~ dat$D ) / sum(dat$N)

plot(NULL,xlim=c(-0.2,0.3),ylim=c(0,25),xlab="
Gender contrast (probability)",ylab="Density")
for ( i in 1:6 ) dens( diff_prob_D_[,i] ,
lwd=2+20*w[i] , col=1+i , add=TRUE )
abline(v=0,lty=3)
```

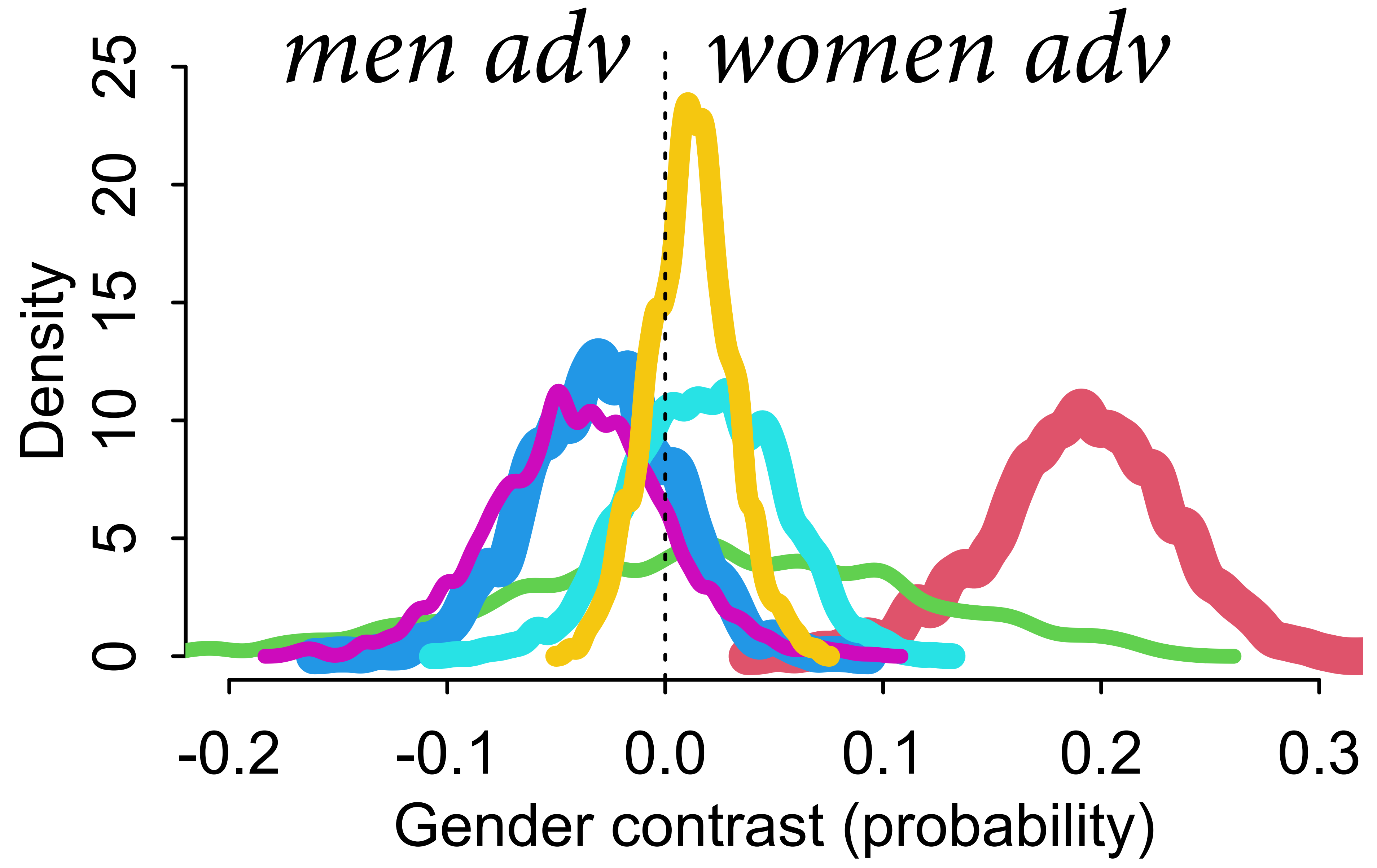


Post-stratification

Description, prediction & causal inference often require post-stratification

Post-stratification: Re-weighting estimates for target population

At a different university, distribution of applications will differ => predicted consequence of intervention different



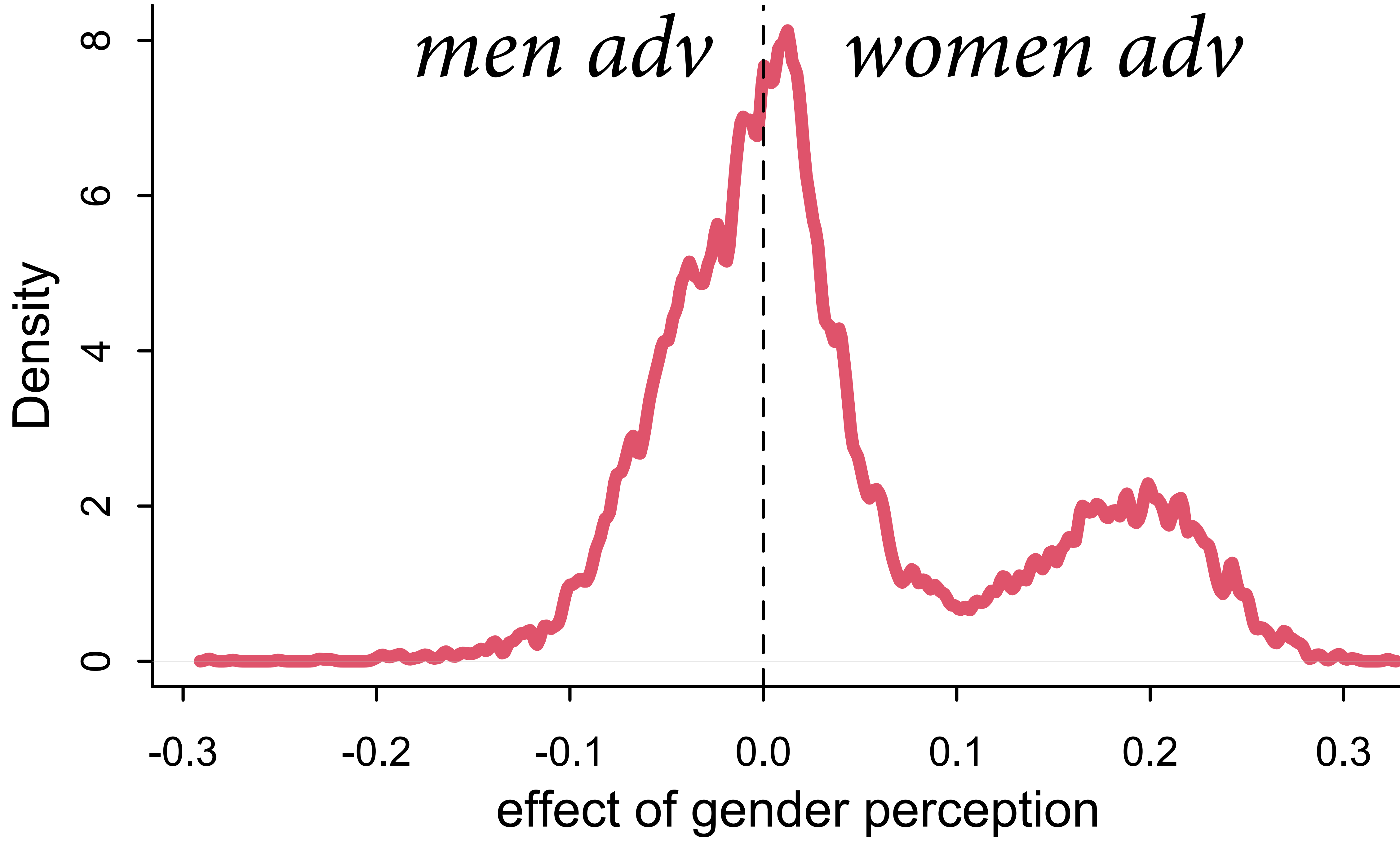
Admissions so far

Evidence for discrimination?

Big structural effects, but

(1) Distribution of applications can be a consequence of discrimination (data do not speak to this)

(2) Confounds likely



Gender Gaps at the Academies

David Card, Stefano DellaVigna, Patricia Funk & Nagore Iriberri

WORKING PAPER 30510 **DOI** 10.3386/w30510 **ISSUE DATE** September 2022

Historically, a large majority of the newly elected members of the National Academy of Science (NAS) and the American Academy of Arts and Science (AAAS) were men. Within the past two decades, however, that situation has changed, and in the last 3 years women made up about 40 percent of the new members in both academies. We build lists of active scholars from publications in the top journals in three fields – Psychology, Mathematics and Economics – and develop a series of models to compare changes in the probability of selection of women as members of the NAS and AAAS from the 1960s to today, controlling for publications and citations. In the early years of our sample, women were less likely to be selected as members than men with similar records. By the 1990s, the selection