GLM for count data: Poisson regression

Types of response variable

- Gaussian: `lm`

Types of response variable

- Gaussian: `lm`
- Bernouilli / Binomial: `glm` (family `binomial / quasibinomial`)

Types of response variable

- Gaussian: `lm`
- Bernouilli / Binomial: `glm` (family `binomial / quasibinomial`)
- Counts: `glm` (family `poisson / quasipoisson`)

Poisson regression

- Response variable: Counts (0, 1, 2, 3...) - discrete

Then

$$log(N) = a + bx$$
$$N = e^{a+bx}$$

Poisson regression

- Response variable: Counts (0, 1, 2, 3...) - discrete
- Link function: `log`

Then

$$log(N) = a + bx$$
$$N = e^{a+bx}$$

Example dataset: Seedling counts in quadrats

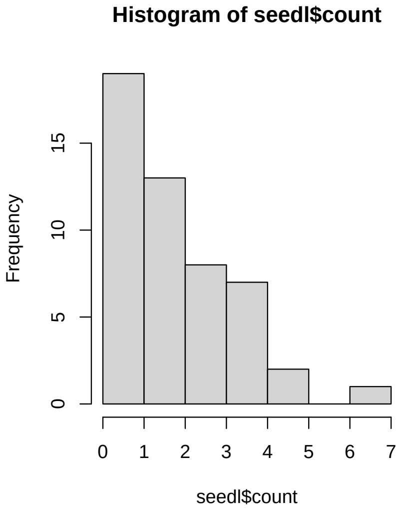
```r
seedl <- read.csv("data/seedlings.csv")
```

```
       X             count          row          col          l
 Min.   : 1.00   Min.   :0.00   Min.   :1   Min.   : 1.0   Min.
 1st Qu.:13.25   1st Qu.:1.00   1st Qu.:2   1st Qu.: 3.0   1st Q
 Median :25.50   Median :2.00   Median :3   Median : 5.5   Media
 Mean   :25.50   Mean   :2.14   Mean   :3   Mean   : 5.5   Mean
 3rd Qu.:37.75   3rd Qu.:3.00   3rd Qu.:4   3rd Qu.: 8.0   3rd Q
 Max.   :50.00   Max.   :7.00   Max.   :5   Max.   :10.0   Max.
      area
 Min.   :0.25
 1st Qu.:0.25
 Median :0.50
 Mean   :0.62
 3rd Qu.:1.00
 Max.   :1.00
```

EDA

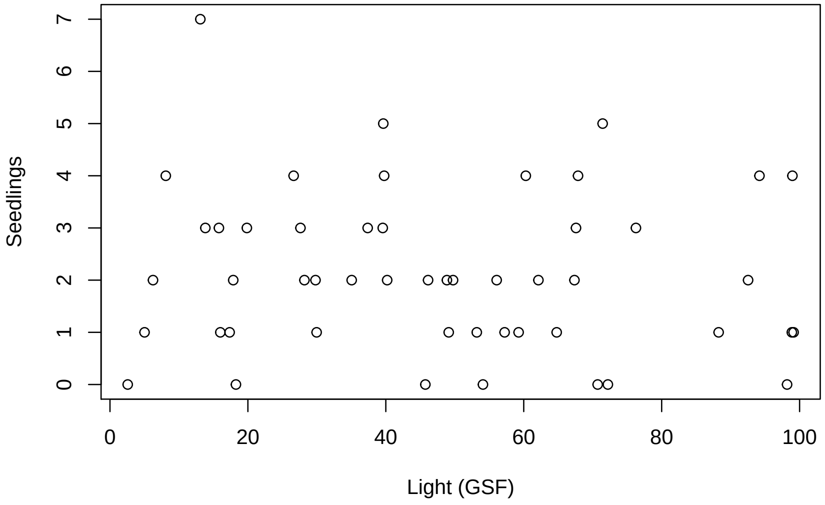
```
table(seedl$count)
```

```

 0  1  2  3  4  5  7
 7 12 13  8  7  2  1
```



Q: Relationship between Nseedlings and light?

```
plot(seedl$light, seedl$count, xlab = "Light (GSF)", ylab = "See
```



Let's fit model (Poisson regression)

```r
seedl.glm <- glm(count ~ light, data = seedl, family = poisson)
summary(seedl.glm)
```

```
Call:
glm(formula = count ~ light, family = poisson, data = seedl)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.1906  -0.8466  -0.1110   0.5220   2.4577

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.881805   0.188892   4.668 3.04e-06 ***
light       -0.002576   0.003528  -0.730    0.465
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 63.029  on 49  degrees of freedom
Residual deviance: 62.492  on 48  degrees of freedom
AIC: 182.03

Number of Fisher Scoring iterations: 5
```

