NRES 776 Lecture 18

Binomial regression

Sunny Tseng

Our schedule today

- Announcement (3 min)
  - zoom recording
  - You choose the lab 10 topic (https://forms.gle/gjqQsMFPdmp86yX98)
- Overview of Binomial regression (17 min)
- Fit Binomial regression in R (25 min)
- Wrap up (5 min)

Overview of Binomial data

Applications

- Predict the winner of a sport game (team A or team B)
- Predict animal behaviour (eat or not eat)
- Evaluate business decisions (invest or not)

Data requirement

- Binary data (0 or 1)
- Survival data (alive, dead)
- Choice or behaviour (yes or no)
- Result (pass or fail)

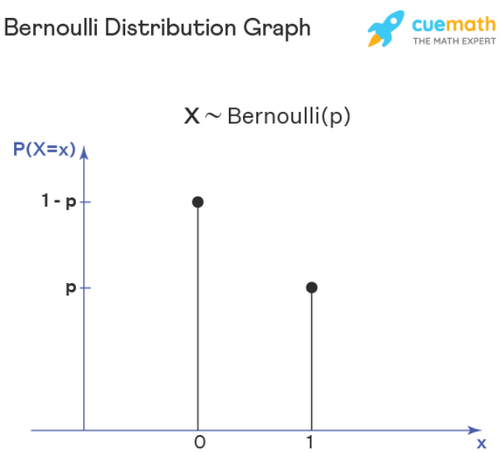
In short

- Use binomial regression when $y \sim Binomial(p)$

Binomial distribution

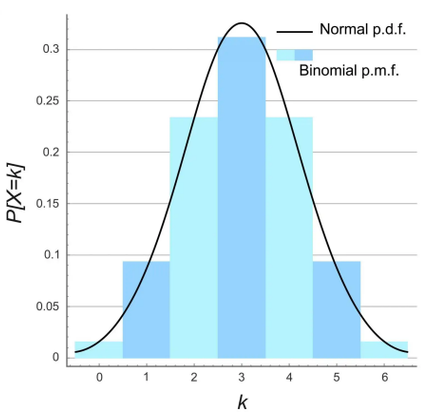
Bernoulli distribution

- Describe a variable which takes the value 1 with probability p and the value 0 with probability $1 - p$
- The probability of front/back by flipping one coin.
- $f(k; p) = p^k (1 - p)^{1-k}$ for $k \in \{0, 1\}$



Binomial distribution

- The # of successes in a sequence of n independant experiments.
- The probability of having k coins facing up after tossing n coins.
- *[Math Processing Error]*
- Bernoulli distribution is a special case of Binomial distribution when $n = 1$.



Overview of Binomial regression

1. Systematic component

$$\eta_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \ldots + \beta_p x_{pi}$$

2. Link function $g()$ –> most often **logit** (log odds), another common one is “probit”

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

3. Random component

$$var(y_i) = n_i p_i (1-p_i)$$

Overview of Binomial regression (con'd)

Equation for binomial regression

$$logit(\mu_i) = logit(p_i) = log(\frac{p_i}{1-p_i}) = \beta_0 + \beta_1 x_{1i} + \ldots + \beta_p x_{pi}$$

Back transformation to get probability

$$\mu_i = p_i = logit^{-1}(\beta_0 + \beta_1 x_{1i} + \ldots + \beta_p x_{pi}) = \frac{1}{1 + exp(\beta_0 + \beta_1 x_{1i} + \ldots)}$$

Or, back transformation to get odds

$$Odds = \frac{p_i}{1-p_i} = exp(\beta_0 + \beta_1 x_{1i} + \ldots + \beta_p x_{pi})$$

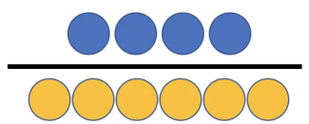
Probability, Odds, Odds Ratio (OR)

From probability to Odds

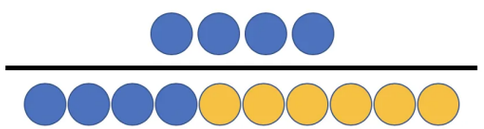
$$Odds = \frac{p_i}{1 - p_i} = exp(\beta_0 + \beta_1 x_{1i} + \ldots + \beta_p x_{pi})$$

