

Multivariate Statistics in Ecology and
Quantitative Genetics
Generalized Linear Models (GLMs)

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http://evol.bio.lmu.de/_statgen

23. July 2012

Contents

Poisson GLMs for counting data

- Intro to Poisson GLM

- Daphnia and Deviance

- County size and cancer risk, now with Poisson

Binomial GLMs for Ratios

- Intro to binomial GLMs and logistic regression

- Odorant preferences in flies

- Sex ratio in ants

Other GLMs

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```
> daph <- read.table("daphnia_justina.csv",h=T)
> mod1 <- lm(counts~foodlevel+species,data=daph)
> mod2 <- lm(counts~foodlevel*species,data=daph)
> anova(mod1,mod2)
```

Analysis of Variance Table

Model 1: counts ~ foodlevel + species

Model 2: counts ~ foodlevel * species

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)		
1	9	710.00						
2	8	176.67	1	533.33	24.151	0.001172	**	

Signif. codes:	0	***	0.001	**	0.01	*	0.05	. 0.1 1
>								

```
> daph
  counts foodlevel species
1     68      high  magna
2     54      high  magna
3     59      high  magna
4     24      high galeata
5     27      high galeata
6     16      high galeata
7     20      low   magna
8     18      low   magna
9     18      low   magna
10     5      low   galeata
11     8      low   galeata
12     9      low   galeata
```

The normal distribution $\mathcal{N}(\mu, \sigma^2)$ is a continuous distribution and thus not suitable to model distributions on small numbers.

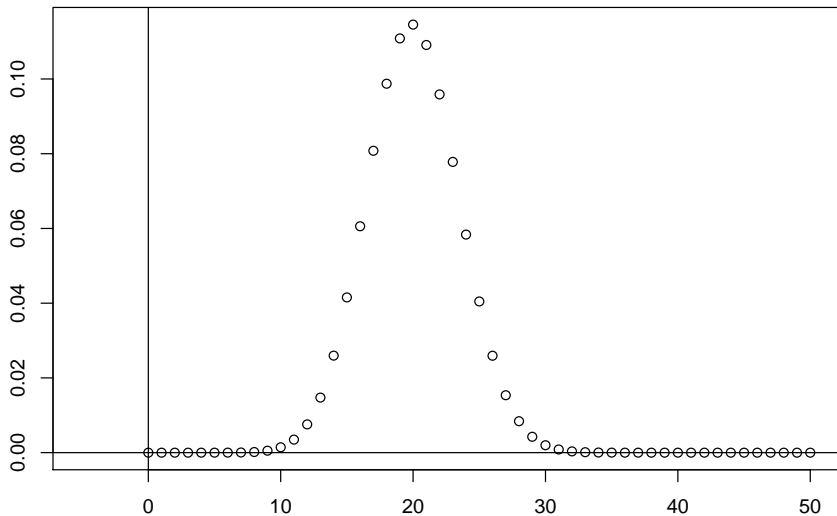
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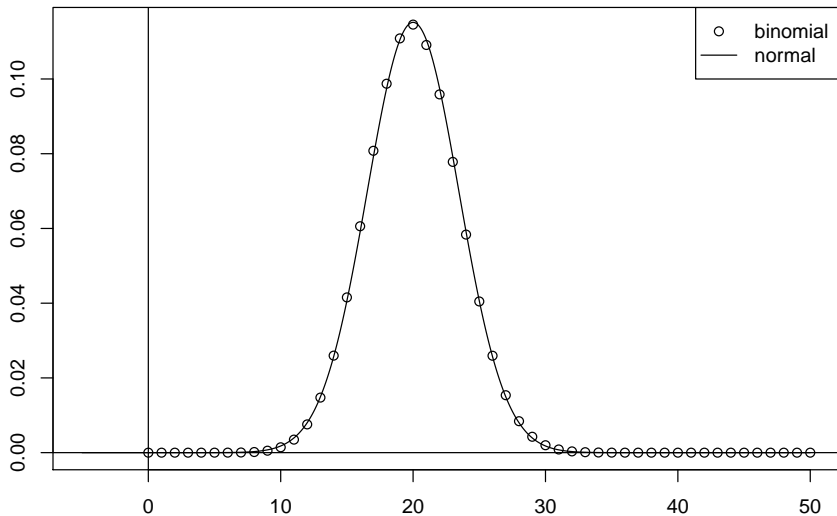
The Poisson distribution $\text{Pois}(\lambda)$ is a distribution on $\{0, 1, 2, 3, \dots\}$.

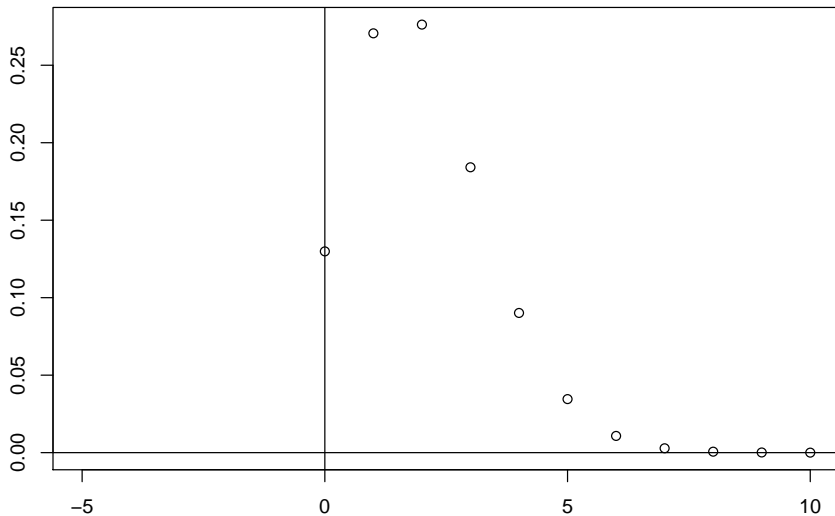
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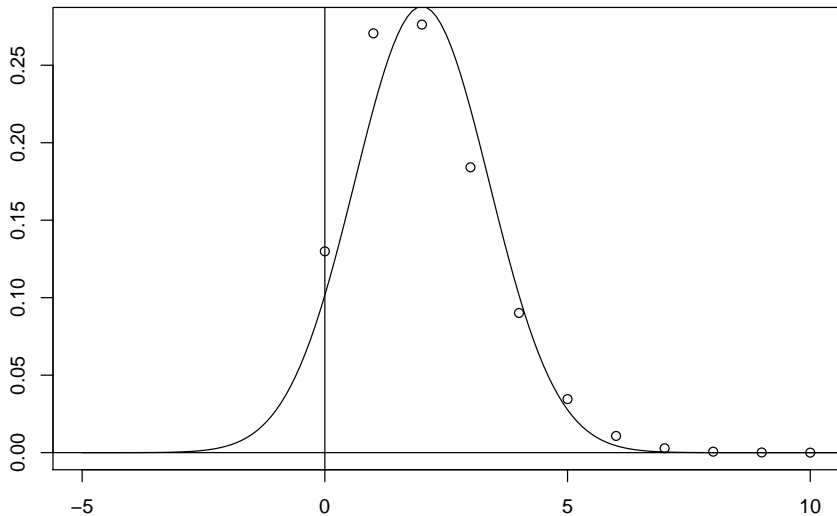
The Poisson distribution $\text{Pois}(\lambda)$ is a distribution on $\{0, 1, 2, 3, \dots\}$.

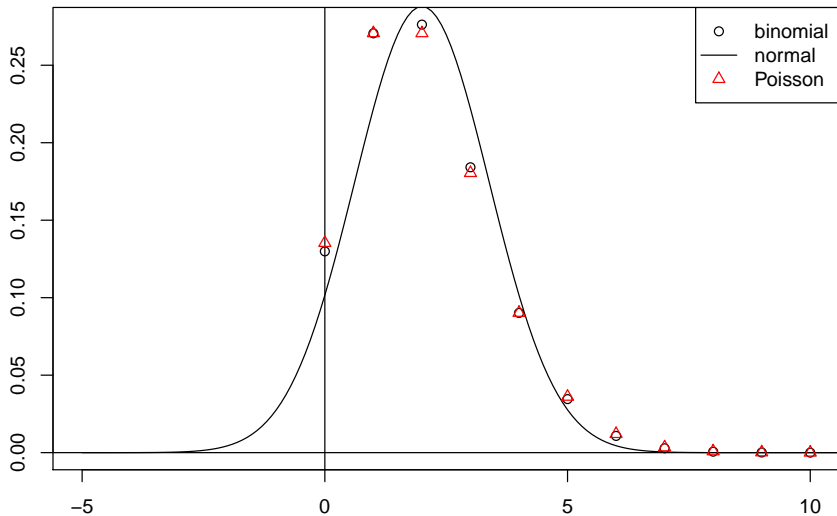
$\mathcal{N}(\mu = n \cdot p, \sigma^2 = n \cdot p \cdot (1 - p))$ approximates the binomial distribution $\text{Bin}(n, p)$ if $n \cdot p \cdot (1 - p)$ is not too small (rule of thumb: $n \cdot p \cdot (1 - p) > 9$), $\text{Pois}(\lambda = n \cdot p)$ gives a better approximation when p is small.

n=50, p=0.4

n=50, p=0.4

n=50, p=0.04

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n=50, p=0.04

If Y is $\text{Pois}(\lambda)$ -distributed, then

$$\Pr(Y = k) = \frac{\lambda^k}{k!} \cdot e^{-\lambda} \quad \text{for } k = 0, 1, 2, \dots$$

$$\mathbb{E}Y = \lambda$$

$$\text{Var}(Y) = \lambda$$

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Is there a linear model with $\text{Pois}(\lambda)$ instead of $\mathcal{N}(\mu, \sigma^2)$?

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$$\text{Var}(Y) = \lambda$$

Is there a linear model with $\text{Pois}(\lambda)$ instead of $\mathcal{N}(\mu, \sigma^2)$?

Yes, the **Generalized Linear Model (GLM) of type Poisson**.

Remember the normal linear model:

$$Y_j = b_0 + b_1 \cdot X_{1,j} + \cdots + b_k \cdot X_{k,j} + \varepsilon_j \quad \text{with } \varepsilon_j \sim \mathcal{N}(0, \sigma^2)$$

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or equivalently:

$$\begin{aligned} \eta_i &= b_0 + b_1 \cdot X_{1,i} + \cdots + b_k \cdot X_{k,i} \\ Y_i &\sim \mathcal{N}(\eta_i, \sigma^2) \end{aligned}$$

η is called the *linear predictor*.

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η is called the *linear predictor*.

This also works for the Poisson distribution:

$$\begin{aligned} \eta_i &= b_0 + b_1 \cdot X_{1,i} + \cdots + b_k \cdot X_{k,i} \\ Y_i &\sim \text{Pois}(\eta_i) \end{aligned}$$

(but note that the additional σ^2 is missing!)

Instead of using η directly as parameter of the Poisson distribution, it is common to apply a transformation:

$$\begin{aligned}\ell(\mu_i) = \eta_i &= b_0 + b_1 \cdot X_{1,i} + \cdots + b_k \cdot X_{k,i} \\ Y_i &\sim \text{Pois}(\mu_i)\end{aligned}$$

$\ell(\cdot)$ is called the *link function*.

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$\ell(\cdot)$ is called the *link function*.

The default link function for Poisson GLMs is log, the natural logarithm.

Thus,

$$\mathbb{E} Y_i = \mu_i = e^{\eta_i} = e^{b_0 + b_1 \cdot X_{1,i} + \dots + b_k \cdot X_{k,i}} = e^{b_0} \cdot e^{b_1 \cdot X_{1,i}} \dots e^{b_k \cdot X_{k,i}}$$

and the Poisson GLM with this default link is multiplicative model rather than an additive one.

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```
> pmod1 <- glm(counts~foodlevel+species,data=daph,
                family=poisson)
> summary(pmod1)
[...]
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	3.1166	0.1105	28.215	< 2e-16	***
foodlevellow	-1.1567	0.1298	-8.910	< 2e-16	***
speciesmagna	0.9794	0.1243	7.878	3.32e-15	***

