#### **STAT 120 C**

Introduction to Probability and Statistics III

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### Categorical Data Analysis

In categorical data analysis, we consider observations that belong to sets of categories.

#### **Examples**

- Are carriers of a particular gene more susceptible to cancer?
- Is heart attack incidence associated with blood type?
- Is gender associated with likelihood of promotion?
- Do STEM degrees or humanities degrees have lower unemployment?

# Categorical Data Analysis

- Nominal variables have categorical values
- For example, Blood Type takes values over 8 categories (A+, A-, B+, B-, O+, O-, AB+, AB-).
- Each person's measured blood type will belong to exactly one of these categories.
- A sample of 100 individuals may have blood type distributed as:

Blood Type	<b>A</b> +	<b>A</b> -	B+	B-	0+	0-	AB+	AB-
Count	34	40	7	3	8	7	1	0

#### Review of Multinomial Distribution

- ullet Consider a random vector of count data  $X=(N_1,N_2,\ldots,N_c)$  , where each  $N_i$  is a count of elements in category i.
- ullet X follows a multinomial distribution if it has probability mass function

$$p(N_1=n_1,N_2=n_2,\cdots,N_c=n_c) = \left(rac{n!}{n_1!n_2!\cdots n_c!}
ight)\pi_1^{n_1}\pi_2^{n_2}\cdots\pi_c^{n_c},$$

where

$$\sum_{i=1}^{c} n_i = n$$

$$\sum_{i=1}^c \pi_i = 1$$

ullet We write  $X \sim Multi(n,(\pi_1,\ldots,\pi_c))$  .

#### Review of Multinomial Distribution

#### **Properties**

$$\mathbb{E}(N_i) = n\pi_i 
onumber 
o$$

#### **Marginal Distribution**

$$N_i \sim Binom(n,\pi_i)$$

#### **Conditional Distribution**

$$(N_1,\cdots,N_{c-1})|(N_c=n_c)\sim Multi\left(n-n_c,rac{pi_1}{1-\pi_c},\ldots,rac{\pi_{c-1}}{1-\pi_c}
ight)$$

**Note** that when c=2, the multinomial distribution reduces to the binomial distribution.

#### Review of Multinomial Distribution

#### **Example**

The distribution of the blood type data may follow a multinomial:

$$X \sim Multi(100, (0.374, 0.357, 0.085, 0.034, 0.066, 0.063, 0.015, 0.006))$$

The count data from the table is a realization of this random variable from a random sample of 100 people.

<b>Blood Type</b>	<b>A</b> +	<b>A</b> -	B+	B-	0+	0-	AB+	AB-
Count	34	40	7	3	8	7	1	0

Consider a two-way contingency table

$n_{11}$	$n_{12}$		$n_{1J}$	$n_1$ .
$n_{21}$	$n_{22}$	• • •	$n_{1J}$ $n_{2J}$	$n_1$ . $n_2$ .
÷	÷	:	:	:
$n_{I1}$	$n_{J2}$		$n_{IJ}$	$n_I$ .
n.1	n2		nJ	n

#### where

- ullet  $n_{ij}$  is the observed count in row i and column j
- ullet  $n_{i\cdot} = \sum_{j=1}^{J}$  is the total number of observations in row i
- ullet  $n_{\cdot j} = \sum_{i=1}^{I} n_{ij}$  is the total number of observations in column j
- $n_{\cdot \cdot \cdot} = \sum_{i=1}^{I} \sum_{j=1}^{J} n_{ij}$  is the total number of observations

- If we have two factors, the Chi-squared test can be used to determine:
  - Are the two factors independent?
  - Are subpopulations homogeneous (i.e. equally distributed)?
- Which question we are answering depends on the data we have and the goal of the analysis.

The test statistic is

$$T = \sum_{i=1}^c rac{(Obs_i - Exp_i)^2}{Exp_i},$$

where

- ullet c is the total number of cells (e.g. c=IJ for an I imes J table),
- $Obs_i$  is the observed count for cell i,
- ullet  $Exp_i$  is the expected count for cell i under some specific null hypothesis.
- ullet The value of  $Exp_i$  can be calculated from the MLE of the parameters under the null hypothesis.

