

## Part II: Generalized Linear Models

## Load Packages

Again, we must load the packages that will be used in the first part of this workshop.

```
library(pastecs, quietly = TRUE)
library(lm.beta, quietly = TRUE)
library(lmtest, quietly = TRUE)
library(foreign, quietly = TRUE)
library(lattice, quietly = TRUE)
library(lme4, quietly = TRUE)
library(nlme, quietly = TRUE)
library(survival, quietly = TRUE)
library(dplyr, quietly = TRUE)
library(ggfortify, quietly = TRUE)
library(survminer, quietly = TRUE)
library(rms, quietly = TRUE)
library(MASS, quietly = TRUE)
library(pscl, quietly = TRUE)
```

A generalized linear model (GLM) has three components:

- ▶ a random component with mean  $\mu$ . Generally, the random component is the response variable  $Y_i$ .
- ▶ a systematic component,  $\eta_i$ , that relates the explanatory variables,

$$\eta_i = \sum_{j=1}^n \beta_j x_{ij}$$

- ▶ a link function that relates the mean of the random to the systematic component

$$g(\mu) = \eta_i$$

## Logistic regression

Logistic regression is a GLM used the model binary (0 or 1) data. The response variable must be binary and is assumed to follow a bernoulli distribution.

That said, logistic regression has the following components:

- ▶ a response binary variable,  $Y_i$ , that follows a bernoulli distribution with mean  $\pi_i$ .
- ▶ a systematic component,  $\eta_i$ , that relates the explanatory variables,

$$\eta_i = \sum_{j=1}^n \beta_j x_{ij}$$

- ▶ a link function that relates the mean of the random to the systematic component

$$\log \left( \frac{\pi_i}{1 - \pi_i} \right) = \sum_{j=1}^n \beta_j x_{ij}.$$

$\log (\pi_i/(1 - \pi_i))$  is known as the log odds.

# Logistic regression

## Data

Using the iris data, we create binary data. We add the column `Sepal.Width_binary` to `iris`. If the `Sepal.Width` is greater than the median then the associated value in `Sepal.Width_binary` is 1. Otherwise, `Sepal.Width_binary` is 0.

```
data <- iris
data$Sepal.Width_binary <- ifelse(data$Sepal.Width
                                  >= median(data$Sepal.Width
                                             1, 0)
```

# Logistic regression

## Logistic Regression with only the constant term

Fitting only a constant term, the systematic component is

$$\eta_i = \beta_0.$$

```
logit <- glm(Sepal.Width_binary ~ 1, data = data, family = "binomial")
summary(logit)
```

```
##
## Call:
## glm(formula = Sepal.Width_binary ~ 1, family = "binomial", data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.3911  -1.3911   0.9778   0.9778   0.9778
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.4895     0.1682    2.91  0.00361 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 199.22  on 149  degrees of freedom
## Residual deviance: 199.22  on 149  degrees of freedom
## AIC: 201.22
##
```

# Logistic regression

## Logistic Regression with only the constant term

```
p_avg <- mean(data$Sepal.Width_binary)
log_odds_avg <- log(p_avg/(1-p_avg))
print(log_odds_avg)
```

```
## [1] 0.4895482
```

# Logistic regression

## Logistic Regression with Species

Fitting the species term, the systematic component is

$$\eta_i = 1 + \beta_2 X_{1i} + \beta_3 X_{2i}.$$

where

$$X_{1i} = \begin{cases} 1 & \text{if } i\text{th data point is versicolor} \\ 0 & \text{otherwise} \end{cases},$$

$$X_{2i} = \begin{cases} 1 & \text{if } i\text{th data point is virginica} \\ 0 & \text{otherwise} \end{cases}.$$



# Logistic regression

## Logistic Regression with Species

```
logit <- glm(Sepal.Width_binary ~ as.factor(Species), data = data, family = "binomial")
summary(logit)
```

```
##
## Call:
## glm(formula = Sepal.Width_binary ~ as.factor(Species), family = "binomial",
##      data = data)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.5373  -0.8782   0.2857   1.0438   1.5096
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      3.1781     0.7215   4.405 1.06e-05 ***
## as.factor(Species)versicolor  -3.9318     0.7826  -5.024 5.06e-07 ***
## as.factor(Species)virginica   -2.8553     0.7763  -3.678 0.000235 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 199.22  on 149  degrees of freedom
## Residual deviance: 147.51  on 147  degrees of freedom
## AIC: 153.51
##
## Number of Fisher Scoring iterations: 5
```

# Logistic regression

## Logistic Regression with Species

Let's compare the results to the average log odds of each Species group

```
log_odds_avg_fun <- function(data){  
  p_avg <- mean(data)  
  log_odds_avg <- log(p_avg/(1-p_avg))  
  return(log_odds_avg)  
}  
  
tapply(data$Sepal.Width_binary,  
        data$Species, log_odds_avg_fun)
```

```
##      setosa versicolor virginica  
## 3.1780538 -0.7537718  0.3227734
```

The intercept corresponds to the average log odds of setosa as we would expect. However, the other coefficients do not correspond to the average log odds of the other species. Why?

# Logistic regression

## Logistic Regression with Species

From the formula,  $\eta_i = 1 + \beta_2 X_{2i} + \beta_3 X_{3i}$ , the log odds of versicolor actually corresponds to  $1 + \beta_2$ . The log odds of versicolor actually corresponds to  $1 + \beta_3$ .

```
coefficients<-unnname(coef(logit))  
print(c(coefficients[1],coefficients[1]+coefficients[2],  
        coefficients[1]+coefficients[3]))
```

```
## [1] 3.1780537 -0.7537718 0.3227734
```

# Logistic regression

Logistic Regression with continuous variable

COMPLETE

# Logistic regression

## Logistic Regression with continuous variable, Sepal.Length

Fitting the species term, the systematic component is

$$\eta_i = \beta_3 X_{1i}.$$

where  $X_{1i}$  = Sepal.Length of the  $i$ th data point.

```
logit <- glm(Sepal.Width_binary ~ Sepal.Length,  
             data = data, family = "binomial")  
summary(logit)
```

# Logistic regression

## Logistic Regression with continuous variable, Sepal.Length

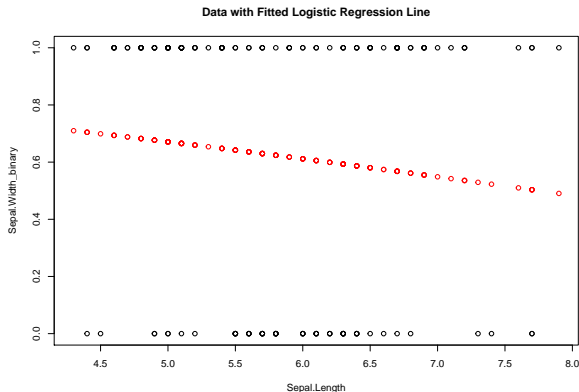
```
logit <- glm(Sepal.Width_binary ~ Sepal.Length,  
             data = data, family = "binomial")  
summary(logit)
```

```
##  
## Call:  
## glm(formula = Sepal.Width_binary ~ Sepal.Length, family = "binomial",  
##      data = data)  
##  
## Deviance Residuals:  
##      Min       1Q   Median       3Q      Max   
## -1.5614  -1.3524   0.8883   0.9890   1.1936   
##  
## Coefficients:  
##              Estimate Std. Error z value Pr(>|z|)      
## (Intercept)    2.0088     1.2176   1.650   0.099 .      
## Sepal.Length  -0.2591     0.2050  -1.264   0.206      
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## (Dispersion parameter for binomial family taken to be 1)  
##  
##      Null deviance: 199.22  on 149  degrees of freedom  
## Residual deviance: 197.61  on 148  degrees of freedom  
## AIC: 201.61  
##  
## Number of Fisher Scoring iterations: 4
```

# Logistic regression

## Logistic Regression with continuous variable, Sepal.Length

```
plot(Sepal.Width_binary~Sepal.Length, data=data)
points(data$Sepal.Length[order(data$Sepal.Length)],
       logit$fitted[order(data$Sepal.Length)], col="red")
title(main="Data with Fitted Logistic Regression Line")
```



# Logistic regression

## Logistic Regression with Species and Sepal.Length

Fitting the species term, the systematic component is

$$\eta_i = 1 + \beta_2 X_{1i} + \beta_3 X_{2i} + \beta_3 X_{3i}.$$

where

$$X_{1i} = \begin{cases} 1 & \text{if } i\text{th data point is versicolor} \\ 0 & \text{otherwise} \end{cases},$$

$$X_{2i} = \begin{cases} 1 & \text{if } i\text{th data point is virginica} \\ 0 & \text{otherwise} \end{cases}$$

and  $X_{3i} = \text{Sepal.Length}$  of the  $i$ th data point.



