

# Module 3, Part 1: Generalized Linear Models

BIOS 526

## Concepts

- Link function.
- Logistic regression and odds ratio.
- Probit regression.
- Poisson regression.

## Readings

- Chapter 3, Wood, S. *Generalized Additive Models*, 2017. Has a nice, self-contained introduction to generalized linear models.

# Linear Regression Model

Consider the following multiple linear regression model. For  $i = 1, \dots, n$ ,

$$y_i = \beta_0 + \sum_{k=1}^p \beta_k x_{ik} + \epsilon_i \quad \epsilon_i \stackrel{iid}{\sim} N(0, \sigma^2),$$

where  $x_{ik}$  is the  $k$ th linear predictor for observation  $i$ .

The above model assumes

- $\beta_0, \beta_1, \dots, \beta_p$  are fixed unknown constants;
- only the residual error  $\epsilon_i$  is **random**.

Therefore,

1.  $y_i$  follows a normal distribution.
2.  $E[y_i | \mathbf{x}_i] = \beta_0 + \sum_{k=1}^p \beta_k x_{ik}$ .

The **linear regression** part is used to model only the **mean function** of  $y_i$ .

# Generalized Linear Regression Model

A generalized linear model (GLM) extends linear regression to other distributions, where the response variable is generated from a distribution in the **exponential family**.

A GLM involves three ingredients:

1. An exponential family of probability distributions.
2. A linear model  $\mathbf{x}'_i\boldsymbol{\beta}$ .
3. A **link function**  $g()$  and its inverse  $g^{-1}()$  relates the linear model to its expectation:

$$E[y_i | \mathbf{x}_i] = \mu_i = g^{-1}(\mathbf{x}'_i\boldsymbol{\beta})$$
$$Var[y_i | \mathbf{x}_i] = V(\mu_i) = V(g^{-1}(\mathbf{x}'_i\boldsymbol{\beta}))$$

Note: unlike ordinary least squares, the basic form of the GLM does not involve a noise variance (no  $\sigma^2$ ).

# Exponential Family

The basic form for an exponential family density is

$$f_{\theta}(y) = \exp [\{y\theta - b(\theta)\} / a(\phi) + c(y, \phi)],$$

where  $b$ ,  $a$ , and  $c$  are known functions, and  $\phi$  is a known scale parameter. There is only **one** unknown parameter:  $\theta$ .

In the GLM,  $\theta$  will be a function of  $x_i'\beta$ .

Examples of distributions in the exponential family include: normal distribution with **known** variance (link = identity), Bernoulli (logit or probit link), binomial (with fixed number of trials), gamma, exponential (link: negative inverse), and others.

[https://en.wikipedia.org/wiki/Generalized\\_linear\\_model](https://en.wikipedia.org/wiki/Generalized_linear_model)

Rather than derive expressions for the general case, we will focus on the two most popular models:

1. Binary outcome:  $y_i \stackrel{ind}{\sim}$  Bernoulli ( $p_i$ ), where  $p_i$  is the probability of success.
2. Poisson outcome:  $y_i \stackrel{ind}{\sim}$  Poisson ( $\lambda_i$ ),  $\lambda_i$  is the rate parameter, equal to expected number of events.

# GLMs

The mean and variance function of  $y_i$  can be expressed as a function of the distribution parameters (i.e.  $p_i$  for Bernoulli and  $\lambda_i$  for Poisson).

1. Binary outcome:

$$E[y_i] = \mu_i = p_i,$$

$$\text{Var}[y_i] = V[\mu_i] = V[p_i] = p_i(1 - p_i).$$

2. Poisson outcome:

$$E[y_i] = \mu_i = \lambda_i,$$

$$\text{Var}[y_i] = V[\mu_i] = V[\lambda_i] = \lambda_i.$$

A natural approach is to model the mean as a function of linear predictors. A difficulty in modeling non-normal data is that the distributional parameters often have constraints.

1. Binary outcome has expected value  $p_i \in (0, 1)$
2. Poisson outcome has expected value  $\lambda_i > 0$ .

# Workspace

# Generalized Linear Regression Model

Our solution is to model the **transformed** mean function:

$$g(\mu_i) = \beta_0 + \sum_{k=1}^p \beta_k x_{ik}.$$

The function  $g(\cdot)$  is known as the **link function**.

The link function should have some desirable properties:

1.  $g(\cdot)$  should have a range of  $(-\infty, \infty)$  because  $\beta_k$  and  $x_{ik}$  can take any real value.
2.  $g(\cdot)$  should have a domain that corresponds to possible values of  $\mu_i$ . (i.e.  $(0, 1)$  for binary outcome and  $(0, \infty)$  for Poisson outcome.
3.  $g(\cdot)$  should be 1-to-1. Then,

$$\mu_i = g^{-1}\left(\beta_0 + \sum_{k=1}^p \beta_k x_{ik}\right).$$

A strictly increasing or decreasing function will satisfy this.