```
[...]
```

Note that the Poisson model has log as its default link function. Thus, the model `pmod1` assumes that the number of Daphnia in row i is Poisson distributed with mean λ_i , i.e.

$$\Pr(X = k) = \frac{\lambda_i^k}{k!} e^{-\lambda}, \text{ and}$$

$$\log(\lambda_i) \approx 3.12 - 1.15 \cdot I_{\text{lowfoodlevel}} + 0.979 \cdot I_{\text{magna}}$$

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$$\Pr(X = k) = \frac{\lambda_i^k}{k!} e^{-\lambda}, \text{ and}$$

$$\log(\lambda_i) \approx 3.12 - 1.15 \cdot I_{\text{lowfoodlevel}} + 0.979 \cdot I_{\text{magna}}$$

or, equivalently,

$$\lambda_i \approx e^{3.12} \cdot e^{-1.15 I_{\text{lowfoodlevel}}} \cdot e^{0.979 I_{\text{magna}}} \approx 22.6 \cdot 0.317^{I_{\text{lowfoodlevel}}} \cdot 2.66^{I_{\text{magna}}}$$

Thus, this Poisson model assumes multiplicative effects.

```
> pmod1 <- glm(counts~foodlevel+species,  
               data=daph,family=poisson)  
> pmod2 <- glm(counts~foodlevel*species,  
               data=daph,family=poisson)  
> anova(pmod1,pmod2,test="F")
```

```
> pmod1 <- glm(counts~foodlevel+species,
                data=daph,family=poisson)
> pmod2 <- glm(counts~foodlevel*species,
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> anova(pmod1,pmod2,test="F")
```

Analysis of Deviance Table

Model 1: counts ~ foodlevel + species

Model 2: counts ~ foodlevel * species

	Resid. Df	Resid. Dev	Df	Deviance	F	Pr(>F)
1	9	6.1162				
2	8	6.0741	1	0.042071	0.0421	0.8375

Warning message:

F-Test not appropriate for family 'poisson'

Note:

- ▶ The `anova` command gives us an “analysis of deviance” instead of an analysis of variance!

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- ▶ The anova command gives us an “analysis of deviance” instead of an analysis of variance!
- ▶ What is a deviance?
- ▶ There is a Warning “F-Test not appropriate for family 'poisson' ”.
- ▶ Why?
- ▶ Which test should we apply?

What is the deviance?

Let $\hat{b}_0, \dots, \hat{b}_k$ be our fitted model coefficients and

$$\hat{\mu}_i = \ell^{-1} \left(\hat{b}_0 + \hat{b}_1 X_{1i} + \dots + \hat{b}_k X_{ki} \right)$$

be the predicted means for all observations. The Likelihood of the fitted parameter values is the probability of the observations assuming the fitted parameter values:

$$L(\hat{\mu}) = \frac{\hat{\mu}_1^{Y_1}}{Y_1!} e^{-\hat{\mu}_1} \cdot \frac{\hat{\mu}_2^{Y_2}}{Y_2!} e^{-\hat{\mu}_2} \dots \frac{\hat{\mu}_k^{Y_k}}{Y_k!} e^{-\hat{\mu}_k}$$

Now we compare this to a *saturated* Poisson GLM model, i.e. a model with so many parameters such that we can get a perfect fit of $\tilde{\mu}_i = Y_i$. This leads to the highest possible likelihood $L(\tilde{\mu})$.

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Now we compare this to a *saturated* Poisson GLM model, i.e. a model with so many parameters such that we can get a perfect fit of $\tilde{\mu}_i = Y_i$. This leads to the highest possible likelihood $L(\tilde{\mu})$. In practice such a model is not desirable because it leads to overfitting.

What is the deviance?

$$\text{our model: } L(\hat{\mu}) = \frac{\hat{\mu}_1^{Y_1}}{Y_1!} e^{-\hat{\mu}_1} \cdot \frac{\hat{\mu}_2^{Y_2}}{Y_2!} e^{-\hat{\mu}_2} \dots \frac{\hat{\mu}_k^{Y_k}}{Y_k!} e^{-\hat{\mu}_k}$$

$$\text{saturated model: } L(\tilde{\mu}) = \frac{Y_1^{Y_1}}{Y_1!} e^{-Y_1} \cdot \frac{Y_2^{Y_2}}{Y_2!} e^{-Y_2} \dots \frac{Y_k^{Y_k}}{Y_k!} e^{-Y_k}$$

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The *residual deviance* of our model is defined as

$$2 \cdot [\log(L(\hat{\mu})) - \log(L(\tilde{\mu}))].$$

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The *residual deviance* of our model is defined as

$$2 \cdot [\log(L(\hat{\mu})) - \log(L(\tilde{\mu}))].$$

It measures how far our model is away from the theoretical optimum.

- ▶ The deviance is approximately χ_{df}^2 distributed, where df is the degrees of freedom of our model.

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Analysis of deviance:

If D_1 and D_2 are the deviances of models M_1 with p_1 parameters and M_2 with p_2 parameters, and M_1 is nested in M_2 (i.e. the parameters of M_1 are a subset of the parameters of M_2), then $D_1 - D_2$ is approximately $\chi_{p_2-p_1}^2$ -distributed.

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Analysis of deviance:

If D_1 and D_2 are the deviances of models M_1 with p_1 parameters and M_2 with p_2 parameters, and M_1 is nested in M_2 (i.e. the parameters of M_1 are a subset of the parameters of M_2), then

$D_1 - D_2$ is approximately $\chi_{p_2-p_1}^2$ -distributed.

This Test is the classical likelihood-ratio test. (Note that $D_1 - D_2$ is 2x the log of the likelihood-ratio of the two models.)

