GLM for count data: Poisson regression

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Types of response variable

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- **Binary**: glm (family `binomial / quasibinomial`)

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- **Gaussian**: lm
- **Binary**: glm (family `binomial / quasibinomial`)
- **Counts**: glm (family `poisson / quasipoisson`)

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

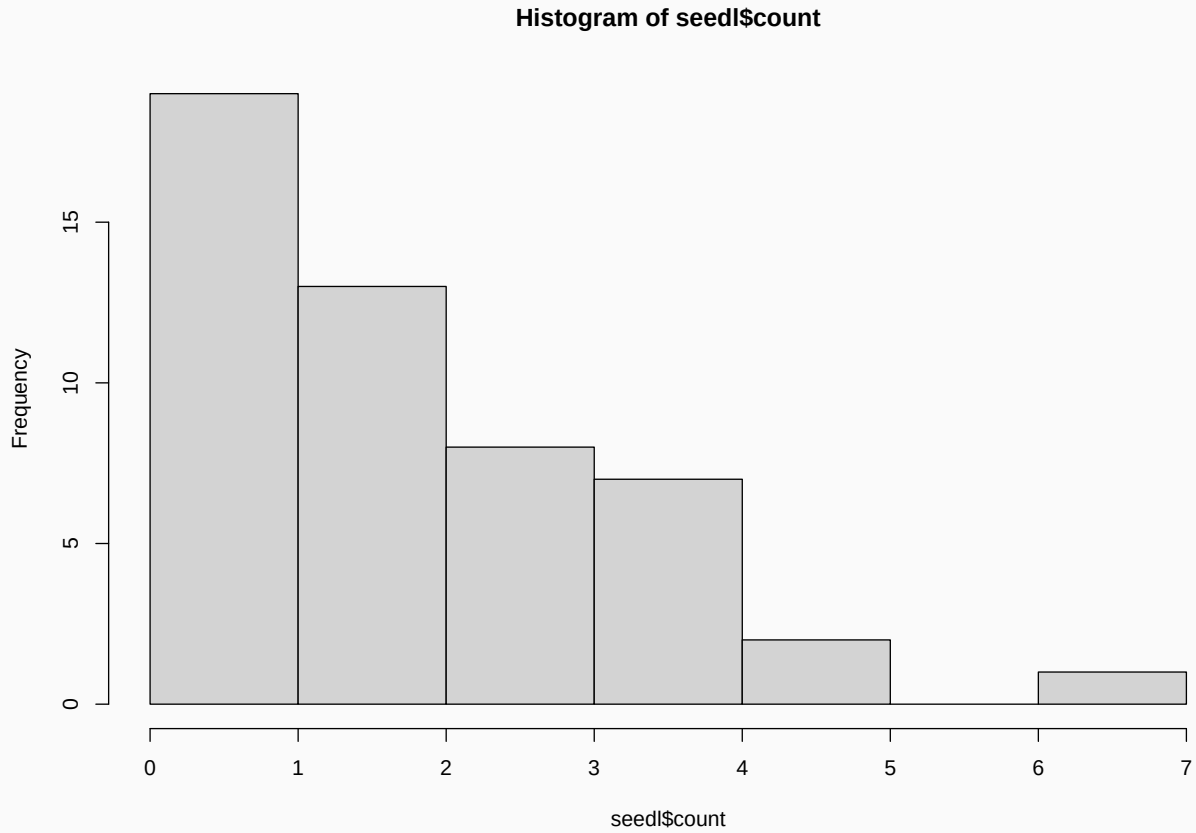
```
seedl <- read.csv("data/seedlings.csv")
```

```
     sample          count           light             area       
 Min.   : 1.00   Min.   :0.00   Min.   : 2.571   Min.   :0.25  
 1st Qu.:13.25   1st Qu.:1.00   1st Qu.:26.879   1st Qu.:0.25  
 Median :25.50   Median :2.00   Median :47.493   Median :0.50  
 Mean   :25.50   Mean   :2.14   Mean   :47.959   Mean   :0.62  
 3rd Qu.:37.75   3rd Qu.:3.00   3rd Qu.:67.522   3rd Qu.:1.00  
 Max.   :50.00   Max.   :7.00   Max.   :99.135   Max.   :1.00  
```