#### Idea of the test

- The Central Limit Theorem tells us that sums of random variables will be approximately normally distributed.
- ullet Quadratic forms of normal random variables will follow a  $\chi^2$  distribution.
- Combining these properties, we can derive the (approximate) null distribution for the test statistic

#### **Theoretical Justification**

- Consider a multinomial sample  $(n_1, n_2, \ldots, n_c)$  of size n.
- The marginal distribution of  $n_i$  is  $Binom(n,\pi_i)$ .
- $\bullet$  For large n, the CLT tells us that

$$\hat{\pi} = \left(rac{n_1}{n}, rac{n_2}{n}, \ldots, rac{n_{c-1}}{n}
ight)^T$$

has an approximate multivariate normal distribution.

#### **Theoretical Justification**

• Let  $\Sigma_0$  be the null covariance matrix of  $\sqrt{n}\,\hat{\pi}$ , and let

$$\pi_0 = (\pi_{10}, \pi_{20}, \dots, \pi_{c-1,0})^T$$

be the expectation of  $\pi$  under the null hypothesis.

• Then, by the CLT

$$\sqrt{n}(\hat{\pi}-\pi_0) o\mathcal{N}(0,\Sigma_0)$$

• Therefore, by results on the distribution of quadratic forms

$$n(\hat{\pi}-\pi_0)^T\Sigma_0^{-1}(\hat{\pi}-\pi_0) o\chi_{c-1}^2$$

#### **Theoretical Justification**

• The covariance matrix  $\Sigma$  of  $\sqrt{n}\,\hat{\pi}$  has elements

$$\Sigma = egin{pmatrix} \pi_1(1-\pi_1) & -\pi_1\pi_2 & \dots & -\pi_1\pi_{c-1} \ -\pi_1\pi_2 & \pi_2(1-\pi_2) & \dots & -\pi_2\pi_{c-1} \ dots & dots & dots & dots \ -\pi_1\pi_{c-1} & \dots & \pi_{c-1}(1-\pi_{c-1}) \end{pmatrix}$$

- Under a null hypothesis giving values  $\pi_0=(\pi_{10},\ldots,\pi_{c-1,0})^T$  , we plug in these values into  $\Sigma$  to obtain  $\Sigma_0$ .
- It can be shown that the Pearson Chi-squared test statistic is equal to

$$T = n(\hat{\pi} - \pi_0)^T \Sigma_0^{-1} (\hat{\pi} - \pi_0).$$

ullet Thus, the null distribution is  $T\stackrel{H_0}{\sim}\chi^2_{c-1}$  .

- Suppose we wish to test whether the factors are independent in a two-way contingency table
- The null hypothesis is

$$H_0:\pi_{ij}=\pi_{i\cdot}\pi_{\cdot j},$$

by the definition of independence

• The likelihood for the multinomial can be written

$$\mathcal{L}(\pi_{11},\ldots,\pi_{IJ}) = \left(rac{n_{..}!}{n_{11}!\cdots n_{IJ}!}
ight)\pi_{11}^{n_{11}}\pi_{12}^{n_{21}}\cdots\pi_{IJ}^{n_{IJ}}$$

• Under the null hypothesis, the likelihood can be written

$$\mathcal{L}_0 \propto \prod_{i=1}^I \prod_{j=1}^J [\pi_{i\cdot}\pi_{j\cdot}]^{n_{ij}}$$
 .

• The log-likelihood is

$$egin{aligned} \ell_0 &= \log(\mathcal{L}_0) = \sum_{i=1}^I \sum_{j=1}^J [n_{ij} \log(\pi_{i\cdot}\pi_{\cdot j})] + const \ &= \sum_i \sum_j n_{ij} \log(\pi_{i\cdot}) + \sum_i \sum_j n_{ij} \log(\pi_{\cdot j}) + const \ &= \sum_i n_{i\cdot} \log(\pi_{i\cdot}) + \sum_j n_{\cdot j} \log(\pi_{\cdot j}) + const \end{aligned}$$

• It can be shown that the MLEs are

$$egin{aligned} \hat{\pi}_{i\cdot} &= rac{n_{i\cdot}}{n_{\cdot\cdot}}, & ext{for } i = 1, \cdots, I \ \ \hat{\pi}_{\cdot j} &= rac{n_{\cdot j}}{n_{\cdot\cdot}}, & ext{for } j = 1, \cdots, J. \end{aligned}$$

