BIOS621 Session 2

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Welcome and outline - session 2

- brief overview of multiple regression (Chapter 4)
- Linear Regression as a Generalized Linear Model (Chapter 5)
- Statistical inference for logistic regression

Learning objectives - session 2

- define generalized linear models (GLM)
- define linear and logistic regression as special cases of GLMs
- distinguish between additive and multiplicative models
- define Pearson and deviance residuals
- additional familiarity with R, including `dplyr` and `ggplot2`

Multiple Linear Regression Model

Systematic component:

$$E[y|x] = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + ... + \beta_p x_p$$

- x_p are the predictors or independent variables
- y is the outcome, response, or dependent variable
- $E[y|x]$ is the expected value of y given x
- β_p are the regression coefficients

Multiple Linear Regression Model

Systematic plus random component:

$y_i = E[y|x] + \epsilon_i$

$y_i = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + ... + \beta_p x_p + \epsilon_i$

Assumption: $\epsilon_i \overset{iid}{\sim} N(0, \sigma_\epsilon^2)$

- Normal distribution
- Mean zero at every value of predictors
- Constant variance at every value of predictors
- Values that are statistically independent

Generalized Linear Models

- Linear regression is a special case of a broad family of models called "Generalized Linear Models" (GLM)
- This unifying approach allows to fit a large set of models using maximum likelihood estimation methods (MLE) (Nelder & Wedderburn, 1972)
- Can model many types of data directly using appropriate distributions, e.g. Poisson distribution for count data
- Transformations of Y not needed

Components of GLM

- **Random component** specifies the conditional distribution for the response variable
  - doesn't have to be normal
  - can be any distribution in the "exponential" family of distributions
- **Systematic component** specifies linear function of predictors (linear predictor)
- **Link** [denoted by g(.)] specifies the relationship between the expected value of the random component and the systematic component
  - can be linear or nonlinear

Linear Regression as GLM

- **The model**:
  $y_i = E[y|x] + \epsilon_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + ... + \beta_p x_{pi} + \epsilon_i$
- **Random component** of y_i is normally distributed:
  $\epsilon_i \overset{iid}{\sim} N(0, \sigma_\epsilon^2)$
- **Systematic component** (linear predictor):
  $\beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + ... + \beta_p x_{pi}$
- **Link function** here is the *identity link*: $g(E(y|x)) = E(y|x)$.
  We are modeling the mean directly, no transformation.

Logistic Regression as GLM

- **The model**:

$$Logit(P(x)) = log\left(\frac{P(x)}{1-P(x)}\right) = \beta_0+\beta_1 x_{1i}+\beta_2 x_{2i}+...+\beta_p x_{pi}$$

- **Random component**: y_i follows a Binomial distribution (outcome is a binary variable)
- **Systematic component**: linear predictor

$$\beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + ... + \beta_p x_{pi}$$

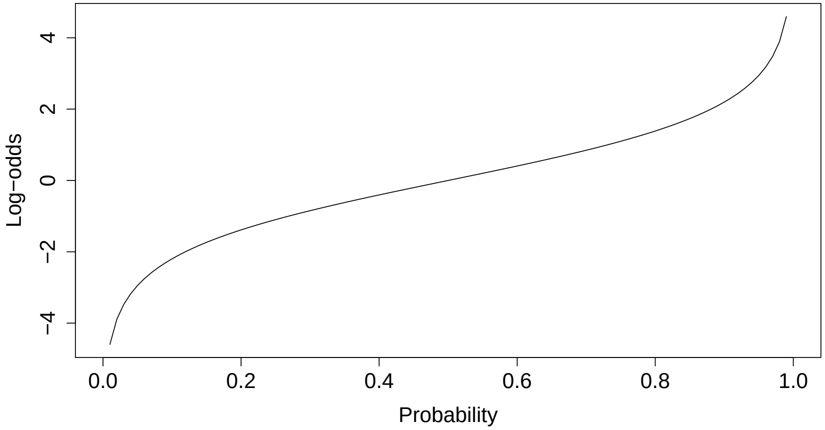
- **Link function**: *logit* (log of the odds that the event occurs)

$$g(P(x)) = logit(P(x)) = log\left(\frac{P(x)}{1-P(x)}\right)$$

$$P(x) = g^{-1}\left(\beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + ... + \beta_p x_{pi}\right)$$

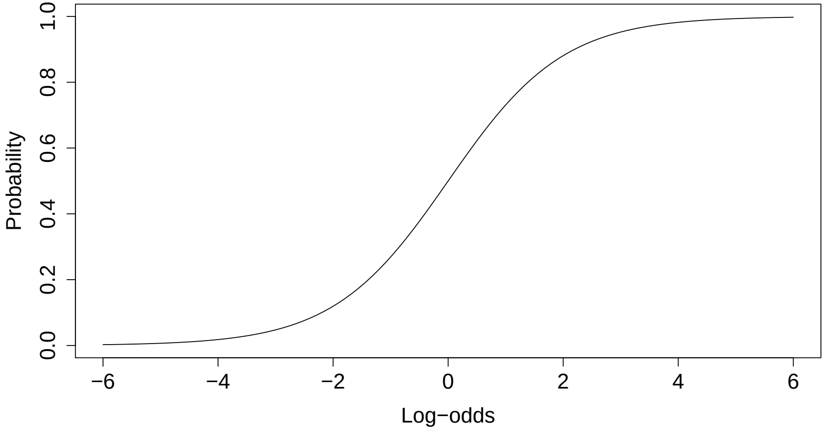
logit function

```
logit <- function(P) log(P/(1-P))
plot(logit, xlab="Probability", ylab="Log-odds",
     cex.lab=1.5, cex.axis=1.5)
```



