

# Statistical Modeling

## BANA 7042

Lecture 6: Modeling count data

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# What is count data?

- A type of data in which the observations take non-negative integer values  $\{0, 1, 2, 3, \dots\}$ .
- Examples
  - The number of patients who come to the ER of Children's Hospital between 9PM and 1AM.
  - The number of shoppers in Kenwood Towne Centre on a calendar day.
  - The number of Google searches (in a week) for flights to Shanghai right before Lunar New Year.

# Compared to other data types ...

- In which ways, count data is different from binomial data or rank (ordinal) data?
- Binomial data (e.g., the no. of damages out of 6 O-rings) has an upper bound, whereas count data is unbounded from above.
- Ordinal data (e.g., ratings of a product) only reflects ranks, its values  $\{0,1,2,3\}$  should not be interpreted as numbers. The values of count data  $\{0,1,2,\dots\}$  are the numbers of the occurrence of a specific event.

# What distribution to model count data?

- Poisson distribution

$$\Pr\{Y = y\} = \frac{e^{-\mu} \mu^y}{y!}, \quad y = 0, 1, 2, \dots$$

- How many parameters used in Poisson distribution?

$$\mu = E(Y) = Var(Y)$$

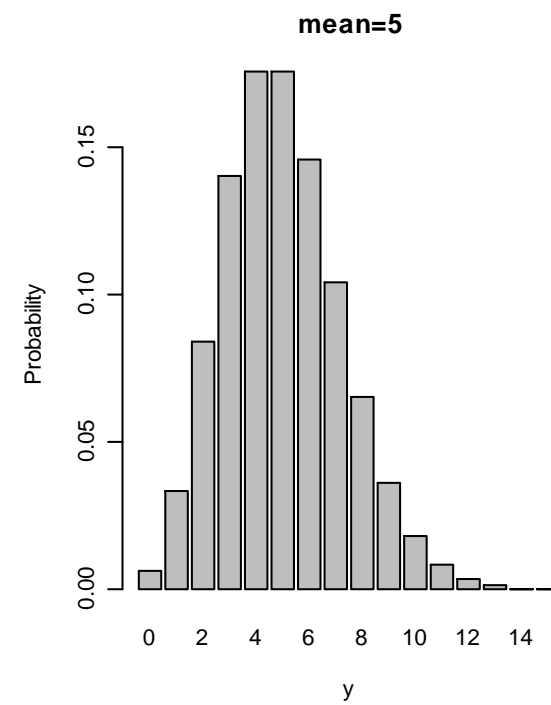
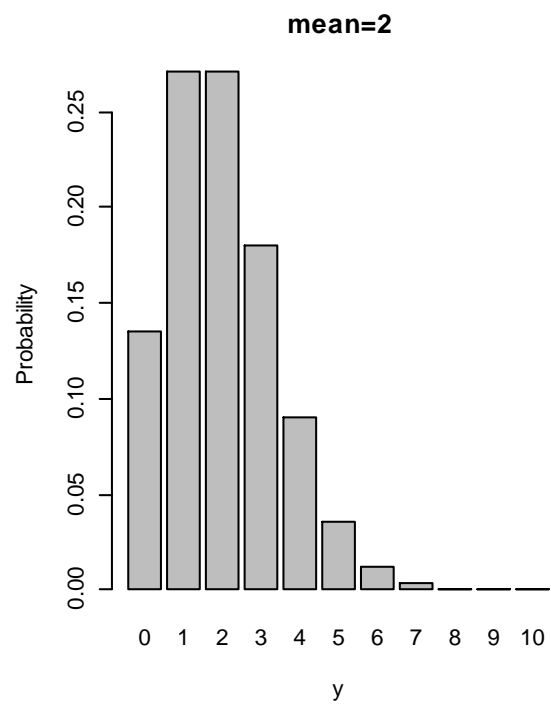
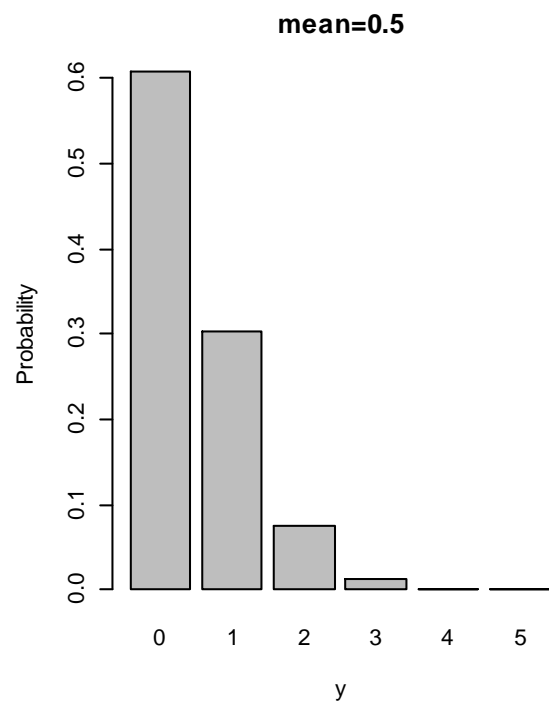
# The impact of the mean parameter

```
par(mfrow=c(1,3))
```

```
barplot(dpois(0:5,0.5),xlab="y",ylab="Probability",names=0:5,main="mean=0.5")
```

```
barplot(dpois(0:10,2),xlab="y",ylab="Probability",names=0:10,main="mean=2")
```

```
barplot(dpois(0:15,5),xlab="y",ylab="Probability",names=0:15,main="mean=5")
```





