This course was developed as a part of the VLIR-UOS Cross-Cutting project s:

- Statistics: 2011-2016, 2017.
- Statistics: 2017.
- Statistics for development : 2018-2020.

The >eR-Biostat initiative

Making R based education materials in statistics accessible for all

Applied Generalized Linear Models (GLM) using R (PART 2)

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LAST UPDATE: 31/02/2018

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Reference list

- Main reference
  - Dobson (2002): An introduction to generalized linear models.
- Other references:
  - McCillagh and Nelder (1983): Generalized linear models (first edition).
  - Collet D(1994): Modeling Binary data.
  - Lindsey (1997): Applying generalized linear models.

Software

- Two main R functions:
  - Linear models in R: the `lm()` function.
  - Generalized linear models in R: the `glm()` function in R.

- All R programs for the examples presented in the slides are available online:

https://github.com/eR-Biostat/Courses/tree/master/Statistical%20modeling%20(1)/glm/R%20programs

YouTube tutorials

- YouTube tutorials are available for:
  - Generalized, linear, and generalized least squares models (host: Christoph Scherber): https://www.youtube.com/watch?v=P-WYkSZp9lY
  - Generalized Linear Models in R (host: Clark Gaylord): https://www.youtube.com/watch?v=H7y24LlNNl0
  - Generalized Linear Modeling in R (host: Chris Mack): https://www.youtube.com/watch?v=kffIgjHxdpw

- Link to the YouTube tutorials about GLMs:

https://github.com/eR-Biostat/Courses/tree/master/Statistical%20modeling%20(1)/glm/YouTube%20tutorials

Datasets

- Data are given as a part of R programs for the course.

- External datasets (which are not given as a part of the R code) and used for illustration are available online:

https://github.com/eR-Biostat/Courses/tree/master/Statistical%20modeling%20(1)/glm/Data

Topics (part 2)

11. Poisson Regression
12. Beyond Poisson and binomial distributions: models with different link functions and/or distributions
13. Poisson regression and log linear models
14. Over dispersion

Chapter 11:
Poisson Regression

Donson: chapter 7.

Lindsey: Appendix B.

McCullagh & Nelder: chapter 2.

Count data

Count data:

- counts per unit of time/area/distance, etc
- contingency tables: counts cross-classified by categorical variables
- Covariates: categorical or continuous

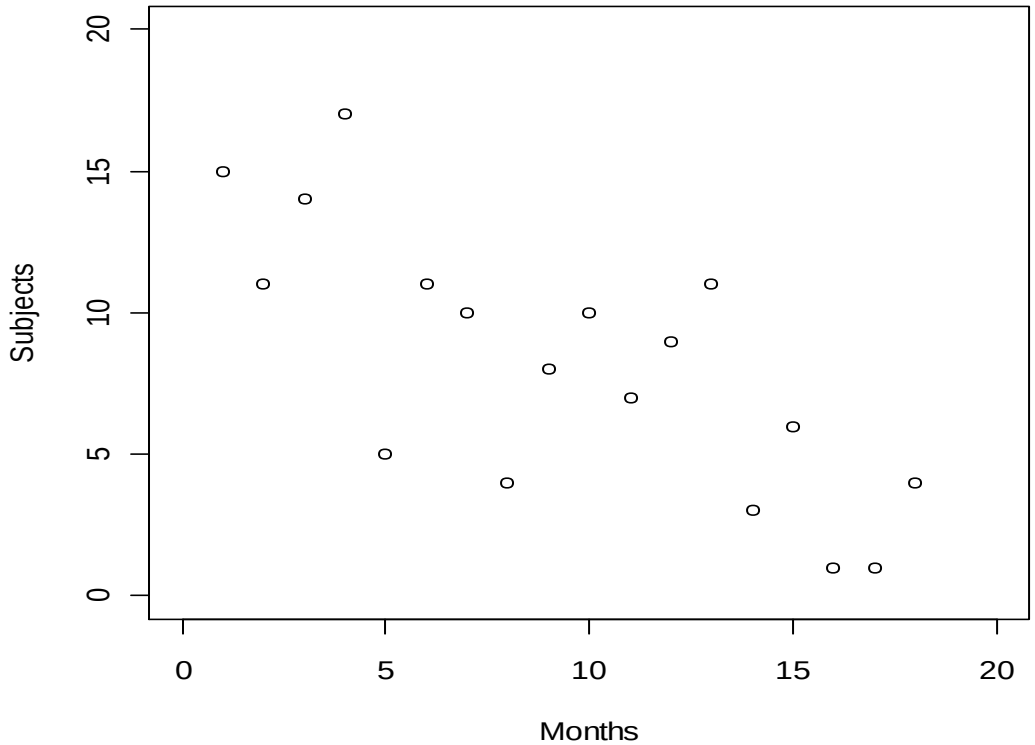
Example 1: Stress data

- One randomly chosen member from each randomly chosen household in a sample from Oakaland, California, USA was interviewed. In a list of 41 events, respondents were asked to note which had occurred within the last 18 months. The result is given as:

Month	1	2	3	4	5	6	7	8	9
Respondents	15	11	14	17	5	11	10	4	8
Month	10	11	12	13	14	15	16	17	18
Respondents	10	7	9	11	3	6	1	1	14

Data in R

```
> stress <- read.table("C:...../stress.txt", sep=",",header=TRUE)
> attach(stress)
plot(respondents ~ month, xlab = "Months",ylab = "Subjects",
     xlim=c(0,20), ylim=c(0,20))
```



Model formulation

The distribution of the response variable

$$Y_t \sim Poisson(\mu_t)$$

$$f(Y_t, \mu) = \frac{\mu^{y_i} e^{-\mu}}{Y_t!}$$

$$E(Y_t) = \mu_t$$

The dependency on the predictor

$$\mu_t = f(month)$$

A proposal ?

$$\mu_t = \beta_0 + \beta_1 t$$

Model formulation

The distribution of the response variable

$$Y_t \sim Poisson(\mu_t)$$

$$E(Y_t) = \mu_t$$

The linear predictor

$$\mu_t = f(month)$$

$$\eta = \beta_0 + \beta_1 M_t$$

$$\mu_t = e^{\eta} = e^{\beta_0 + \beta_1 M_t}$$

$$g(E(Y_t)) = \log(\mu_t) = \eta$$

GLM for Poisson regression using glm()

$$\eta = \beta_0 + \beta_1 t$$

```
> respGLM <- glm(respondents ~ month,
                 family=poisson, data=stress)
```

The relative risk

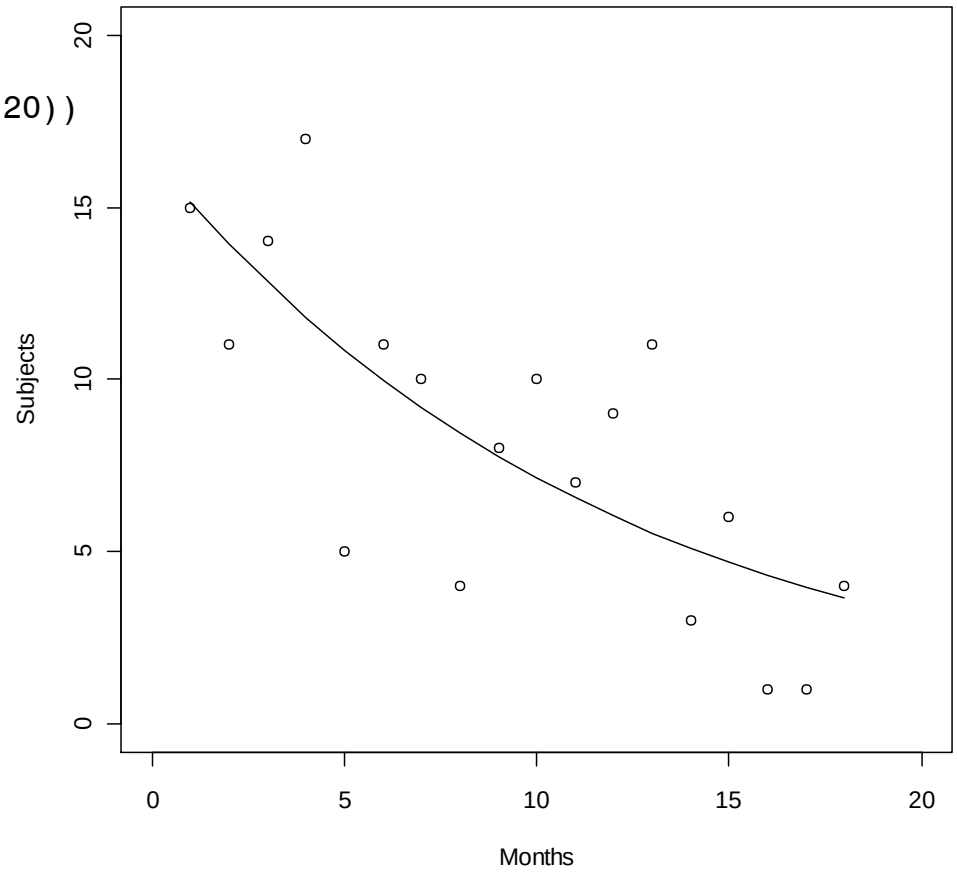
$$RR = \frac{E(Y_t \mid t+1)}{E(Y_t \mid t)} = \frac{e^{\beta_0 + \beta_1 (t+1)}}{e^{\beta_0 + \beta_1 t}} = e^{\beta_1}$$

GLM for Poisson regression using glm()

```
> summary(respGLM)
Call:
glm(formula = respondents ~ month, family = poisson, data = stress)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.9886  -0.9631   0.1737   0.5131   2.0362

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.80316    0.14816  18.920  < 2e-16 ***
month       -0.08377    0.01680  -4.986 6.15e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 50.843  on 17  degrees of freedom
Residual deviance: 24.570  on 16  degrees of freedom
AIC: 95.825
Number of Fisher Scoring iterations: 5
```

Data and fitted model

```
plot(respondents ~ month, xlab = "Months",
ylab = "Subjects", xlim=c(0,20), ylim=c(0,20))
lines(month,respGLM$fit)
```



Example 2: Ministerial resignation

- On October 18, 1995, `The Independent' reported on the numbers of ministerial resignations because of different reason. The years start in 1945-1951, with a Labour government, and 7 Resignations.

Term	45-51	51-57	55-57	57-63	63-64	64-70	70-74	74-76	76-79	79-90	90-95	97-05
Gov	Lab	con	con	con	con	lab	con	lab	lab	con	con	lab
Res	7	1	2	7	1	5	6	5	4	1	1	1
Year	6	4	2	6	1	6	4	2	3	1	5	8

- Main question: Is there any difference between Government (Labor and Conservative) in the rate of resignations?