Inverse logit function

```r
invLogit <- function(x) 1/(1+exp(-x))
```



Additive vs. Multiplicative models

- Linear regression is an *additive* model
  - *e.g.* for two binary variables $\beta_1 = 1.5$, $\beta_2 = 1.5$.
  - If $x_1 = 1$ and $x_2 = 1$, this adds 3.0 to $E(y|x)$
- Logistic regression is a *multiplicative* model
  - If $x_1 = 1$ and $x_2 = 1$, this adds 3.0 to $log(\frac{P}{1-P})$
  - Odds-ratio $\frac{P}{1-P}$ increases 20-fold: $exp(1.5 + 1.5)$ or $exp(1.5) * exp(1.5)$

Motivating example: contraceptive use data

From http://data.princeton.edu/wws509/datasets/#cuse

```
##      age             education         wantsMore
##  Length:16          Length:16          Length:16
##  Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character
##
##
##
##      using
##  Min.   : 4.00
##  1st Qu.: 9.50
##  Median :29.00
##  Mean   :31.69
##  3rd Qu.:49.00
##  Max.   :80.00
```

Motivating example: contraceptive use data

No interactions:

```r
fit1 <- glm(cbind(using, notUsing) ~ age + education + wantsMore,
           data=cuse, family=binomial("logit"))
summary(fit1)
```

```
##
## Call:
## glm(formula = cbind(using, notUsing) ~ age + education + wantsMore,
##     family = binomial("logit"), data = cuse)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.5148  -0.9376   0.2408   0.9822   1.7333
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.8082     0.1590  -5.083 3.71e-07 ***
## age25-29       0.3894     0.1759   2.214  0.02681 *
## age30-39       0.9086     0.1646   5.519 3.40e-08 ***
## age40-49       1.1892     0.2144   5.546 2.92e-08 ***
## educationlow  -0.3250     0.1240  -2.620  0.00879 **
## wantsMoreyes  -0.8330     0.1175  -7.091 1.33e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 165.772  on 15  degrees of freedom
## Residual deviance:  29.917  on 10  degrees of freedom
## AIC: 113.43
##
## Number of Fisher Scoring iterations: 4
```

Pearson residuals for logistic regression

Take the difference between observed and fitted values (on probability scale 0-1), and divide by the standard deviation of the observed value.

- Let $\hat{y}_i$ be the best-fit predicted probability for each data point, i.e. $g^{-1}(\beta_0 + \beta_1 x_{1i} + ...)$
- y_i is the observed value, either 0 or 1.

$$r_i = \frac{y_i - \hat{y}_i}{\sqrt{Var(\hat{y}_i)}}$$

Summing the squared Pearson residuals produces the *Pearson Chi-squared statistic*:

$$\chi^2 = \sum_i r_i^2$$

Deviance residuals for logistic regression

- Deviance residuals and Pearson residuals converge for high degrees of freedom
- Deviance residuals indicate the contribution of each point to the model *likelihood*
- Definition of deviance residuals:

$$d_i = s_i \sqrt{-2(y_i \log \hat{y}_i + (1 - y_i) \log(1 - \hat{y}_i))}$$

Where $s_i = 1$ if $y_i = 1$ and $s_i = -1$ if $y_i = 0$.

- Summing the deviances gives the overall deviance: $D = \sum_i d_i^2$

Model likelihood and deviance

- The *likelihood* of a model is the probability of the observed outcomes given the model, sometimes written as:
  - $L(\theta|data) = P(data|\theta)$.
- Deviance residuals and the difference in log-likelihood between two models are related by:

$$\Delta(\mathrm{D}) = -2 * \Delta(\text{log likelihood})$$

Likelihood Ratio Test

- Use to assess whether the reduction in deviance provided by a more complicated model indicates a better fit
- It is equivalent of the nested Analysis of Variance is a nested Analysis of Deviance
- The difference in deviance under H_0 is *chi-square distributed*, with df equal to the difference in df of the two models.

Likelihood Ratio Test (cont'd)

```
fit0 <- glm(cbind(using, notUsing) ~ -1, data=cuse,
            family=binomial("logit"))
anova(fit0, fit1, test="LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: cbind(using, notUsing) ~ -1
## Model 2: cbind(using, notUsing) ~ age + education + wantsMore
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1        16     389.85
## 2        10      29.92  6   359.94 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Wald test for individual regression coefficients

- Can use partial Wald test for a single coefficient:
  - $\frac{\hat{\beta}}{\sqrt{var(\hat{\beta})}} \sim t_{n-1}$
  - $\frac{\left(\hat{\beta}-\beta_0\right)^2}{var(\hat{\beta})} \sim \chi^2_{df=1}$ (large sample)
- Wald CI for β: $\hat{\beta} \pm t_{1-\alpha/2,n-1}\sqrt{var(\hat{\beta})}$
- Wald CI for odds-ratio: $e^{\hat{\beta} \pm t_{1-\alpha/2,n-1}\sqrt{var(\hat{\beta})}}$

Note: Wald test confidence intervals on coefficients can provide poor coverage in some cases, even with relatively large samples