```
> pmod1 <- glm(counts~foodlevel+species,
                data=daph,family=poisson)
> pmod2 <- glm(counts~foodlevel*species,
                data=daph,family=poisson)
> anova(pmod1,pmod2,test="Chisq")
```

Analysis of Deviance Table

Model 1: counts ~ foodlevel + species

Model 2: counts ~ foodlevel * species

	Resid.	Df	Resid.	Dev	Df	Deviance	P(> Chi)
1		9		6.1162			
2		8		6.0741	1	0.042071	0.8375

Why not the F -test?

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Remember that we did not estimate a variance σ^2 for the Poisson distribution.

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Example: *overdispersed Poisson*, also called *quasipoisson* GLM. Here, $\mathbb{E} Y_i = \mu_i$ but $\text{Var} Y_i = \phi \cdot \mu_i$ with the dispersion parameter $\phi > 1$.

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Since the dispersion parameter is estimated, one can apply an F approximation in the analysis of deviance.

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Example: *overdispersed Poisson*, also called *quasipoisson* GLM. Here, $\mathbb{E} Y_i = \mu_i$ but $\text{Var} Y_i = \phi \cdot \mu_i$ with the dispersion parameter $\phi > 1$.

This is often used to model the influence of unknown external factors.

Since the dispersion parameter is estimated, one can apply an F approximation in the analysis of deviance. But also χ^2 is still an option.

```
> qpmod1 <- glm(counts~foodlevel+species,data=daph,
                 family=quasipoisson)
> qpmod2 <- glm(counts~foodlevel*species,data=daph,
                 family=quasipoisson)
> anova(qpmod1,qpmod2,test="F")
```

Analysis of Deviance Table

Model 1: counts ~ foodlevel + species

Model 2: counts ~ foodlevel * species

	Resid. Df	Resid. Dev	Df	Deviance	F	Pr(>F)
1	9	6.1162				
2	8	6.0741	1	0.042071	0.0572	0.817

```
> anova(qpmod1, qpmod2, test="Chisq")
```

```
Analysis of Deviance Table
```

```
Model 1: counts ~ foodlevel + species
```

```
Model 2: counts ~ foodlevel * species
```

	Resid. Df	Resid. Dev	Df	Deviance	P(> Chi)
1	9	6.1162			
2	8	6.0741	1	0.042071	0.811

```
> expect <- predict(pmod1,type="response")
> sim <- rpois(12,expect)
> smod1 <- lm(sim~foodlevel+species,data=daph)
> smod2 <- lm(sim~foodlevel*species,data=daph)
> anova(smod1,smod2)
```

```

> expect <- predict(pmod1,type="response")
> sim <- rpois(12,expect)
> smod1 <- lm(sim~foodlevel+species,data=daph)
> smod2 <- lm(sim~foodlevel*species,data=daph)
> anova(smod1,smod2)

```

Analysis of Variance Table

Model 1: sim ~ foodlevel + species

Model 2: sim ~ foodlevel * species

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	9	1289.42				
2	8	109.33	1	1180.1	86.348	1.464e-05 ***

Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 1

What is the problem? Normal distribution assumption or additivity?

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How about a multiplicative linear model?

```
> expect <- predict(pmod1,type="response")
> sim <- rpois(12,expect)
> smod1 <- lm(log(sim)~foodlevel+species,data=daph)
> smod2 <- lm(log(sim)~foodlevel*species,data=daph)
> anova(smod1,smod2)
```

```
> expect <- predict(pmod1,type="response")
> sim <- rpois(12,expect)
> smod1 <- lm(log(sim)~foodlevel+species,data=daph)
> smod2 <- lm(log(sim)~foodlevel*species,data=daph)
> anova(smod1,smod2)
```

Analysis of Variance Table

Model 1: $\log(\text{sim}) \sim \text{foodlevel} + \text{species}$

Model 2: $\log(\text{sim}) \sim \text{foodlevel} * \text{species}$

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	9	0.19216				
2	8	0.19115	1	0.0010162	0.0425	0.8418

This solves the biggest problem, but what does the model say?

```
> lmod1 <- lm(log(counts)~foodlevel+species,data=daph)
[...]
```

Coefficients:

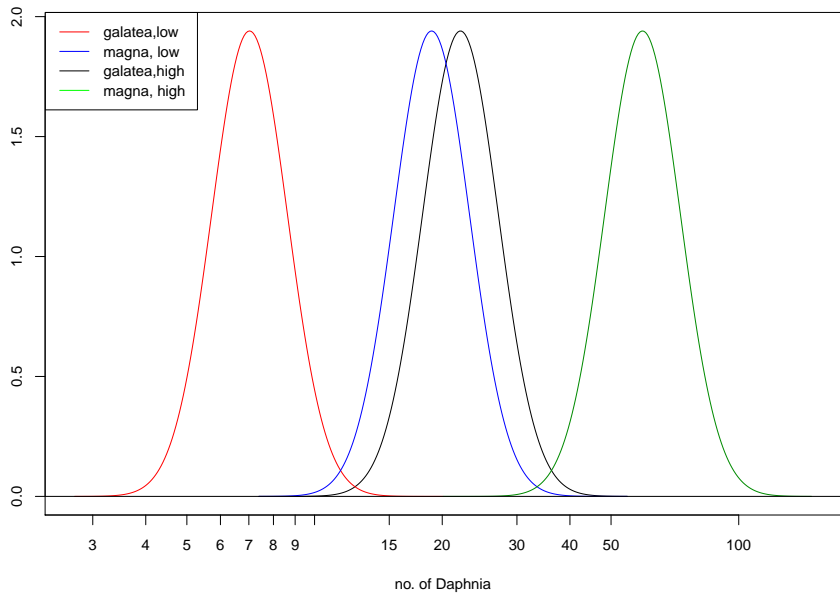
	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	3.0946	0.1028	30.104	2.41e-10	***
foodlevellow	-1.1450	0.1187	-9.646	4.83e-06	***
speciesmagna	0.9883	0.1187	8.326	1.61e-05	***

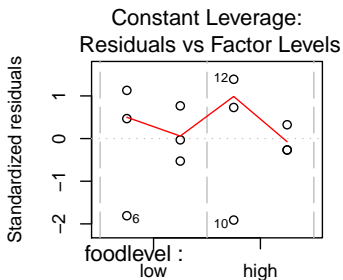
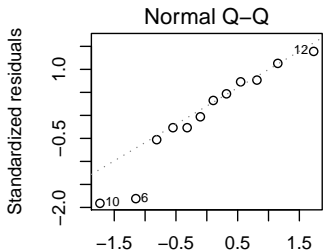
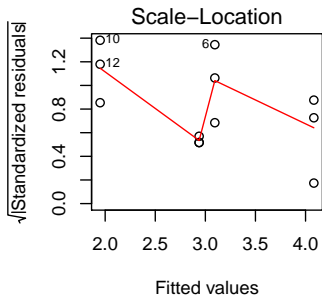
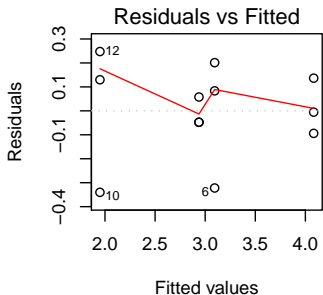
```
[...]
```

Residual standard error: 0.2056 on 9 degrees of freedom

