Generalized linear mixed models

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Duke STA 610

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;
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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
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## 5     37  1368           62        1   2     1
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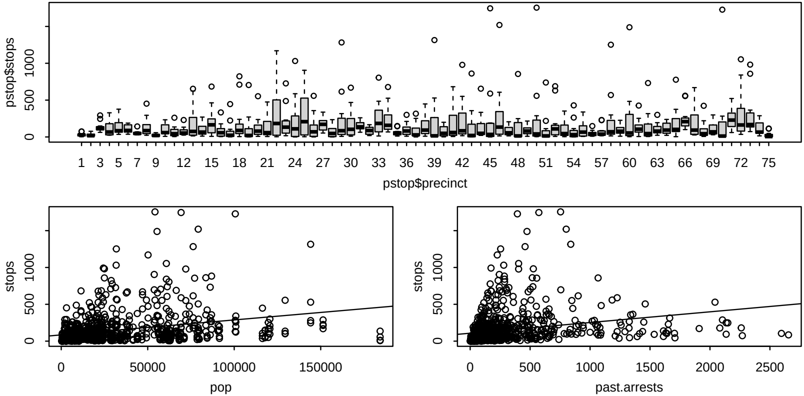
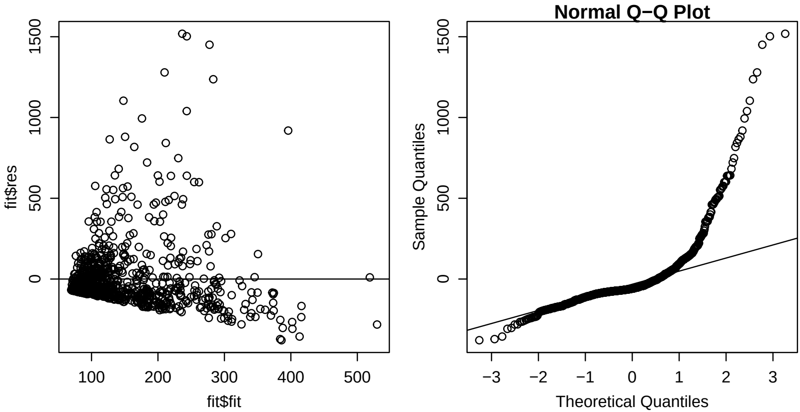


Example: Police stop data

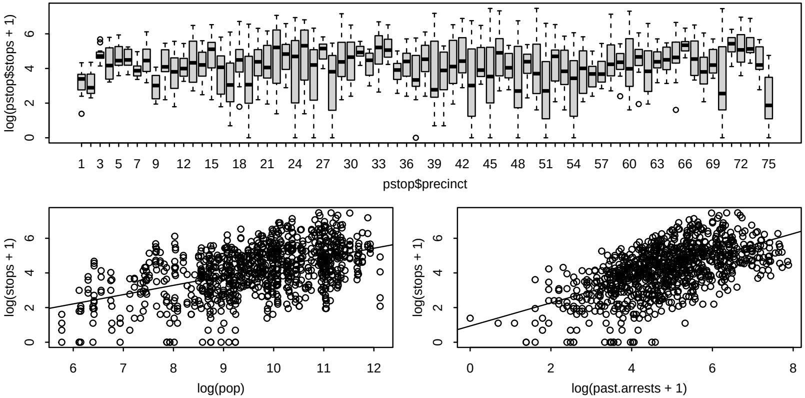
```
fit<-lm(stops~pop+past.arrests,data=pstop)

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
```



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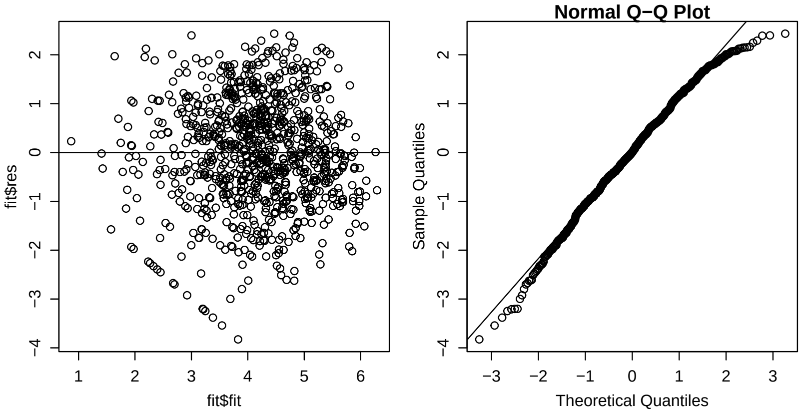