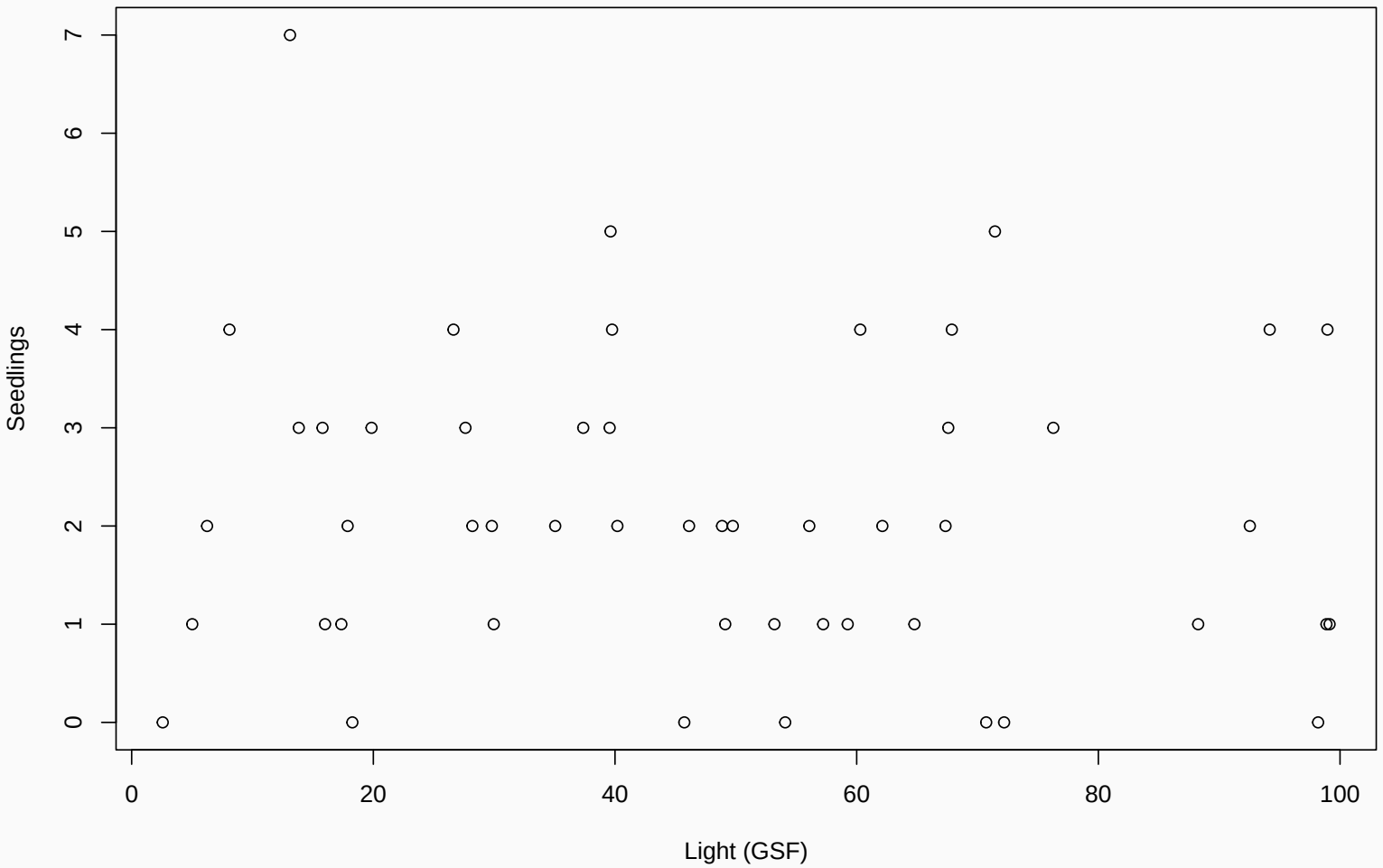
Exploring the data

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

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



Relationship between Nseedlings and light?



Poisson regression

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

which corresponds to

```
equatiomatic::extract_eq(seedl.glm)
```

$$\log(E(\text{count})) = \alpha + \beta_1(\text{light}) \tag{1}$$

Interpreting Poisson 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
```

Parameter estimates are in log scale!

Parameter estimates (log scale):

```
coef(seedl.glm)[1]
```

```
(Intercept)
   0.881805
```

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

```
exp(coef(seedl.glm)[1])
```

```
(Intercept)
   2.415255
```

Using effects package

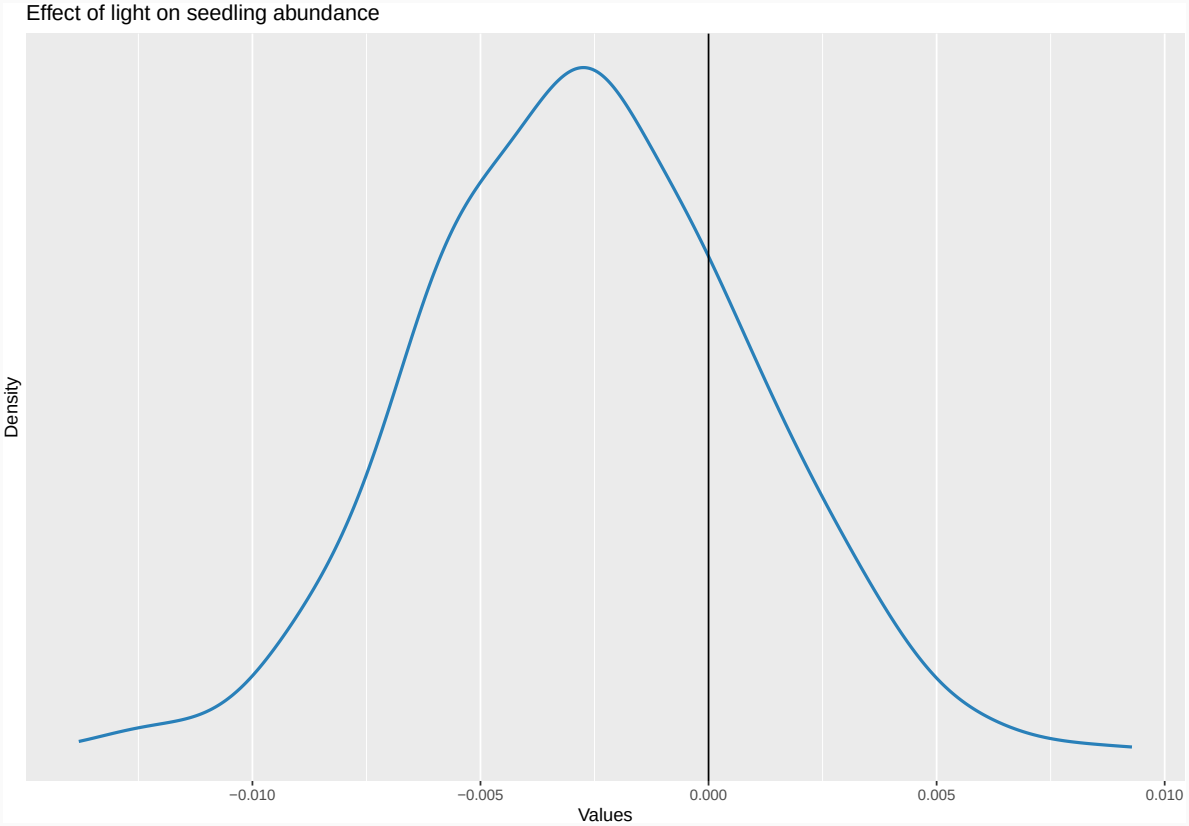
```
allEffects(seedl.glm)
```