## GLM for Binary Outcome

For  $i = 1, \dots, n$ , assume

$$y_i \stackrel{\text{ind}}{\sim} \text{Bernoulli}(p_i),$$

where  $y_i \in \{0, 1\}$ ,  $y_i|p_i$  for  $i = 1, \dots, n$  are independent, and  $p_i$  is the probability  $y_i = 1$ . The probability mass function is given by

$$f(y_i|p_i) = p_i^{y_i} (1 - p_i)^{1-y_i}.$$

We know that

$$\mu_i = p_i = P(Y_i = 1).$$

So we wish to model

$$g[P(Y_i = 1)] = \beta_0 + \sum_{k=1}^p \beta_k x_{ik}.$$

The two most commonly used link functions are the **logistic function** and the **probit function**.

# Logistic Regression

The logistic regression is formulated as follows. For  $i = 1, \dots, n$ ,

$$y_i \overset{\text{ind}}{\sim} \text{Bernoulli}(p_i)$$

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \sum_{k=1}^p \beta_k x_{ik}.$$

- $g(\mu_i)$  is the **log odds** of success probability.
- $\log\left(\frac{p_i}{1-p_i}\right) \rightarrow -\infty$  when  $p_i \rightarrow 0$ ; and  $\log\left(\frac{p_i}{1-p_i}\right) \rightarrow \infty$  when  $p_i \rightarrow 1$
- $\log\left(\frac{p_i}{1-p_i}\right)$  is strictly increasing.

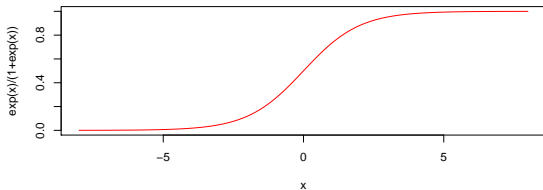
## Likelihood function: logistic regression

$$\begin{aligned}\ell(\boldsymbol{\beta}; \mathbf{y}, \mathbf{x}) &= \log \prod_{i=1}^n p_i^{y_i} (1 - p_i)^{1-y_i} \\ &= \sum_{i=1}^n y_i \log \left( \frac{e^{\boldsymbol{\beta}' \mathbf{x}_i}}{1 + e^{\boldsymbol{\beta}' \mathbf{x}_i}} \right) + (1 - y_i) \log \left( \frac{1}{1 + e^{\boldsymbol{\beta}' \mathbf{x}_i}} \right) \\ &= \sum_{i=1}^n y_i \boldsymbol{\beta}' \mathbf{x}_i - \log(1 + \exp(\boldsymbol{\beta}' \mathbf{x}_i))\end{aligned}$$

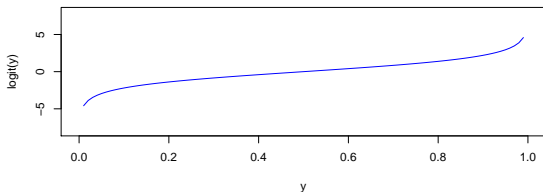
In practice, GLMs are estimated using iteratively reweighted least squares. We won't go into details, but see p. 107 in Wood for more info.

The **logistic** function:

$$p(g) = \exp(g)/(1 + \exp(g)) = 1/(1 + \exp(-g)), \quad (-\infty, \infty) \rightarrow (0, 1).$$



The **logit** function:  $g(p) = \log(p/(1 - p))$ ,  $(0, 1) \rightarrow (-\infty, \infty)$ .



# Logistic Regression: Interpretation

Consider a simple logistic model with only one predictor:

$$y_i \overset{\text{ind}}{\sim} \text{Bernoulli}(p_i)$$
$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 x_i.$$

When  $x_i = 0$ :

- $\log\left(\frac{p_i}{1-p_i}\right) = \beta_0$ .
- $\beta_0$  is interpreted as the **baseline log odds**.  
Function of the probability of success at baseline:

$$p_i = \frac{e^{\beta_0}}{1 + e^{\beta_0}}.$$

- Note that the above function satisfies
  - $p_i \in (0, 1)$  for  $\beta_0 \in \mathbb{R}$ .
  - $p_i$  a strictly increasing function of  $\beta_0$ .

## Logistic Regression: Log odds and log odds ratio

Now we consider the effect of a unit change in  $x_i$ :

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 x_i \quad \text{versus} \quad \log\left(\frac{p_i^*}{1-p_i^*}\right) = \beta_0 + \beta_1 (x_i + 1).$$

Then,

$$\begin{aligned} \log\left(\frac{p_i^*}{1-p_i^*}\right) - \log\left(\frac{p_i}{1-p_i}\right) &= \beta_0 + \beta_1 (x_i + 1) - (\beta_0 + \beta_1 x_i) \\ &= \beta_1. \end{aligned}$$

In words:  $\beta_1$  is the change in log odds per unit change in  $x_i$ .