Example: Grouseticks

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

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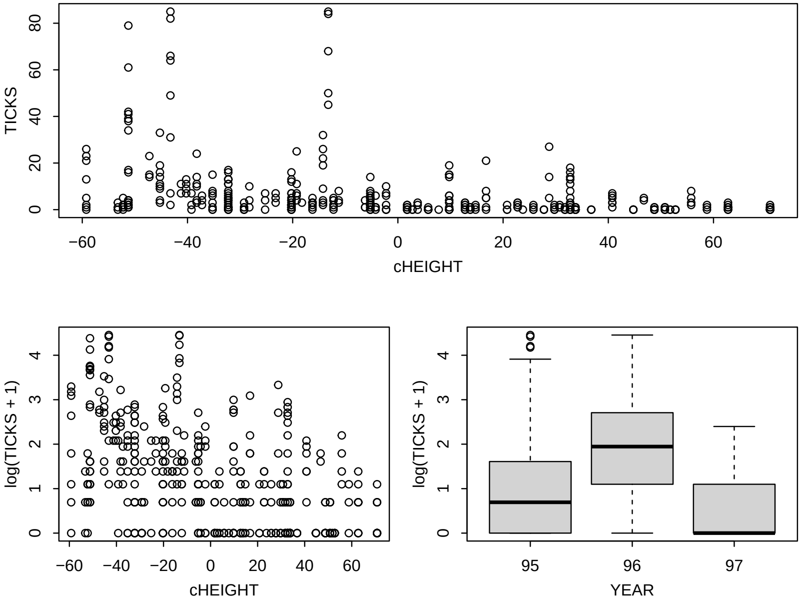

Example: Grouseticks

```
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
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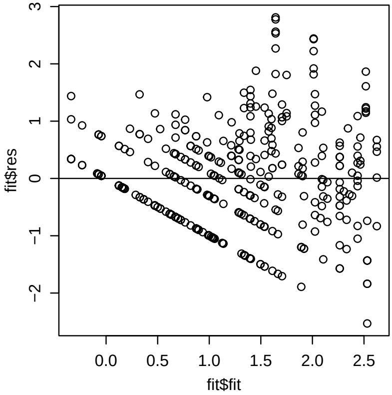

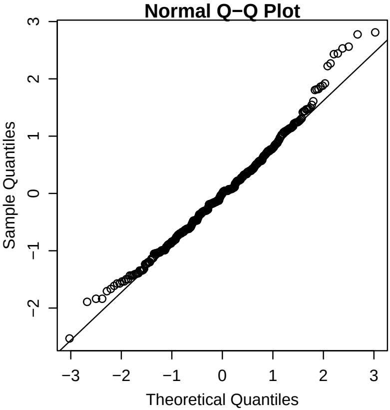

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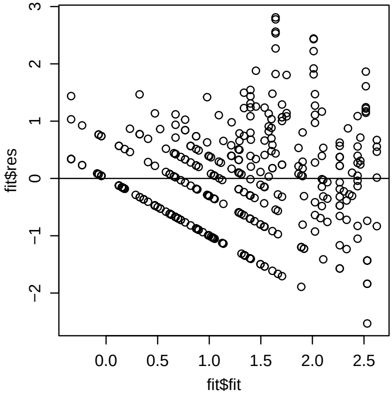

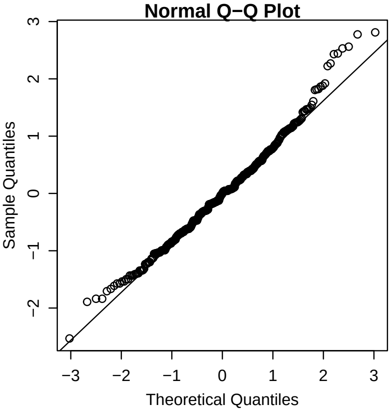

Transformably normal

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.

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Logistic regression

Logistic regression:

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

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

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
. .   .   .
. .   .   .
```

```r
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
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.  .   .   .   .
.  .   .   .   .
```