Interpreting Poisson regression output

Parameter estimates (log scale):

```r
coef(seedl.glm)
```

```
 (Intercept)        light 
 0.881805022 -0.002575656 
```

We need to back-transform: apply the inverse of the logarithm

```r
exp(coef(seedl.glm))
```

```
(Intercept)       light 
  2.4152554   0.9974277 
```

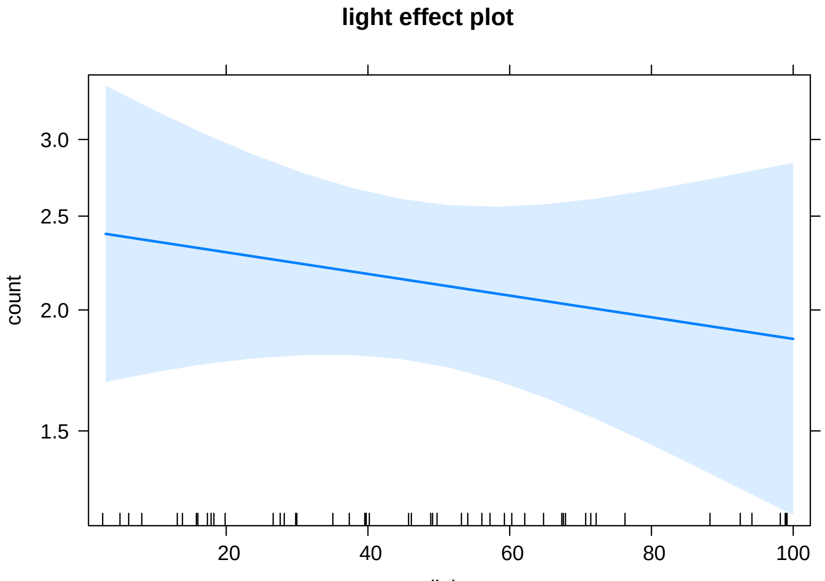
Using effects package

```r
summary(allEffects(seedl.glm))
```

```
 model: count ~ light

 light effect
light
       3       30       50       70      100
2.396665 2.235657 2.123408 2.016794 1.866826

 Lower 95 Percent Confidence Limits
light
       3       30       50       70      100
1.684579 1.795202 1.753373 1.567785 1.228247

 Upper 95 Percent Confidence Limits
light
       3       30       50       70      100
3.409754 2.784179 2.571535 2.594398 2.837408
```

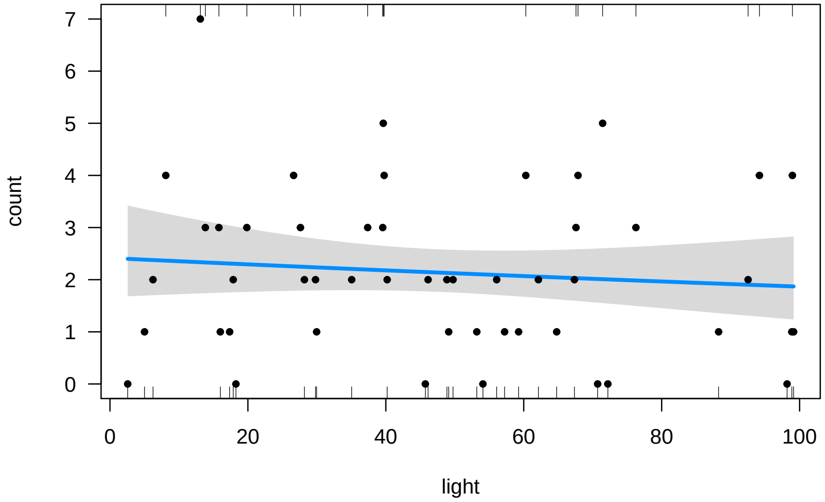
So what's the relationship between Nseedlings and light?

```
plot(allEffects(seedl.glm))
```