```
 model: count ~ light

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

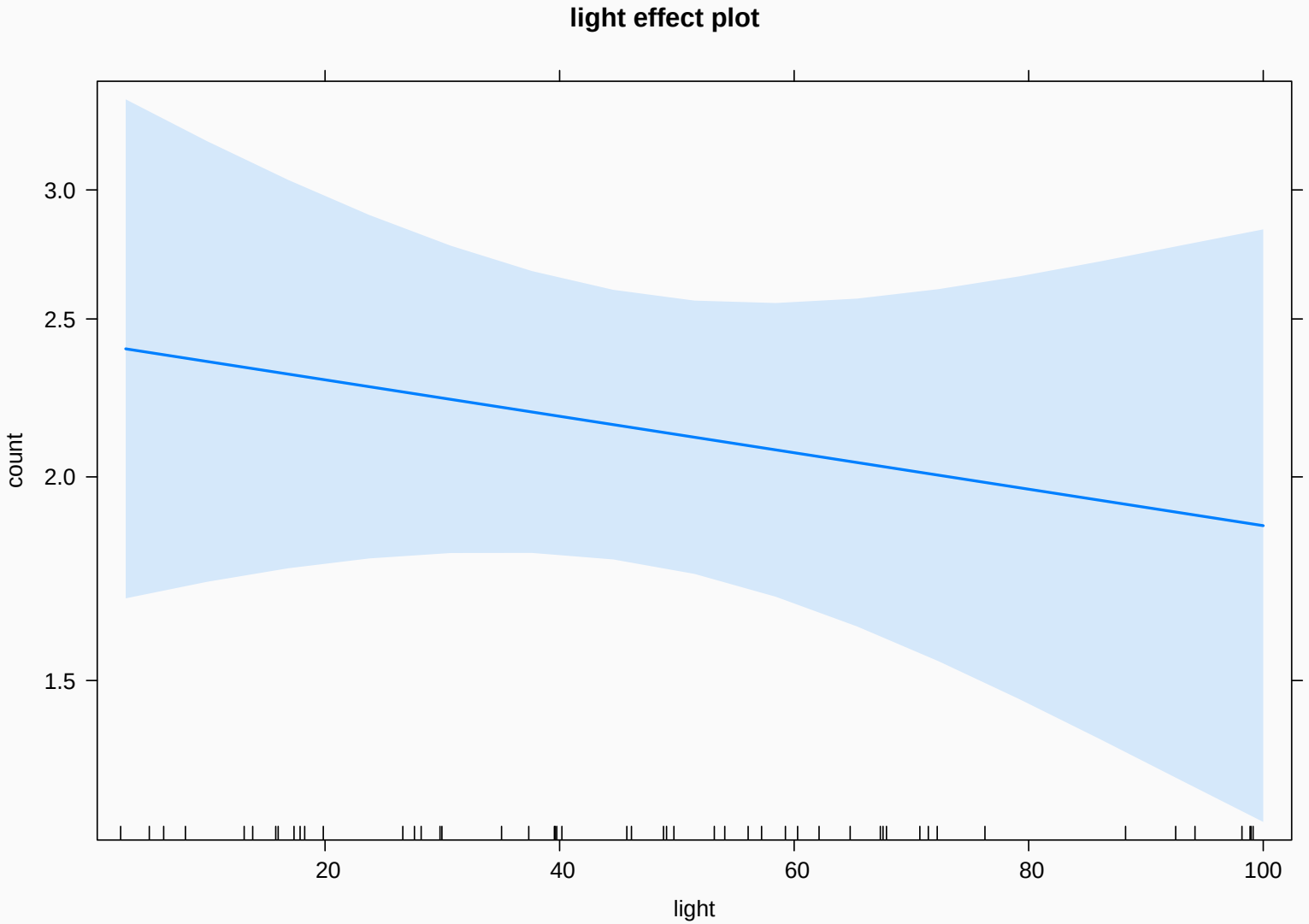
Estimated distribution of the slope parameter

```
library("parameters")
plot(simulate_parameters(seedl.glm)) +
  geom_vline(xintercept = 0) +
  ggtitle("Effect of light on seedling abundance")
```



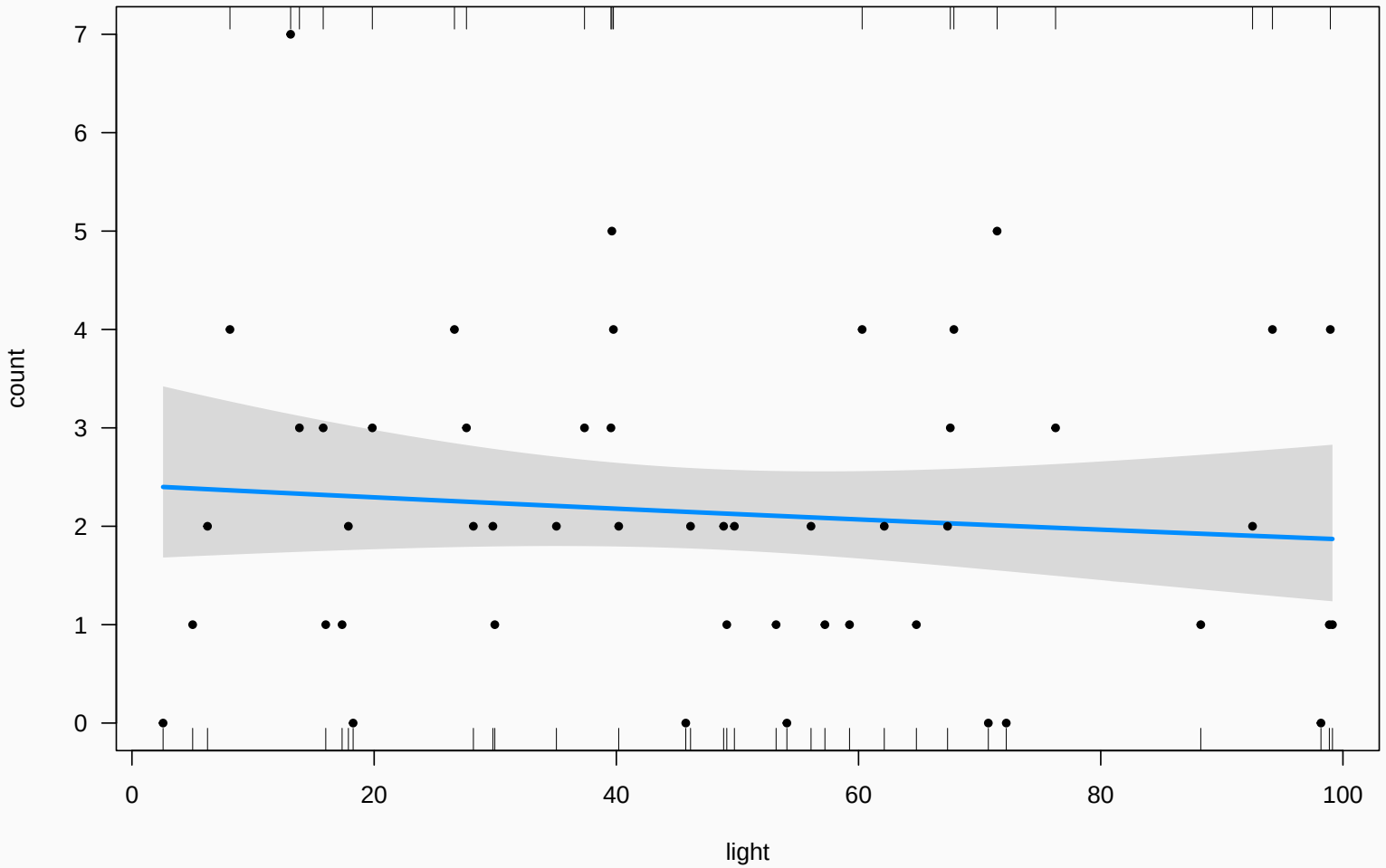
So what's the relationship between Nseedlings and light?

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



Using visreg

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



Low R-squared

```
library("performance")
r2(seedl.glm)
```

```
# R2 for Generalized Linear Regression
  Nagelkerke's R2: 0.015
```

Describing the model results

```
library("report")
report(seedl.glm)
```

We fitted a poisson model (estimated using ML) to predict count with light (formula: count ~ light). The model's explanatory power is very weak (Nagelkerke's R2 = 0.01). The model's intercept, corresponding to light = 0, is at 0.88 (95% CI [0.50, 1.24], p < .001). Within this model:

- The effect of light is statistically non-significant and negative (beta = -2.58e-03, 95% CI [-9.57e-03, 4.28e-03], p = 0.465; Std. beta = -0.07, 95% CI [-0.27, 0.12])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald z-distribution approximation.