Here, the model is

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

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

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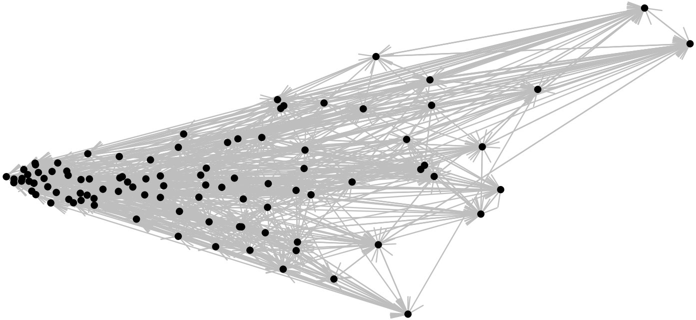

Example: Social network analysis

```
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 1 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) -3.3963777162 0.06823249 -49.7765466 0.000000e+00
## Xrgpa        0.2654852784 0.05086973   5.2189240 1.799656e-07
## Xrsmoke      0.3108504175 0.05915817   5.2545649 1.483748e-07
## Xcgpa        0.2752593480 0.05035810   5.4660390 4.602032e-08
## Xcsmoke      0.2506464322 0.05986543   4.1868306 2.828768e-05
## Xigrade      1.5465497415 0.08209840  18.8377564 3.703344e-79
## Xigpa       -0.0007701432 0.04687819  -0.0164286 9.868925e-01
## Xismoke      0.1119389182 0.07453943   1.5017410 1.331640e-01
```

Do you think the observations are independent?

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## Xcsmoke      0.2506464322 0.05986543   4.1868306 2.828768e-05
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## Xigpa       -0.0007701432 0.04687819  -0.0164286 9.868925e-01
## Xismoke      0.1119389182 0.07453943   1.5017410 1.331640e-01
```

Do you think the observations are independent?

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{aligned}
\Pr(Y = 0|\theta = 2.1) = &\quad (2.1)^0 e^{-2.1}/(0!) = &\quad .12 \\
\Pr(Y = 1|\theta = 2.1) = &\quad (2.1)^1 e^{-2.1}/(1!) = &\quad .26 \\
\Pr(Y = 2|\theta = 2.1) = &\quad (2.1)^2 e^{-2.1}/(2!) = &\quad .27 \\
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Poisson regression

In Poisson regression, we relate the mean θ 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:

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

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Multiplicative mean model

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

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

Here, β_1 represents the *multiplicative effect* of x on Y:

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

So an increase of x by one results in the mean being e^{β_1} times as large.

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

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

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

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

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

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

MLE: The log-likelihood, as a function of β, is given by

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

= `sum( log( dpois( y,exp(X%*%beta) ) ) )`

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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
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## log(past.arrests + 1)  0.7346374 0.07750595  9.478465 4.320869e-18
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Example: Grouse tick data

```r
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
```

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

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##                        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
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Generalized linear models

Generalized linear model (glm): A model in which the mean 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:

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

Generalized linear models

Normal, Poisson and logistic regression are all GLMs:

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

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

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

- $\log \theta = \beta^T \mathbf{x}$, so g is the log link
- γ is not present
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The logistic regression model: $Y \sim \text{binomial}(n, \frac{\exp[\beta^T \mathbf{x}]}{1+\exp[\beta^T \mathbf{x}]})$

- when $n = 1$, $E[Y|\mathbf{x}] = \Pr(Y = 1|\mathbf{x}) = \frac{\exp[\beta^T \mathbf{x}]}{1+\exp[\beta^T \mathbf{x}]}$)
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Normal, Poisson and logistic regression are all GLMs:

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Recall the general form of a LME:

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

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

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In this model,

- the $\text{mvn}(\mathbf{0}, \Psi)$ distribution represents across-group heterogeneity
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The fixed (non-group specific) parameters to estimate in include $\{\boldsymbol{\beta}, \Psi, \gamma\}$.

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Estimation

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

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

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where Σ depends on Ψ, $\mathbf{Z}_j$ and σ^2.

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

Obtaining MLEs requires iteration of the following:

- approximating (derivatives of) the above integral;
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$$\left.\begin{array}{rl} \mathbf{y}_{i,j} & \sim f(y_{i,j}|\mathbf{x}_{i,j}^{\top}\boldsymbol{\beta}+\mathbf{z}_{i,j}^{\top}\mathbf{b}_j) \\ \mathbf{b}_j & \sim N(\mathbf{0},\Psi) \end{array}\right\} \Rightarrow p(\mathbf{y}_j|\boldsymbol{\beta},\mathbf{X}_j,\mathbf{Z}_j) = \int p(\mathbf{y}_j|\boldsymbol{\beta},\mathbf{X}_j,\mathbf{Z}_j,\mathbf{b}_j)\times p(\mathbf{b}_j|\Psi)\; d$$

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

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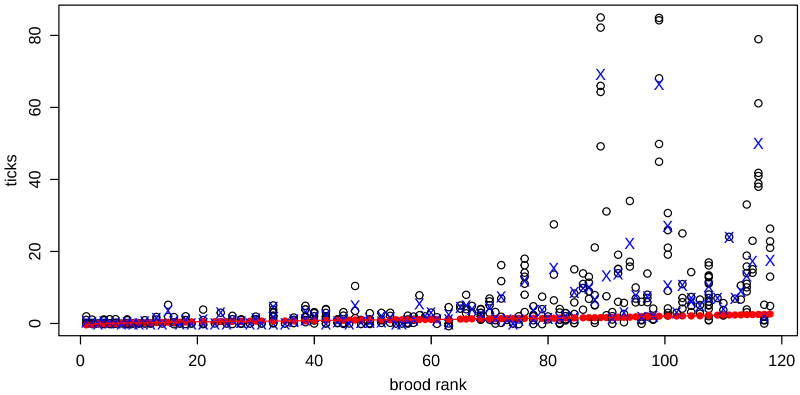
Grousetick example

