# Generalized linear mixed models

## 560 Hierarchical modeling

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# Non-normal data

**Assumption so far:**
Within-group heterogeneity is well-represented by a normal distribution.

**Reality:**
Not a good assumption in many applications.

Examples of data that are generally not normally distributed include

- income, hospital costs or other monetary data (often highly skewed);
- time to an event;
- number of children or other count data;
- binary indicator variables.

# Example: Police stop data

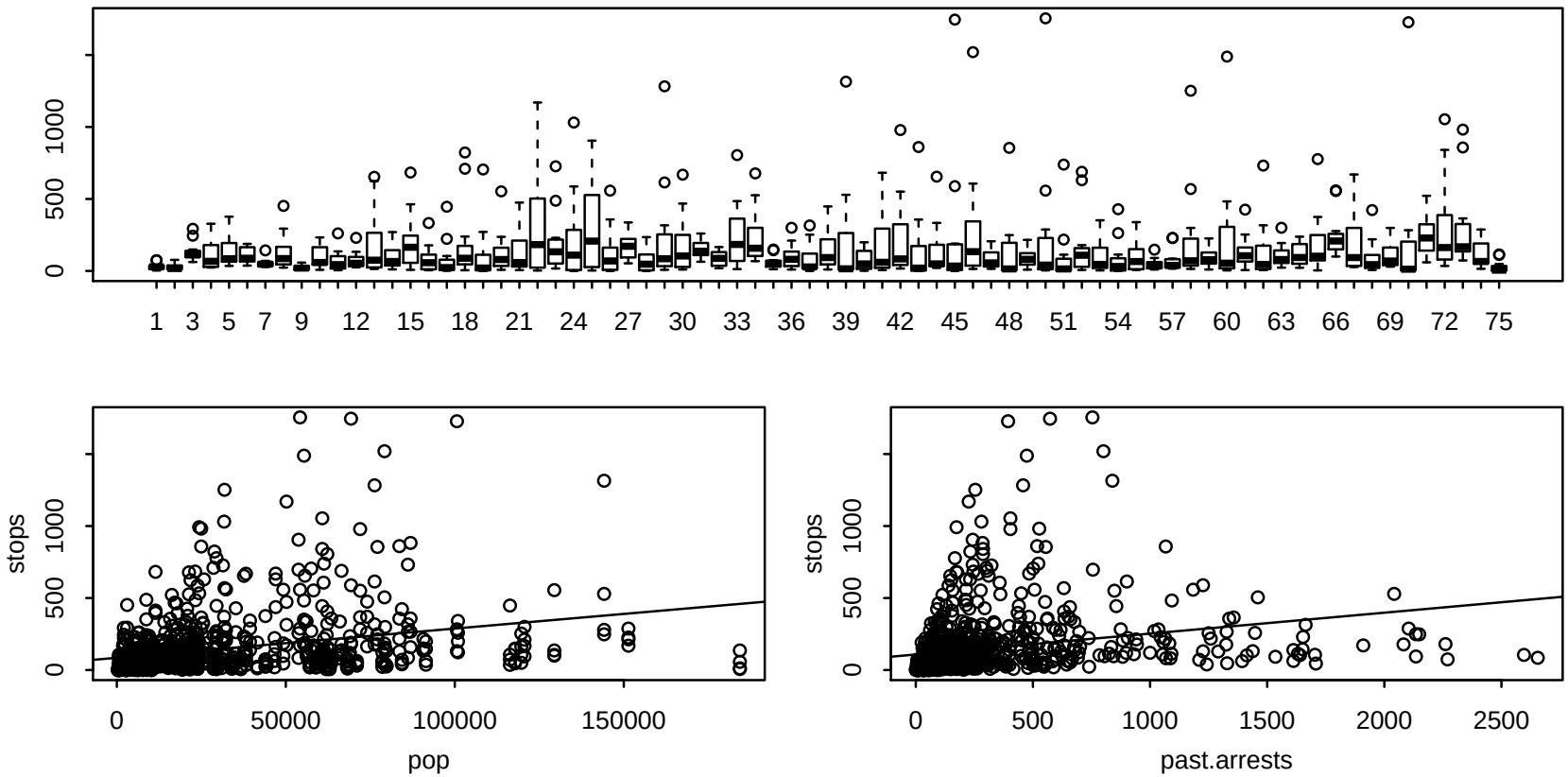
A 1999 study of the NYC police department gathered data on police searches in 75 city precincts, including

- `stops:` number of stops in a given precinct;
- `pop:` the population of the precinct;
- `past.arrests:` number of arrests in the precinct in a previous year.
- `eth, crime:` stops broken down by ethnicity and crime type.

```
pstop[1:15,]
```

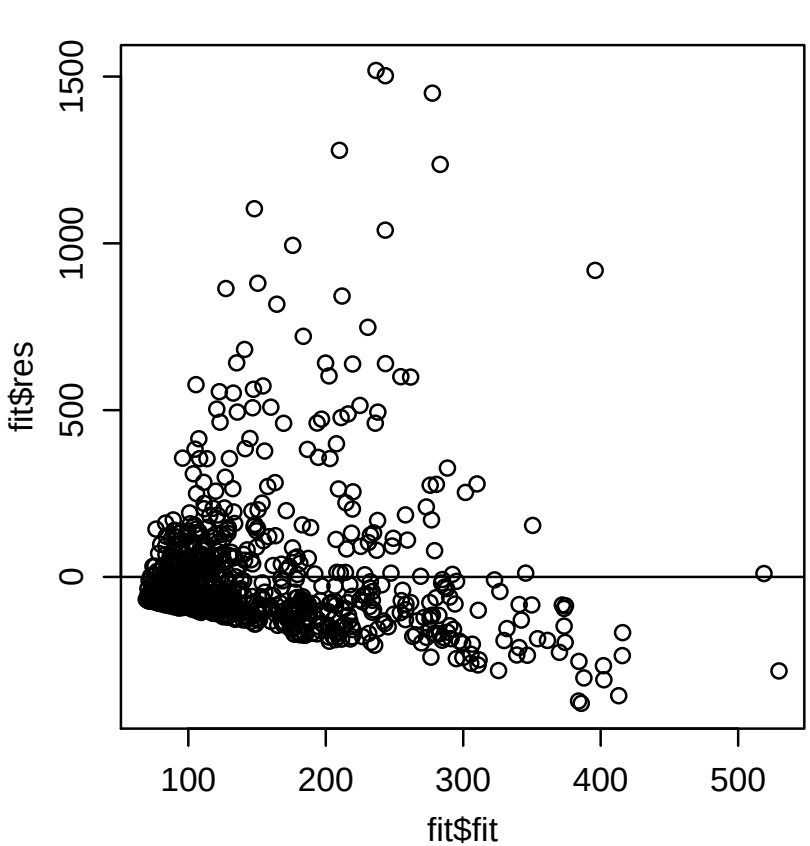
```
##    stops   pop past.arrests precinct eth crime
## 1     75  1720          191        1   1     1
## 2     36  1720           57        1   1     2
## 3     74  1720          599        1   1     3
## 4     17  1720          133        1   1     4
## 5     37  1368           62        1   2     1
## 6     39  1368           27        1   2     2
## 7     23  1368          149        1   2     3
## 8      3  1368           57        1   2     4
## 9     26 23854          135        1   3     1
## 10    32 23854           16        1   3     2
## 11    10 23854          107        1   3     3
## 12    13 23854          123        1   3     4
## 13    73  2596          227        2   1     1
## 14    37  2596           56        2   1     2
## 15     9  2596          246        2   1     3
```