How can we model a count response  
using a number of covariates?



# Model the number of species on the Galapagos Islands













# Species diversity on the Galapagos Islands

There are 30 Galapagos islands and 7 variables in the dataset. The relationship between the number of plant species and several geographic variables is of interest.

```
library("faraway")  
data(gala)  
str(gala)  
?gala  
gala<-gala[,-2] ### Remove the second variable  
summary(gala)
```

#### Species

the number of plant species found on the island

#### Endemics

the number of endemic species

#### Area

the area of the island ( $\text{km}^2$ )

#### Elevation

the highest elevation of the island (m)

#### Nearest

the distance from the nearest island (km)

#### Scruz

the distance from Santa Cruz island (km)

#### Adjacent

the area of the adjacent island (square km)

#### Source

M. P. Johnson and P. H. Raven (1973) "Species number and endemism: The Galapagos Archipelago revisited" Science, 179, 893-895



# Summary statistics

```
> summary(gala)
```

Species	Area	Elevation	Nearest
Min. : 2.00	Min. : 0.010	Min. : 25.00	Min. : 0.20
1st Qu.: 13.00	1st Qu.: 0.258	1st Qu.: 97.75	1st Qu.: 0.80
Median : 42.00	Median : 2.590	Median : 192.00	Median : 3.05
Mean : 85.23	Mean : 261.709	Mean : 368.03	Mean : 10.06
3rd Qu.: 96.00	3rd Qu.: 59.237	3rd Qu.: 435.25	3rd Qu.: 10.03
Max. : 444.00	Max. : 4669.320	Max. : 1707.00	Max. : 47.40

Scruz	Adjacent
Min. : 0.00	Min. : 0.03
1st Qu.: 11.03	1st Qu.: 0.52
Median : 46.65	Median : 2.59
Mean : 56.98	Mean : 261.10
3rd Qu.: 81.08	3rd Qu.: 59.24
Max. : 290.20	Max. : 4669.32

