model help

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Seed detections distribution

Empirical density

Cumulative distribution
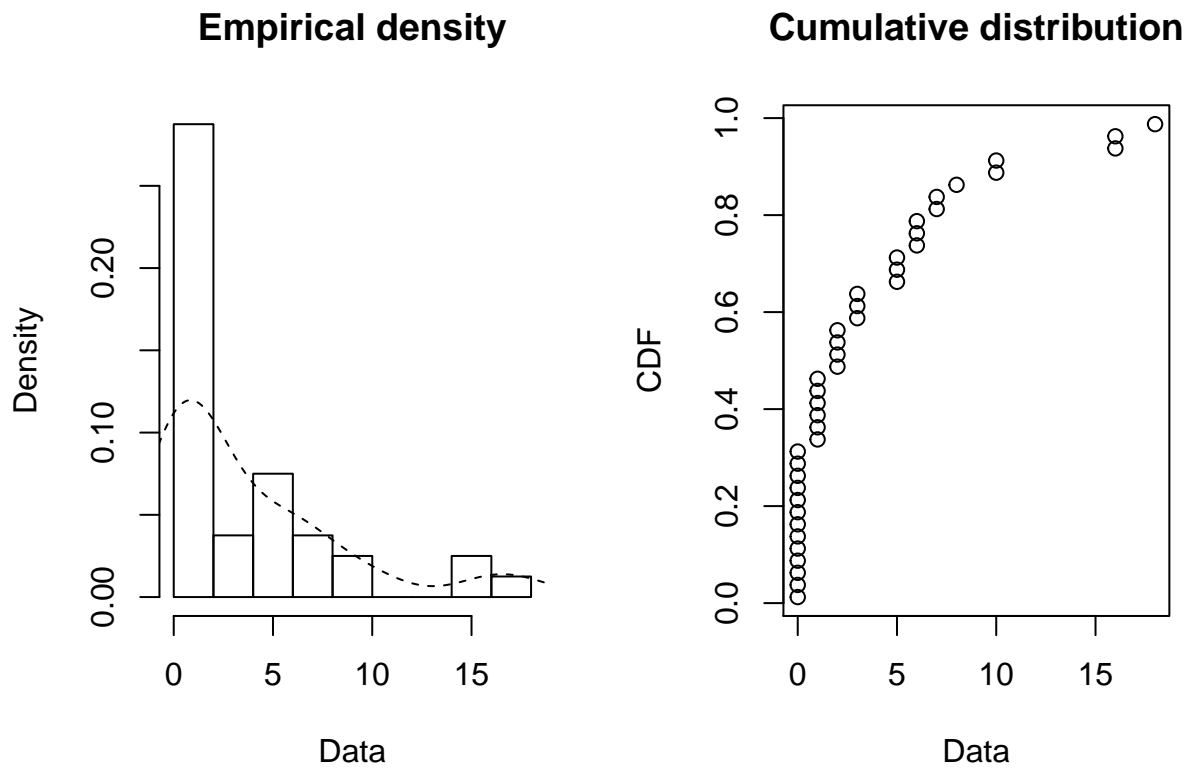
Cullen and Frey graph
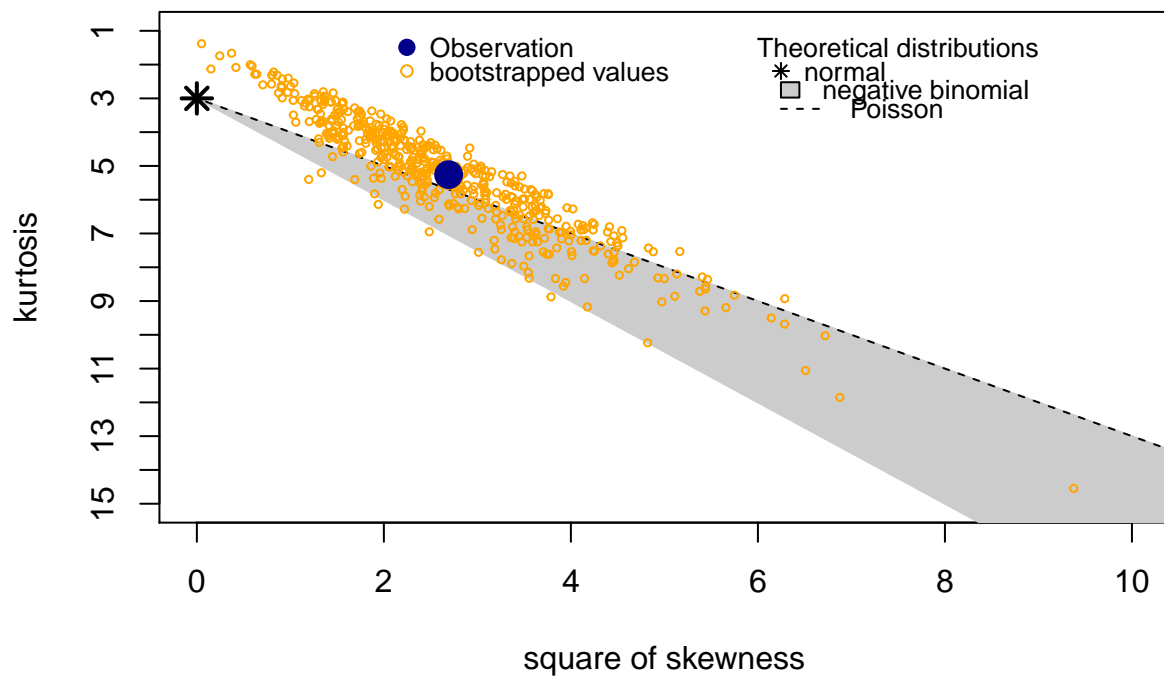
```
## summary statistics
## ------
## min:  0   max:  18
## median:  2
## mean:  3.7
## estimated sd:  4.756642
## estimated skewness:  1.64098
## estimated kurtosis:  5.258471
```