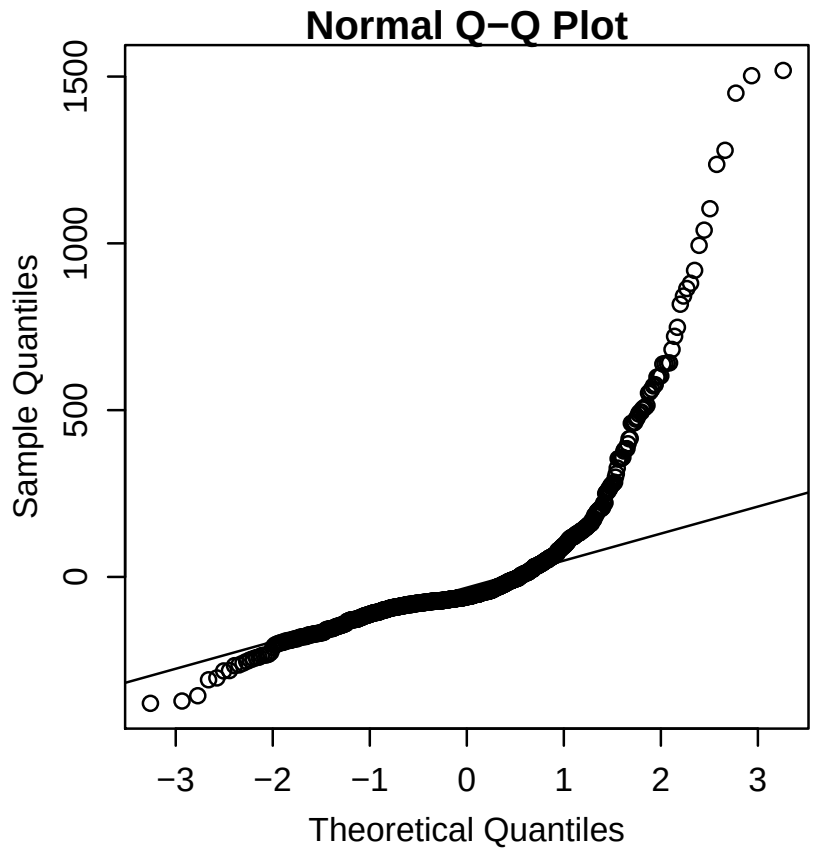
# Example: Police stop data



# Example: Police stop data

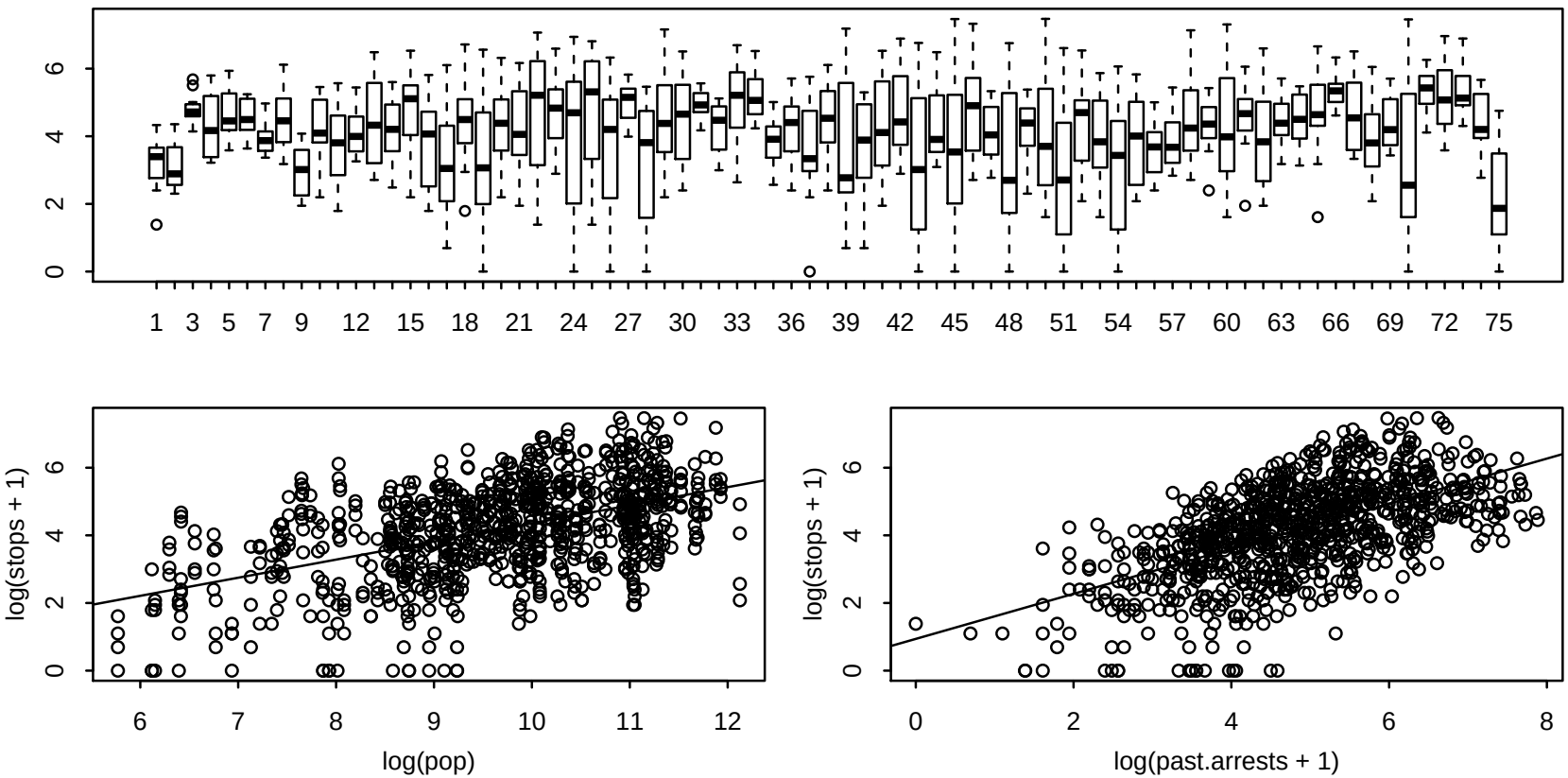
```
fit<-lm(stops~pop+past.arrests,data=pstop)

mpar(mfrow=c(1,2))
plot(fit$res~fit$fit) ; abline(h=0)
qqnorm(fit$res) ; qqline(fit$res)
```



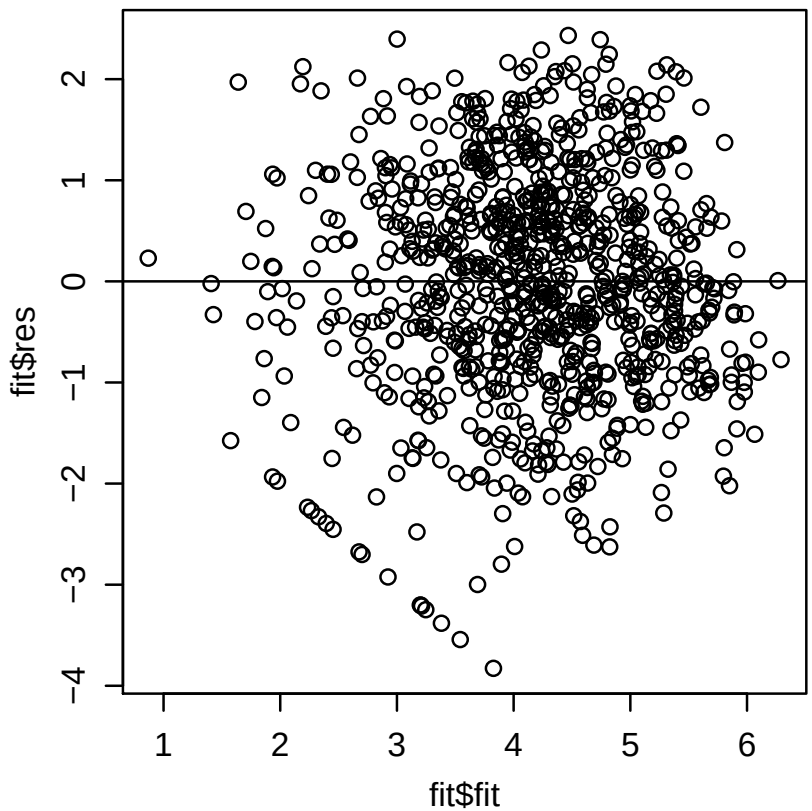
# Example: Police stop data

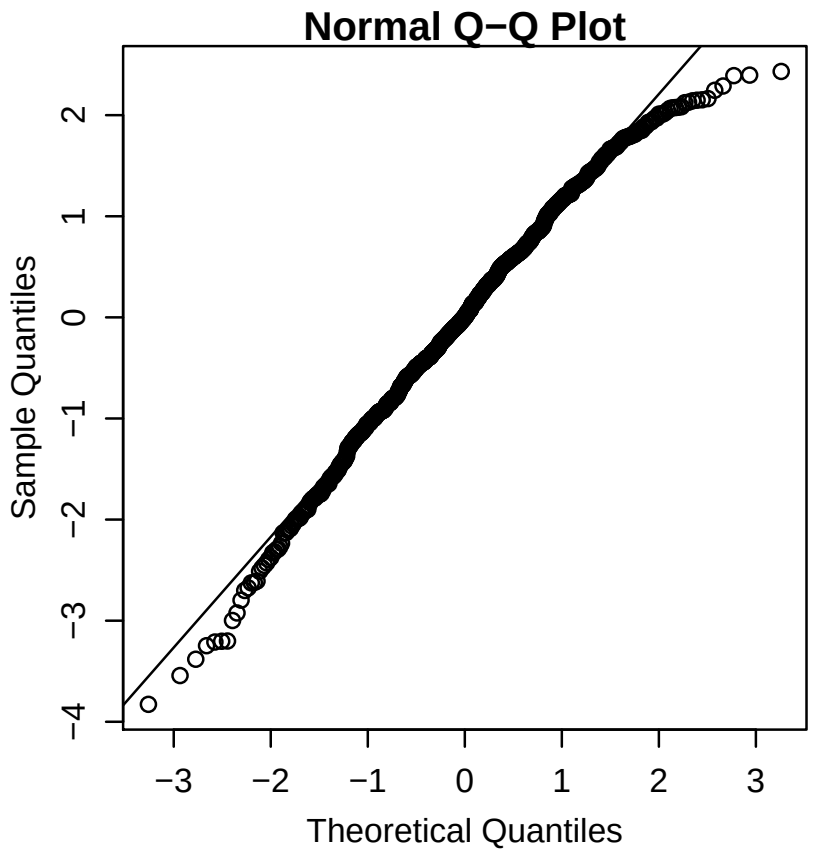
```
mpar()
layout(matrix(c(1,2,1,3),2,2)  )
boxplot(log(pstop$stops+1)~pstop$precinct)
plot(log(stops+1)~log(pop),data=pstop) ; abline(lm(log(stops+1)~log(pop),data=pstop))
plot(log(stops+1)~log(past.arrests+1),data=pstop) ; abline(lm(log(stops+1)~log(past.arrests
```



# Example: Police stop data

```
fit<-lm(log(stops+1)~log(pop)+log(past.arrests+1),data=pstop)

mpar(mfrow=c(1,2))
plot(fit$res~fit$fit) ; abline(h=0)
qqnorm(fit$res) ; qqline(fit$res)
```



