Generalized Linear Models
Consider the normal theory Gauss–Markov linear model

\[ y = X\beta + \varepsilon, \quad \varepsilon \sim N(0, \sigma^2 I). \]

Another way to write this model is

\[ y_i \sim N(m_i, \sigma^2), \quad \text{where} \]

\[ m_i = x_i' \beta \quad \text{for all } i = 1, \ldots, N \quad \text{and} \]

\[ y_1, \ldots, y_n \text{ independent.} \]
This is a special case of what is known as a generalized linear model.

Here is another special case:

\[ Y_i \sim \text{Bernoulli}(\pi_i), \text{ where} \]

\[ \pi_i = \frac{\exp(x_i' \beta)}{1 + \exp(x_i' \beta)} \quad \text{for all } i = 1, \ldots, N \text{ and} \]

\[ Y_1, \ldots, Y_n \text{ are independent.} \]
In each example, all responses are independent and each response is a draw from one type of distribution whose parameters may depend on explanatory variables through a linear predictor $X_i\beta$. 
The second model, for the case of a binary response, is often called a **logistic regression model**.

Binary responses are common (success/failure, survive/die, good customer/bad customer, win/lose, etc.)

The logistic regression model can help us understand how explanatory variables are related to the probability of "success."

In health study to investigate an epidemic outbreak of a disease that is spread by mosquitoes, individuals were randomly sampled within two sectors in a city to determine if the person had recently contracted the disease under study.

\[ y_i = 1 \text{ (person i has the disease)} \]

\[ y_i = 0 \text{ (person does not have the disease)} \]
Potential explanatory variables include

age in years

socioeconomic status (1 = upper, 2 = middle, 3 = lower)

sector (1 or 2)

These variables were recorded for 196 randomly selected individuals.

Are any of these variables associated with the probability of disease and if so how?
We will demonstrate how to use R to fit a logistic regression model to this data set.

Before delving more deeply into logistic regression, we will review the basic facts of the Bernoulli distribution.
$y \sim \text{Bernoulli } (\pi)$ has probability mass function

$$f(y) = \begin{cases} \pi^y (1-\pi)^{1-y} & \text{for } y \in \{0,1\} \\ 0 & \text{otherwise} \end{cases}$$

Thus, $Pr(y=0) = \pi^0 (1-\pi)^{1-0} = 1-\pi$

and $Pr(y=1) = \pi^1 (1-\pi)^{1-1} = \pi$. 
\[ E(y) = \sum y \cdot f(y) = 0 \cdot (1-\pi) + 1 \cdot \pi = \pi. \]

\[ E(y^2) = \sum y^2 \cdot f(y) = 0^2 \cdot (1-\pi) + 1^2 \cdot \pi = \pi. \]

\[ \text{Var}(y) = E(y) - \{E(y)^2\}^2 = \pi - \pi^2 = \pi (1-\pi). \]

Note that \( \text{Var}(y) \) is a function of \( E(y) \).
The Logistic Regression Model

For $i=1, \ldots, N$, $Y_i \sim \text{Bernoulli}(\pi_i)$,

where $\pi_i = \frac{\exp(\mathbf{x}_i' \beta)}{1 + \exp(\mathbf{x}_i' \beta)}$ and $Y_1, \ldots, Y_n$ are independent.
The function $g(\pi) = \log \left( \frac{\pi}{1-\pi} \right)$ is called the logit function.

The logit function maps the interval $(0, 1)$ to the real line $(-\infty, \infty)$. If $\pi$ is a probability, so $\log \left( \frac{\pi}{1-\pi} \right)$ is the log ("odds").

\[
\text{Odds of event } A \equiv \frac{\Pr(A)}{1-\Pr(A)}.
\]
Note that

\[ g(\Pi_i) = \log \left( \frac{\Pi_i}{1-\Pi_i} \right) \]

\[ = \log \left[ \frac{\exp(x_i'\beta)}{1 + \exp(x_i'\beta)} / \frac{1}{1 + \exp(x_i'\beta)} \right] \]

\[ = \log \left[ \exp(x_i'\beta) \right] = x_i'\beta. \]
Thus, the logistic regression model says that

\[ Y_i \sim \text{Bernoulli}(\pi_i) \text{ where} \]

\[ \log \left( \frac{\pi_i}{1-\pi_i} \right) = x_i' \beta. \]

In Generalized Linear Models terminology, the logit is called the link function because it "links" the mean of \( Y_i \) (\( \pi_i \)) to the linear predictor \( x_i' \beta \).
For Generalized Linear Models, it is not necessarily that the mean of $y_i$ be a linear function of $\beta$.