Model checking

Assumptions of Poisson regression

- Linearity (log response ~ predictors)

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- Observations are independent

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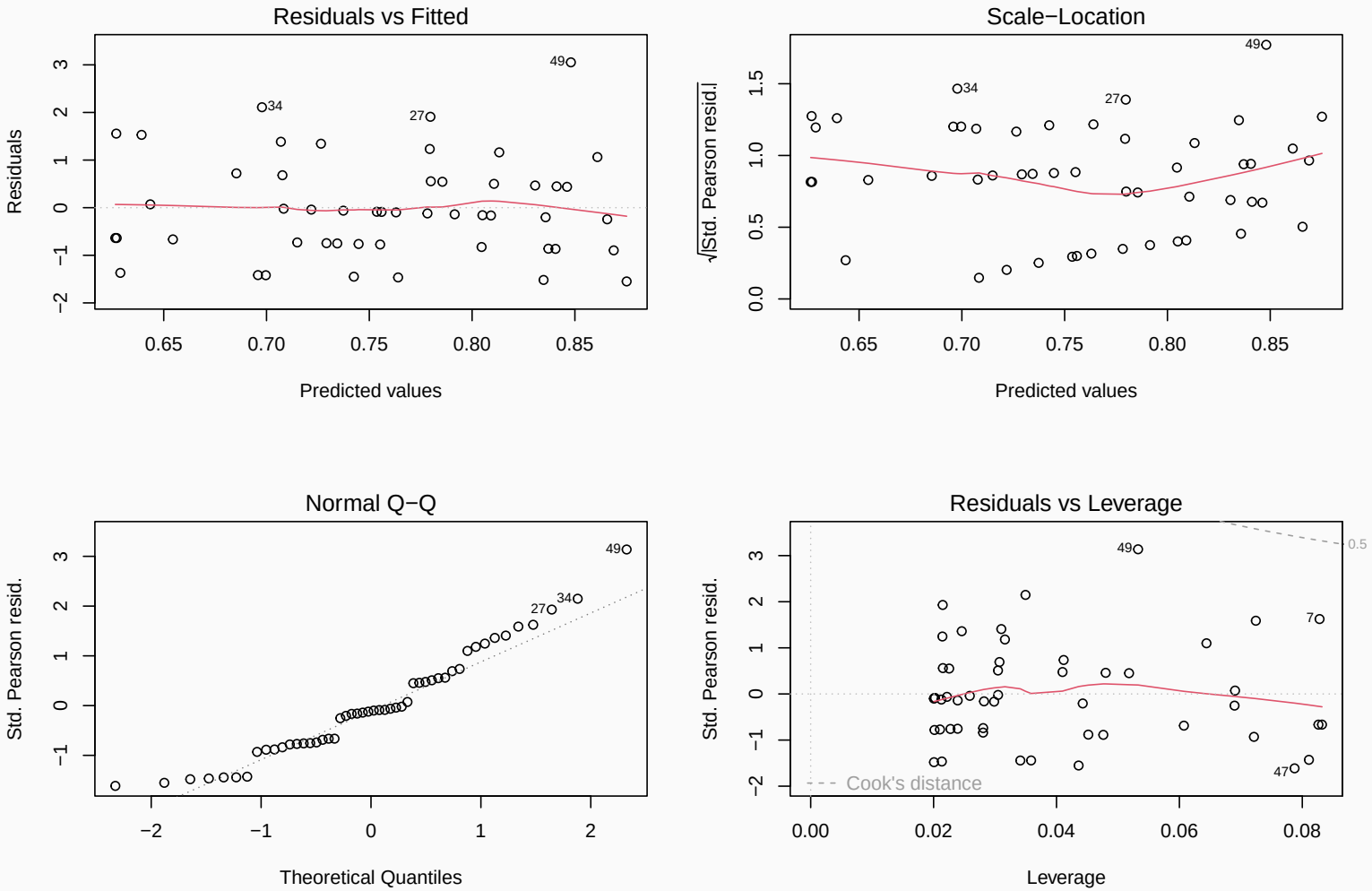
- Observations are independent
- Mean = Variance

Checking Poisson GLM

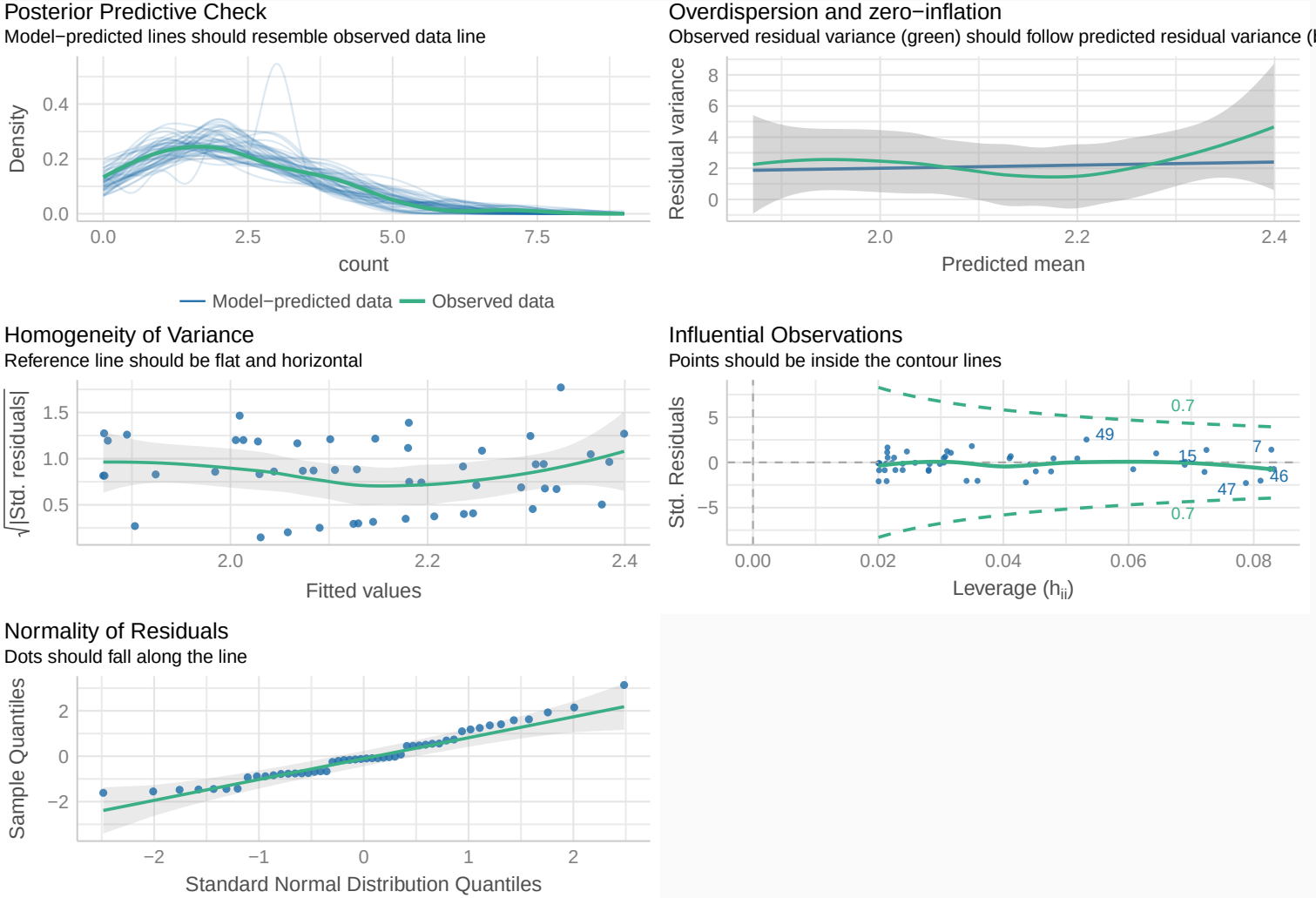
```
plot(seedl.glm)
```




```
null device
```