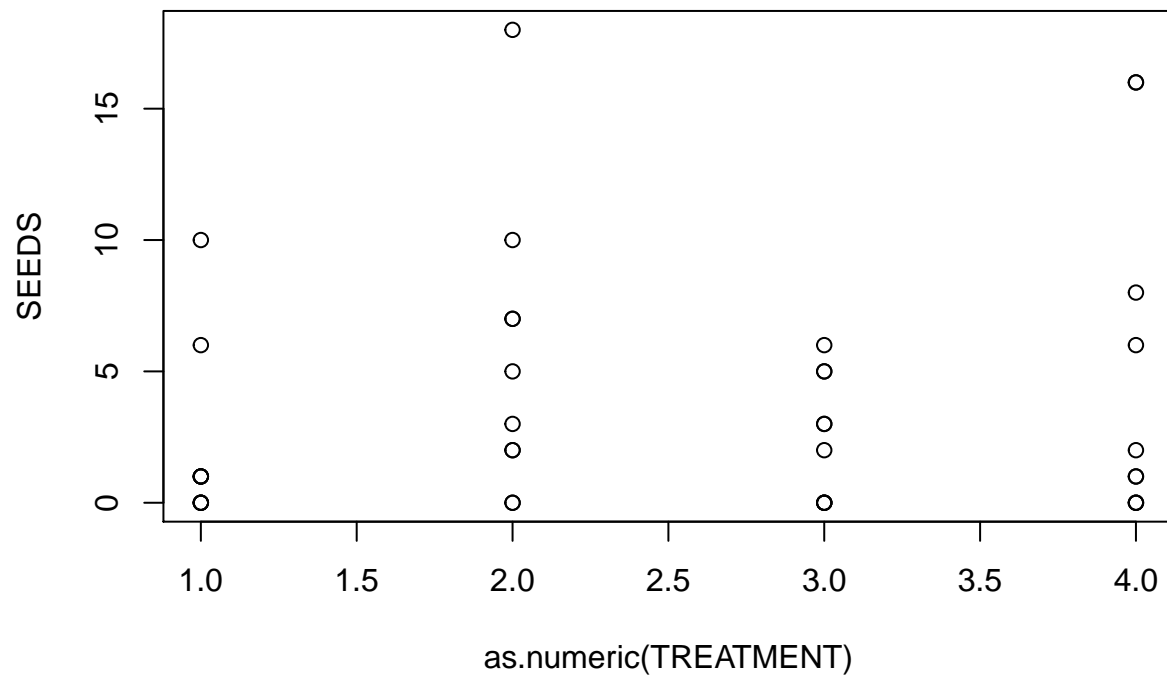# Negative binomial and poisson model fits for seed detections

```r
# neg binom fit
seeds.obs.fit.nb <- glmer.nb(SEEDS ~ TREATMENT + (1 | BLOCK),
                             data = seed.obs)
```

```
## boundary (singular) fit: see ?isSingular
```
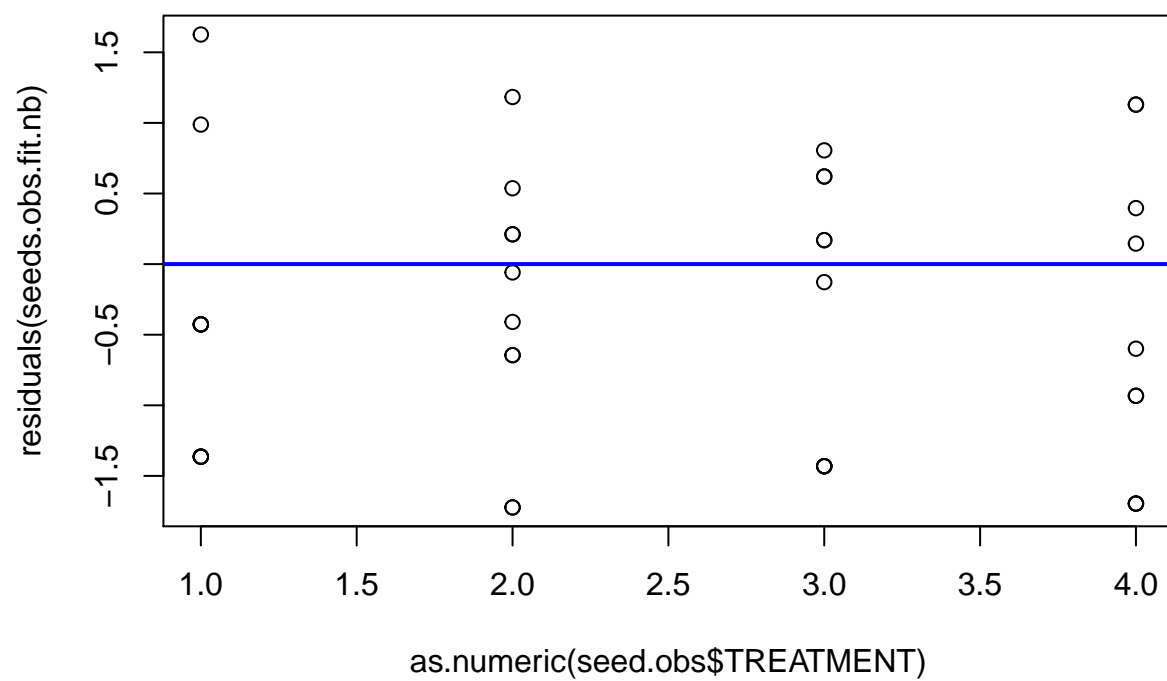
```r
# poisson fit
seed.obs.fit.pois <- glmer(SEEDS ~ TREATMENT + (1 | BLOCK),
                           data = seed.obs, family = poisson(link = "log"))
```