```
[...]
```

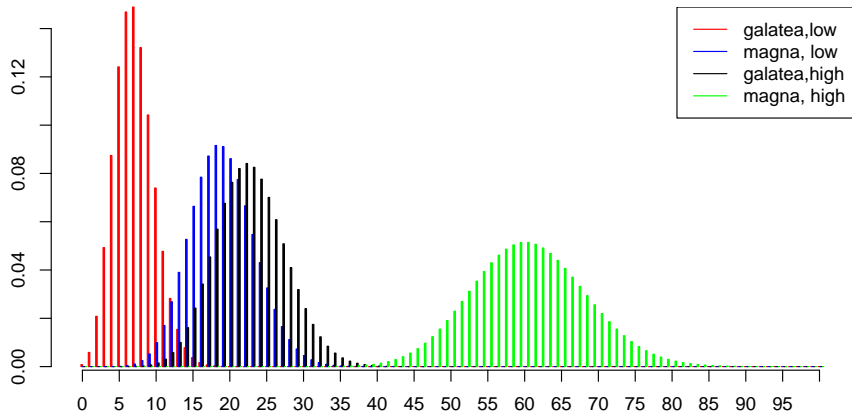
prediction of log-linear model

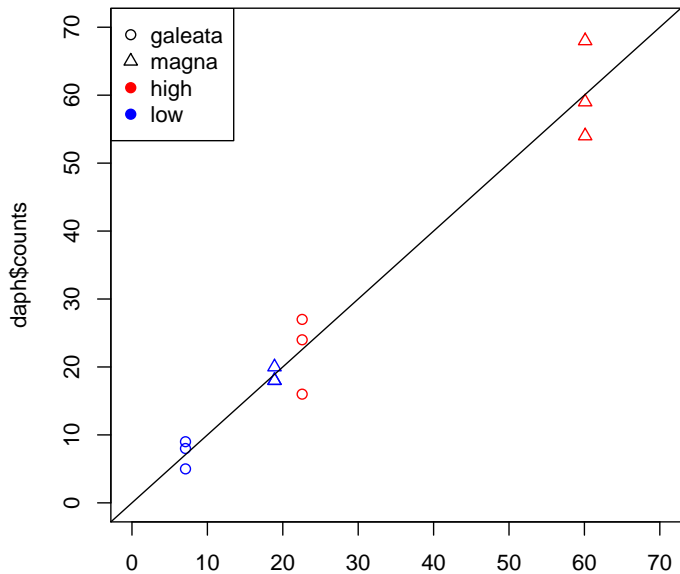





```
> summary(pmod1)
[.]
glm(formula = counts ~ foodlevel + species,
     family = poisson, data = daph)
[.]

              Estimate Std. Error z value Pr(>|z|)
(Intercept)    3.1166     0.1105  28.215 < 2e-16 ***
foodlevellow  -1.1567     0.1298  -8.910 < 2e-16 ***
speciesmagna   0.9794     0.1243   7.878 3.32e-15 ***
[.]
(Dispersion parameter for poisson family taken to be 1)
[.]
Residual deviance:  6.1162  on  9  degrees of freedom
AIC: 70.497
```





Since the variance is proportional to the expectation value in the Poisson model, usual residuals are not so informative.

Since the variance is proportional to the expectation value in the Poisson model, usual residuals are not so informative.

Instead use *deviance residuals*. Let d_i be the contribution of observation i (row i in the data table) to the Deviance, then the deviance residual of observation i is

$$\text{sign}(Y_i - \hat{\mu}_i) \cdot \sqrt{d_i}.$$

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The deviance residuals are the default residuals given by R for GLMs. They have similar properties as the standard residuals in the normal linear model.

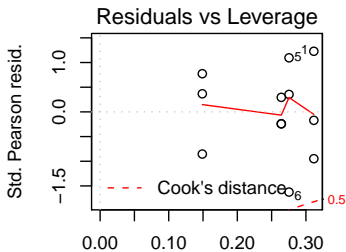
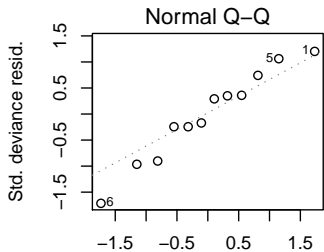
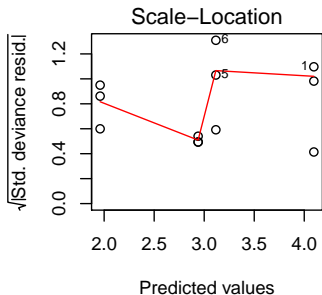
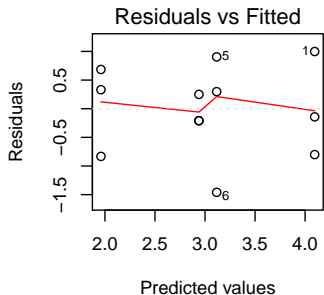
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Instead use *deviance residuals*. Let d_i be the contribution of observation i (row i in the data table) to the Deviance, then the deviance residual of observation i is

$$\text{sign}(Y_i - \hat{\mu}_i) \cdot \sqrt{d_i}.$$

The deviance residuals are the default residuals given by R for GLMs. They have similar properties as the standard residuals in the normal linear model.

In the following plot obtained with `plot(pmod1)` the word “residual” always refers to deviance residuals.



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Other GLMs

In the lecture about linear regression we analysed a data set to find out whether the county size (number of females living in a county) has an effect on the risk of dying by breast cancer. Since the response variable in this data set are deaths counts, it seems natural to fit a Poisson GLM.

```
> str(canc)
'data.frame': 301 obs. of 2 variables:
 $ deaths      : int  1 0 3 4 3 4 1 5 5 5 ...
 $ inhabitants: int  445 559 677 681 746 869 950 976 ...
```

First trial:

```
> mod0 <- glm(deaths~inhabitants,data=canc,family=poisson)
> summary(mod0)
```

Call:

```
glm(formula = deaths ~ inhabitants, family = poisson,
data = canc)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-13.8783	-2.6449	-0.8845	1.8160	6.9909

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	2.961e+00	1.320e-02	224.2	<2e-16	***
inhabitants	4.044e-05	3.374e-07	119.9	<2e-16	***

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

Before we complain about the large residual deviance... we ask ourselves whether this is a plausible model.

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Let D_i be the *expected* number of deaths in county i and S_i its size. Then the model assumes

$$\log(D_i) = a + b \cdot S_i$$

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this is not a plausible model.

Solution: take the log of S_i .

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or, equivalently,

$$D_i = e^{a+b \cdot \log(S_i)} = e^a \cdot (e^{\log(S_i)})^b = e^a \cdot S_i^b$$

If $b = 1$, then e^a is just the individual risk to die by breast cancer (during the time span of the survey).

```
> mod1 <- glm(deaths~log(inhabitants),data=canc,family=poisson)
> summary(mod1)
```

```
[..]
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -5.531496   0.093003  -59.48  <2e-16 ***
log(inhabitants) 0.988350   0.009406  105.08  <2e-16 ***
```

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

```
(Dispersion parameter for poisson family taken to be 1)
```

```
Null deviance: 12994.06  on 300  degrees of freedom
Residual deviance:   785.85  on 299  degrees of freedom
AIC: 2282.9
```

```
> mod1 <- glm(deaths~log(inhabitants),data=canc,family=poisson)
> summary(mod1)
```

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

```
(Dispersion parameter for poisson family taken to be 1)
```

```
Null deviance: 12994.06  on 300  degrees of freedom
Residual deviance:   785.85  on 299  degrees of freedom
AIC: 2282.9
```

Too much residual deviance for $df=299 \Rightarrow$ Let's allow for overdispersion!

```
> mod2 <- glm(deaths~log(inhabitants),data=canc,family=quasipoisson)
> summary(mod2)
[...]
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-5.53150	0.14865	-37.21	<2e-16	***
log(inhabitants)	0.98835	0.01503	65.75	<2e-16	***

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

