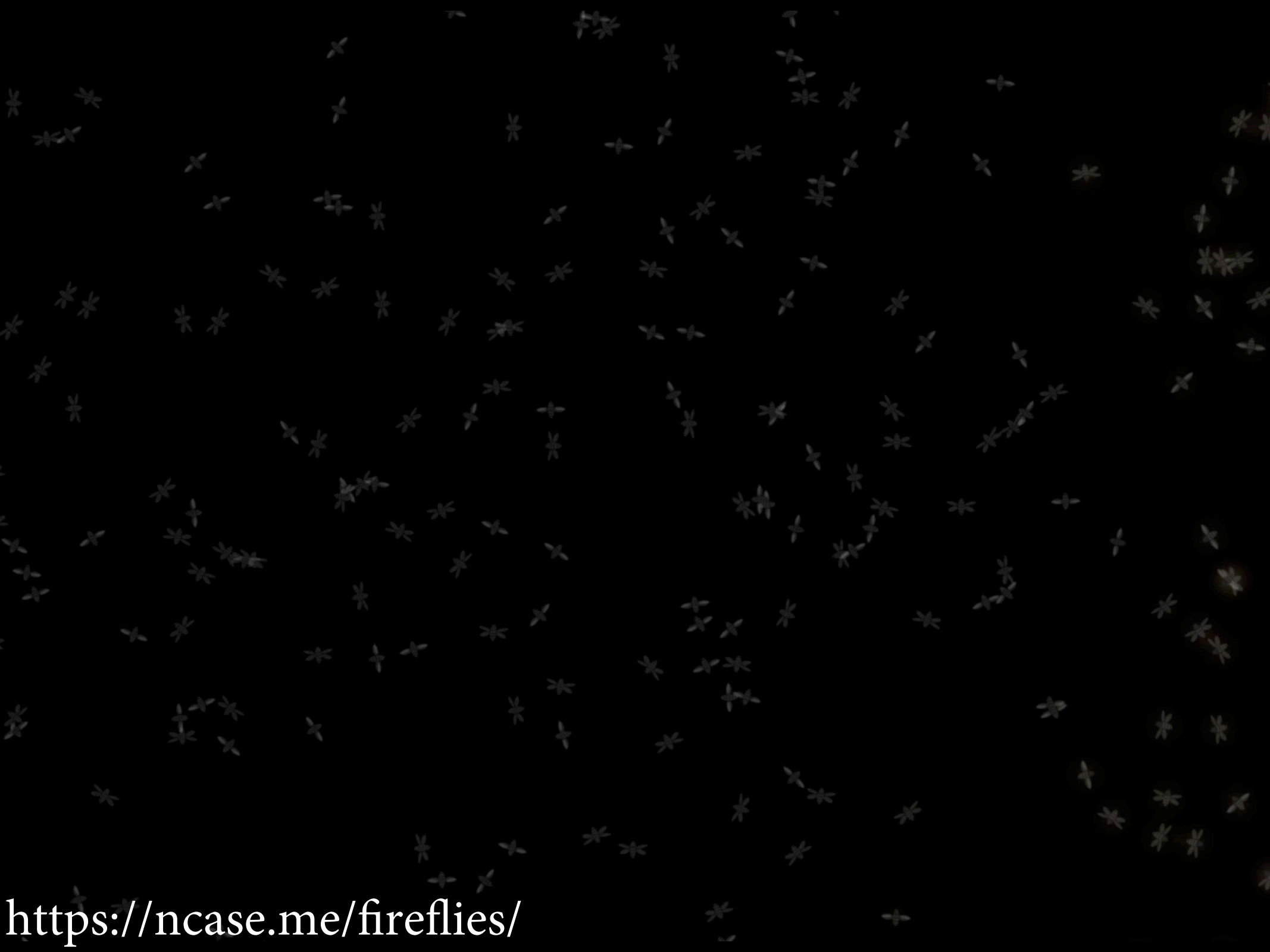
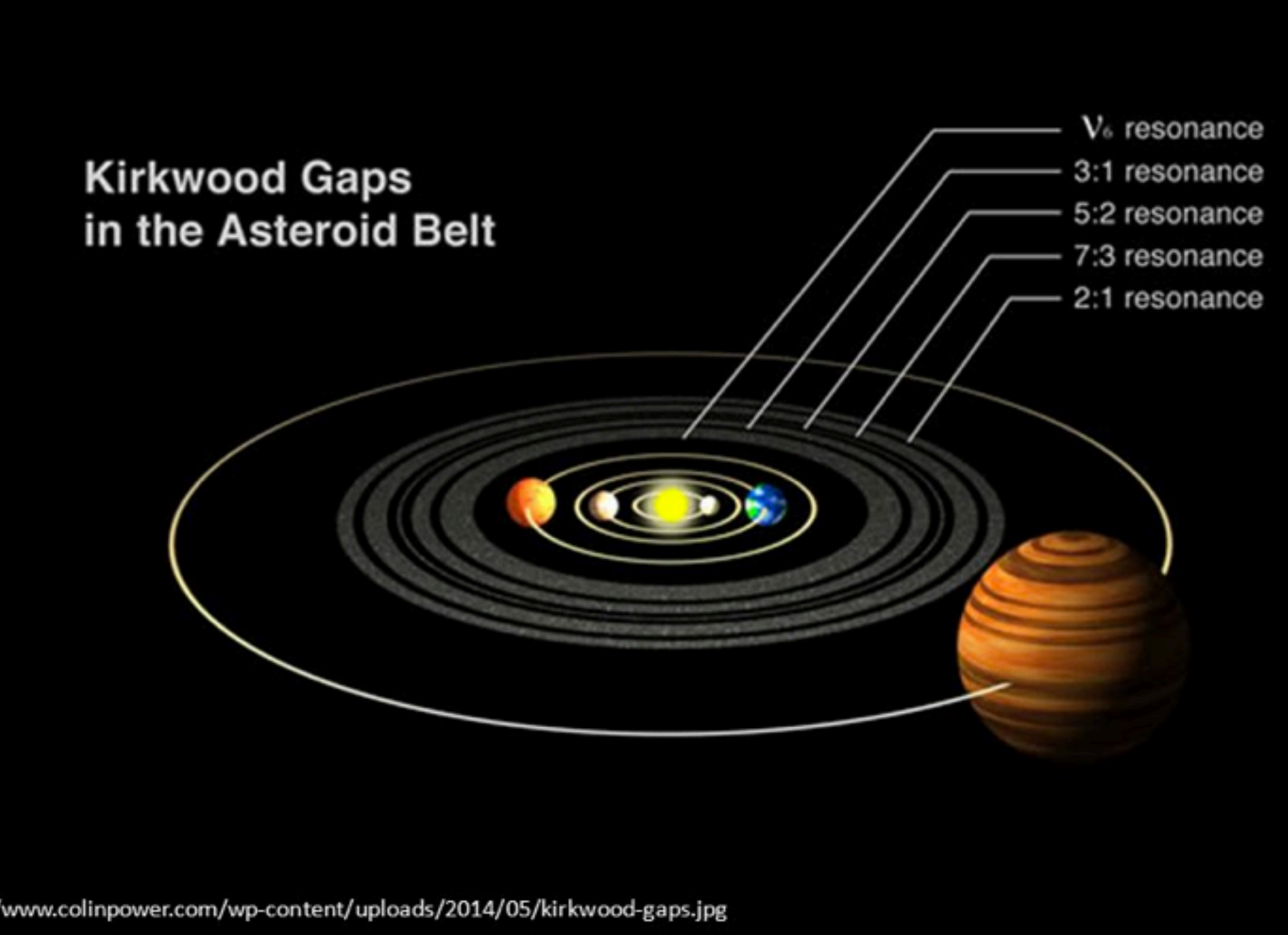
# Statistical Rethinking
# Winter 2019

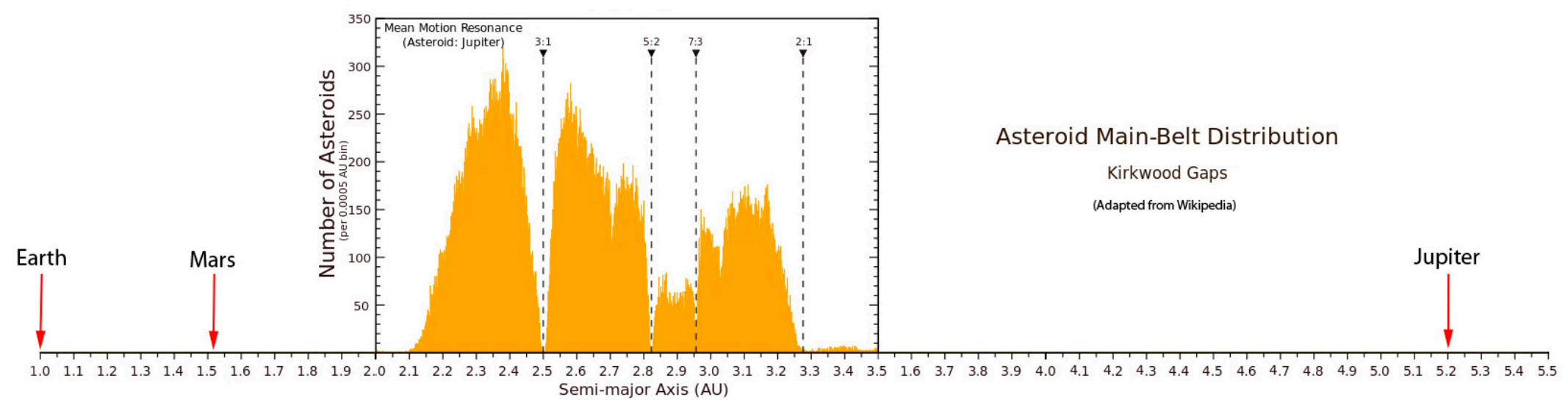
Lecture 12 / Week 6

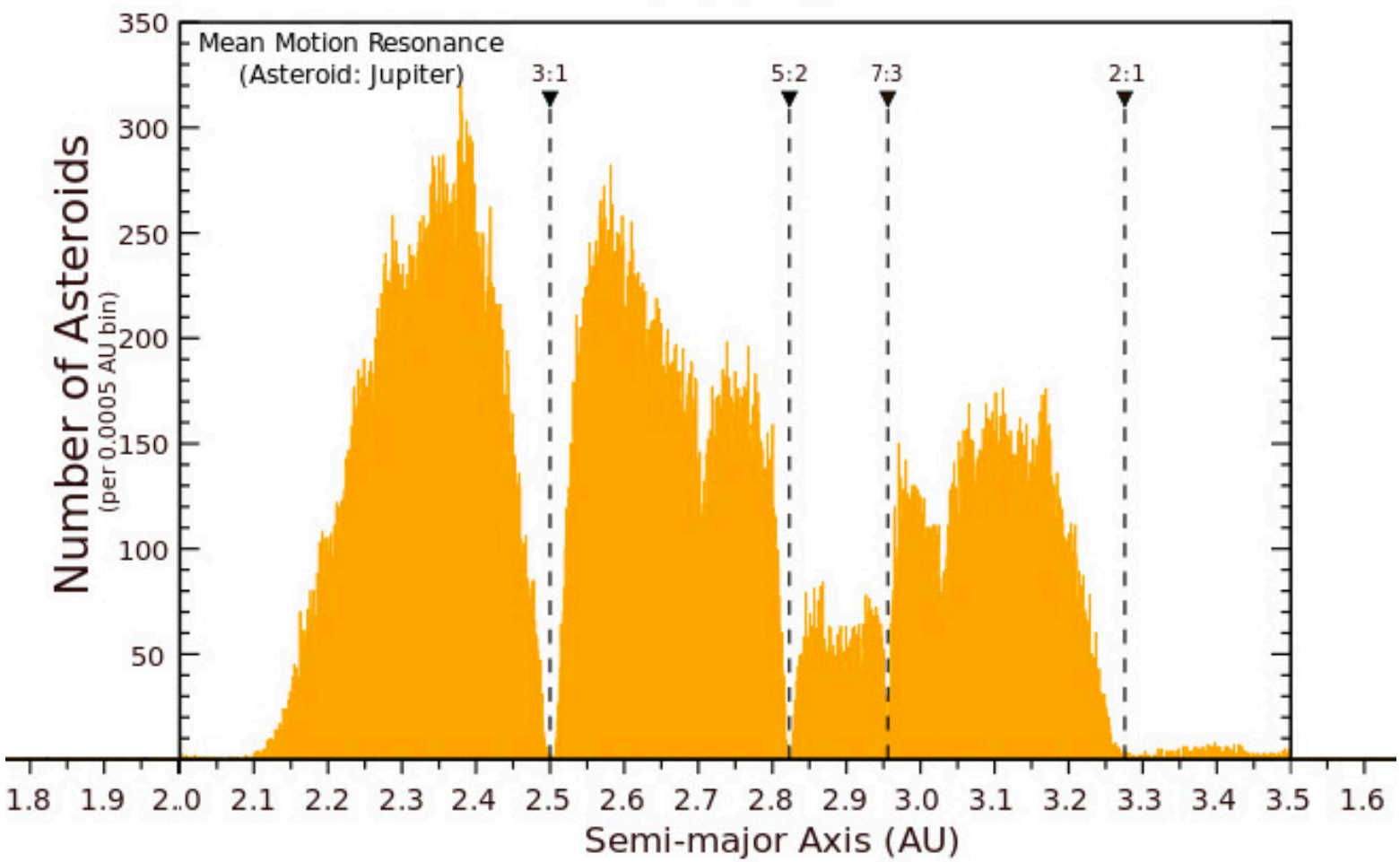
# God Spiked
# The Integers


https://ncase.me/fireflies/




/www.colinpower.com/wp-content/uploads/2014/05/kirkwood-gaps.jpg


Mean Motion Resonance
(Asteroid: Jupiter)
3:1
5:2
7:3
2:1
Number of Asteroids
(per 0.0005 AU bin)
Asteroid Main-Belt Distribution
Kirkwood Gaps
(Adapted from Wikipedia)
Earth
Mars
Jupiter
Semi-major Axis (AU)

