

hw13 for stat341

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Q: 10E1, 10E2, 10M1, 10M3, 10H1, 10H2, 10H3

10E1. If an event has probability 0.35, what are the log-odds of this event?

Solutions:

```
logit(0.35)
```

```
## [1] -0.6190392
```

log-odds of this event is -0.619.

10E2. If an event has log-odds 3.2, what is the probability of this event? (or use logistic)

Solutions:

```
ilogit(3.2)
```

```
## [1] 0.9608343
```

the probability of this event is 0.96.

10M1. As explained in the chapter, binomial data can be organized in aggregated and disaggregated forms, without any impact on inference. But the likelihood of the data does change when the data are converted between the two formats. Can you explain why?

Solutions:

Because in an aggregated binomial each “point” is a bunch of independent trials that happen to share predictor values. And binomial distribution in aggregated form has a lead coefficient that is the multiplicity. This coefficient does not change the inference, since it isn't the function of the parameter. But it change the values of log-likelihood and deviance.

10M3. Explain why the logit link is appropriate for a binomial generalized linear model.

Solutions:

Because the logit link is good for doing multinomial distribution. log scale make the range of probability always be positive.

10H1. Use map to construct a quadratic approximate posterior distribution for the chimpanzee model that includes a unique intercept for each actor, m10.4 (page 299). Compare the quadratic approximation to the posterior distribution produced instead from MCMC. Can you explain both the differences and the similarities between the approximate and the MCMC distributions?

Solutions:

```
Chimps <- chimpanzees %>%
  mutate( combo = paste0(prosoc_left, "/", condition) )

m10.4map <- map(
  alist(
    pulled_left ~ dbinom(1, p),
    logit(p) <- a[actor] + (bp + bpC * condition) * prosoc_left,
    a[actor] ~ dnorm(0, 10),
    bp ~ dnorm(0, 10),
```

be sure you can do them by 'hands' too

particular chimps can
the

```

    bpC ~ dnorm(0, 10)
  ),
  data = Chimps)

precis(m10.4map, depth = 3)

```

```

##           Mean StdDev  5.5% 94.5%
## a[1] -0.73    0.27 -1.16 -0.30
## a[2]  6.67    3.60  0.92 12.41
## a[3] -1.03    0.28 -1.48 -0.59
## a[4] -1.03    0.28 -1.48 -0.59
## a[5] -0.73    0.27 -1.16 -0.30
## a[6]  0.21    0.27 -0.21  0.64
## a[7]  1.75    0.38  1.14  2.37
## bp    0.82    0.26  0.41  1.24
## bpC  -0.13    0.30 -0.61  0.34

```

```
show(m10.4stan)
```

```

## map2stan model fit
## 8000 samples from 4 chains
##
## Formula:
## pulled_left ~ dbinom(1, p)
## logit(p) <- a[actor] + (bp + bpC * condition) * prosoc_left
## a[actor] ~ dnorm(0, 10)
## bp ~ dnorm(0, 10)
## bpC ~ dnorm(0, 10)
##
## Log-likelihood at expected values: -256.53
## Deviance: 513.07
## DIC: 529.61
## Effective number of parameters (pD): 8.27
##
## WAIC (SE): 529.87 (19.9)
## pWAIC: 8.33

```

Use Stan for all

Compare m10.4 from maps and the stan, the difference of WAIC is quite small, and it implies that the

```
compare(m10.4map, m10.4stan)
```

```

## Warning in compare(m10.4map, m10.4stan): Not all model fits of same class.
## This is usually a bad idea, because it implies they were fit by different algorithms.
## Check yourself, before you wreck yourself.

```

```

##           WAIC pWAIC dWAIC weight    SE dSE
## m10.4stan 529.9    8.3   0.0      1 19.92  NA
## m10.4map  565.6   23.0  35.7      0 17.98  4.07

```

10H2. Use WAIC to compare the chimpanzee model that includes a unique intercept for each actor, m10.4 (page 299), to the simpler models fit in the same section.