# Example: Grouseticks

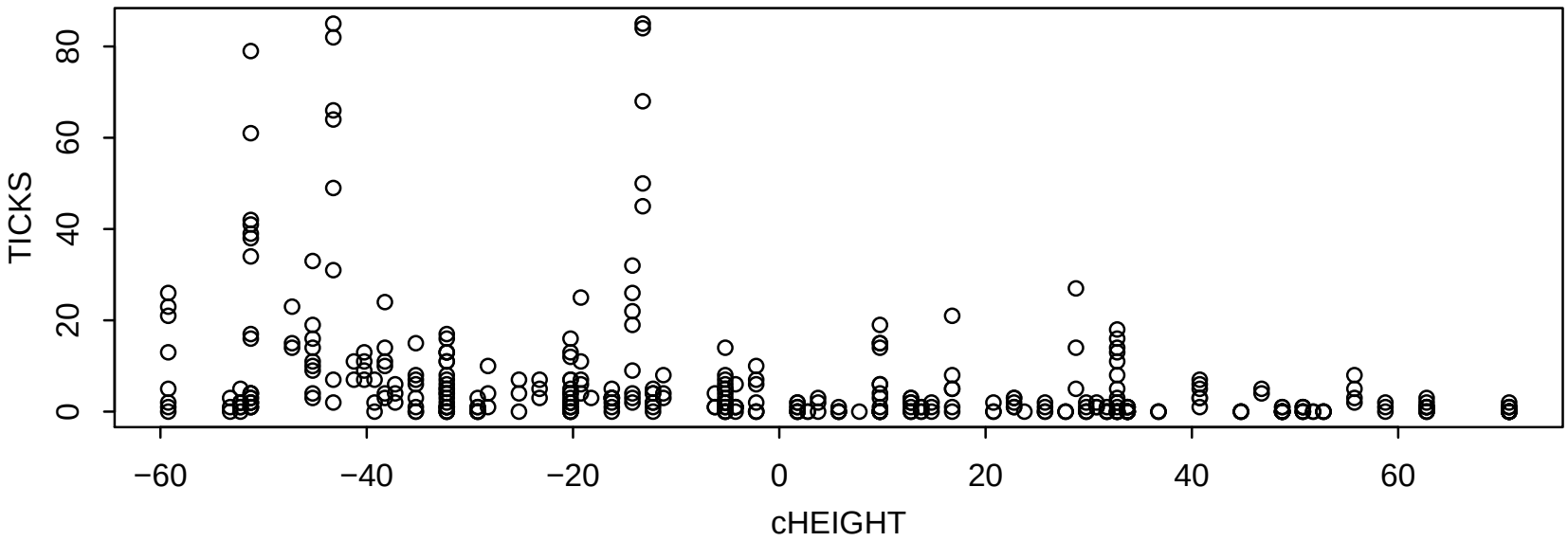
Some variables:

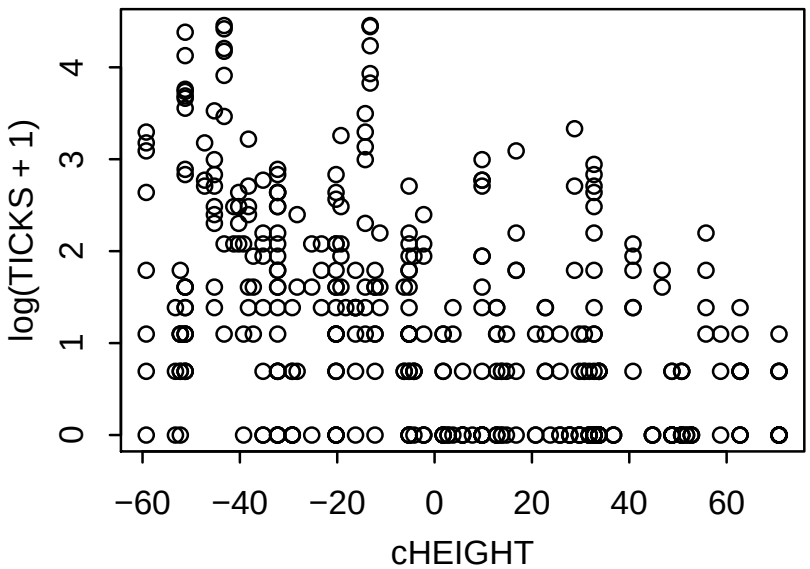
- `TICKS`: number of ticks on a chicks head
- `BROOD`: brood number
- `cHEIGHT`: height above sea level (centered)
- `YEAR`: year of study

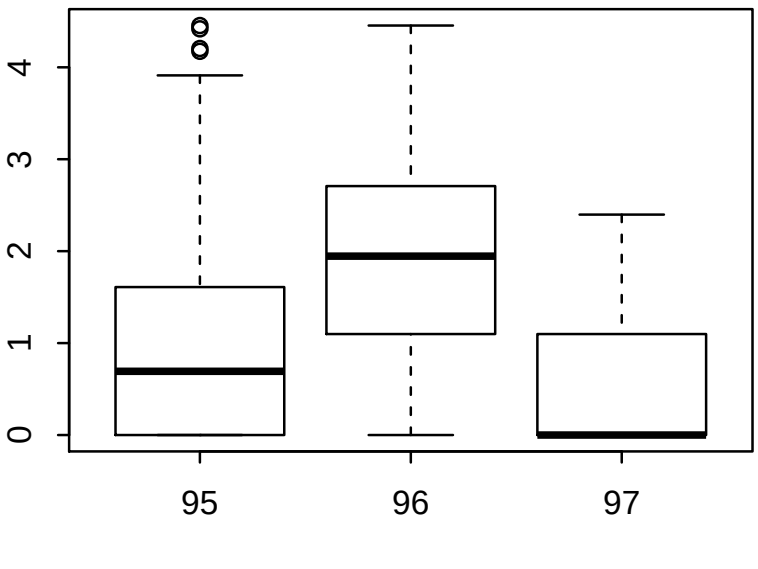
```
grouseticks[1:15,]

##    INDEX TICKS BROOD HEIGHT YEAR LOCATION   cHEIGHT
## 1      1     0   501    465   95       32  2.759305
## 2      2     0   501    465   95       32  2.759305
## 3      3     0   502    472   95       36  9.759305
## 4      4     0   503    475   95       37 12.759305
## 5      5     0   503    475   95       37 12.759305
## 6      6     3   503    475   95       37 12.759305
## 7      7     2   503    475   95       37 12.759305
## 8      8     0   504    488   95       44 25.759305
## 9      9     0   504    488   95       44 25.759305
## 10    10     2   504    488   95       44 25.759305
## 11    11     0   505    492   95       47 29.759305
## 12    12     0   505    492   95       47 29.759305
## 13    13     0   505    492   95       47 29.759305
## 14    14     0   506    490   95       45 27.759305
## 15    15     0   506    490   95       45 27.759305
```

Almost 20% of broods have a zero count for all chicks.

# Example: Grouseticks

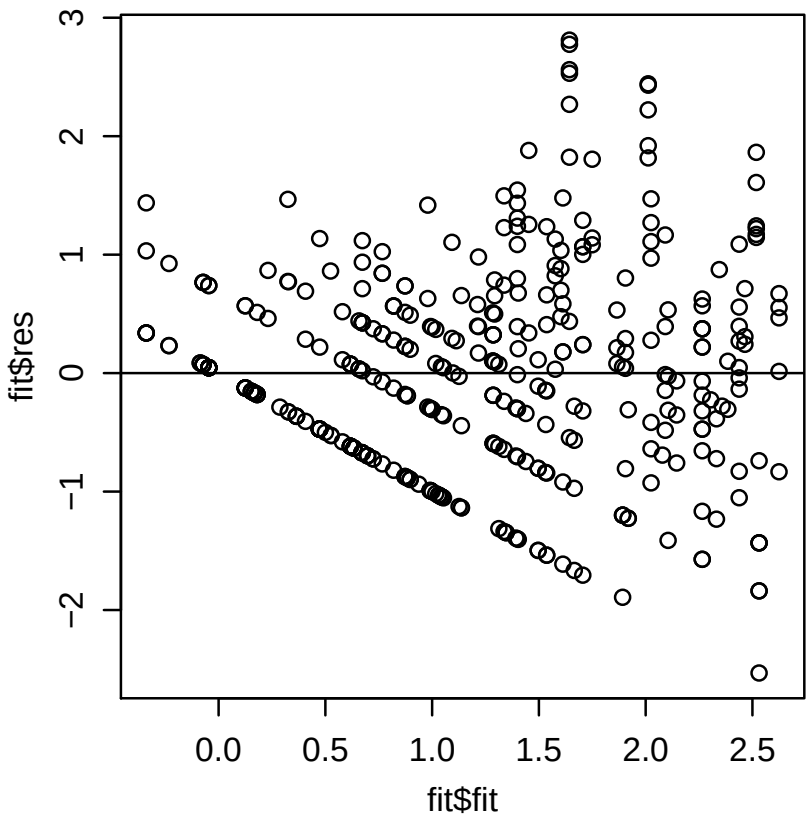


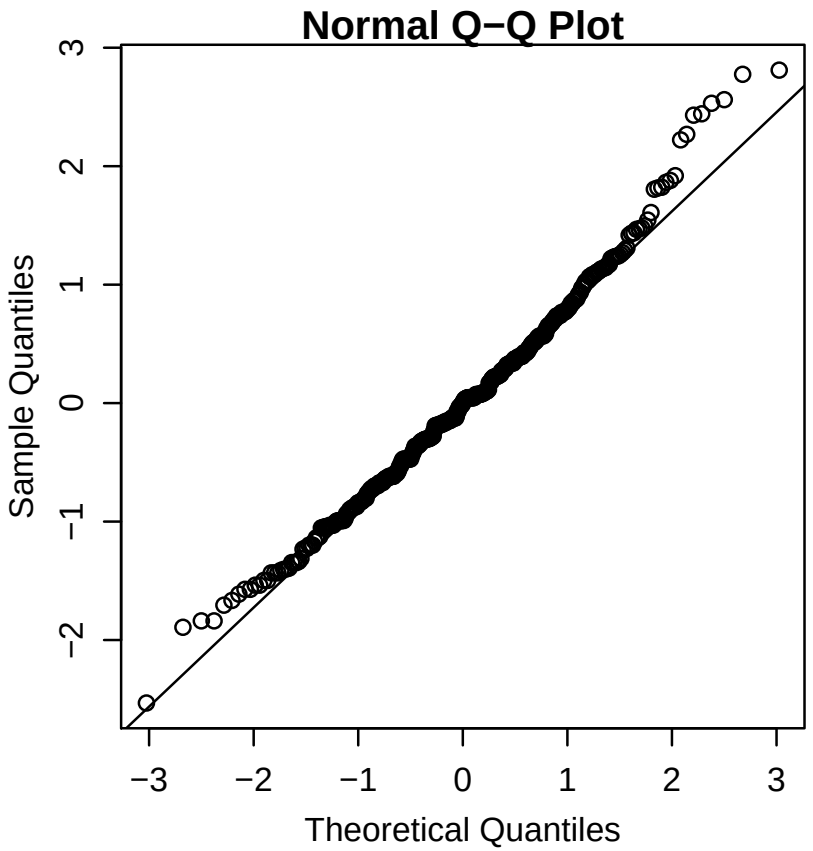



# Example: Grouseticks

```
fit<-lm( log(TICKS+1)~ cHEIGHT + as.factor(YEAR) ,data=grouseticks)

summary(fit)$coef

##                        Estimate Std. Error    t value     Pr(>|t|)
## (Intercept)         1.06715919 0.07961023  13.404799 4.356064e-34
## cHEIGHT            -0.01331815 0.00120441 -11.057815 5.646538e-25
## as.factor(YEAR)96   0.76833413 0.10607991   7.242975 2.280915e-12
## as.factor(YEAR)97  -0.46374571 0.10926018  -4.244417 2.728417e-05
```



# Transformably normal

Many outcomes can be transformed so that distributional assumptions are almost met:

- mean-variance relationships can be stabilized;
- residuals have a distribution close to normal.