# Logistic regression

## Logistic Regression with continuous variable, Sepal.Length

Fitting the logistic model accordingly,

```
logit <- glm(Sepal.Width_binary ~ Species + Sepal.Length,  
             data = data, family = "binomial")  
summary(logit)
```

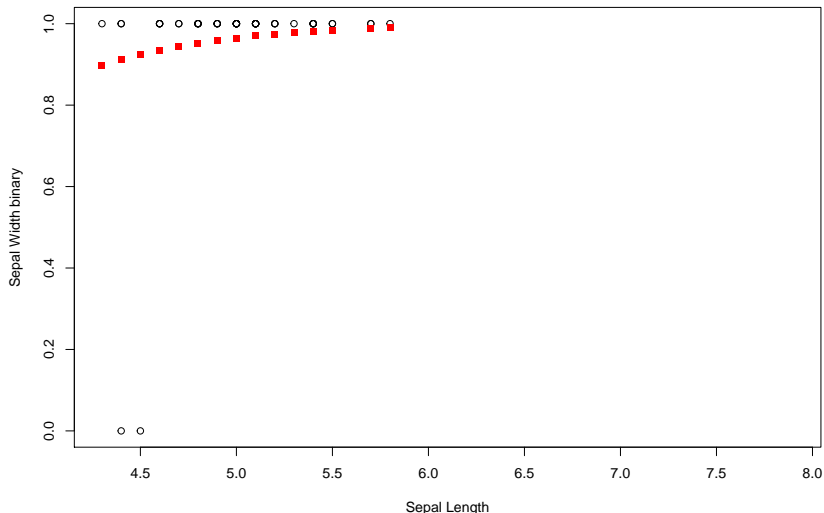
```
##  
## Call:  
## glm(formula = Sepal.Width_binary ~ Species + Sepal.Length, family = "binomial",  
##      data = data)  
##  
## Deviance Residuals:  
##      Min       1Q   Median       3Q      Max   
## -2.2710  -0.7538   0.2472   0.7020   1.9477   
##  
## Coefficients:  
##              Estimate Std. Error z value Pr(>|z|)      
## (Intercept)   -4.7988     2.2981  -2.088 0.036784 *      
## Speciesversicolor -5.6936     0.9686  -5.878 4.16e-09 ***   
## Speciesvirginica  -5.4812     1.0879  -5.039 4.69e-07 ***   
## Sepal.Length     1.6219     0.4510   3.596 0.000323 ***   
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## (Dispersion parameter for binomial family taken to be 1)  
##  
##      Null deviance: 199.22  on 149  degrees of freedom  
## Residual deviance: 131.27  on 146  degrees of freedom  
## AIC: 139.27  
##
```

# Logistic regression

## Logistic Regression with continuous variable, Sepal.Length

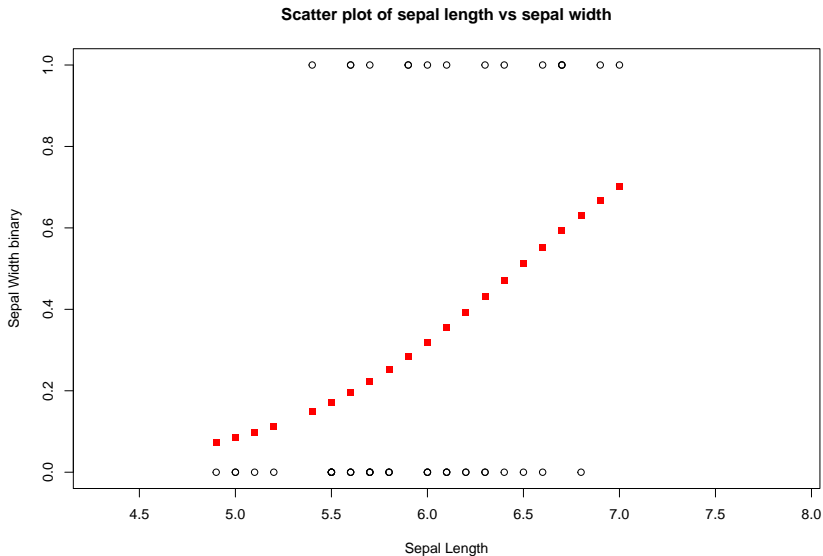
Plot the results for each species, we get that

Scatter plot of sepal length vs sepal width



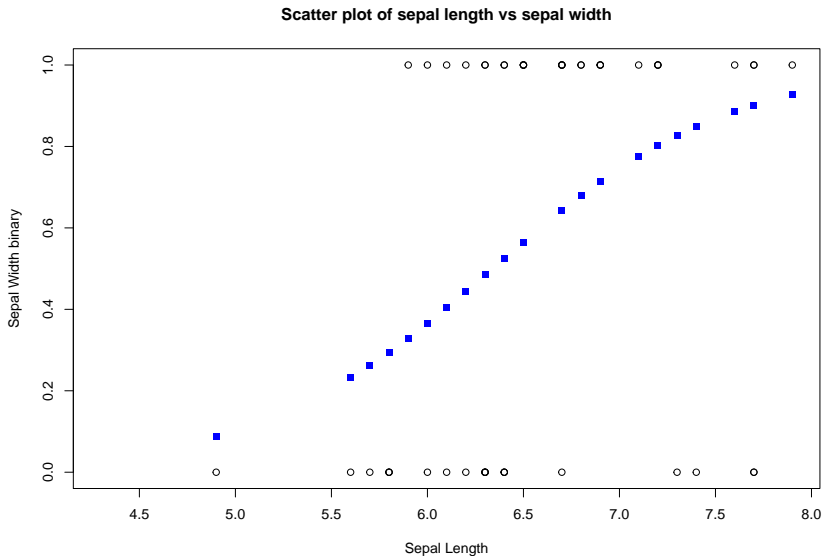
# Logistic regression

## Logistic Regression with continuous variable, Sepal.Length



# Logistic regression

## Logistic Regression with continuous variable, Sepal.Length



# Logistic regression

## Goodness of Fit

### Deviance

For general linear models, we use *deviance* to compare model pairs. Deviance is the difference in log likelihood of the models multiplied by 2.

For a linear model, *deviance* is equivalent the sum of squares error of the residual.

# Logistic regression

## Goodness of Fit

### Saturated Model

Let's consider model in which each data point has its own mean and coefficients. This is called the saturated model. It basically replicates the data at hand.

Using deviance, we can compare our fitted model to a saturated model.

If the fitted model behaves similar to the saturated model, then the deviance can be well approximated by a chi-squared distribution with  $m - n$  degrees of freedom.  $m$  is the number of the data points and  $n$  is the number of coefficients in our fitted model.

# Logistic regression

## Goodness of Fit

### Saturated Model

This statistical property of the deviance allows us perform a hypothesis test

$H_0$  : the fitted model is equivalent to the saturated model

$H_\alpha$  : the fitted model is not equivalent to the saturated model

# Logistic regression

## Goodness of Fit

### Saturated Model

`logit$deviance` is the deviance between saturated model and fitted model.

`logit$df.residual` is equal to number of observations minus the number of coefficients in the fitted model.

Using this, we can calculate the p value for the hypothesis test above.

```
p_value = pchisq(logit$deviance,  
                 logit$df.residual, lower.tail = F)  
print(p_value)
```

```
## [1] 0.8032738
```

Since the p value is greater than 0.05, we fail to reject the null hypothesis. (This is a good thing.)



# Logistic regression

## Goodness of Fit

### Null Model

We can also use deviance to determine if our fitted model is better than the null model. The null model is a model with only a linear term.

Like above, we can design a hypothesis test comparing the null model to the fitted model.

# Logistic regression

Goodness of Fit

Null Model

$H_0 =$  the fitted model is equivalent to the null model

$H_\alpha =$  the fitted model is not equivalent to the null model

In the limit of large data, it is known that the deviance follows a chi-squared distribution with parameter  $n - 1$ .

# Logistic regression

## Goodness of Fit

### Null Model

`logit$deviance` is the deviance between saturated model and fitted model. `logit$df.residual` is equal to number of observations minus the number of coefficients in the fitted model.

`logit$null.deviance` is the deviance between saturated model and the null model. `logit$df.null` is the number of observations minus 1.

# Logistic regression

## Goodness of Fit

## Null Model

Using this information, we can calculate the p value for the hypothesis test above.

```
p_value = pchisq(logit$null.deviance-logit$deviance,  
                 logit$df.null-logit$df.residual,  
                 lower.tail = F)  
print(p_value)
```

```
## [1] 1.173879e-14
```

Since the p value is less than one, we reject our null hypothesis.  
(This is a good thing.)

# Logistic regression

## Goodness of Fit

## Anova

`anova` with argument `test="Chisq"` allows us to compare change in deviance after sequentially adding terms our model.

```
anova(logit,test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model: binomial, link: logit
##
## Response: Sepal.Width_binary
##
## Terms added sequentially (first to last)
##
##
```

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
## NULL			149	199.22	
## Species	2	51.709	147	147.51	5.910e-12 ***
## Sepal.Length	1	16.239	146	131.27	5.583e-05 ***

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

# Poisson Generalized Linear Model

A poisson GLM is used to study *count* data (i.e. discrete numbers,  $0, 1, 2, \dots$ ). *Count* data describes the number of events that occur within a given time frame.

insert plot of poisson distribution here

# Poisson Generalized Linear Model

A Poisson GLM is most useful when studying data in which the mean and variance are approximately equal. If they are not equal, the standard error of the model terms must be adjusted to account for the assumption violation.

# Poisson Generalized Linear Model

Poisson Regression has the following components:

- ▶ response count variables,  $Y_i$ , that follows a Poisson distribution with mean  $\mu_i$
- ▶ a systematic component,  $\eta_i$ , that relates the explanatory variables,  $\eta_i = \sum_{j=1}^n \beta_j x_{ij}$
- ▶ a link function,  $\log(\mu_i) = \sum_{j=1}^n \beta_j x_{ij}$

From Poisson regression, we learn the *mean* of each  $Y_i$  given the associated explanatory variables.



# Poisson Generalized Linear Model

## Data

We will be consider the bioChemists data set in this section.