process at both academies was approximately gender-neutral, conditional on publications and citations. In the past 20 years, however, a positive preference for female members has emerged and strengthened in all three fields. Currently, women are 3-15 times more likely to be selected as members of the AAAS and NAS than men with similar publication and citation records.

PNAS BRIEF REPORT | SOCIAL SCIENCES COMPUTER SCIENCES

Gendered citation patterns among the scientific elite

Kristina Lerman[a,1], Yulin Yu[b], Fred Morstatter[a], and Jay Pujara[a]

Edited by Susan Fiske, Princeton University, Princeton, NJ; received April 8, 2022; accepted August 22, 2022

Diversity in science is necessary to improve innovation and increase the capacity of the scientific workforce. Despite decades-long efforts to increase gender diversity, however, women remain a small minority in many fields, especially in senior positions. The dearth of elite women scientists, in turn, leaves fewer women to serve as mentors and role models for young women scientists. To shed light on gender disparities in science, we study prominent scholars who were elected to the National Academy of Sciences. We construct author citation networks that capture the structure of recognition among scholars' peers. We identify gender disparities in the patterns of peer citations and show that these differences are strong enough to accurately predict the scholar's gender. In contrast, we do not observe disparities due to prestige, with few significant differences in the structure of citations of scholars affiliated with high-ranked and low-ranked institutions. These results provide further evidence that a scholar's gender plays a role in the mechanisms of success in science.