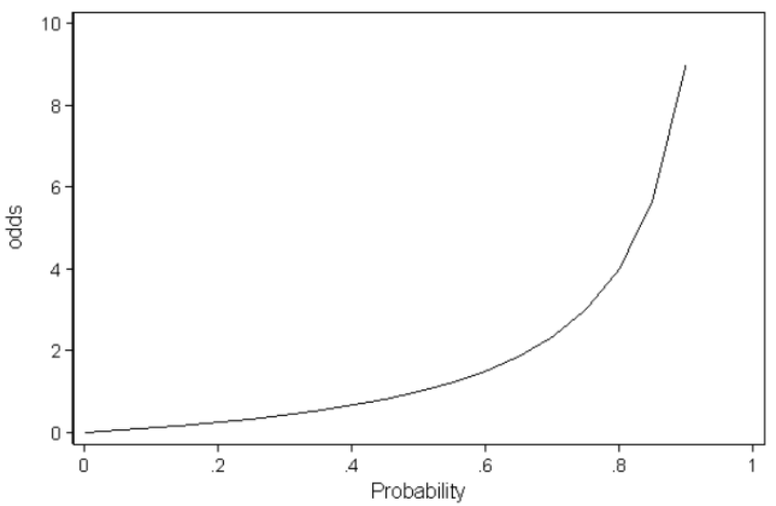
- The probability that the event will occur divided by the probability that the event will not occur.
- Odds increases as the probability increases.

Odds =



Probability =

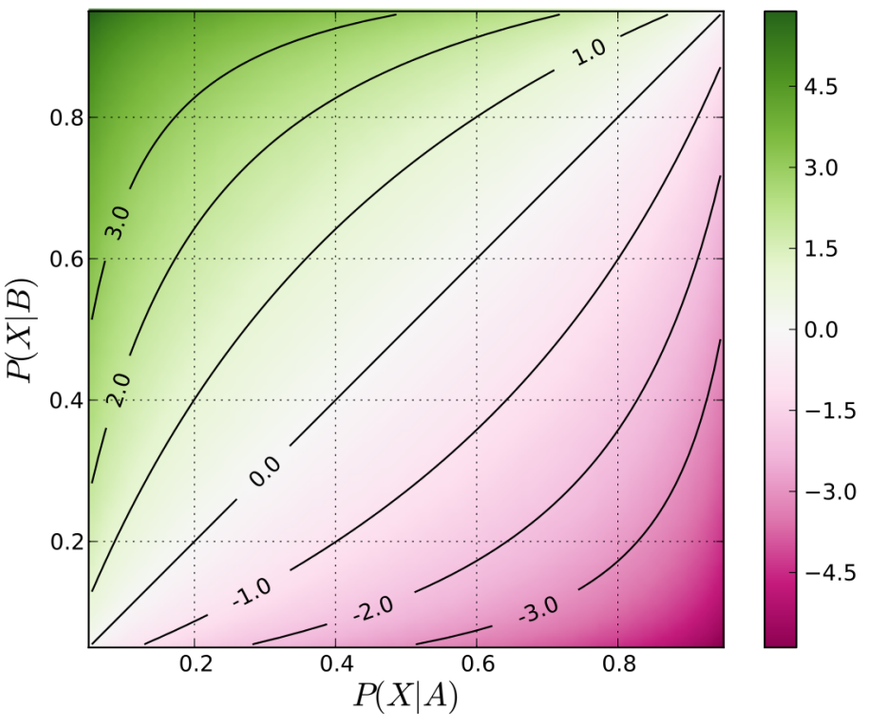




Probability, Odds, Odds Ratio (OR) (con'd)

From Odds to Odds Ratio (OR)

- Odd ratios compare the odds of an event in two different groups
- $OR = \frac{Odds(A)}{Odds(B)} = \frac{p_A/(1-p_A)}{p_B/(1-p_B)}$
- $OR = 1$, no difference between groups
- $OR < 1$, treatment decreases odds
- $OR > 1$, treatment increases odds



Note: the figure is showing log(OR), but the idea is the same. OR, or log(OR) is higher when the event has higher probability compared to another one. Figure

Binomial regression in R

- By default `family = binomial(link = "logit")`
- The variance for this distribution is `variance = "mu(1-mu)"`, and you cannot change it from the default.

```
glm_binomial <- glm(formula = incidence ~ area,
                    data = bird_incidence,
                    family = "binomial")
glm_binomial %>% summary
```

```
Call:
glm(formula = incidence ~ area, family = "binomial", data = bird_incidence)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5709  -0.9052   0.3183   0.6588   1.8424

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.1554     0.7545  -2.857 0.004278 **
area          0.6272     0.1861   3.370 0.000753 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 68.029  on 49  degrees of freedom
Residual deviance: 50.172  on 48  degrees of freedom
AIC: 54.172

Number of Fisher Scoring iterations: 5
```

Long vs wide format

A survey was done on 50 islands for the incidence of a bird species Grasshopper Warbler. Researchers want to know whether the incidence is related to the area and/or the isolation level of the islands.

