GLM for count data: Poisson regression

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- ▶ Gaussian: 1m
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- ► 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

```
seedl <- read.csv("data/seedlings.csv")</pre>
      X
                   count
                                            col
                                 row
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. :10.0
Max. :50.00
               Max. :7.00
                             Max. :5
                                                     Max.
     area
Min.
       :0.25
```

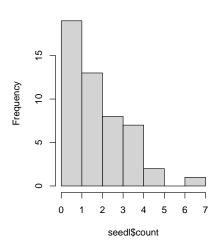
Min. :0.25 1st Qu::0.25 Median :0.50 Mean :0.62 3rd Qu::1.00 Max. :1.00

EDA

table(seedl\$count)

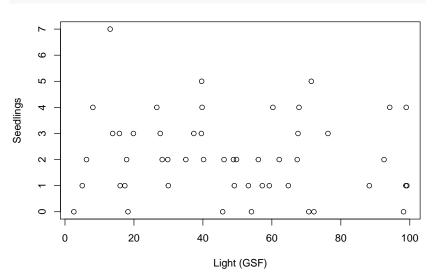
0 1 2 3 4 5 7 7 12 13 8 7 2 1

Histogram of seedl\$count



Q: Relationship between Nseedlings and light?

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



Let's fit model (Poisson regression)

```
seedl.glm <- glm(count ~ light. data = seedl. family = poisson)</pre>
summary(seedl.glm)
Call:
glm(formula = count ~ light, family = poisson, data = seedl)
Deviance Residuals:
   Min
             10 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 '**' 0.05 '.' 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):

coef(seedl.glm)

(Intercept) light
0.881805022 -0.002575656

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

exp(coef(seedl.glm))

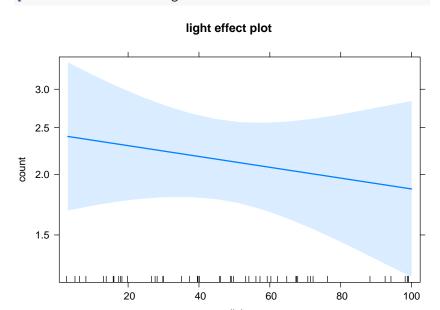
(Intercept) light
2.4152554 0.9974277
```

Using effects package

```
summary(allEffects(seedl.glm))
model: count ~ light
light effect
light
                        50
               30
                                 70
                                          100
2.396665 2.235657 2.123408 2.016794 1.866826
 Lower 95 Percent Confidence Limits
light
               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
```

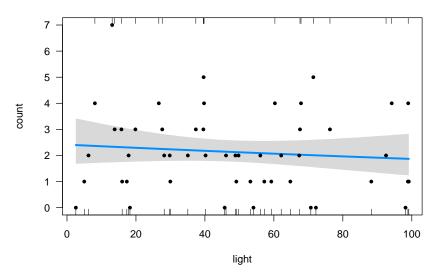
So what's the relationship between Nseedlings and light?

plot(allEffects(seedl.glm))



Using visreg

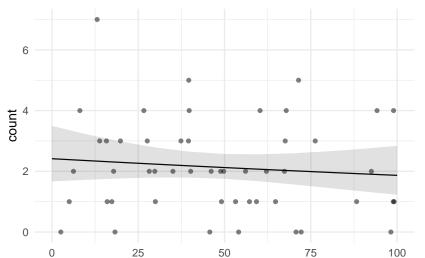
```
visreg(seedl.glm, scale = "response", ylim = c(0, 7))
points(count ~ light, data = seedl, pch = 20)
```



Using sjPlot

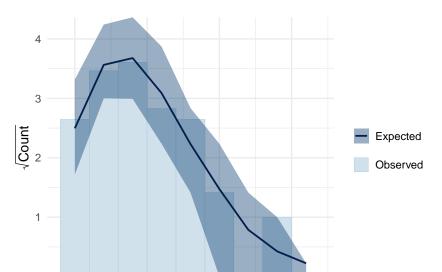
```
sjPlot::plot_model(seedl.glm, type = "eff", show.data = TRUE)
$light
```