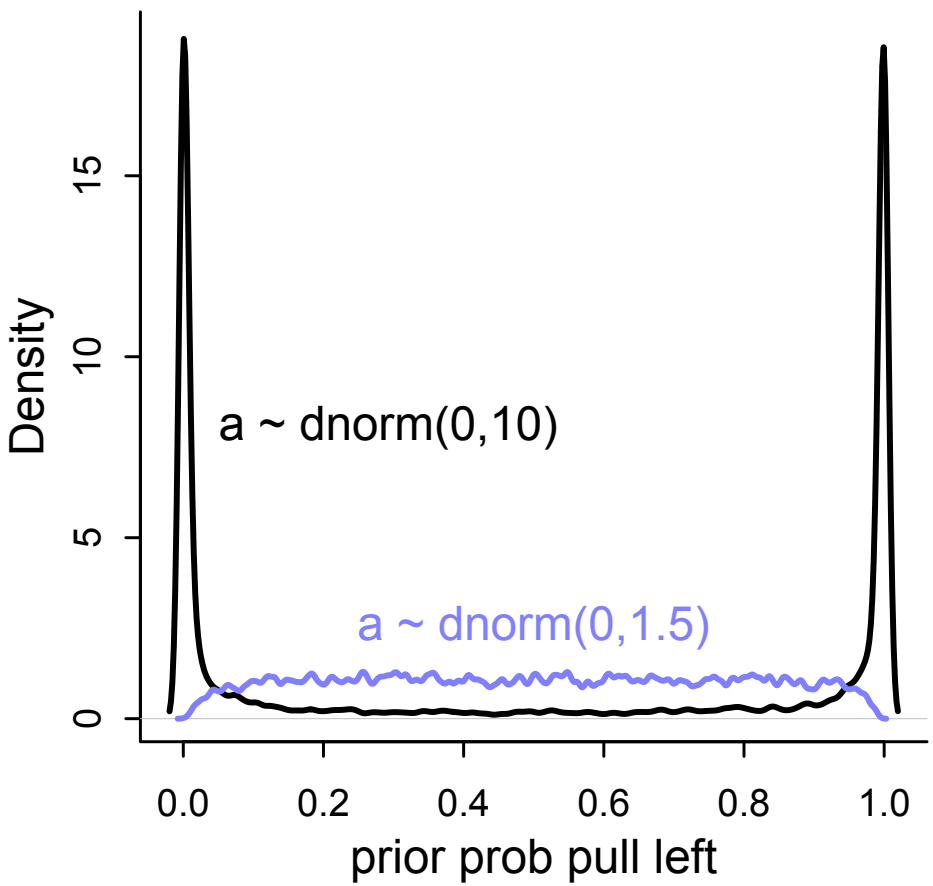

Mean Motion Resonance
(Asteroid: Jupiter)
3:1
5:2
7:3
2:1
Number of Asteroids
(per 0.0005 AU bin)
Semi-major Axis (AU)

# Logit link priors

- What about treatments?

R code 11.7

```
m11.2 <- quap(
    alist(
        pulled_left ~ dbinom( 1 , p ) ,
        logit(p) <- a + b[treatment] ,
        a ~ dnorm( 0 , 1.5 ),
        b[treatment] ~ dnorm( 0 , 10 )
    ) , data=d )
```


Density
0
5
10
15
a ~ dnorm(0,10)
a ~ dnorm(0,1.5)
0.0
0.2
0.4
0.6
0.8
1.0
prior prob pull left

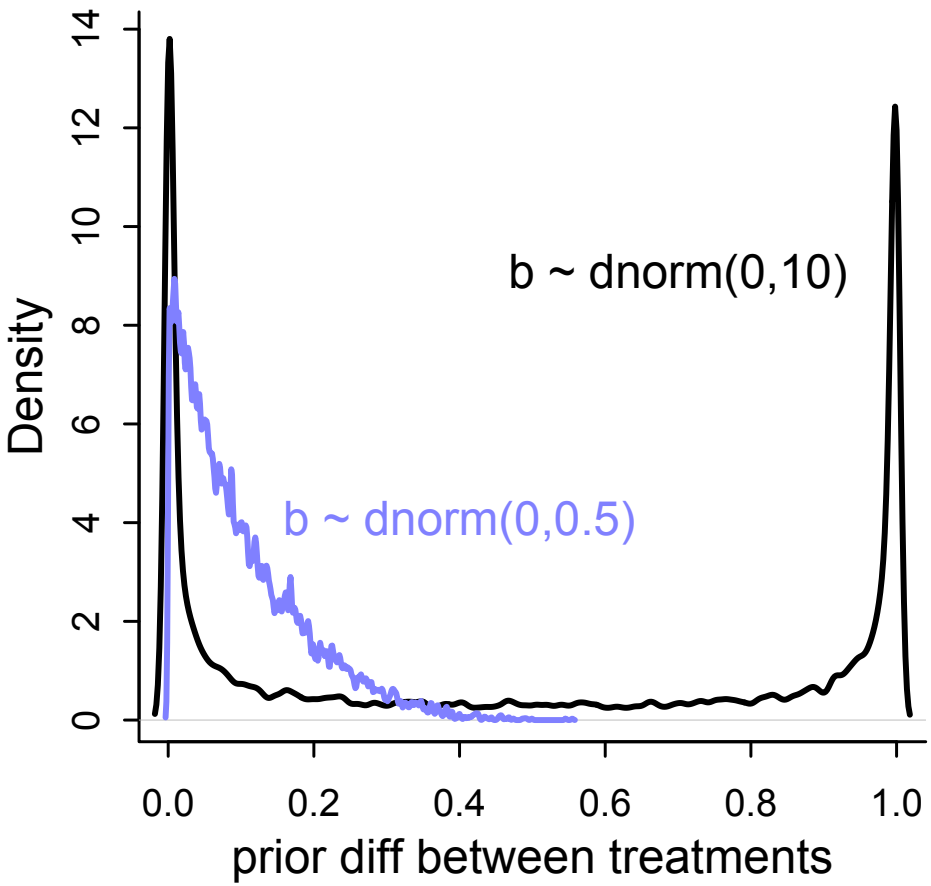

Density
0
2
4
6
8
10
12
14
b ~ dnorm(0,10)
b ~ dnorm(0,0.5)
0.0
0.2
0.4
0.6
0.8
1.0
prior diff between treatments

Figure 11.3

```
# particles in 11-dimensional space
m11.4 <- ulam(
    alist(
        pulled_left ~ dbinom( 1 , p ) ,
        logit(p) <- a[actor] + b[treatment] ,
        a[actor] ~ dnorm( 0 , 1.5 ),
        b[treatment] ~ dnorm( 0 , 0.5 )
    ) ,
    data=dat_list , chains=4 )
precis( m11.4 , depth=2 )
```

| | mean | sd | 5.5% | 94.5% | n_eff | Rhat |
|---|---|---|---|---|---|---|
| a[1] | -0.44 | 0.34 | -0.97 | 0.11 | 736 | 1 |
| a[2] | 3.90 | 0.77 | 2.78 | 5.22 | 921 | 1 |
| a[3] | -0.75 | 0.34 | -1.29 | -0.20 | 886 | 1 |
| a[4] | -0.74 | 0.34 | -1.28 | -0.19 | 770 | 1 |
| a[5] | -0.44 | 0.34 | -0.98 | 0.08 | 832 | 1 |
| a[6] | 0.48 | 0.34 | -0.08 | 1.02 | 854 | 1 |
| a[7] | 1.96 | 0.41 | 1.29 | 2.61 | 847 | 1 |
| b[1] | -0.05 | 0.29 | -0.51 | 0.42 | 781 | 1 |
| b[2] | 0.48 | 0.29 | 0.03 | 0.94 | 657 | 1 |
| b[3] | -0.39 | 0.28 | -0.83 | 0.07 | 669 | 1 |
| b[4] | 0.36 | 0.29 | -0.11 | 0.81 | 732 | 1 |

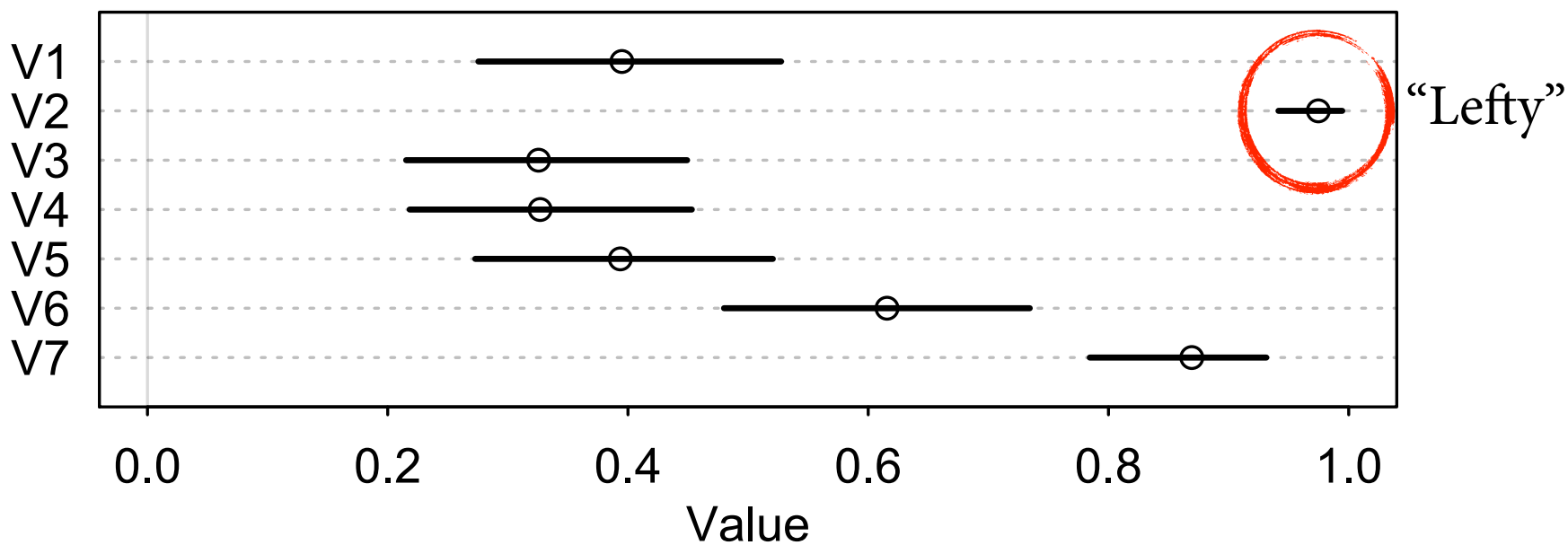
Chimpanzees

Treatments: RN, LN, RP, LP

# Individual differences

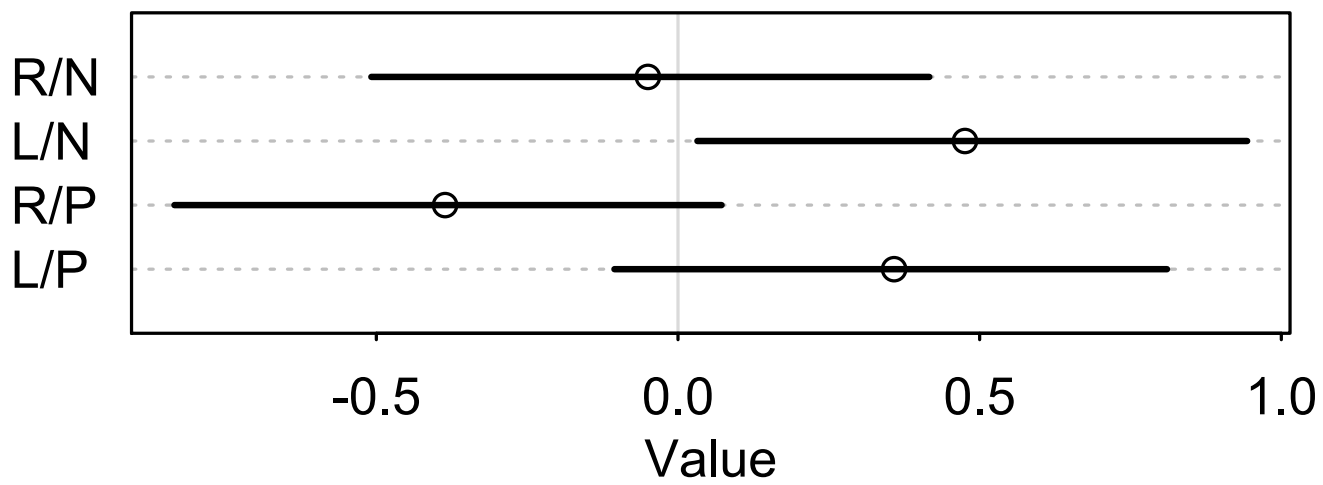
R code 11.11

```
post <- extract.samples(m11.4)
p_left <- inv_logit( post$a )
plot( precis( as.data.frame(p_left) ) , xlim=c(0,1) )
```