```
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=grousetick
```

```
BIC(fit1)
```

```
## [1] 2008.07
```

```
BIC(fit0)
```

```
## [1] 4398.807
```

```
summary(fit1)$coef
```

```
##                        Estimate  Std. Error   z value     Pr(>|z|)
## (Intercept)          0.50919618 0.186616637  2.728568 6.360998e-03
## cHEIGHT             -0.02386615 0.003010643 -7.927260 2.240344e-15
## as.factor(YEAR)96    1.13587983 0.242387482  4.686215 2.783040e-06
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GLMMs with glmer

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```

```
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```

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,
BIC(fit2)
## [1] 2011.87
BIC(fit1)
## [1] 2008.07
```

We'll continue with `fit1`.

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BIC(fit2)

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```

We'll continue with `fit1`.

Checking assumptions

The fitted mean for each brood j is given by

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

The fitted model for data within brood j is

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

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 ≈ sample variance.
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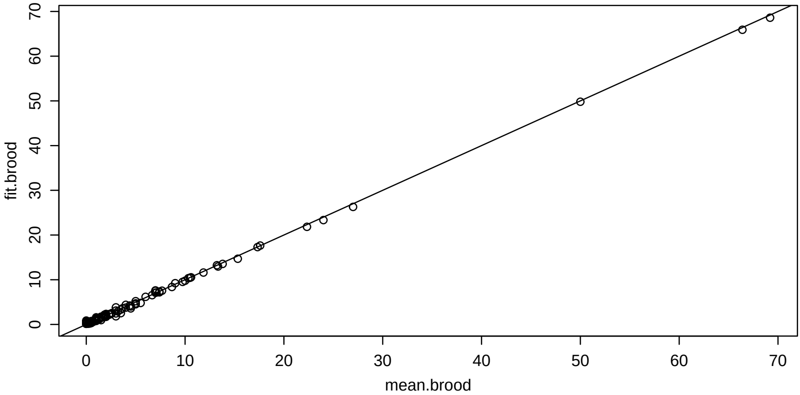
Checking assumptions

```
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?

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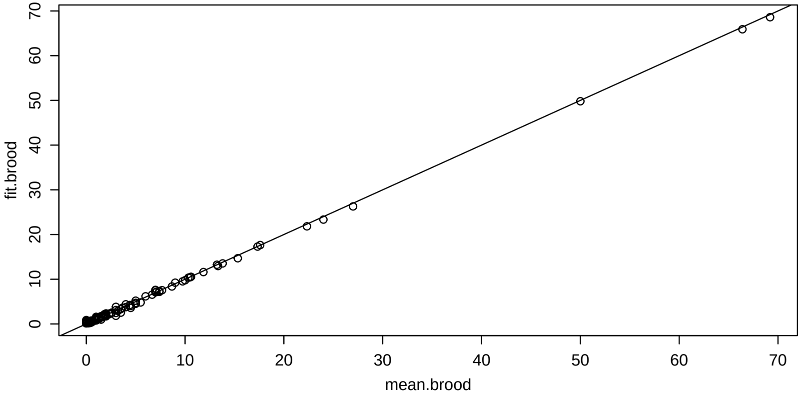

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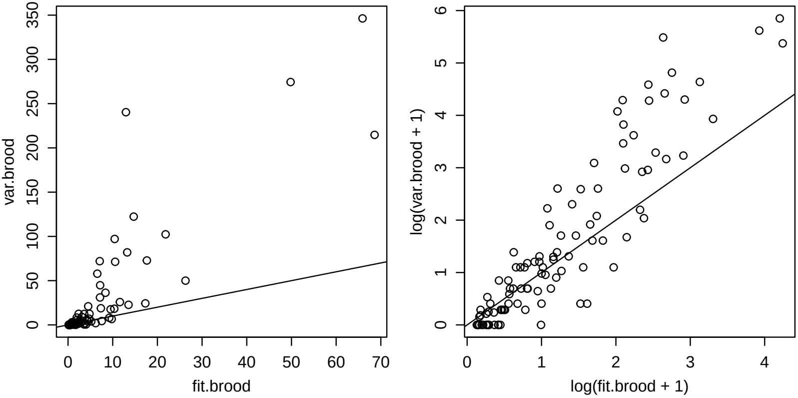

These data are generally *overdispersed* relative to a Poisson model.