This data set contains number of articles produced by PhD biochemistry student during the last 3 years of their PhD.

```
attach(bioChemists)
summary(bioChemists)
```

```
##          art          fem          mar          kid5
## Min.    : 0.000   Men :494   Single :309   Min.    :0.0000
## 1st Qu.: 0.000   Women:421   Married:606   1st Qu.:0.0000
## Median : 1.000                                Median :0.0000
## Mean    : 1.693                                Mean    :0.4951
## 3rd Qu.: 2.000                                3rd Qu.:1.0000
## Max.    :19.000                                Max.    :3.0000
##          phd          ment
## Min.    :0.755   Min.    : 0.000
## 1st Qu.:2.260   1st Qu.: 3.000
## Median :3.150   Median : 6.000
## Mean    :3.103   Mean    : 8.767
## 3rd Qu.:3.920   3rd Qu.:12.000
## Max.    :4.620   Max.    :77.000
```

# Poisson Generalized Linear Model

## Data

The data set also contains demographic data associated with each student. The data set has five variables:

- ▶ *art* - number of articles produced by the student in the last 3 years of their PhD
- ▶ *fem* - gender
- ▶ *mar* - marital status
- ▶ *kid5* - number of children less than 5
- ▶ *phd* - prestige of PhD program
- ▶ *ment* - number of articles of the mentor in the last 3 years

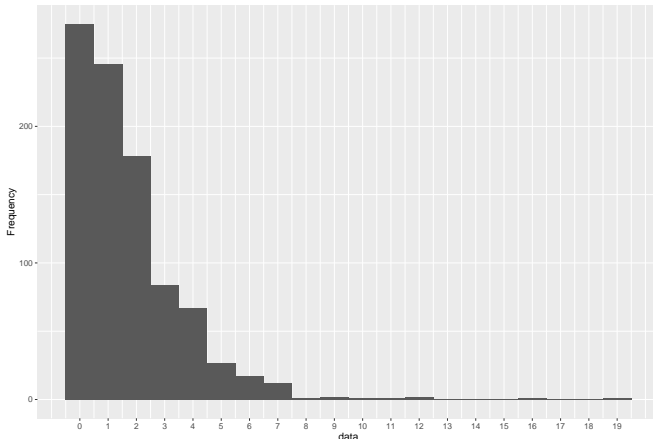


# Poisson Generalized Linear Model

## Data Visualization

Plotting the bar graph of `bioChemists$art`, we can see that the data looks Poisson-like since there is a large number of observations at 0.

Histogram plot of the number of articles published by biochemist phd students in last 3 years



# Poisson Generalized Linear Model

## Data

We can “quantify” the Poisson-ness by analyzing the mean and variance of the data.

```
mean(bioChemists$art)
```

```
## [1] 1.692896
```

```
var(bioChemists$art)
```

```
## [1] 3.709742
```

Although mean and variance are not equal, we will still fit it to Poisson distribution.

# Poisson Generalized Linear Model

## Poisson Regression with constant term

To model only the constant term, I use the formula  $\text{art} \sim 1$ . This formula is equivalent to

$$\log \mu_i = \beta_0.$$

# Poisson Generalized Linear Model

## Poisson Regression with constant term

```
poisson_model = glm(art ~ 1, family=poisson(link=log),data=bioChemists)
summary(poisson_model)
```

```
##
## Call:
## glm(formula = art ~ 1, family = poisson(link = log), data = bioChemists)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8401  -1.8401  -0.5770   0.2294   7.5677
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.52644    0.02541   20.72  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 1817.4  on 914  degrees of freedom
## Residual deviance: 1817.4  on 914  degrees of freedom
## AIC: 3487.1
##
## Number of Fisher Scoring iterations: 5
```

# Poisson Generalized Linear Model

## Poisson Regression with constant term

Note that the constant term is the log mean number of counts.

```
print(coef(poisson_model))
```

```
## (Intercept)  
##      0.5264408
```

```
print(log(mean(bioChemists$art)))
```

```
## [1] 0.5264408
```



## Goodness of fit

### Saturated model

We can again compare the current model to the saturated model (best possible fit).

```
p_value = pchisq(poisson_model$deviance,  
                 poisson_model$df.residual,  
                 lower.tail = F)  
print(p_value)
```

```
## [1] 3.304511e-62
```

Since our p value is less than 0.05, we reject the null hypothesis. The models are not equivalent.

## Goodness of fit

### Null model

We can also compare the current model to the null model (worst possible fit).

```
p_value = pchisq(poisson_model$null.deviance  
                 -poisson_model$deviance,  
                 poisson_model$df.null  
                 -poisson_model$df.residual,  
                 lower.tail = F)  
print(p_value)
```

```
## [1] 1
```

We fail to reject the null hypothesis. This makes sense since the models are literally the same thing.

## Poisson Regression with marital status covariate

To model the marital status covariate, I use the formula `art ~ 1+mar`. This formula is equivalent to

$$\log \mu_i = \beta_0 + \beta_1 X_{1i}$$

where

$$X_{1i} = \begin{cases} 1 & \text{if mar = Married} \\ 0 & \text{otherwise} \end{cases}.$$

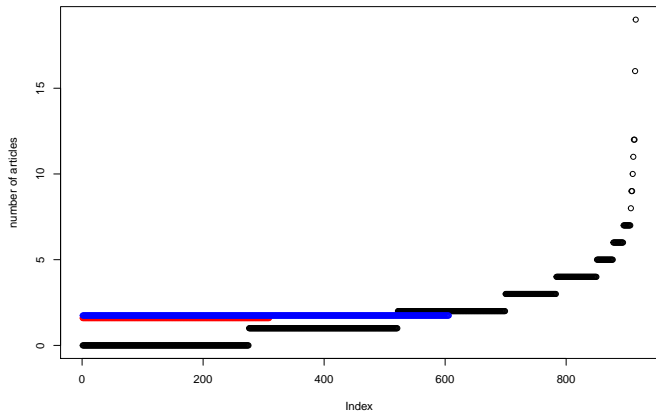
## Poisson Regression with marital status covariate

```
poisson_model = glm(art~1+mar , family=poisson(link=log),data=bioChemists)
summary(poisson_model)
```

```
##
## Call:
## glm(formula = art ~ 1 + mar, family = poisson(link = log), data = bioChemists)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8677  -1.7845  -0.5042   0.3107   7.4992
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.46514    0.04508  10.317  <2e-16 ***
## marMarried   0.09117    0.05458   1.671   0.0948 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 1817.4  on 914  degrees of freedom
## Residual deviance: 1814.6  on 913  degrees of freedom
## AIC: 3486.3
##
## Number of Fisher Scoring iterations: 5
```

## Poisson Regression with marital status covariate

```
plot(bioChemists$art,ylab='number of articles',xlab = 'Index')  
points(poisson_model$fitted[bioChemists$mar=="Single"],col="red")  
points(poisson_model$fitted[bioChemists$mar=="Married"],col="blue")
```



Graphically, we can see that marital status is not a good indicator of number articles published.

## Goodness of fit

### Saturated model

We can again compare the current model to the saturated model (best possible fit).

```
p_value = pchisq(poisson_model$deviance,  
                 poisson_model$df.residual,  
                 lower.tail = F)  
print(p_value)
```

```
## [1] 4.731233e-62
```

Since our p value is less than 0.05, we reject the null hypothesis. The models are not equivalent and our model is a bad fit.

## Goodness of fit

### Null model

We can also compare the current model to the null model (worst possible fit).

```
p_value = pchisq(poisson_model$null.deviance-logit$deviance,  
                 poisson_model$df.null-logit$df.residual, lower.tail = F)  
print(p_value)
```

```
## [1] 1.016236e-70
```

Since our p value is less than 0.05, we reject the null hypothesis. The models are not equivalent. Though our current model does not capture much deviance, the current model captures much more variance than the null model.

# Anova

```
anova(poisson_model,test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: art
##
## Terms added sequentially (first to last)
##
##
##      Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                914      1817.4
## mar    1    2.8211     913      1814.6 0.09304 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



## Possion Regression with martial status and children covariate

To model the martial status and children as covariates, I use the formula `art ~ 1+mar + kid5`. This formula is equivalent to

$$\log \mu_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \beta_4 X_{4i}$$

where

$$X_{1i} = \begin{cases} 1 & \text{if the } i\text{th data point is married} \\ 0 & \text{otherwise} \end{cases},$$

$$X_{2i} = \begin{cases} 1 & \text{if the number of children of } i\text{th data point is 1} \\ 0 & \text{otherwise} \end{cases},$$

$$X_{3i} = \begin{cases} 1 & \text{if the number of children of } i\text{th data point is 2} \\ 0 & \text{otherwise} \end{cases}$$

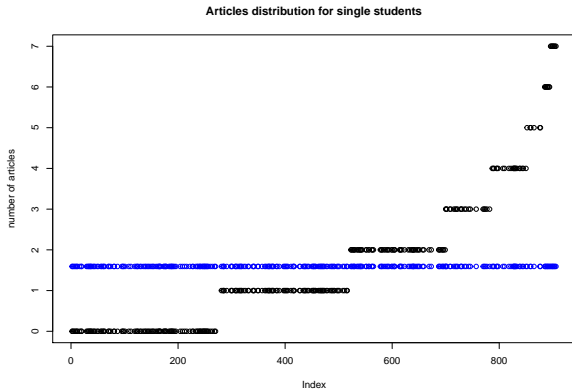
$$\text{and } X_{4i} = \begin{cases} 1 & \text{if the number of children of } i\text{th data point is 3} \\ 0 & \text{otherwise} \end{cases}.$$

# Poisson Regression with marital status and children covariate

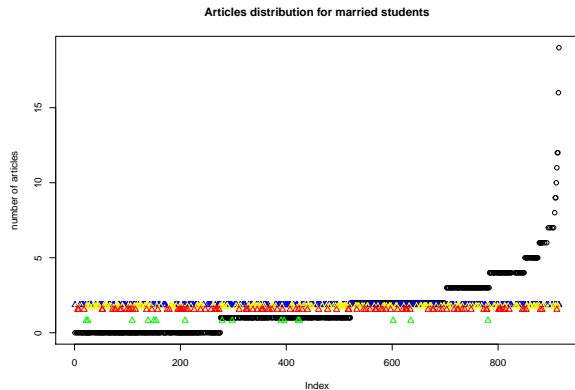
```
poisson_model = glm(art ~ 1 + kid5 + mar,  
                    family=poisson(link=log),data=bioChemists)  
summary(poisson_model)
```