Long format

- Each row is an individual observation
- Binary output

```
# A tibble: 50 × 3
   incidence  area isolation
   <fct>     <dbl> <fct>
 1 1          7.93 low
 2 0          1.92 high
 3 1          2.04 median
 4 0          4.78 median
 5 0          1.54 median
 6 1          7.37 low
 7 1          8.60 low
 8 0          2.42 high
 9 1          6.40 median
10 1          7.20 median
# … with 40 more rows
```

Wide format

- Each row is a group observation
- Ratio, or proportion

```
# A tibble: 3 × 6
  presence absence total proportion mean_area isolation
     <int>   <int> <int>      <dbl>     <dbl> <fct>
1       15       0    15      1          6.03 low
2       14       8    22      0.636      3.93 median
3        0      13    13      0          3.01 high
```

Long vs wide format (con'd)

Long format

- Directly put y as the Binary output

```
glm_long <- glm(formula = incidence ~ isolation,
                data = data_long,
                family = "binomial")

glm_long %>% coef()
```

```
   (Intercept) isolationmedian    isolationhigh
      20.56607       -20.00645       -41.13214
```

Wide format

- Use the number of presence and absence

```
glm_wide <- glm(formula =
                  cbind(presence, absence) ~ isolati
                data = data_wide,
                family = "binomial")

glm_wide %>% coef()
```

```
   (Intercept) isolationmedian    isolationhigh
      25.48433       -24.92472       -50.83786
```

- Or, give R the proportion and the total count

```
glm_wide <- glm(formula = proportion ~ isolation,
                weights = total,
                data = data_wide,
                family = "binomial")

glm_wide %>% coef()
```

```
   (Intercept) isolationmedian    isolationhigh
      25.48433       -24.92472       -50.83786
```

Long vs wide format (con’d)

What’s the same

- The raw data used
- The “direction” of coefficients

What’s the difference

- The coefficient values (Note: These would be the same if the data is balanced)

When to use what

- What’s your raw data structure?
- Which variables you have? individual or group?
- Do you want to make inference to group or individual?
    - e.g., probability of eggs hatching in a nest -> nest success? or success of individual eggs?

Research question (1 categorical x)

A survey was done on 50 islands for the incidence of a bird species Grasshopper Warbler. Researchers want to know whether the incidence is related to the area and/or the isolation level of the islands.

Use long format as input

```
# A tibble: 50 × 3
   incidence  area isolation
   <fct>     <dbl> <fct>
 1 1          7.93 low
 2 0          1.92 high
 3 1          2.04 median
 4 0          4.78 median
 5 0          1.54 median
 6 1          7.37 low
 7 1          8.60 low
 8 0          2.42 high
 9 1          6.40 median
10 1          7.20 median
# … with 40 more rows
```

Take a look at the group means

```
# A tibble: 3 × 3
  proportion total isolation
       <dbl> <int> <fct>
1      1        15 low
2      0.636    22 median
3      0        13 high
```

Model formulation

$$logit(p_i) = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i}$$

```r
incidence_binom <- glm(formula = incidence ~ isolation,
                       data = data_long,
                       family = "binomial")

incidence_binom %>% summary
```

```
Call:
glm(formula = incidence ~ isolation, family = "binomial", data = data_long)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.42239  -0.00005   0.00005   0.95077   0.95077

Coefficients:
               Estimate Std. Error z value Pr(>|z|)
(Intercept)       20.57    4577.96   0.004    0.996
isolationmedian  -20.01    4577.96  -0.004    0.997
isolationhigh    -41.13    6718.61  -0.006    0.995

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 68.029  on 49  degrees of freedom
Residual deviance: 28.841  on 47  degrees of freedom
AIC: 34.841

Number of Fisher Scoring iterations: 19
```