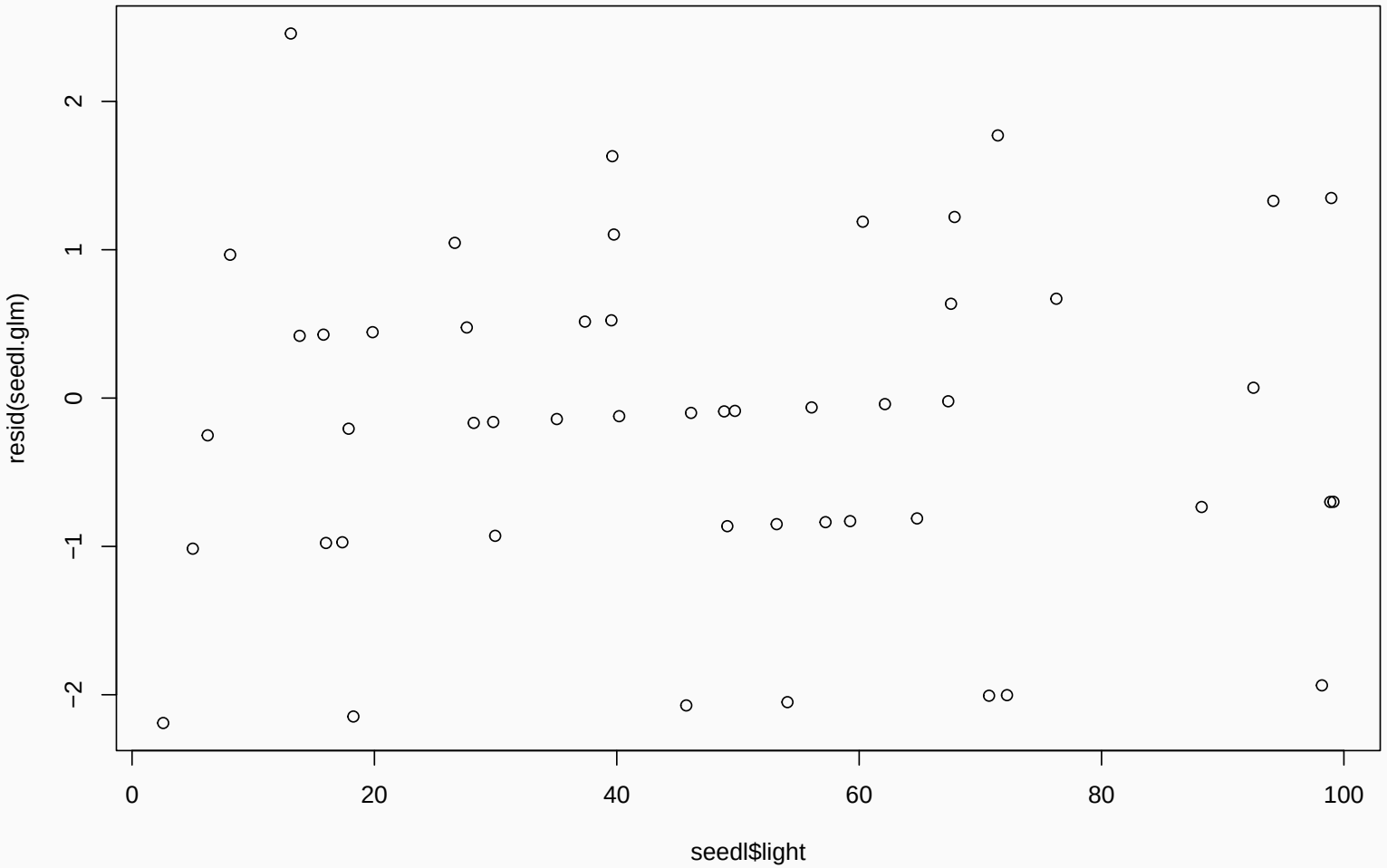
Checking Poisson GLM

```
check_model(seedl.glm)
```



Is there pattern of residuals along predictor?