```
##  
## Call:  
## glm(formula = art ~ 1 + kid5 + mar, family = poisson(link = log),  
##      data = bioChemists)  
##  
## Deviance Residuals:  
##      Min        1Q      Median        3Q        Max   
## -1.9280  -1.7845  -0.5042   0.3518   7.3520   
##  
## Coefficients:  
##              Estimate Std. Error z value Pr(>|z|)      
## (Intercept)  0.46514    0.04508  10.317  <2e-16 ***  
## kid51        -0.05510    0.06907  -0.798   0.4250      
## kid52        -0.18620    0.08960  -2.078   0.0377 *      
## kid53        -0.82747    0.28067  -2.948   0.0032 **     
## marMarried   0.15470    0.06235   2.481   0.0131 *      
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
##  
## (Dispersion parameter for poisson family taken to be 1)  
##  
##      Null deviance: 1817.4  on 914  degrees of freedom  
## Residual deviance: 1799.9  on 910  degrees of freedom  
## AIC: 3477.7  
##  
## Number of Fisher Scoring iterations: 5
```

## Possion Regression with martial status and children covariate



## Possion Regression with martial status and children covariate



Graphically, we can see than that martial status and number of children is not good indicator of number articles published.

## Goodness of Fit

### Saturated model

We can again compare the current model to the saturated model (best possible fit).

```
p_value = pchisq(poisson_model$deviance,  
                 poisson_model$df.residual,  
                 lower.tail = F)  
print(p_value)
```

```
## [1] 6.462874e-61
```

Since our p value is less than 0.05, we reject the null hypothesis. The models are not equivalent.

## Goodness of fit

### Null model

We can also compare the current model to the null model (worst possible fit).

```
p_value = pchisq(poisson_model$null.deviance  
                 -poisson_model$deviance,  
                 poisson_model$df.null  
                 -poisson_model$df.residual,  
                 lower.tail = F)  
print(p_value)
```

```
## [1] 0.001567133
```

## Goodness of fit

### Anova

We can also determine the model terms that cause a significance reduction in deviance.

```
anova(poisson_model, test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: art
##
## Terms added sequentially (first to last)
##
##
##      Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                914      1817.4
## kid5  3   11.3045      911      1806.1 0.01019 *
## mar   1    6.1638      910      1799.9 0.01304 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Poisson Regression with continuous variables, mentor articles and marital status

To model the marital status and number of mentor articles as covariates, I use the formula `art ~ 1+mar + ment`. This formula is equivalent to

$$\log \mu_i = \beta_0 + \beta_1 X_{1i} + X_{2i}$$

where

$$X_{1i} = \begin{cases} 1 & \text{if the } i \text{ data point is Married} \\ 0 & \text{otherwise} \end{cases}$$

and  $X_{2i}$  is the number of publications of the  $i$ th data point's mentor.



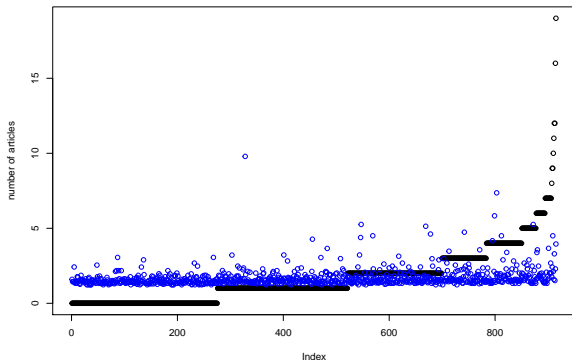
# Poisson Regression with continuous variables, mentor articles and marital status

```
poisson_model = glm(art ~ 1 + ment + mar,
                    family=poisson(link=log),data=bioChemists)
summary(poisson_model)

##
## Call:
## glm(formula = art ~ 1 + ment + mar, family = poisson(link = log),
##      data = bioChemists)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.6086  -1.6317  -0.3608   0.5039   5.8942
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.210726   0.049847   4.227 2.36e-05 ***
## ment         0.025917   0.001915  13.530 < 2e-16 ***
## marMarried   0.075332   0.054643   1.379  0.168
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 1817.4  on 914  degrees of freedom
## Residual deviance: 1667.6  on 912  degrees of freedom
## AIC: 3341.4
##
## Number of Fisher Scoring iterations: 5
```

## Possion Regression with continuous variables, mentor articles and martial status

```
plot(bioChemists$art,ylab='number of articles',xlab = 'Index')  
points(poisson_model$fitted,col="blue",pch=1)
```



Graphically, we can see than that martial status and number of children is not good indicator of number articles published.

## Goodness of Fit

### Saturated model

We can again compare the current model to the saturated model (best possible fit).

```
p_value = pchisq(poisson_model$deviance,  
                 poisson_model$df.residual,  
                 lower.tail = F)  
print(p_value)
```

```
## [1] 6.132629e-47
```

Since our p value is less than 0.05, we reject the null hypothesis. The models are not equivalent.

## Goodness of fit

### Null model

We can also compare the current model to the null model (worst possible fit).

```
p_value = pchisq(poisson_model$null.deviance  
                 -poisson_model$deviance,  
                 poisson_model$df.null  
                 -poisson_model$df.residual,  
                 lower.tail = F)  
print(p_value)
```

```
## [1] 2.993003e-33
```

Since our p value is less than 0.05, we reject the null hypothesis. The models are not equivalent.

## Goodness of fit

### Anova

We can also determine the model terms that cause a significance reduction in deviance.

```
anova(poisson_model, test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: art
##
## Terms added sequentially (first to last)
##
##
##      Df Deviance Resid. Df Resid. Dev Pr(>Chi)
## NULL                                914      1817.4
## ment  1  147.860             913      1669.5 <2e-16 ***
## mar   1    1.918             912      1667.6  0.1661
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Log-Linear Regression

Contingency table displays number of observations for a given combination of factors.

	low mentor articles	high mentor articles
low articles published	321	200
high articles published	171	223

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Log-linear model to model the group mean count of each cell of the contingency table

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Log-linear models allow us to model association between two or more variables.



## Log-Linear Regression

Contingency table displays number of observations for a given combination of factors.

	low mentor articles	high mentor articles
low articles published	321	200
high articles published	171	223

Log-linear model to model the group mean count of each cell of the contingency table

Log-linear models allow us to model association between two or more variables.

There are no well defined explanatory/response variables. This is because we are more focused on the interaction between two variables.

# Log-Linear Regression

## Contingency Table

Contingency table displays number of observations for all combinations of levels of given discrete variables.

We would like to learn a contingency table for the `biochemist` data set using number of articles published, number of mentor articles published and number of children.

First, we discretize our continuous variables.

```
bioChemists$art_binary <- sapply(bioChemists$art,  
                                function(x) ifelse(x > 1, 1, 0))  
bioChemists$ment_binary <- sapply(bioChemists$ment,  
                                  function(x)  
                                  ifelse(x > median(bioChemists$ment),  
                                         1, 0))
```

# Log-Linear Regression

## Contingency Table

### One-Way Contingency Table

A one-way contingency table shows the counts according to one covariate.

```
table(art_relative=bioChemists$art_binary)
```

```
## art_relative  
##    0    1  
## 521 394
```

This one-way contingency table shows that:

- ▶ there are 521 biochemists with 1 or less papers
- ▶ there are 394 biochemists with greater than 1 papers.

# Log-Linear Regression

## Contingency Table

### Two-Way Contingency Table

A two-way contingency table shows the counts according to two covariates.

```
table(art_relative=bioChemists$art_binary,ment=bioChemists$ment_binary)
```

```
##           ment
## art_relative  0   1
##           0 321 200
##           1 171 223
```

This two-way contingency table shows that:

- ▶ there are 321 biochemists with 1 or less papers and with a mentor that produced less than or equal to 6 papers
- ▶ there are 200 biochemists with 1 or less papers and with a mentor that produced more than 6 papers

# Log-Linear Regression

## Contingency Table

### Two-Way Contingency Table

A two-way contingency table shows the counts according to two covariates.

```
table(art_relative=bioChemists$art_binary,ment=bioChemists$ment_binary)
```

```
##           ment
## art_relative  0   1
##           0 321 200
##           1 171 223
```

- ▶ there are 171 biochemists with more than 1 paper and with a mentor that produced less than or equal to 6 papers
- ▶ there are 200 biochemists with more than 1 paper and with a mentor that produced more than 6 papers

# Log-Linear Regression

## Contingency Table

### Three-Way Contingency Table

A three-way contingency table shows the counts according to three covariates.