Using visreg

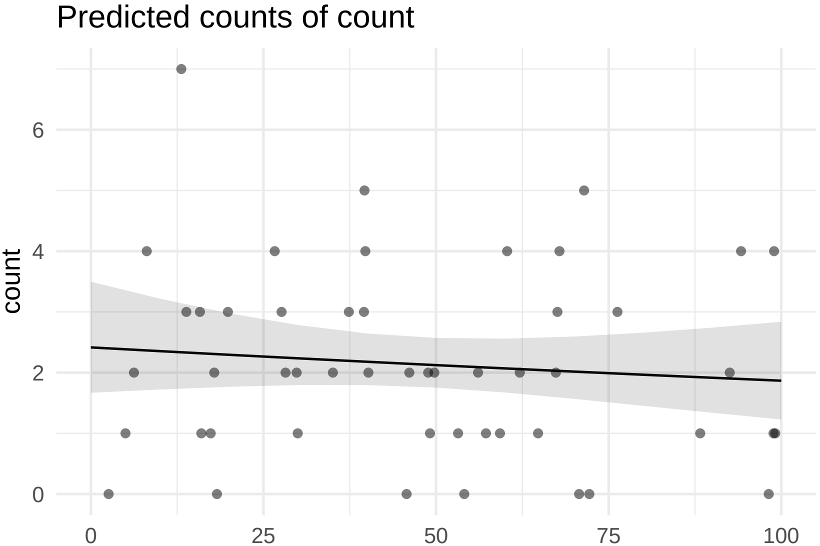
```
visreg(seedl.glm, scale = "response", ylim = c(0, 7))
points(count ~ light, data = seedl, pch = 20)
```



Using sjPlot

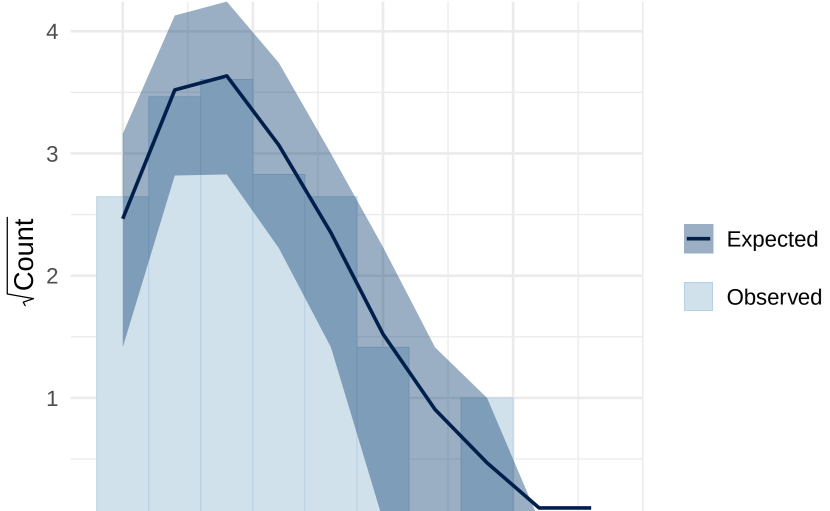
```r
sjPlot::plot_model(seedl.glm, type = "eff", show.data = TRUE)
```

```
$light
```

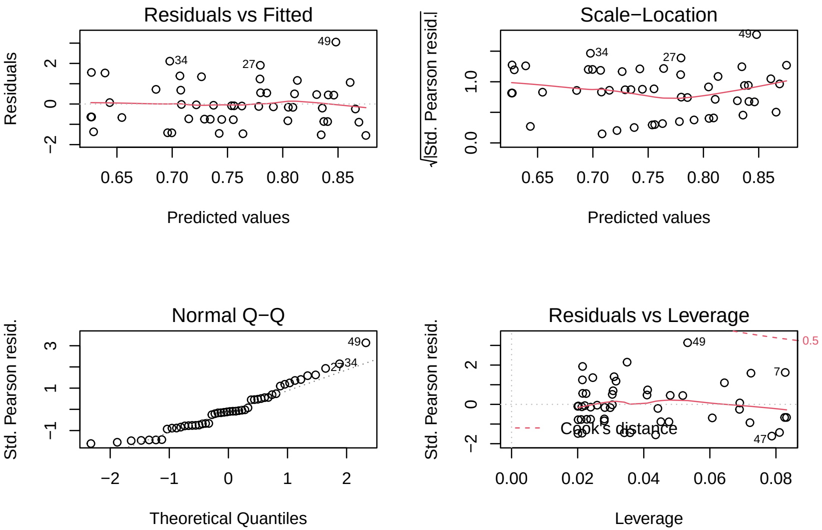


Calibration plot with count data: rootograms

```r
sims <- simulate(seedl.glm, nsim = 100)
yrep <- t(as.matrix(sims))
bayesplot::ppc_rootogram(seedl$count, yrep)
```