# Treatments

```
labs <- c("R/N","L/N","R/P","L/P")
plot( precis( m11.4 , depth=2 , pars="b" ) , labels=labs )
```



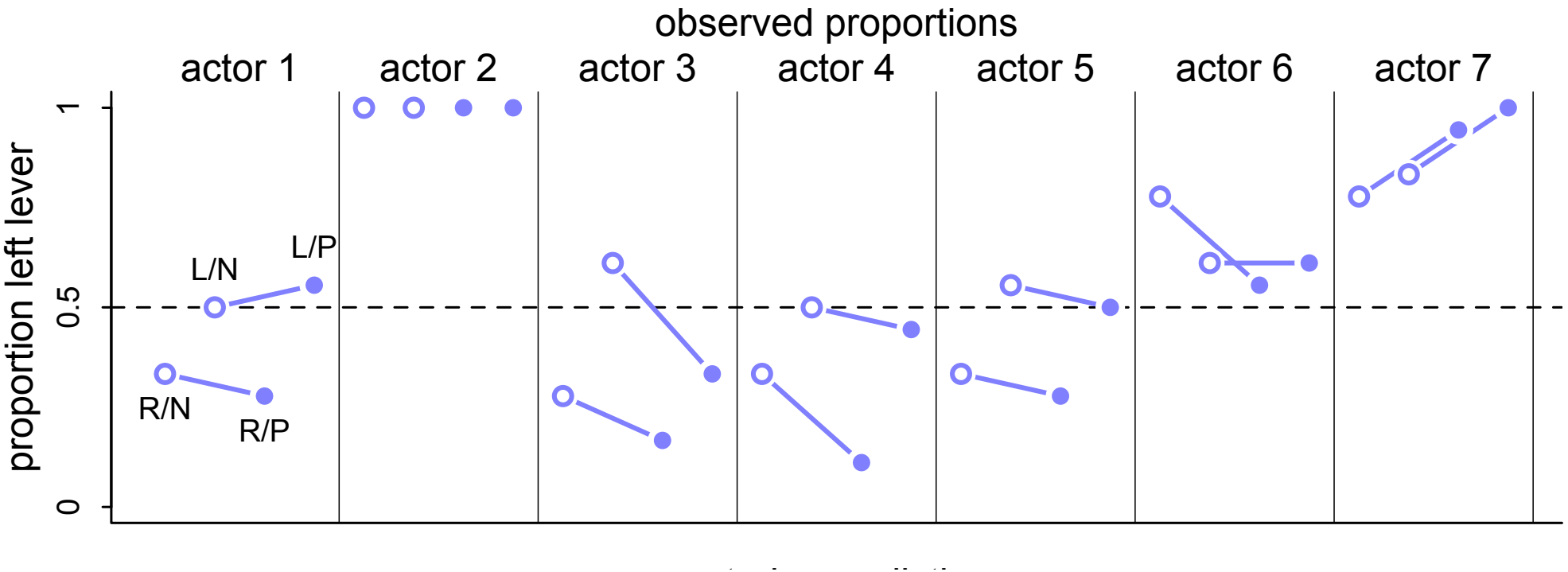

observed proportions
actor 1
actor 2
actor 3
actor 4
actor 5
actor 6
actor 7
proportion left lever
1
0.5
0
L/N
L/P
R/N
R/P

Figure 11.4

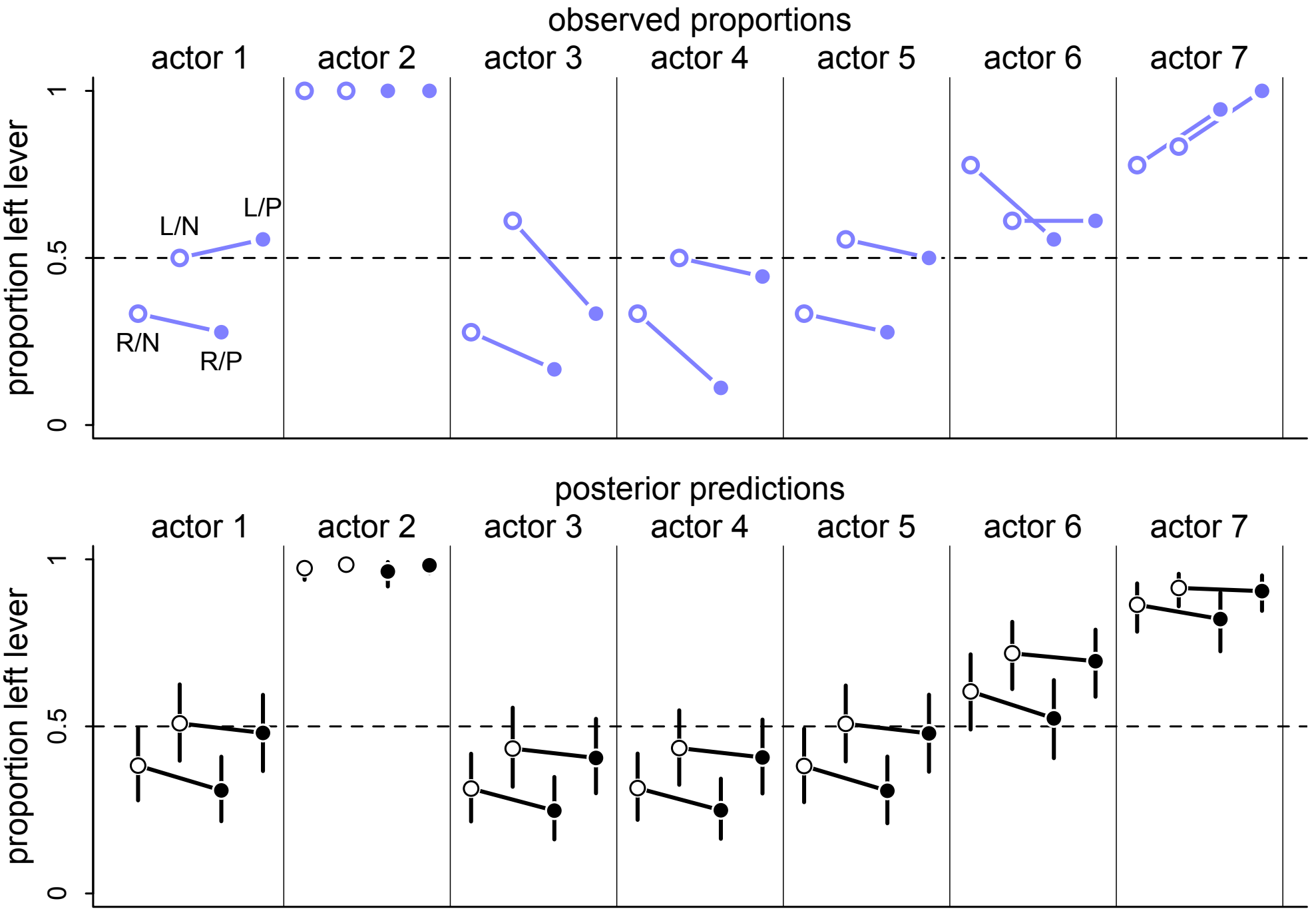

observed proportions
actor 1
actor 2
actor 3
actor 4
actor 5
actor 6
actor 7
proportion left lever
0
0.5
1
L/N
L/P
R/N
R/P
posterior predictions
actor 1
actor 2
actor 3
actor 4
actor 5
actor 6
actor 7
proportion left lever
0
0.5
1

Figure 11.4

# Comparing no-interaction

```
m11.5 <- ulam(
    alist(
        pulled_left ~ dbinom( 1 , p ) ,
        logit(p) <- a[actor] + bs[side] + bc[cond] ,
        a[actor] ~ dnorm( 0 , 1.5 ),
        bs[side] ~ dnorm( 0 , 0.5 ),
        bc[cond] ~ dnorm( 0 , 0.5 )
    ) ,
    data=dat_list2 , chains=4 , log_lik=TRUE )
```

R code 11.19

```
compare( m11.5 , m11.4 , func=LOO )
```

```
        LOO pLOO dLOO weight    SE  dSE
m11.5 531.2  7.9  0.0   0.66 19.17   NA
m11.4 532.6  8.7  1.4   0.34 19.01 1.28
```

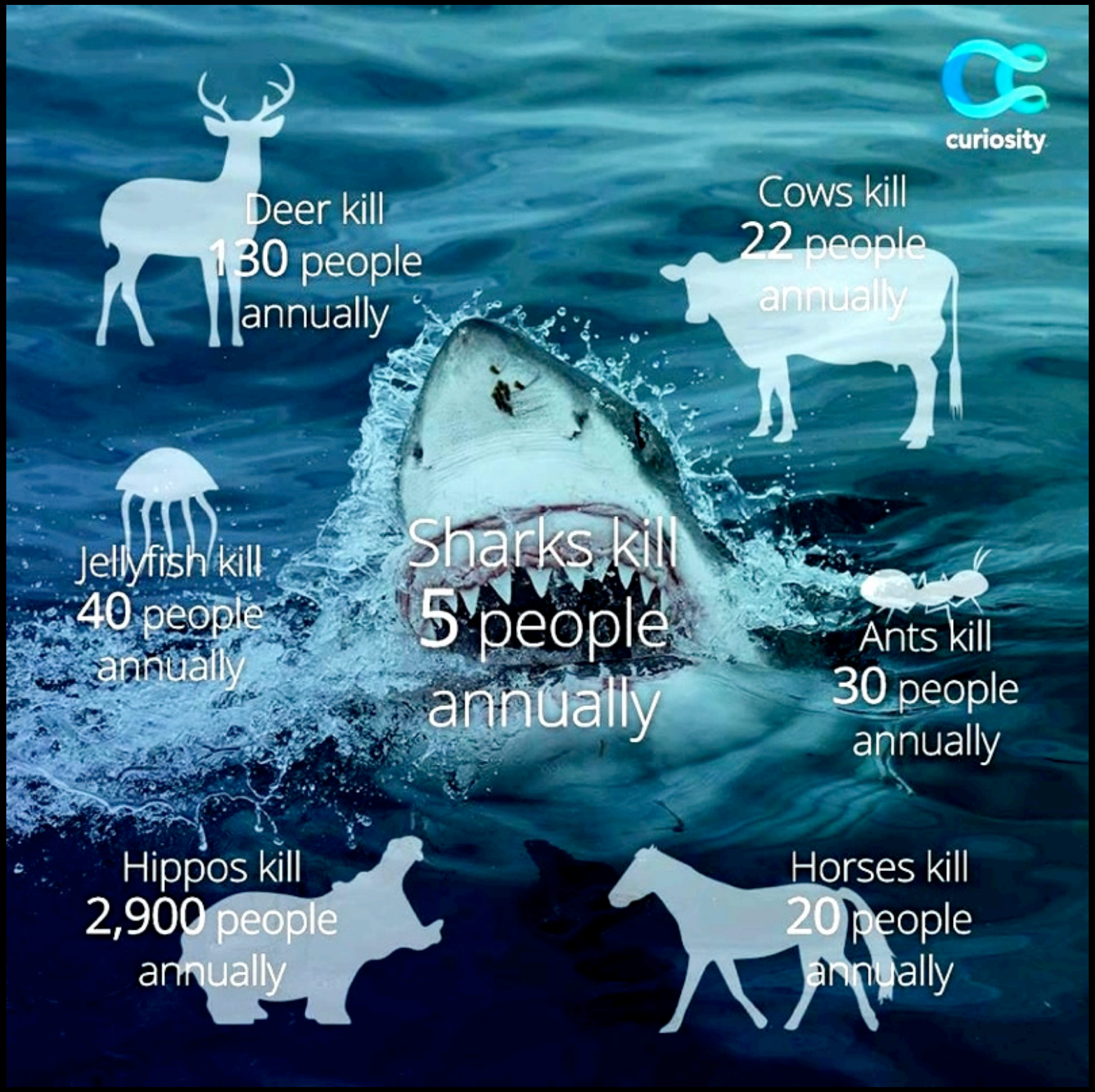
# Relative and absolute effects

- Parameters on *relative* effect scale
- Predictions on *absolute* effect scale
- Proportional odds: Relative effect measure

R code 11.22

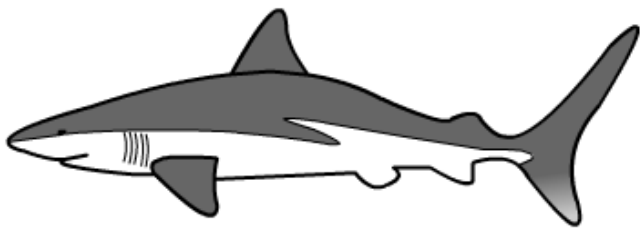
```
post <- extract.samples(m11.4)
mean( exp(post$b[,4]-post$b[,2]) )
```

```
[1] 0.9206479
```


curiosity
Deer kill
130 people
annually
Cows kill
22 people
annually
Jellyfish kill
40 people
annually
Sharks kill
5 people
annually
Ants kill
30 people
annually
Hippos kill
2,900 people
annually
Horses kill
20 people
annually

# Relative and absolute effects

- Parameters on *relative* effect scale
- Predictions on *absolute* effect scale
- Using relative effects may exaggerate importance of predictor
  - Good for scaring people, getting published
  - Not so good for public health, scientific progress
  - But needed for causal inference



*relative shark*

*absolute penguin*

# Risk communication

- Many people mistake relative risk for absolute risk
- Example:
  - 1/1000 women develop blood clots
  - 3/1000 women on birth control develop blood clots
  - => 200% increase in blood clots!
  - Change in probability is only 0.002
  - Pregnancy much more dangerous than blood clots

# Aggregated Binomial

R code 11.28

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

- Numbers accepted/rejected to 6 PhD programs at UC Berkeley (largest depts in 1973)
- Evidence of gender discrimination? Dean was afraid of lawsuit.
- Call in the statisticians!