```
table(art_relative=bioChemists$art_binary,ment=bioChemists$ment_binary,  
      kid5=bioChemists$kid5)
```

```
## , , kid5 = 0  
##  
##          ment  
## art_relative  0  1  
##           0 208 128  
##           1 116 147  
##  
## , , kid5 = 1  
##  
##          ment  
## art_relative  0  1  
##           0  66  46  
##           1  38  45  
##  
## , , kid5 = 2  
##  
##          ment  
## art_relative  0  1  
##           0  39  21
```

# Log-Linear Regression

## Contingency Table

## Three-Way Contingency Table

This three-way contingency table shows that:

- ▶ With no children,
  - ▶ there are 208 biochemists with 1 or less papers and with a mentor that produced less than or equal to 6 papers
  - ▶ there are 128 biochemists with 1 or less papers and with a mentor that produced more than 6 papers
  - ▶ there are 116 biochemists with more than 1 paper and with a mentor that produced less than or equal to 6 papers
  - ▶ there are 147 biochemists with more than 1 paper and with a mentor that produced more than 6 papers

## Log-linear Regression for two way contingency table

For a two-way contingency table, log-linear GLMs have the following components:

- ▶ count response variables,  $Y_{ij}$ , which is the number of entries in the (i,j)th cell of the table.  $Y_{ij}$  follows a Poisson distribution with mean  $\mu_{ij}$



## Log-linear Regression for two way contingency table

For a two-way contingency table, log-linear GLMs have the following components:

- ▶ count response variables,  $Y_{ij}$ , which is the number of entries in the  $(i,j)$ th cell of the table.  $Y_{ij}$  follows a Poisson distribution with mean  $\mu_{ij}$
- ▶ a systematic component,  $\eta_{ij}$ , that relates the explanatory variables,

$$\eta_{ij} = \beta_0 + \sum_{k=1}^n \sum_{i=1}^{m-1} \beta_{ki} X_{ki}$$

where  $n$  is the number of covariates,  $m$  is the number of covariate class of  $X_k$  and  $X_{ki}$  is the total number of observations with  $i$ th covariate class of  $X_k$

## Log-linear Regression for two way contingency table

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- ▶ count response variables,  $Y_{ij}$ , which is the number of entries in the  $(i,j)$ th cell of the table.  $Y_{ij}$  follows a Poisson distribution with mean  $\mu_{ij}$
- ▶ a systematic component,  $\eta_{ij}$ , that relates the explanatory variables,

$$\eta_{ij} = \beta_0 + \sum_{k=1}^n \sum_{i=1}^{m-1} \beta_{ki} X_{ki}$$

where  $n$  is the number of covariates,  $m$  is the number of covariate class of  $X_k$  and  $X_{ki}$  is the total number of observations with  $i$ th covariate class of  $X_k$

- ▶ a link function that relates the mean of the random to the systematic component

$$\log \mu_{ij} = \beta_0 + \sum_{k=1}^n \sum_{i=1}^{m-1} \beta_{ki} X_{ki}$$

## Independent Model for two-way contingency table

Remember, using a log-linear model, our primary goal is to learn the interaction effects between covariates.

Again, we build the same two-way contingency table. We need to convert the contingency table in a form that is acceptable to glm.

```
contingency_table = table(art_relative=bioChemists$art_binary,  
                           ment=bioChemists$ment_binary)  
contingency_table.df = as.data.frame(contingency_table)
```

## Independent Model for two-way contingency table

```
print(contingency_table.df)
```

```
##   art_relative ment Freq
## 1           0    0  321
## 2           1    0  171
## 3           0    1  200
## 4           1    1  223
```

## Independent Model for two-way contingency table

Assuming each number of articles and mentor do not affect each other, we build a model of the cell count that does not take into account interaction effects. Such a model is called the *independent* model.

To do this, we use formula `Freq ~ art_relative + ment`.

```
log_linear_model_int <- glm(Freq ~ art_relative + ment,  
                             data = contingency_table.df, family = poisson)
```

## Independent Model for two-way contingency table

```
summary(log_linear_model_int)
```

```
##
## Call:
## glm(formula = Freq ~ art_relative + ment, family = poisson, data = contingency_table.df)
##
## Deviance Residuals:
##      1      2      3      4
##  2.385 -2.905 -2.713  2.923
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   5.63530    0.05347 105.392 < 2e-16 ***
## art_relative1 -0.27940    0.06676  -4.185 2.85e-05 ***
## ment1         -0.15111    0.06631  -2.279  0.0227 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 52.927  on 3  degrees of freedom
## Residual deviance: 30.035  on 1  degrees of freedom
## AIC: 65.008
##
## Number of Fisher Scoring iterations: 4
```

## Independent Model for two-way contingency table

### Goodness of fit

We compare the current model to the saturated model (best possible fit).

```
p_value = pchisq(log_linear_model_int$deviance,  
                  log_linear_model_int$df.residual,  
                  lower.tail = F)  
print(p_value)
```

```
## [1] 4.243721e-08
```

Since our p value is less than 0.05, we reject the null hypothesis. The models are not equivalent.

## Independent Model for two-way contingency table

## Saturated Model for the two-way contingency table

Assuming each number of articles and mentor affect each other, we build a model of the cell count that takes into account all interaction effects. Such a model is called the *saturated* model. To do this, we use formula `Freq ~ art_relative*ment`.

```
log_linear_model_sat <- glm(Freq ~ art_relative*ment,  
                             data = contingency_table.df,  
                             family = poisson)
```



## Independent Model for two-way contingency table

## Saturated Model for the two-way contingency table

```
summary(log_linear_model_sat)
```

```
##
## Call:
## glm(formula = Freq ~ art_relative * ment, family = poisson, data = contingency_table.df)
##
## Deviance Residuals:
## [1]  0  0  0  0  0
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      5.77144    0.05581 103.404 < 2e-16 ***
## art_relative1    -0.62978    0.09467  -6.652 2.89e-11 ***
## ment1            -0.47312    0.09008  -5.252 1.50e-07 ***
## art_relative1:ment1  0.73863    0.13582   5.438 5.38e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##    Null deviance: 5.2927e+01  on 3  degrees of freedom
## Residual deviance: 1.8874e-14  on 0  degrees of freedom
## AIC: 36.973
##
## Number of Fisher Scoring iterations: 2
```

## Independent Model for two-way contingency table

### Goodness of fit

We compare the current model to the saturated model (best possible fit).

```
p_value = pchisq(0,
                  log_linear_model_sat$df.residual,
                  lower.tail = F)
print(p_value)
```

```
## [1] 1
```

We fail to reject the null hypothesis. This makes sense since the models are literally the same thing.

## Independent Model for two-way contingency table

### Model Comparison

We use `anova` with `test='Chisq'` to compare the independent and saturated model.

```
anova(log_linear_model_int, log_linear_model_sat,
      test='Chisq')

## Analysis of Deviance Table
##
## Model 1: Freq ~ art_relative + ment
## Model 2: Freq ~ art_relative * ment
##   Resid. Df Resid. Dev Df Deviance  Pr(>Chi)
## 1          1      30.035
## 2          0       0.000  1   30.035 4.244e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From `anova`, we can see that the saturated model provides a statistically significant result.

# Independent Model for two-way contingency table

## Anova

We use also anova to determine what caused the significant decrease in the deviance.

```
anova(log_linear_model_sat, test='Chisq')
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Freq
##
## Terms added sequentially (first to last)
##
##
```

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
## NULL			3	52.927	
## art_relative	1	17.6844	2	35.243	2.608e-05 ***
## ment	1	5.2082	1	30.035	0.02248 *
## art_relative:ment	1	30.0348	0	0.000	4.244e-08 ***

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Adding art\_relative:ment to the independent model caused significant decrease in deviance.

## Independent Model for the three-way contingency table

Again, we build the same three-way contingency table. We need to convert the contingency table in a form that is acceptable to `glm`.

To create the *independent* model for the three-way contingency table, we use formula `Freq ~ art_relative + ment + kid5`.

```
log_linear_model_int <- glm(Freq ~ art_relative + ment + kid5,  
                             data = contingency_table.df, family = poisson)
```

# Independent Model for the three-way contingency table

```
summary(log_linear_model_int)
```

```
##
## Call:
## glm(formula = Freq ~ art_relative + ment + kid5, family = poisson,
##      data = contingency_table.df)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -2.4439  -1.4070  -0.1702   1.1974   2.4521
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    5.21164    0.05861  88.915 < 2e-16 ***
## art_relative1 -0.27940    0.06676  -4.185 2.85e-05 ***
## ment1         -0.15111    0.06631  -2.279  0.0227 *
## kid51         -1.12226    0.08245 -13.612 < 2e-16 ***
## kid52         -1.74130    0.10580 -16.459 < 2e-16 ***
## kid53         -3.62267    0.25331 -14.301 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 901.879  on 15  degrees of freedom
## Residual deviance:  36.651  on 10  degrees of freedom
## AIC: 131.03
##
## Number of Fisher Scoring iterations: 4
```

## Goodness of fit

We compare the current model to the saturated model (best possible fit).

```
p_value = pchisq(log_linear_model_int$deviance,  
                 log_linear_model_int$df.residual, lower.tail = F)  
print(p_value)
```

```
## [1] 6.50121e-05
```

Since our p value is less than 0.05, we reject the null hypothesis. The models are not equivalent.