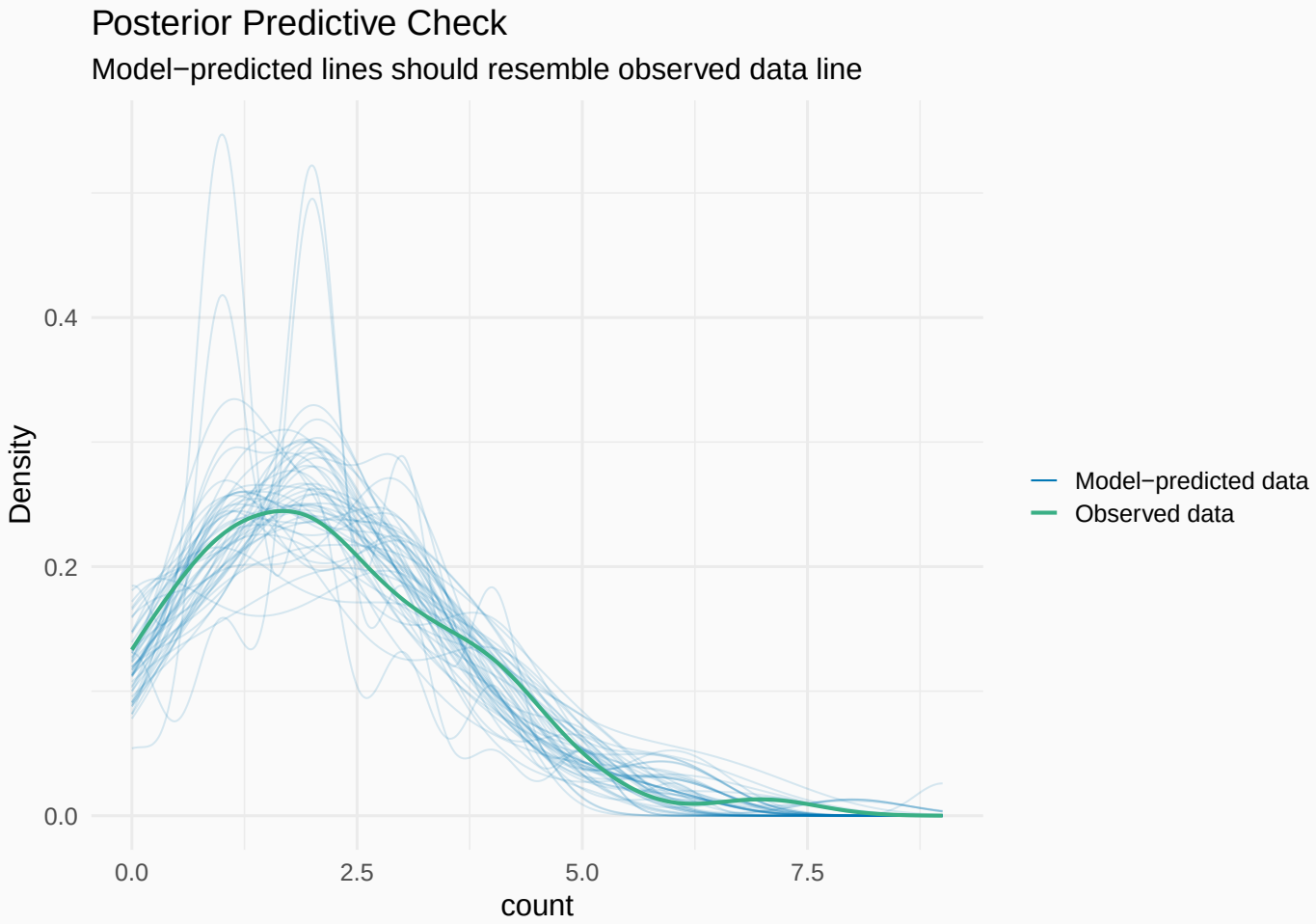
```
plot(seedl$light, resid(seedl.glm))
```



Posterior predictive checking

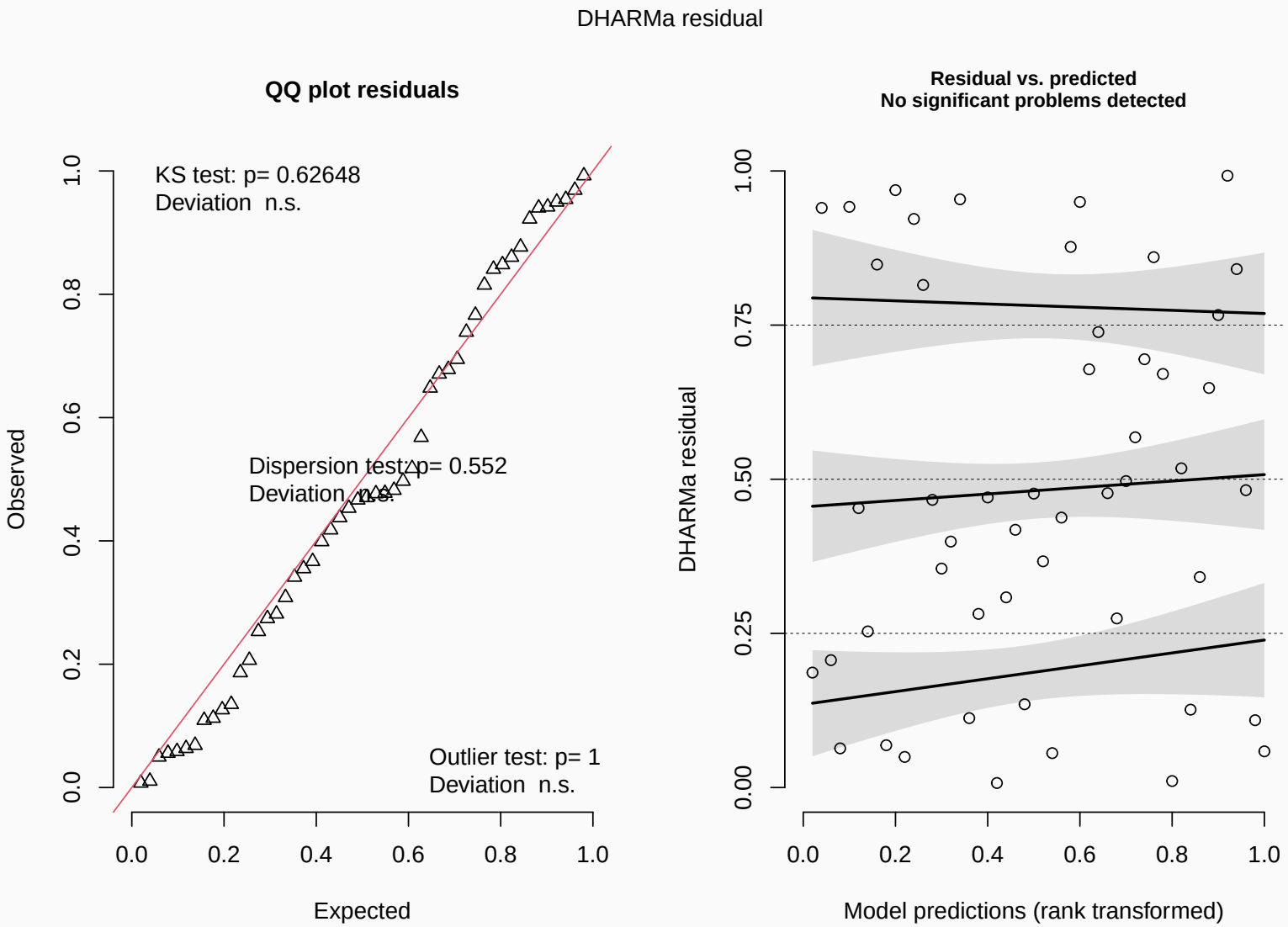
Simulate data from fitted model (`yrep`) and compare with observed data (`y`)

```
check_predictions(seedl.glm)
```