Equivalently, it is the log odds ratio per unit change in  $x_i$ :

$$\beta_1 = \log \left[ \frac{p_i^*/(1-p_i^*)}{p_i/(1-p_i)} \right].$$

# Logistic Regression: Odds ratio

$e^{\beta_1}$  is the **odds ratio**:

$$e^{\beta_1} = \frac{p_i^*/(1 - p_i^*)}{p_i/(1 - p_i)}.$$

Odds ratio interpretation helpful for indicator variables. Let  $x_i = 1$  in exposed group,  $x_i = 0$  in unexposed group. Then:

$$\begin{aligned} e^{\beta_1} &= \frac{\left\{ \frac{P(y_i=1|x_i=1)}{P(y_i=0|x_i=1)} \right\}}{\left\{ \frac{P(y_i=1|x_i=0)}{P(y_i=0|x_i=0)} \right\}} \\ &= \text{odds(Exposed)}/\text{odds(Unexposed)}. \end{aligned}$$

# Logistic Regression: Background

- Logistic regression is commonly used because the slope coefficient corresponds to the log odds ratio (OR), a commonly used measure in epidemiology.
- OR is different from relative risk.
- Risk ratio (RR) is  $P(y_i = 1|x_i = 1)/P(y_i = 1|x_i = 0)$
- OR is close to RR when the event  $y_i = 1$  is rare, but in general, you need a different model to estimate RR.
- OR can be used in retrospective and observational studies.



# Logistic Regression: Probability

The effect of a unit change in  $x_i$  depends on  $x_i$  on the probability scale.

E.g.,  $\beta_0 = 0$  and  $\beta_1 = 2$ :

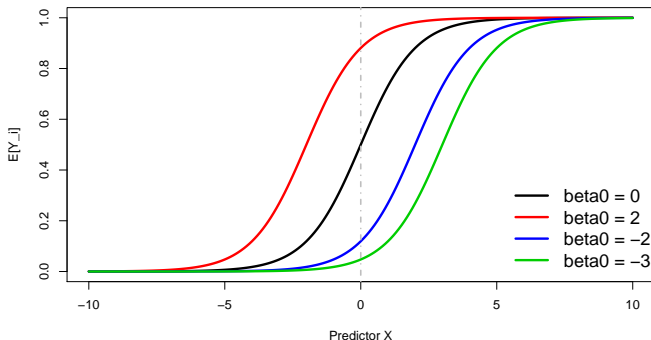
$$\frac{e^{2(0+1)}}{1 + e^{2(0+1)}} - \frac{e^{2(0)}}{1 + e^{2(0)}} \neq \frac{e^{2(1+1)}}{1 + e^{2(1+1)}} - \frac{e^{2(1)}}{1 + e^{2(1)}}$$

A change in  $x_i$  from 0 to 1 increases the probability by 0.38, but a change in  $x_i$  from 1 to 2 increases the probability by 0.10.

Intuitively, this has to be the case in order for the probability to max out at 1:  $\frac{e^{2(100+1)}}{1+e^{2(100+1)}} - \frac{e^{2(100)}}{1+e^{2(100)}} \approx 1 - 1$ .

# Logistic Regression: Effects of Baseline Odds

$$\text{logit}(p_i) = \beta_0 + x_i.$$
$$\mu_i = P(Y_i = 1) = \frac{e^{\beta_0 + x_i}}{1 + e^{\beta_0 + x_i}}.$$



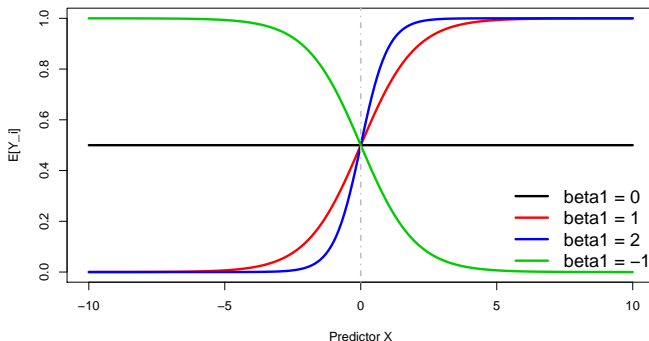
Note:

- The **shape** is maintained.
- The baseline (intercept) probability changes.

# Logistic Regression: Effects of Slope

$$\text{logit}(\mu_i) = \beta_1 x_i.$$

$$\mu_i = P(Y_i = 1) = \frac{e^{\beta_1 x_i}}{1 + e^{\beta_1 x_i}}.$$



Note:

- How the steepness changes.
- How the direction of effect changes.

# Logistic Regression: Interpretation

In multiple logistic regression, for  $i = 1, \dots, n$ ,

$$y_i \stackrel{\text{ind}}{\sim} \text{Bernoulli}(p_i) = \text{Bernoulli}(\mu_i)$$

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \sum_{k=1}^p \beta_k x_{ik}.$$

- $\beta_0$  is the log odds when all covariate values equal zero.
- $\beta_k$  is the log odds ratio associated with covariate  $k$  while controlling for other covariates.