## Saturated Model

To create the *saturated* model for the three-way contingency table, we use formula `Freq ~ art_relative*ment*kid5`.

```
log_linear_model_sat <- glm(Freq ~ art_relative*ment*kid5,  
                             data = contingency_table.df, family = poisson)
```



# Saturated Model

```
summary(log_linear_model_sat)
```

```
##
## Call:
## glm(formula = Freq ~ art_relative * ment * kid5, family = poisson,
##      data = contingency_table.df)
##
## Deviance Residuals:
##      [1]  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0  0
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      5.33754    0.06934   76.979 < 2e-16 ***
## art_relative1     -0.58395    0.11588   -5.039 4.67e-07 ***
## ment1             -0.48551    0.11234   -4.322 1.55e-05 ***
## kid51             -1.14788    0.14128   -8.125 4.47e-16 ***
## kid52             -1.67398    0.17450   -9.593 < 2e-16 ***
## kid53             -3.25810    0.36029   -9.043 < 2e-16 ***
## art_relative1:ment1  0.72235    0.16746    4.314 1.61e-05 ***
## art_relative1:kid51  0.03188    0.23430    0.136  0.892
## art_relative1:kid52 -0.30703    0.31870   -0.963  0.335
## art_relative1:kid53 -1.49549    1.06697   -1.402  0.161
## ment1:kid51        0.12449    0.22251    0.559  0.576
## ment1:kid52       -0.13353    0.29305   -0.456  0.649
## ment1:kid53        0.01550    0.58105    0.027  0.979
## art_relative1:ment1:kid51 -0.19226    0.33686   -0.571  0.568
## art_relative1:ment1:kid52  0.49140    0.44529    1.104  0.270
## art_relative1:ment1:kid53  0.44080    1.36126    0.324  0.746
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
```

## Goodness of fit

We compare the current model to the saturated model (best possible fit).

```
p_value = pchisq(log_linear_model_sat$deviance,  
                 log_linear_model_sat$df.residual, lower.tail = F)  
print(p_value)
```

```
## [1] 1
```

We fail to reject the null hypothesis. This makes sense since the models are literally the same thing.

## Model Comparison

We use `anova` with `test='Chisq'` to compare the independent and saturated model.

```
anova(log_linear_model_int,log_linear_model_sat,test='Chisq')
```

```
## Analysis of Deviance Table
##
## Model 1: Freq ~ art_relative + ment + kid5
## Model 2: Freq ~ art_relative * ment * kid5
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      10      36.651
## 2       0       0.000 10   36.651 6.501e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From `anova`, we can see that the saturated model provides a statistically significant result.

## Model Comparison

We use also anova to determine what caused the significant decrease in the deviance.

```
anova(log_linear_model_sat, test='Chisq')
```

```
## Analysis of Deviance Table
##
## Model: poisson, link: log
##
## Response: Freq
##
## Terms added sequentially (first to last)
##
##
##              Df Deviance Resid. Df Resid. Dev  Pr(>Chi)
## NULL                      15      901.88
## art_relative             1    17.68      14    884.20 2.608e-05 ***
## ment                     1     5.21      13    878.99 0.02248 *
## kid5                     3   842.34      10    36.65 < 2.2e-16 ***
## art_relative:ment        1    30.03       9     6.62 4.244e-08 ***
## art_relative:kid5        3     4.45       6     2.17 0.21665
## ment:kid5                3     0.19       3     1.97 0.97873
## art_relative:ment:kid5   3     1.97       0     0.00 0.57819
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Adding art\_relative:ment to the independent model caused significant decrease in deviance.

# Hierarchical modeling

## Data Wrangling

```
student_data <- read.csv("hsb1.csv")
school_data  <- read.csv("hsb2.csv")
student_data$ses_grandmean <- student_data$ses -
  mean(student_data$ses) # Grand-mean centered student SES
school_data$sm_ses_grandmean <- school_data$meanses -
  mean(school_data$meanses) # Grand-mean centered school SES

data <- merge(student_data, school_data, by = "id")
```

# Hierarchical modeling

## Data Wrangling

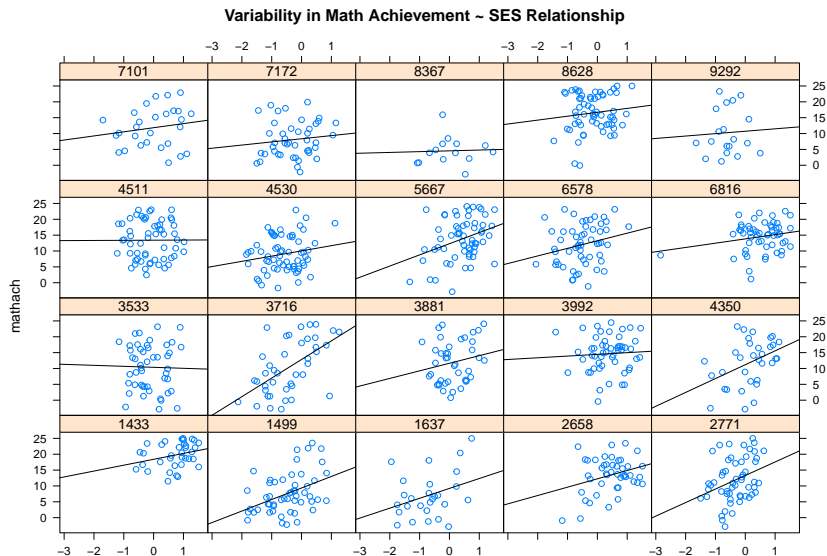
```
# Group-mean centered student SES
ses_group_mean <- aggregate(data$ses, list(data$id),
                             FUN = mean, data = data)

names(ses_group_mean) <- c('id', 'groupmeanSES')
data <- merge(data, ses_group_mean, by = "id")

groups <- unique(data$id)[sample(1:160, 20)]
subset <- data[data$id %in% groups, ]
```

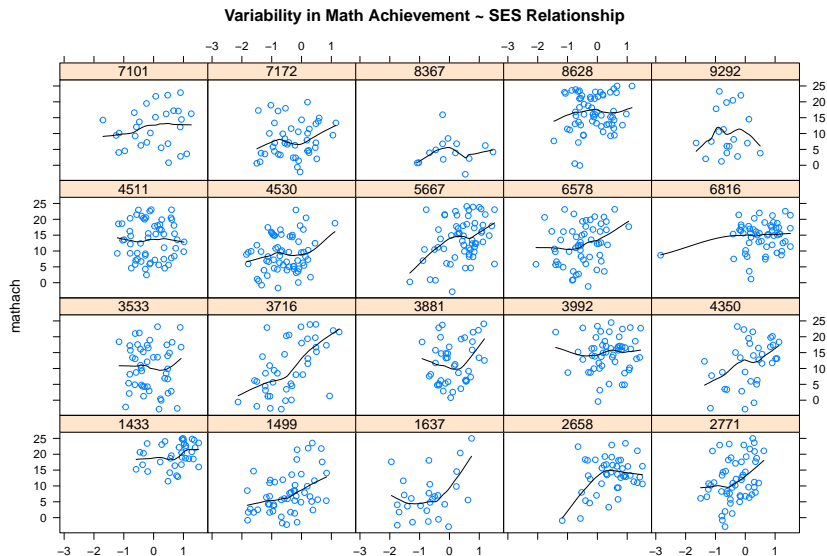
# Hierarchical modeling

```
xyplot(mathach ~ ses | as.factor(id), subset,  
       col.line = 'black',  
       type = c("p", "r"),  
       main = 'Variability in Math Achievement ~ SES Relationship')
```



# Hierarchical modeling

```
xyplot(mathach ~ ses | as.factor(id), subset,  
       col.line = 'black',  
       type = c("p", "smooth"),  
       main = 'Variability in Math Achievement ~ SES Relationship')
```





# Hierarchical modeling

```
unconditional <- lmer(mathach ~ 1 + (1|id), data = data)
summary(unconditional) # on p-values in nlme: https://stat.ethz.ch/pipermail/r-help/2006-May/094765.html
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: mathach ~ 1 + (1 | id)
## Data: data
##
## REML criterion at convergence: 47116.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.0631 -0.7539  0.0267  0.7606  2.7426
##
## Random effects:
## Groups   Name                Variance Std.Dev.
## id      (Intercept)          8.614    2.935
## Residual                    39.148    6.257
## Number of obs: 7185, groups: id, 160
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  12.6370    0.2444   51.71
```

## Hierarchical modeling

```
confint(unconditional) # you can also just calculate an app
```

```
## Computing profile confidence intervals ...
```

```
##           2.5 %    97.5 %  
## .sig01      2.594729  3.315880  
## .sigma      6.154803  6.361786  
## (Intercept) 12.156289 13.117121
```

# Hierarchical modeling

```
unconditional_2 <- lme(mathach ~ 1, random = ~ 1 | id, data = data)
summary(unconditional_2)
```

```
## Linear mixed-effects model fit by REML
## Data: data
##      AIC      BIC    logLik
##  47122.79 47143.43 -23558.4
##
## Random effects:
## Formula: ~1 | id
##      (Intercept) Residual
## StdDev:      2.934966 6.256862
##
## Fixed effects: mathach ~ 1
##              Value Std.Error   DF  t-value p-value
## (Intercept) 12.63697 0.2443936 7025  51.70747      0
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.06312473 -0.75387398  0.02670132  0.76062171  2.74262579
##
## Number of Observations: 7185
## Number of Groups: 160
```

# Hierarchical modeling

```
random_intercept_fixed_slope <- lmer(mathach ~ 1 + groupmeanSES + (1|id), data = data)
summary(random_intercept_fixed_slope)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: mathach ~ 1 + groupmeanSES + (1 | id)
## Data: data
##
## REML criterion at convergence: 46961.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.13493 -0.75254  0.02413  0.76766  2.78515
##
## Random effects:
## Groups Name Variance Std.Dev.
## id (Intercept) 2.639 1.624
## Residual 39.157 6.258
## Number of obs: 7185, groups: id, 160
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 12.6846 0.1493 84.97
## groupmeanSES 5.8635 0.3615 16.22
##
## Correlation of Fixed Effects:
## (Intr)
## groupmenSES 0.010
```