```
(Dispersion parameter for quasipoisson family taken to be 2.554585)
```

```
Null deviance: 12994.06 on 300 degrees of freedom
Residual deviance: 785.85 on 299 degrees of freedom
```

```
> mod2 <- glm(deaths~log(inhabitants),data=canc,family=quasipoisson)
> summary(mod2)
[...]
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-5.53150	0.14865	-37.21	<2e-16	***
log(inhabitants)	0.98835	0.01503	65.75	<2e-16	***

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(Dispersion parameter for quasipoisson family taken to be 2.554585)

Null deviance: 12994.06 on 300 degrees of freedom
Residual deviance: 785.85 on 299 degrees of freedom

What does the highly significant p -value for $\log(\text{inhabitants})$ say?

```
> mod2 <- glm(deaths~log(inhabitants),data=canc,family=quasipoisson)
> summary(mod2)
[...]
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-5.53150	0.14865	-37.21	<2e-16	***
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(Dispersion parameter for quasipoisson family taken to be 2.554585)

Null deviance: 12994.06 on 300 degrees of freedom
 Residual deviance: 785.85 on 299 degrees of freedom

What does the highly significant p -value for $\log(\text{inhabitants})$ say?
 It says that the coefficient b is significantly different from 0.


```
> mod2 <- glm(deaths~log(inhabitants),data=canc,family=quasipoisson)
> summary(mod2)
[...]
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-5.53150	0.14865	-37.21	<2e-16	***
log(inhabitants)	0.98835	0.01503	65.75	<2e-16	***

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

(Dispersion parameter for quasipoisson family taken to be 2.554585)

Null deviance: 12994.06 on 300 degrees of freedom
 Residual deviance: 785.85 on 299 degrees of freedom

What does the highly significant p -value for $\log(\text{inhabitants})$ say?
 It says that the coefficient b is significantly different from 0.

But our question is rather whether b is significantly different from 1!

Trick: Fit a model

$$\log(D_i) = a + \log(S_i) + b \cdot \log(S_i)$$

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which is equivalent to

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Then the question is whether b is significantly different from 0.

Trick: Fit a model

$$\log(D_i) = a + \log(S_i) + b \cdot \log(S_i)$$

which is equivalent to

$$D_i = e^a \cdot S_i \cdot S_i^b.$$

Then the question is whether b is significantly different from 0.

in R: use the command `offset` to tell R not to estimate a coefficient for the first $\log(S_i)$

```
> mod3 <- glm(deaths~offset(log(inhabitants))+log(inhabitants),
              data=canc,family=quasipoisson)
> summary(mod3)
[...]
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-5.53150	0.14865	-37.212	<2e-16	***
log(inhabitants)	-0.01165	0.01503	-0.775	0.439	

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

(Dispersion parameter for quasipoisson family taken to be 2.554585)
```

```
> mod3 <- glm(deaths~offset(log(inhabitants))+log(inhabitants),  
              data=canc,family=quasipoisson)
```

```
> summary(mod3)
```

```
[...]
```

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-5.53150	0.14865	-37.212	<2e-16	***
log(inhabitants)	-0.01165	0.01503	-0.775	0.439	

```
---
```

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

```
(Dispersion parameter for quasipoisson family taken to be 2.554585)
```

Thus, the expected number of deaths seems to be just proportional to the number of inhabitants. No significant dependence of the death rate on the county size was found.

Another way of testing this:

```
> mod4 <- glm(deaths~offset(log(inhabitants)),
              data=canc,family=quasipoisson)
```

```
> anova(mod4,mod3,test="F")
```

Analysis of Deviance Table

Model 1:

```
deaths ~ offset(log(inhabitants))
```

Model 2:

```
deaths ~ offset(log(inhabitants)) + log(inhabitants)
```

	Resid.	Df	Resid.	Dev	Df	Deviance	F	Pr(>F)
1		300		787.38				
2		299		785.85	1	1.5315	0.5995	0.4394

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```
> fly <- read.csv("Flies_AnaCatalan.csv",h=T,sep=";")
> fly
```

	odorant	resp	air	PI	sex	day	species
1	C02	1	29	NA	males	1	mel
2	C02	2	28	NA	males	1	mel
3	C02	1	25	NA	males	1	mel
.
.
.
753	30C02	4	7	NA	females	2	vir
754	30C02	6	12	NA	females	2	vir
755	30C02	6	11	NA	females	2	vir
756	30C02	6	15	NA	females	2	vir

```
> str(fly)
'data.frame': 756 obs. of 7 variables:
 $ odorant: Factor w/ 3 levels "30CO2","CO2",...: 2 2 2 2 ...
 $ resp   : int  1 2 1 2 5 4 9 5 5 11 ...
 $ air    : int  29 28 25 17 36 42 38 13 19 25 ...
 $ PI     : logi  NA NA NA NA NA NA ...
 $ sex    : Factor w/ 2 levels "females","males": 2 2 2 2 ...
 $ day    : int  1 1 1 1 1 1 2 2 2 2 ...
 $ species: Factor w/ 11 levels "ana","atr","ere",...: 5 5
```

Model

In experiment i (row i of the data table) there are n_i flies. Each of these flies decided independently of all other to go to the odorant with probability p_i and, thus, to go to the fresh air with probability $(1 - p_i)$.

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$$Y_i \sim \text{bin}(n_i, p_i)$$
$$\Pr(Y_i = k) = \binom{n_i}{k} \cdot p_i^k \cdot (1 - p_i)^{n_i - k}$$

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$$\begin{aligned} Y_i &\sim \text{bin}(n_i, p_i) \\ \Pr(Y_i = k) &= \binom{n_i}{k} \cdot p_i^k \cdot (1 - p_i)^{n_i - k} \\ \mathbb{E} Y_i &= n_i \cdot p_i \end{aligned}$$

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Model

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Thus, the number Y_i of flies which went to the odorant is binomially distributed:

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How does p_i depend on the odorant and on the species?

Binomial GLM with logit link

Similar as in Poisson GLMs we assume:

$$\ell(\boldsymbol{p}_i) = \eta_i = b_0 + b_1 \cdot X_{1,i} + \dots + b_k \cdot X_{k,i}$$

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The default link of the Binomial GLM is the logit link:

$$\eta = \text{logit}(p) = \log(p/(1 - p))$$

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Its inverse is the logistic function

$$p = \frac{1}{1 + e^{-\eta}}$$

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The default link of the Binomial GLM is the logit link:

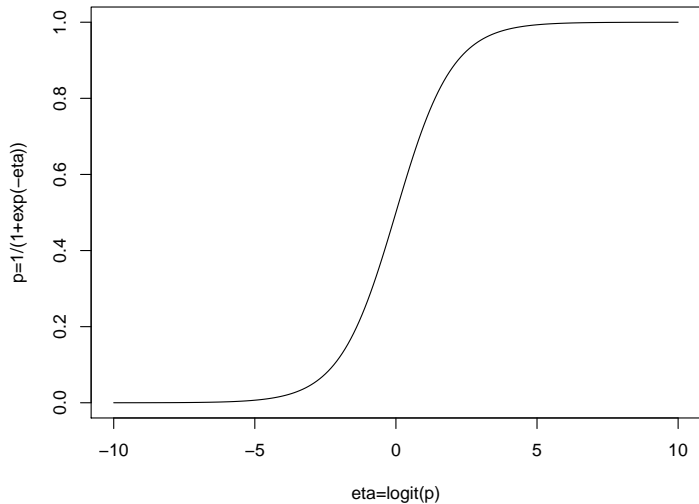
$$\eta = \text{logit}(p) = \log(p/(1 - p))$$

Its inverse is the logistic function

$$p = \frac{1}{1 + e^{-\eta}}$$

Binomial GLM with the logit link is also called *logistic regression*.

The logistic function $1/(1+\exp(-\eta))$



Likelihood and Deviance

If $\hat{p}_1, \dots, \hat{p}_k$ are the estimated p_i in our model, then the likelihood of the fitted parameters is

$$L(\hat{p}) = \binom{n_1}{Y_1} \hat{p}_1^{Y_1} (1 - \hat{p}_1)^{n_1 - Y_1} \cdot \binom{n_2}{Y_2} \hat{p}_2^{Y_2} (1 - \hat{p}_2)^{n_2 - Y_2} \dots \\ \dots \binom{n_k}{Y_k} \hat{p}_k^{Y_k} (1 - \hat{p}_k)^{n_k - Y_k}$$

Using this likelihood, the *deviance* and the deviance residuals are defined like in the Poisson GLM.

Analysis of deviance and overdispersion

Note that, like in the Poisson model, $\text{Var} Y_i = n_i \cdot p_i \cdot (1 - p_i)$ is fixed for given $\mathbb{E} Y_i = n_i p_i$. Thus, the χ^2 approximation should be used in the analysis of deviance.

Analysis of deviance and overdispersion

Note that, like in the Poisson model, $\text{Var} Y_i = n_i \cdot p_i \cdot (1 - p_i)$ is fixed for given $\mathbb{E} Y_i = n_i p_i$. Thus, the χ^2 approximation should be used in the analysis of deviance.

There is an overdispersed binomial GLM (available in R with the option `family=quasibinomial`) with an additional dispersion parameter. For these models one can use both χ^2 approximation and F approximations in analyses of deviance.

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```
> fly <- read.csv("Flies_AnaCatalan.csv",h=T,sep=";")
> fly
```