Model formulation

The distribution of the response variable

$$Y_t \sim Poisson(\mu_t)$$

$$E(Y_t) = \mu_t$$

The linear predictor

$$\mu_t = f(gov : L/C)$$

$$G_t = \begin{cases} 1 & L \\ 0 & C \end{cases}$$

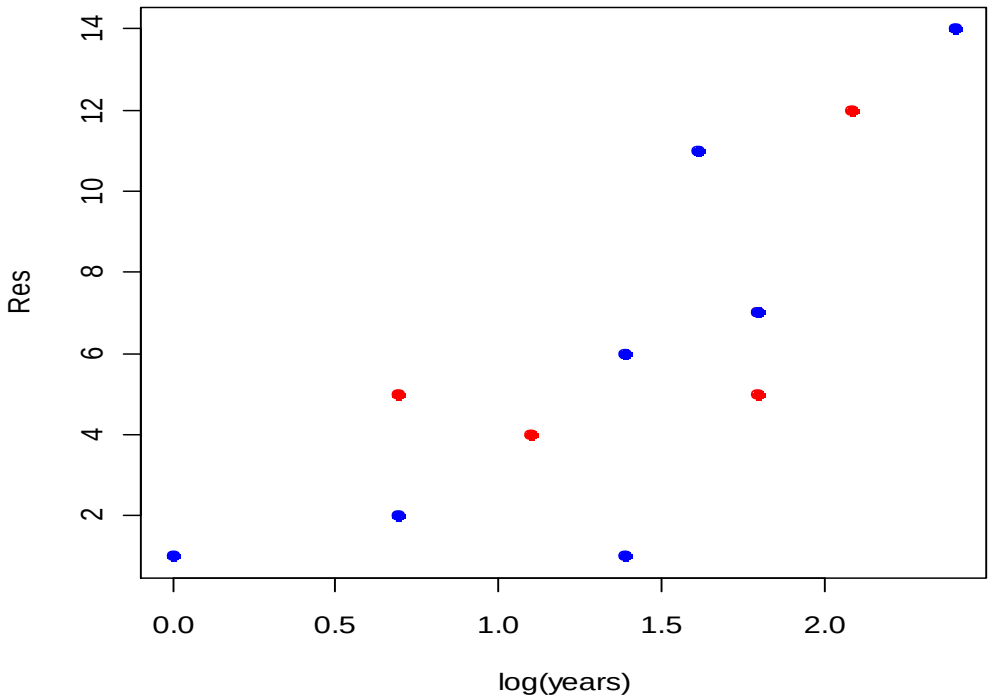
$$\eta = \beta_0 + \beta_1 G_t$$

$$\mu_t = e^{\eta} = e^{\beta_0 + \beta_1 G_t}$$

$$g(E(Y_t)) = \log(\mu_t) = \eta$$

The data in R

```
>Resignations <- read.table("C:...../resign.txt",header=T)
>attach(Resignations)
>plot(Res ~ log(years), pch=19, col=c(4,2)[Gov])
```



Model formulation (1)

```
> first.glm <- glm(Res ~ Gov , poisson)
```

$$\eta = \log(\mu_t) = \beta_0 + \beta_1 G_t$$

The relative risk

$$RR = \frac{E(Y_t \mid L)}{E(Y_t \mid C)} = \frac{e^{\beta_0 + \beta_1}}{e^{\beta_0}} = e^{\beta_1}$$

Model 1 output in R

```
> first.glm <- glm(Res ~ Gov, poisson);
> summary(first.glm)
Call:
glm(formula = Res ~ Gov, family = poisson)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.5331  -1.2942  -0.3255   0.7548   2.7793
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.79176    0.15430   11.61   <2e-16 ***
Govlab       0.09531    0.23262    0.41    0.682
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Dispersion parameter for poisson family taken to be 1)
    Null deviance: 33.436  on 11  degrees of freedom
Residual deviance: 33.269  on 10  degrees of freedom
AIC: 78.459

Number of Fisher Scoring iterations: 5
```

Model formulation (2)

How can we take the number of government years into account ?

$$\mu_t = e^{\eta} = e^{\beta_0 + \beta_1 G_t + \beta_2 \underbrace{\log(years_t)}}$$

$$\eta = \log(\mu_t) = \beta_0 + \beta_1 G_t + \beta_2 \log(years_t)$$

GLM with Poisson family

```
> first.glm <- glm(Res ~ Gov + log(years), poisson)
```

The same slope for log(year)

$$\eta = \log(\mu_t) = \beta_0 + \beta_1 G_t + \beta_2 \log(years_t)$$

Model 2: R output

```
glm(formula = Res ~ Gov + log(years), family = poisson)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.2417  -0.3469  -0.1250   0.3917   1.6513
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.29973    0.41598   0.721    0.471
Govlab       0.03541    0.23271   0.152    0.879
log(years)   0.96636    0.22258   4.342 1.41e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 33.436  on 11  degrees of freedom
Residual deviance: 11.276  on  9  degrees of freedom
AIC: 58.466

Number of Fisher Scoring iterations: 4
```

Model 3: model formulation

Different intercepts and slopes

```
>  first.glm3 <- glm(Res ~ log(years)+Gov+Gov:log(years),
                     poisson)
```

$$\eta = \beta_0 + \beta_1 G_t + \beta_2 \log(years_t) + \beta_3 G_t \log(year_t)$$

Model 3 output in R

```
> summary(first.glm)
Call:
glm(formula = Res ~ log(years) +Gov+ Gov:log(years), family= poisson)

Estimate Std. Error z value Pr(>|z|)
(Intercept)        0.04443    0.51085   0.087    0.931
log(years)         1.11144    0.27306   4.070 4.69e-05 ***
Govlab             0.81973    0.82744   0.991    0.322
log(years):Govlab -0.46049    0.46880  -0.982    0.326


Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Dispersion parameter for poisson family taken to be 1)
    Null deviance: 33.436  on 11  degrees of freedom
Residual deviance: 10.336  on  8  degrees of freedom
AIC: 59.526
Number of Fisher Scoring iterations: 4
```

Model 4: GLM with an offset variable: model formulation

Number of resignation per government year:

$$\frac{Y_t}{year_t} \sim Poisson(\mu_t)$$

$$Y_t \sim Poisson(years_t \times \mu_t)$$

Model 4: GLM with an offset variable - model formulation

$$Y_t \sim Poisson(years_t \times \mu_t)$$

$$E(Y_t) = years_t \times \mu_t = years_t \times e^{\beta_0 + \beta_1 G_t}$$

$$g(E(Y_t)) = g(years_t \times \mu_t) = \log(years_t \times e^{\beta_0 + \beta_1 G_t})$$

$$g(E(Y_t)) = \underbrace{\log(years_t)}_{\text{offset variable}} + \beta_0 + \beta_1 G_t = \eta$$

A model with offset in R

```
> next.glm<- glm(Res ~ Gov + offset(log(years)), poisson)
```

$$\beta_0 + \beta_1 G_t + \log(years_t)$$

Model 4 GLM with offset output in R

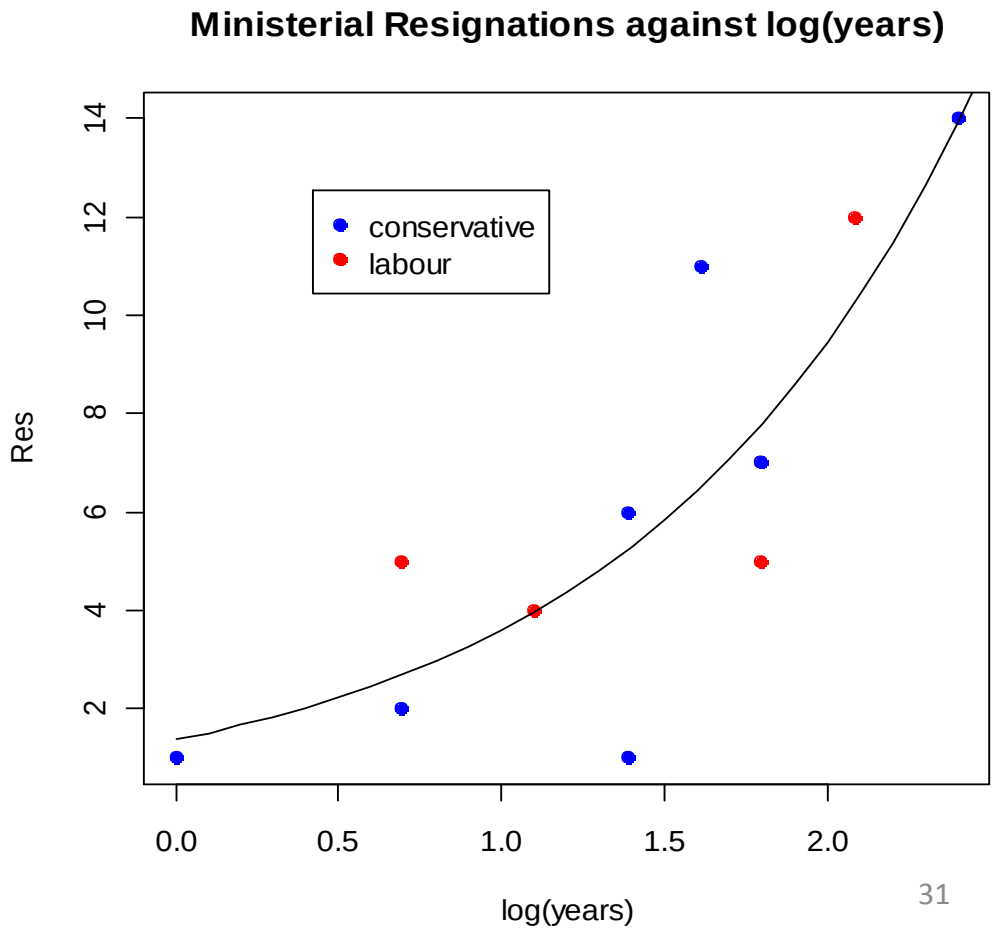
```
summary(first.glm4)
Call:
glm(formula = Res ~ Gov + offset(log(years)), family = poisson)


Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.24116    0.15430   1.563    0.118
Govlab       0.03647    0.23262   0.157    0.875


(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 11.323  on 11  degrees of freedom
Residual deviance: 11.299  on 10  degrees of freedom
AIC: 56.488

Number of Fisher Scoring iterations: 4
```

$\hat{\beta}_0$

$\hat{\beta}_1$

Data and predicted models

```
 plot(Res ~ log(years), pch=19, col=c(4,2)[Gov]) # Use palette() to find out which colour
corresponds
> legend(locator(1), legend= c("conservative", "labour"), col=c(4,2), pch=19)
> l <- (0:25)/10
> fv <- exp(0.3168 + 0.9654*l)# to plot fitted curve under last.glm
> lines(l,fv)
```



AIC for the different models

MODEL	No parameters	Deviance	AIC
1	2	33.269	78.45861
2	3	11.276	58.46574
3	4	10.336	59.52603
4	2	11.299	56.48846

$$g(E(Y_t)) = \log(years_t) + \beta_0 + \beta_1 G_t$$

Confidence interval for β_2 for model 2

```
first.glm2 <- glm(Res ~ log(years)+Gov, poisson); summary(first.glm)

> confint(first.glm2, level=0.95)
Waiting for profiling to be done...
                 2.5 %    97.5 %
(Intercept) -0.5701863 1.0636716
log(years)   0.5447242 1.4185361
Govlab      -0.4268576 0.4893354
```

ANOVA for model 3 and model 2

```
> anova(first.glm3,first.glm2, test = "Chisq")
Analysis of Deviance Table

Model 1: Res ~ log(years) + Gov + Gov:log(years)
Model 2: Res ~ log(years) + Gov
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1         8     10.336
2         9     11.276 -1 -0.93971    0.3324
```

Model selection (II): the step() function in R

```
> step(first.glm, direction = "backward")
Start:  AIC=59.53
Res ~ log(years) + Gov + Gov:log(years)
                 Df Deviance    AIC
- log(years):Gov  1   11.276 58.466
<none>                10.336 59.526
Step:  AIC=58.47
Res ~ log(years) + Gov
             Df Deviance    AIC
- Gov         1   11.299 56.489
<none>            11.276 58.466
-  log(years)  1   33.269 78.459
```

```
Step:  AIC=56.49
Res ~ log(years)
             Df Deviance    AIC
<none>            11.299 56.489
-log(years)  1   33.436 76.626
-Call:  glm(formula = Res ~
log(years), family = poisson)
Coefficients:
(Intercept)   log(years)
     0.3168       0.9654
Degrees of Freedom: 11 Total (i.e.
Null);  10 Residual
Null Deviance:      33.44
Residual Deviance: 11.3
AIC: 56.49
```