Predicted counts of count

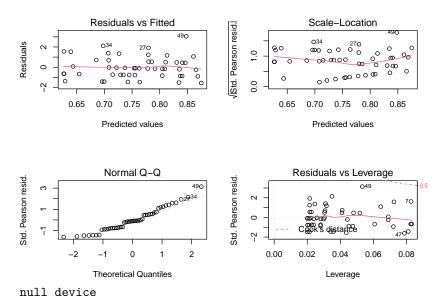


Calibration plot with count data: rootograms

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



Poisson regression: model checking

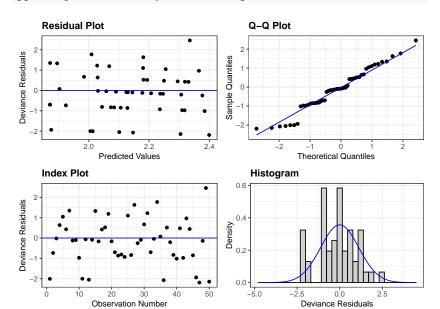


nurr devic

.

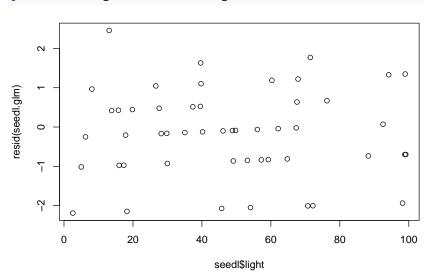
Poisson regression: model checking

ggResidpanel::resid_panel(seedl.glm)



Is there pattern of residuals along predictor?

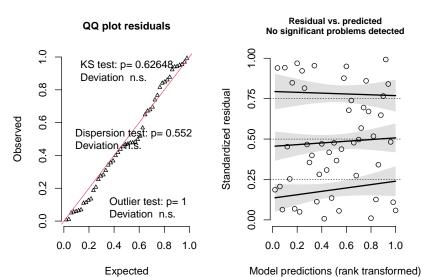
plot(seedl\$light, resid(seedl.glm))



Residuals diagnostics with DHARMa

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

DHARMa residual diagnostics



Poisson regression: Overdispersion

Always check overdispersion with count data

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

DHARMa nonparametric dispersion test via mean deviance residus. simulated-refitted

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

Accounting for overdispersion in count data

Use family quasipoisson

```
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:

Call:

```
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

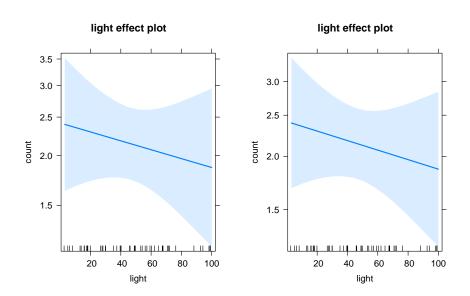
(Dispersion parameter for quasipoisson family taken to be 1.1349

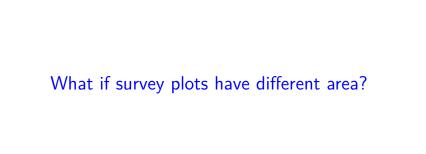
Null deviance: 63.029 on 49 degrees of freedom Residual deviance: 62.492 on 48 degrees of freedom $\Lambda TC \cdot M\Lambda$

Mean estimates do not change after accounting for overdispersion

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

But standard errors may change





Avoid regression of ratios

seedlings/area ~ 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)</pre>
```

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

```
Min 1Q Median 3Q Max -2.6926 -0.8532 0.1491 0.5211 3.1051
```

Deviance Residuals:

Residual deviance: 68.535

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
```

```
Null deviance: 70.263 on 49 degrees of freedom
```

(Dispersion parameter for poisson family taken to be 1)

on 48 degrees of freedom

Note estimates now referred to area units

```
exp(coef(seedl.offset))
(Intercept) light
1.3491422 0.9955123
```

Other examples

► Infant mortality ~ GDP

Other examples

- ► Infant mortality ~ GDP
- Number of cones consumed by squirrels (data)