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:
  $\epsilon_i \overset{iid}{\sim} N(0, \sigma^2_\epsilon)$
- **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

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

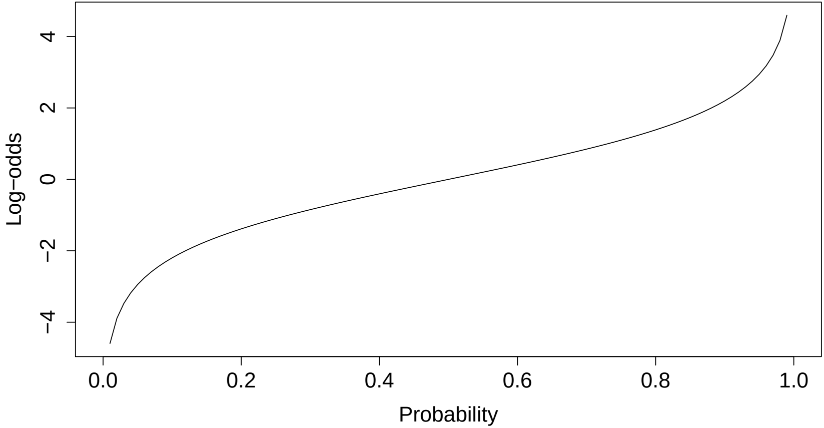
- **Link function**: *logit* (log of the odds that the event occurs)

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

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

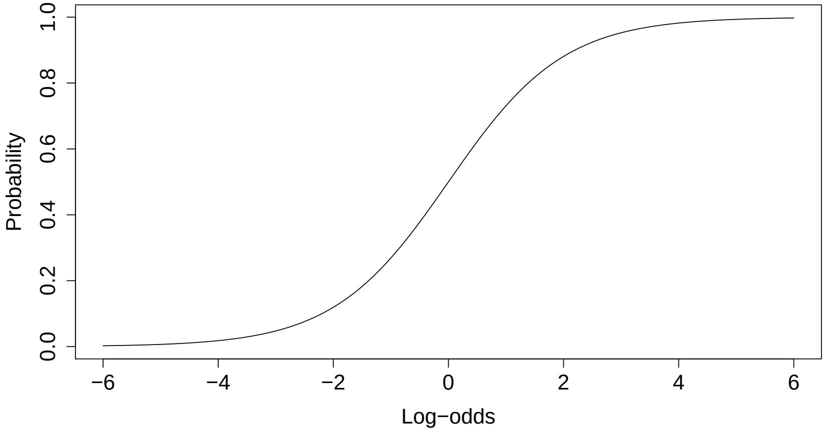
logit function

```r
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

```
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    notUsing           usi
##  <25  :4   high:8    no :8      Min.    :  8.00   Min.    :
##  25-29:4   low :8    yes:8      1st Qu.: 31.00   1st Qu.:
##  30-39:4                        Median : 56.50   Median :
##  40-49:4                        Mean   : 68.75   Mean   :
##                                 3rd Qu.: 85.75   3rd Qu.:
##                                 Max.   :212.00   Max.   :
```

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:

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

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)

```r
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

Lab Exercises

1. What is the mean fraction of women using birth control for each age group? Each education level? For women who do or don't want more children?
   - Hint: look at the "data wrangling" cheat sheet functions `mutate`, `group_by`, and `summarize`
2. Based on `fit1`, write on paper the model for expected probability of using birth control. Don't forget the logit function.
3. Based on `fit1`, what is the expected probability of an individual 25-29 years old, with high education, who wants more children, using birth control? Calculate it manually, and using `predict(fit1)`
4. Based on `fit1`: Relative to women under 25 who want to have children, what is the predicted increase in odds that a woman 40-49 years old who does *not* want to have children will be taking birth control?
5. Using a likelihood ratio test, is there evidence that a model with interactions improves on `fit1` (no interactions)?