# UCB admissions

R code 11.28

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

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

# Trials vary by row

$$
\begin{aligned}
A_i &\sim \text{Binomial}(N_i, p_i) \\
\text{logit}(p_i) &= \alpha_{\text{GID}[i]} \\
\alpha_j &\sim \text{Normal}(0, 1.5)
\end{aligned}
$$

```
d$gid <- ifelse( d$applicant.gender=="male" , 1 , 2 )
m11.7 <- quap(
    alist(
        admit ~ dbinom( applications , p ) ,
        logit(p) <- a[gid] ,
        a[gid] ~ dnorm( 0 , 1.5 )
    ) , data=d )
precis( m11.7 , depth=2 )
```

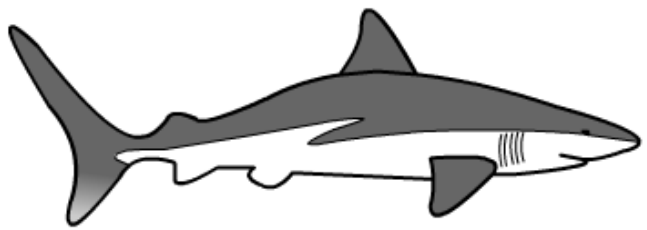
```
      mean   sd  5.5% 94.5%
a[1] -0.22 0.04 -0.28 -0.16
a[2] -0.83 0.05 -0.91 -0.75
```

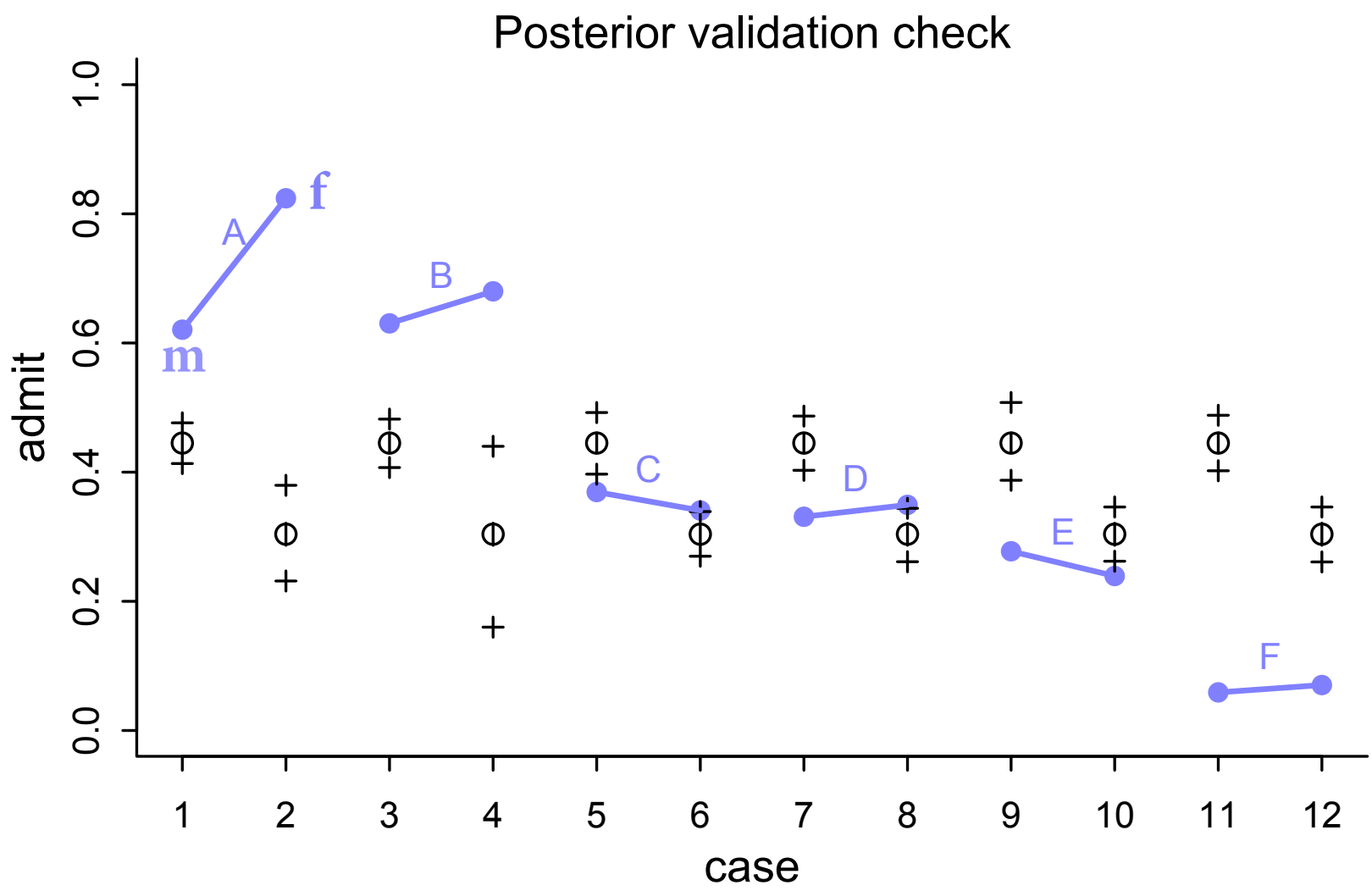
# Posterior contrast

- Compute the contrast between genders
- On both logit (shark) and prob (penguin) scales

```
post <- extract.samples(m11.7)
diff_a <- post$a[,1] - post$a[,2]
diff_p <- inv_logit(post$a[,1]) - inv_logit(post$a[,2])
precis( list( diff_a=diff_a , diff_p=diff_p ) )
```

```
'data.frame': 10000 obs. of 2 variables:
       mean   sd 5.5% 94.5%     histogram
diff_a 0.61 0.06 0.51  0.71   ▁▁▁▂▇▇▃▁▁▁
diff_p 0.14 0.01 0.12  0.16 ▁▁▁▂▅▇▇▃▁▁▁▁
```



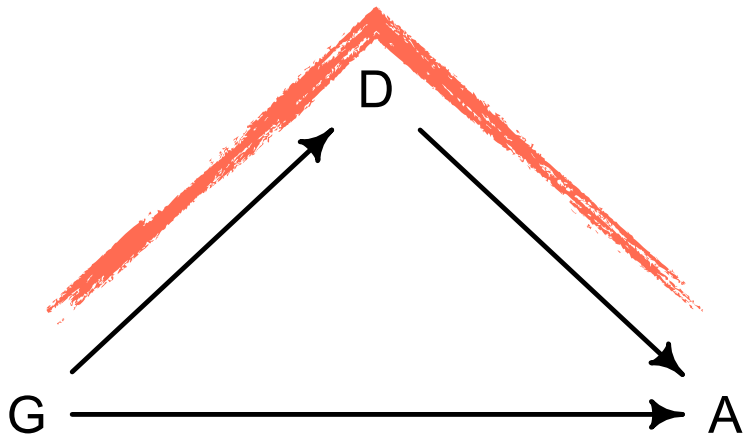



Females admitted more in all but 2 departments!

Figure 11.5

# Backdoor admissions

- Backdoor path through department
- Use unique intercepts to adjust for that path




$$
\begin{aligned}
A_i &\sim \text{Binomial}(N_i, p_i) \\
\text{logit}(p_i) &= \alpha_{\text{GID}[i]} + \delta_{\text{DEPT}[i]} \\
\alpha_j &\sim \text{Normal}(0, 1.5) \\
\delta_k &\sim \text{Normal}(0, 1.5)
\end{aligned}
$$

# Stratification by department

$$
\begin{aligned}
A_i &\sim \text{Binomial}(N_i, p_i) \\
\text{logit}(p_i) &= \alpha_{\text{GID}[i]} \\
\alpha_j &\sim \text{Normal}(0, 1.5)
\end{aligned}
$$

*Stat Q: What are the average probabilities of admission for females and males across all departments?*

*Causal Q: What is the TOTAL influence of gender?*

# Stratification by department

$$A_i \sim \text{Binomial}(N_i, p_i)$$
$$\text{logit}(p_i) = \alpha_{\text{GID}[i]}$$
$$\alpha_j \sim \text{Normal}(0, 1.5)$$

*Stat Q: What are the average probabilities of admission for females and males across all departments?*

*Causal Q: What is the TOTAL influence of gender?*

$$A_i \sim \text{Binomial}(N_i, p_i)$$
$$\text{logit}(p_i) = \alpha_{\text{GID}[i]} + \delta_{\text{DEPT}[i]}$$
$$\alpha_j \sim \text{Normal}(0, 1.5)$$
$$\delta_k \sim \text{Normal}(0, 1.5)$$

*Stat Q: What is the average difference in probability of admission for females and males within departments?*

*Causal Q: What is the DIRECT influence of gender?*

# Stratification by department

```
d$dept_id <- rep(1:6,each=2)
m11.8 <- quap(
    alist(
        admit ~ dbinom( applications , p ) ,
        logit(p) <- a[gid] + delta[dept_id] ,
        a[gid] ~ dnorm( 0 , 1.5 ) ,
        delta[dept_id] ~ dnorm( 0 , 1.5 )
    ) , data=d )
precis( m11.8 , depth=2 )
```

```
           mean   sd  5.5% 94.5%
a[1]     -0.53 0.53 -1.38  0.32
a[2]     -0.43 0.53 -1.28  0.42
delta[1]  1.11 0.54  0.25  1.96
delta[2]  1.06 0.54  0.20  1.92
delta[3] -0.15 0.53 -1.00  0.70
delta[4] -0.18 0.54 -1.04  0.67
delta[5] -0.62 0.54 -1.48  0.23
delta[6] -2.17 0.55 -3.05 -1.30
```

# Again with shark & penguin

- Difference on logit and probability scales

R code 11.33

```
post <- extract.samples(m11.8)
diff_a <- post$a[,1] - post$a[,2]
diff_p <- inv_logit(post$a[,1]) - inv_logit(post$a[,2])
precis( list( diff_a=diff_a , diff_p=diff_p ) )
```

```
'data.frame': 10000 obs. of 2 variables:
        mean   sd  5.5% 94.5%      histogram
diff_a -0.10 0.08 -0.22  0.03 ▁▁▁▁▂▆▆▃▁▁▁▁
diff_p -0.02 0.02 -0.05  0.01    ▁▁▂▆▆▂▁▁
```

# Backdoor admissions

- What happened? Females apply more to most selective departments. So overall rate of admission lower.
- Proportions of m/f applications by department:

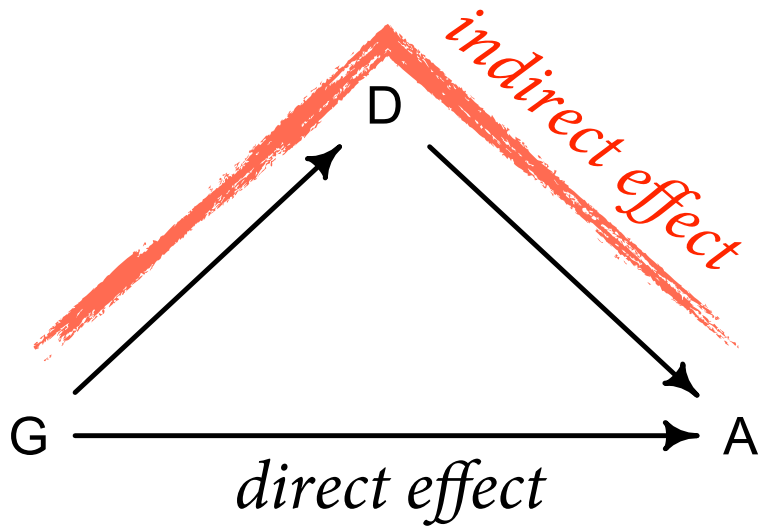
R code 11.34

```
pg <- sapply( 1:6 , function(k)
    d$applications[d$dept_id==k]/sum(d$applications[d$dept_id==k]) )
rownames(pg) <- c("male","female")
colnames(pg) <- unique(d$dept)
round( pg , 2 )
```

```
           A    B    C    D    E    F
male    0.88 0.96 0.35 0.53 0.33 0.52
female 0.12 0.04 0.65 0.47 0.67 0.48
```

# Backdoor admissions

- Careful about casual interpretation
- No evidence for direct path G –> A
- Lots of evidence of indirect path G –> D –> A
- Total causal influence of G still strong
- Still results in disenfranchisement
- But effective intervention very different