However, sometimes such transformations are not feasible or desirable:

- For some discrete data it is difficult or impossible to find an appropriate transformation (eg., binary data).
- Even if a transformation could be found, there are advantages to analyzing the data on its original scale.

In such cases we will modify our regression models to account for non-normality.

# Logistic regression

**Logistic regression:**

$$\Pr(y_i = 1) = \theta_i = \frac{e^{\beta^T x_i}}{1 + e^{\beta^T x_i}}$$

$$\log \frac{\theta_i}{1-\theta_i} = \boldsymbol{\beta}^T \mathbf{x}_i$$

# Data types for logistic regression

## Binary data

| y | x1 | x2 |
|---|---|---|
| 0 | 2.3 | 3.2 |
| 0 | 2.3 | 2.1 |
| 1 | 2.3 | 5.4 |
| 0 | 4.1 | 1.6 |
| 1 | 4.1 | 3.2 |
| 1 | 4.1 | 1.2 |
| . | . | . |
| . | . | . |

```
fit <- glm( y ~ x1 + x2 , family=binomial )
```

# Data types for logistic regression

## Binomial data

| y | n | x1 | x2 |
|---|---|---|---|
| 4 | 10 | 2.3 | 3.2 |
| 2 | 12 | 2.3 | 2.1 |
| 5 | 8 | 2.3 | 5.4 |
| 3 | 10 | 4.1 | 1.6 |
| 6 | 16 | 4.1 | 3.2 |
| 8 | 9 | 4.1 | 1.2 |
| . | . | . | . |
| . | . | . | . |

Here, the model is

$$y_i \sim \text{binomial}(\theta_i, n_i)$$

```
fit <- glm( cbind(y,n-y) ~ x1 + x2 , family=binomial )
```

# Example: Social network analysis

**Network and relational data:** Data measured on pairs (dyads) of units.

**Friendship study:** What characteristics of people lead to friendship ties?

**Data:**

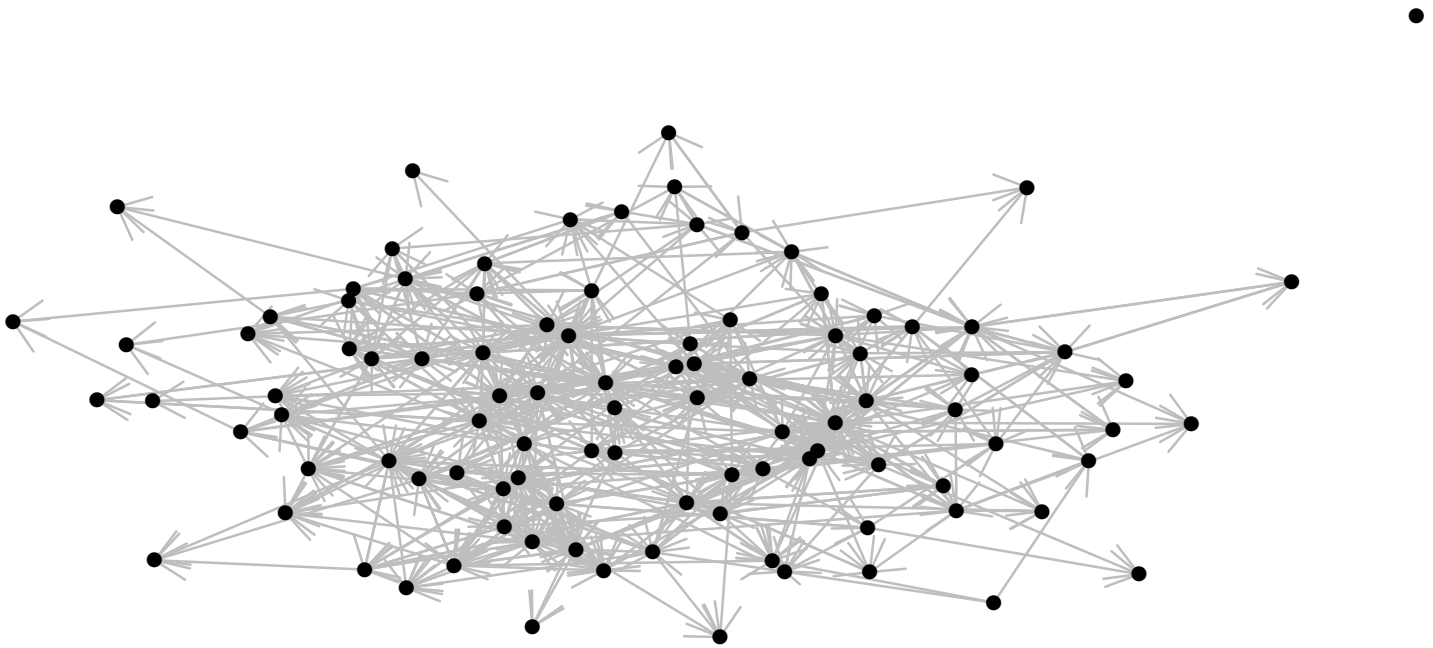
friendship: binary indicator of (directed) friendship

gpa: GPA

smoke: smoking score

grade: year in school

# Example: Social network analysis



# Example: Social network analysis

```
X[1:15,]
```

```
##        rgpa rsmoke cgpa csmoke igrade  igpa ismoke
##  [1,]  0.71   0.62 0.41  -0.07      1  0.29  -0.04
##  [2,]  0.85   0.98 0.41  -0.07      1  0.35  -0.07
##  [3,]  0.86  -0.12 0.41  -0.07      0  0.35   0.01
##  [4,]  0.41   0.64 0.41  -0.07      0  0.17  -0.05
##  [5,]  0.66   0.63 0.41  -0.07      0  0.27  -0.04
##  [6,] -0.54   0.87 0.41  -0.07      0 -0.22  -0.06
##  [7,]  0.69   0.66 0.41  -0.07      0  0.28  -0.05
##  [8,] -0.29  -0.64 0.41  -0.07      0 -0.12   0.05
##  [9,] -0.51  -0.68 0.41  -0.07      1 -0.21   0.05
## [10,]  0.41   0.64 0.41  -0.07      0  0.17  -0.05
## [11,]  2.17  -1.04 0.41  -0.07      0  0.89   0.07
## [12,] -0.28   0.00 0.41  -0.07      0 -0.11   0.00
## [13,]  0.69  -0.61 0.41  -0.07      1  0.28   0.04
## [14,]  1.52  -0.60 0.41  -0.07      0  0.62   0.04
## [15,] -0.30   1.51 0.41  -0.07      0 -0.12  -0.11
```

```
y[1:15]
```

```
##  [1] 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0
```

# Logistic regression

```
fit0<-glm( y ~ X, family=binomial)
```

```
summary(fit0)$coef
```

```
##                Estimate Std. Error     z value     Pr(>|z|)
## (Intercept) -4.12113655 0.09146103 -45.0589348 0.000000e+00
## Xrgpa        0.36857711 0.06091581   6.0505990 1.443082e-09
## Xrsmoke      0.44406283 0.06842175   6.4900832 8.578901e-11
## Xcgpa        0.37325974 0.05980462   6.2413199 4.338938e-10
## Xcsmoke      0.33401415 0.06961131   4.7982741 1.600387e-06
## Xigrade      2.06330014 0.09901610  20.8380263 1.957441e-96
## Xigpa        0.04612661 0.05488132   0.8404793 4.006397e-01
## Xismoke      0.02072443 0.08501630   0.2437701 8.074089e-01
```

# Poisson model

A natural model for count data is the *Poisson model*: $Y \sim \text{Pois}(\theta)$ if

$$\Pr(Y = y|\theta) = \text{dpois}(y, \theta) = \theta^y e^{-\theta}/y!.$$

For example, if $\theta = 2.1$ (the 2006 U.S. fertility rate),

$$\begin{array}{lll}
\Pr(Y = 0|\theta = 2.1) = & (2.1)^0 e^{-2.1}/(0!) = & .12 \\
\Pr(Y = 1|\theta = 2.1) = & (2.1)^1 e^{-2.1}/(1!) = & .26 \\
\Pr(Y = 2|\theta = 2.1) = & (2.1)^2 e^{-2.1}/(2!) = & .27 \\
\Pr(Y = 3|\theta = 2.1) = & (2.1)^3 e^{-2.1}/(3!) = & .19 \\
\vdots & \vdots & \vdots
\end{array}$$

# Poisson regression

In Poisson regression, we relate the mean $\theta$ to explanatory variables $x$

One possibility would be to just write $\theta(x)$ as a linear regression:

$$\theta(x) = \beta_0 + \beta_1 x.$$

However, this allows for negative values of $\theta(x)$, which doesn't make sense:

$$Y \in \{0, 1, 2, \ldots\} \Rightarrow \mathsf{E}[Y|x] = \theta(x) \geq 0 \text{ for all } x$$

# Multiplicative mean model

One way to impose this constraint is to write $\theta(x)$ in terms of multiplicative effects, via the exponential function:

$$\mathsf{E}[Y|x] = \theta(x) = \exp(\beta_0 + \beta_1 x) = e^{\beta_0+\beta_1 x}$$

Here, $\beta_1$ represents the *multiplicative effect* of $x$ on $Y$:

$$\begin{aligned} \mathsf{E}[Y|x+1]/\mathsf{E}[Y|x] &= \frac{e^{\beta_0+\beta_1(x+1)}}{e^{\beta_0+\beta_1 x}} \\ &= e^{\beta_1} \end{aligned}$$

So an increase of $x$ by one results in the mean being $e^{\beta_1}$ times as large.