# Hierarchical modeling

```
confint(random_intercept_fixed_slope)
```

```
## Computing profile confidence intervals ...
```

```
##           2.5 %    97.5 %  
## .sig01      1.385193  1.871127  
## .sigma      6.155502  6.362511  
## (Intercept) 12.391774 12.976903  
## groupmeanSES 5.155743  6.572440
```

# Hierarchical modeling

```
random_intercept_fixed_slope_2 <- lme(mathach ~ 1 + groupmeanSES, random = ~ 1 | id, data = data)
summary(random_intercept_fixed_slope_2)
```

```
## Linear mixed-effects model fit by REML
## Data: data
##      AIC      BIC    logLik
## 46969.29 46996.81 -23480.65
##
## Random effects:
## Formula: ~1 | id
##      (Intercept) Residual
## StdDev:      1.624462 6.257562
##
## Fixed effects: mathach ~ 1 + groupmeanSES
##              Value Std.Error   DF t-value p-value
## (Intercept) 12.684609 0.1492900 7025 84.96624      0
## groupmeanSES  5.863539 0.3614712 158 16.22132      0
## Correlation:
##              (Intr)
## groupmeanSES 0.01
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.13493066 -0.75254260 0.02413095 0.76766113 2.78515398
##
## Number of Observations: 7185
## Number of Groups: 160
```

# Hierarchical modeling

```
summary(random_intercept_random_slope)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: mathach ~ 1 + groupmeanSES + (1 + groupmeanSES | id)
## Data: data
##
## REML criterion at convergence: 46960.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.13245 -0.75164  0.02212  0.76876  2.79449
##
## Random effects:
##   Groups      Name                Variance Std.Dev. Corr
##   id          (Intercept)         2.62707  1.6208
##             groupmeanSES         0.05417  0.2327   -1.00
## Residual                        39.15798  6.2576
## Number of obs: 7185, groups: id, 160
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  12.6832     0.1491   85.04
## groupmeanSES   5.8379     0.3644   16.02
##
## Correlation of Fixed Effects:
##              (Intr)
## groupmenSES -0.078
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

# Hierarchical modeling

```
random_intercept_random_slope_2 <- lme(mathach ~ 1 + groupmeanSES,  
                                         random = ~ 1 + groupmeanSES | id,  
                                         data = data)  
summary(random_intercept_random_slope_2)
```

```
## Linear mixed-effects model fit by REML  
## Data: data  
##      AIC      BIC    logLik  
## 46973.29 47014.57 -23480.65  
##  
## Random effects:  
## Formula: ~1 + groupmeanSES | id  
## Structure: General positive-definite, Log-Cholesky parametrization  
##           StdDev      Corr  
## (Intercept) 1.624460932 (Intr)  
## groupmeanSES 0.008272356 -0.003  
## Residual      6.257561467  
##  
## Fixed effects: mathach ~ 1 + groupmeanSES  
##           Value Std.Error   DF t-value p-value  
## (Intercept) 12.684610 0.1492901 7025 84.96616      0  
## groupmeanSES 5.863533 0.3614729 158 16.22122      0  
## Correlation:  
##           (Intr)  
## groupmeanSES 0.01  
##  
## Standardized Within-Group Residuals:  
##           Min           Q1           Med           Q3           Max  
## -3.13493049 -0.75254293  0.02413128  0.76766157  2.78515572  
##  
## Number of Observations: 7185  
## Number of Groups: 160
```



# Hierarchical modeling

```
fixed_intercept_random_slope <- lmer(mathach ~ 1 + groupmeanSES + (0 + groupmeanSES|id), data = data)
summary(fixed_intercept_random_slope)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: mathach ~ 1 + groupmeanSES + (0 + groupmeanSES | id)
##      Data: data
##
## REML criterion at convergence: 47065
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.1150 -0.7431  0.0317  0.7651  2.8202
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##    id      groupmeanSES  27.05     5.201
## Residual              39.75     6.304
## Number of obs: 7185, groups: id, 160
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)   12.7640    0.1226  104.07
## groupmeanSES   5.4202    0.5271   10.28
##
## Correlation of Fixed Effects:
##              (Intr)
## groupmenSES -0.045
```

# Hierarchical modeling

```
fixed_intercept_random_slope_2 <- lme(mathach ~ 1 + groupmeanSES,  
                                       random = ~ 0 + groupmeanSES | id, data = data)  
summary(fixed_intercept_random_slope_2)
```

```
## Linear mixed-effects model fit by REML  
## Data: data  
##      AIC      BIC    logLik  
## 47072.99 47100.51 -23532.5  
##  
## Random effects:  
## Formula: ~0 + groupmeanSES | id  
##      groupmeanSES Residual  
## StdDev:      5.201045 6.304462  
##  
## Fixed effects: mathach ~ 1 + groupmeanSES  
##              Value Std.Error DF t-value p-value  
## (Intercept) 12.764014 0.1226493 7025 104.06918      0  
## groupmeanSES 5.420157 0.5270957 158 10.28306      0  
## Correlation:  
##              (Intr)  
## groupmeanSES -0.045  
##  
## Standardized Within-Group Residuals:  
##      Min      Q1      Med      Q3      Max  
## -3.11504273 -0.74308714 0.03169931 0.76511017 2.82021818  
##  
## Number of Observations: 7185  
## Number of Groups: 160
```

# Hierarchical modeling

```
fixed_slope_level_two_variable <- lmer(mathach ~ 1 + groupmeanSES
                                       + sm_ses_grandmean + (1|id),
                                       data = data)
summary(fixed_slope_level_two_variable)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: mathach ~ 1 + groupmeanSES + sm_ses_grandmean + (1 | id)
## Data: data
##
## REML criterion at convergence: 46946.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.13127 -0.75215  0.02439  0.76700  2.78177
##
## Random effects:
##  Groups   Name      Variance Std.Dev.
##  id       (Intercept) 2.659    1.631
##  Residual              39.157    6.258
## Number of obs: 7185, groups: id, 160
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)      11.675      3.299   3.539
## groupmeanSES     -157.361     532.675  -0.295
## sm_ses_grandmean  163.223     532.668   0.306
##
## Correlation of Fixed Effects:
##              (Intr) grpSES
## groupmenSES   0.999
## sm_ss_grndm  -0.999 -1.000
```

# Hierarchical modeling

```
fixed_slope_level_two_variable_2 <- lme(mathach ~ 1 + groupmeanSES
                                         + sm_ses_grandmean,
                                         random = ~ 1 | id, data = data)
summary(fixed_slope_level_two_variable_2)
```

```
## Linear mixed-effects model fit by REML
## Data: data
##      AIC      BIC    logLik
## 46956.81 46991.2 -23473.4
##
## Random effects:
## Formula: ~1 | id
##      (Intercept) Residual
## StdDev:      1.630771 6.257562
##
## Fixed effects: mathach ~ 1 + groupmeanSES + sm_ses_grandmean
##              Value Std.Error   DF   t-value p-value
## (Intercept)   11.67469    3.2988 7025   3.539111 0.0004
## groupmeanSES  -157.36077   532.6748  157  -0.295416 0.7681
## sm_ses_grandmean 163.22262   532.6683  157   0.306425 0.7597
## Correlation:
##              (Intr) grpSES
## groupmeanSES    0.999
## sm_ses_grandmean -0.999 -1.000
##
## Standardized Within-Group Residuals:
##      Min      Q1      Med      Q3      Max
## -3.13126623 -0.75215319  0.02439264  0.76699775  2.78176653
##
## Number of Observations: 7185
## Number of Groups: 160
```

# Hierarchical modeling

```
summary(random_slope_level_two_variable)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## mathach ~ 1 + groupmeanSES + sm_ses_grandmean + (1 + groupmeanSES |
##   id)
## Data: data
##
## REML criterion at convergence: 46946.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.12727 -0.74930  0.02286  0.76841  2.79122
##
## Random effects:
## Groups Name Variance Std.Dev. Corr
## id (Intercept) 2.64688 1.6269
## groupmeanSES 0.05901 0.2429 -1.00
## Residual 39.15801 6.2576
## Number of obs: 7185, groups: id, 160
##
## Fixed effects:
## Estimate Std. Error t value
## (Intercept) 11.493 3.292 3.491
## groupmeanSES -186.500 531.608 -0.351
## sm_ses_grandmean 192.333 531.597 0.362
##
## Correlation of Fixed Effects:
## (Intr) grpSES
## groupmenSES 0.999
## sm_ss_grndm -0.999 -1.000
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

# Hierarchical modeling

```
random_slope_level_two_variable_2 <- lme(mathach ~ 1 + groupmeanSES  
    + sm_ses_grandmean,  
    random = ~ 1 + groupmeanSES | id,  
    data = data)
```