There is more *within-brood* variance than can be ascribed to Poisson variation.

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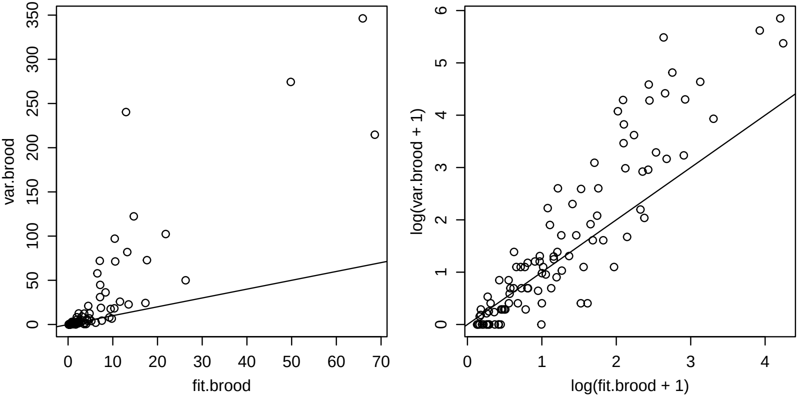

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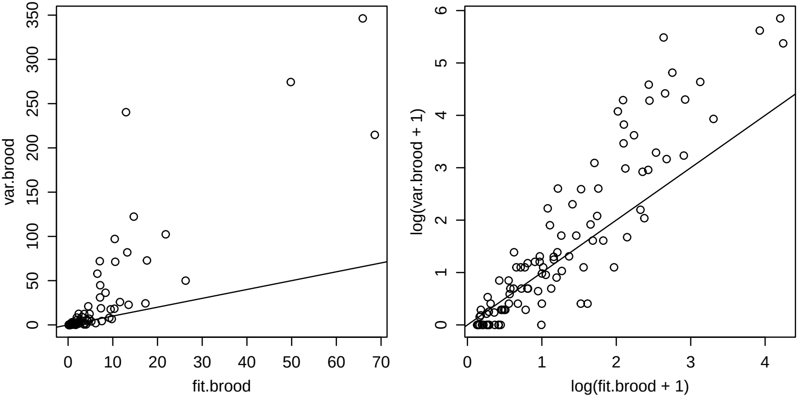

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Models for overdispersion

Consider the following model:

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

- 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:

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

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

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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  as.factor(YEAR)97
##           0.40999           -0.02405            1.14892           -0.99061
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```

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)         0.50919618 0.186616637  2.728568 6.360998e-03
## cHEIGHT            -0.02386615 0.003010643 -7.927260 2.240344e-15
## as.factor(YEAR)96   1.13587983 0.242387482  4.686215 2.783040e-06
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summary(fit.o1)$coef

##                       Estimate  Std. Error   z value     Pr(>|z|)
## (Intercept)         0.40998718 0.190354324  2.153811 3.125502e-02
## cHEIGHT            -0.02404906 0.003044808 -7.898382 2.825465e-15
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```

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 0.188250992  2.807647 4.990486e-03
## cHEIGHT             -0.02390358 0.003014457 -7.929647 2.197695e-15
## as.factor(YEAR)96    1.13183765 0.243944397  4.639736 3.488542e-06
## as.factor(YEAR)97   -0.99381870 0.270617604 -3.672410 2.402741e-04
```