Rather, some function of the mean of $y_i$ is a linear function of $\beta$.

For logistic regression, that function is

$$\text{logit}(\pi_i) = \log \left( \frac{\pi_i}{1 - \pi_i} \right) = \mathbf{x}_i' \mathbf{\beta}.$$
When the response is Bernoulli or, more generally, binomial, the logit link function is one natural choice. However, other link functions can be considered.

Some common choices (that are also available in R) include the following:
logit: \( \log \left( \frac{\pi}{1-\pi} \right) = \beta' x \)

probit: \( \Phi^{-1}(\pi) = \beta' x \)

\[ \text{Inverse of } N(0,1) \text{ CDF.} \]

complementary log-log (cloglog in R):

\( \log \left( -\log (1-\pi) \right) = \beta' x \)
Although any of these link functions (or others) can be used, the logit link has some advantages when it comes to interpreting the results (as we will discuss later).

Thus, the logit link is a good choice if it can provide a good fit to the data.
The likelihood function for logistic regression is

\[
\ell (\beta | Y) = \sum_{i=1}^{n} \log \left[ \pi_i Y_i (1 - \pi_i)^{1 - Y_i} \right]
\]

\[
= \sum_{i=1}^{n} \left[ Y_i \log (\pi_i) + (1 - Y_i) \log (1 - \pi_i) \right]
\]

\[
= \sum_{i=1}^{n} \left[ Y_i \left\{ \log (\pi_i) - \log (1 - \pi_i) \right\} + \log (1 - \pi_i) \right]
\]

\[
= \sum_{i=1}^{n} \left[ Y_i \log \left( \frac{\pi_i}{1 - \pi_i} \right) + \log (1 - \pi_i) \right]
\]

\[
= \sum_{i=1}^{n} \left[ Y_i X_i \beta - \log (1 + \exp \{ X_i \beta \}) \right].
\]
For Generalized Linear Models, Fisher's Scoring Method is typically used to obtain an MLE for $\beta$, denoted by $\hat{\beta}$.

Fisher's Scoring Method is a variation of the Newton-Raphson algorithm in which the Hessian matrix (matrix of second partial derivatives) is replaced by its expected value (-Fisher Information matrix).
For Generalized Linear Models, Fisher's scoring method results in an iterative weighted least squares procedure.

The algorithm is presented for the general case in Section 2.5 of Generalized Linear Models 2nd Edition (1989) by McCullagh and Nelder.
For sufficiently large samples, \( \hat{\beta} \) is approximately normal with mean \( \beta \) and a variance-covariance matrix that can be approximated by the estimated inverse of the Fisher information matrix.
Inference can be conducted using the Wald approach or via likelihood ratio testing as discussed in Slide set 27.
Interpretation of Logistic Regression

Parameters:

Let \( \tilde{x} = (x_1, x_2, \ldots, x_{j-1}, x_j + 1, x_{j+1}, \ldots, x_p) \).

In other words, \( \tilde{x} \) is the same as \( x \) except that the \( j \)th explanatory variable has been increased by one unit.

Let \( \tilde{\pi} = \frac{\exp(x' \beta)}{1 + \exp(x' \beta)} \) and \( \tilde{\pi} = \frac{\exp(\tilde{x}' \beta)}{1 + \exp(\tilde{x}' \beta)} \).
The odds ratio

\[
\frac{\frac{\hat{\pi}}{1-\hat{\pi}}}{\frac{\pi}{1-\pi}} = \exp \left\{ \log \left( \frac{\hat{\pi}}{1-\hat{\pi}} \right) \right\}
\]

\[
= \exp \left\{ \log \left( \frac{\hat{\pi}}{1-\hat{\pi}} \right) - \log \left( \frac{\pi}{1-\pi} \right) \right\}
\]

\[
= \exp \left\{ \frac{\hat{x}_j}{\beta} - \frac{x_j}{\beta} \right\}
\]

\[
= \exp \left\{ (\hat{x}_j + 1) \beta_j - x_j \beta_j \right\}
\]

\[
= \exp \left\{ \beta_j \right\}
\]
Thus, \( \frac{\hat{\pi}}{1-\hat{\pi}} = \exp(\beta_j) \frac{\pi}{1-\pi} \).