Eg., $\beta_1 = \log 2 = 0.693 \Rightarrow$ a unit increase in $x$ leads to a doubling of $\mathsf{E}[Y]$.

# Poisson regression with a log-link

Suppose $\{Y_i, \mathbf{x}_i\}$ are independently sampled from a population.

The *Poisson regression model with a log-link* is

$$Y_i|\mathbf{x}_i \sim \text{Poisson}(\exp[\boldsymbol{\beta}^T\mathbf{x}_i]).$$

**Log-link:** the function linking the regression to the expectation of $Y$ is log:

$$\text{E}[Y|\mathbf{x}] = \exp(\boldsymbol{\beta}^T\mathbf{x}) \Leftrightarrow \log \text{E}[Y|\mathbf{x}] = \boldsymbol{\beta}^T\mathbf{x}$$

**MLE**: The log-likelihood, as a function of $\boldsymbol{\beta}$, is given by

$$\begin{aligned} l(\boldsymbol{\beta} : \mathbf{y}, \mathbf{X}) &= \log \text{Pr}(\mathbf{y}|\mathbf{X}, \boldsymbol{\beta}) \\ &= \log \prod_{i=1}^{n} p(y_i|\mathbf{x}_i, \boldsymbol{\beta}) \\ &= \sum_{i=1}^{n} \log \texttt{dpois}(y_i, \exp(\boldsymbol{\beta}^T\mathbf{x}_i)) \\ &= \texttt{sum( log( dpois( y,exp(X\%*\%beta) ) ) )} \end{aligned}$$

# Example: Police stop data

```
fit.pstop<-glm( stops ~ log(pop) + log(past.arrests+1) + as.factor(eth) ,
                        family=poisson, data=pstop[pstop$crime==1,])

summary(fit.pstop)$coef

##                          Estimate  Std. Error   z value      Pr(>|z|)
## (Intercept)            1.26242170 0.051554721  24.48702 2.030854e-132
## log(pop)               0.07275764 0.009306141   7.81824  5.356706e-15
## log(past.arrests + 1)  0.59150963 0.012420654  47.62307  0.000000e+00
## as.factor(eth)2       -0.32832680 0.014383023 -22.82739 2.451891e-115
## as.factor(eth)3       -1.00964834 0.027073122 -37.29338 2.100727e-304
```

```
fit.tpstop<-lm(log(stops+1) ~ log(pop) + log(past.arrests+1) + as.factor(eth) ,
                        data=pstop[pstop$crime==1,])

summary(fit.tpstop)$coef

##                          Estimate Std. Error   t value     Pr(>|t|)
## (Intercept)            -0.7092861 0.32676005 -2.170664 3.102700e-02
## log(pop)                0.1881834 0.05655829  3.327248 1.027900e-03
## log(past.arrests + 1)   0.7346374 0.07750595  9.478465 4.320869e-18
## as.factor(eth)2        -0.4813409 0.12046354 -3.995739 8.798892e-05
## as.factor(eth)3        -1.3316453 0.15791405 -8.432723 4.472171e-15
```

# Example: Grouse tick data

```
fit.gtick<-glm( TICKS ~ cHEIGHT + as.factor(YEAR) , family=poisson, data=grouseticks)

summary(fit.gtick)$coef

##                      Estimate   Std. Error    z value      Pr(>|z|)
## (Intercept)        1.61599798 0.0401455805  40.253447  0.000000e+00
## cHEIGHT           -0.02145184 0.0007103969 -30.196982 2.594875e-200
## as.factor(YEAR)96  0.40964577 0.0453477934   9.033422  1.663851e-19
## as.factor(YEAR)97 -1.68514105 0.0898007151 -18.765341  1.450635e-78
```

```
fit.tgtick<-lm(log(TICKS+1) ~ cHEIGHT + as.factor(YEAR) , data=grouseticks)

summary(fit.tgtick)$coef

##                      Estimate Std. Error    t value     Pr(>|t|)
## (Intercept)        1.06715919 0.07961023  13.404799 4.356064e-34
## cHEIGHT           -0.01331815 0.00120441 -11.057815 5.646538e-25
## as.factor(YEAR)96  0.76833413 0.10607991   7.242975 2.280915e-12
## as.factor(YEAR)97 -0.46374571 0.10926018  -4.244417 2.728417e-05
```

# Generalized linear models

**Generalized linear model (glm):** A model in which the mean $\mathsf{E}[Y]$ of an outcome is related to some specified function of a linear predictor $\boldsymbol{\beta}^T\mathbf{x}$ via a *link function* $g$:

$$\begin{aligned} g(\mathsf{E}[Y|\mathbf{x}]) &= \boldsymbol{\beta}^T\mathbf{x} \\ \theta = \mathsf{E}[Y|\mathbf{x}] &= g^{-1}(\boldsymbol{\beta}^T\mathbf{x}) \\ Y &\sim f(y|\theta,\gamma) \end{aligned}$$

# Generalized linear models

Normal, Poisson and logistic regression are all GLMs:

The normal regression model: $Y \sim \text{normal}(\boldsymbol{\beta}^T\mathbf{x}, \sigma^2)$

- $\theta = \boldsymbol{\beta}^T\mathbf{x}$, so $g$ is the identity link
- $\gamma = \sigma^2$
- $f(y|\theta,\gamma) = \text{dnorm}(y,\theta,\gamma)$

The Poisson regression model: $Y \sim \text{Poisson}(\exp[\boldsymbol{\beta}^T\mathbf{x}])$

- $\log\theta = \boldsymbol{\beta}^T\mathbf{x}$, so $g$ is the log link
- $\gamma$ is not present
- $f(y|\theta) = \text{dpois}(y,\theta)$

The logistic regression model: $Y \sim \text{binomial}(n, \frac{\exp[\boldsymbol{\beta}^T\mathbf{x}]}{1+\exp[\boldsymbol{\beta}^T\mathbf{x}]})$

- when $n = 1$, $\text{E}[Y|x] = \Pr(Y = 1|x) = \frac{\exp[\boldsymbol{\beta}^T\mathbf{x}]}{1+\exp[\boldsymbol{\beta}^T\mathbf{x}]})$
- $\log(\theta/[1-\theta]) = \boldsymbol{\beta}^T\mathbf{x}$, so $g$ is the logit link
- $\gamma$ is not present
- $f(y|\theta) = \text{dbinom}(y,n,\theta)$

# GLMMs

Recall the general form of a LME:

$$\begin{aligned} y_{i,j} &\sim N(\theta_{i,j}, \sigma^2) \\ \theta_{i,j} &= \boldsymbol{\beta}^T \mathbf{x}_{i,j} + \mathbf{b}_j^T \mathbf{z}_j \\ \mathbf{b}_1, \ldots, \mathbf{b}_m &\sim \text{i.i.d. mvn}(\mathbf{0}, \Psi) \end{aligned}$$

A *generalized linear mixed model* is the same model, but with the normal distribution replaced with a glm:

$$\begin{aligned} y_{i,j} &\sim f(y|\theta_{i,j}, \gamma) \\ \theta_{i,j} &= \boldsymbol{\beta}^T \mathbf{x}_{i,j} + \mathbf{b}_j^T \mathbf{z}_j \\ \mathbf{b}_1, \ldots, \mathbf{b}_m &\sim \text{i.i.d. mvn}(\mathbf{0}, \Psi) \end{aligned}$$

In this model,

- the mvn$(\mathbf{0}, \Psi)$ distribution represents across-group heterogeneity
- $f(y|\theta, \gamma)$ represents within-group heterogeneity.

The fixed (non-group specific) parameters to estimate in include $\{\boldsymbol{\beta}, \Psi, \gamma)$.

# Estimation

**LMMs:** Estimation for LMMs is faciliated by the following fact:

$$\left.\begin{array}{rcl} \mathbf{y}_j & = & \mathbf{X}_j\boldsymbol{\beta} + \mathbf{Z}_j\mathbf{b}_j + \boldsymbol{\epsilon}_j \\ \mathbf{b}_j & \sim & N(\mathbf{0}, \Psi) \end{array}\right\} \Rightarrow p(\mathbf{y}|\boldsymbol{\beta}, \mathbf{X}_j, \mathbf{Z}_j) = \int p(\mathbf{y}|\boldsymbol{\beta}, \mathbf{X}_j, \mathbf{Z}_j, \mathbf{b}_j) \times p(\mathbf{b}_j|\Psi)\ d\mathbf{b}_j$$

$$= \texttt{dnorm}(\mathbf{X}_j\boldsymbol{\beta}, \Sigma),$$

where $\Sigma$ depends on $\Psi$, $\mathbf{Z}_j$ and $\sigma^2$.

The likelihood based on this normal density can be written down and optimized.

# Estimation

**GLMMs:** Estimation for GLMMs is more difficult:

$$\left.\begin{array}{rcl} \mathbf{y}_j & = \mathbf{X}_j\beta + \mathbf{Z}_j\mathbf{b}_j + \boldsymbol{\epsilon}_j \\ \mathbf{b}_j & \sim & N(\mathbf{0}, \Psi) \end{array}\right\} \Rightarrow p(\mathbf{y}|\beta, \mathbf{X}_j, \mathbf{Z}_j) = \int p(\mathbf{y}|\beta, \mathbf{X}_j, \mathbf{Z}_j, \mathbf{b}_j) \times p(\mathbf{b}_j|\Psi)\ d\mathbf{b}_j$$

is not a normal density

The likelihood can't be written down in a closed form.