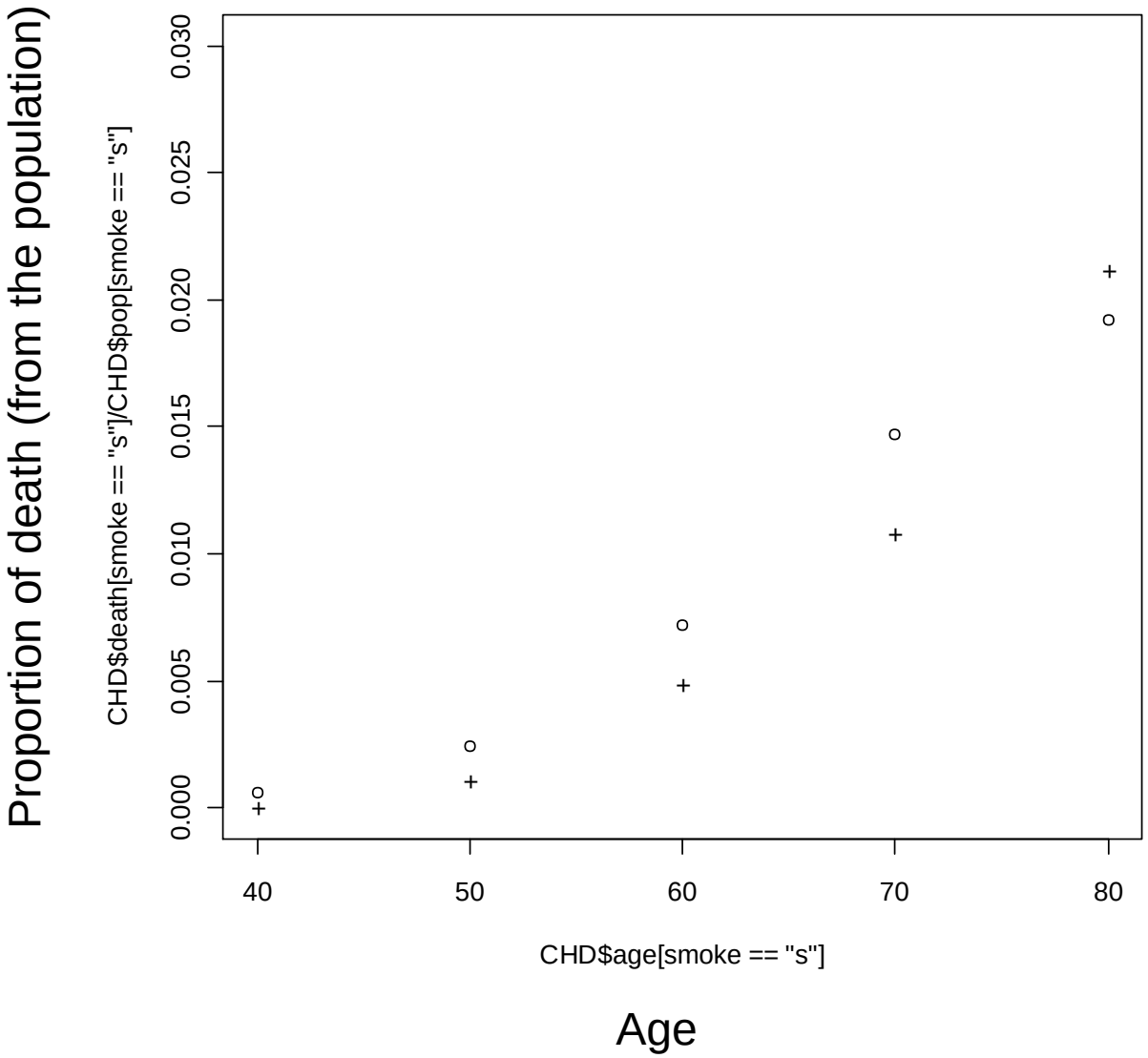
Model 4 with the offset variable is not included here.

Example 3: smoking and coronary death

```
> CHD
   age smoke death   pop
1   40     s    32 52407
2   50     s   104 43248
3   60     s   206 28612
4   70     s   186 12663
5   80     s   102  5317
6   40    ns     2 18790
7   50    ns    12 10673
8   60    ns    28  5710
9   70    ns    28  2585
10  80    ns    31  1462
```

A study about tobacco consumption and coronary heart disease among British doctors.

Smoking and coronary death: the data



GLM with an offset variable: model formulation

Number of deaths per population size:

$$\frac{Y_i}{n_i} \sim Poisson(\mu_i)$$

$$Y_i \sim Poisson(n_i \times \mu_i)$$

$$g(\mu_i) = X\beta$$

Smoking and coronary death

- Is the death rate higher for smokers than non smokers ?
- If so, by how much ?
- Is there differential effects of age ?

GLM with an offset variable: model formulation

Number of deaths per population size:

$$\frac{Y_i}{n_i} \sim Poisson(\mu_i)$$

$$Y_i \sim Poisson(n_i \times \mu_i)$$

$$g(\mu_i) = X\beta = \log(n_i) + \log(\mu_i)$$

Offset variable

$$\beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + ...$$

Linear predictor:

$$\eta = f(age, smoking, pop.)$$

3 models

$$M_1 : \eta = \boxed{\log(pop.)} + \beta_1 age + \beta_2 smoke$$

$$M_2 : \eta = \boxed{\log(pop.)} + \beta_1 age + \beta_2 smoke + \beta_3 age \times smoke$$

$$M_3 : \eta = \boxed{\log(pop.)} + \beta_{11} age + \beta_{12} age^2 + \beta_2 smoke + \beta_3 age \times smoke$$

```
>fit.chd1<-glm(death ~ age + smoke+offset(log(pop)), poisson)
>fit.chd2<-glm(death ~ age + smoke+age:smoke+offset(log(pop)), poisson)
>age2<-age^2
>fit.chd3<-glm(death ~ age+age2+smoke+age:smoke+offset(log(pop)), poisson)
```

Model selection

```
> extractAIC(fit.chd1, k=2)
[1]   3.0000 130.2500
> extractAIC(fit.chd2, k=2)
[1]   4.0000 122.9614
> extractAIC(fit.chd3, k=2)
[1]  5.00000 66.70331
```

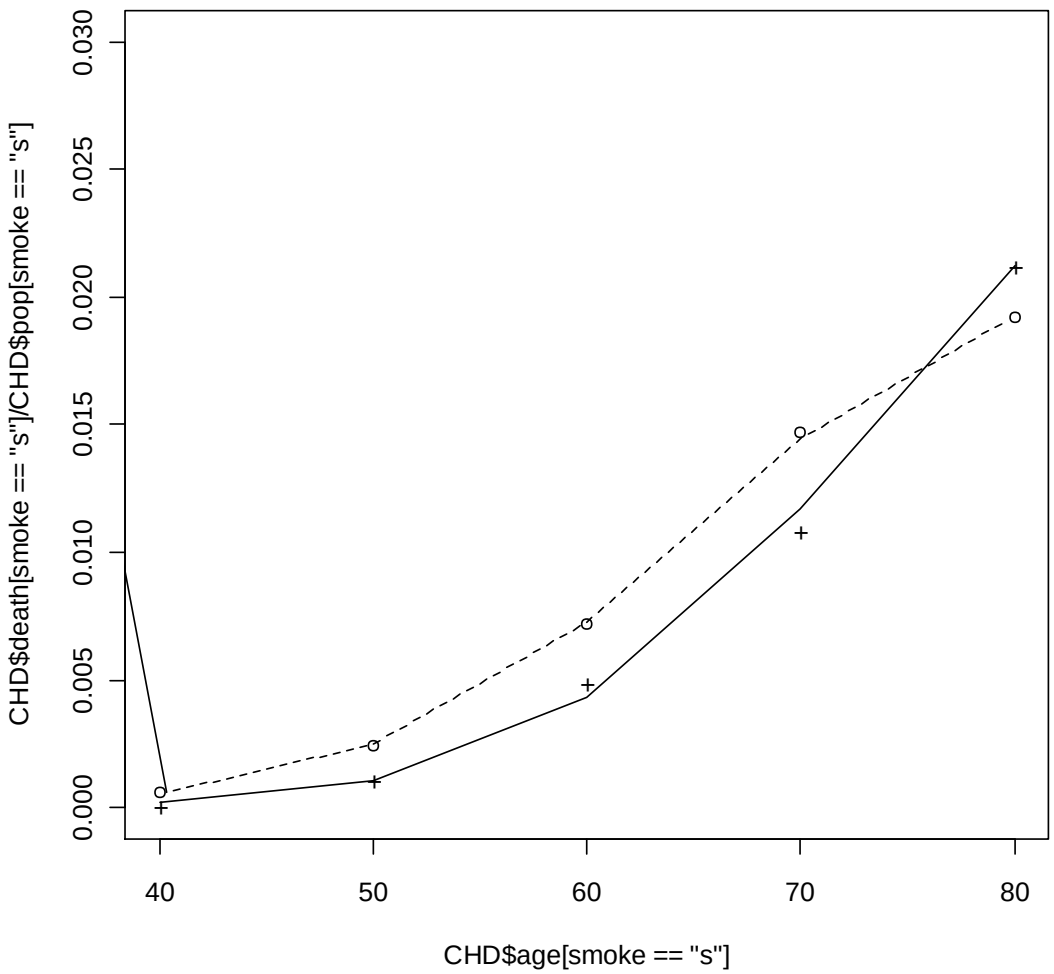
The model with quadratic age effect has the best goodness-of-fit.

R output (model 3)

```
> summary(fit.chd3)

Call:
glm(formula = death ~ age + age2 + smoke + age:smoke + offset(log(pop)),
    family = poisson)


Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.970e+01  1.253e+00 -15.717  < 2e-16 ***
age          3.563e-01  3.632e-02   9.810  < 2e-16 ***
age2        -1.977e-03  2.737e-04  -7.223 5.08e-13 ***
smokes       2.364e+00  6.562e-01   3.602 0.000316 ***
age:smokes  -3.075e-02  9.704e-03  -3.169 0.001528 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 935.0673  on 9  degrees of freedom
Residual deviance:   1.6354  on 5  degrees of freedom
AIC: 66.703

Number of Fisher Scoring iterations: 4
```

Data and predicted model

$$\hat{E}(Y_i) = n_i \times \exp(\mu_i) = n_i \times \exp(X\hat{\beta})$$



Chapter 12:
Beyond Poisson and binomial distributions: Models with different link functions and/or distributions

Lindsey: Chapter 4.

Example 1: Employment duration

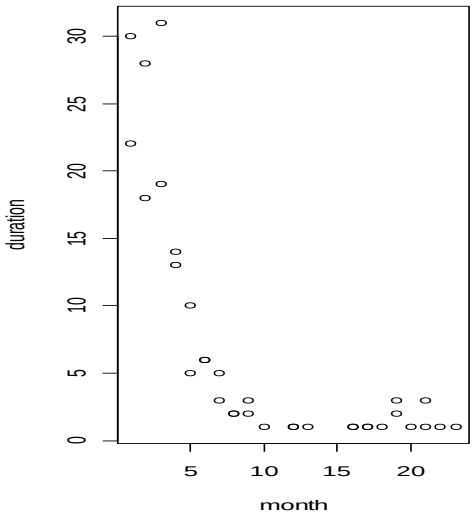
- The employment duration of staff, age 25 to 44, recruited to the British post office in the first quarter of 1973 and classified in to two grades.

Month	Grade 1	Grade2	Month	Grade1	Grade2
1	22	30	13	0	1
2	18	28	14	0	0
3	19	31	15	0	0
4	13	14	16	1	1
5	5	10	17	1	1
6	6	6	18	1	0
7	3	5	19	3	2
8	2	2	20	1	0
9	2	3	21	1	3
10	1	0	22	0	1
11	0	0	23	0	1
12	1	1	24	0	0

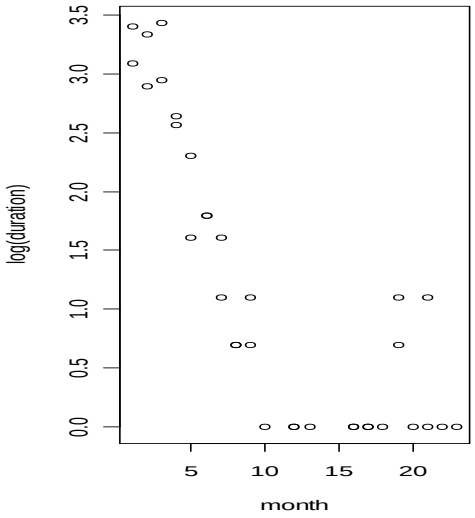
The data in R

```
> employ <- read.table("C:.... /employ.txt",header=TRUE)
> attach(employ)
> employ
   month grade duration
1      1     1       22
2      1     2       30
3      2     1       18
4      2     2       28
5      3     1       19
6      3     2       31
7      4     1       13
8      4     2       14
9      5     1        5
10     5     2       10
.      .     .        .
```

Original sacle.



log transformation.