All other explanatory variables held constant, the odds of success at \( X_j + 1 \) are \( \exp(\beta_j) \) times the odds of success at \( X_j \).

This is true regardless of the initial value \( X_j \).
A 1 unit increase in the $j$th explanatory variable (with all other explanatory variables held constant) is associated with a multiplicative change in the odds of success by the factor $\exp(\beta_j)$. 
If \((L_j, U_j)\) is a 100\((1-\alpha)\)% confidence interval for \(\beta_j\), then

\[\exp\{L_j\}, \exp\{U_j\}\]

is a 100\((1-\alpha)\)% confidence interval for \(\exp\{\beta_j\}\).
Also, note that

\[ \Pi = \frac{\exp(x/\beta)}{1 + \exp(x/\beta)} = \frac{1}{\exp(x/\beta) + 1} = \frac{1}{1 + \exp(-x/\beta)}. \]

Thus, if \((L_j, U_j)\) is a \(100(1-\alpha)\%\) confidence interval for \(x/\beta\), then a \(100(1-\alpha)\%\) confidence interval for \(\Pi\) is \(\left( \frac{1}{1 + \exp(-L_j)}, \frac{1}{1 + \exp(-U_j)} \right)\).
d=read.delim("http://www.public.iastate.edu/~dnett/S511/Disease.txt")

head(d)

<table>
<thead>
<tr>
<th>id</th>
<th>age</th>
<th>ses</th>
<th>sector</th>
<th>disease</th>
<th>savings</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>33</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>35</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>3</td>
<td>6</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>4</td>
<td>60</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>5</td>
<td>18</td>
<td>3</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>6</td>
<td>26</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

d$ses=as.factor(d$ses)
d$sector=as.factor(d$sector)
o=glm(disease~age+ses+sector,  
   family=binomial(link=logit),  
   data=d)

summary(o)

Call:
glm(formula = disease ~ age + ses + sector, family =  
   binomial(link = logit),  
   data = d)

Deviance Residuals:

       Min        1Q   Median        3Q       Max
-1.6576   -0.8295  -0.5652   1.0092   2.0842
Coefficients:

|             | Estimate | Std. Error | z value | Pr(>|z|)   |
|-------------|----------|------------|---------|-----------|
| (Intercept) | -2.293933| 0.436769   | -5.252  | 1.50e-07  *** |
| age         | 0.026991 | 0.008675   | 3.111   | 0.001862  **  |
| ses2        | 0.044609 | 0.432490   | 0.103   | 0.917849  |
| ses3        | 0.253433 | 0.405532   | 0.625   | 0.532011  |
| sector2     | 1.243630 | 0.352271   | 3.530   | 0.000415  *** |

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 236.33  on 195  degrees of freedom
Residual deviance: 211.22  on 191  degrees of freedom
AIC: 221.22

Number of Fisher Scoring iterations: 3
coef(o)

(Intercept)         age        ses2        ses3     sector2   -2.29393347  0.02699100  0.04460863  0.25343316  1.24363036

v=vcov(o)

round(v,3)

(Intercept)    age   ses2   ses3 sector2
(Intercept)       0.191 -0.002 -0.083 -0.102  -0.080 age              -0.002  0.000  0.000  0.000   0.000
ses2             -0.083  0.000  0.187  0.072   0.003 ses3             -0.102  0.000  0.072  0.164   0.039 sector2          -0.080  0.000  0.003  0.039   0.124

confint(o)

Waiting for profiling to be done...