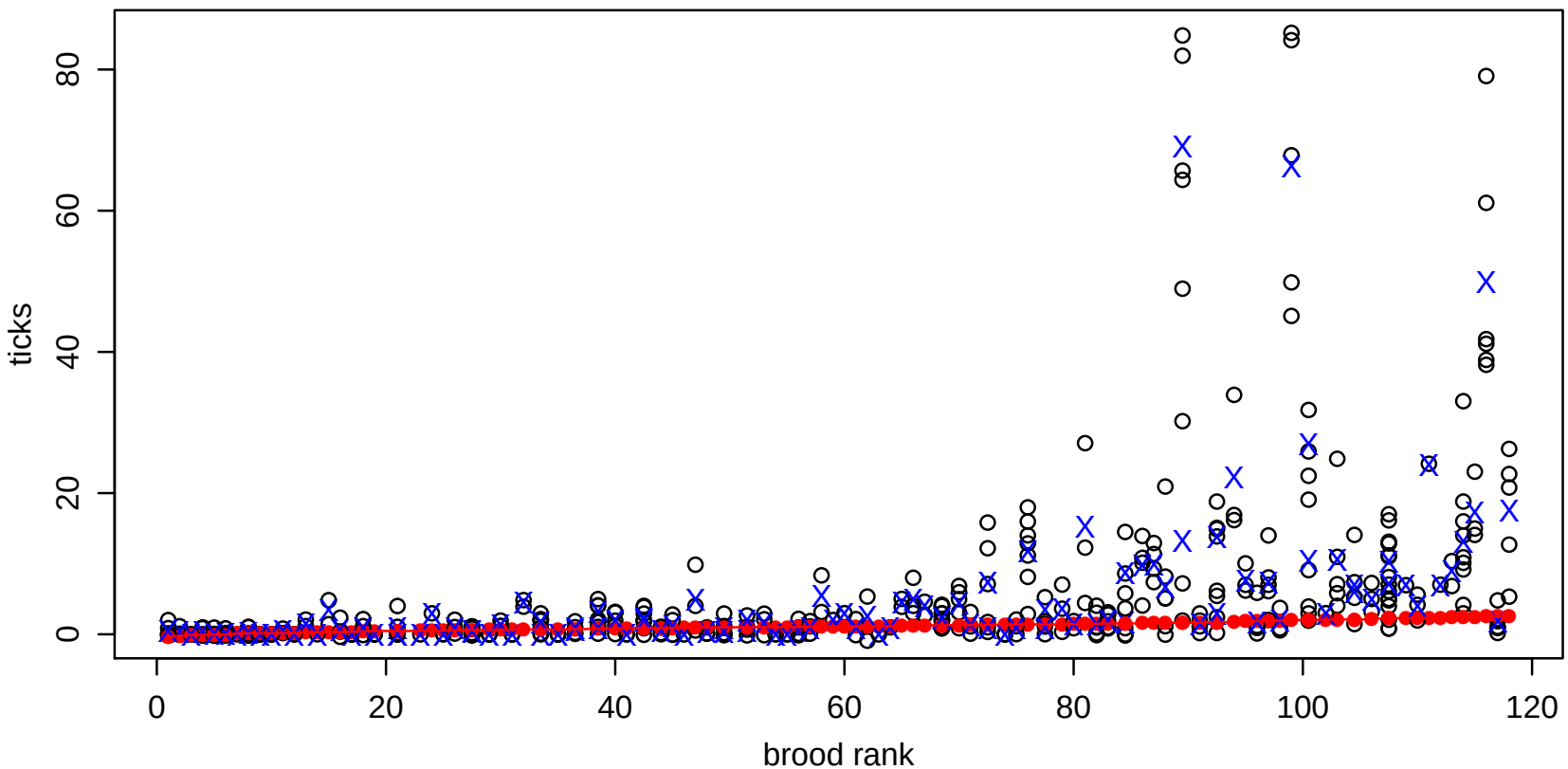
Obtaining MLEs requires iteration of the following:

- approximating (derivatives of) the above integral;
- optimization steps to find the MLE.

Non-convergence of optimization procedures for parameter estimation in such models is common.

# Grousetick example

```
fit0<-glm( TICKS~ cHEIGHT+as.factor(YEAR),family=poisson,data=grouseticks)

summary(fit)$coef

##                       Estimate Std. Error    t value     Pr(>|t|)
## (Intercept)         1.06715919 0.07961023  13.404799 4.356064e-34
## cHEIGHT            -0.01331815 0.00120441 -11.057815 5.646538e-25
## as.factor(YEAR)96   0.76833413 0.10607991   7.242975 2.280915e-12
## as.factor(YEAR)97  -0.46374571 0.10926018  -4.244417 2.728417e-05
```



# GLMMs with glmer

```
fit1<-glmer( TICKS ~ cHEIGHT + as.factor(YEAR) + (1|BROOD) ,family=poisson,data=grouseticks

BIC(fit1)

## [1] 2008.07

BIC(fit0)

## [1] 4398.807
```

```
summary(fit1)$coef

##                      Estimate  Std. Error   z value     Pr(>|z|)
## (Intercept)        0.50917345 0.186618205  2.728423 6.363790e-03
## cHEIGHT           -0.02386609 0.003010673 -7.927161 2.242130e-15
## as.factor(YEAR)96  1.13590090 0.242388921  4.686274 2.782237e-06
## as.factor(YEAR)97 -1.00112997 0.269687357 -3.712187 2.054759e-04
```

# Nested nests

Another variable is **LOCATION**, specifying spatial location of each brood.

**Question:** What are the grouping factors, and how are they related?

**Answer:** BROOD is nested within LOCATION
(but note, each brood already has a unique identifier)

```
fit2<-glmer( TICKS ~ cHEIGHT + as.factor(YEAR) + (1|BROOD) + (1|LOCATION) ,family=poisson,c

BIC(fit2)

## [1] 2011.87

BIC(fit1)

## [1] 2008.07
```

We'll continue with `fit1`.

# Checking assumptions

The fitted mean for each brood is given by

$$\hat{\theta}_j = \hat{\beta}_1 + \hat{\beta}_2 \times \text{cHEIGHT}_j + \widehat{\text{YEAR}}_j + \hat{b}_j$$

The fitted model for data within brood $j$ is

$$\hat{p}(y_{i,j}) = \texttt{dpois}(\hat{\theta}_j)$$
$$\hat{E}[y_{i,j}] = \hat{\theta}_j$$
$$\hat{V}[y_{i,j}] = \hat{\theta}_j$$

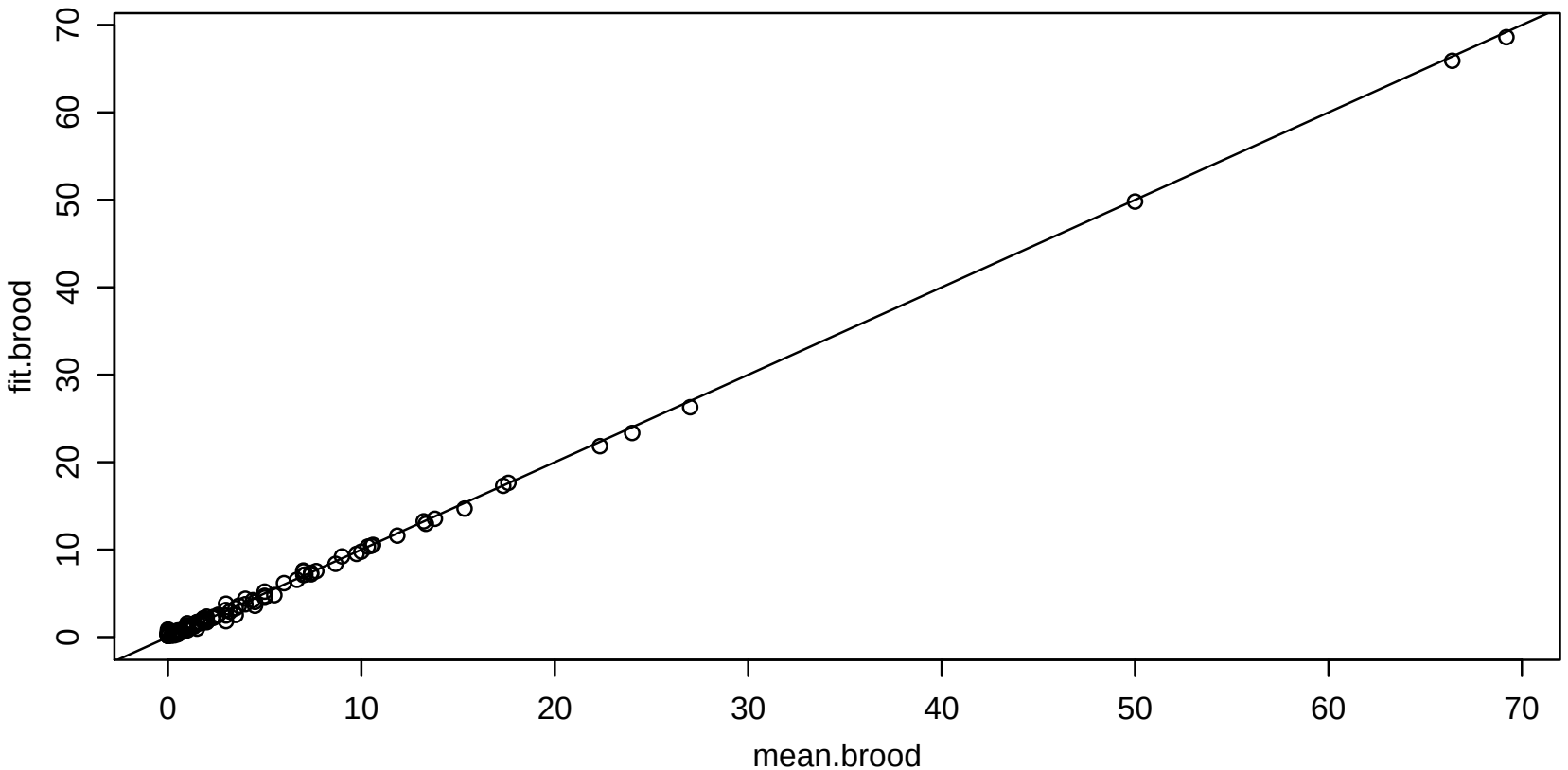
**Question:** How can we check (one aspect of ) this assumption?