# Hierarchical modeling

```
summary(random_slope_level_two_variable_2)
```

```
## Linear mixed-effects model fit by REML
## Data: data
##      AIC      BIC    logLik
## 46960.81 47008.96 -23473.4
##
## Random effects:
## Formula: ~1 + groupmeanSES | id
## Structure: General positive-definite, Log-Cholesky parametrization
##           StdDev    Corr
## (Intercept) 1.6307657 (Intr)
## groupmeanSES 0.0130297 -0.005
## Residual     6.2575620
##
## Fixed effects: mathach ~ 1 + groupmeanSES + sm_ses_grandmean
##              Value Std.Error DF   t-value p-value
## (Intercept)   11.67466   3.2988 7025   3.539092  0.0004
## groupmeanSES  -157.36607  532.6762  157  -0.295425  0.7681
## sm_ses_grandmean 163.22790  532.6697  157   0.306434  0.7597
## Correlation:
##              (Intr) grpSES
## groupmeanSES    0.999
## sm_ses_grandmean -0.999 -1.000
##
## Standardized Within-Group Residuals:
##           Min           Q1           Med           Q3           Max
## -3.13126549 -0.75215462  0.02439169  0.76699807  2.78177069
##
## Number of Observations: 7185
## Number of Groups: 160
```

# Hierarchical modeling

```
fixed_slope_cl_interaction <- lmer(mathach ~ 1 + groupmeanSES*sm_ses_grandmean
                                   + (1|id), data = data)
summary(fixed_slope_cl_interaction)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: mathach ~ 1 + groupmeanSES * sm_ses_grandmean + (1 | id)
## Data: data
##
## REML criterion at convergence: 46945
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.11930 -0.75112  0.02448  0.76597  2.78831
##
## Random effects:
## Groups Name Variance Std.Dev.
## id (Intercept) 2.664 1.632
## Residual 39.158 6.258
## Number of obs: 7185, groups: id, 160
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)    11.4252     3.3155   3.446
## groupmeanSES   -213.6963    537.6427  -0.397
## sm_ses_grandmean 219.4884    537.6248   0.408
## groupmeanSES:sm_ses_grandmean -0.5799     0.7253  -0.800
##
## Correlation of Fixed Effects:
##              (Intr) grpSES sm_ss_
## groupmenSES  0.998
## sm_ss_grndm -0.998 -1.000
## grpmnSES:__  0.094  0.131 -0.131
```



# Hierarchical modeling

```
fixed_slope_cl_interaction_2 <- lme(mathach ~ 1 + groupmeanSES*sm_ses_grandmean,  
                                   random = ~ 1 | id, data = data)  
summary(fixed_slope_cl_interaction_2)
```

```
## Linear mixed-effects model fit by REML  
## Data: data  
##      AIC      BIC    logLik  
## 46956.97 46998.25 -23472.49  
##  
## Random effects:  
## Formula: ~1 | id  
##      (Intercept) Residual  
## StdDev:      1.632105 6.257638  
##  
## Fixed effects: mathach ~ 1 + groupmeanSES * sm_ses_grandmean  
##              Value Std.Error   DF   t-value p-value  
## (Intercept)      11.42519    3.3155 7025   3.445968 0.0006  
## groupmeanSES      -213.69625   537.6427  156  -0.397469 0.6916  
## sm_ses_grandmean      219.48842   537.6248  156   0.408256 0.6836  
## groupmeanSES:sm_ses_grandmean    -0.57991    0.7253  156  -0.799543 0.4252  
## Correlation:  
##              (Intr) grpSES sm_ss_  
## groupmeanSES      0.998  
## sm_ses_grandmean    -0.998 -1.000  
## groupmeanSES:sm_ses_grandmean  0.094  0.131 -0.131  
##  
## Standardized Within-Group Residuals:  
##      Min      Q1      Med      Q3      Max  
## -3.11929841 -0.75112002 0.02448373 0.76596673 2.78831371  
##  
## Number of Observations: 7185  
## Number of Groups: 160
```

# Hierarchical modeling

```
random_slope_cl_interaction <- lmer(mathach ~ 1 + groupmeanSES*sm_ses_grandmean  
                                   + (1 + groupmeanSES|id), data = data)
```

```
## boundary (singular) fit: see ?isSingular
```

# Hierarchical modeling

```
summary(random_slope_cl_interaction)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula:
## mathach ~ 1 + groupmeanSES * sm_ses_grandmean + (1 + groupmeanSES |
##   id)
## Data: data
##
## REML criterion at convergence: 46944.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.11654 -0.75065  0.02247  0.76812  2.79659
##
## Random effects:
## Groups Name Variance Std.Dev. Corr
## id      (Intercept) 2.65355 1.6290
##          groupmeanSES 0.04692 0.2166 -1.00
## Residual 39.15898 6.2577
## Number of obs: 7185, groups: id, 160
##
## Fixed effects:
##                                     Estimate Std. Error t value
## (Intercept)                        11.3252      3.3070  3.425
## groupmeanSES                       -228.1145    536.0175 -0.426
## sm_ses_grandmean                   233.9132    536.0005  0.436
## groupmeanSES:sm_ses_grandmean      -0.5251      0.7363 -0.713
##
## Correlation of Fixed Effects:
##      (Intr) grpSES sm_ss_
## groupmenSES 0.998
## sm_ss_grndm -0.998 -1.000
## grpmnSES:__ 0.080 0.118 -0.118
## convergence code: 0
```

# Hierarchical modeling

```
random_slope_cl_interaction_2 <- lme(mathach ~ 1 + groupmeanSES*sm_ses_grandmean,  
                                     random = ~ 1 + groupmeanSES | id,  
                                     data = data)
```

# Hierarchical modeling

```
summary(random_slope_cl_interaction_2)
```

```
## Linear mixed-effects model fit by REML
## Data: data
##      AIC      BIC    logLik
## 46960.97 47016.01 -23472.49
##
## Random effects:
## Formula: ~1 + groupmeanSES | id
## Structure: General positive-definite, Log-Cholesky parametrization
##           StdDev      Corr
## (Intercept) 1.632105137 (Intr)
## groupmeanSES 0.005745282 -0.002
## Residual     6.257637586
##
## Fixed effects: mathach ~ 1 + groupmeanSES * sm_ses_grandmean
##                                     Value Std.Error   DF   t-value p-value
## (Intercept)             11.42519     3.3155 7025   3.445964 0.0006
## groupmeanSES             -213.69606    537.6432  156  -0.397468 0.6916
## sm_ses_grandmean         219.48823    537.6253  156   0.408255 0.6836
## groupmeanSES:sm_ses_grandmean  -0.57990     0.7253  156  -0.799534 0.4252
## Correlation:
##                                     (Intr) grpSES sm_ss_
## groupmeanSES                      0.998
## sm_ses_grandmean                  -0.998 -1.000
## groupmeanSES:sm_ses_grandmean  0.094  0.131 -0.131
##
## Standardized Within-Group Residuals:
##           Min           Q1           Med           Q3           Max
## -3.11929848 -0.75111989  0.02448355  0.76596678  2.78831459
##
## Number of Observations: 7185
## Number of Groups: 160
```

# Hierarchical modeling

```
logit_random_intercept_and_slope <- glmer(minority ~ groupmeanSES +  
      (1 + groupmeanSES | id),  
      data = data, family = binomial(link="logit"))
```

# Hierarchical modeling

```
summary(logit_random_intercept_and_slope)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
## Approximation) [glmerMod]
## Family: binomial ( logit )
## Formula: minority ~ groupmeanSES + (1 + groupmeanSES | id)
## Data: data
##
##           AIC          BIC    logLik deviance df.resid
##    5453.9    5488.3   -2721.9   5443.9      7180
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -6.2886 -0.3942 -0.2073  0.1590  6.1544
##
## Random effects:
## Groups Name          Variance Std.Dev. Corr
## id      (Intercept)    2.529    1.590
##          groupmeanSES 11.445    3.383   -0.32
## Number of obs: 7185, groups: id, 160
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -1.7382    0.1678  -10.359 < 2e-16 ***
## groupmeanSES  -2.0523    0.5370   -3.822 0.000132 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## groupmenSES -0.230
```

# Hierarchical modeling

```
specified_variance_covariance_matrix_for_random_effects <- lme(mathach ~ 1  
  +groupmeanSES*sm_ses_grandmean,  
  random = ~ 1 + groupmeanSES | id,  
  correlation = corAR1(),  
  data = data)
```

*# just an example, not needed in this case (useful for growth curve models)!*



# Hierarchical modeling

```
summary(specified_variance_covariance_matrix_for_random_effects)
```

```
## Linear mixed-effects model fit by REML
## Data: data
##      AIC      BIC    logLik
## 46962.8 47024.71 -23472.4
##
## Random effects:
## Formula: ~1 + groupmeanSES | id
## Structure: General positive-definite, Log-Cholesky parametrization
##              StdDev    Corr
## (Intercept)  1.62876592 (Intr)
## groupmeanSES 0.07080922 -0.039
## Residual     6.25836130
##
## Correlation Structure: AR(1)
## Formula: ~1 | id
## Parameter estimate(s):
##      Phi
## 0.005104377
## Fixed effects: mathach ~ 1 + groupmeanSES * sm_ses_grandmean
##              Value Std.Error DF   t-value p-value
## (Intercept)    11.42446   3.3152 7025   3.446083  0.0006
## groupmeanSES   -213.84493  537.5895  156  -0.397785  0.6913
## sm_ses_grandmean  219.63651  537.5716  156   0.408572  0.6834
## groupmeanSES:sm_ses_grandmean -0.57970   0.7256  156  -0.798894  0.4256
## Correlation:
##              (Intr) grpSES sm_ss_
## groupmeanSES    0.998
## sm_ses_grandmean -0.998 -1.000
## groupmeanSES:sm_ses_grandmean  0.094  0.131 -0.131
##
## Standardized Within-Group Residuals:
##              Min      Q1      Med      Q3      Max
```