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```
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## [1] 1815.938

summary(fit.o2)$coef

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Random effects logistic regression

Logistic regression:

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

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

Mixed effects logistic regression:

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

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

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

Mixed effects logistic regression:

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

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

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
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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

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

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

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```
y  n  g   x1  x2
4 10  1  2.3 3.2
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5  8  1  2.3 5.4
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.  .  .   .   .
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.	.	.	.	.
.	.	.	.	.

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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?

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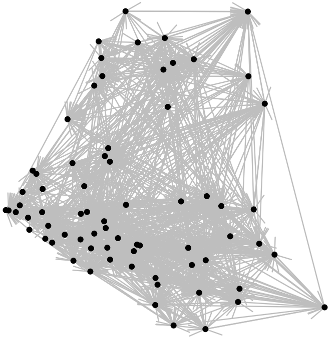

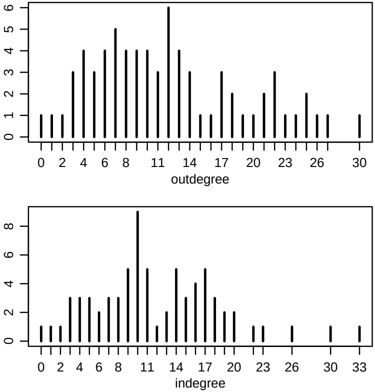

Example: Social network analysis

```
dim(Y)

## [1] 71 71

dim(X)

## [1] 71 71  2

dimnames(X)[[3]]

## [1] "advice"       "samepractice"
```

Logistic regression

```
X[1:10,]

##       advice samepractice
##  [1,]      1            0
##  [2,]      0            1
##  [3,]      1            0
##  [4,]      1            1
##  [5,]      0            1
##  [6,]      0            0
##  [7,]      1            1
##  [8,]      0            0
##  [9,]      0            0
## [10,]      1            1

y[1:10]

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

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

```
summary(fit0)$coef

##                 Estimate Std. Error   z value      Pr(>|z|)
## (Intercept)   -2.3043528 0.07069337 -32.59645 4.604979e-233
## Xadvice        0.3059047 0.10852842   2.81866  4.822457e-03
## Xsamepractice  1.1521500 0.08320930  13.84641  1.337308e-43
```

Network dependence

Do you think the 71×70 network ties are independent?

What sort of dependence might you expect? What are the grouping factors?

- sender (row)
- receiver (column)
- dyad (pair)

Network dependence

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Simulate and compare

```
ysim<-rbinom(length(y),1,fit0$fitted)

mean(ysim)

## [1] 0.178672

mean(y)

## [1] 0.171831

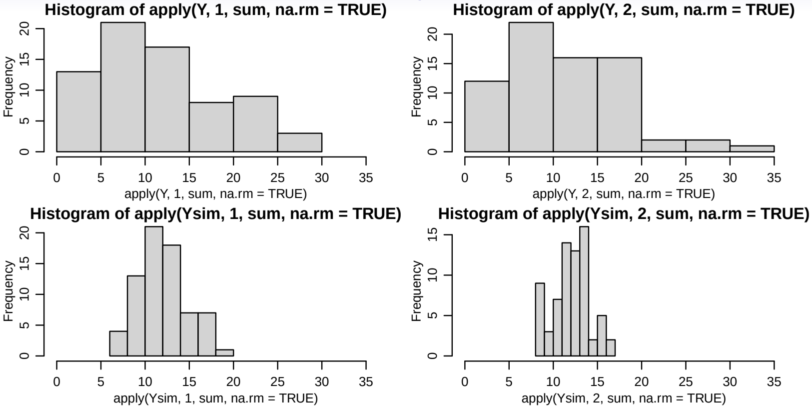
fit0sim<-glm( ysim ~ X, family=binomial)
fit0sim$coef

##   (Intercept)       Xadvice Xsamepractice
##    -2.2481936     0.2360881     1.1571658

fit0$coef

##   (Intercept)       Xadvice Xsamepractice
##    -2.3043528     0.3059047     1.1521500
```

Network dependence



```
cor( Y[upper.tri(Y)],t(Y)[upper.tri(Y)],use="pairwise.complete")