Coef. interpretation

- For Low isolation:

$$logit(p_L) = log(\frac{p_L}{1-p_L}) = \beta_0$$

$$\frac{p_L}{1-p_L} = Odd(p_L) = exp(\beta_0) = exp(20.57) = 8.5 * 10^8$$

- For Median isolation (use odd ratio):

$$logit(p_M) = \beta_0 + \beta_1$$

$$logit(p_M) - logit(p_L) = \beta_1 = log(\frac{Odd(p_M)}{Odd(p_L)})$$

$$\frac{Odd(p_M)}{Odd(p_L)} = exp(\beta_1) = exp(-20.01) = 2.04 * 10^{-9}$$

Coef. interpretation (con’d)

- For High isolation (use odd ratio):

$$logit(p_M) = \beta_0 + \beta_2$$

$$\frac{Odd(p_H)}{Odd(p_L)} = exp(\beta_2) = exp(-41.13) = 1.36 * 10^{-18}$$

Output interpretation

Odd ratio (OR)

- $OR = 1$, no difference between groups
- $OR < 1$, treatment decreases odds
- $OR > 1$, treatment increases odds

R output

- **Intercept (20.57)**: The odd of the bird being present on low isolation island is $exp(20.57)$
- **isolationmedian (-20.01)**: The odd ratio of bird being present on median isolation island compared to low isolation island is $exp(-20.01)$
- **isolationhigh (-41.13)**: The odd ratio of bird being present on median isolation island compared to low isolation island is $exp(-41.13)$
- **Dispersion parameter (1)**: wonderful. Need to consider other methods if dispersion larger than 1 (over-dispersion) or smaller than 1 (under-dispersion)
- **AIC (34.841)**: Can be used to compare the goodness of fit between models

Model goodness of fit: Likelihood ratio test

```r
incidence_binom_null <- glm(formula = incidence ~ 1,
                            data = data_long,
                            family = "binomial")
```

H_0: The model performance is the same as a null model (making predictions by chance)

H_1: The model performance is significantly different comparing to a null model

- Use `lrtest()` function in the `lmtest` package

```r
lrtest(incidence_binom, incidence_binom_null)
```

```
Likelihood ratio test

Model 1: incidence ~ isolation
Model 2: incidence ~ 1
  #Df  LogLik Df  Chisq Pr(>Chisq)
1   3 -14.421
2   1 -34.015 -2 39.188  3.093e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model goodness of fit: Likelihood ratio test

```r
incidence_binom_null <- glm(formula = incidence ~ 1,
                            data = data_long,
                            family = "binomial")
```

H_0: The model performance is the same as a null model (making predictions by chance)

H_1: The model performance is significantly different comparing to a null model

- Or, Use `anova()` and specify `test = "Chisq"`

```r
anova(incidence_binom, incidence_binom_null, test = "Chisq")
```

```
Analysis of Deviance Table

Model 1: incidence ~ isolation
Model 2: incidence ~ 1
  Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
1        47     28.841
2        49     68.029 -2  -39.188 3.093e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Predictor significance: Likelihood ratio test

- Test whether adding one more variable `area` could increase the model performance

H_0: The full model performance is the same as a reduced model (whichever model have fewer predictors)

H_1: The full model performance is significantly different comparing to a reduced model

```
incidence_binom_add <- glm(formula = incidence ~ isolation + area,
                           data = data_long,
                           family = "binomial")

lrtest(incidence_binom, incidence_binom_add)
```

```
Likelihood ratio test

Model 1: incidence ~ isolation
Model 2: incidence ~ isolation + area
  #Df  LogLik Df  Chisq Pr(>Chisq)
1   3 -14.421
2   4 -11.607  1 5.6277    0.01768 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model prediction

- Use `predict()` and specify `type = "response"` to get back transformed y_i

```
incidence_p <- data_long %>%
  mutate(incidence_p = predict(incidence_binom_add, type = "response"))

incidence_p
```

```
# A tibble: 50 × 4
   incidence  area isolation incidence_p
   <fct>     <dbl> <fct>           <dbl>
 1 1          7.93 low          1.00e+ 0
 2 0          1.92 high         6.11e-10
 3 1          2.04 median       4.80e- 1
 4 0          4.78 median       7.79e- 1
 5 0          1.54 median       4.19e- 1
 6 1          7.37 low          1.00e+ 0
 7 1          8.60 low          1.00e+ 0
 8 0          2.42 high         7.79e-10
 9 1          6.40 median       8.86e- 1
10 1          7.20 median       9.20e- 1
# … with 40 more rows
```

Model prediction

- Or, use `fitted()`, which provides back transformed y_i by default