	odorant	resp	air	PI	sex	day	species
1	C02	1	29	NA	males	1	mel
2	C02	2	28	NA	males	1	mel
3	C02	1	25	NA	males	1	mel
.
.
.
753	30C02	4	7	NA	females	2	vir
754	30C02	6	12	NA	females	2	vir
755	30C02	6	11	NA	females	2	vir
756	30C02	6	15	NA	females	2	vir

```
> modelbin <- glm(cbind(resp,air)~(sex+species)*odorant+day,
+                 subset=odorant!="oct",
+                 data=fly,family=binomial)
> summary(modelbin)
```

Call:

```
glm(formula = cbind(resp, air) ~ (sex + species) * odorant +
     day, family = binomial, data = fly,
     subset = odorant != "oct")
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-3.3735	-0.9693	-0.1187	0.7240	4.4994

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-1.376503	0.123901	-11.110	< 2e-16	***
sexmales	0.131066	0.053810	2.436	0.014863	*
speciesatr	0.227528	0.145096	1.568	0.116854	
speciesere	0.057917	0.150061	0.386	0.699528	
speciesmau	0.141718	0.163017	0.869	0.384658	

speciesmel	-1.128202	0.164920	-6.841	7.87e-12	***
speciespse	1.318299	0.143279	9.201	< 2e-16	***
speciessec	-0.518238	0.143658	-3.607	0.000309	***
speciessim	0.427407	0.136345	3.135	0.001720	**
speciestei	-0.266130	0.144181	-1.846	0.064921	.
speciesvir	0.424609	0.173881	2.442	0.014608	*
speciesyak	-0.454361	0.170760	-2.661	0.007795	**
odorantC02	-0.922118	0.171020	-5.392	6.97e-08	***
day	-0.008059	0.014922	-0.540	0.589129	
sexmales:odorantC02	-0.023450	0.067791	-0.346	0.729408	
speciesatr:odorantC02	1.180104	0.194524	6.067	1.31e-09	***
speciesere:odorantC02	1.473309	0.200023	7.366	1.76e-13	***
speciesmau:odorantC02	1.214336	0.222429	5.459	4.78e-08	***
speciesmel:odorantC02	1.530291	0.219269	6.979	2.97e-12	***
speciespse:odorantC02	0.384300	0.195086	1.970	0.048849	*
speciessec:odorantC02	2.046612	0.194380	10.529	< 2e-16	***
speciessim:odorantC02	1.369519	0.189228	7.237	4.57e-13	***

speciestei:odorantC02	1.033078	0.199579	5.176	2.26e-07	***
speciesvir:odorantC02	1.262574	0.225086	5.609	2.03e-08	***
speciesyak:odorantC02	1.919994	0.215587	8.906	< 2e-16	***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2429.1 on 663 degrees of freedom
Residual deviance: 1187.1 on 639 degrees of freedom
AIC: 3430.7

Number of Fisher Scoring iterations: 4

A residual deviance of 1187.1 on 639 degrees of freedom is very high and indicates that the model parameters cannot fully explain the data.

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⇒ Fit an overdispersed model!

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⇒ Fit an overdispersed model!

There is a price we have to pay for overdispersion: Since it is not a clearly defined distribution, AIC is not available for model selection.

A residual deviance of 1187.1 on 639 degrees of freedom is very high and indicates that the model parameters cannot fully explain the data.

⇒ Fit an overdispersed model!

There is a price we have to pay for overdispersion: Since it is not a clearly defined distribution, AIC is not available for model selection.

Select parameters

1. that seem important to you from the biological context
2. or have low p -values.

```
> model <- glm(cbind(resp,air)~(sex+species)*odorant+day,
+             subset=odorant!="oct",
+             data=fly,family=quasibinomial)
> drop1(model,test="F")
Single term deletions
```

Model:

```
cbind(resp, air) ~ (sex + species) * odorant + day
```

	Df	Deviance	F value	Pr(F)
<none>		1187.1		
day	1	1187.3	0.1571	0.6920
sex:odorant	1	1187.2	0.0644	0.7997
species:odorant	10	1431.1	13.1365	<2e-16 ***

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

```
> model2 <- update(model, ~.-day)
```

```
> drop1(model2, test="F")
```

```
Single term deletions
```

```
Model:
```

```
cbind(resp, air) ~ sex + species + odorant + sex:odorant
```

	Df	Deviance	F value	Pr(F)
<none>		1187.3		
sex:odorant	1	1187.5	0.0673	0.7953
species:odorant	10	1432.6	13.2215	<2e-16 ***

```
---
```

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

```
> model3 <- update(model2, ~.-sex:odorant)
```

```
> drop1(model3, test="F")
```

```
Single term deletions
```

```
Model:
```

```
cbind(resp, air) ~ sex + species + odorant + species:odorant
```

	Df	Deviance	F value	Pr(F)	
<none>		1187.5			
sex	1	1200.0	6.7785	0.00944	**
species:odorant	10	1432.7	13.2366	< 2e-16	***

```
---
```

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

```
> model4 <- glm(cbind(resp,air)~sex+species+odorant
+               +species:odorant+species:sex,
+               subset=odorant!="oct",
+               data=fly,family=quasibinomial)
> anova(model3,model4,test="F")
```

Analysis of Deviance Table

Model 1: cbind(resp, air) ~ sex + species + odorant + spe

Model 2: cbind(resp, air) ~ sex + species + odorant + spe
species:sex

	Resid. Df	Resid. Dev	Df	Deviance	F	Pr(>F)
1	641	1187.5				
2	631	1157.1	10	30.395	1.7232	0.072 .

Signif. codes: 0 *** 0.001 ** 0.01 * 0.05 . 0.1 1

```
> drop1(model4, test="F")
```

```
Single term deletions
```

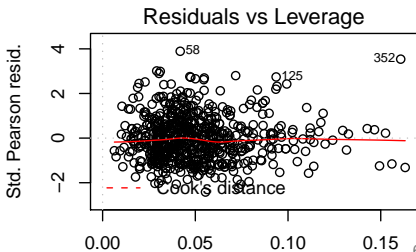
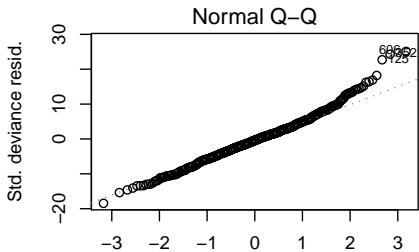
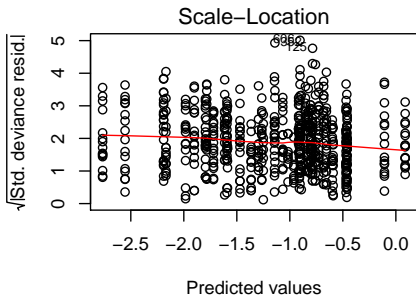
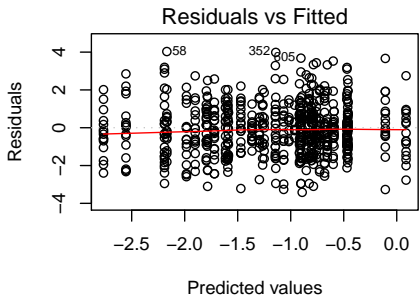
```
Model:
```