2.5 %      97.5 %
(Intercept) -3.19560769 -1.47574975
age          0.01024152  0.04445014
ses2         -0.81499026  0.89014587
ses3         -0.53951033  1.05825383
sector2      0.56319260  1.94992969
oreduced=glm(disease~age+sector,
    family=binomial(link=logit),
    data=d)

anova(oreduced,o,test="Chisq")

Analysis of Deviance Table

Model 1: disease ~ age + sector
Model 2: disease ~ age + ses + sector

| Resid. Df | Resid. Dev | Df | Deviance | P(>|Chi|) |
|-----------|------------|----|----------|----------|
| 1         | 193        |    | 211.64   |          |
| 2         | 191        | 2  | 211.22   | 0.4193   | 0.8109   |
```
o=oreduced

anova(o,test="Chisq")

Analysis of Deviance Table

Model: binomial, link: logit

Response: disease

Terms added sequentially (first to last)

| Df | Deviance | Resid. Df | Resid. Dev | P(>|Chi|)    |
|----|----------|-----------|------------|-------------|
| NULL | 195 | 236.33 |
| age | 1 | 12.013 | 194 | 224.32 | 0.0005283 *** |
| sector | 1 | 12.677 | 193 | 211.64 | 0.0003702 *** |
```
head(model.matrix(o))

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>age</th>
<th>sector2</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>33</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>35</td>
<td>0</td>
</tr>
<tr>
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<td>1</td>
<td>6</td>
<td>0</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>60</td>
<td>0</td>
</tr>
<tr>
<td>5</td>
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<td>18</td>
<td>0</td>
</tr>
<tr>
<td>6</td>
<td>1</td>
<td>26</td>
<td>0</td>
</tr>
</tbody>
</table>

b=coef(o)

b

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>-2.15965912</td>
<td>0.02681289</td>
<td>1.18169345</td>
</tr>
</tbody>
</table>

ci=confint(o)

Waiting for profiling to be done...

<p>| | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>-2.86990940</td>
<td>-1.51605906</td>
<td></td>
</tr>
<tr>
<td>age</td>
<td>0.01010532</td>
<td>0.04421365</td>
<td></td>
</tr>
<tr>
<td>sector2</td>
<td>0.52854584</td>
<td>1.85407936</td>
<td></td>
</tr>
</tbody>
</table>
How should we interpret our estimate of the slope coefficient on age?

\[ \exp(b[2]) \]

age
1.027176

All else equal, the odds of disease are about 1.027 times greater for someone age \( x+1 \) than for someone age \( x \). An increase of one year in age is associated with an increase in the odds of disease by about 2.7%. A 95% confidence interval for the multiplicative increase factor is

\[ \exp(ci[2,]) \]

2.5 % 97.5 %
1.010157 1.045206
How should we interpret our estimate of the slope coefficient on sector?

\( \exp(b[3]) \)
sector2
3.25989

All else equal, the odds of disease are about 3.26 times greater for someone living in sector 2 than for someone living in sector 1.

A 95% confidence interval for the multiplicative increase factor is

\( \exp(ci[3,]) \)
  
  2.5 %  97.5 %

1.696464  6.385816
#Estimate the probability that a randomly selected 40-year-old living in sector 2 has the disease.

\[ x = c(1, 40, 1) \]

\[
\frac{1}{1 + \exp(-t(x) \times b)}
\]

\[
\begin{bmatrix}
[1,] & 0.5236198
\end{bmatrix}
\]

#Approximate 95% confidence interval for the probability in question.

\[
\text{sexb} = \sqrt{t(x) \times \text{vcov}(o) \times x}
\]

\[
\text{cixb} = c(t(x) \times b - 2 \times \text{sexb}, t(x) \times b + 2 \times \text{sexb})
\]

\[
\frac{1}{1 + \exp(-\text{cixb})}
\]

\[
\begin{bmatrix}
[1] & 0.3965921 & 0.6476635
\end{bmatrix}
\]
Now suppose that instead of a Bernoulli response, we have a binomial response for each unit in an experiment or an observational study.

As an example, consider the trout data set discussed on page 641 of *The Statistical Sleuth*, second edition, by Ramsey and Schafer.

Five doses of toxic substance were assigned to a total of 20 fish tanks using a completely randomized design with four tanks per dose.