## [1] 0.1926326

cor( Ysim[upper.tri(Y)],t(Ysim)[upper.tri(Y)],use="pairwise.complete")

## [1] 0.06496955
```

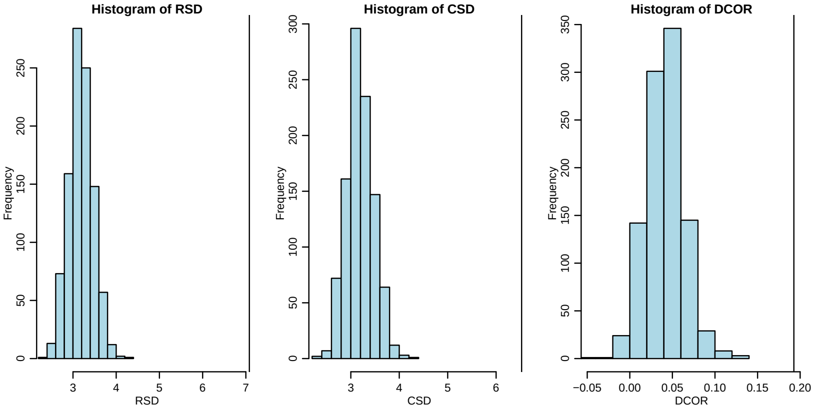
Simulation study

```
RSD<-CSD<-DCOR<-NULL
for(s in 1:1000){

  ysim<-rbinom(length(y),1,fit0$fitted)
  Ysim<-Y ; Ysim[!is.na(Ysim)]<-ysim

  RSD<-c(RSD,sd(apply(Ysim,1,sum,na.rm=TRUE)))
  CSD<-c(CSD,sd(apply(Ysim,2,sum,na.rm=TRUE)))
  DCOR<-c(DCOR,cor(Ysim[upper.tri(Y)],t(Ysim)[upper.tri(Y)],
          use="pairwise.complete"))
}
```

Lack of fit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Frequency
0
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0
50
100
150
200
250
300
350
−0.05
0.00
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0.15
0.20
DCOR

Social relations model

We would like a model that allows for

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

$$\begin{aligned} \log \frac{\theta_{i,j}}{1-\theta_{i,j}} &= \boldsymbol{\beta}^T \mathbf{x}_{i,j} + a_i + b_j + \epsilon_{\{i,j\}} \\ a_1, \ldots, a_n &\sim \text{ i.i.d. } N(0, \tau_a^2) \\ b_1, \ldots, b_n &\sim \text{ i.i.d. } N(0, \tau_b^2) \\ \{\epsilon_{\{i,j\}}\} &\sim \text{ i.i.d. } N(0, \sigma^2) \end{aligned}$$

Note $\theta_{i,j}$ and $\theta_{j,i}$ share *the same* $\epsilon_{\{i,j\}}$.

- $\{a_i\}$ represent heterogeneity across senders of ties (sociability)
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Fitting the SRM-lite with `glmer`

```
rows<-matrix(1:nrow(Y),nrow(Y),nrow(Y))
rlab<-c(rows)[!is.na(c(Y))]
clab<-c(t(rows))[!is.na(c(Y))]
dlab<-t(apply(cbind(rlab,clab) ,1,sort) )
dlab<-paste(dlab[,1],dlab[,2],sep=".")
G<-as.data.frame(cbind(rlab,clab,dlab) )
```

```
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
```

Fitting the SRM-lite with `glmer`

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 best we can do is the following:

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

```
BIC(fit.ab)

## [1] 4078.228

BIC(fit0)

## [1] 4363.334
```

```
VarCorr(fit.ab)

##  Groups Name        Std.Dev.
##  G$rlab (Intercept) 0.74527
##  G$clab (Intercept) 0.67392

summary(fit.ab)$coef

##                 Estimate Std. Error     z value     Pr(>|z|)
## (Intercept)   -2.61297936 0.14374547 -18.1778200 7.734797e-74
## Xadvice        0.02158876 0.12699036   0.1700031 8.650077e-01
## Xsamepractice  1.25084242 0.08953187  13.9709187 2.345810e-44
```

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```

Simulation study