• Thus,

$$Exp_{ij}=n_{\cdot\cdot}\hat{\pi}_{ij}=n_{\cdot\cdot}\hat{\pi}_{i\cdot}\hat{\pi}{\cdot}j=rac{n_{i\cdot}n_{\cdot j}}{n_{\cdot\cdot}}$$

ullet The resulting  $\chi^2$  test statistic can be written

$$T = \sum_{i=1}^{I} \sum_{j=1}^{J} rac{(n_{ij} - n_{i\cdot} n_{\cdot j}/n_{\cdot \cdot})^2}{n_{i\cdot} n_{\cdot j}/n_{\cdot \cdot}}.$$

ullet This statistic has reference distribution  $T\stackrel{H_0}{\sim}\chi^2_{(I-1)(J-1)}$  under the null hypothesis of independence.

#### **Example**

200 students were surveyed on their preference between two political candidates A and B. The following table shows the responses by major subject area.

#### **Observed Counts**

	Bio.	Eng.	Soc. Sci.	Other	Totals
А	24	24	17	27	92
В	23	14	8	19	64
Undecided	12	10	13	9	44
Totals	59	48	38	55	200

#### **Observed Counts**

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#### **Expected Counts under null hypothesis of independence**

	Bio.	Eng.	Soc. Sci.	Other	Totals
А	27.14	22.08	17.48	25.3	92
В	18.88	15.36	12.16	17.60	64
Undecided	12.98	10.56	8.36	12.10	44
Totals	59	48	38	55	200

- ullet The statistic is  $T=\sumrac{\left(Obs-Exp
  ight)^{2}}{Exp}=6.68$
- ullet Since I=3,J=4 , the null distribution is  $\chi^2_6$  , where 6=(I-1)(J-1)
- The upper 5% tail of  $\chi^2_6$  has cutoff 12.59.
- We conclude then that there is insufficient evidence to reject the hypothesis that candidate preference is independent of major type, at significance level 0.05.
- That is, we conclude that candidate preference is associated with major type, at significance level 0.05.

- Suppose now that instead of a simple random sample, the data results from a stratified sample.
- In this setting, we can instead test for homogeneity across the subgroups.
- For instance, suppose that in the above example, the data were obtained by sampling 59 students from Bio, 48 students from Soc Sci, etc. (rather than just sampling 200 students randomly).
- The test for homogeneity determines if candidate preferences have the same distribution within each major.

- Let  $\pi_{ij}$  be the probability that an observation in the jth population is in category i.
- Organized as a table, the parameters are:

Pop. 1	Pop. 2		Pop. J
$\pi_{11}$	$\pi_{12}$		$\pi_{1J}$
$\pi_{21}$	$\pi_{22}$		$\pi_{2J}$
÷	:	÷	÷
$\pi_{I1}$	$\pi_{I2}$		$\pi_{IJ}$

Table 1: Full set of parameters.

• The null hypothesis for the test of homogeneity is

$$H_0: \pi_{ij}=\pi_i, \quad i=1,\ldots,I; j=1,\ldots,J$$

ullet The parameters under  $H_0$  reduce to

Pop. 1	Pop. 2		Pop. J
$\pi_1$	$\pi_1$		$\pi_1$
$\pi_2$	$\pi_2$		$\pi_2$
÷	÷	:	÷
$\pi_I$	$\pi_I$		$\pi_I$

Table 2: Parameters under  $H_0$ .

- ullet To test the homogeneity null hypothesis  $H_0$  , we can use the Likelihood Ratio Test.
- ullet Using the constraint  $\sum_{i=1}^I \pi_i = 1$ , we can write the null likelihood as

$$\mathcal{L}_0(\pi_1,\ldots,\pi_I) \propto \pi_1^{n_1} \pi_2^{n_2} \ldots (1-\sum_{i=1}^{I-1} \pi_i)^{n_I}.$$

• The log-likelihood is

$$\ell_0(\pi_1,\ldots,\pi_I) = n_1\log(\pi_1) + \cdots + n_{I-1}\log(\pi_{I-1}) + n_I\log(1 - \sum_{i=1}^{I-1}\pi_i)$$