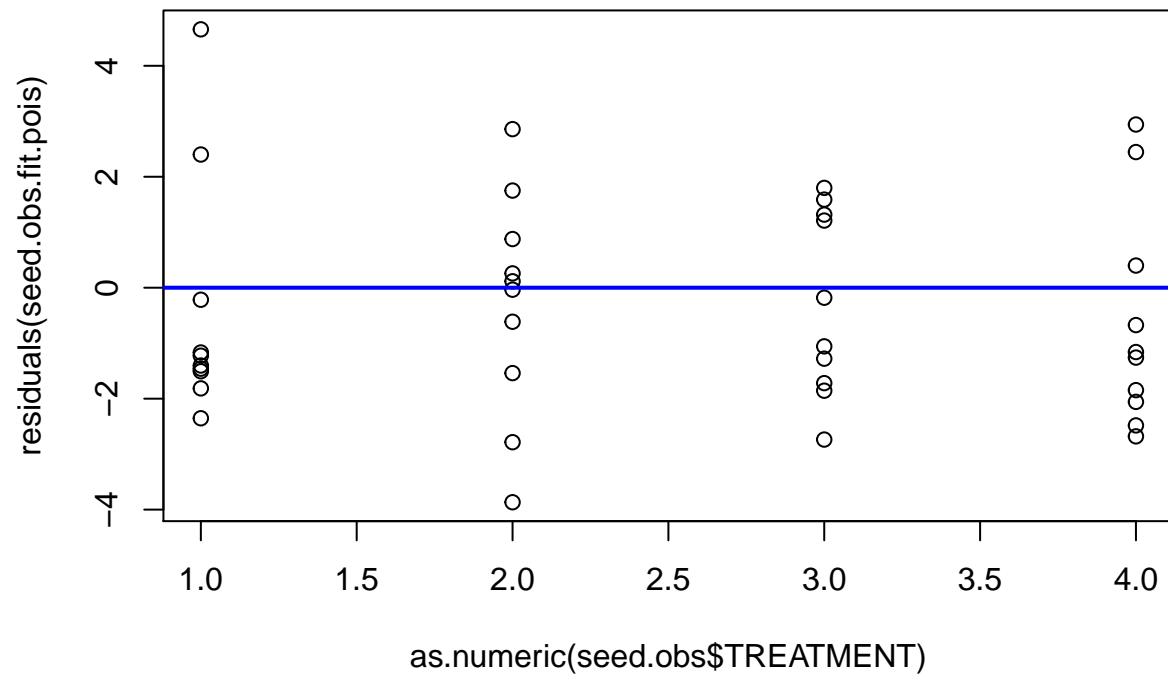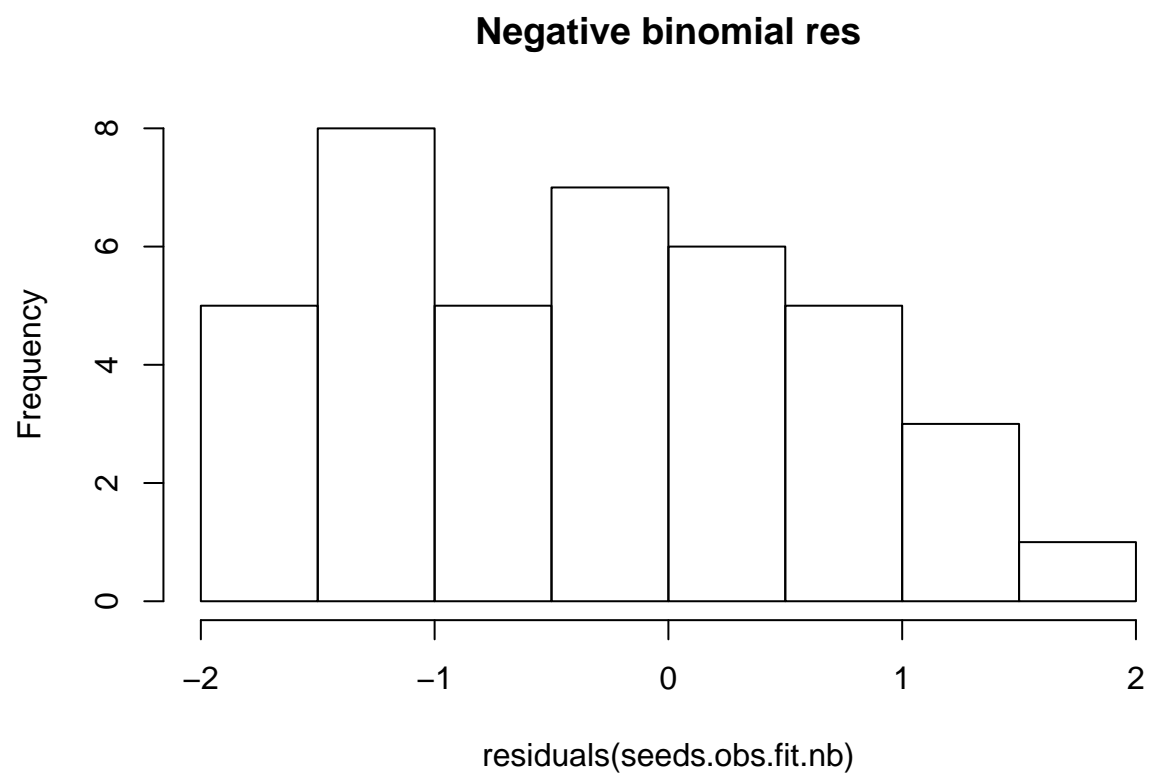