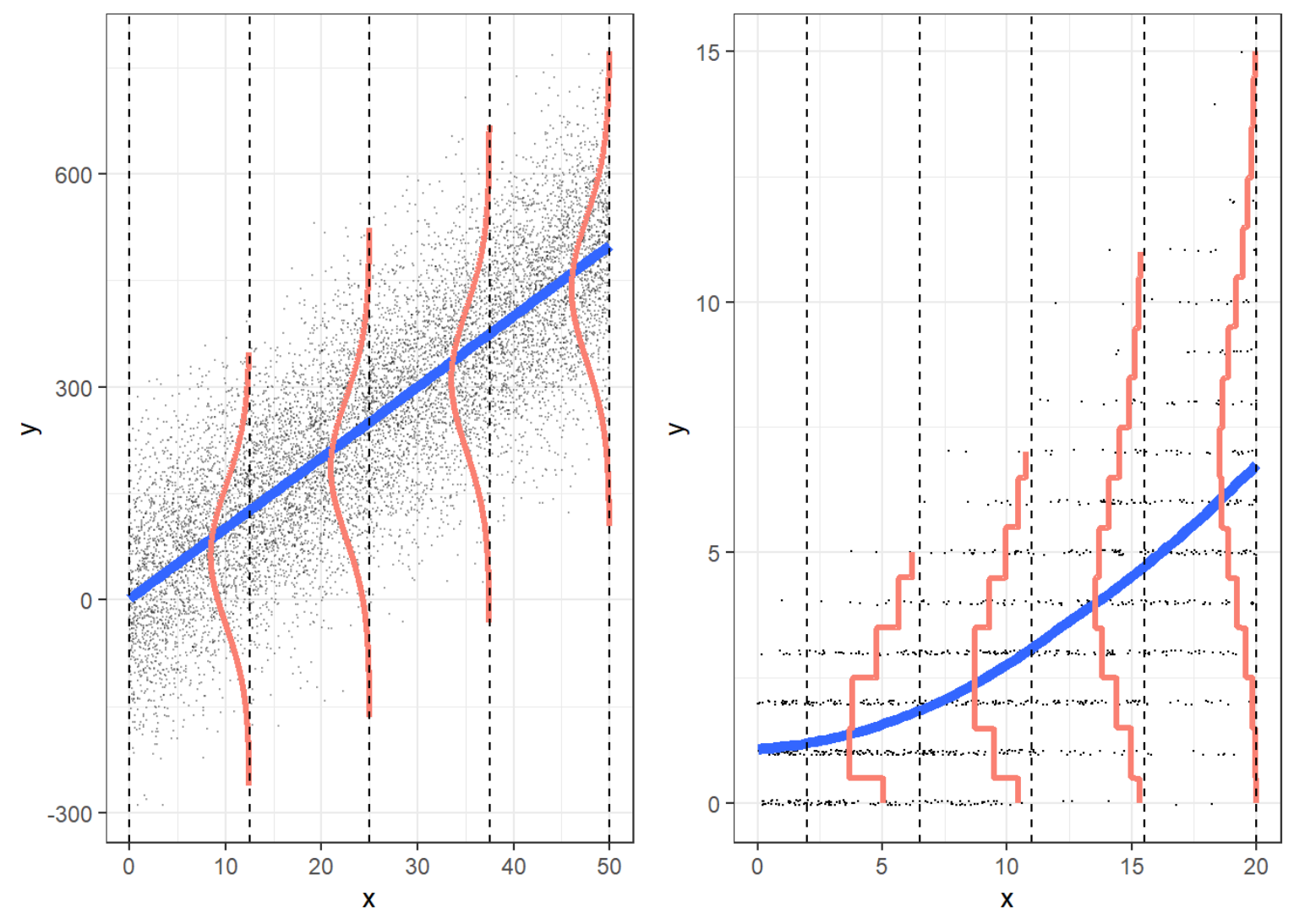
Residuals diagnostics with DHARMa

```
simulateResiduals(seedl.glm, plot = TRUE)
```



Overdispersion

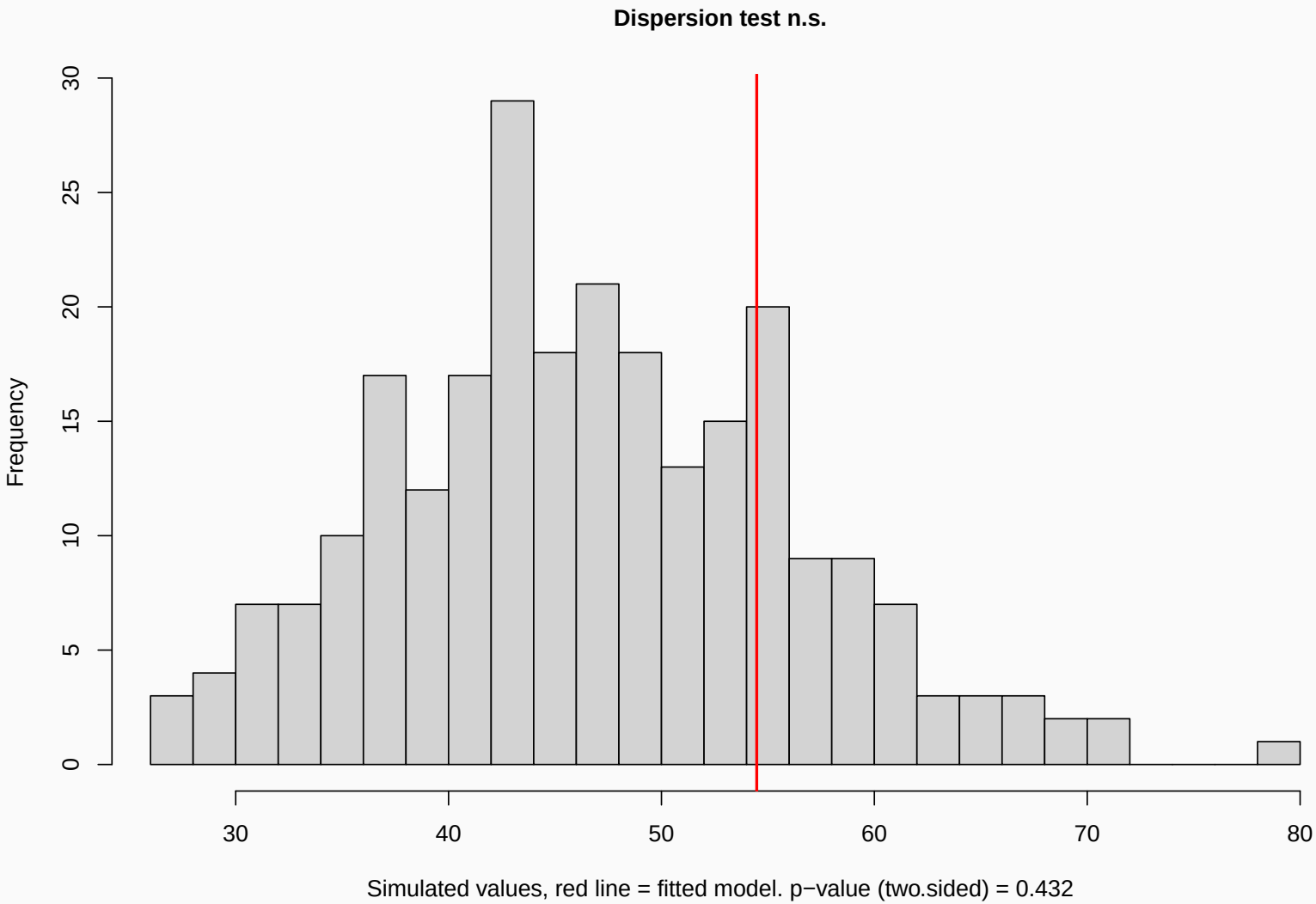
Poisson GLM assumes mean = variance



Roback & Legler 2021

Always check overdispersion with count data

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



Accounting for overdispersion in count data

- Use family `quasipoisson`

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- Use family `quasipoisson`
- Use negative binomial distribution (`MASS::glm.nb`)
- Include observation-level random effect (e.g. see Harrison 2014)