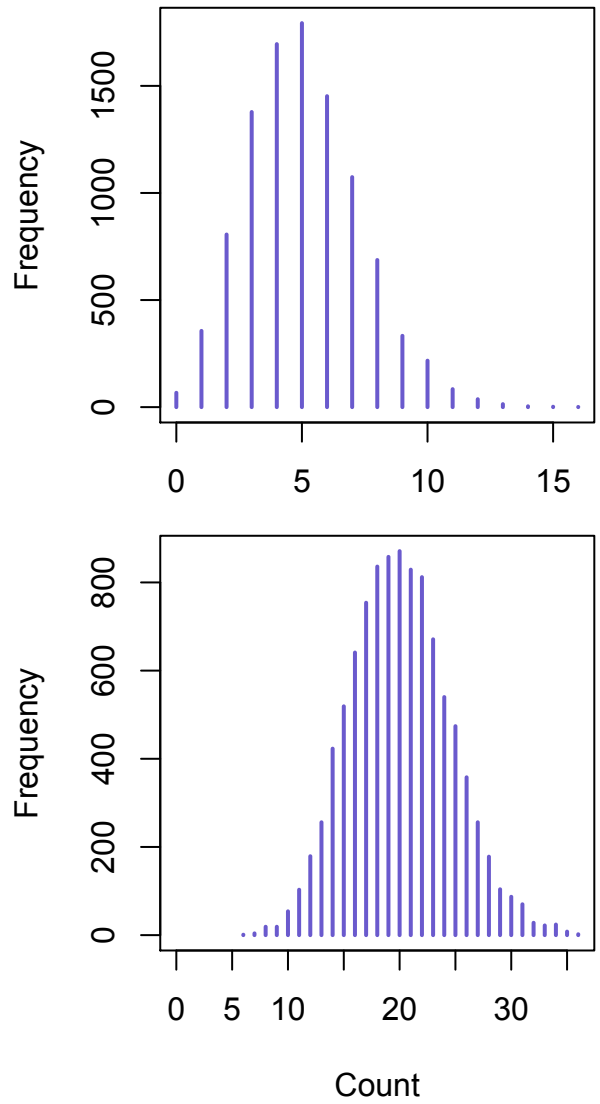
# Poisson GLMs

$$y \sim \text{Poisson}(\lambda)$$

$$\text{E}(y) = \lambda$$

$$\text{var}(y) = \lambda$$

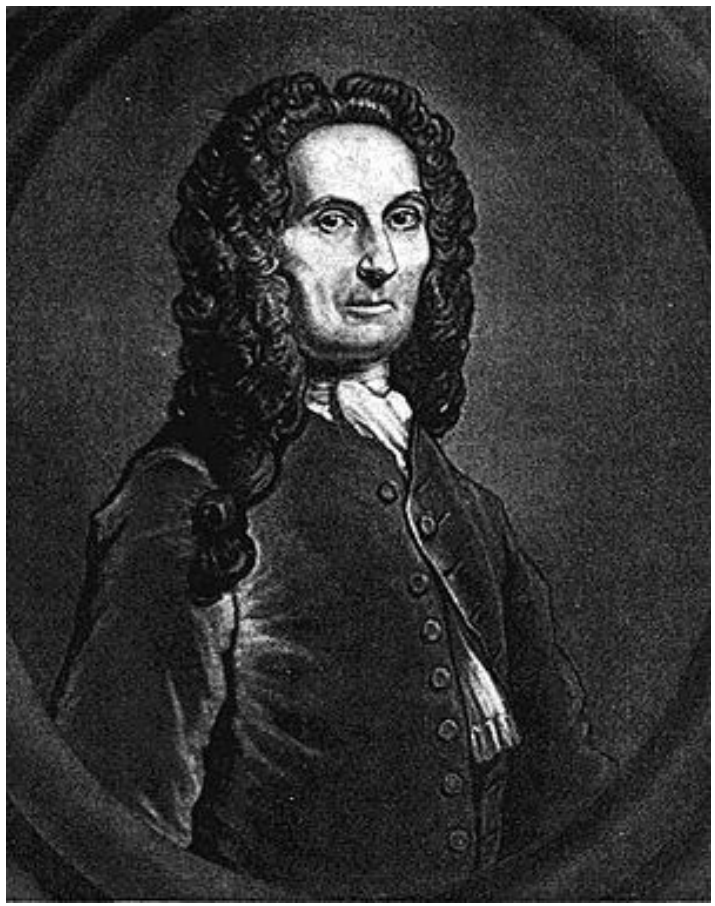
- Counts without upper limit, constant expected value
- Single parameter: events per unit time/distance
- Variance equal to mean



# Poisson GLMs

- Examples: Soccer goals, fission events, photons striking a detector, DNA mutations, soldiers killed by horses

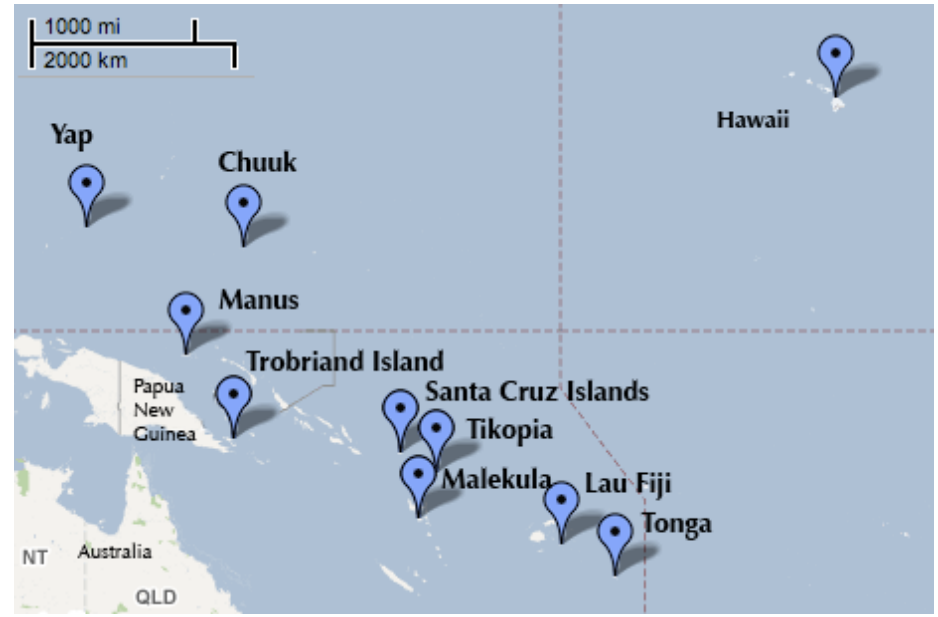
Siméon Denis Poisson (1781–1840)



Abraham de Moivre (1667–1754)

# Oceanic tool complexity

| culture | population | contact | total_tools | mean_TU |
|---|---|---|---|---|
| Malekula | 1100 | low | 13 | 3.2 |
| Tikopia | 1500 | low | 22 | 4.7 |
| Santa Cruz | 3600 | low | 24 | 4.0 |
| Yap | 4791 | high | 43 | 5.0 |
| Lau Fiji | 7400 | high | 33 | 5.0 |
| Trobriand | 8000 | high | 19 | 4.0 |
| Chuuk | 9200 | high | 40 | 3.8 |
| Manus | 13000 | low | 28 | 6.6 |
| Tonga | 17500 | high | 55 | 5.4 |
| Hawaii | 275000 | low | 71 | 6.6 |




(1) Complexity of toolkit proportional to magnitude of population?

(2) Contact with other islands moderates impact?

Dr. Michelle Kline (Simon Fraser U)

# Anatomy of Poisson GLM

total_tools (*outcome*)

expected tools for case $i$

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

log link

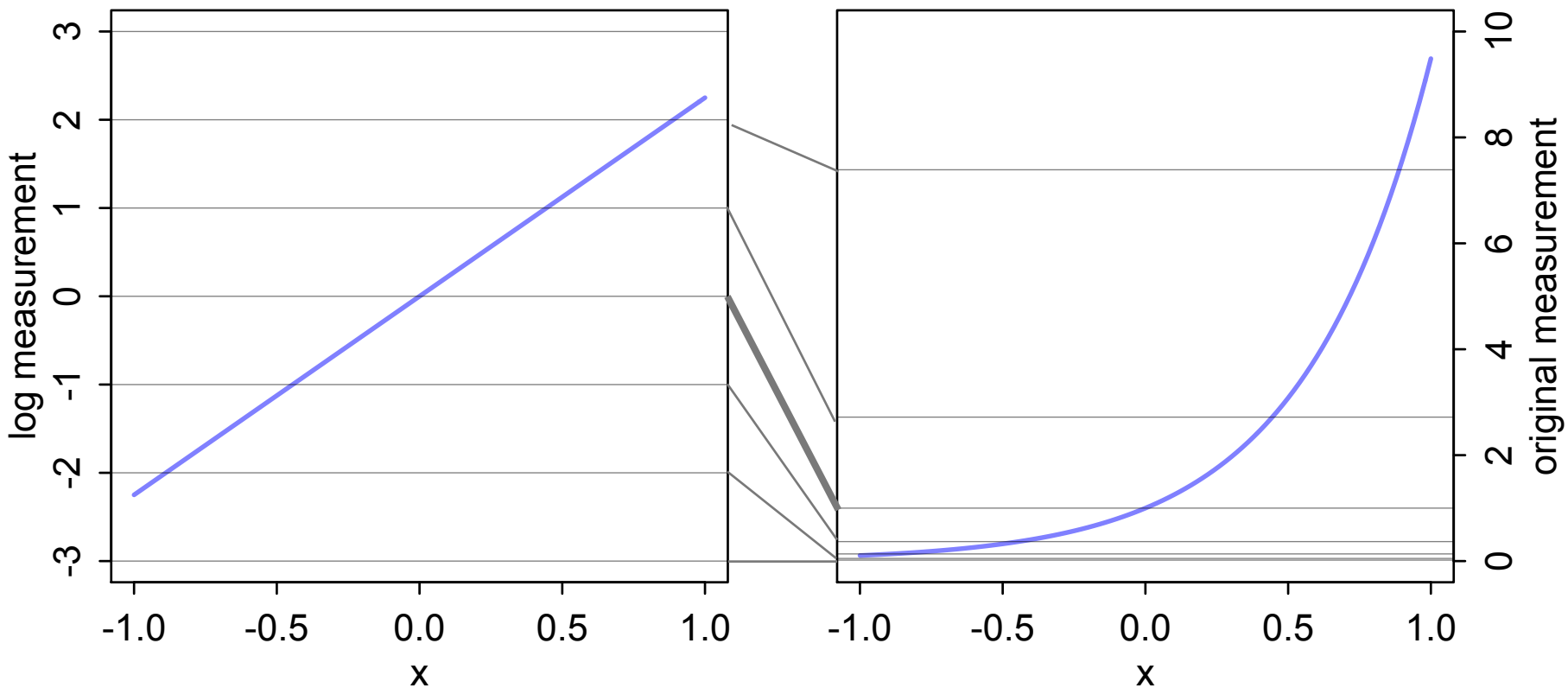
$$\log \lambda_i = \alpha_{\text{CID}[i]} + \beta_{\text{CID}[i]} \log P_i$$

$$\alpha_j \sim \text{to be determined}$$

$$\beta_j \sim \text{to be determined}$$

# Log link

- Goal: Map linear model to positive reals
- Log link maps all negative numbers to [0,1]
- All positive numbers to [1,infinity]



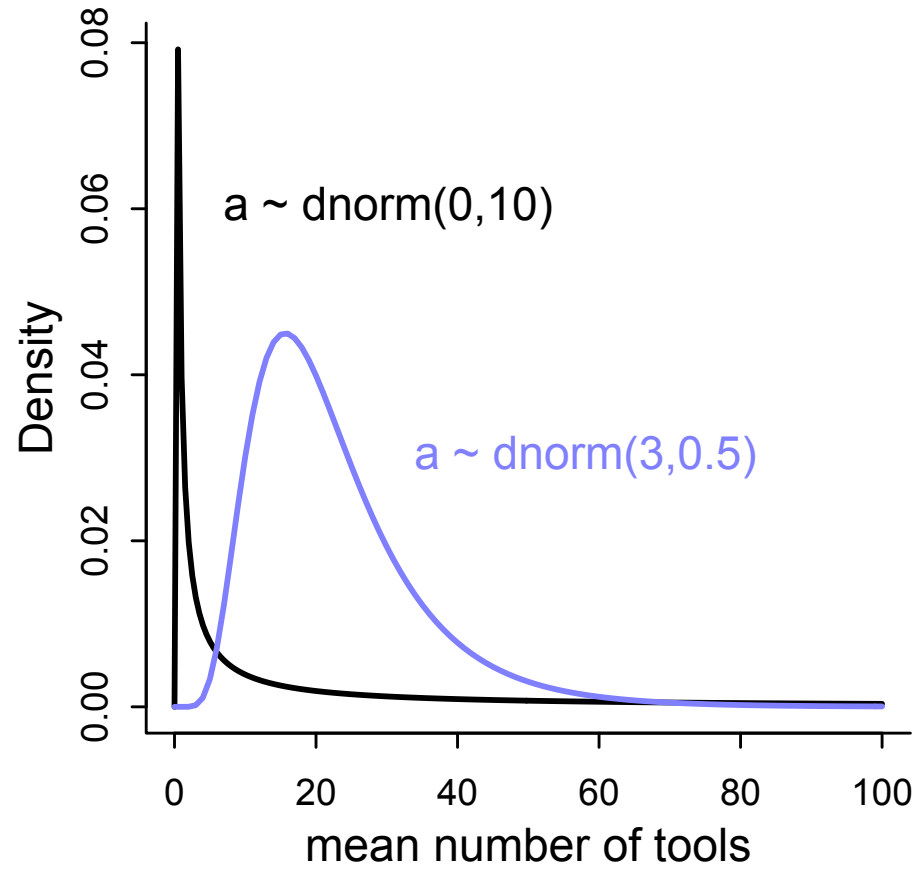
# Priors & the log link

- Log link not intuitive — simulate

$$T_i \sim \text{Poisson}(\lambda_i)$$
$$\log \lambda_i = \alpha$$
$$\alpha \sim \text{Normal}(0, 10)$$