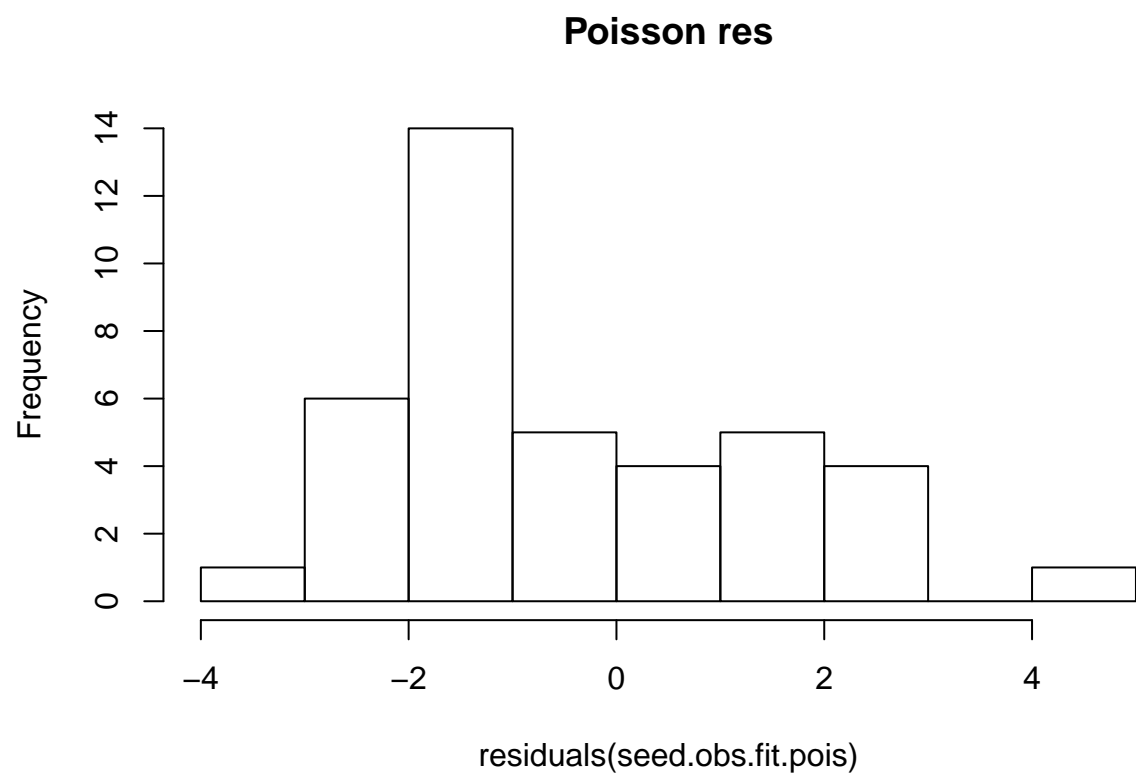# Check some assumptions (seed detection models)