Model formulation

Models with normal error.

$$Y_t \sim N(\mu_t, \sigma^2)$$

$$\eta = \beta_0 + \beta_1 t + \beta_2 G$$

$$\mu = \beta_0 + \beta_1 t + \beta_2 G$$

identity link

$$\log(\mu) = \beta_0 + \beta_1 t + \beta_2 G$$

$$\mu = e^{\beta_0 + \beta_1 t + \beta_2 G}$$

Log link

$$\frac{1}{\mu} = \beta_0 + \beta_1 t + \beta_2 G$$

$$\mu = \frac{1}{\beta_0 + \beta_1 t + \beta_2 G}$$

invesre link

Models with normal error in R

```
m.normal.idt <- glm(duration ~ month + grade + month:grade,data = employ,
family = gaussian(link = identity))

m.normal.inv <- glm(duration ~ month + grade + month:grade,data = employ,
family = gaussian(link = inverse))

m.normal.log <- glm(duration ~ month + grade + month:grade,data = employ,
family = gaussian(link = log))

m.normal.log1 <- glm(duration ~ month + grade ,data = employ,
family = gaussian(link = log))
```

Model selection

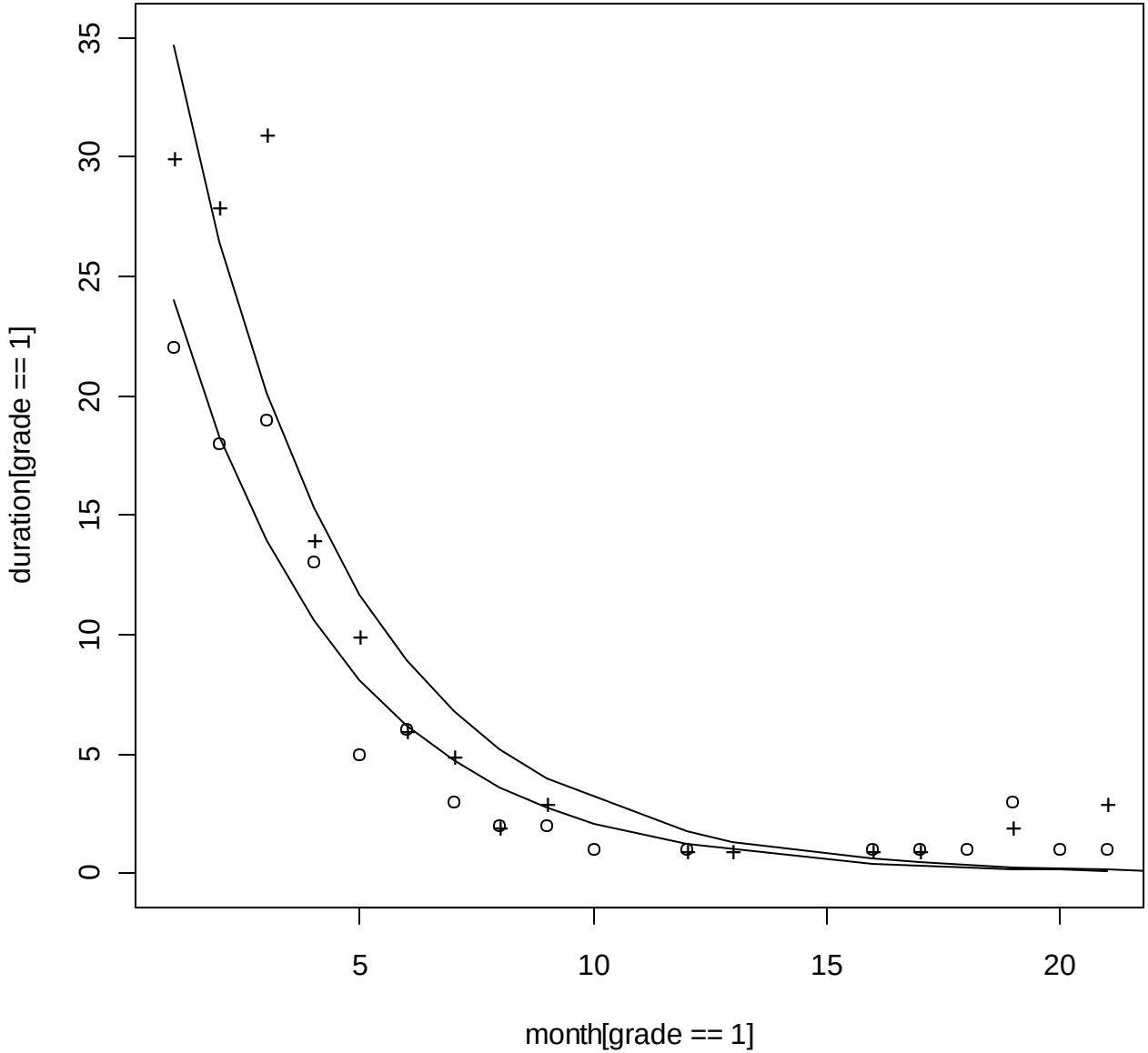
```
> extractAIC(m.normal.idt, k=2)
[1]   4.0000 228.5094
> extractAIC(m.normal.inv, k=2)
[1]   4.0000 198.3163
> extractAIC(m.normal.log, k=2)
[1]   4.0000 173.8542
> extractAIC(m.normal.log1, k=2)
[1]   3.0000 171.8545
```

The model with log link has the smallest AIC value.

GLM with normal error and log link in R

```
> m.normal.log <- glm(duration ~ month + grade + month:grade,data = employ1, family =
gaussian(link = log))
> summary(m.normal.log)

Call:
glm(formula = duration ~ month + grade + month:grade, family = gaussian(link = log),
    data = employ1)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.6676  -1.5332  -0.2005   0.8915  10.8676

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)   3.4476971  0.1304802  26.423  < 2e-16 ***
month        -0.2709521  0.0444746  -6.092 1.08e-06 ***
grade2        0.3698490  0.1591805   2.323   0.0271 *
month:grade2 -0.0007872  0.0545143  -0.014   0.9886
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 8.219982)

    Null deviance: 2771.88  on 33  degrees of freedom
Residual deviance:  246.59  on 30  degrees of freedom
AIC: 173.85

Number of Fisher Scoring iterations: 7
```

Data and fitted model



Other models

- Different distributions:
  - Normal.
  - Gamma.
  - …

$$Y_t \sim H(\mu_t)$$

$$g(\mu_t) = \eta = \beta_0 + \beta_1 t + \beta_2 G$$

$$\mu = \beta_0 + \beta_1 t + \beta_2 G$$

identity link

$$\log(\mu) = \beta_0 + \beta_1 t + \beta_2 G$$

$$\mu = e^{\beta_0 + \beta_1 t + \beta_2 G}$$

Log link

$$\frac{1}{\mu} = \beta_0 + \beta_1 t + \beta_2 G$$

$$\mu = \frac{1}{\beta_0 + \beta_1 t + \beta_2 G}$$

invesre link

Model formulation (model 1)

```
m.normal.log <- glm(duration ~ month + grade + month:grade,
data = employ1, family = gaussian(link = log))
```

$$\eta = \log(\mu_i) = \beta_0 + \beta_2 t_i + \beta_1 G_i + \beta_3 t_i \times G_i$$

A model with normal error and log link:

$$Y_i \sim N(\mu_i, \sigma^2)$$

$$g(\mu) = \eta, \ \log(\mu) = \eta$$

R output : model 1

```
> m.normal.log <- glm(duration ~ month + grade + month:grade, data = employ, family =
    gaussian(link = log))
> summary(m.normal.log)

Call:
glm(formula = duration ~ month + grade + month:grade, family = gaussian(link = log),
    data = employ)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-4.6676  -1.5332  -0.2005   0.8915  10.8676

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  3.0778481  0.2764302  11.134 3.54e-12 ***
month       -0.2701650  0.0943705  -2.863  0.00759 **
grade        0.3698490  0.1591805   2.323  0.02712 *
month:grade -0.0007872  0.0545143  -0.014  0.98857
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for gaussian family taken to be 8.219982)

    Null deviance: 2771.88  on 33  degrees of freedom
Residual deviance:  246.59  on 30  degrees of freedom
AIC: 173.85
```

Model with gamma error and inverse link function: model formulation (model 2)

```
m.gamma.log <- glm(duration ~ month + grade + month:grade,
                   data = employ1,
                   family = Gamma(link = inverse))
```

$$\eta = 1/\mu_i = \beta_0 + \beta_2 t_i + \beta_1 G_i + \beta_3 t \times G_i$$

A model with gamma error and inverse:

$$Y_i \sim Gamma(\mu_i)$$

$$\frac{1}{\mu_i} = \eta_i$$

R output: model 2

```
> m.gamma.inv <- glm(duration ~ month + grade + month:grade, data = employ, family =
    Gamma(link = inverse))
> summary(m.gamma.inv )

Call:
glm(formula = duration ~ month + grade + month:grade, family = Gamma(link = inverse),
    data = employ)


Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.0122937  0.0396403  -0.310  0.75861
month        0.0492390  0.0154143   3.194  0.00329 **
grade       -0.0008403  0.0226236  -0.037  0.97062
month:grade -0.0089011  0.0090337  -0.985  0.33235
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Gamma family taken to be 0.3661260)

    Null deviance: 51.752  on 33  degrees of freedom
Residual deviance:  9.887  on 30  degrees of freedom
AIC: 147.27
```

Model with gamma error and inverse link function: model formulation (model 3)

Grade is not included in the model:

$$\eta = 1/\mu_i = \beta_0 + \beta_2 t_i$$

A model with gamma error and inverse:

$$Y_i \sim Gamma(\mu_i)$$

$$\frac{1}{\mu_i} = \eta_i$$

R output: model 3

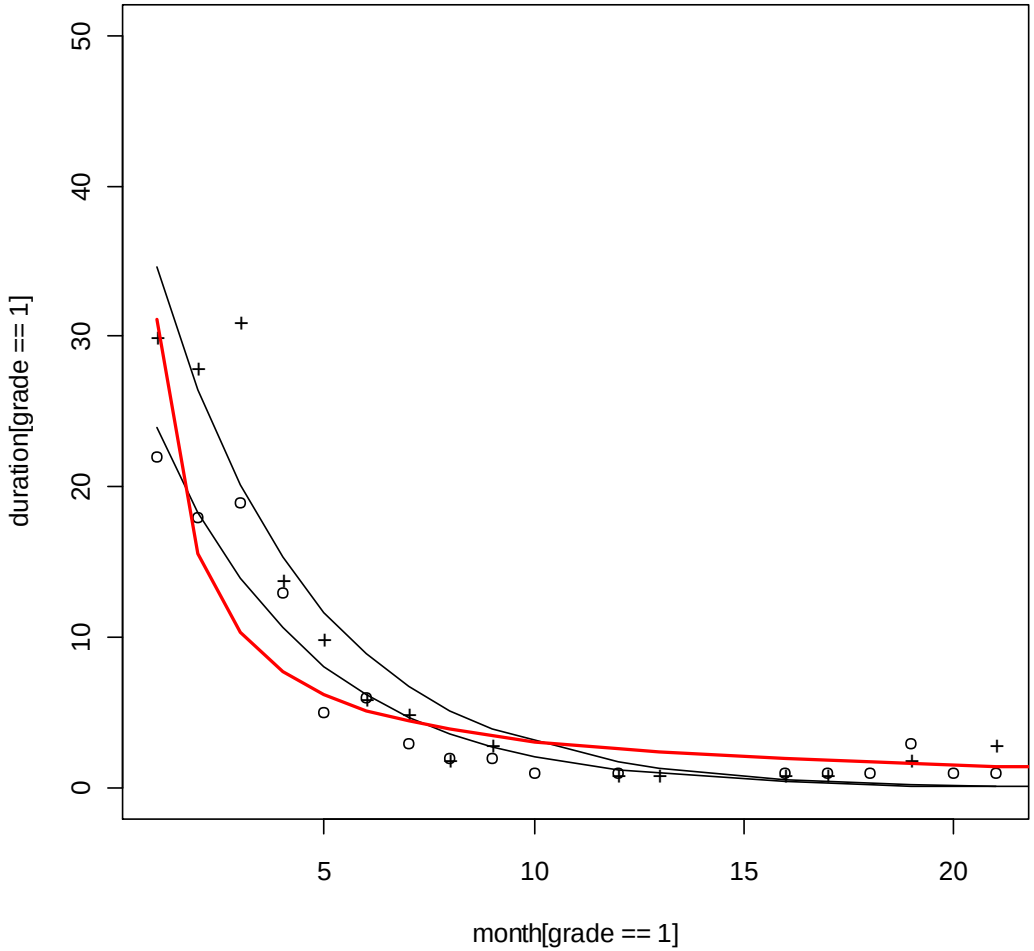
```
> m.gamma.inv1 <- glm(duration ~ month , data = employ, family = Gamma(link = inverse))
> summary(m.gamma.inv1)

Call:
glm(formula = duration ~ month, family = Gamma(link = inverse),
    data = employ)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9163  -0.5284  -0.2795   0.2599   1.2685

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.014033   0.010821  -1.297    0.204
month        0.035353   0.004445   7.954 4.45e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for Gamma family taken to be 0.3762360)

    Null deviance: 51.752  on 33  degrees of freedom
Residual deviance: 10.562  on 32  degrees of freedom
AIC: 145.63

Number of Fisher Scoring iterations: 6
```

Model selection

```
> AIC(m.normal.log)
[1] 173.8542
> AIC(m.gamma.inv)
[1] 147.2748
> AIC(m.gamma.inv1)
[1] 145.6314
> AIC(m.gamma.inv2)
[1] 145.3437
```

The model which give small AIC is the gamma model with inverse line and only duration in the model

Data and fitted models



Chapter 13:
Poisson regression and log linear models

Based on Dobson: Chapter 9

Log linear models

The general frame work of Poisson regression is given by:

$$Y_i \sim Poisson(\mu_i)$$

$$g(\mu_i) = \log(\mu_i) = X\beta$$

Example 1: melanoma

	Site			
Tumor Type	Head & neck	Trunk	Extere mities	total
Hutchinson	22	2	10	34
Superficial melanoma	16	54	115	185
Nodular	19	33	73	125
Indeterminate	11	17	28	56
Total	68	106	226	400

Cross sectional study of patients with form of skin cancer.