Solutions: Compared with the simpler models, the model.

```

m10.1 <-
  map(
    alist(pulled_left ~ dbinom(1, p),
          logit(p) <- a,

```

cuz is bad

```

      a ~ dnorm(0, 10)),
    data = Chimps)
precis(m10.1)

```

```

##      Mean StdDev 5.5% 94.5%
## a 0.32    0.09 0.18  0.46

```

```

m10.2 <-
  map(
    alist(
      pulled_left ~ dbinom(1, p),
      logit(p) <- a + bp * prosoc_left,
      a ~ dnorm(0, 10),
      bp ~ dnorm(0, 10)
    ),
    data = Chimps)

m10.3 <-
  map(
    alist(
      pulled_left ~ dbinom(1, p),
      logit(p) <- a + (bp + bpC * condition) * prosoc_left,
      a ~ dnorm(0, 10),
      bp ~ dnorm(0, 10),
      bpC ~ dnorm(0, 10)
    ),
    data = Chimps)
compare(m10.1, m10.2, m10.3, m10.4map)

```

```

##           WAIC pWAIC dWAIC weight      SE  dSE
## m10.4map  539.0   10.7   0.0       1 19.05   NA
## m10.2     680.6    2.1 141.7       0  9.31 18.43
## m10.3     682.3    3.0 143.3       0  9.45 18.40
## m10.1     687.7    0.9 148.8       0  7.12 19.22

```

10H3. The data contained in `library(MASS); data(eagles)` are records of salmon pirating attempts by Bald Eagles in Washington State. See `eagles` for details. While one eagle feeds, sometimes another will swoop in and try to steal the salmon from it. Call the feeding eagle the “victim” and the thief the “pirate”. Use the available data to build a binomial GLM of successful pirating attempts. (a) Consider the following model:

$$y_i \sim \text{Binomial}(n_i, p_i) \quad \log \frac{p_i}{1-p_i} = \alpha + \beta_P P_i + \beta_V V_i + \beta_A A_i$$

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

$$\beta_P \sim \text{Normal}(0, 5)$$

$$\beta_V \sim \text{Normal}(0, 5)$$

$$\beta_A \sim \text{Normal}(0, 5)$$

where y is the number of successful attempts, n is the total number of attempts, P is a dummy variable indicating whether or not the pirate had large body size, V is a dummy variable indicating whether or not the victim had large body size, and finally A is a dummy variable indicating whether or not the pirate was an adult. Fit the model above to the `eagles` data, using both `map` and `map2stan`. Is the quadratic approximation okay? (b) Now interpret the estimates. If the quadratic approximation turned out okay, then it’s okay to use the `map` estimates. Otherwise stick to `map2stan` estimates. Then plot the posterior predictions. Compute and display both (1) the predicted probability of success and its 89% interval for each row (i) in the data, as well as (2) the predicted success count and its 89% interval. What different information does each type of

posterior prediction provide? (c) Now try to improve the model. Consider an interaction between the pirate's size and age (immature or adult). Compare this model to the previous one, using WAIC. Interpret.

Solutions:

- (a) try parameterize the data, let P="L" be 1, A="A" be 1, and V="L" be 1. since logic function not working use dumb way to make data frame

```
eaglesnew <- data.frame("y" = c(17,29,17,20,1,15,0,1), "n" = c(24,29,27,20,12,16,28,4), "P" = c(1,1,1,1,1,1,1,1), "A" = c(1,1,1,1,1,1,1,1), "V" = c(1,1,1,1,1,1,1,1))
```

```
##      y  n P A V
## 1 17 24 1 1 1
## 2 29 29 1 1 0
## 3 17 27 1 0 1
## 4 20 20 1 0 0
## 5  1 12 0 1 1
## 6 15 16 0 1 0
## 7  0 28 0 0 1
## 8  1  4 0 0 0
```

map

```
eaglemap<- map(
  alist(
    y ~ dbinom(n, p),
    logit(p) <- a+ bp*P+ bv*V +ba*A,
    a~ dnorm(0, 10),
    bp ~ dnorm(0, 5),
    bv ~ dnorm(0, 5),
    ba ~ dnorm(0, 5)
  ),
  data = eaglesnew)
```

map2stan

```
eaglestan<- map2stan(
  alist(
    y ~ dbinom(n, p),
    logit(p) <- a+ bp*P+ bv*V +ba*A,
    a~ dnorm(0, 10),
    bp ~ dnorm(0, 5),
    bv ~ dnorm(0, 5),
    ba ~ dnorm(0, 5)
  ),
  data = eaglesnew, chains = 4, cores = 4,
  refresh = 0
)
```

show stan if code is working

```
show(eaglestan)
```

```
compare(eaglemap,eaglestan)
```

- (b) the estimates is determined by WAIC

- (c)