gender | bibliometrics | science of science | gender disparities

Gender disparities persist in many fields of science. Despite long-running efforts to increase women's representation in the scientific workforce, they continue to face barriers to advancement. Women are less likely than their male peers to be mentored by eminent faculty (1) and to be hired and promoted (2, 3). Women publish in less prestigious journals (4), have fewer collaborators (5), and are underrepresented among journal reviewers and editors (6), and their papers receive fewer citations (7, 8). The multifaceted gender disparities create a "glass ceiling," an invisible barrier that fundamentally limits professional recognition for even the best women scientists (9). As a result, the share of women in higher academic positions decreases steadily (3), with relatively few becoming full professors or receiving prestigious awards. For example, among physics faculty in 4-y colleges and universities, women represent 23% of assistant professors and 18% of associate professors

BONUS

Survival Analysis

Counts often modeled as time-to-event

Tricky, because cannot ignore *censored* cases

Left-censored: Don't know when time started

Right-censored: Observation ended before event

Ignoring censored cases leads to inferential error

Imagine estimating time-to-PhD: Time in program before dropping out is info about rate

Survival Analysis

Example: Cat adoptions

data(AustinCats)

20-thousand cats

Estimand: Adoption rates of black and non-black cats

Events: (1) adopted or (2) something else

Something else could be: death, escape, **censored**

Austin Cats

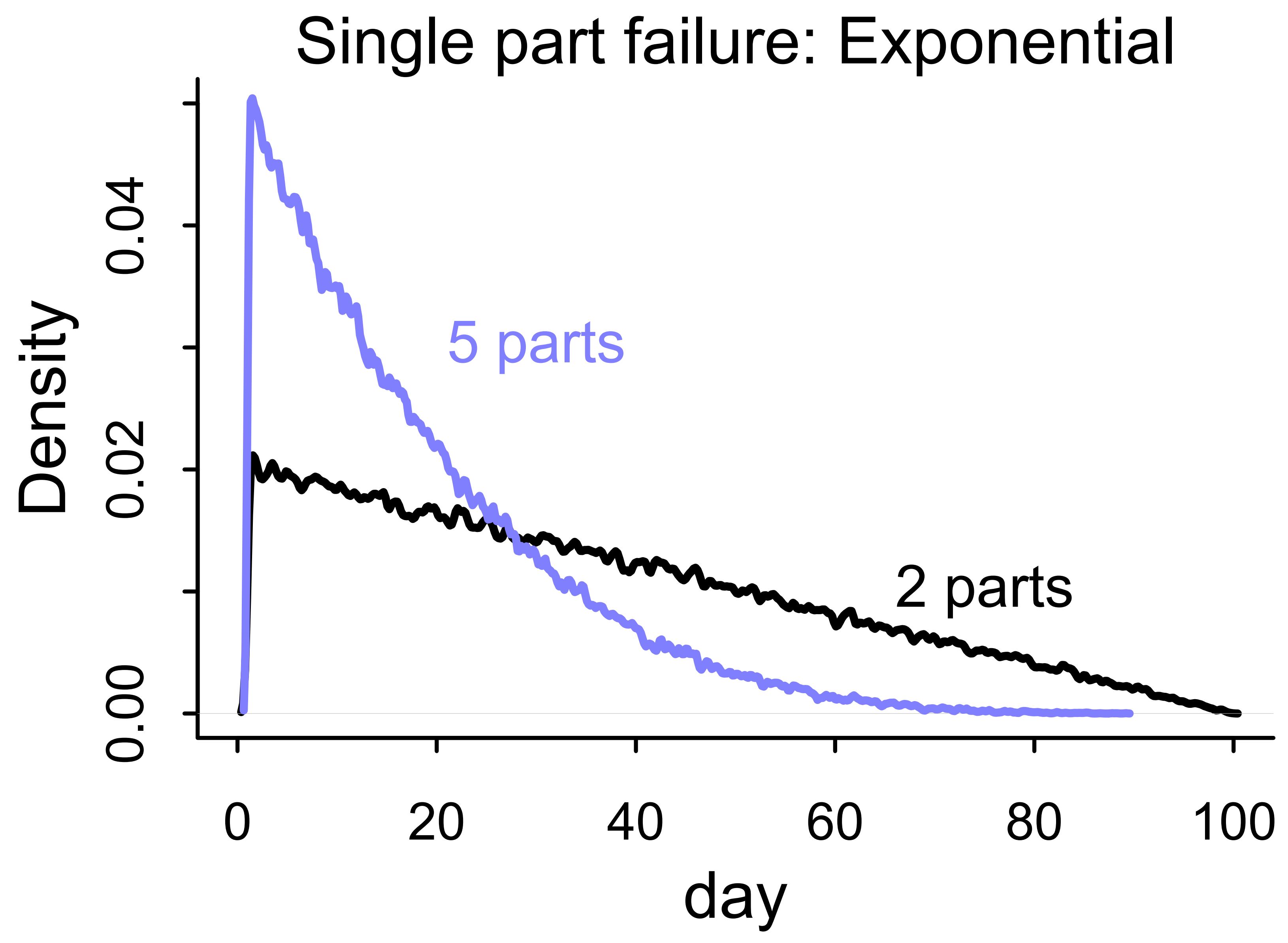
Outcome variable: days_to_event

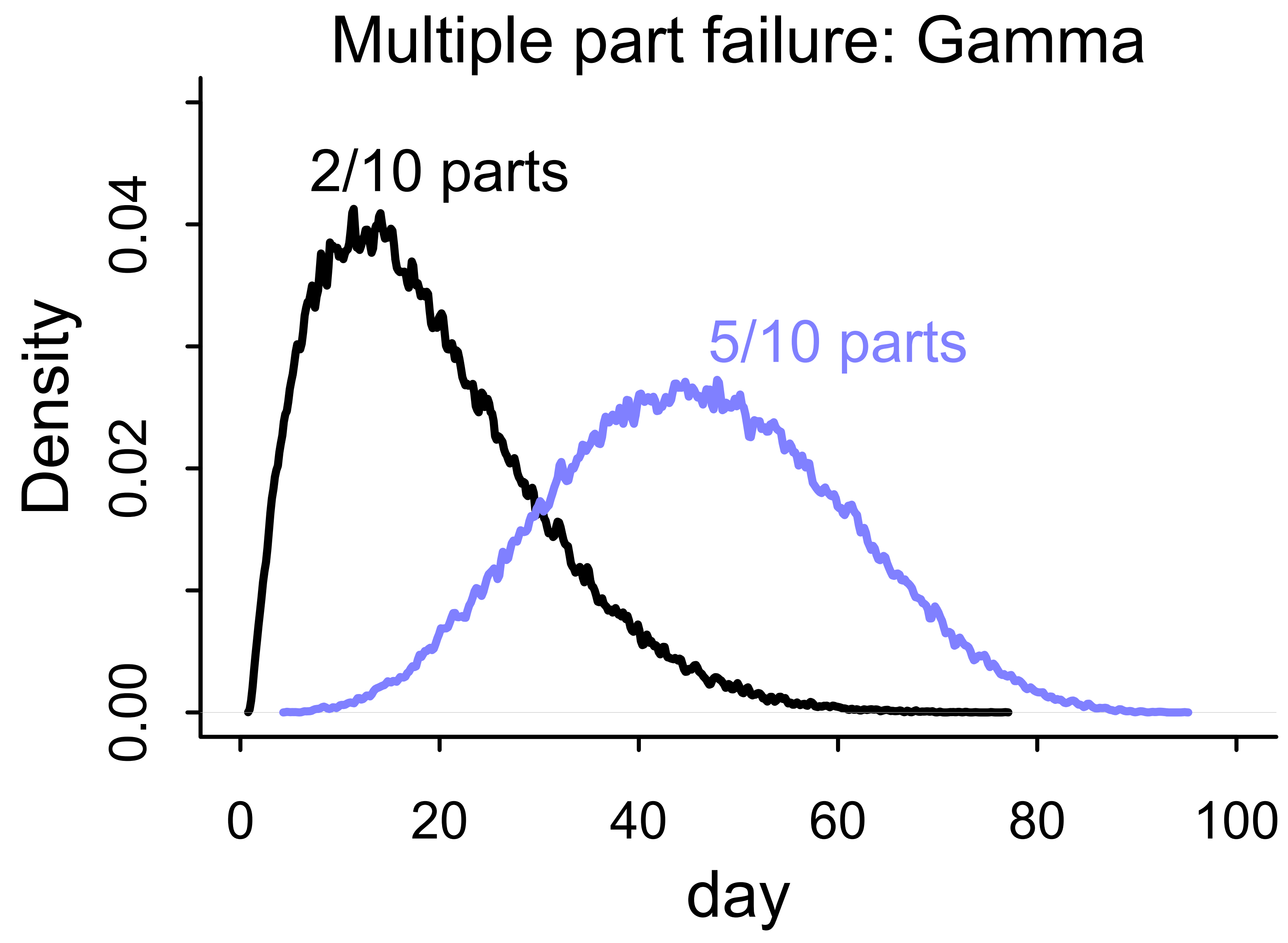
What is a good distribution?