Different sites & different tumor types.

Example 1

	Site			
Tumor Type	Head & neck	Trunk	Extere mities	total
Hutchinson	22	2	10	34
Superficial melanoma	16	54	115	185
Nodular	19	33	73	125
Indeterminate	11	17	28	56
Total	68	106	226	400

Y_{ij} Frequency of subjects with tumor type i and site j.

$$Y_{ij} \sim Poisson(\mu_{ij})$$

n Sample size.

Example 1: independence ?

	Site			
Tumor Type	Head & neck	Trunk	Extere mities	total
Hutchinson	22	2	10	34
Superficial melanoma	16	54	115	185
Nodular	19	33	73	125
Indeterminate	11	17	28	56
Total	68	106	226	400

$Y_{i.}$

$Y_{.j}$

Chi-squared statistic for independence:

$$X^2 = \frac{\sum_{ij} \left(Y_{ij} - e_{ij}\right)^2}{e_{ij}}$$

$$e_{ij} = \frac{Y_{i.} \times Y_{.j}}{n}$$

$$e_{11} = \frac{34 \times 68}{400}$$

Example 1: independence ?

$$X^2 = \frac{\sum_{ij}\left(Y_{ij} - e_{ij}\right)^2}{e_{ij}} = \frac{(22-5.78)^2}{5.78} + \ldots + \frac{(28-31.64)^2}{31.64} = 65.8$$

Model formulation

$$Y_{ij} \sim Poisson(\mu_{ij})$$

$g(\mu_{ij}) = \mu$	$g(\mu_{ij}) = \mu + \alpha_i + \beta_j$	$g(\mu_{ij}) = \mu + \alpha_i + \beta_j + \alpha\beta_{ij}$
The minimal model	Independence model	Second ordered interaction model
M1	M2	M3

Data in R

```
> melanoma
   Tumor   Type   y
1     Hu     HN  22
2     Hu  Trunk   2
3     Hu Extrem  10
4     Su     HN  16
5     Su  Trunk  45
6     Su Extrem 115
7    Nod     HN  19
8    Nod  Trunk  33
9    Nod Extrem  73
10   Ind     HN  11
11   Ind  Trunk  17
12   Ind Extrem  28
```

Models in R

```
> M1<-glm(y~1, family=poisson, data=melanoma)
```

$$g(\mu_{ij}) = \mu$$

```
> M2<-glm(y~Tumor+Type, family=poisson, data=melanoma)
```

$$g(\mu_{ij}) = \mu + \alpha_i + \beta_j$$

```
> M3<-glm(y~Tumor+Type+Tumor:Type,family=poisson,
          data=melanoma)
```

$$g(\mu_{ij}) = \mu + \alpha_i + \beta_j + \alpha\beta_{ij}$$

```
> AIC(M1)
[1] 348.8361
> AIC(M2)
[1] 121.5482
> AIC(M3)
[1] 82.9297
```

Likelihood ratio test

```
> anova.glm(M2,M3,test="Chisq")
Analysis of Deviance Table

Model 1: y ~ Tumor + Type
Model 2: y ~ Tumor + Type + Tumor:Type
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1         6     50.618
2         0      0.000  6   50.618 3.533e-09 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘
’ 1
>
```

Example 2: Death penalty

Death penalty verdicts for cases involving multiple murders in Florida between 1976 and 1987. This data is from an article that studied effects of racial characteristics on whether persons convicted of homicide received the death penalty. The 674 subjects classified is in to a 2x2x2 contingency table- two rows, two columns, and two layers.

		Victim's Race			
		White		Black	
		Defendant's Race		Defendant's Race	
		White	Black	White	Black
Death Penalty	Yes	53	11	0	4
	No	414	37	16	139
Percent Yes		11.3	22.9	0.0	2.8

Example 3: Death penalty

		Victim's Race			
		White		Black	
		Defendant's Race		Defendant's Race	
		White	Black	White	Black
Death Penalty	Yes	53	11	0	4
	No	414	37	16	139
Percent Yes		11.3	22.9	0.0	2.8

The response variable: death penalty verdicts

$$Y_{ijk} \sim Poisson(\mu_{ijk})$$

Example 3: Death penalty

		Victim's Race			
		White		Black	
		Defendant's Race		Defendant's Race	
		White	Black	White	Black
Death Penalty	Yes	53	11	0	4
	No	414	37	16	139

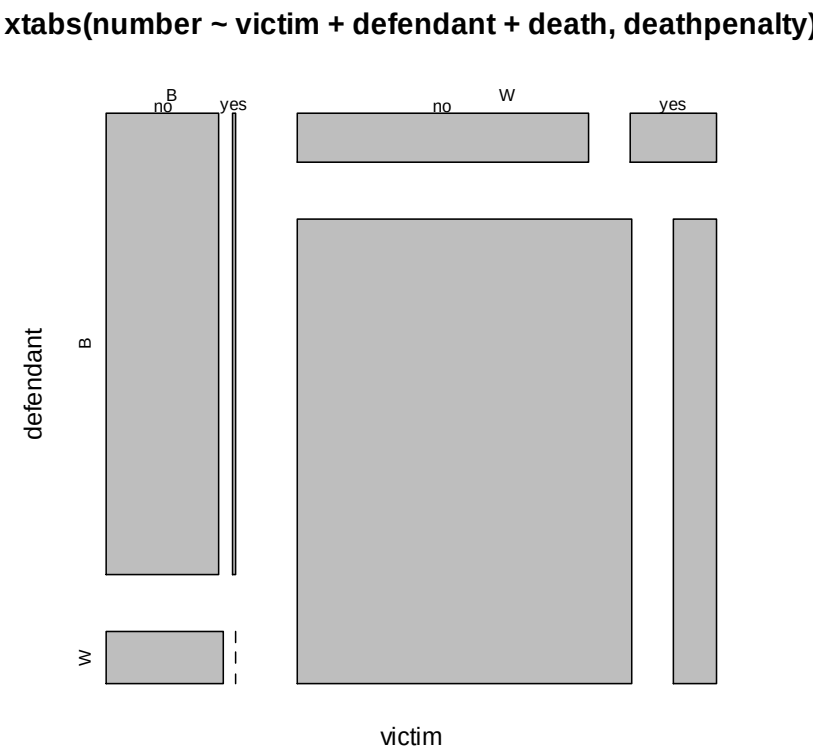
The mean structure

$$\log(\mu_{ijk}) = \mu + v_i + d_j + p_k + \text{interaction}$$

$$\log(\mu_{ijk}) = \mu + v_i + d_j + p_k + vd_{ij} + vp_{ik} + dp_{jk} + vdp_{ijk}$$

Exploring the Data in R

```
> deathpenalty <- data.frame(number = c(53,11,0,4,414,37,16,139),
+ victim = c("W","W","B","B","W","W","B","B"),
+ defendant = c("W","B","W","B","W","B","W","B"),
+ death = rep(c("yes","no"),rep(4,2)))
plot(xtabs(number~ victim + defendant+ death, deathpenalty))
```



The model in R

$$\log(\mu_{ijk}) = \mu + v_i + d_j + p_k + vd_{ij} + vp_{ik} + dp_{jk} + vdp_{ijk}$$

```
M1<-glm(number~victim*defendant*death,
        family=poisson,
        data=deathpenalty)
```

Saturated model with Poisson family

```
> M1<-glm(number~victim*defendant*death, family=poisson, data=deathpenalty)

> summary(M1)
> Call:


Estimate Std. Error z value Pr(>|z|)
(Intercept)                  4.934e+00  8.482e-02  58.177  < 2e-16 ***
victimW                     -1.324e+00  1.850e-01  -7.155 8.38e-13 ***
defendantW                  -2.162e+00  2.640e-01  -8.189 2.63e-16 ***
deathyes                    -3.548e+00  5.071e-01  -6.996 2.63e-12 ***
victimW:defendantW           4.577e+00  3.149e-01  14.536  < 2e-16 ***
victimW:deathyes             2.335e+00  6.125e-01   3.813 0.000137 ***
defendantW:deathyes         -2.153e+01  4.225e+04  -0.001 0.999593
victimW:defendantW:deathyes  2.068e+01  4.225e+04 0.00049 0.999609
---


Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1.2251e+03  on 7  degrees of freedom
Residual deviance: 4.1224e-10  on 0  degrees of freedom
AIC: 54.04
Number of Fisher Scoring iterations: 20
```

Using the step function in R to identify the best model

```
step(the three way interaction model)
```

- A stepwise selection based on AIC.
- Starting point: the three way interaction model.

Step () function for model selection

```
> step(M1)
Start:  AIC=54.04
number ~ victim * defendant * death
                          Df Deviance   AIC
- victim:defendant:death  1  0.37984 52.42
<none>                       0.00000 54.04
Step:  AIC=52.42
number ~ victim + defendant + death +
victim:defendant + victim:death +
    defendant:death
                   Df Deviance    AIC
<none>                   0.38  52.42
- defendant:death   1     5.39  55.43
- victim:death      1    20.73  70.77
- victim:defendant  1   384.43 434.47
```

Starting point (see also slide 79).

Three was interaction is excluded.

Two way interaction are excluded (one at the time).

The best model includes all two way interactions:

$$\log(\mu_{ijk}) = \mu + v_i + d_j + p_k + vd_{ij} + vp_{ik} + dp_{jk}$$

Output of the Step() function

```
Call:  glm(formula = number ~ victim + defendant + death + victim:defendant +
                              victim:death + defendant:death,
                              family = poisson, data = deathpenalty)


Coefficients:
        (Intercept)               victimW            defendantW
             4.9358               -1.3298               -2.1746
           deathyes   victimW:defendantW     victimW:deathyes
            -3.5961                4.5950                2.4044
defendantW:deathyes
            -0.8678

Degrees of Freedom: 7 Total (i.e. Null);  1 Residual

Null Deviance:      1225

Residual Deviance: 0.3798      AIC: 52.42
```

The two way interaction model in R

$$\log(\mu_{ijk}) = \mu + v_i + d_j + p_k + vd_{ij} + vp_{ik} + dp_{jk}$$

```
M2<-glm(number~victim+defendant+death
        +victim:defendant
        +victim:death
        +defendant:death,
        family=poisson, data=deathpenalty)
```

Output in R

```
> summary(M2)

Call:
glm(formula = number ~ victim + defendant + death + victim:defendant +
    victim:death + defendant:death, family = poisson, data = deathpenalty)


Coefficients:
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)          4.93578    0.08471  58.265  < 2e-16 ***
victimW             -1.32980    0.18479  -7.196 6.19e-13 ***
defendantW          -2.17465    0.26377  -8.245  < 2e-16 ***
deathyes            -3.59610    0.50691  -7.094 1.30e-12 ***
victimW:defendantW   4.59497    0.31353  14.656  < 2e-16 ***
victimW:deathyes     2.40444    0.60061   4.003 6.25e-05 ***
defendantW:deathyes -0.86780    0.36707  -2.364   0.0181 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1225.07955  on 7  degrees of freedom
Residual deviance:    0.37984  on 1  degrees of freedom
AIC: 52.42
```

Example 3: Antibiotic prescription

Diagnosis of Respiratory Tract Infections Hueston and Stott (2000) report a study of clinicians' diagnoses of respiratory tract infections over a 14-month period. The aim was to determine whether a reduction in prescription of antibiotics to acute bronchitis patients was due to clinicians assigning an alternative diagnosis.