**Answer:** Check to see if sample variance correponds to fitted variance:

- If some Poisson model is correct, sample mean $\approx$ sample variance.
- If the Poisson regression is correct, fitted mean $\approx$ sample variance.

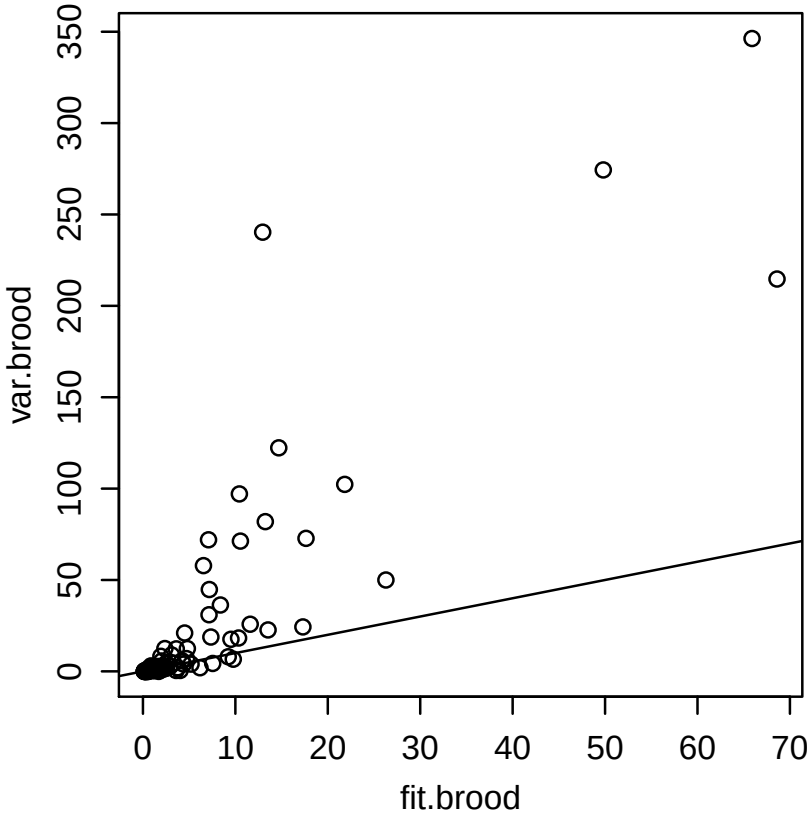
# Checking assumptions

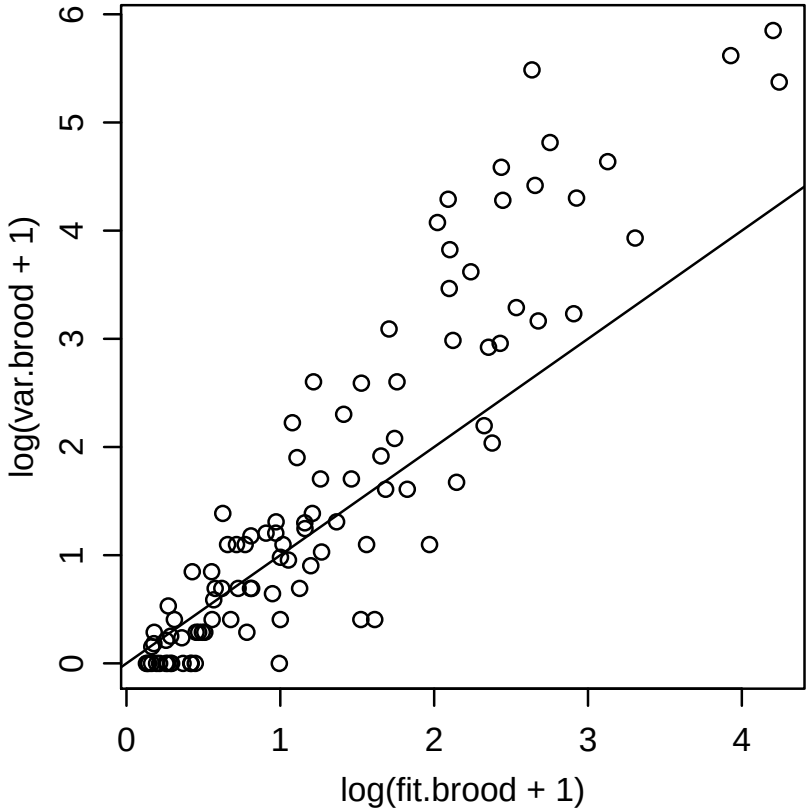
```
var.brood<-tapply(grouseticks$TICKS,grouseticks$BROOD,var)

mean.brood<-tapply(grouseticks$TICKS,grouseticks$BROOD,mean)

fit.brood<-tapply(fitted(fit1),grouseticks$BROOD,mean)
```




Does this plot surpise you? Why or why not?

# Checking assumptions




These data are generally *overdispersed* relative to a Poisson model.
There is more *within-brood* variance than can be ascribed to Poisson variation.

# Models for overdispersion

Consider the following model:

$$\mu_j = \boldsymbol{\beta}^T \mathbf{x}_j + \mathbf{b}_j^T \mathbf{z}_j$$
$$y_{i,j} \sim \text{Poisson}(e^{\mu_j + \epsilon_{i,j}})$$
$$\epsilon_{i,j} \sim \ i.i.d. \ \text{ from some distribution}$$

- If $\text{Var}[\epsilon_{i,j}] = 0$ then the model is the Poisson GLMM;
- If $\text{Var}[\epsilon_{i,j}] > 0$ then the model allows for overdispersion.

**Common overdispersion models:**

$$\epsilon_{i,j} \sim \ i.i.d. \ N(0, \sigma^2)$$
$$\epsilon_{i,j} \sim \ i.i.d. \ \text{log gamma distribution}$$

The latter corresponds to *negative binomial regression*.
Both can be fit in with `glmer`.

# Overdispersed Poisson via random effects

```
grouseticks[1:5,]

##   INDEX TICKS BROOD HEIGHT YEAR LOCATION   cHEIGHT
## 1     1     0   501    465   95       32  2.759305
## 2     2     0   501    465   95       32  2.759305
## 3     3     0   502    472   95       36  9.759305
## 4     4     0   503    475   95       37 12.759305
## 5     5     0   503    475   95       37 12.759305
```

```
fit.o1<-glmer( TICKS ~ cHEIGHT + as.factor(YEAR) + (1|BROOD) + (1|INDEX),family=poisson,dat
```

```
fit.o1

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: TICKS ~ cHEIGHT + as.factor(YEAR) + (1 | BROOD) + (1 | INDEX)
##    Data: grouseticks
##      AIC      BIC   logLik deviance df.resid
## 1794.040 1818.034 -891.020 1782.040      397
## Random effects:
##  Groups Name        Std.Dev.
##  INDEX  (Intercept) 0.5435
##  BROOD  (Intercept) 0.9085
## Number of obs: 403, groups:  INDEX, 403; BROOD, 118
## Fixed Effects:
##       (Intercept)            cHEIGHT  as.factor(YEAR)96
##           0.40999           -0.02405            1.14892
## as.factor(YEAR)97
##          -0.99061
```

# Overdispersed Poisson via random effects

## Comparison to Poisson regression

```
BIC(fit1)

## [1] 2008.07

BIC(fit.o1)

## [1] 1818.034
```

```
summary(fit1)$coef

##                      Estimate  Std. Error   z value     Pr(>|z|)
## (Intercept)        0.50917345 0.186618205  2.728423 6.363790e-03
## cHEIGHT           -0.02386609 0.003010673 -7.927161 2.242130e-15
## as.factor(YEAR)96  1.13590090 0.242388921  4.686274 2.782237e-06
## as.factor(YEAR)97 -1.00112997 0.269687357 -3.712187 2.054759e-04

summary(fit.o1)$coef

##                      Estimate  Std. Error   z value     Pr(>|z|)
## (Intercept)        0.40998716 0.190355432  2.153798 3.125601e-02
## cHEIGHT           -0.02404906 0.003044808 -7.898382 2.825470e-15
## as.factor(YEAR)96  1.14891703 0.246303176  4.664646 3.091494e-06
## as.factor(YEAR)97 -0.99061439 0.273458801 -3.622536 2.917287e-04
```

# Overdispersed Poisson via the negative binomial distribution

```
fit.o2<-glmer.nb(TICKS ~ cHEIGHT + as.factor(YEAR) + (1|BROOD),data=grouseticks)
```

```
BIC(fit.o2)

## [1] 1815.938

summary(fit.o2)$coef

##                      Estimate  Std. Error   z value     Pr(>|z|)
## (Intercept)        0.52854237 0.188249519  2.807669 4.990146e-03
## cHEIGHT           -0.02390358 0.003014457 -7.929647 2.197688e-15
## as.factor(YEAR)96  1.13183765 0.243942814  4.639766 3.488034e-06
## as.factor(YEAR)97 -0.99381870 0.270615475 -3.672439 2.402469e-04
```

# Random effects logistic regression

**Logistic regression:**

$$\Pr(y_i = 1) = \theta_i = \frac{e^{\beta^T x_i}}{1 + e^{\beta^T x_i}}$$

$$\log \frac{\theta_i}{1-\theta_i} = \boldsymbol{\beta}^T \mathbf{x}_i$$

**Mixed effects logistic regression:**

$$\Pr(y_{i,j} = 1) = \theta_{i,j} = \frac{e^{\beta^T x_{i,j} + b_j^T z_{i,j}}}{1 + e^{\beta^T x_i b_j^T z_{i,j}}}$$

$$\log \frac{\theta_{i,j}}{1-\theta_i} = \boldsymbol{\beta}^T \mathbf{x}_{i,j} + \mathbf{b}_j^T \mathbf{z}_{i,j}$$