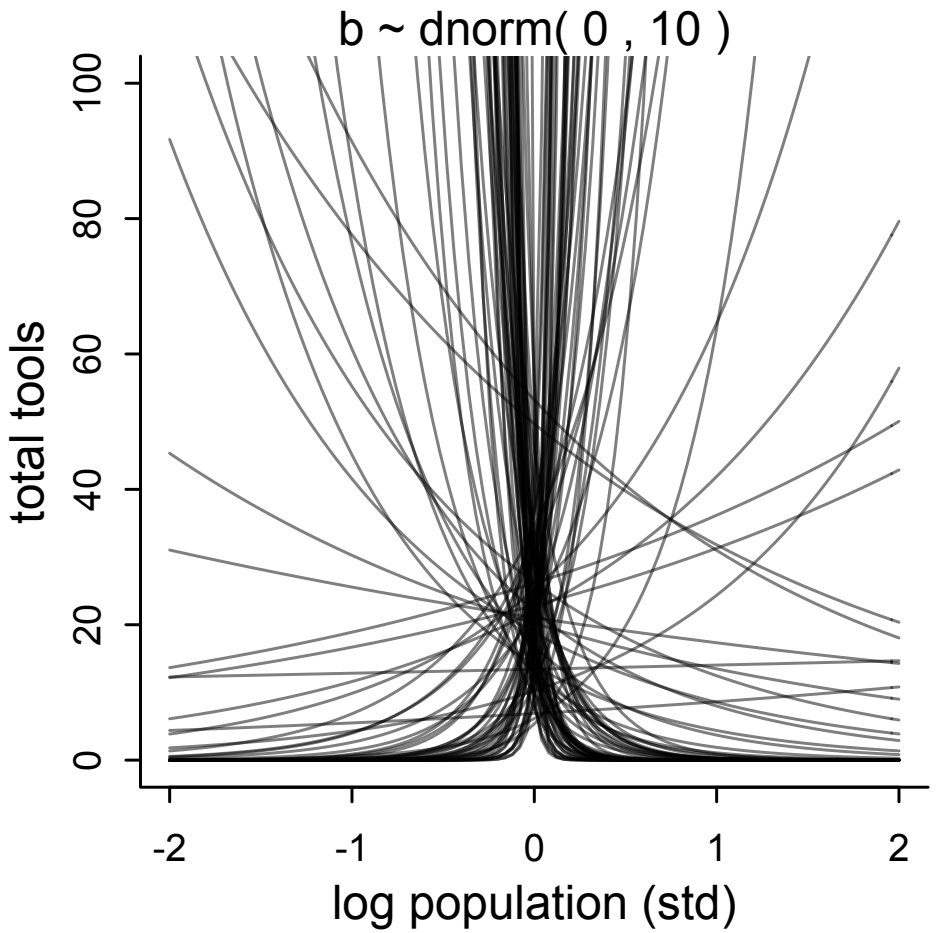
```
a <- rnorm(1e4,0,10)
lambda <- exp(a)
mean( lambda )
```

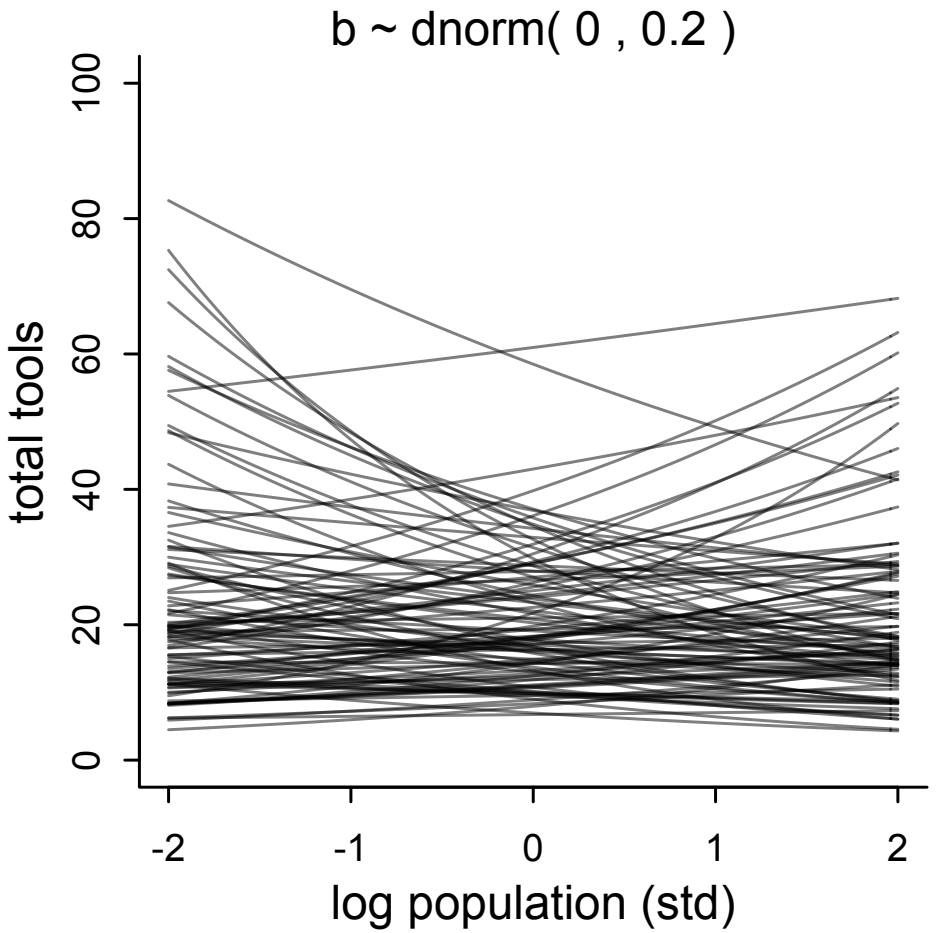
```
[1] 9.622994e+12
```



# Priors & the log link

- Slopes equally unintuitive



# Tools models

R code 11.48

```
dat <- list(
    T = d$total_tools ,
    P = d$P ,
    cid = 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[cid] + b[cid]*P,
        a[cid] ~ dnorm( 3 , 0.5 ),
        b[cid] ~ dnorm( 0 , 0.2 )
    ), data=dat , chains=4 , log_lik=TRUE )
```

# Compare using PSIS-LOO

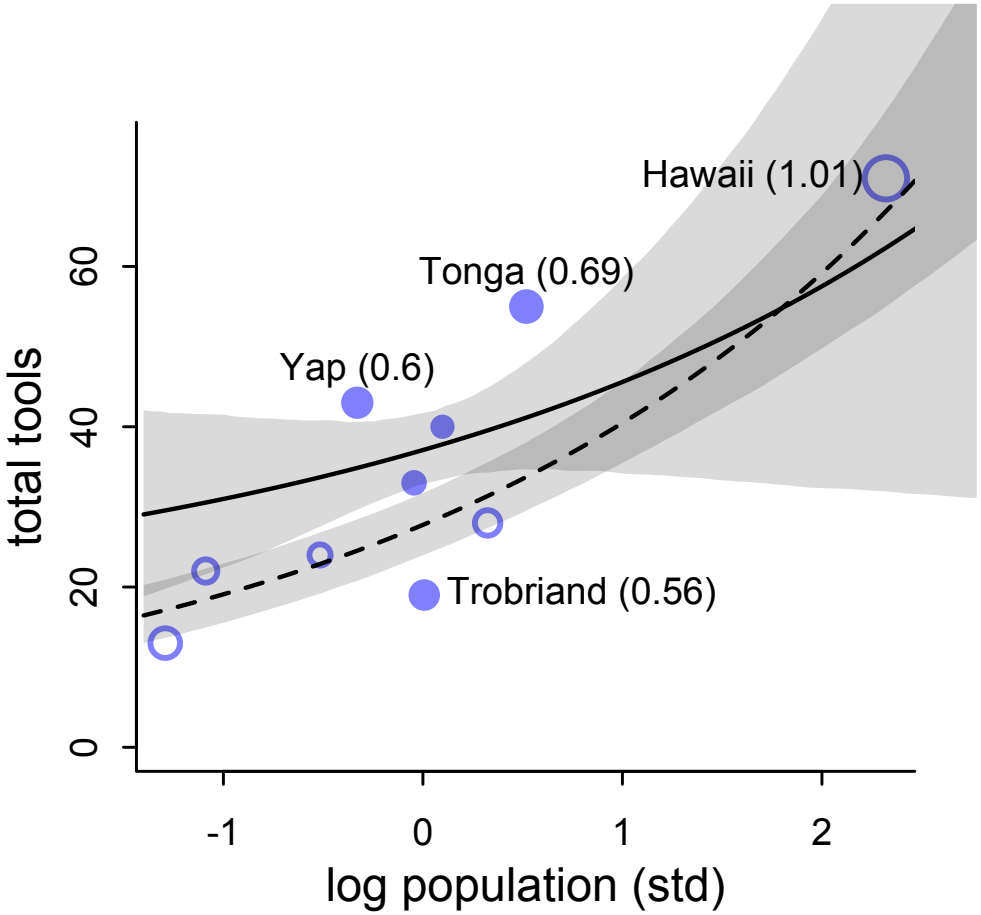
```
compare( m11.9 , m11.10 , func=LOO )
```

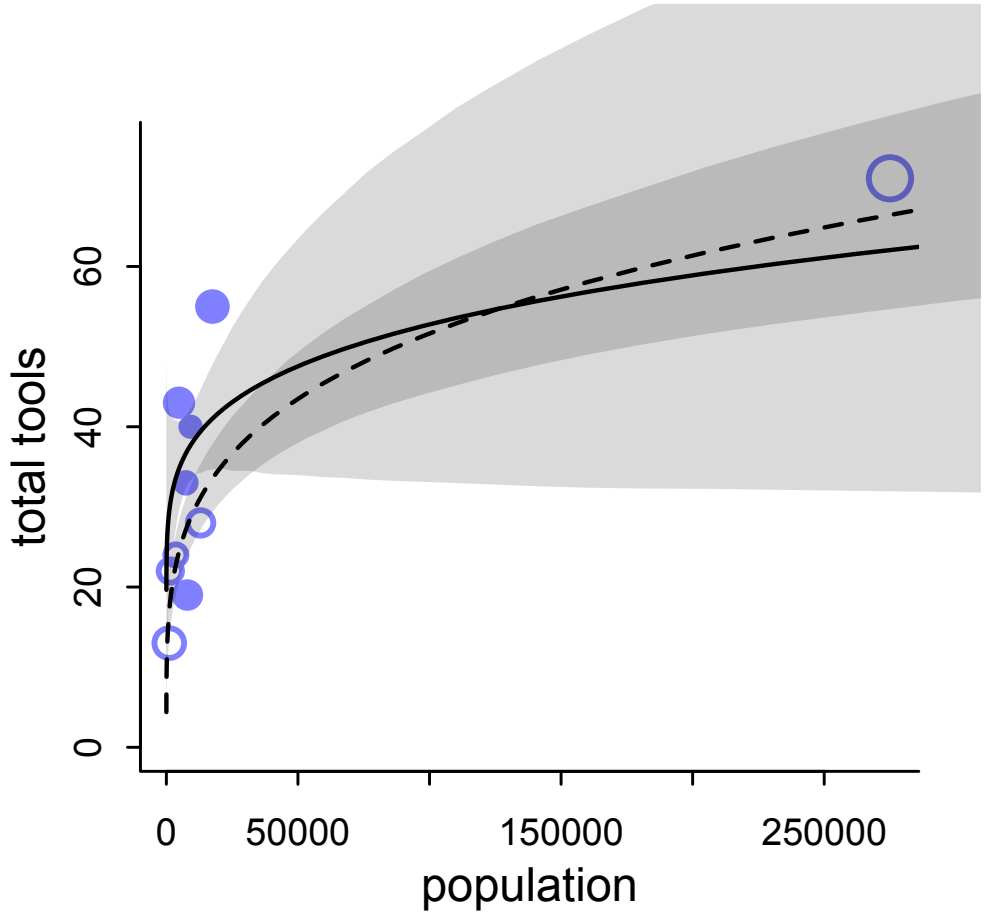
R code
11.49

```
         LOO pLOO dLOO weight    SE   dSE
m11.10  85.5  7.1  0.0      1 13.22    NA
m11.9  141.1  8.0 55.5      0 33.33 32.78
Warning messages:
1: Some Pareto k diagnostic values are too high. See help('pareto-k-diagnostic') for details.
```