```
cbind(resp, air) ~ sex + species + odorant + species:odorant
                  species:sex
```

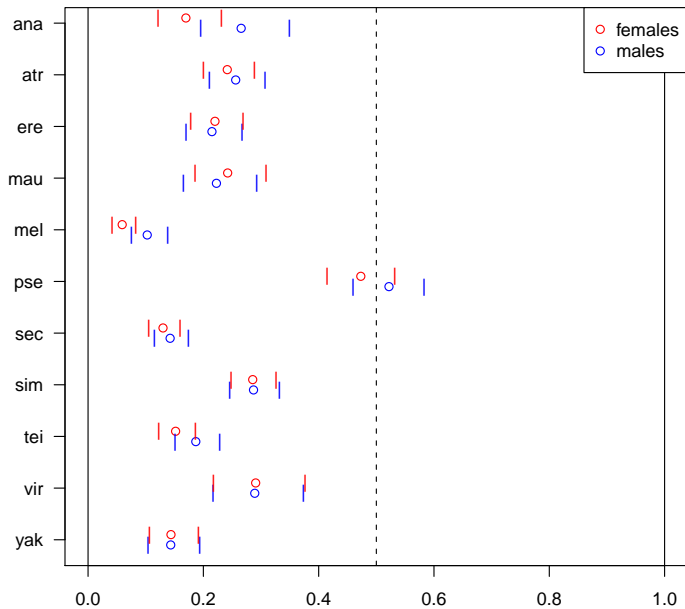
	Df	Deviance	F value	Pr(F)
<none>		1157.1		
species:odorant	10	1402.9	13.4043	< 2e-16 ***
sex:species	10	1187.5	1.6575	0.08708 .

```
---
```

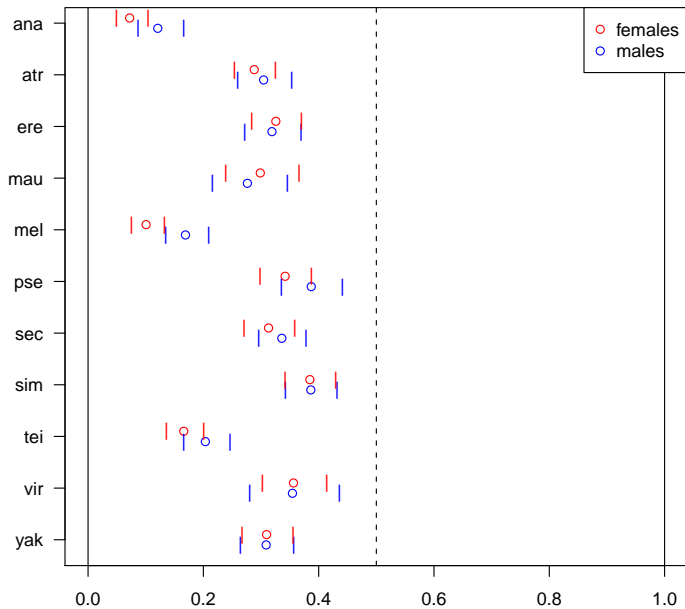
```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**estimated probability of choosing 30CO2
with 95% confidence bands**



estimated probability of choosing CO2 with 95% confidence bands



```
> newdata <- data.frame(species=rep(levels(fly$species),4),
+                        odorant=rep(levels(fly$odorant)[1:2],rep(22,2)),
+                        sex=rep(rep(levels(fly$sex),2),rep(11,4)))
```

```
> newdata
```

	species	odorant	sex
1	ana	30C02	females
2	atr	30C02	females
3	ere	30C02	females
4	mau	30C02	females
5	mel	30C02	females
6	pse	30C02	females
7	sec	30C02	females
8	sim	30C02	females
9	tei	30C02	females
10	vir	30C02	females
11	yak	30C02	females
12	ana	30C02	males
13	atr	30C02	males
14	ere	30C02	males
15	mau	30C02	males
16	mel	30C02	males

23	ana	C02 females
24	atr	C02 females
25	ere	C02 females
26	mau	C02 females
27	mel	C02 females
28	pse	C02 females
29	sec	C02 females
30	sim	C02 females
31	tei	C02 females
32	vir	C02 females
33	yak	C02 females
34	ana	C02 males
35	atr	C02 males
36	ere	C02 males
37	mau	C02 males
38	mel	C02 males
39	pse	C02 males
40	sec	C02 males
41	sim	C02 males
42	tei	C02 males
43	vir	C02 males

```
> predict(model4,newdata,type="link")
```

1	2	3	4	5	
-1.58789551	-1.14469372	-1.26487696	-1.14101650	-2.76586374	-0.1077
7	8	9	10	11	
-1.90097360	-0.91699408	-1.72012424	-0.89185179	-1.78389658	-1.0172
13	14	15	16	17	
-1.06650110	-1.29566564	-1.25030454	-2.16842944	0.08781449	-1.7959
19	20	21	22	23	
-0.91001993	-1.47044203	-0.89969326	-1.78744176	-2.55428808	-0.9039
25	26	27	28	29	
-0.72774118	-0.85332683	-2.19052045	-0.65510800	-0.78579246	-0.4694
31	32	33	34	35	
-1.61457993	-0.59147161	-0.80167681	-1.98367468	-0.82573216	-0.7585
37	38	39	40	41	
-0.96261487	-1.59308615	-0.45953795	-0.68077358	-0.46245135	-1.3648
43	44				
-0.59931308	-0.80522198				

```
> predict(model4,newdata,type="response")
```

	1	2	3	4	5	6
0.16968019	0.24145963	0.22013549	0.24213378	0.05919695	0.47308714	0
8	9	10	11	12	13	
0.28557077	0.15185516	0.29072783	0.14382265	0.26555715	0.25606905	0
15	16	17	18	19	20	
0.22264743	0.10262158	0.52193952	0.14234421	0.28699576	0.18687544	0
22	23	24	25	26	27	
0.14338666	0.07213894	0.28824462	0.32569061	0.29873544	0.10060499	0
29	30	31	32	33	34	
0.31307282	0.38475223	0.16595372	0.35629727	0.30966695	0.12092766	0
36	37	38	39	40	41	
0.31896554	0.27635496	0.16895014	0.38709544	0.33608867	0.38640446	0
43	44					
0.35450087	0.30890960					

Compute an approx. 95% confidence range

```
> case <- data.frame(species="mel",odorant="CO2",sex="males")
> (pred <- predict(model4,case,type="link",se.fit=TRUE) )
$fit
-1.593086
$se.fit
[1] 0.1327248
$residual.scale
[1] 1.328106
> invlink <- function(x) {      ## inverse link function
+   1/(1+exp(-x))
+ }
> invlink(pred$fit)           ## prediction
0.1689501
> invlink(pred$fit-2*pred$se.fit)  ## lower bound
0.1348738
> invlink(pred$fit+2*pred$se.fit)  ## upper bound
0.2095506
```


This can be done simultaneously for a whole data frame (e.g. `newdata`) instead just for one on case (in our example `meI/CO2/males`)

This can be done simultaneously for a whole data frame (e.g. newdata) instead just for one on case (in our example mel/CO2/males)

Should be done on the linear predictor (“link”) scale and not on the response scale because it is based on a normal distribution approximation, which is only (more or less) valid on the linear predictor scale. (Remember: for a normal distribution, $> 95\%$ are within the 2σ -bounds around the mean.)

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Sex ratio in ants

Other GLMs



S. Foitzik, I.M. Kureck, M.H. Rüger, D. Metzler (2010)
Alternative reproductive tactics and the influence of local
competition on sex allocation in the ant *Hypoponera opacior*.
Behavioral Ecology and Sociobiology, to appear.

How does the ratio of queens and males produced by an ant
nest depend on the nest size?

- ▶ Winged sexuals were observed in June, unwinged sexuals in August.
- ▶ New queens and workers have more genetic material in common than new males and workers.
- ▶ Queens are larger than males and thus more costly to produce.
- ▶ Other factors: local resource competition, local mate competition...

Variables in the ants data set.