	Time period				
Diagnosis	1-3/96	4-6/96	7-9/96	10-12/96	1-2/97
Acute bronchitis	113	58	40	108	100
Acute sinusitis	99	37	23	50	32
URI	410	228	125	366	304
Pneumonia	60	43	30	56	45
Total	682	366	218	580	481

The data in R

```
> diag <- rep(c("bron", "sinus", "URI", "pneu"), 5)
> time <- rep(c("win96", "spr96", "sum96", "aut96",
   "spr97"), rep(4, 5))
> rt <- data.frame(diag = factor(diag, unique(diag)),
+ time = factor(time, unique(time)), count = c(113, 99,
   410, 60, 58, 37, 228, 43, 40, 23, 125, 30,
+ 108, 50, 366, 56, 100, 32, 304, 45))
```

Example 3: Antibiotic prescription

	Time period				
Diagnosis	1-3/96	4-6/96	7-9/96	10-12/96	1-2/97
Acute bronchitis	113	58	40	108	100
Acute sinusitis	99	37	23	50	32
URI	410	228	125	366	304
Pneumonia	60	43	30	56	45

Research question:
Diagnostic and time period are independent ?

Data in R

```
> rt
    diag  time count
1   bron win96   113
2  sinus win96    99
3    URI win96   410
4   pneu win96    60
5   bron spr96    58
6  sinus spr96    37
7    URI spr96   228
8   pneu spr96    43
9   bron sum96    40
10 sinus sum96    23
11   URI sum96   125
12  pneu sum96    30
13  bron aut96   108
14 sinus aut96    50
15   URI aut96   366
16  pneu aut96    56
17  bron spr97   100
18 sinus spr97    32
19   URI spr97   304
20  pneu spr97    45
```

Models formulation

$$Y_{ij} \sim Poisson(\mu_{ij})$$

$g(\mu_{ij}) = \mu$	$g(\mu_{ij}) = \mu + D_i + T_j$	$g(\mu_{ij}) = \mu + D_i + T_j + DT_{ij}$
Minimal model	Independence model	Second ordered interaction

Models in R

```
>
> M1 <- glm(count ~ 1, family=poisson, data=rt)
> M2 <- glm(count ~ diag+time, family=poisson, data=rt)
> M3 <- glm(count ~  diag+time+diag:time,family=poisson, data=rt)
>
>
> AIC(M1)
[1] 1915.304
> AIC(M2)
[1] 169.8704
> AIC(M3)
[1] 164.2791
```

Likelihood ratio test

```
> anova.glm(M2,M3,test="Chisq")
Analysis of Deviance Table

Model 1: count ~ diag + time
Model 2: count ~ diag + time + diag:time
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1        12     29.591
2         0      0.000 12   29.591  0.003216 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1
‘ ’ 1
>
```

Independence model is rejected.

Output model 3

```
> summary(M3)

Coefficients:
                    Estimate Std. Error z value Pr(>|z|)
(Intercept)          4.72739    0.09407  50.253  < 2e-16 ***
diagsinus           -0.13227    0.13766  -0.961  0.33664
diagURI              1.28877    0.10625  12.130  < 2e-16 ***
diagpneu            -0.63304    0.15974  -3.963 7.40e-05 ***
timespr96           -0.66694    0.16153  -4.129 3.64e-05 ***
timesum96           -1.03851    0.18398  -5.645 1.66e-08 ***
timeaut96           -0.04526    0.13457  -0.336  0.73664
timespr97           -0.12222    0.13729  -0.890  0.37336
diagsinus:timespr96 -0.31726    0.25143  -1.262  0.20702
diagURI:timespr96    0.08013    0.18143   0.442  0.65872
diagpneu:timespr96   0.33380    0.25693   1.299  0.19388
diagsinus:timesum96 -0.42112    0.29568  -1.424  0.15438
diagURI:timesum96   -0.14934    0.21045  -0.710  0.47795
diagpneu:timesum96   0.34536    0.28957   1.193  0.23300
diagsinus:timeaut96 -0.63784    0.21957  -2.905  0.00367 **
diagURI:timeaut96   -0.06827    0.15258  -0.447  0.65457
diagpneu:timeaut96  -0.02374    0.22942  -0.103  0.91760
diagsinus:timespr97 -1.00717    0.24536  -4.105 4.05e-05 ***
diagURI:timespr97   -0.17691    0.15677  -1.128  0.25913
diagpneu:timespr97  -0.16546    0.24029  -0.689  0.49107
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 1.7890e+03  on 19  degrees of freedom
Residual deviance: 1.5765e-14  on  0  degrees of freedom
AIC: 164.28

Number of Fisher Scoring iterations: 3
```

Chapter 14
Over dispersion

Lindsey: Chapter 3

Over dispersion parameter

- The general form of exponential family is defined as:

$$f(y) = \exp\left\{ \frac{y_i \theta_i - b(\theta_i)}{a_i(\phi)} + c(y_i, \phi) \right\}$$

- Where ϕ is the dispersion parameter.
- a(ϕ): scale parameter.

Example: normal distribution

$$f(y_i;\mu_i,\sigma^2)=\frac{1}{\sqrt{2\pi\sigma^2}}e^{\frac{-(y_i-\mu_i)^2}{2\sigma^2}}$$

$$=\exp\left\{\left[y_i\mu_i-\frac{\mu_i^2}{2}\right]\frac{1}{\sigma^2}-\frac{y_i^2}{2\sigma^2}-\frac{1}{2}\log(2\pi\sigma^2)\right\}$$

The mean and the variance are separated parameters.

$$\theta_i=\mu_i,$$

$$b(\theta_i)=\theta_i^2/2$$

$$a_i(\phi)=\sigma^2$$

$$c(y_i,\ \phi)=-\left[y_i^2/\phi+\log(2\pi\phi)\right]/2.$$

Example: Binomial distribution

$$Z_i = \begin{cases} 1 \\ 0 \end{cases} \Rightarrow Y_i = \sum_{i=1}^{n} Z_i \Rightarrow Y_i \sim B(n, \pi_i)$$

$$p(y_i \mid \theta) = \binom{n_i}{y_i} \theta^{y_i} (1-\theta)^{n-y} =$$

$$\exp\left\{ y_i \log\left[\frac{\theta_i}{1-\theta_i}\right] + n_i \log(1-\theta_i) + \log\binom{n_i}{y_i} \right\}$$

The variance is a function of the mean.

$$a_i(\phi) = 1, \quad b(\theta_i) = \log(1+\exp(\theta_i))$$

$$c(y) = \log\binom{n_i}{y_i}$$

$$E(y) = \mu = b'(\theta_i) = e^{\theta}(1+\exp(\theta_i))^{-1}$$

$$\mathrm{var}(y) = n\mu(1-\mu)$$

Poisson distribution

$$Y_i \sim Poisson(\mu)$$

$$f(y_i, \theta_i) \frac{\theta_i^{y_i} e^{-\theta}}{y_i!}$$

$$a_i(\phi) = 1$$

$$b(\theta) = \exp(\theta)$$

$$c(y) = -\log(y!)$$

E(y)=V(y).

$$E(y) = \mu = b'(\theta) = \exp(\theta)$$

$$\mathrm{var}(y) = \mu$$

Overdispersion

The binomial and Poisson distribution are a members of one parameter exponential family.

$$Y_t \sim Poisson(\mu_t)$$

$$E(Y_t) = V(Y_t) = \mu_t$$

$$Y_i \sim B(n, \pi)$$

$$E(Y_i) = n\pi$$

$$V(Y_i) = n\pi(1-\pi)$$

$$\boxed{a_i(\phi) = 1}$$

Overdispersion

Often, we observed extra variability than expected:

$$V(Y_i) > E(Y_i)$$

$$V(Y_i) > n\pi(1-\pi)$$

$$V(Y_i) = \phi E(Y_i)$$

$$V(Y_i) = \phi n\pi(1-\pi)$$

$\phi = 1 \Rightarrow$ No problem with overdispersion

Estimating over dispersion

Formula

$$\phi = \frac{\chi_p^2}{n-p}$$

where

$$\mathrm{p} = \text{number of parametr in the model}$$

$$\mathrm{n} = \text{number of observations}$$

Example 1: Germination of seeds from Orobanche

o. aegyptiaco 75				o. aegyptiaco 73			
bean		cucumber		bean		cucumber	
germ.	total	germ.	total	germ.	total	germ.	total
10	39	5	6	8	16	3	12
23	62	53	74	10	30	22	41
23	81	55	72	8	28	15	30
26	51	32	51	23	45	32	51
17	39	46	79	0	4	3	7
		10	13				

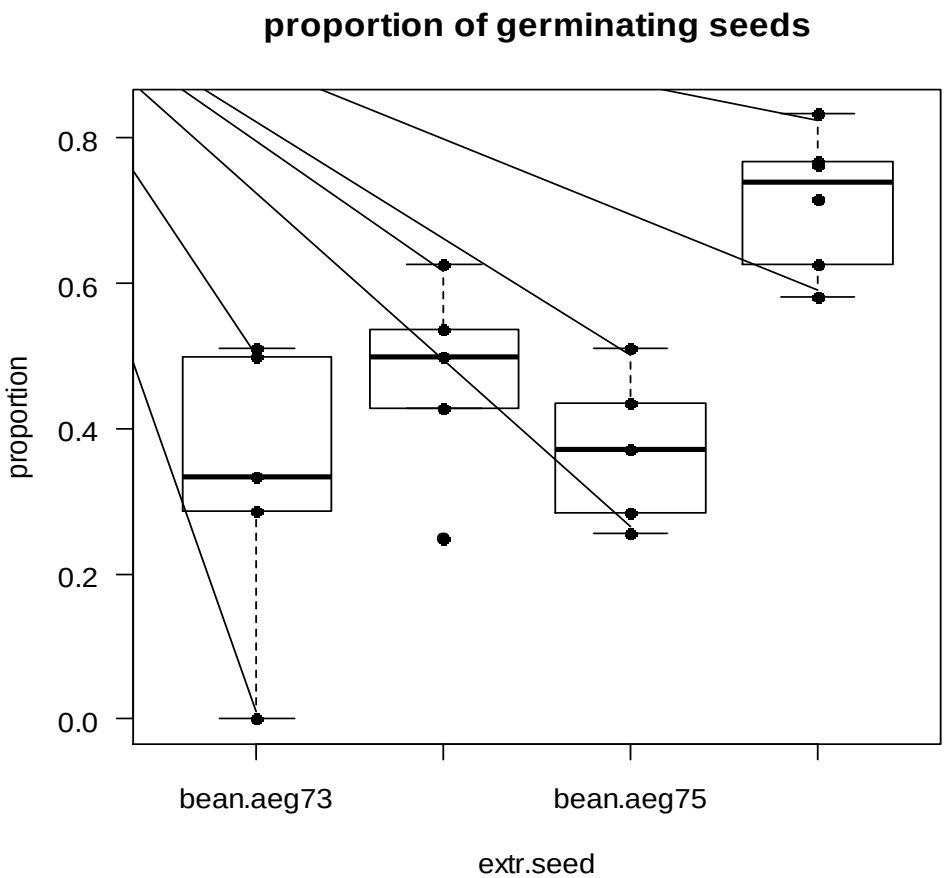
Data in R

```
> fac<-read.table("C:...../seed.txt", header = TRUE)
> fact <- transform(fac, prop = germ/total, extr.seed = interaction(extract,seed))
```

```
 fact
    seed  extract germ total      prop      extr.seed
1  aeg75     bean   10    39 0.2564103     bean.aeg75
2  aeg75     bean   23    62 0.3709677     bean.aeg75
3  aeg75     bean   23    81 0.2839506     bean.aeg75
4  aeg75     bean   26    51 0.5098039     bean.aeg75
5  aeg75     bean   17    39 0.4358974     bean.aeg75
6  aeg75 cucumber    5     6 0.8333333 cucumber.aeg75
7  aeg75 cucumber   53    74 0.7162162 cucumber.aeg75
8  aeg75 cucumber   55    72 0.7638889 cucumber.aeg75
9  aeg75 cucumber   32    51 0.6274510 cucumber.aeg75
10 aeg75 cucumber   46    79 0.5822785 cucumber.aeg75
11 aeg75 cucumber   10    13 0.7692308 cucumber.aeg75
12 aeg73     bean    8    16 0.5000000     bean.aeg73
13 aeg73     bean   10    30 0.3333333     bean.aeg73
14 aeg73     bean    8    28 0.2857143     bean.aeg73
15 aeg73     bean   23    45 0.5111111     bean.aeg73
16 aeg73     bean    0     4 0.0000000     bean.aeg73
17 aeg73 cucumber    3    12 0.2500000 cucumber.aeg73
18 aeg73 cucumber   22    41 0.5365854 cucumber.aeg73
19 aeg73 cucumber   15    30 0.5000000 cucumber.aeg73
20 aeg73 cucumber   32    51 0.6274510 cucumber.aeg73
21 aeg73 cucumber    3     7 0.4285714 cucumber.aeg73
```