```
incidence_p <- data_long %>%
  mutate(incidence_p = fitted(incidence_binom_add))

incidence_p
```

```
# A tibble: 50 × 4
   incidence  area isolation incidence_p
   <fct>     <dbl> <fct>           <dbl>
 1 1          7.93 low          1.00e+ 0
 2 0          1.92 high         6.11e-10
 3 1          2.04 median       4.80e- 1
 4 0          4.78 median       7.79e- 1
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 8 0          2.42 high         7.79e-10
 9 1          6.40 median       8.86e- 1
10 1          7.20 median       9.20e- 1
# … with 40 more rows
```
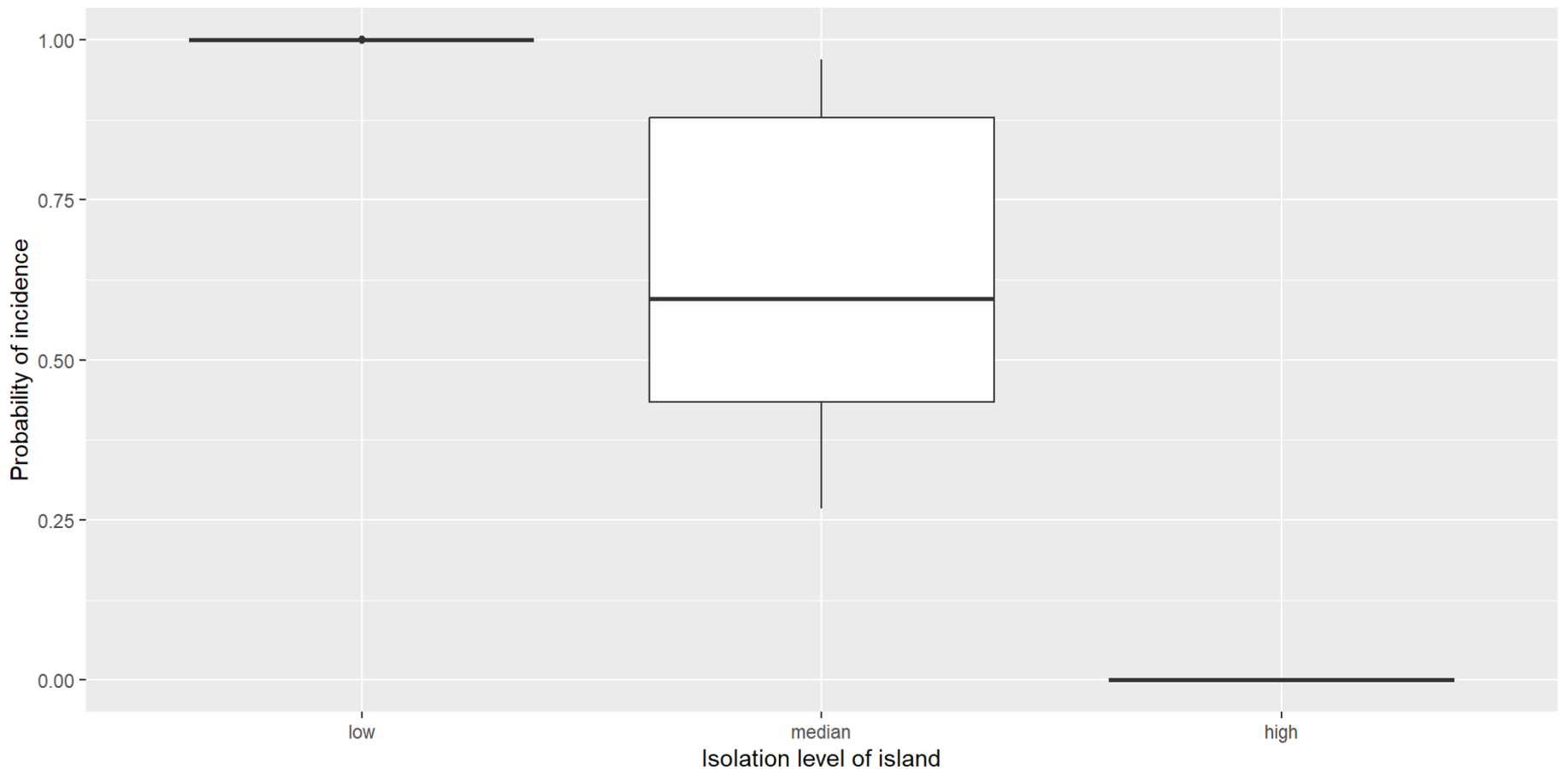

Model visualization