# The idea of modeling a binary response

- Suppose the binary response

$$Y \sim \text{Bernoulli}(p)$$

- We will make two additional assumptions on top of this assumption:
  1.  $Y$  relies on  $X$  only through its mean, e.g.  $Y \sim \text{Bernoulli}(p(X))$
  2. The logit transformation of the parameter  $p$

$$\text{logit}(p) = \log\left(\frac{p}{1-p}\right) = \beta_1 + \beta_2 X$$



# How to extend the idea to modeling a count response?

- Suppose the count response

$$Y \sim \text{Poisson}(\mu)$$

- We will make two additional assumptions on top of this assumption:
  1.  $Y$  relies on  $X$  only through its mean, e.g.  $Y \sim \text{Poisson}(\mu(X))$
  2. The log transformation of the parameter  $\mu$

$$\log(\mu) = \beta_1 + \beta_2 X$$

# Fit a GLM

```
modp<-glm(Species ~ ., family=poisson, gala)
summary(modp)
step(modp)
drop1(modp, test="Chisq")
```

```
> summary(modp)
```

Call:

```
glm(formula = Species ~ ., family = poisson, data = gala)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-8.2752	-4.4966	-0.9443	1.9168	10.1849

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	3.155e+00	5.175e-02	60.963	< 2e-16 ***
Area	-5.799e-04	2.627e-05	-22.074	< 2e-16 ***
Elevation	3.541e-03	8.741e-05	40.507	< 2e-16 ***
Nearest	8.826e-03	1.821e-03	4.846	1.26e-06 ***
Scruz	-5.709e-03	6.256e-04	-9.126	< 2e-16 ***
Adjacent	-6.630e-04	2.933e-05	-22.608	< 2e-16 ***

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 3510.73 on 29 degrees of freedom  
Residual deviance: 716.85 on 24 degrees of freedom  
AIC: 889.68

```
> step(modp)
```

```
Start:  AIC=889.68
```

```
Species ~ Area + Elevation + Nearest + Scrutz +  
Adjacent
```

	Df	Deviance	AIC
<none>		716.85	889.68
- Nearest	1	739.41	910.24
- Scrutz	1	813.62	984.45
- Area	1	1204.35	1375.18
- Adjacent	1	1341.45	1512.29
- Elevation	1	2389.57	2560.40

```
> drop1(modp,test="LRT")
```

Single term deletions

Model:

Species ~ Area + Elevation + Nearest + Scrutz + Adjacent

	Df	Deviance	AIC	LRT	Pr(>Chi)	
<none>		716.85	889.68			
Area	1	1204.35	1375.18	487.51	< 2.2e-16	***
Elevation	1	2389.57	2560.40	1672.72	< 2.2e-16	***
Nearest	1	739.41	910.24	22.57	2.031e-06	***
Scrutz	1	813.62	984.45	96.77	< 2.2e-16	***
Adjacent	1	1341.45	1512.29	624.61	< 2.2e-16	***

# Check the correlation

```
> round(cor(gala), 2)
```

	Species	Area	Elevation	Nearest	Scruz	Adjacent
Species	1.00	0.62	0.74	-0.01	-0.17	0.03
Area	0.62	1.00	0.75	-0.11	-0.10	0.18
Elevation	0.74	0.75	1.00	-0.01	-0.02	0.54
Nearest	-0.01	-0.11	-0.01	1.00	0.62	-0.12
Scruz	-0.17	-0.10	-0.02	0.62	1.00	0.05
Adjacent	0.03	0.18	0.54	-0.12	0.05	1.00

# Prediction

```
> modp$y
```

Baltra	Bartolome	Caldwell	Champion	Coamano	Daphne.Major	Daphne.Minor	Darwin
58	31	3	25	2	18	24	10
Eden	Enderby	Espanola	Fernandina	Gardner1	Gardner2	Genovesa	Isabela
8	2	97	93	58	5	40	347
Marchena	Onslow	Pinta	Pinzon	Las.Plazas	Rabida	SanCristobal	SanSalvador
51	2	104	108	12	70	280	237
SantaCruz	SantaFe	SantaMaria	Seymour	Tortuga	Wolf		
444	62	285	44	16	21		