# Logistic Regression: Interpretation

The estimated (predicted) value is given by

$$\mu_i = p_i = \frac{e^{\beta_0 + \sum_{k=1}^p \beta_k x_{ik}}}{1 + e^{\beta_0 + \sum_{k=1}^p \beta_k x_{ik}}}$$

Again, the above function is non-linear in  $x_k$ , in contrast with normal regression

# Inference: Likelihood Ratio Tests

To conduct inference, we appeal to **asymptotic results** that hold for large-ish  $n$ . There are two approaches:

## 1) Likelihood Ratio Tests (Difference in Deviance)

Let  $\beta_F$  be a vector of coefficients of interest. Then to test  $H_0 : \beta_F = 0$ , we create a full and reduced model. Let  $\ell(\hat{\beta}_{\text{Full}})$  be the log-likelihood of the full model, and  $\ell(\hat{\beta}_{\text{Reduced}})$  be the LL for the reduced model. Then we reject  $H_0$  if

$$-2 \left\{ \ell(\hat{\beta}_{\text{Reduced}}) - \ell(\hat{\beta}_{\text{Full}}) \right\} > \chi^2_{\nu, 1-\alpha}$$

where  $\nu$  is the difference in the number of parameters between the full and reduced, and  $\chi^2_{\nu, 1-\alpha}$  is the critical value from a chi-squared distribution with  $\nu$  degrees of freedom.

## Inference: Wald Tests

2) Wald Tests. Under regularity conditions, asymptotically,

$$\begin{aligned}\hat{\beta} &\sim N(\beta, I(\beta)^{-1}), \\ I(\beta) &= E \left\{ \left( \frac{\partial \ell}{\partial \beta} \right) \left( \frac{\partial \ell}{\partial \beta} \right)' \right\} \\ &= -E \frac{\partial^2 \ell}{\partial \beta \partial \beta'},\end{aligned}$$

where the Hessian  $I(\beta)$  is called the Fisher information matrix. See Wood p. 106 for details of the expected Hessian which is calculated during iteratively re-weighted least squares.

We can write  $\hat{\beta} \sim N(\beta, (\mathbf{X}'\mathbf{W}\mathbf{X})^{-1}\phi)$  where  $\mathbf{W}$  contains the “Fisher weights” and  $\phi = 1$  in the usual (not overdispersed) GLM.

In R, the default `summary(glmmodel)` is a Wald-type test:  $\hat{\beta}_j/se(\hat{\beta}_j)$ , where  $se(\hat{\beta}_j)$  is extracted from the square root of the  $j$ th diagonal of the above covariance.

## Binary Outcome Example

Dataset: a cohort of live births from Georgia born in the year 2001 ( $N = 77,340$ ).

Variables:

- *ptb*: indicator for whether the baby from pregnancy  $i$  was born preterm ( $< 37$  weeks).
- *age*: the mother's age at delivery (centered at age 25).
- *male*: indicator of the baby's sex (1 = male; 0=female).
- *tobacco*: indicator for mother's tobacco use during pregnancy (1 = yes; 0 = no)



# The *glm* ( ) Function

Fitting a GLM model in R is very similar to a linear regression model. We need to specify the distribution (**binomial**) and the link function (**logit**).

```
glm(formula = ptb ~ age + male + tobacco, family = binomial(link = "logit"),  
    data = dat)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.5160	-0.4236	-0.4103	-0.4088	2.2500

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-2.4370033	0.0200791	-121.370	< 2e-16 ***
age	-0.0006295	0.0021596	-0.291	0.77068
maleM	0.0723659	0.0258672	2.798	0.00515 **
tobacco	0.4096495	0.0534627	7.662	1.83e-14 ***

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## Birth Outcome Analysis

- Preterm delivery was significantly associated with male babies ( $p$ -value= 0.005) when controlling for age and mother's smoking status. The odds ratio of a preterm birth for a male baby versus a female baby was 1.07 (95% CI: 1.02, 1.13).

$$\text{OR} = e^{0.0723} = 1.07$$

$$\text{CI} = e^{(0.0723 \pm 1.96 * 0.0258)} = (1.02, 1.13)$$

- Note: **transform the intervals**. Do NOT transform standard errors (requires delta method).
- Preterm delivery was significantly associated with whether the mother smoked during pregnancy ( $p < 0.001$ ) when controlling for age and the baby's sex. The odds ratio for mother's that smoked versus did not smoke was  $e^{0.409} = 1.51$  (95% CI: 1.36, 1.67).

## Birth outcome analysis, cont.

- The baseline proportion (female babies born to mother of age 25 who didn't smoke) of preterm delivery was

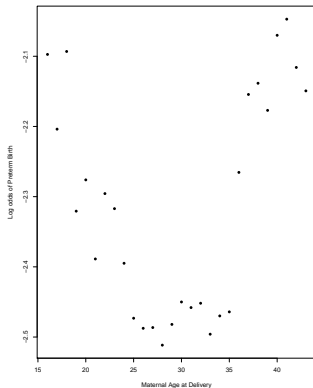
$$\frac{e^{-2.437}}{1 + e^{-2.437}} = 0.080.$$

- We didn't find an effect of mother's age.

## Birth Outcome Analysis - Mother's Age

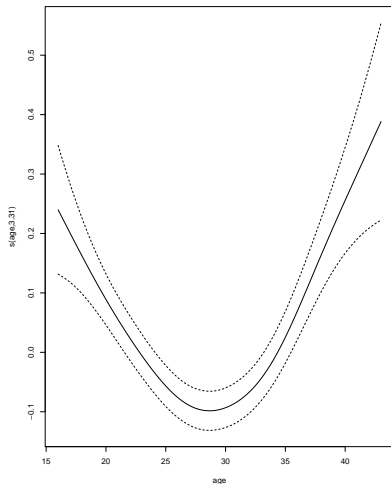
We assumed that the mother's age has a linear effect on log odds of preterm birth. Is this a reasonable assumption?

Explore this by calculating % preterm births for each age group.



# Generalized Additive Model

In Module 5, we will model this non-linearly using splines:



## P-values using LRTs