For each tank, the total number of fish and the number of fish that developed liver tumors were recorded.
```r
# Load the dataset

d = read.delim("http://www.public.iastate.edu/~dnett/S511/Trout.txt")

d
   dose tumor total
   1 0.010 9  87
   2 0.010 5  86
   3 0.010 2  89
   4 0.010 9  85
   5 0.025 30  86
   6 0.025 41  86
   7 0.025 27  86
   8 0.025 34  88
   9 0.050 54  89
  10 0.050 53  86
  11 0.050 64  90
  12 0.050 55  88
  13 0.100 71  88
  14 0.100 73  89
  15 0.100 65  88
  16 0.100 72  90
  17 0.250 66  86
  18 0.250 75  82
  19 0.250 72  81
  20 0.250 73  89
```
One way to analyze this data would be to convert the binomial counts and totals into Bernoulli responses.

For example, the first line of the data set could be converted into 9 ones and 87-9=78 zeros. Each of these 87 observations would have dose 0.01 as their explanatory variable value.

We could then use the logistic regression modeling strategy for Bernoulli response as described above.

A simpler and equivalent way to deal with this data is to consider a logistic regression model for the binomial counts directly.
Logistic Regression Model for Binomial Count Data:

For all $i=1, \ldots, N$, $Y_i \sim \text{Binomial} \left( M_i, T_i \right)$, where $M_i$ is a known number of trials for observation $i$,

\[
T_i = \frac{\exp(x_i' \beta)}{1 + \exp(x_i' \beta)}, \quad \text{and}
\]

\[Y_i, \ldots, Y_n \text{ are independent.}\]
Recall that for $Y_i \sim \text{Binomial}(M_i, \Pi_i)$,

$$E(Y_i) = M_i \Pi_i \quad \text{Var}(Y_i) = M_i \Pi_i (1-\Pi_i)$$

$$f(Y_i) = \binom{M_i}{Y_i} \Pi_i^{Y_i} (1-\Pi_i)^{M_i-Y_i} \quad \text{for } Y_i = 0, \ldots, M_i$$

$$\lambda(\beta | X) = \sum_{i=1}^{n} \left[ Y_i \log \left( \frac{\Pi_i}{1-\Pi_i} \right) + M_i \log (1-\Pi_i) \right] + \text{const}$$

$$= \sum_{i=1}^{n} \left[ Y_i X_i \beta - M_i \log (1+\exp \{-X_i \beta\}) \right] + \text{const}.$$
The function $l(\beta | y)$ can be maximized over $\beta \in \mathbb{R}^p$ as discussed previously to obtain an MLE $\hat{\beta}$.

We can compare the fit of a logistic regression model to what is known as a "Saturated" model.

The saturated model uses one parameter for each observation. In this case, there is one parameter for each $y_i$. 
Logistic Regression Model

\[ Y_i \sim \text{Binomial} \left( M_i, \Pi_i \right) \]

\[ Y_1, \ldots, Y_n \text{ independent} \]

\[ \Pi_i = \frac{\exp(\mathbf{x}_i' \beta)}{1 + \exp(\mathbf{x}_i' \beta)} \]

for some \( \beta \in \mathbb{R}^p \)

\( p \) parameters

Saturated Model

\[ Y_i \sim \text{Binomial} \left( M_i, \Pi_i \right) \]

\[ Y_1, \ldots, Y_n \text{ independent} \]

\[ \Pi_i \in [0,1] \text{ for } i = 1, \ldots, n \]

with no other restrictions.

\( n \) parameters
Let \( \hat{\pi}_i = \frac{\exp (x_i' \hat{\beta})}{1 + \exp (x_i' \hat{\beta})} \) for all \( i = 1, \ldots, N \).

Then the likelihood ratio statistic for testing the logistic regression model as the reduced model vs. the saturated model as the full model is

\[
\sum_{i=1}^{n} 2 \left[ y_i \log \left( \frac{y_i}{m_i \hat{\pi}_i} \right) + (m_i - y_i) \log \left( \frac{m_i - y_i}{m_i - m_i \hat{\pi}_i} \right) \right]
\]
This statistic is sometimes called the Deviance Statistic, the Residual Deviance, or just the Deviance.

The statistic can be compared to the $X^2_{n-p}$ distribution to check the goodness of fit of the logistic regression model.
The $\chi^2$ approximation to the null distribution works reasonably well if $m_i \geq 5$ for most $i$.