- Warning indicates strongly influential points
- Look at those pLOO values: No relationship to parameter count — not unusual & not a mistake

# Hawaii has leverage

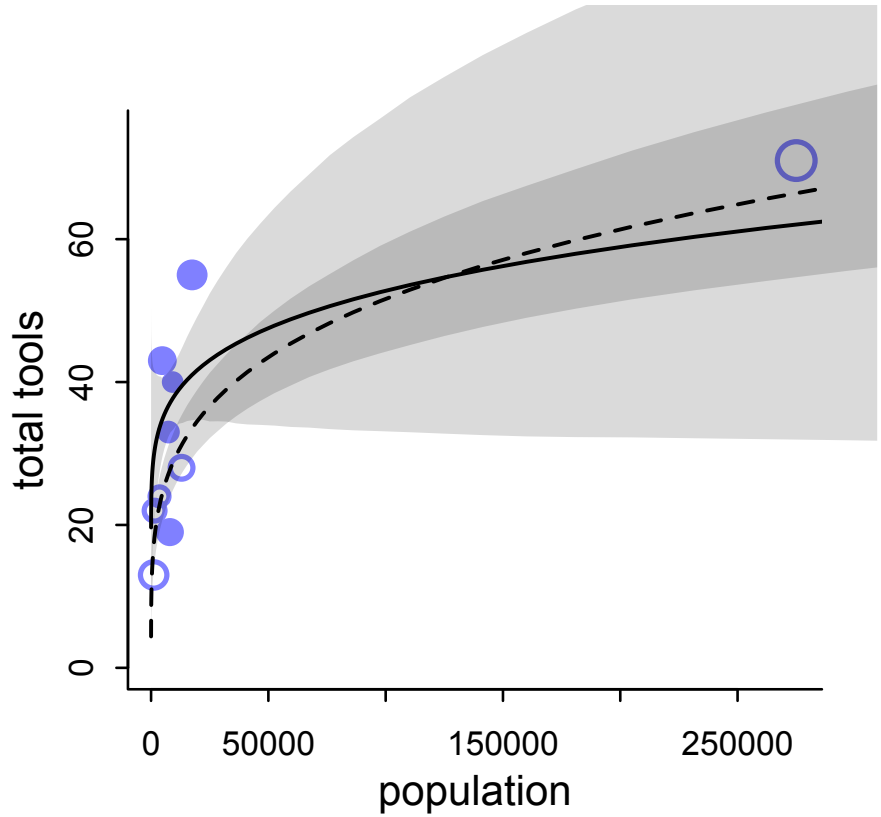



- Point size proportional to Pareto-*k* diagnostic value

# Generalized Linear Madness

- This model is terrible:
- Intercepts don't pass through origin
- Zero population = zero tools
- We can do better by thinking *scientifically* instead of *statistically*



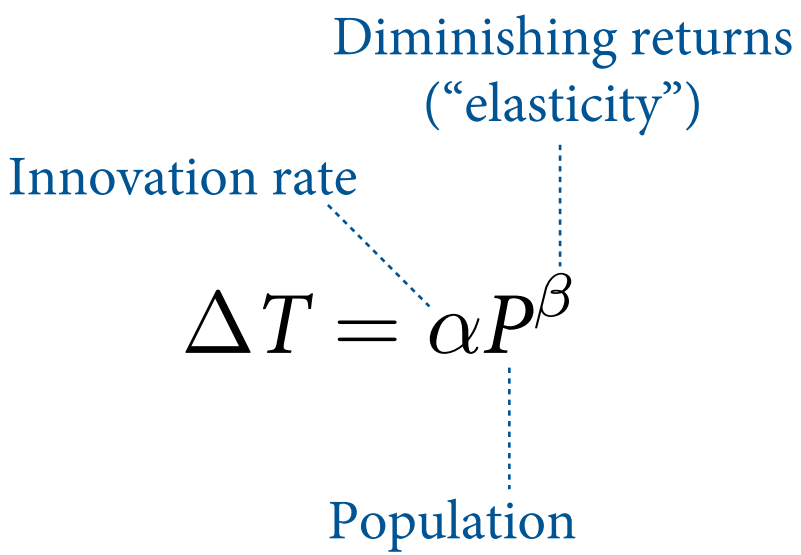
# Scientific model

- Change in tools per unit time:

$$\Delta T =$$

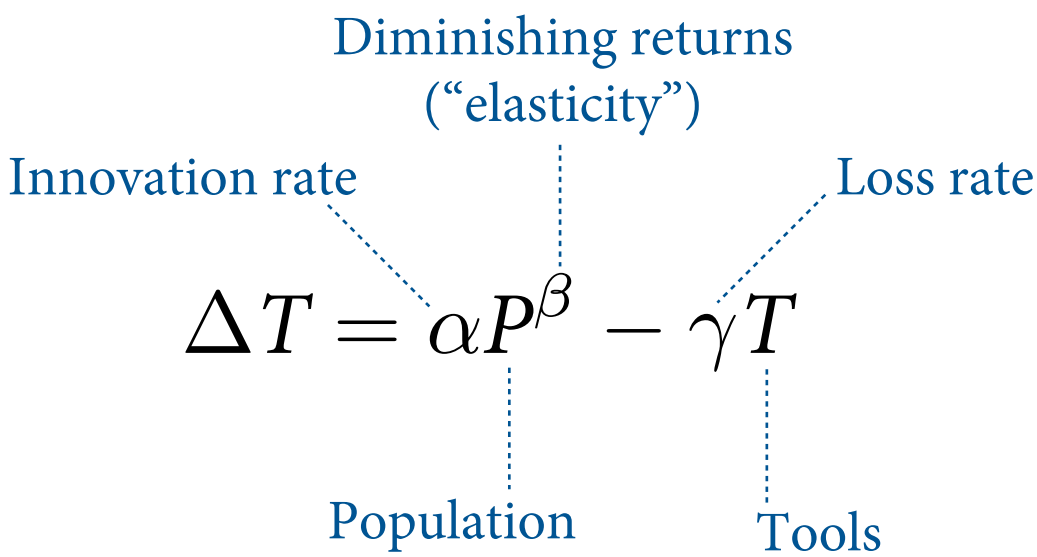
# Scientific model

- Change in tools per unit time:



# Scientific model

- Change in tools per unit time:



# Scientific model

- Solve for steady state expected number of tools
- Where $\Delta T = 0$

$$\hat{T} = \frac{\alpha P^{\beta}}{\gamma}$$

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

$$\lambda_i = \alpha P_i^{\beta} / \gamma$$

No *ad hoc* link function!

# Scientific model

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

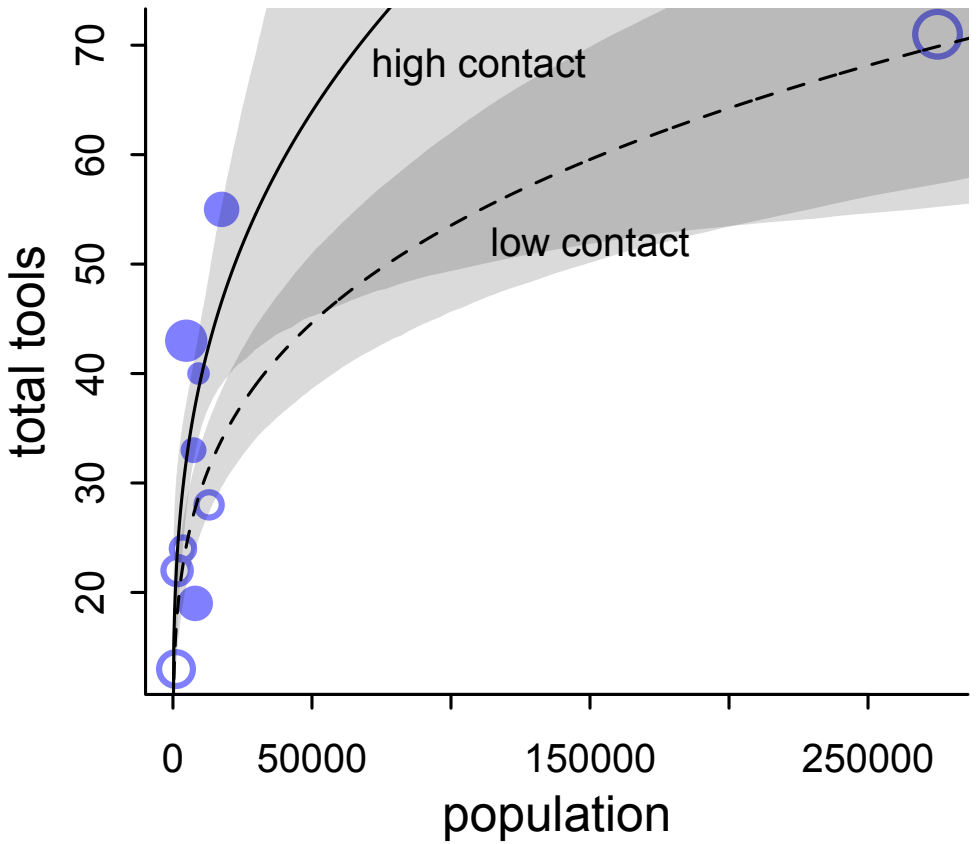
$$\lambda_i = \alpha P_i^{\beta} / \gamma$$

R code 11.52

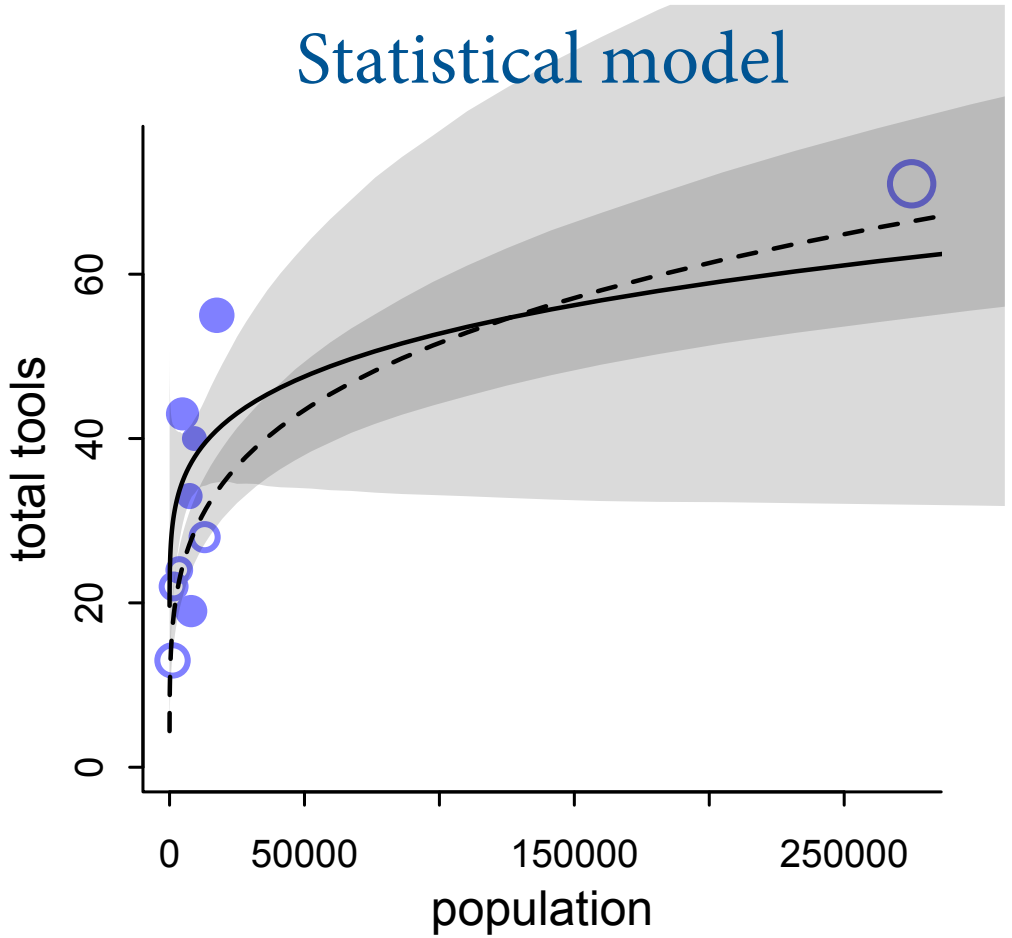
```
dat2 <- list( T=d$total_tools, P=d$population, cid=d$contact_id )
m11.11 <- ulam(
    alist(
        T ~ dpois( lambda ),
        lambda <- exp(a[cid])*P^b[cid]/g,
        a[cid] ~ dnorm(1,1),
        b[cid] ~ dexp(1),
        g ~ dexp(1)
    ), data=dat2 , chains=4 , log_lik=TRUE )
```

# Science pays

## Scientific model




## Statistical model




Model violations now mean something.

Parameters now mean something.