```
> library(car)
> # LRTs:
> Anova(fit)
Analysis of Deviance Table (Type II tests)
```

Response: ptb

	LR	Chisq	Df	Pr(>Chisq)
age	0.085	1	0.770669	
male	7.834	1	0.005126 **	
tobacco	53.648	1	2.399e-13 ***	

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# Probit Regression

Probit regression is an alternative approach to model binary data. It still assumes the Bernoulli model, but uses a different **link** function. For

$i = 1, \dots, n$ ,

$$y_i \stackrel{ind}{\sim} \text{Bernoulli}(p_i)$$

$$\Phi^{-1}(p_i) = \beta_0 + \sum_{k=1}^p \beta_k x_{ik},$$

where  $\Phi^{-1}$  is the **inverse cumulative distribution function** of a standard normal distribution. Recall  $\Phi^{-1}(x)$  asks what Z-value gives a cumulative probability of  $x$ ?

- Example:  $\Phi^{-1}(0.5) = 0$  and  $\Phi^{-1}(0.975) = 1.96$ .
- Note  $\Phi^{-1}(p_i)$  is strictly increasing, has range  $(-\infty, \infty)$  and domain  $(0, 1)$ .

# Probit Regression

The probit link function results in

$$p_i = \Phi\left(\beta_0 + \sum_{k=1}^p \beta_k x_{ik}\right).$$

Therefore,  $P(y_i = 1)$  is viewed as the probability of a standard normal variable being less than  $\beta_0 + \sum_{k=1}^p \beta_k x_{ik}$ .

Probit regression has a very attractive **latent variable** (i.e., unobserved) interpretation. Let  $Z_i$  denote a latent variable associated with each binary outcome.

$$Z_i \stackrel{ind}{\sim} N\left(\beta_0 + \sum_{k=1}^p \beta_k x_{ik}, 1\right).$$

Then

$$\begin{aligned} P(Z_i > 0) &= 1 - P(Z_i < 0) = 1 - P\left(\frac{0 - (\beta_0 + \sum_{k=1}^p \beta_k x_{ik})}{1} < 0\right) \\ &= 1 - \Phi\left(-(\beta_0 + \sum_{k=1}^p \beta_k x_{ik})\right) = \Phi\left(\beta_0 + \sum_{k=1}^p \beta_k x_{ik}\right). \end{aligned}$$



# Probit Regression: Latent Variable Representation

We can rewrite

$$y_i \stackrel{ind}{\sim} \text{Bernoulli}(p_i) \quad \Phi^{-1}(p_i) = \beta_0 + \sum_{k=1}^p \beta_k x_{ik}$$

as a hierarchical model:

$$\begin{aligned} 1. \quad & Z_i \stackrel{ind}{\sim} N\left(\beta_0 + \sum_{k=1}^p \beta_k x_{ik}, 1\right) \\ 2. \quad & y_i = \begin{cases} 0 & \text{if } Z_i < 0 \\ 1 & \text{if } Z_i > 0 \end{cases} \end{aligned}$$

Therefore we assume the binary outcome  $y_i = 1$  when its latent variable  $Z_i$  passes the threshold 0.

The probability of this occurring depends on the mean of the latent variable  $Z_i$ . Larger mean  $(\beta_0 + \sum_{k=1}^p \beta_k x_{ik})$  increases the the probability of  $y_i = 1$ .

# Probit Regression: Interpretation

Consider a simple probit model with only one predictor:

$$y_i \stackrel{ind}{\sim} \text{Bernoulli}(p_i)$$

$$p_i = \Phi(\beta_0 + \beta_1 x_i).$$

Interpretation of the regression coefficients is arguably more challenging.  
Represents change in z-score.

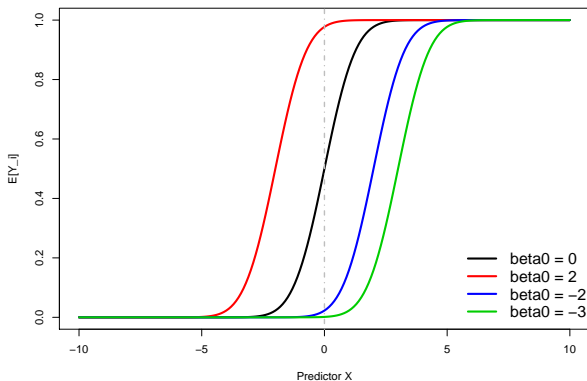
- The baseline probability is  $\Phi(\beta_0)$ .
- The effect of a unit increase in  $x_i$  on  $P(y_i = 1)$  is

$$\Phi(\beta_0 + \beta_1 x_i + \beta_1) - \Phi(\beta_0 + \beta_1 x_i),$$

which again depends on the value of  $x_i$ .

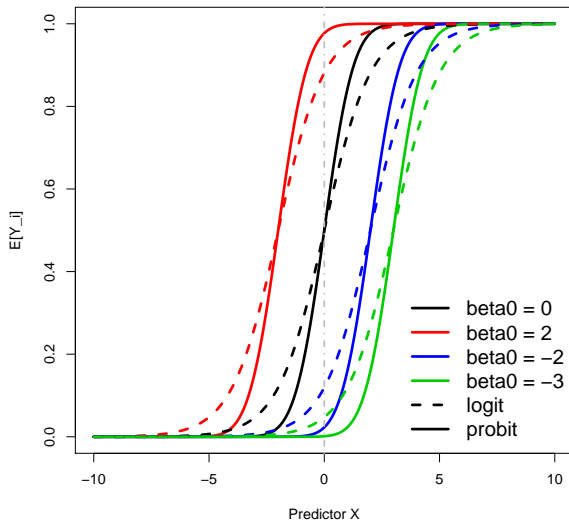
## Probit Regression: Effects of Intercept

$$p_i = \mu_i = \Phi(\beta_0 + \beta_1 x_i).$$



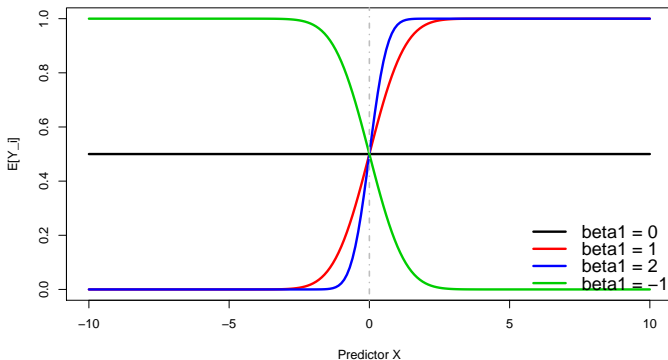
Very similar behaviors as logistic regression. Slightly different tail behaviors compared to a logit link function.

# Logit and Probit Regression: Effects of Intercept



# Probit Regression: Effects of Slope

$$p_i = \mu_i = \Phi(\beta_1 x_i).$$



## The *glm* ( ) Function with probit