The term

$$d_i = \text{sign} (y_i - m_i \hat{\pi}_i) \sqrt{2 \left[ y_i \log \left( \frac{y_i}{m_i \hat{\pi}_i} \right) + (m_i - y_i) \log \left( \frac{m_i - y_i}{m_i - m_i \hat{\pi}_i} \right) \right]}$$

is called a **deviance residual**.

Note that the residual deviance statistic $= \sum_{i=1}^{n} d_i^2$. 
Another goodness of fit statistic that is approximately $X^2_{n-p}$ under the null is Pearson's Chi-Square Statistic

$$X^2 = \sum_{i=1}^{n} \left( \frac{Y_i - \hat{E}(Y_i)}{\sqrt{\text{Var}(Y_i)}} \right)^2$$
\[ r_i = \frac{Y_i - \hat{M}_i \hat{\Pi}_i}{\sqrt{\hat{M}_i \hat{\Pi}_i (1 - \hat{\Pi}_i)}} \]

is known as a Pearson residual.

\[ \chi^2 = \sum_{i=1}^{n} r_i^2. \]

For large \( m_i \)'s, both \( d_i \) and \( r_i \) should behave like standard normal random variables if the logistic regression model is correct.
# Let's plot observed tumor proportions for each tank.

plot(d$dose, d$tumor/d$total, col=4, pch=19, xlab="Dose", ylab="Proportion of Fish with Tumor")
# Let's fit a logistic regression model
# dose is a quantitative explanatory variable.

```r
o = glm(cbind(tumor, total - tumor) ~ dose,
       family = binomial(link = logit),
       data = d)
```

```r
summary(o)
```

Call:
`glm(formula = cbind(tumor, total - tumor) ~ dose, family = binomial(link = logit), data = d)`

Deviance Residuals:
```
     Min      1Q  Median      3Q     Max
-7.3577 -4.0473 -0.1515  2.9109  4.7729
```

```r
```
Coefficients:

|            | Estimate | Std. Error | z value | Pr(>|z|) |
|------------|----------|------------|---------|----------|
| (Intercept)| -0.86705 | 0.07673    | -11.30  | <2e-16 *** |
| dose       | 14.33377 | 0.93695    | 15.30   | <2e-16 *** |

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 667.20 on 19 degrees of freedom
Residual deviance: 277.05 on 18 degrees of freedom
AIC: 368.44

Number of Fisher Scoring iterations: 5
#Let's plot the fitted curve.

```r
b = coef(o)
u = seq(0, .25, by = 0.001)
pihat = 1 / (1 + exp(-xb))
lines(u, pihat, col = 2, lwd = 1.3)
```
#Let's use a reduced versus full model likelihood ratio test to test for lack of fit relative to the saturated model.

```
1-pchisq(deviance(o), df.residual(o))
```

[1] 0

#We could try adding higher-order polynomial terms, but let's just skip right to the model with dose as a categorical variable.
d$dosef=gl(5,4)

d
<table>
<thead>
<tr>
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<th>tumor</th>
<th>total</th>
<th>dosef</th>
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<td>54</td>
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<tr>
<td>0.250</td>
<td>73</td>
<td>89</td>
<td>5</td>
</tr>
</tbody>
</table>
```R
o = glm(cbind(tumor, total - tumor) ~ dosef, 
       family = binomial(link = logit), 
       data = d)

summary(o)

Call:
  glm(formula = cbind(tumor, total - tumor) ~ dosef, 
       family = binomial(link = logit), 
       data = d)

Deviance Residuals:
     Min       1Q   Median       3Q      Max
-2.0966  -0.6564  -0.1015   1.0793   1.8513
```
Coefficients:

|                | Estimate | Std. Error | z value | Pr(>|z|) |
|----------------|----------|------------|---------|----------|
| (Intercept)    | -2.5557  | 0.2076     | -12.310 | <2e-16 *** |
| dosef2         | 2.0725   | 0.2353     | 8.809   | <2e-16 *** |
| dosef3         | 3.1320   | 0.2354     | 13.306  | <2e-16 *** |
| dosef4         | 3.8900   | 0.2453     | 15.857  | <2e-16 *** |
| dosef5         | 4.2604   | 0.2566     | 16.605  | <2e-16 *** |