```
ggplot(aes(x = isolation, y = incidence_p), data = incidence_p) +
  geom_boxplot() +
  labs(y = "Probability of incidence", x = "Isolation level of island")
```



Research question (1 continuous x)

A survey was done on 50 islands for the incidence of a bird species Grasshopper Warbler. Researchers want to know whether the incidence is related to the area and/or the isolation level of the islands.

Use long format as input

```
# A tibble: 50 × 3
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 4 0          4.78 median
 5 0          1.54 median
 6 1          7.37 low
 7 1          8.60 low
 8 0          2.42 high
 9 1          6.40 median
10 1          7.20 median
# … with 40 more rows
```

Take a look at the relationship

```
# A tibble: 3 × 3
  proportion total mean_area
       <dbl> <int>     <dbl>
1      1        15      6.03
2      0.636    22      3.93
3      0        13      3.01
```

Model formulation

$$logit(p_i) = \beta_0 + \beta_1 x_{1i}$$

```r
incidence_binom <- glm(formula = incidence ~ area,
                       data = data_long,
                       family = "binomial")

incidence_binom %>% summary
```

```
Call:
glm(formula = incidence ~ area, family = "binomial", data = data_long)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5709  -0.9052   0.3183   0.6588   1.8424

Coefficients:
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(Intercept)  -2.1554     0.7545  -2.857 0.004278 **
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---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 68.029  on 49  degrees of freedom
Residual deviance: 50.172  on 48  degrees of freedom
AIC: 54.172
```

Coef. interpretation

- For island with area as 0 (baseline):

$$logit(p_i) = log(\frac{p_i}{1-p_i}) = \beta_0$$

$$\frac{p_i}{1-p_i} = Odd(p_i) = exp(\beta_0) = exp(-2.15) = 0.11$$

- The odd for the intercept is not often interpreted by itself.

Coef. interpretation (con'd)

- For island with non-0 area:

$$logit(p_i) = \beta_0 + \beta_1 x_{1i}$$

$$logit(p_i') = \beta_0 + \beta_1 (x_{1i} + 1)$$

$$logit(p_i') - logit(p_i) = \beta_1 = log(\frac{Odd(p_i')}{Odd(p_i)})$$

$$\frac{Odd(p_i')}{Odd(p_i)} = exp(\beta_1) = exp(0.62) = 1.87$$

- For one unit increase in `area`, the odds of the bird species being present increase by a factor of 1.87.

Output interpretation

Odd ratio (OR)

- $OR = 1$, no difference between groups
- $OR < 1$, treatment decreases odds
- $OR > 1$, treatment increases odds

R output

- **Intercept (-2.15)**: The odd of the bird being present on 0 area island is $exp(-2.15)$
- **area (0.62)**: For one unit increase in `area`, the odds of the bird species being present increase by a factor of $exp(0.62)$
- **Dispersion parameter (1)**: wonderful. Need to consider other methods if dispersion larger than 1 (over-dispersion) or smaller than 1 (under-dispersion)
- **AIC (54.172)**: Can be used to compare the goodness of fit between models

Model goodness of fit: Likelihood ratio test

```r
incidence_binom_null <- glm(formula = incidence ~ 1,
                            data = data_long,
                            family = "binomial")
```

H_0: The model performance is the same as a null model (making predictions by chance)

H_1: The model performance is significantly different comparing to a null model

- Use `lrtest()` function in the `lmtest` package

```r
lrtest(incidence_binom, incidence_binom_null)
```

```
Likelihood ratio test

Model 1: incidence ~ area
Model 2: incidence ~ 1
  #Df  LogLik Df  Chisq Pr(>Chisq)
1   2 -25.086
2   1 -34.015 -1 17.857  2.382e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model prediction