• We can find the MLEs through the derivative:

$$egin{align} rac{\partial \ell_0}{\partial \pi_i} &= rac{n_{i\cdot}}{\pi_i} - rac{n_{I\cdot}}{1 - \sum_{i=1}^{I-1} \pi_i} = rac{n_{i\cdot}}{\pi_i} - rac{n_{I\cdot}}{\pi_I} = 0 \ \hat{\pi}_i &= rac{\hat{\pi}_I n_{i\cdot}}{n_{I\cdot}} \end{aligned}$$

ullet Plugging these estimates into the constraint  $\sum \pi_i = 1$  ,

$$\hat{\pi}_i = rac{n_i.}{n_i.}, \quad i=1,\ldots,I.$$

• The expected number of observations in each cell under the null hypothesis is

$$Exp_{ij} = n_{\cdot j}\hat{\pi}_i = rac{n_{i\cdot}n_{\cdot j}}{n_{\cdot i\cdot}}$$

The test statistic is then

$$T = \sum_{i=1}^{I} \sum_{j=1}^{J} rac{(n_{ij} - n_{i.} n_{.j} / n_{..})^2}{n_{i.} n_{.j} / n_{..}},$$

which has approximate null distribution

$$T\stackrel{H_0}{\sim}\chi^2_{(I-1)(J-1)}.$$

- The degrees of freedom are calculated as the difference of the number of parameters in the full model vs the reduced model:
  - $\circ$  **Full Model**: (I-1)J total free parameters.
  - $\circ$  **Reduced Model**: (I-1) free parameters.
  - $\circ$  Difference =(I-1)J-(I-1)=(I-1)(J-1)

- **NOTE** Pearson's tests are based on asymptotic properties, and thus are only appropriate when the sample size is moderately large *in each cell*.
- Often times in tabular data, some cells are sparse, and the results of Pearson's chisquared test may be invalid
- The usual rule of thumb is to only apply Pearson's chi-squared test when there are at at least 5 observations per cell.
- When we have fewer observations, it is usually better to use an alternative, such as *Fisher's Exact Test*.

#### Application to Forgery Detection

- The chi-squared test for homogeneity can be used to evaluate the authorship of a given text
- Consider the works of Jane Austen, including *Sense and Sensibility, Emma*, and *Sanditon*. This last novel was only partially completed by Austen before her death.
- A literary admirer of Austen completed Sanditon, attempting to emulate her style.
- We can evaluate whether the prose by the admirer matches Austen's style, or if it is significantly different, using the chi-squared test for homogeneity.

We can consider the distribution of words in works known to be authored by Austen (S
 & S, Emma, Sanditon I), and compare these to the work of suspect authorship (Sanditon II)

Word	Sense and Sensibility	Emma	Sanditon I	Sanditon II
a	147	186	101	83
an	25	26	11	29
this	32	39	15	15
that	94	105	37	22
with	59	74	28	43
without	18	10	10	4
Total	375	440	202	196

- Calculate expected counts assuming the distributions are the same in each subpopulation (text) known to be authored by Austen
- ullet The expected count for the ijth cell is  $Exp_{ij}=rac{n_i.n_{\cdot j}}{n_{\cdot \cdot}}$  .
- ullet For instance,  $Exp_{12}=rac{434\cdot 440}{375+440+202}=187.8$

Word	Sense and Sensibility	Emma	Sanditon I
a	147 (160.0)	186 (187.8)	101 (86.2)
an	25 (22.9)	26 (26.8)	11 (12.3)
this	32 (31.7)	39 (37.2)	15 (17.1)
that	94 (87.0)	105 (102.1)	37 (46.9)
with	59 (59.4)	74 (69.7)	28 (32.0)
without	18 (14.0)	10 (16.4)	10 (7.5)

• The resulting test statistic is

$$T = \sum_{i=1}^{I} \sum_{j=1}^{J} rac{(Obs_{ij} - Exp_{ij})^2}{Exp_{ij}} = 12.27.$$

- Under the null hypothesis that the works have the same relative distribution of word counts,  $T\stackrel{H_0}{\sim}\chi_{10}^2$  , where (I-1)(J-1)=(6-1)\*(3-1)=10.
- The 10% cutoff for  $\chi^2_{10}$  is 15.99. Thus, since T=12.27<15.99, the works are consistent with the hypothesis of equal word distributions. (That is, Austen did not change the relative frequencies of these words across her different works.)

• We can now test whether *Sanditon II*, which was not written by Austen, follows the same word distribution.