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 667.195 on 19 degrees of freedom
Residual deviance: 25.961 on 15 degrees of freedom
AIC: 123.36

Number of Fisher Scoring iterations: 4
# Let's add the new fitted values to our plot.

```r
fitted(o)
```

```
 1 2 3 4 5 6 7
0.07204611 0.07204611 0.07204611 0.07204611 0.38150289 0.38150289 0.38150289
 8 9 10 11 12 13 14
0.38150289 0.64022663 0.64022663 0.64022663 0.64022663 0.79154930 0.79154930
 15 16 17 18 19 20
0.79154930 0.79154930 0.84615385 0.84615385 0.84615385 0.84615385
```

```r
points(d$dose, fitted(o), pch="_", cex=3, col=3)
```
#The fit looks good, but let's formally test for lack of fit.

1-pchisq(deviance(o), df.residual(o))
[1] 0.03843272

#There is still a significant lack of fit when comparing to the saturated model.

#The problem is over dispersion, otherwise known in this case as extra binomial variation.
Overdispersion:

In the Generalized Linear Models framework, it's often the case that \( \text{Var}(Y_i) \) is a function of \( E(Y_i) \).

That is the case for logistic regression where

\[
\text{Var}(Y_i) = m_i \pi_i (1-\pi_i) = m_i \pi_i - \frac{(m_i \pi_i)^2}{m_i} \\
= E(Y_i) - \frac{[E(Y_i)]^2}{m}.
\]
Thus, when we fit a logistic regression model and obtain estimates of the mean of the response, we get estimates of the variance of the response as well.

If the variability of our response is greater than we should expect based on our estimates of the mean, we say that there is overdispersion.
If either the likelihood ratio-based or the Pearson Chi Square-based test of goodness of fit (or lack of fit), suggests a lack of fit that cannot be explained by other reasons (e.g., poor model fit for the mean or a few extreme outliers) overdispersion may be the problem.
If there is overdispersion, a quasi-likelihood approach may be used.

In the binomial case we make all the same assumptions as before except that we assume \( \text{Var}(Y_i) = \phi M_i \Pi_i (1 - \Pi_i) \) for some unknown dispersion parameter \( \phi > 1 \).
The dispersion parameter $\phi$ can be estimated by
\[
\frac{\sum_{i=1}^{n} d_i^2}{n-p}
\] or
\[
\frac{\sum_{i=1}^{n} r_i^2}{n-p}
\].

Residual Deviance Statistic

Pearson Chi-Square Statistic
All analyses are as before except that

1. The estimated variance of \( \hat{\beta} \) is multiplied by \( \phi \).

2. For Wald type inferences, the standard normal null distribution is replaced by \( t \) with \( n-p \) degrees of freedom.

3. A test statistic \( T \) that was assumed \( X_2^2 \) under \( H_0 \) is replaced with \( T/(q, \phi) \) and compared to an \( F \) distribution with \( q \) and \( n-p \) degrees of freedom.
These changes to the inference strategy in the presence of overdispersion are analogous to the changes that would take place in normal theory Gauss-Markov linear model analysis if we switched from assuming $\sigma^2$ was known to be 1 to assuming $\sigma^2$ was unknown and estimating it with MSE. (Here $\phi$ is like $\sigma^2$ and $\hat{\phi}$ is like MSE.)
Whether there is overdispersion or not, all the usual ways of conducting generalized linear models inference are approximate except for the special case of normal theory linear models.
#Let's estimate the dispersion parameter.

```r
phihat = deviance(o)/df.residual(o)
phihat
[1] 1.730745
```

#We can obtain the same estimate by using the deviance residuals.

```r
di = residuals(o, type="deviance")
sum(di^2)/df.residual(o)
[1] 1.730745
```

#We can obtain an alternative estimate by using the Pearson residuals.

```r
ri = residuals(o, type="pearson")
sum(ri^2)/df.residual(o)
[1] 1.671226
```
Now let's test for effect of dose on the response.

drop1(o, scale=phihat, test="F")