# Poisson exposure (*offsets*)

- Poisson outcome: events per unit time/distance
- Q: What if time/distance varies across cases?
- A: Use an *exposure*, aka *offset*

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

$$\log \lambda_i = \log \frac{\mu_i}{\tau_i} = \alpha + \beta x_i$$

*exposure*

*expected count*

$$y_i \sim \text{Poisson}(\mu_i)$$

$$\log \mu_i = \log \tau_i + \alpha + \beta x_i$$

# Additional count distributions

- Multinomial/categorical: generalized binomial, more than 2 un-ordered outcomes
- Geometric: number of trials until specific event
- Mixtures, coping with heterogeneity:
  - Beta-binomial: varying probabilities
  - gamma-Poisson: aka negative-Binomial, varying rates
  - others (e.g. Dirichlet-multinomial)

# Survival Analysis

- Count models are fundamentally about rates
  - Rate of heads per coin toss
  - Rate of tools per person
- Can also estimate rates by modeling time-to-event
- Tricky, because cannot ignore *censored* cases
  - Left-censored: Don't know when time started
  - Right-censored: Something cut observation off before event occurred
- Ignoring censored cases leads to inferential error
  - Imagine estimating time-to-PhD but ignoring people who drop out
  - Time in program before dropping out is info about rate

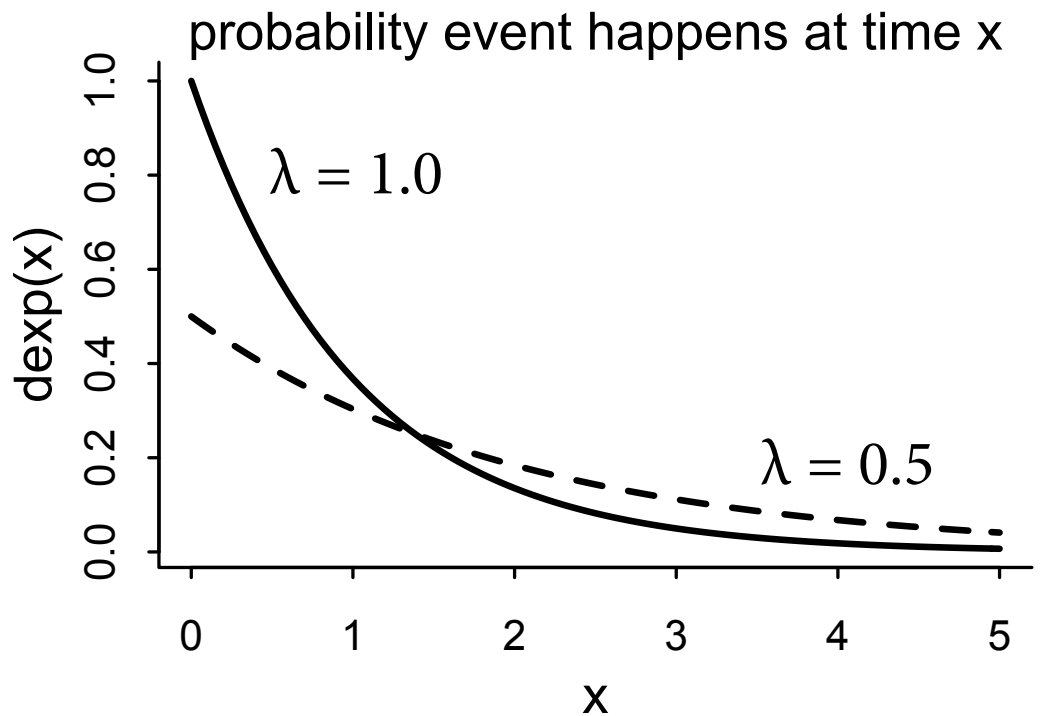
# Survival Analysis

- Example: Cat adoptions
- data(AustinCats)
  - 20-thousand cats
  - time-to-event
  - Event either: (1) adopted or (2) something else
  - Something else could be: death, escape, **censored**

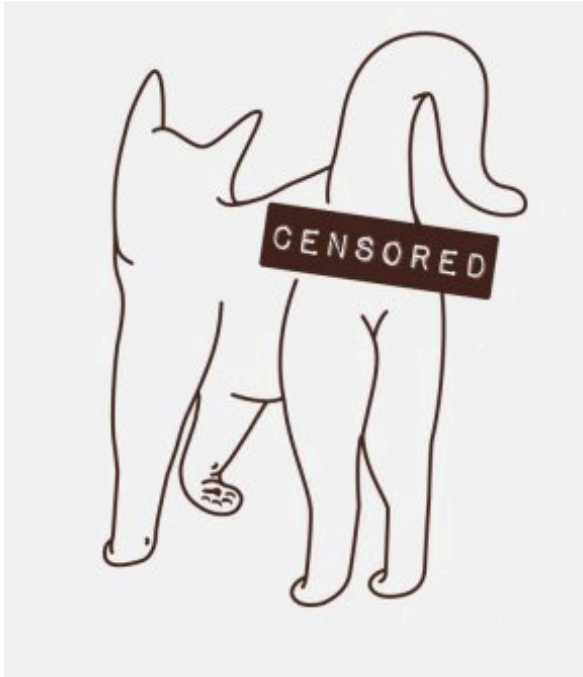
# Un-censored observations

- For observed adoptions, just need:

$$D_i \sim \text{Exponential}(\lambda_i) \qquad p(D_i|\lambda_i) = \lambda_i \exp(-\lambda_i D_i)$$

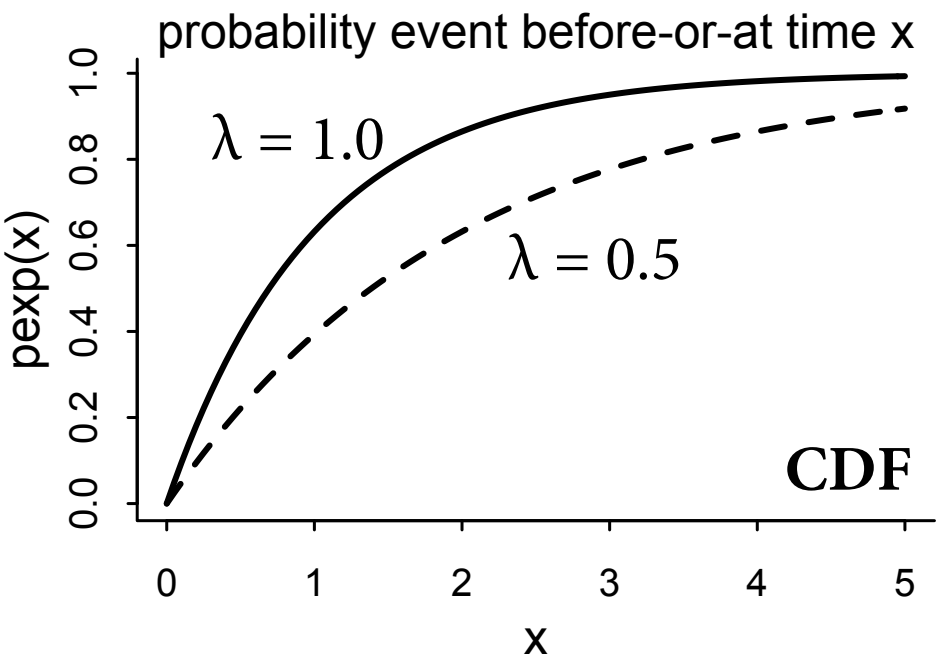


# Censored cats

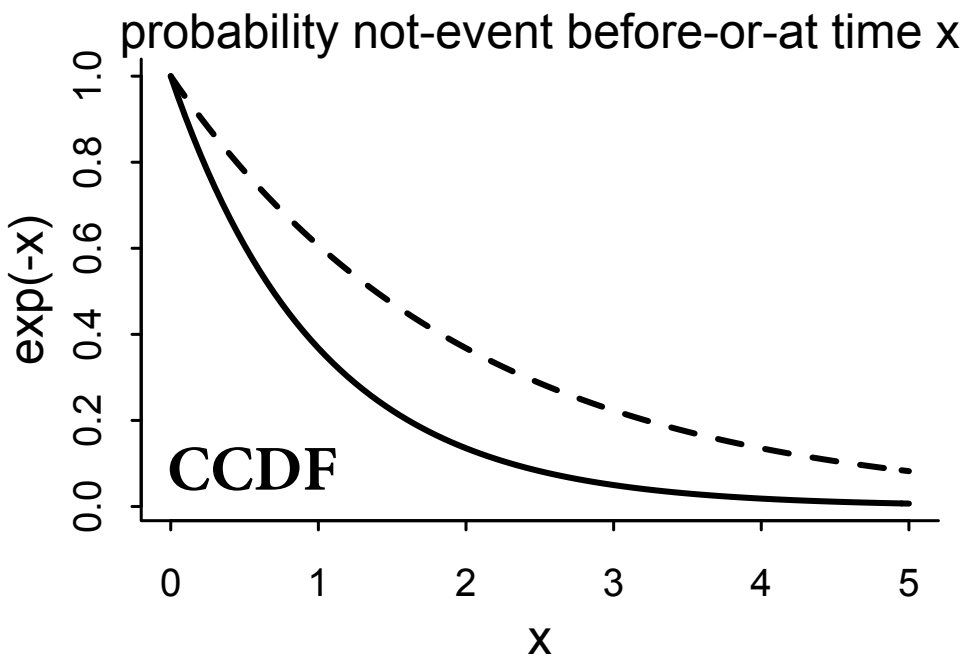



- Cumulative distribution (CDF): Probability event before-or-at time $x$
- Complementary cumulative distribution (CCDF): Probability not-event-yet

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




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



# Cat code

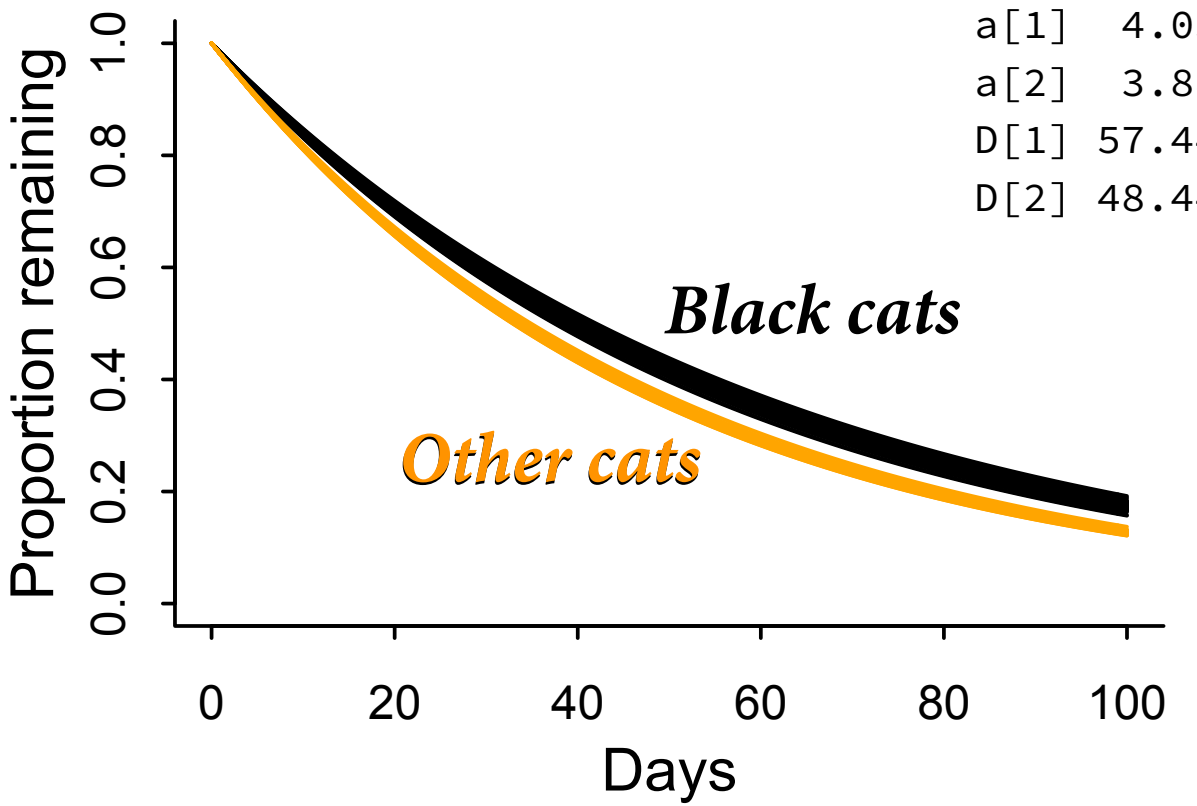
$$
\begin{aligned}
D_i | A_i = 1 &\sim \text{Exponential}(\lambda_i) \\
D_i | A_i = 0 &\sim \text{Exponential-CCDF}(\lambda_i) \\
\lambda_i &= 1/\mu_i \\
\log \mu_i &= \alpha_{\text{CID}[i]}
\end{aligned}
$$

```
m11.14 <- ulam(
    alist(
        days_to_event|adopted==1 ~ exponential( lambda ),
        days_to_event|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 )
```

# Posterior survival curves

```
post <- extract.samples( m11.14 )
post$D <- exp(post$a)
precis( post , 2 )
```

```
'data.frame': 2000 obs. of 4 variables:
      mean   sd  5.5% 94.5%   histogram
a[1]  4.05 0.03  4.01  4.09
a[2]  3.88 0.01  3.87  3.90
D[1] 57.44 1.47 55.11 59.77
D[2] 48.44 0.49 47.71 49.22
```



# Homework

- 3 problems, 2 data sets, multiple good DAGs
- One of the data sets (NWOGrants) is new in rethinking 1.83, so update
- Next week: More adventures with integers