```
glm(formula = ptb ~ age + male + tobacco, family = binomial(link = "probit"),  
    data = dat)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.5158	-0.4237	-0.4104	-0.4087	2.2509

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	-1.4024285	0.0099738	-140.612	< 2e-16	***
age	-0.0003746	0.0010793	-0.347	0.7285	
maleM	0.0363566	0.0129215	2.814	0.0049	**
tobacco	0.2102264	0.0281156	7.477	7.59e-14	***

Comparing the logistic and probit regression model, we note the regression coefficients are **qualitatively** similar but the magnitude differs.

# Poisson Regression

A Poisson regression is specified as follows. For  $i = 1, \dots, n$ ,

$$y_i \stackrel{ind}{\sim} \text{Poisson}(\lambda_i)$$

$$\log(\lambda_i) = \beta_0 + \sum_{k=1}^p \beta_k x_{ik}.$$

For a Poisson distributed random variable,

$$E y_i = \lambda_i,$$

$$V y_i = \lambda_i$$

Poisson regression is often used to model **count data**. Examples include daily mortality in a city, number of HIV infected individuals in a neighborhood, and number of medical errors at a hospital.

- Here the link function is  $\log(\cdot)$ .
- $\log(\cdot)$  has domain  $(0, \infty)$  and range  $(-\infty, \infty)$ , and is strictly increasing.

# Poisson Regression Interpretation

Consider a simple Poisson regression model with only one covariate:

$$y_i \overset{ind}{\sim} \text{Poisson}(\lambda_i)$$

$$\log(\lambda_i) = \beta_0 + \beta_1 x_i.$$

When  $x_i = 0$ ,  $\log(\lambda_i) = \beta_0$ .

- $e^{\beta_0} = \lambda_i$  is the **baseline expected counts**.



# Poisson Regression Interpretation

Now consider a unit change in  $x$

$$\log(\lambda_i) = \beta_0 + \beta_1 x_i \quad \log(\lambda_i^*) = \beta_0 + \beta_1 (x_i + 1).$$

Note that

$$\beta_1 = \log(\lambda_i^*) - \log(\lambda_i)$$

- $e^{\beta_1} = \lambda_i^* / \lambda_i$  is the **relative change in count** per unit change in  $x$ . Also called the relative rate. Also called the incident rate ratio.
- For continuous variables with  $\beta_1 > 0$ , the rate increases by  $100 * (e^{\beta_1} - 1)\%$  for every unit increase in  $x$ .
- For factors with  $\beta_j > 0$ , the rate increases by  $100 * (e^{\beta_j} - 1)\%$  for level  $j$  relative to baseline.