Nest.size number of workers in the nest

Puppen pupae produced by the nest

New.Males new males produced by the nest

New.Queens new queens produced by the nest

month 6=June, 8=August

(Many more variables in full dataset)

```
> str(ants)
'data.frame': 229 obs. of 5 variables:
 $ Puppen      : int  71 16 7 6 12 13 330 12 180 0 ...
 $ Nest.size   : int  39 6 5 2 5 4 18 9 47 10 ...
 $ New.Males   : int  0 1 3 0 0 0 2 2 0 0 ...
 $ New.Queens  : int  1 3 9 0 2 0 2 1 0 0 ...
 $ month       : int  6 6 6 6 6 6 6 6 6 6 ...
> attach(ants)
> productivity <- ( Puppen + New.Males +
                   New.Queens )/ (Nest.size)
```

```

> M0 <- glm(cbind(New.Queens,New.Males)~(as.factor(month)
+           +Nest.size+productivity)^2,family=binomial)
> summary(M0)
[...]
```

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-0.428	0.3175	-1.3	0.1776	
as.factor(month)8	-0.205	0.3664	-0.5	0.5757	
Nest.size	0.066	0.0177	3.7	0.0001	***
productivity	0.002	0.0178	0.1	0.8670	
as.factor(month)8:Nest.size	-0.030	0.0171	-1.8	0.0710	.
as.factor(month)8:productivity	-0.016	0.0165	-0.9	0.3225	
Nest.size:productivity	-0.000	0.0007	-0.5	0.5988	

```

[..]
Null deviance: 494.61 on 138 degrees of freedom
Residual deviance: 354.96 on 132 degrees of freedom
(10 observations deleted due to missingness)
AIC: 529.5
```


We already have lots of parameters and interactions in the model, but the residual deviance of 354.96 is still too high for 132 degrees of freedom.

We already have lots of parameters and interactions in the model, but the residual deviance of 354.96 is still too high for 132 degrees of freedom.

⇒ Use *overdispersed* binomial (quasibinomial).

```

> M1 <- glm(cbind(New.Queens,New.Males)~(as.factor(month)
+       +Nest.size+productivity)^2,family=quasibinomial)
> summary(M1)
[..]

```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-0.4281	0.470	-0.9	0.36
as.factor(month)8	-0.2050	0.542	-0.3	0.70
Nest.size	0.0667	0.026	2.5	0.01 *
productivity	0.0029	0.026	0.1	0.91
as.factor(month)8:Nest.size	-0.0309	0.025	-1.2	0.22
as.factor(month)8:productivity	-0.0164	0.024	-0.6	0.50
Nest.size:productivity	-0.0003	0.001	-0.3	0.72

```

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

(Dispersion parameter for quasibinomial family 2.190267)

Null deviance: 494.61  on 138  degrees of freedom
Residual deviance: 354.96  on 132  degrees of freedom
(10 observations deleted due to missingness)
AIC: NA

```

- ▶ Less significance now.
- ▶ Residual deviance still the same, but no reason to worry for overdispersed models
- ▶ AIC not available anymore; that's a real pity!

```
> drop1(M1,test="F")  
Single term deletions
```

Model:

```
cbind(New.Queens, New.Males) ~ (as.factor(month)  
+ Nest.size + productivity)^2
```

	Df	Deviance	F value	Pr(F)
<none>		354.96		
as.factor(month):Nest.size	1	358.39	1.2754	0.2608
as.factor(month):productivity	1	355.94	0.3642	0.5472
Nest.size:productivity	1	355.24	0.1035	0.7482

Model selection when AIC is not available.

- ▶ Apply backward model selection strategy: apply drop1 and remove the variable with the highest p-value. Apply drop1 on the reduced model and repeat this again and again until you only variables are left which are significant or almost significant.
- ▶ Variables will not be removed if they are involved in interactions, because drop1 won't show those variables.
- ▶ Do not remove a variable if there is a good biological reason why it should be in the model.

```
> M2 <- update(M1, ~.-as.factor(month):productivity)
```

```
> drop1(M2, test="F")
```

Single term deletions

Model:

```
cbind(New.Queens, New.Males) ~ as.factor(month)
+ Nest.size + productivity + as.factor(month):Nest.size
+ Nest.size:productivity
```

	Df	Deviance	F value	Pr(F)
<none>		355.94		
as.factor(month):Nest.size	1	358.86	1.0911	0.2981
Nest.size:productivity	1	355.96	0.0067	0.9349

```
> M3 <- update(M2, ~.-Nest.size:productivity)
> drop1(M3, test="F")
```

Single term deletions

Model:

```
cbind(New.Queens, New.Males) ~ as.factor(month) +
  Nest.size + productivity +
  as.factor(month):Nest.size
```

	Df	Deviance	F value	Pr(F)
<none>		355.96		
productivity	1	358.57	0.9832	0.3232
as.factor(month):Nest.size	1	359.40	1.2952	0.2571


```
> M4 <- update(M3, ~.-productivity )
> drop1(M4, test="F")
Single term deletions
```

Model:

```
cbind(New.Queens, New.Males) ~ as.factor(month) +
  Nest.size + as.factor(month):Nest.size
```

	Df	Deviance	F value	Pr(F)
<none>		358.57		
as.factor(month):Nest.size	1	360.07	0.5626	0.4545

```
> M5 <- update(M4, ~.-as.factor(month):Nest.size)
```

```
> drop1(M5, test="F")
```

Single term deletions

Model:

```
cbind(New.Queens, New.Males) ~ as.factor(month) + Nest.size
```

	Df	Deviance	F value	Pr(F)	
<none>		360.07			
as.factor(month)	1	399.32	14.828	0.0001806	***
Nest.size	1	417.47	21.684	7.559e-06	***

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

```
> summary(M5)
```

Call:

```
glm(formula = cbind(New.Queens, New.Males) ~ as.factor(month) +  
     Nest.size, family = quasibinomial)
```

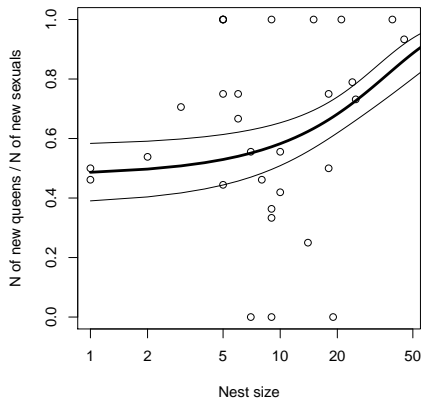
Deviance Residuals:

Min	1Q	Median	3Q	Max
-3.5049	-0.8569	0.0000	0.3521	4.2843

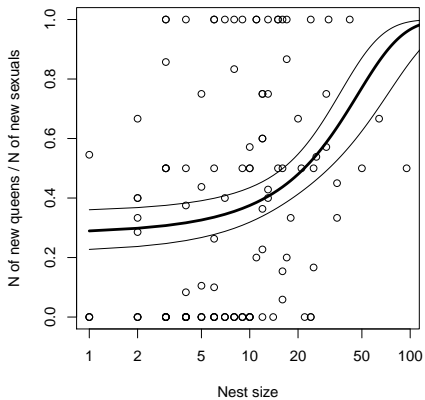
Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	-0.156142	0.236048	-0.661	0.509	
as.factor(month)8	-0.839253	0.202793	-4.138	6.10e-05	***
Nest.size	0.045656	0.009749	4.683	6.76e-06	***

June



August



```
plot(Nest.size[month==6],  
     New.Queens[month==6]/(New.Males[month==6]+New.Queens[month==6]),  
     main="June", log="x", xlab="Nest size",  
     ylab="N of new queens / N of new sexuals")  
  
hypotheticaljune <- data.frame(month=6,Nest.size=0:200)  
  
pred <- predict(M5,hypotheticaljune,type="link",se.fit=TRUE)  
  
lines(0:200,1/(1+exp(-pred$fit)),lwd=3)  
  
lines(0:200,1/(1+exp(-(pred$fit+2*pred$se.fit))))  
  
lines(0:200,1/(1+exp(-(pred$fit-2*pred$se.fit))))
```

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GLMs and their links (canonical links first)

Poisson $\log(\mu)$, μ , $\sqrt{\mu}$

binomial logit, probit, cloglog

gaussian μ

Gamma $-1/\mu$, μ , $\log(\mu)$

inverse gaussian $-2/\mu^2$

Also interesting: **negative binomial** as alternative to overdispersed Poisson.