Basic choices: Exponential or gamma

Maximum entropy distributions for waiting times

Generative story: *X* things required before event



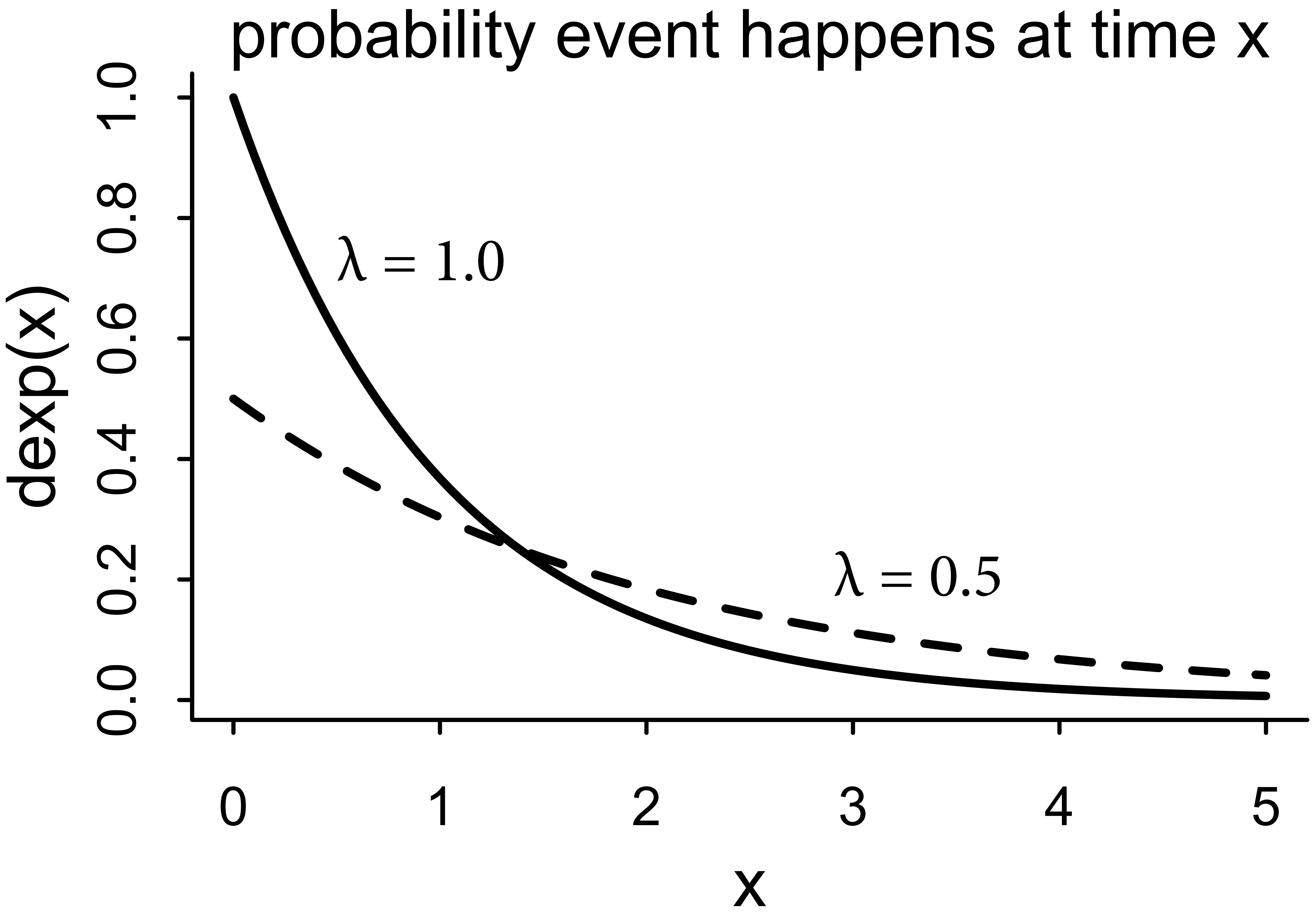


Un-censored observations

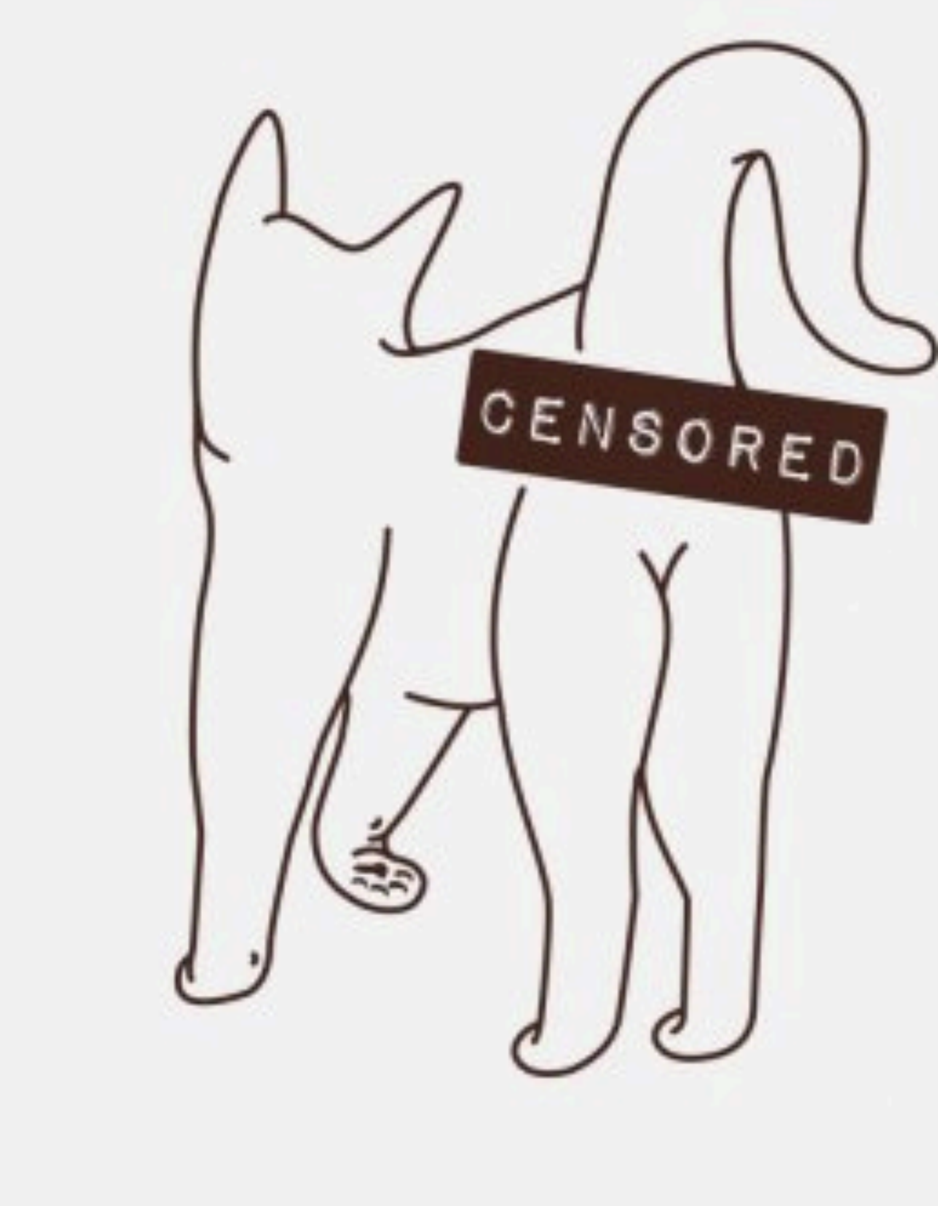
For observed adoptions, just need:

$$D_i \sim \text{Exponential}(\lambda_i)$$

$$p(D_i|\lambda_i) = \lambda_i \exp(-\lambda_i D_i)$$

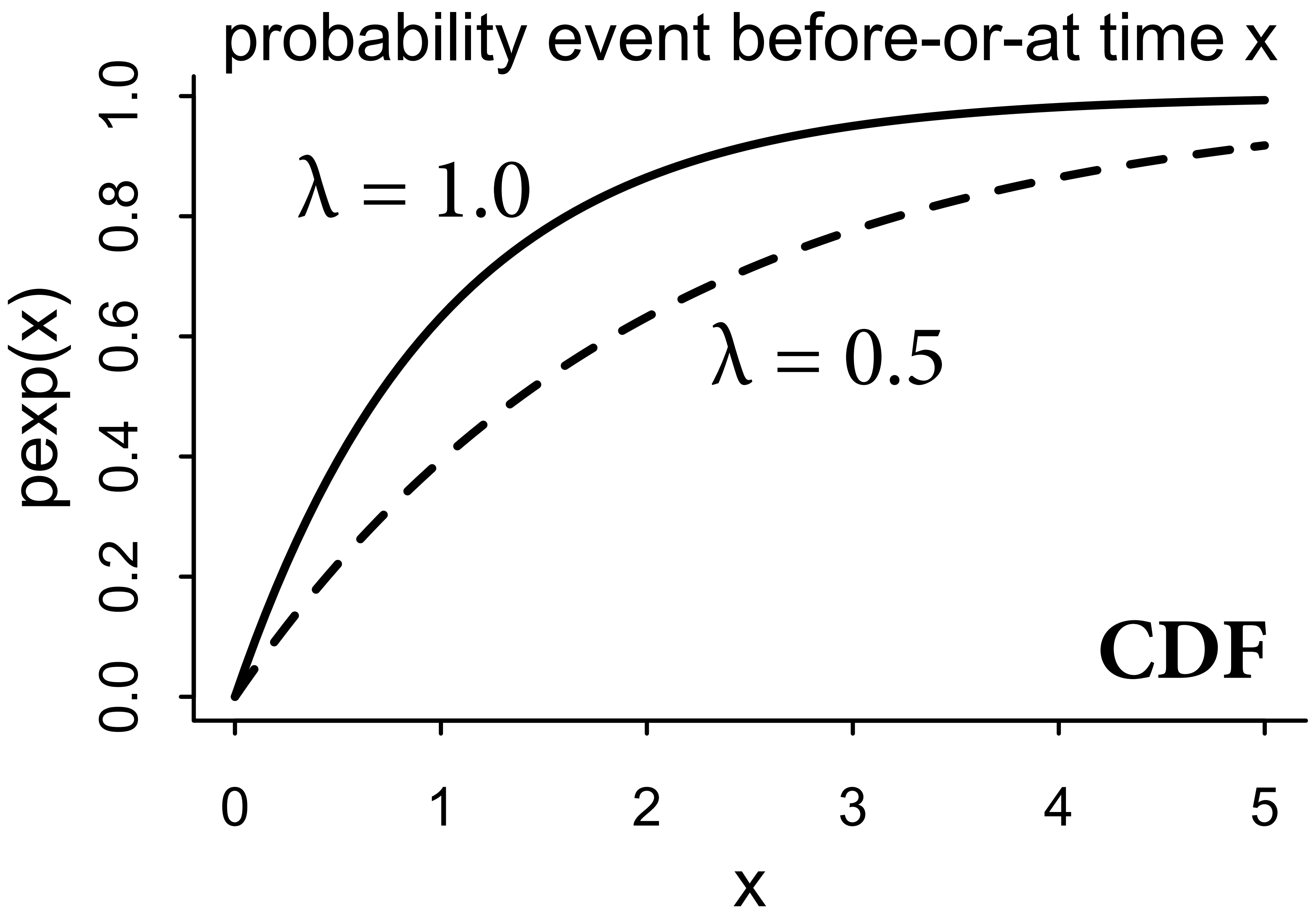


Censored cats



Event happened

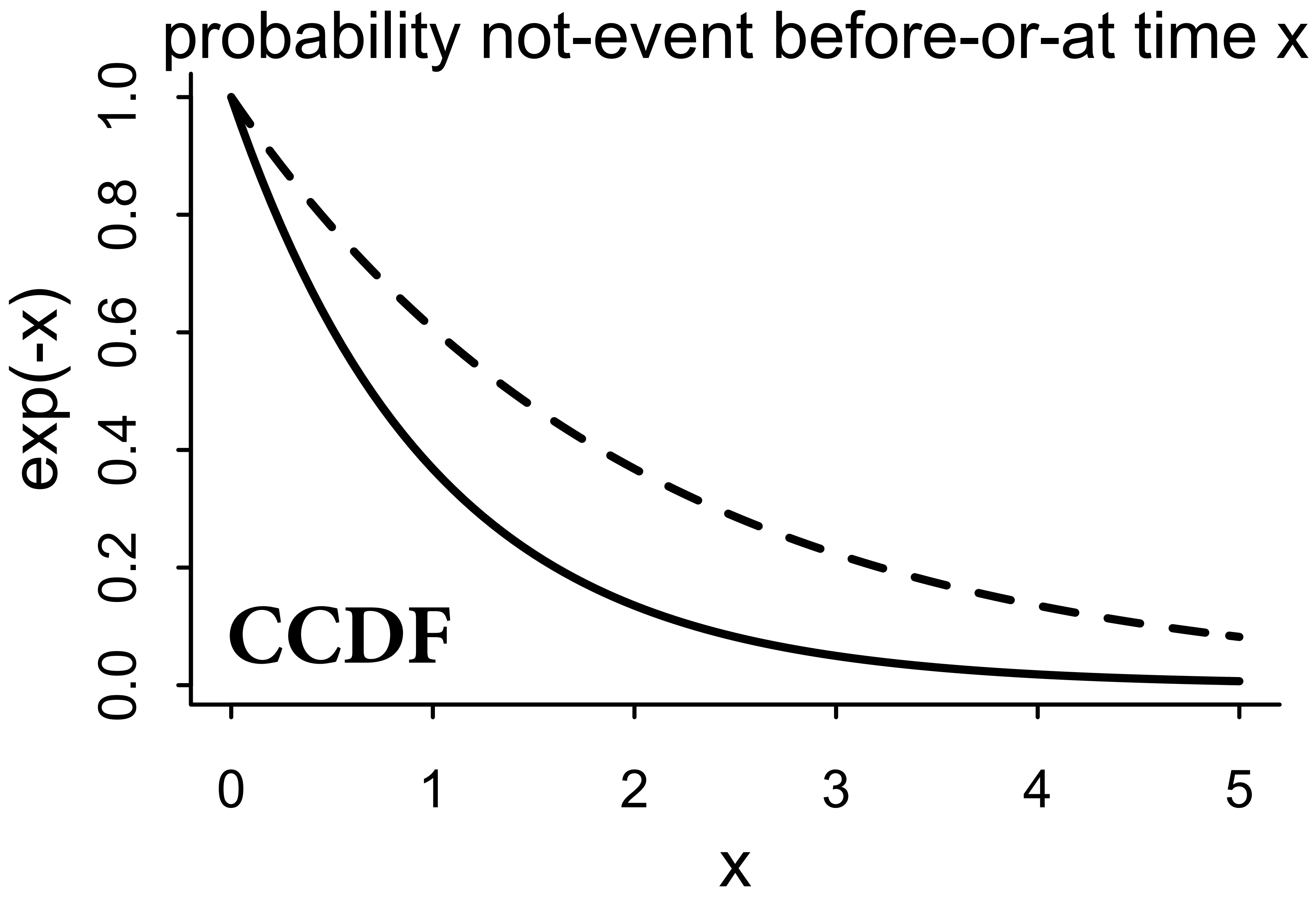
$$\Pr(D_i|\lambda_i) = 1 - \exp(-\lambda_i D_i)$$