Covariate impacts are **multiplicative** rather than additive (applies to log models in general) on the count scale:

$$E y_i = e^{\beta_0} e^{\beta_1 x_{i1}} \dots e^{\beta_p x_{ip}}$$

## Example: bacteria counts

Dataset: antibiotic resistance in a mutation of *E. coli*.

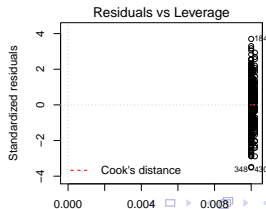
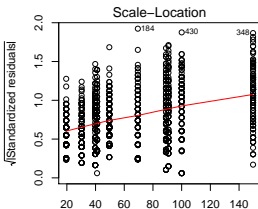
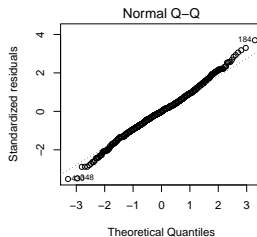
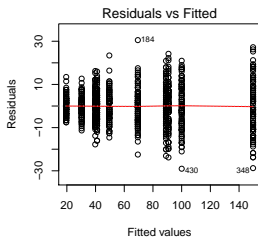
Variables:

- *Colony*: the number of ampicillin-resistant mutant colonies
- *Conc*: the concentration of novobiocin ( $\mu\text{g}/\text{ml}$ )
- *Media*: the type of media used for bacterial growth.

The experiment involved two media preparations (LB and M9), 5 concentrations of novobiocin, and 100 replicates for each media-concentration combination. TNTC (too numerous to count) were recorded when the number of colonies exceeded 300.

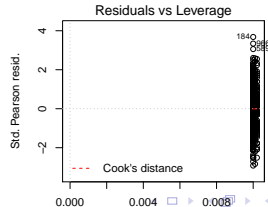
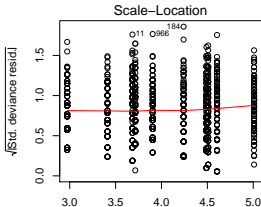
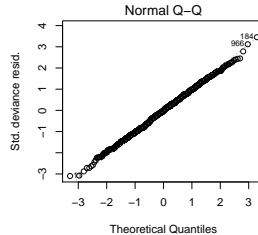
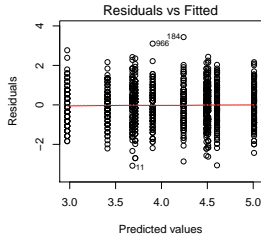
# Modeling count data

```
lm_colony = lm(Colony_numeric~factor(Conc)*Media,data=colonydata)
```



# Modeling count data: Poisson

```
glm_colony = glm(Colony_numeric~factor(Conc)*Media,data=colonydata,family = "poisson")
```



# Residuals in glms

The usual plot of residual versus fitted is not useful in GLMs because of the relationship between the mean and variance.

The **deviance residuals** have an approximate normal distribution.

The deviance residual is

$$\hat{\epsilon}_i^d = \text{sign}(y_i - \hat{\mu}_i) \sqrt{d_i}.$$

where  $d_i$  is the  $i$ th term in the calculation of the deviance. For details, see p.113 in Wood 2017. (This plot is not useful for 0/1 data as common in logistic regression.)

## Goodness of fit tests, quasipoisson

In glms, the **deviance** performs a role similar to the sum of squared errors in OLS:

$$D(\hat{\beta}) = 2 \left\{ \ell(\hat{\beta}_{\max}; \mathbf{y}) - \ell(\hat{\beta}; \mathbf{y}) \right\}$$

where  $\ell(\hat{\beta}_{\max}; \mathbf{y})$  is the “saturated model,” equal to likelihood evaluated at  $\hat{\mu}_i = y_i$ .

Asymptotically,  $D(\hat{\beta}) \sim \chi^2_{n-p}$

One can perform a deviance test to examine goodness of fit. The null hypothesis is that the model fits the data.  $p < 0.05$  indicates a problem (i.e., lack of fit).

```
with(glm_colony, cbind(res.deviance = deviance, df = df.residual,  
p = pchisq(deviance, df.residual, lower.tail=FALSE)))
```

```
res.deviance  df      p  
[1,]      973.8841 987 0.6108368
```

Here,  $p > 0.05$ , from which we conclude that the model provides an adequate fit.

# Overdispersion

In Poisson, the assumption that  $Ey_i = Vy_i$  is often violated.

One can add an additional **overdispersion parameter**, also called a **scale parameter**.

One can adjust the parameter variances by the scale parameter:

$$\hat{\beta} \sim N(0, I(\beta)^{-1} \phi)$$

We will see this again in GEEs.

Section 3.1.5 in Wood describes three different estimators of  $\phi$ .