Word	Imitator	Austen
a	83 (83.5)	434 (433.5)
an	29 (14.7)	62 (76.3)
this	15 (16.3)	86 (84.7)
that	22 (41.7)	236 (216.3)
with	43 (33.0)	161 (171.0)
without	4 (6.8)	38 (35.1)

- ullet The resulting statistic is T=32.81, with 5 degrees of freedom, resulting in a P-value < 0.001
- Thus, we conclude that the work of the imitator follows a different word distribution, with significance at least 0.05.

• To determine which words are contributing to this deviation, we can consider  $(Exp-Obs)^2/Exp$  for each cell.

Word	Imitator	Austen
a	0.00	0.00
an	13.9	2.68
this	0.11	0.02
that	9.3	1.79
with	3.06	0.59
without	1.14	0.22

• So we see that the imitator used "an" and "that" much more frequently than Austen.

#### Application to Cryptography

- The chi-squared test for homogeneity can be used to help decode messages for many cipher types
- The simple *Caesar cipher* encodes a message by shifting each letter a fixed number of characters
- E.g., a Caesar cipher with a shift of 3 will map
  - ∘ A -> D
  - ∘ B -> E
  - ∘ C -> F

•••

∘ Z -> C

Here is an example taken from the website Practical Cryptography

#### **Example**

Here's an example of encoding a message with a Caesar cipher with a shift of 1

Plaintext defendtheeastwallofthecastle

Ciphertext efgfoeuiffbtuxbmmpguifdbtumf

#### Idea:

- Consider the relative frequencies of letters in the "decoded" message for different shift lengths
- Assuming the correct cipher will decode to English, we can automatically search for the most likely cipher by computing the chi-squared statistic for each possible shift.
- The smallest test statistic will correspond to the cipher that yields a decoded message that most closely resembles the relative frequencies of letters in English

Here is an example taken from the website Practical Cryptography

• Consider the following encoded text:

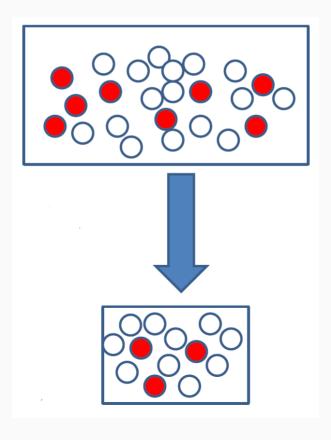
aoljhlzhyjpwolypzvulvmaollhysplzaruvduhukzptwslzajpwoly zpapzhafwlvmzbizapabapvujpwolypudopjolhjoslaalypuaolwsh pualeapzzopmalkhjlyahpuubtilyvmwshjlzkvduaolhswohila

- The chi-squared statistic for each shift is a mesaure of how closely the decoded message matches the frequencies of English.
- The minimum statistic should correspond to the shift that is most likely to be the correct cipher.

decryption key		plaintext	chi-squared
0	AOLJHLZHYJPI	WOLYPZVULVMAOL	1634.09
1	ZNKIGKYGXIO	/NKXOYUTKULZNK	3441.13
2	YMJHFJXFWHNI	CMYXTSJTKYMJ	2973.71
3	XLIGEIWEVGM <sup>-</sup>	TLIVMWSRISJXLI	1551.67
4	WKHFDHVDUFLS	SKHULVRQHRIWKH	1199.40
5	VJGECGUCTEKI	RJGTKUQPGQHVJG	1466.62
6	UIFDBFTBSDJ	QIFSJTPOFPGUIF	1782.26
7	THECAESARCI	PHERISONEOFTHE	33.67
8	SGDBZDRZQBH	OGDQHRNMDNESGD	1747.07
9	RFCAYCQYPAGI	NFCPGQMLCMDRFC	1386.62
10	QEBZXBPXOZFI	MEBOFPLKBLCQEB	3423.96
11	PDAYWAOWNYE	_DANEOKJAKBPDA	809.38
12	OCZXVZNVMXDI	CZMDNJIZJAOCZ	4646.96
13	NBYWUYMULWC:	JBYLCMIHYIZNBY	724.11
14	MAXVTXLTKVB:	[AXKBLHGXHYMAX	2159.43
15	LZWUSWKSJUAŁ	HZWJAKGFWGXLZW	1787.26
16	KYVTRVJRITZ	GYVIZJFEVFWKYV	3527.17
17	JXUSQUIQHSYI	XUHYIEDUEVJXU	2967.66
18	IWTRPTHPGRXI	EWTGXHDCTDUIWT	1368.70
19	HVSQOSGOFQWI	OVSFWGCBSCTHVS	929.17
20	GURPNRFNEPV	CUREVFBARBSGUR	461.19

# Review of Hypergeometric Distribution

- ullet Consider a box containing n balls total, with r red balls, and n-r white balls.
- ullet Suppose we randomly select m balls from the box without replacement.
- The number of red balls selected will follow a hypergeometric distribution.