Single term deletions

Model:
cbind(tumor, total - tumor) ~ dosef

scale: 1.730745

<table>
<thead>
<tr>
<th>Df</th>
<th>Deviance</th>
<th>AIC</th>
<th>F value</th>
<th>Pr(F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;none&gt;</td>
<td>25.96</td>
<td>123.36</td>
<td></td>
<td></td>
</tr>
<tr>
<td>dosef</td>
<td>4</td>
<td>667.20</td>
<td>485.86</td>
<td>92.624 2.187e-10 ***</td>
</tr>
</tbody>
</table>

Warning message:
In drop1.glm(o, scale = phihat, test = "F") :
  F test assumes 'quasibinomial' family
There is strong evidence that the probability of tumor formation is different for different doses of the toxicant.
# Let's test for a difference between the top two doses.

\[
b = \text{coef}(o)
\]

\[
b
\]

(Intercept) dosef2 dosef3 dosef4 dosef5
-2.555676  2.072502  3.132024  3.889965  4.260424

\[
v = \text{vcov}(o, \text{dispersion} = \text{phihat})
\]

\[
v
\]

(Intercept) dosef2 dosef3 dosef4 dosef5
(Intercept) 0.07460394 -0.07460394 -0.07460394 -0.07460394 -0.07460394
dosef2 -0.07460394  0.09580324  0.07460394  0.07460394  0.07460394
dosef3 -0.07460394  0.07460394  0.09589002  0.07460394  0.07460394
dosef4 -0.07460394  0.07460394  0.07460394  0.10415162  0.07460394
dosef5 -0.07460394  0.07460394  0.07460394  0.07460394  0.11393904

\[
\text{se} = \sqrt{\text{t}(c(0,0,0,-1,1)) \% \% \% \text{v} \% \% \% c(0,0,0,-1,1)}
\]

\[
tstat = (b[5] - b[4]) / \text{se}
\]

\[
pval = 2 * (1 - \text{pt}(\text{abs}(tstat), \text{df.residual(o)}))
\]

pval

[1,] 0.1785000
We have discussed the case of Bernoulli or binomial response, where logistic regression modeling is a natural generalized linear modeling strategy.
Another commonly encountered special case of generalized linear modeling involves Poisson response.

We begin with a review of the basics of the Poisson distribution.
\( Y \sim \text{Poisson}(\mu) \implies \)

\[
f(y) = \begin{cases} 
  \frac{\mu^y e^{-\mu}}{y!} & \text{for } y = 0, 1, 2, \ldots \\
  0 & \text{otherwise.}
\end{cases}
\]

\( \mathbb{E}(y) = \mu \quad \text{Var}(y) = \mu \)
The usual Generalized Linear Model for Poisson response:

For all $i = 1, \ldots, n$:

$Y_i \sim \text{Poisson}(M_i)$, where

$M_i = \exp(X_i \beta)$ and

$Y_1, \ldots, Y_n$ are independent.
Note that

$$M_i = \exp (x_i' \beta) \iff \log (M_i) = x_i' \beta.$$ 

Thus, $\log$ is the link function in this case.

All the subsequent details for the Poisson case are analogous to those we discussed for the binomial response case.
The general case: For $i=1, \ldots, N$, suppose $Y_i$ has density (or p.m.f.)

$$\exp \left\{ \frac{(y_i - b(\theta_i))}{a(\phi)} + c(y_i, \phi) \right\},$$

where $a(\cdot)$, $b(\cdot)$, and $c(\cdot)$ are known functions and $\Theta_i$ is an unknown parameter and $\phi$ is either a known or unknown parameter depending on the special case.
For all $i = 1, \ldots, N$,

let $\mu_i = E(Y_i)$ and assume that $g(\mu_i) = \frac{X_i' \beta}{\beta}$ for some link function $g(\cdot)$, known vector of explanatory variables $X_i$, and unknown parameter vector $\beta \in \mathbb{R}^p$.

Finally, suppose $Y_1, \ldots, Y_n$ independent.
Analysis Strategy:

1. Find MLE for $\beta$ using the method of Fisher Scoring which results in an iterative weighted least squares approach. In this case.

2. Obtain an estimate of the inverse Fisher information matrix that can be used for Wald type inference concerning $\beta$ and/or conduct likelihood ratio based inference of reduced vs. full models.