Cumulative distribution (CDF)

Event didn't happen yet

$$\Pr(D_i|\lambda_i) = \exp(-\lambda_i D_i)$$



Complementary cumulative distribution (CCDF)

$$
\begin{aligned}
D_i | A_i = 1 &\sim \text{Exponential}(\lambda_i) \\
D_i | A_i = 0 &\sim \text{Exponential-CCDF}(\lambda_i) \\
\lambda_i &= 1/\mu_i \\
\log \mu_i &= \alpha_{\text{CID}[i]}
\end{aligned}
$$

Observed adoptions

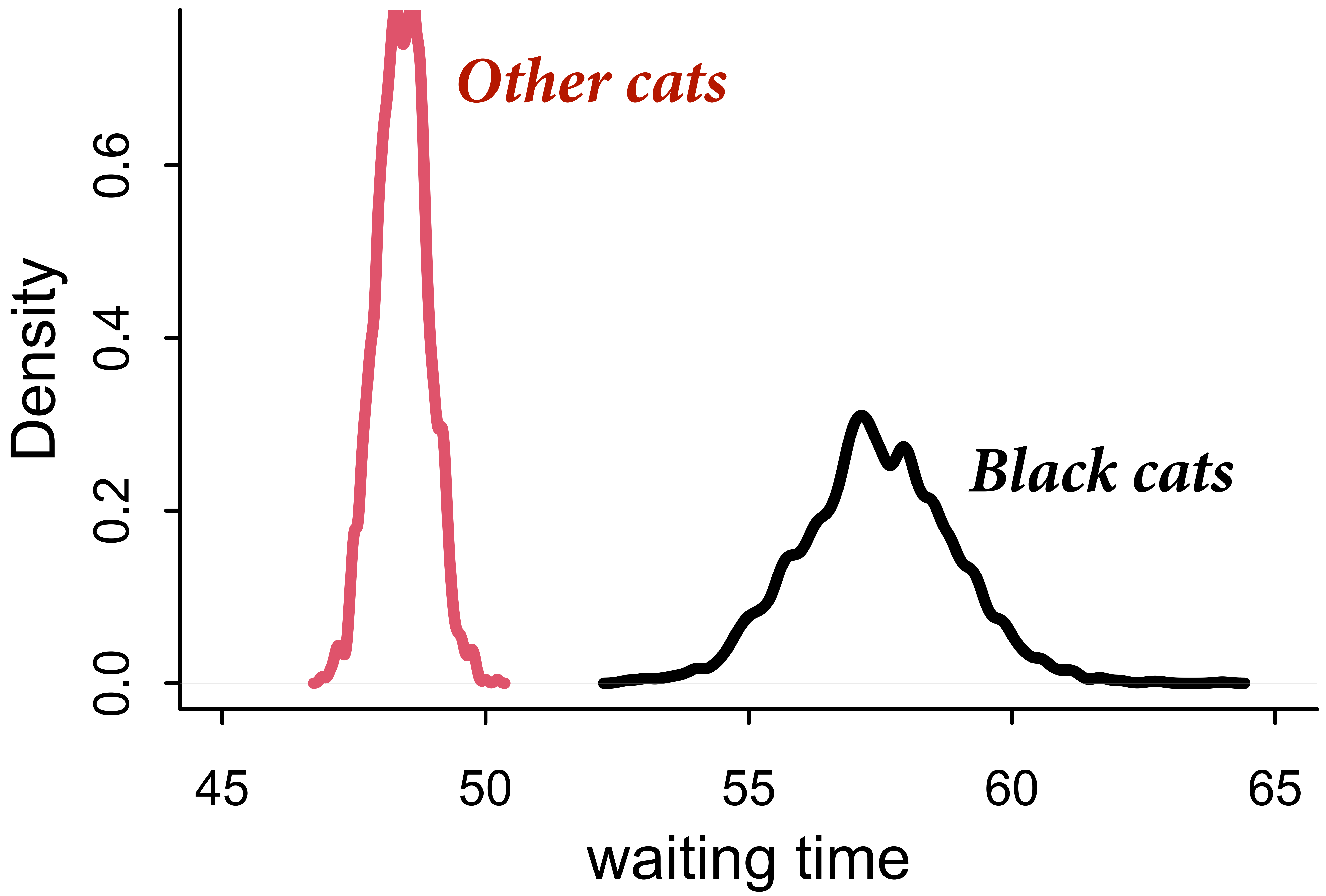
Not-yet-adoptions

$$
\begin{aligned}
D_i | A_i = 1 &\sim \text{Exponential}(\lambda_i) \\
D_i | A_i = 0 &\sim \text{Exponential-CCDF}(\lambda_i) \\