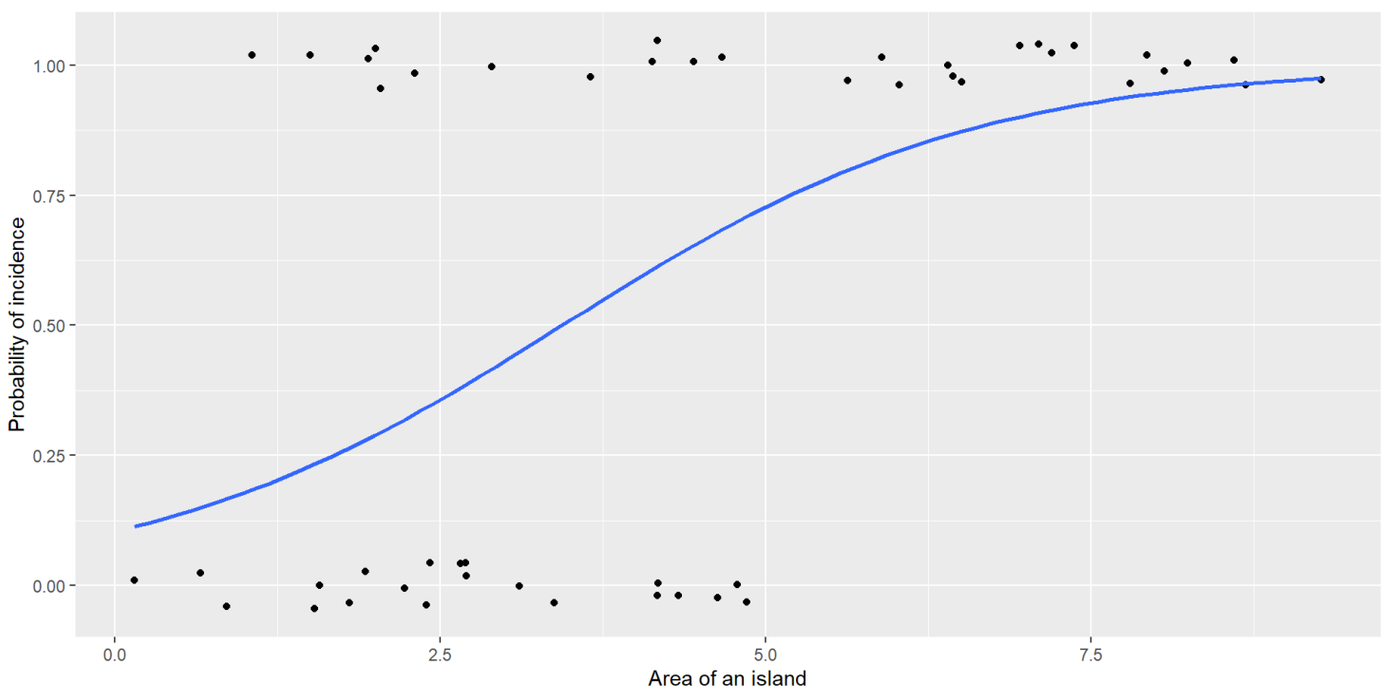
- Use `predict()` and specify `type = "response"` to get back transformed y_i

```
incidence_p <- data_long %>%
  mutate(incidence_p = predict(incidence_binom_add, type = "response"))
incidence_p
```

```
# A tibble: 50 × 4
   incidence  area isolation incidence_p
   <fct>     <dbl> <fct>           <dbl>
 1 1          7.93 low          1.00e+ 0
 2 0          1.92 high         6.11e-10
 3 1          2.04 median       4.80e- 1
 4 0          4.78 median       7.79e- 1
 5 0          1.54 median       4.19e- 1
 6 1          7.37 low          1.00e+ 0
 7 1          8.60 low          1.00e+ 0
 8 0          2.42 high         7.79e-10
 9 1          6.40 median       8.86e- 1
10 1          7.20 median       9.20e- 1
# … with 40 more rows
```

Model visualization

```
data_long %>%
  mutate(incidence = incidence %>% as.numeric() - 1) %>%
  ggplot(aes(x = area, y = incidence), data = .) +
  geom_jitter(width = 0, height = 0.05) +
  geom_smooth(method =  "glm",
              method.args = list(family = "binomial"),
              se = FALSE) +
  labs(y = "Probability of incidence", x = "Area of an island")
```



What we learned today

- What is Binomial distribution
- We can use long data or wide data to fit binomial regression
- Binomial regression coefficient interpretation
- Goodness of fit
- Visualization

Wrap up

Before we meet again

- Vote for the lab 10 topic (https://forms.gle/gjqQsMFPdmp86yX98)

Next time

- Next Thursday morning 8 am lab, virtual on zoom