Exploring the data: Box-Plot

```
> plot(prop ~ extr.seed, data = fact, las = 1, ylab = "proportion")
> points(prop ~ extr.seed, data = fact, pch = 16)
> title("proportion of germinating seeds")
```



Model 1 formulation

- Binomial model

$$yi \sim Bin(n_i, \pi_i)$$

$$g(\pi_i) = \eta, \ \log it(\pi_i) = \eta$$

$$\log it(\pi_i) = \beta_0 + \beta_1 ext + \beta_2 seed + \beta_3 ext \times seed$$

Model 1: binomial family

```
> g <- glm(cbind(germ, total - germ) ~ extract + seed +
   extract:seed, family = binomial, data = fact)
> r.pears<-residuals(g, type="pearson")
> summary(g)
```

The assumption here is over dispersion parameter is $\Phi=1$

Model 1 output

```
Call:
glm(formula = cbind(germ, total - germ) ~ extract + seed + extract:seed,
    family = binomial, data = fact)
Deviance Residuals:
     Min        1Q    Median        3Q       Max
-2.01617  -1.24398   0.05995   0.84695   2.12123
Coefficients:
                          Estimate Std. Error z value Pr(>|z|)
(Intercept)                -0.4122     0.1842  -2.238   0.0252 *
extractcucumber             0.5401     0.2498   2.162   0.0306 *
seedaeg75                  -0.1459     0.2232  -0.654   0.5132
extractcucumber:seedaeg75   0.7781     0.3064   2.539   0.0111 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Dispersion parameter for binomial family taken to be 1)
    Null deviance: 98.719  on 20  degrees of freedom
Residual deviance: 33.278  on 17  degrees of freedom
AIC: 117.87

Number of Fisher Scoring iterations: 4
```

Estimating over dispersion in R

```
> X2 <- sum(residuals(g, type = "pearson")^2)
> X2
[1] 31.65114
> phi <- X2/g$df.residual
> phi
[1] 1.861832
> phi <- g$deviance/g$df.residual
> phi
[1] 1.957517
```

As we can see from the R output, the over dispersion parameter is greater than 1 and hence this is an indication of the presence of over dispersion

Confidence interval for model 1

```
> g <- glm(cbind(germ, total - germ) ~ extract +
  seed + extract:seed, family = binomial, data =
  fact)
> confint(g)
Waiting for profiling to be done...
                              2.5 %      97.5 %
(Intercept)               -0.77866159 -0.05469853
extractcucumber            0.05275108  1.03329024
seedaeg75                 -0.58184899  0.29428969
extractcucumber:seedaeg75  0.17619697  1.37823747
```

Taking into account overdispersion in R

```
glm(model, family = quasibinomial,...)
```

Output quasi-binomial model 2

```
> g.over <- glm(cbind(germ, total - germ) ~ extract + seed + extract:seed, family =
    quasibinomial, data = fact)
> summary(g.over)

Call:
glm(formula = cbind(germ, total - germ) ~ extract + seed + extract:seed,
    family = quasibinomial, data = fact)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-2.01617  -1.24398   0.05995   0.84695   2.12123

Coefficients:
                          Estimate Std. Error t value Pr(>|t|)
(Intercept)                -0.4122     0.2513  -1.640   0.1193
extractcucumber             0.5401     0.3409   1.584   0.1315
seedaeg75                  -0.1459     0.3045  -0.479   0.6379
extractcucumber:seedaeg75   0.7781     0.4181   1.861   0.0801 .
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 1.861832)

    Null deviance: 98.719  on 20  degrees of freedom
Residual deviance: 33.278  on 17  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 4

> summary(g.over)$dispersion
[1] 1.861832
```

Confidence Interval model2

```
> library(MASS)
> fact$prop <- with(fact, germ/total)
> g.over.alt <- glm(prop ~ extract + seed +
  extract:seed,
+ weights = total, family = quasibinomial, data =
  fact)
> confint(g.over.alt)
Waiting for profiling to be done...
                              2.5 %     97.5 %
(Intercept)               -0.91562380 0.07457178
extractcucumber           -0.12415989 1.21529201
seedaeg75                 -0.74043242 0.45663323
extractcucumber:seedaeg75 -0.04413964 1.59702376
```

Estimates and CI for proportion with and without over dispersion

	$\hat{\pi}$	2.5%	97.5%
$\phi = 1$	0.36	0.31	0.42
$\hat{\phi} = 1.86$	0.36	0.28	0.45

To calculate this you need to install the R packages:

```
library(doBy)
library(R2HTML)
```

Example 2: Habitat preferences of lizards

- A study consists of two lizards type: Grohami and Opalinus.
- Response: number of sites (from the total) occupied by Grahami lizards.

- Covariates:

1. Height of the site (H).
2. Diameter (D).
3. Sun condition of the site (S, sun/ shade).
4. Time of the day (T).

Habitat preferences of lizards

```
> habitat
    G Total  S  D  H     T
1  20    22 S1 D1 H1 Early
2   8     9 S1 D1 H1   Mid
3   4     8 S1 D1 H1  Late
4  13    13 S1 D1 H2 Early
5   8     8 S1 D1 H2   Mid
6  12    12 S1 D1 H2  Late
7   8    11 S1 D2 H1 Early
8   4     5 S1 D2 H1   Mid
9   5     8 S1 D2 H1  Late
10  6     6 S1 D2 H2 Early
11  0     0 S1 D2 H2   Mid
12  1     2 S1 D2 H2  Late
13 34    45 S2 D1 H1 Early
14 69    89 S2 D1 H1   Mid
15 18    28 S2 D1 H1  Late
16 31    36 S2 D1 H2 Early
17 55    59 S2 D1 H2   Mid
18 13    16 S2 D1 H2  Late
19 17    32 S2 D2 H1 Early
20 60    92 S2 D2 H1   Mid
21  8    16 S2 D2 H1  Late
22 12    13 S2 D2 H2 Early
23 21    26 S2 D2 H2   Mid
24  4     8 S2 D2 H2  Late
```

S: sun conditions sun / shade).
D: diameter (<2 / > 2).
H: hight (< 5 / > 5).
T: time of day (early/ mid day/late).

Habitat preferences of lizards: model formulation

$$y_{ijkl} \sim B(n_{ijkl}, \pi_{ijkl})$$

Total ample size.

Number of sites occupied by Grahami lizards.

$\pi_{ijkl} =$ The probability that a site is occupied by Grahami lizards.

$$g(\pi_{ijkl}) = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l + \ldots$$

Habitat preferences of lizards: model formulation in R

Main effects model in R

$$g(\pi_{ijkl}) = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l$$

```
> f1<-glm((G/Total)~H+D+S+T,family="binomial",data=habitat)
```

R output

```
> summary(f1)

Call:
glm(formula = (G/Total) ~ H + D + S + T, family = "binomial",
    data = habitat)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.50878  -0.11019   0.02009   0.26466   0.52322

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   2.0618     1.4060   1.466    0.143
HH2           1.0631     1.1222   0.947    0.343
DD2          -0.8798     1.0841  -0.812    0.417
SS2          -0.6415     1.0884  -0.589    0.556
TLate        -1.2054     1.2761  -0.945    0.345
TMid          0.0587     1.4590   0.040    0.968

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 4.6730  on 22  degrees of freedom
Residual deviance: 1.5417  on 17  degrees of freedom
  (1 observation deleted due to missingness)
AIC: 28.658
```

Interpretation

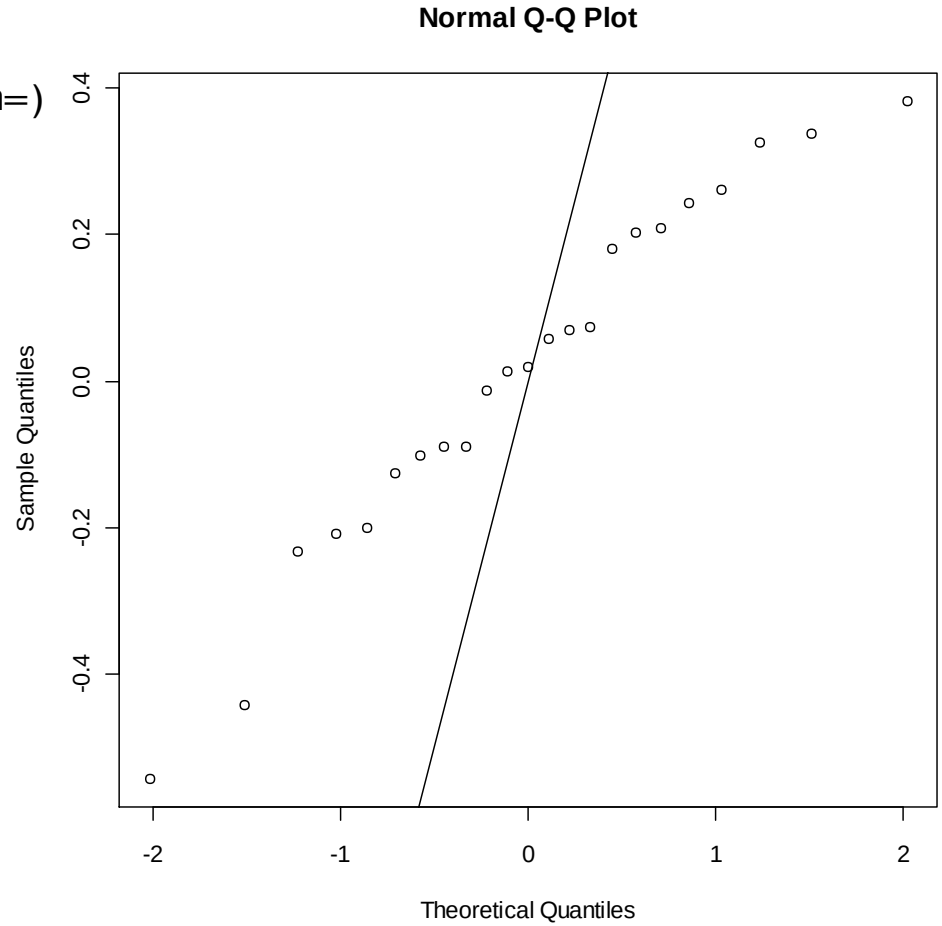
```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   2.0618     1.4060   1.466    0.143
HH2           1.0631     1.1222   0.947    0.343
DD2          -0.8798     1.0841  -0.812    0.417
SS2          -0.6415     1.0884  -0.589    0.556
TLate        -1.2054     1.2761  -0.945    0.345
TMid          0.0587     1.4590   0.040    0.968
```

All the parameters estimates are not significant.

diagnostic

```
>r.pearson<-resid(f1, type="pearson=)
> par(mfrow=c(1,1))
> qqnorm(r.pearson)
> abline(0,1)
```