```
RSD<-CSD<-DCOR<-NULL
for(s in 1:1000){

  ysim<-rbinom(length(y),1,fitted(fit.ab))
  Ysim<-Y ; Ysim[!is.na(Ysim)]<-ysim

  RSD<-c(RSD,sd(apply(Ysim,1,sum,na.rm=TRUE)))
  CSD<-c(CSD,sd(apply(Ysim,2,sum,na.rm=TRUE)))
  DCOR<-c(DCOR,cor(Ysim[upper.tri(Y)],t(Ysim)[upper.tri(Y)],
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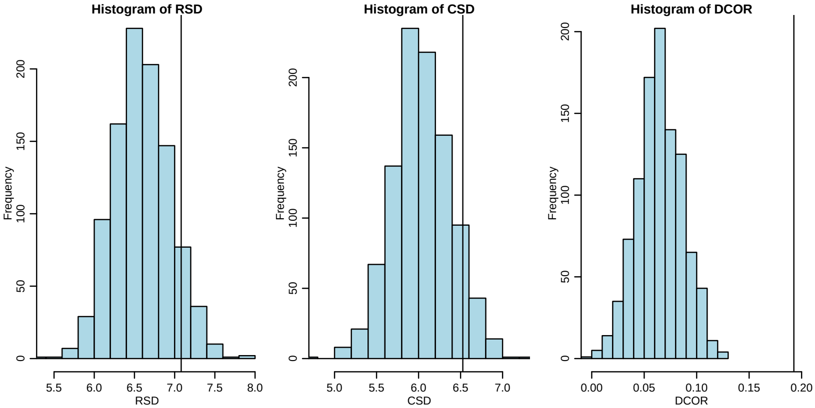
Lack of fit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Frequency
0
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100
150
200
5.0
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6.0
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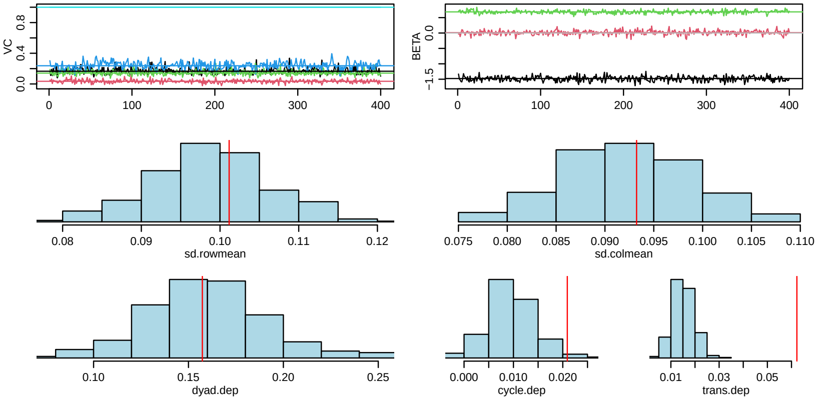
7.0
CSD
Histogram of DCOR
Frequency
0
50
100
150
200
0.00
0.05
0.10
0.15
0.20
DCOR

```
ame                   package:amen                    R Documentation

AME model fitting routine

Description:

     An MCMC routine providing a fit to an additive and multiplicative
     effects (AME) regression model to relational data of various types

Usage:

     ame(Y, Xdyad=NULL, Xrow=NULL, Xcol=NULL, family, R=0, rvar = !(fam
     cvar = TRUE,  dcor = !symmetric, nvar=TRUE,
     intercept=!is.element(family,c("rrl","ord")),
     symmetric=FALSE,
     odmax=rep(max(apply(Y>0,1,sum,na.rm=TRUE)),nrow(Y)), seed = 1, nsc
     10000, burn = 500, odens = 25, plot=TRUE, print = TRUE, gof=TRUE,
     prior=list())

Arguments:

       Y: an n x n square relational matrix of relations. See family
```

Fitting the SRM

```
library(amen)
fitSRRM<-ame(Y, Xd=X, family="bin")
```



Fitting the SRM

```
summary(fitSRRM)

##
## Regression coefficients:
##                    pmean   psd  z-stat p-val
## intercept         -1.483 0.081 -18.301 0.000
## advice.dyad        0.014 0.072   0.194 0.846
## samepractice.dyad  0.685 0.052  13.039 0.000
##
## Variance parameters:
##     pmean   psd
## va  0.171 0.039
## cab 0.035 0.022
## vb  0.144 0.031
## rho 0.241 0.048
## ve  1.000 0.000
```