Accounting for overdispersion with 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 1.134907)

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

Number of Fisher Scoring iterations: 5
```

Mean estimates do not change after accounting for overdispersion

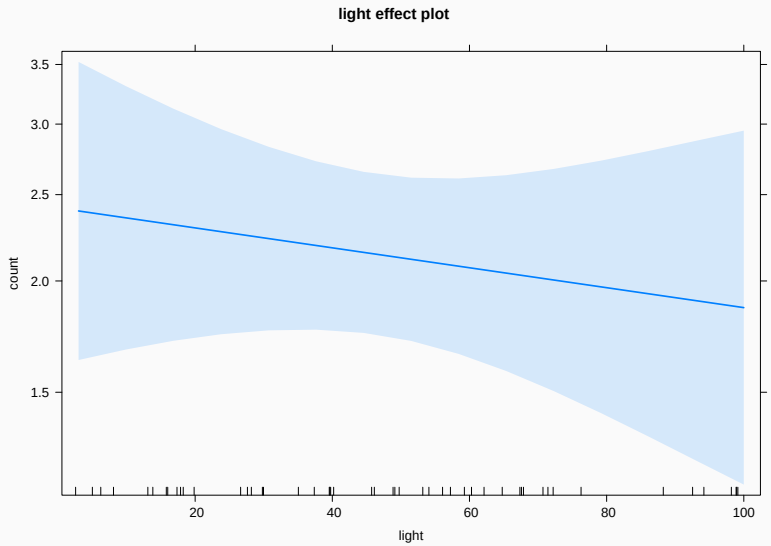
```
allEffects(seedl.overdisp)
```

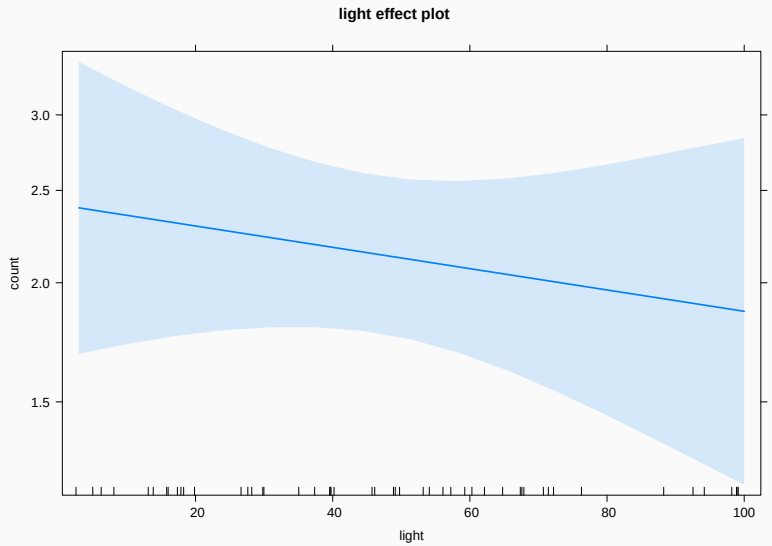
```
 model: count ~ light

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

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

```
 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





Accounting for overdispersion using negative binomial

```
library("MASS")
seedl.nb <- glm.nb(count ~ light, data = seedl)
```

```
Call:
glm.nb(formula = count ~ light, data = seedl, init.theta = 22.23419419,
    link = log)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.1349  -0.8162  -0.1061   0.4954   2.2814

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.881996   0.198213   4.450  8.6e-06 ***
light       -0.002580   0.003691  -0.699    0.485
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Negative Binomial(22.2342) family taken to be 1)

    Null deviance: 58.247  on 49  degrees of freedom
```

Comparing Poisson and Negative Binomial

```
compare_models(seedl.glm, seedl.nb)
```

```
Parameter    |               seedl.glm |                seedl.nb
-----------------------------------------------------------------
(Intercept)  |      0.88 ( 0.51, 1.25) |      0.88 ( 0.49, 1.27)
light        | -2.58e-03 (-0.01, 0.00) | -2.58e-03 (-0.01, 0.00)
-----------------------------------------------------------------
Observations |                      50 |                      50
```

```
compare_performance(seedl.glm, seedl.nb)
```

```
# Comparison of Model Performance Indices

Name      |  Model |     AIC | AIC weights |     BIC | BIC weights | Nagelkerke's R2 |  RMSE |
-------------------------------------------------------------------------------------------------
seedl.glm |    glm | 182.034 |       0.710 | 185.858 |       0.864 |           0.015 | 1.529 |
seedl.nb  | negbin | 183.827 |       0.290 | 189.563 |       0.136 |           0.014 | 1.529 |
```

What if survey plots have different area?

Shall we *standardise* counts dividing by sampling plot area?

Model would be: count/area ~ light

	sample	count	light	area
1	1	0	70.71854	0.50
2	2	1	88.26021	0.25
3	3	2	67.35133	0.50
4	4	3	67.57850	1.00
5	5	4	26.63098	0.25
6	6	3	15.79433	1.00

Avoid regression of ratios

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†

https://doi.org/10.2307/2983064

Use `offset` to account for variable sampling effort

```
seedl.offset <- glm(count ~ light,
                    offset = log(area),
                    data = seedl,
                    family = poisson)
```

Note estimates now referred to area units!

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

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.9918  -1.0142   0.1673   0.8401   3.8230

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.513185   0.183245   8.258   <2e-16 ***
light       -0.005674   0.003384  -1.677   0.0936 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

Note estimates now referred to area units!

```
exp(coef(seedl.offset)[1])
```

```
(Intercept)
   4.541173
```

Prediction

Predicting number of seedlings given light

```
new.lights <- data.frame(light = c(10, 90))
predict(seedl.glm, newdata = new.lights, type = "response", se.fit
```

```
$fit
       1        2
2.353841 1.915533

$se.fit
        1         2
0.3756992 0.3502446

$residual.scale
[1] 1
```

Poisson GLM: more examples

- Infant mortality ~ GDP

Poisson GLM: more examples

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

Poisson GLM: more examples

- Infant mortality ~ GDP
- Number of cones consumed by squirrels (data)
- Elephant matings (Poole 1989)