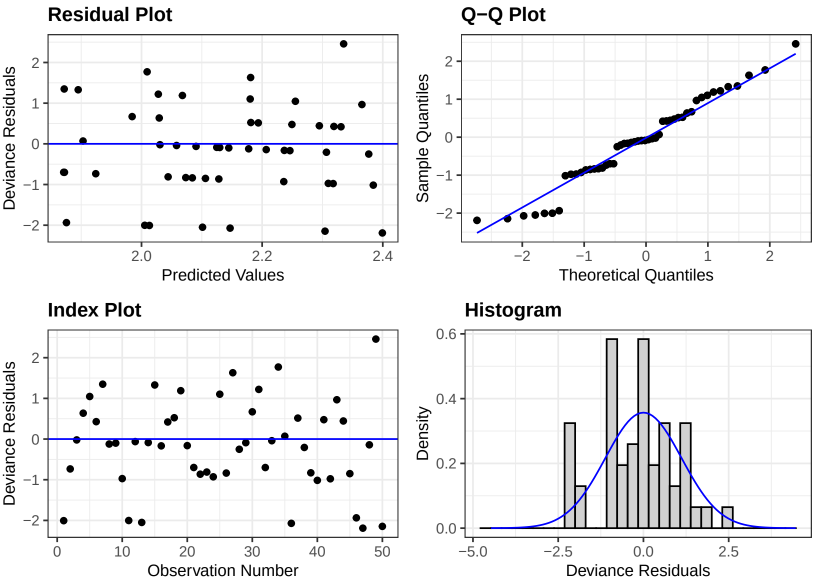
Poisson regression: model checking




```
null device
          1
```

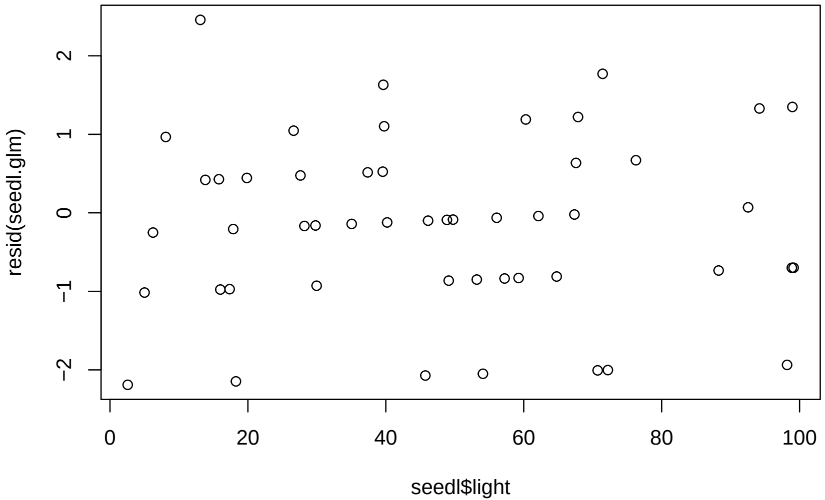
Poisson regression: model checking

```
ggResidpanel::resid_panel(seedl.glm)
```



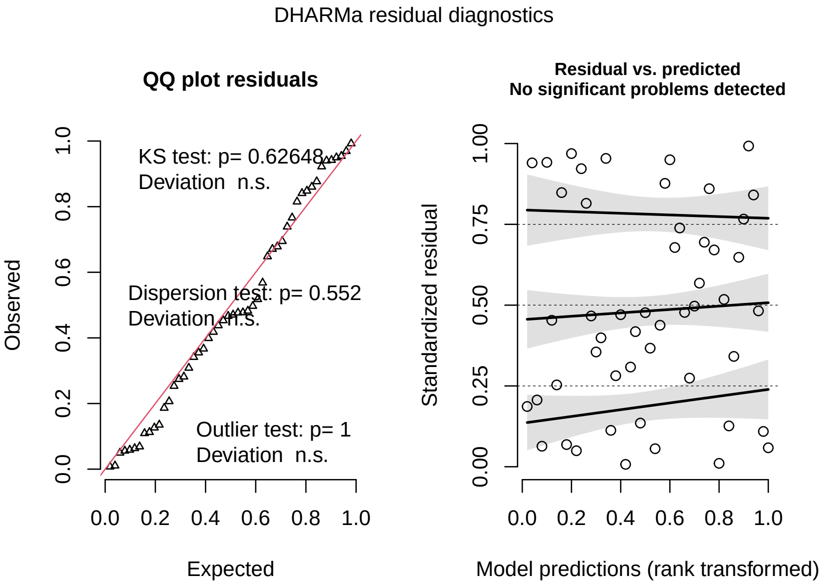
Is there pattern of residuals along predictor?

```
plot(seedl$light, resid(seedl.glm))
```