# Quasipoisson in GLM

```
> glm_colony_quasi = glm(Colony_numeric~factor(Conc)*Media,data=colonydata,family = "quasi")
> summary(glm_colony_quasi)
```

Call:

```
glm(formula = Colony_numeric ~ factor(Conc) * Media, family = "quasipoisson",
    data = colonydata)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-3.0815	-0.7615	-0.0047	0.6573	3.4344

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.683308	0.015807	233.023	< 2e-16 ***
factor(Conc)100	0.557587	0.019786	28.181	< 2e-16 ***
factor(Conc)200	0.806339	0.018981	42.481	< 2e-16 ***
factor(Conc)250	1.325726	0.017764	74.631	< 2e-16 ***
factor(Conc)300	0.922162	0.018660	49.418	< 2e-16 ***
MediaM9	-0.710845	0.027448	-25.898	< 2e-16 ***
factor(Conc)100:MediaM9	-0.118573	0.034923	-3.395	0.000713 ***
factor(Conc)200:MediaM9	-0.064499	0.033221	-1.942	0.052480 .
factor(Conc)250:MediaM9	0.210650	0.030490	6.909	8.75e-12 ***
factor(Conc)300:MediaM9	0.009164	0.032406	0.283	0.777404

---

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

(Dispersion parameter for quasipoisson family taken to be 0.983908)



## Back to original model

When the data are slightly underdispersed, i.e., dispersion parameter  $< 1$ , and there is no evidence of lack of fit, I suggest using the original model:

```
> summary(glm_colony)
```

Call:

```
glm(formula = Colony_numeric ~ factor(Conc) * Media, family = "poisson",  
    data = colonydata)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-3.0815	-0.7615	-0.0047	0.6573	3.4344

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	3.683308	0.015935	231.140	< 2e-16 ***
factor(Conc)100	0.557587	0.019947	27.953	< 2e-16 ***
factor(Conc)200	0.806339	0.019136	42.138	< 2e-16 ***
factor(Conc)250	1.325726	0.017908	74.028	< 2e-16 ***
factor(Conc)300	0.922162	0.018812	49.019	< 2e-16 ***
MediaM9	-0.710845	0.027671	-25.689	< 2e-16 ***
factor(Conc)100:MediaM9	-0.118573	0.035208	-3.368	0.000758 ***
factor(Conc)200:MediaM9	-0.064499	0.033491	-1.926	0.054126 .
factor(Conc)250:MediaM9	0.210650	0.030738	6.853	7.23e-12 ***
factor(Conc)300:MediaM9	0.009164	0.032670	0.280	0.779097

---

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

# Interpretation

- The rate here is colonies per petri dish (for some fixed amount of time).
- Intercept: the log of the expected count is 3.68 in LB media with no novobiocin. Equivalently, the log rate is 3.68 in LB media with no novobiocin.
- The estimated number of colonies and 95% CI for this baseline is  $e^{3.68}$ ,  $e^{3.68-1.96*0.016} - e^{3.68+1.96(0.016)} = 39.6$  (38.4 - 41).
- The ratio of counts in Media M9 with concentration of novobiocin equal to 300 to counts in Media LB with no novobiocin is  $e^{0.009}$ , i.e., the rate increases by 0.9%, which is not significant ( $p > 0.05$ ).

## Example with overdispersion

For educational purposes, consider this poor fitting model:

```
> glm_nomedia_quasi = glm(Colony_numeric~factor(Conc),data=colonydata,  
family = "quasipoisson")  
> summary(glm_nomedia_quasi)
```

Call:

```
glm(formula = Colony_numeric ~ factor(Conc), family = "quasipoisson",  
data = colonydata)
```

Deviance Residuals:

	Min	1Q	Median	3Q	Max
	-5.6832	-2.8772	-0.2983	2.5557	6.2330

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.38805	0.03727	90.90	<2e-16 ***
factor(Conc)100	0.52177	0.04701	11.10	<2e-16 ***
factor(Conc)200	0.78726	0.04493	17.52	<2e-16 ***
factor(Conc)250	1.40432	0.04162	33.74	<2e-16 ***
factor(Conc)300	0.92691	0.04400	21.06	<2e-16 ***

---

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

(Dispersion parameter for quasipoisson family taken to be 8.185913)

Null deviance: 21484.0 on 996 degrees of freedom  
Residual deviance: 8249.4 on 992 degrees of freedom  
AIC: NA

# GOF test

```
> glm_nomedia = glm(Colony_numeric~factor(Conc),data=colonydata,family = "poisson")
> summary(glm_nomedia)
```

Call:

```
glm(formula = Colony_numeric ~ factor(Conc), family = "poisson",
     data = colonydata)
```

...

(Dispersion parameter for poisson family taken to be 1)

```
Null deviance: 21484.0 on 996 degrees of freedom
Residual deviance: 8249.4 on 992 degrees of freedom
AIC: 14127
```

```
> # versus:
```

```
> with(glm_nomedia, cbind(res.deviance = deviance, df = df.residual, p = pchisq(deviance, df.residual)
  res.deviance df p
[1,]      8249.368 992 0
```