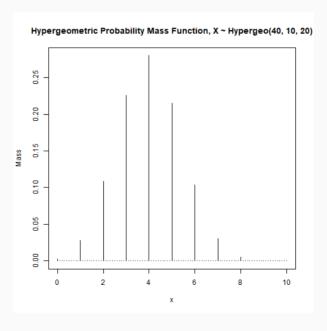


# Review of Hypergeometric Distribution

A random variable  $X \sim Hypergeo(n,m,r)$  following a hypergeometric distribution has probability mass function

$$P(X=k) = rac{inom{r}{k}inom{n-r}{m-k}}{inom{n}{m}}$$

The mean is  $\mathbb{E}(X) = m \cdot \frac{r}{n}$ .



- Suppose we wish to determine whether carriers of the APOE4 gene are more likely to have Alzheimer's Disease by age 70.
- ullet We can consider a sample of data arranged as a 2 imes 2 table.

	APOE4 Yes	APOE4 No	Total
AD Yes	$N_{11}$	$N_{12}$	$n_1$ .
AD No	$N_{21}$	$N_{22}$	$n_2$ .
Total	$n_{\cdot 1}$	$n_{\cdot 2}$	<i>n</i>

Table 3: Set up for Fisher's Exact Test.

#### **Asummptions**

- Independent observations
- ullet Fixed marginal counts  $(n_1, n_2, n_{\cdot 1}, n_{\cdot 2}, n_{\cdot \cdot})$
- Each observation belongs to exactly one cell in the table

#### **Null Hypothesis**

- ullet  $H_0$ : There is no association between membership in the row categories and membership in the column categories.
- In our example:
- ullet  $H_0:$  There is no association between carrying the APOE4 gene and occurrence of AD.

#### **Test Statistic**

- There are four random variables in the  $2 \times 2$  table.
- Because the marginal counts are fixed, if we know one of the cell values, the remaining three cells are fixed.
- ullet Consequently, we can use any of the cell values from observed data as our test statistic, e.g.  $N_{11}$ .
- ullet To find the rejection region, we need the distribution of  $N_{11}$  under the null hypothesis.
- Under the null hypothesis of no association,  $N_{11}$  will follow a hypergeometric distribution.

$$P(N_{11}=n_{11})\stackrel{H_0}{=}rac{inom{n_{1\cdot}}{n_{11}}inom{n_{2\cdot}}{n_{\cdot 1}-n_{11}}}{inom{n_{\cdot \cdot}}{n_{\cdot \cdot 1}}}=rac{inom{n_{1\cdot}}{n_{11}}inom{n_{2\cdot}}{n_{21}}}{inom{n_{\cdot \cdot}}{n_{\cdot \cdot 1}}}$$

• Suppose we observe the following data

	APOE4 Yes	APOE4 No	Total
AD Yes	4	1	5
AD No	2	7	9
Total	6	8	14

Table 4: Example data for Fisher's Exact Test.

- ullet Under  $H_0$  of no association, the  $N_{11}$  cell follows a hypergeometric distribution with n=14, m=6, r=5 .
- ullet We can compute the P-value for Fisher's Exact test in  ${ t R}$ :

```
dat \leftarrow matrix(c(4, 2, 1, 7), 2, 2)
 fisher.test(dat)
##
       Fisher's Exact Test for Count Data
###
###
## data: dat
## p-value = 0.09091
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
      0.6418261 779.1595463
## sample estimates:
## odds ratio
     10.98111
###
```

- ullet The P-value is 0.0909, thus we do not have sufficient evidence to reject the null hypothesis at the 0.05 level of significance.
- That is, we do not have sufficient evidence to conclude that there is a significant association between APOE4 and occurrence of AD, at the 0.05 level of significance.