Residuals diagnostics with DHARMa

```r
DHARMa::simulateResiduals(seedl.glm, plot = TRUE)
```



Poisson regression: Overdispersion

Always check overdispersion with count data

```r
simres <- simulateResiduals(seedl.glm, refit = TRUE)
testDispersion(simres, plot = FALSE)
```

```
	DHARMa nonparametric dispersion test via mean deviance resid
	vs. simulated-refitted

data:  simres
dispersion = 1.1655, p-value = 0.432
alternative hypothesis: two.sided
```

Accounting for overdispersion in count data

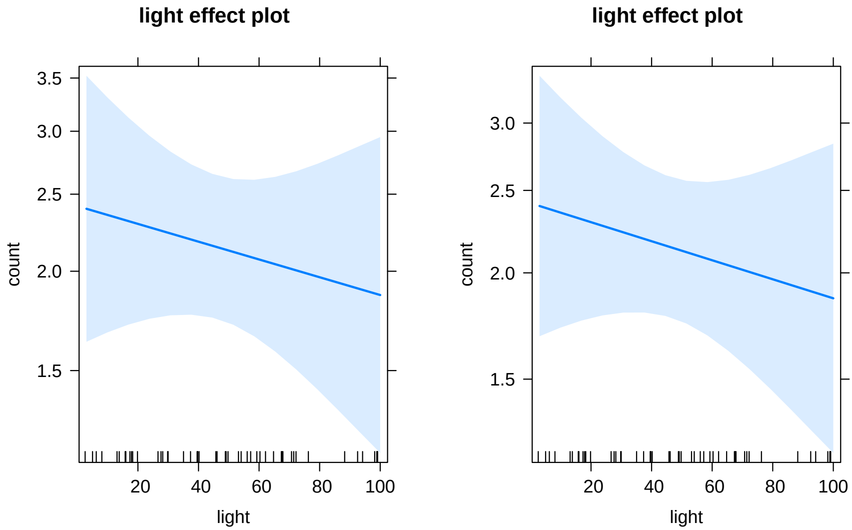
Use family quasipoisson

```
Call:
glm(formula = count ~ light, family = quasipoisson, data = seedl

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.1906  -0.8466  -0.1110   0.5220   2.4577

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.881805   0.201230   4.382 6.37e-05 ***
light       -0.002576   0.003758  -0.685    0.496
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasipoisson family taken to be 1.1349

    Null deviance: 63.029  on 49  degrees of freedom
Residual deviance: 62.492  on 48  degrees of freedom
AIC: NA
```

Mean estimates do not change after accounting for overdispersion

```
 model: count ~ light

 light effect
light
       3       30       50       70      100
2.396665 2.235657 2.123408 2.016794 1.866826
 model: count ~ light

 light effect
light
       3       30       50       70      100
2.396665 2.235657 2.123408 2.016794 1.866826
```

But standard errors may change



What if survey plots have different area?

Avoid regression of ratios

seedlings/area $\sim$ light

J. R. Statist. Soc. A (1993)
156, *Part* 3, *pp*. 379–392

Spurious Correlation and the Fallacy of the Ratio Standard Revisited

By RICHARD A. KRONMAL†

Use offset to standardise response variables in GLMs

```
seedl.offset <- glm(count ~ light, offset = seedl$area, data = s
summary(seedl.offset)
```

```

Call:
glm(formula = count ~ light, family = poisson, data = seedl,
    offset = seedl$area)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.6926  -0.8532   0.1491   0.5211   3.1051

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.299469   0.185468   1.615    0.106
light       -0.004498   0.003441  -1.307    0.191

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 70.263  on 49  degrees of freedom
Residual deviance: 68.535  on 48  degrees of freedom
```

Note estimates now referred to area units

```r
exp(coef(seedl.offset))
```

```
(Intercept)       light
  1.3491422   0.9955123
```

Other examples

- Infant mortality $\sim$ GDP

Other examples

- Infant mortality $\sim$ GDP
- Number of cones consumed by squirrels (data)