# Data types for logistic regression

## Binary data

| y | g | x1 | x2 |
|---|---|---|---|
| 0 | 1 | 2.3 | 3.2 |
| 0 | 1 | 2.3 | 2.1 |
| 1 | 1 | 2.3 | 5.4 |
| 0 | 2 | 4.1 | 1.6 |
| 1 | 2 | 4.1 | 3.2 |
| 1 | 2 | 4.1 | 1.2 |
| . | . | . | . |
| . | . | . | . |

```
fit <- glmer( y ~ x1 + x2 + (x2|g) , family=binomial )
```

# Data types for logistic regression

## Binomial data

| y | n | g | x1 | x2 |
|---|---|---|---|---|
| 4 | 10 | 1 | 2.3 | 3.2 |
| 2 | 12 | 1 | 2.3 | 2.1 |
| 5 | 8 | 1 | 2.3 | 5.4 |
| 3 | 10 | 2 | 4.1 | 1.6 |
| 6 | 16 | 2 | 4.1 | 3.2 |
| 8 | 9 | 2 | 4.1 | 1.2 |
| . | . | . | . | . |
| . | . | . | . | . |

Here, the model is

$$y_{i,j} \sim \text{binomial}(\theta_{i,j}, n_{i,j})$$

```
fit <- glmer( cbind(y,n-y) ~ x1 + x2 + (x2|g) , family=binomial )
```

# Example: Social network analysis

**Network and relational data:** Data measured on pairs (dyads) of units.

**Friendship study:** What characteristics of people lead to friendship ties?

**Data:**

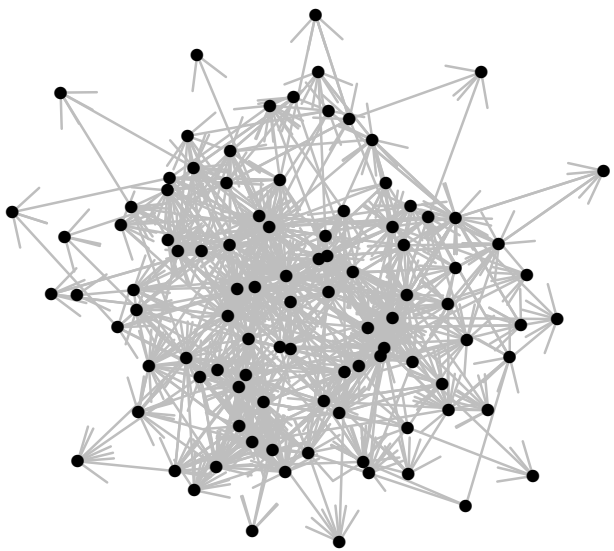
friendship: binary indicator of (directed) friendship

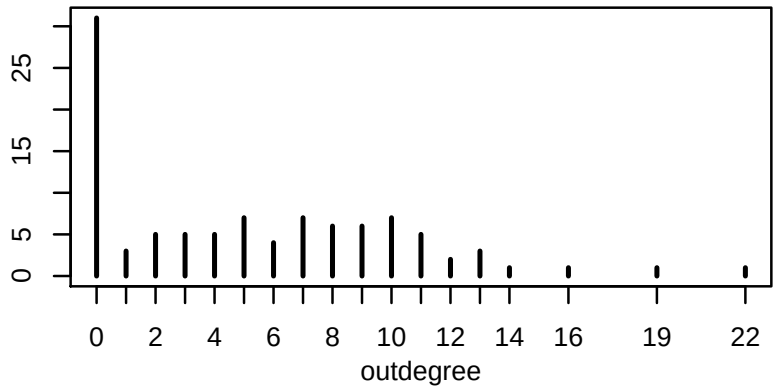
gpa: GPA

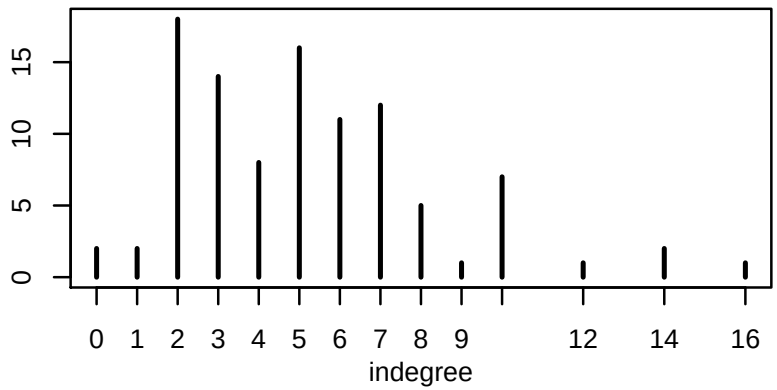
smoke: smoking score

grade: year in school

# Example: Social network analysis





# Example: Social network analysis

```
X[1:15,]
```

```
##         rgpa rsmoke cgpa csmoke igrade  igpa ismoke
##  [1,]  0.71   0.62 0.41  -0.07      1  0.29  -0.04
##  [2,]  0.85   0.98 0.41  -0.07      1  0.35  -0.07
##  [3,]  0.86  -0.12 0.41  -0.07      0  0.35   0.01
##  [4,]  0.41   0.64 0.41  -0.07      0  0.17  -0.05
##  [5,]  0.66   0.63 0.41  -0.07      0  0.27  -0.04
##  [6,] -0.54   0.87 0.41  -0.07      0 -0.22  -0.06
##  [7,]  0.69   0.66 0.41  -0.07      0  0.28  -0.05
##  [8,] -0.29  -0.64 0.41  -0.07      0 -0.12   0.05
##  [9,] -0.51  -0.68 0.41  -0.07      1 -0.21   0.05
## [10,]  0.41   0.64 0.41  -0.07      0  0.17  -0.05
## [11,]  2.17  -1.04 0.41  -0.07      0  0.89   0.07
## [12,] -0.28   0.00 0.41  -0.07      0 -0.11   0.00
## [13,]  0.69  -0.61 0.41  -0.07      1  0.28   0.04
## [14,]  1.52  -0.60 0.41  -0.07      0  0.62   0.04
## [15,] -0.30   1.51 0.41  -0.07      0 -0.12  -0.11
```

```
y[1:15]
```

```
##  [1] 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0
```

# Logistic regression

```
fit0<-glm( y ~ X, family=binomial)
```

```
summary(fit0)$coef
```

```
##                Estimate Std. Error     z value     Pr(>|z|)
## (Intercept) -4.12113655 0.09146103 -45.0589348 0.000000e+00
## Xrgpa        0.36857711 0.06091581   6.0505990 1.443082e-09
## Xrsmoke      0.44406283 0.06842175   6.4900832 8.578901e-11
## Xcgpa        0.37325974 0.05980462   6.2413199 4.338938e-10
## Xcsmoke      0.33401415 0.06961131   4.7982741 1.600387e-06
## Xigrade      2.06330014 0.09901610  20.8380263 1.957441e-96
## Xigpa        0.04612661 0.05488132   0.8404793 4.006397e-01
## Xismoke      0.02072443 0.08501630   0.2437701 8.074089e-01
```

# Network dependence

Do you think the $100 \times 99$ network ties are independent?

What sort of dependence might you expect?

**Social relations model:** The SRM allows for

- across-sender heterogeneity in outdegrees
- across-receiver heterogeneity in indegrees
- within dyad reciprocity

# Fitting the SRM-lite with `glmer`

$$\log \frac{\theta_{i,j}}{1-\theta_{i,j}} = \boldsymbol{\beta}^T \mathbf{x}_{i,j} + a_i + b_j + \epsilon_{\{i,j\}}$$

- $\{a_i\}$ represent heterogeneity across senders of ties (sociability)
- $\{b_j\}$ represent heterogeneity across recievers of ties (popularity)
- $\{\epsilon_{\{i,j\}}\}$ represents similarity within a dyad (reciprocity)

# Fitting the SRM-lite with glmer

```
G[1:10,]

##    rlab clab dlab
## 1     2    1  1.2
## 2     3    1  1.3
## 3     4    1  1.4
## 4     5    1  1.5
## 5     6    1  1.6
## 6     7    1  1.7
## 7     8    1  1.8
## 8     9    1  1.9
## 9    10    1 1.10
## 10   11    1 1.11
```

**Question:** How can we fit the logistic SRM?

```
fit.srm<-glmer( y ~ X + (1|G$rlab) + (1|G$clab) + (1|G$dlab) , family=binomial)
```

Unfortunately, this stumps glmer. The package amen can fit it using MCMC.

```
fit.ab<-glmer( y ~ X + (1|G$rlab) + (1|G$clab) , family=binomial)
```

# Fitting the SRM-lite with glmer

```
BIC(fit.ab)

## [1] 3316.515

BIC(fit0)

## [1] 3541.197
```

```
VarCorr(fit.ab)

##  Groups Name        Std.Dev.
##  G$rlab (Intercept) 1.34299
##  G$clab (Intercept) 0.29877

summary(fit.ab)$coef

##                 Estimate Std. Error     z value      Pr(>|z|)
## (Intercept) -4.840796412 0.19065173 -25.3907815 3.188238e-142
## Xrgpa        0.392489177 0.16953292   2.3151207  2.060633e-02
## Xrsmoke      0.584473776 0.21667891   2.6974188  6.987933e-03
## Xcgpa        0.401574544 0.07007841   5.7303607  1.002173e-08
## Xcsmoke      0.336422908 0.08437207   3.9873730  6.680894e-05
## Xigrade      2.225383589 0.10231915  21.7494346 6.993629e-105
## Xigpa        0.082526478 0.05778840   1.4280803  1.532687e-01
## Xismoke      0.007935361 0.08559484   0.0927084  9.261352e-01
```