\lambda_i &= 1/\mu_i \\
\log \mu_i &= \alpha_{\text{CID}[i]}
\end{aligned}
$$

log average time to adoption

$$D_i | A_i = 1 \sim \text{Exponential}(\lambda_i)$$
$$D_i | A_i = 0 \sim \text{Exponential-CCDF}(\lambda_i)$$
$$\lambda_i = 1/\mu_i$$
$$\log \mu_i = \alpha_{\text{CID}[i]}$$

```
library(rethinking)
data(AustinCats)
d <- AustinCats

dat <- list(
    days = d$days_to_event,
    adopted = ifelse( d$out_event=="Adoption" , 1 , 0 ),
    color_id = ifelse( d$color=="Black" , 1 , 2 ) )

meow <- ulam(
    alist(
        days|adopted==1 ~ exponential(lambda),
        days|adopted==0 ~ custom(exponential_lccdf(!Y|lambda)),
        lambda <- 1.0/mu,
        log(mu) <- a[color_id],
        a[color_id] ~ normal(0,1)
    ) , data=dat , chains=4 , cores=4 )
```


Other cats
Black cats
Density
0.0
0.2
0.4
0.6
45
50
55
60
65
waiting time

```r
post <- extract.samples(meow)
blank2()

plot(NULL,xlim=c(0,100),ylim=c(0,1),xlab=
"days until adoption",ylab="fraction")

for ( i in 1:50 ) curve(exp(-x/
exp(post$a[i,1])),add=TRUE,col=1)
for ( i in 1:50 ) curve(exp(-x/
exp(post$a[i,2])),add=TRUE,col=2)
```