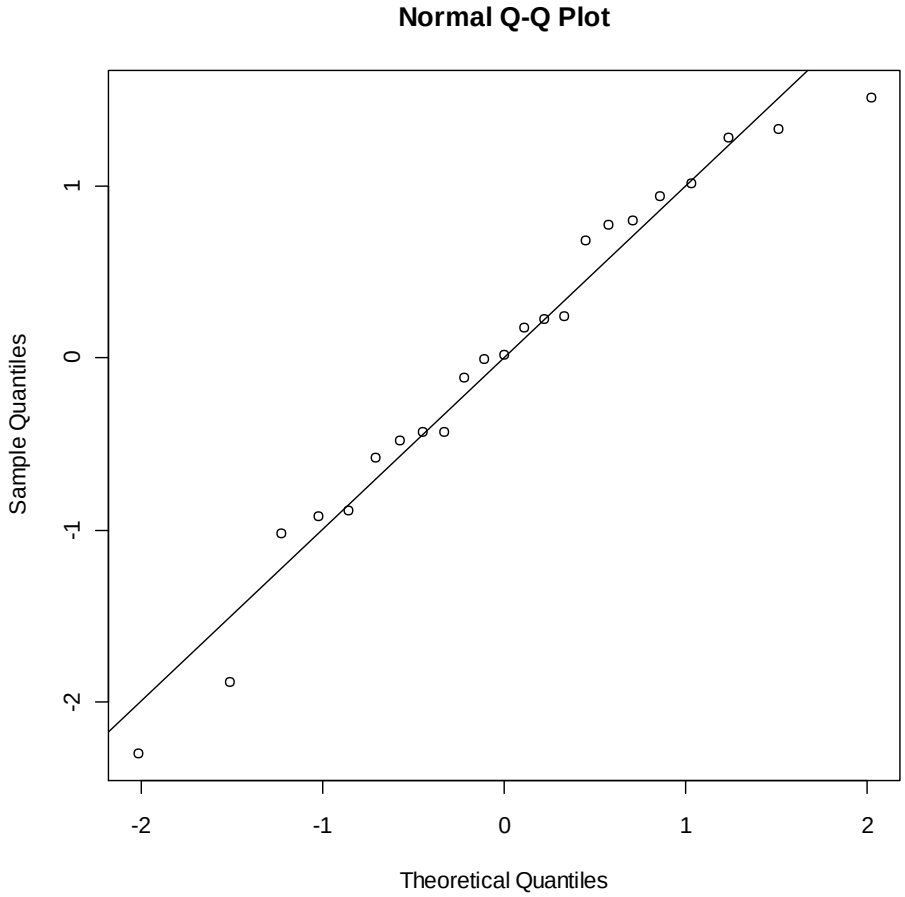
$$r_i^P = \frac{y_i - \hat{\mu}_i}{\sqrt{V(\hat{\mu}_i)}} \sim N(0,1)$$



diagnostic

```
> mean(r.pearson)
[1] 0.01454735
> var(r.pearson)
[1] 0.05871372

>r.s<-(r.pearson-mean(r.pearson))/
      sqrt((var(r.pearson)))

> qqnorm(r.s)
> abline(0,1)
```

The variance of pearson residual is much smaller than 1



Taking into account overdispersion

```
glm((G/Total)~H+D+S+T,family="binomial",data=habitat)
```

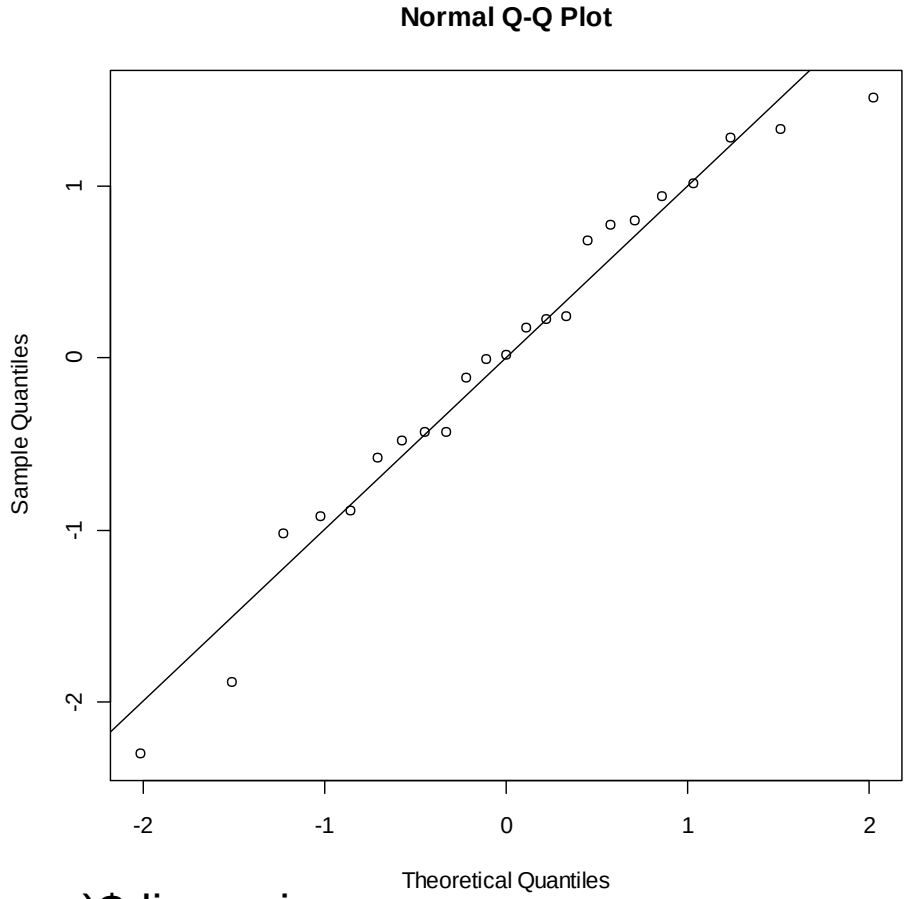
```
glm((G/Total)~H+D+S+T,family=quasibinomial,data= habitat)
```

Taking into account overdispersion

```
> f1.over <- glm((G/Total)~H+D+S+T,family=quasibinomial,data= habitat)
> summary(f1.over)

Call:
glm(formula = (G/Total) ~ H + D + S + T, family = quasibinomial,
    data = habitat)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-0.50878  -0.11019   0.02009   0.26466   0.52322

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   2.0618     0.3883   5.310 5.76e-05 ***
HH2           1.0631     0.3099   3.430  0.00319 **
DD2          -0.8798     0.2994  -2.939  0.00918 **
SS2          -0.6415     0.3006  -2.134  0.04768 *
TLate        -1.2054     0.3524  -3.420  0.00326 **
TMid          0.0587     0.4029   0.146  0.88588
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for quasibinomial family taken to be 0.07626879)

    Null deviance: 4.6730  on 22  degrees of freedom
Residual deviance: 1.5417  on 17  degrees of freedom
  (1 observation deleted due to missingness)
AIC: NA

Number of Fisher Scoring iterations: 5
```

Diagnostic

```
> mean(r.pearson)
[1] 0.01454735
> var(r.pearson)
[1] 0.05871372

>r.s<-(r.pearson-mean(r.pearson))/
      sqrt((var(r.pearson)))

> qqnorm(r.s)
> abline(0,1)
```



The variance of pearson residual is much smaller than 1

```
> summary(f1.over)$dispersion
[1] 0.07626879
```

Example 3: ship damage

- The ships data from the MASS package concern a type of damage caused by waves to the forward section of cargo-carrying vessels.
- The variables are
  - incidents number of damage incidents
  - service aggregate months of service
  - period period of operation : 1960-74, 75-79
  - year year of construction: 1960-64, 65-69, 70-74, 75-79
  - type type: '"A"' to '"E"'
- Here it makes sense to model the expected number of incidents per aggregate months of service.

Data in R

The data is available in the R the MASS library as:

```
> library(MASS)
> data(ships)
> ships2 <- subset(ships, service > 0)
> ships2$year <- as.factor(ships2$year)
➢  ships2$period <- as.factor(ships2$period)
> ships
   type year period service incidents
1     A   60     60     127         0
2     A   60     75      63         0
3     A   65     60    1095         3
4     A   65     75    1095         4
5     A   70     60    1512         6
.     .    .      .      .           .
37    E   70     60    1157         5
38    E   70     75    2161        12
39    E   75     60       0         0
40    E   75     75     542         1
```

Mean structure and model formulation in R

Model formulation:

$$Y_{ijk} \sim Poisson(\mu_{ijk})$$

$$g(\mu_{ijk}) = \mu + Tyep_i + Year_j + Period_k + \underbrace{\log(servise)}_{\text{offset}}$$

Model formulation in R:

```
> glm1 <- glm(formula = incidents ~ type + year + period,
+             family = poisson(link = "log"), data = ships2,
+             offset = log(service))
```

$$\phi = 1$$

R output

```
> glm1 <- glm(formula = incidents ~ type + year + period,
+     family = poisson(link = "log"), data = ships2,
+     offset = log(service))
> summary(glm1)
Call:
glm(formula = incidents ~ type + year + period, family = poisson(link = "log"),
    data = ships2, offset = log(service))
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.6768  -0.8293  -0.4370   0.5058   2.7912
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -6.40590    0.21744 -29.460  < 2e-16 ***
typeB       -0.54334    0.17759  -3.060  0.00222 **
typeC       -0.68740    0.32904  -2.089  0.03670 *
typeD       -0.07596    0.29058  -0.261  0.79377
typeE        0.32558    0.23588   1.380  0.16750
year65       0.69714    0.14964   4.659 3.18e-06 ***
year70       0.81843    0.16977   4.821 1.43e-06 ***
year75       0.45343    0.23317   1.945  0.05182 .
period75     0.38447    0.11827   3.251  0.00115 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Dispersion parameter for poisson family taken to be 1)
    Null deviance: 146.328  on 33  degrees of freedom
Residual deviance:  38.695  on 25  degrees of freedom
AIC: 154.56

Number of Fisher Scoring iterations: 5
```

Model 1: quasi-poisson log linear

```
> glm2 <- update(glm1, family = quasipoisson(link = "log"))
```

$$\phi \neq 1$$

```
> summary(glm2)
> Call:
glm(formula = incidents ~ type + year + period, family = quasipoisson(link = "log"),
    data = ships2, offset = log(service))


Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -6.40590    0.28276 -22.655  < 2e-16 ***
typeB       -0.54334    0.23094  -2.353  0.02681 *
typeC       -0.68740    0.42789  -1.607  0.12072
typeD       -0.07596    0.37787  -0.201  0.84230
typeE        0.32558    0.30674   1.061  0.29864
year65       0.69714    0.19459   3.583  0.00143 **
year70       0.81843    0.22077   3.707  0.00105 **
year75       0.45343    0.30321   1.495  0.14733
period75     0.38447    0.15380   2.500  0.01935 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
(Dispersion parameter for quasipoisson family taken to be 1.691028)
    Null deviance: 146.328  on 33  degrees of freedom
Residual deviance:  38.695  on 25  degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

Standard errors are changed since Φ>1.

Estimation of over dispersion parameter

```
> X2 <- sum(residuals(glm2, type = "pearson")^2)
> X2
[1] 42.27525
> phi <- X2/glm2$df.residual
> phi
[1] 1.69101
> phi <- g$deviance/glm2$df.residual
> phi
[1] 1.331111
```

CI for the parameters

```
> confint(glm2)
```

```
                2.5 %      97.5 %
(Intercept) -6.9789252 -5.86832189
typeB       -0.9793495 -0.07040017
typeC       -1.6043341  0.09972077
typeD       -0.8628299  0.63543426
typeE       -0.2880598  0.92322467
year65       0.3217115  1.08674462
year70       0.3882167  1.25564720
year75      -0.1562814  1.03712256
period75     0.0841713  0.68792187
```

Summary

- ANOVA table without and with assuming over dispersion

Effect	DF	$\phi = 1$	$\hat{\phi} = 1.67$
		P(>|χ^2|)	P(>F)
Type	4	2.63E-11	2.29E-04
Period	1	1.1E-03	1.888E-02
Year	3	5.038e-09	5.777E-04