```
> round(predict(modp,type="response"),1)
```

Baltra	Bartolome	Caldwell	Champion	Coamano	Daphne.Major	Daphne.Minor	Darwin
78.7	20.4	25.7	21.4	17.0	36.6	32.1	10.9
Eden	Enderby	Espanola	Fernandina	Gardner1	Gardner2	Genovesa	Isabela
29.8	26.8	27.9	87.7	15.9	38.2	25.0	370.8
Marchena	Onslow	Pinta	Pinzon	Las.Plazas	Rabida	SanCristobal	SanSalvador
55.8	20.3	212.6	121.4	32.2	53.1	218.8	371.0
SantaCruz	SantaFe	SantaMaria	Seymour	Tortuga	Wolf		
297.3	60.9	158.2	36.9	35.5	18.1		

# Goodness of fit measure

- Pearson's  $X^2$  statistic

$$X^2 = \sum_{i=1}^n \frac{(y_i - \hat{\mu}_i)^2}{\hat{\mu}_i}$$

```
gof<-sum(residuals(modp,type="pearson")^2)
pchisq(gof,df.residual(modp),lower=F)
```



```
> gof    ### Pearson's goodness of fit statistic
[1] 761.9792
> df.residual(modp)    ### Degrees of freedom
[1] 24
> pchisq(gof, df.residual(modp), lower=F)    ### P-value
[1] 2.18719e-145
```

The model does not fit the data well. Why?

# The mean and variance parameters are not separatable

$$Y \sim \text{Poisson}(\mu)$$

- The mean is  $E(Y) = \mu$
- The variance is  $Var(Y) = \mu$
- Once the mean is specified by the Poisson regression, the variance is determined at the same time! This is different from the case of linear regression models.

# What would you do?

$$Y \sim \text{Poisson}(\mu)$$

- Suppose the mean  $E(Y) = \mu$  is correctly captured by the Poisson regression model.
- But the data suggest that the variance is consistently **greater** than

$$\text{Var}(Y) = \mu$$

# Dispersion parameter

- Suppose the count response

$$Y \sim \text{Poisson}(\mu)$$

- We will make **three** additional assumptions on top of this assumption:
  1. Y relies on X only through its mean, e.g  $Y \sim \text{Poisson}(\mu(X))$
  2. The log transformation of the parameter  $\mu$

$$\log(\mu) = \beta_1 + \beta_2 X$$

3. The variance  $\text{Var}(Y) = \phi\mu$ , where the **dispersion parameter**  $\phi$  allows one more layer of flexibility of the model.

# Estimating the dispersion parameter

$$\hat{\sigma}^2 = \frac{X^2}{n-q}$$

- Here,  $X^2$  is the usual Pearson goodness-of-fit statistic,  $n$  is the number of sample cases (number of rows in the dataset we are modeling), and  $q$  is the number of parameters.
- Please try:
- `dp<-gof/modp$df.res`

# Updating the model

```
> dp  
[1] 31.74914
```

```
> summary(modp, dispersion=dp)
```

```
Call:  
glm(formula = Species ~ ., family = poisson, data = gala)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	3.1548079	0.2915897	10.819	< 2e-16	***
Area	-0.0005799	0.0001480	-3.918	8.95e-05	***
Elevation	0.0035406	0.0004925	7.189	6.53e-13	***
Nearest	0.0088256	0.0102621	0.860	0.390	
Scruz	-0.0057094	0.0035251	-1.620	0.105	
Adjacent	-0.0006630	0.0001653	-4.012	6.01e-05	***

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 31.74914)

Null deviance: 3510.73 on 29 degrees of freedom  
Residual deviance: 716.85 on 24 degrees of freedom  
AIC: 889.68

# Further reading

- Zero inflated count models
- Rate models