Seed detections by treatment
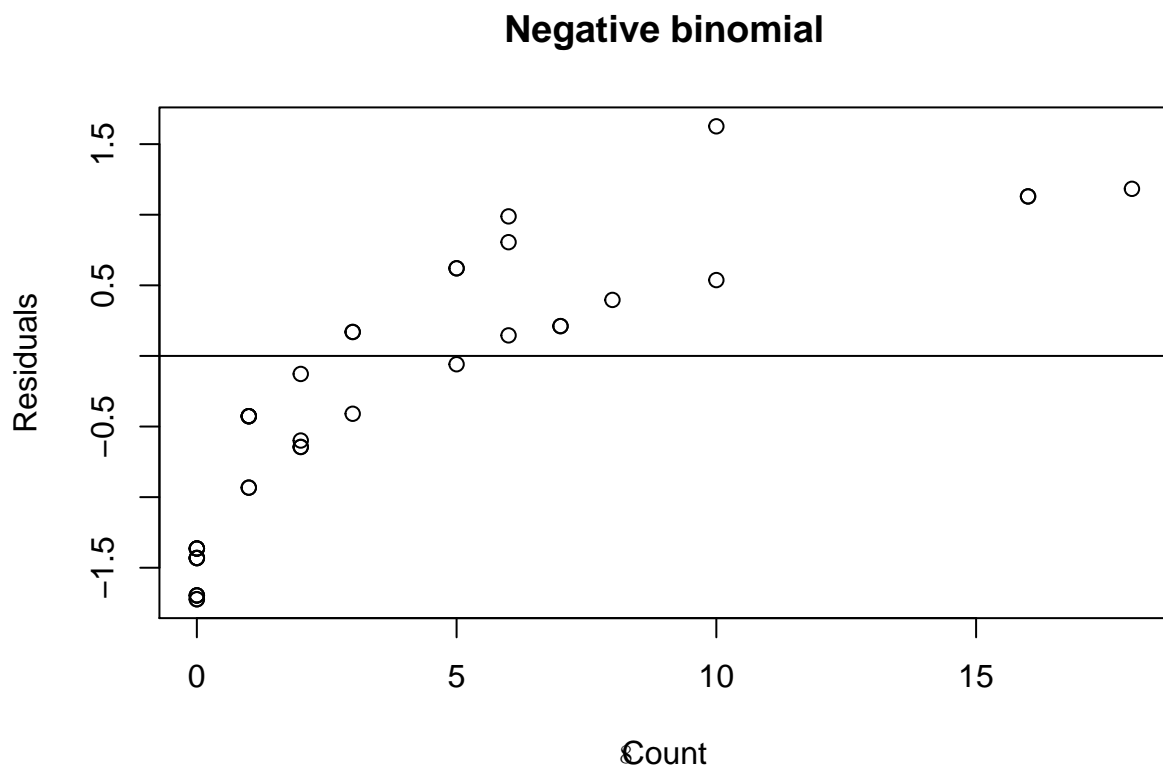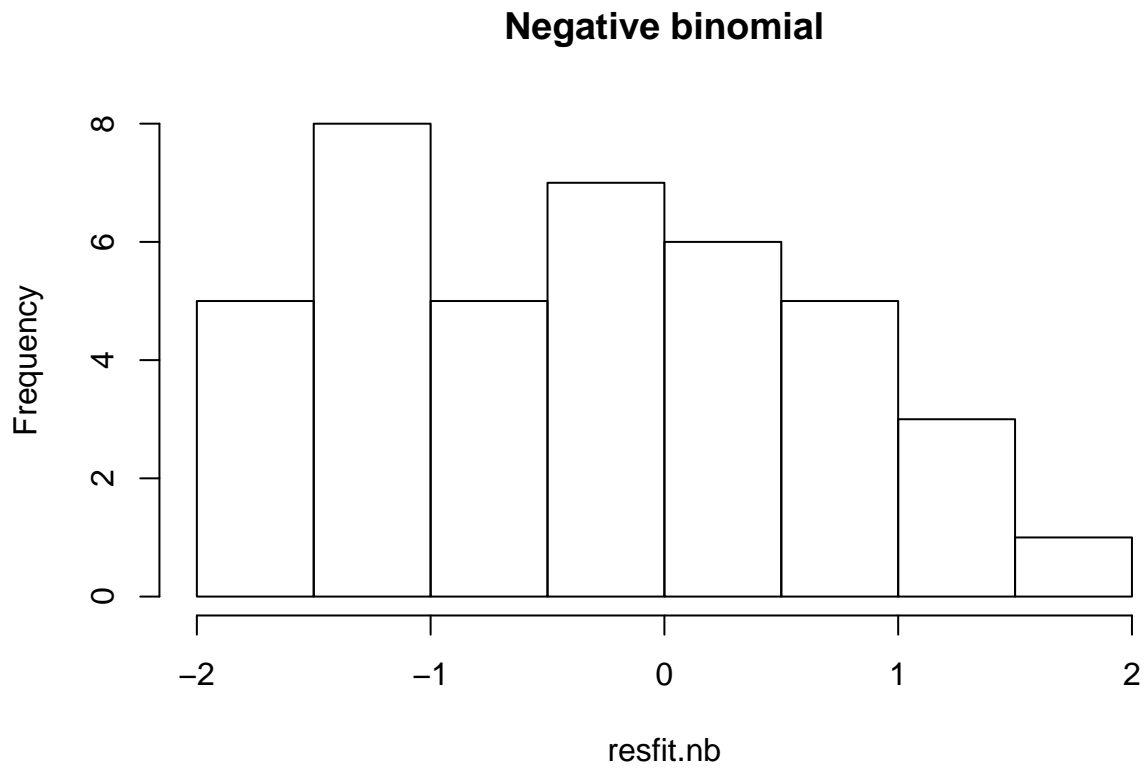

Negative binomial residuals by treatment

Poisson residuals by treatment

Negative binomial res

residuals(seeds.obs.fit.nb)

Poisson res
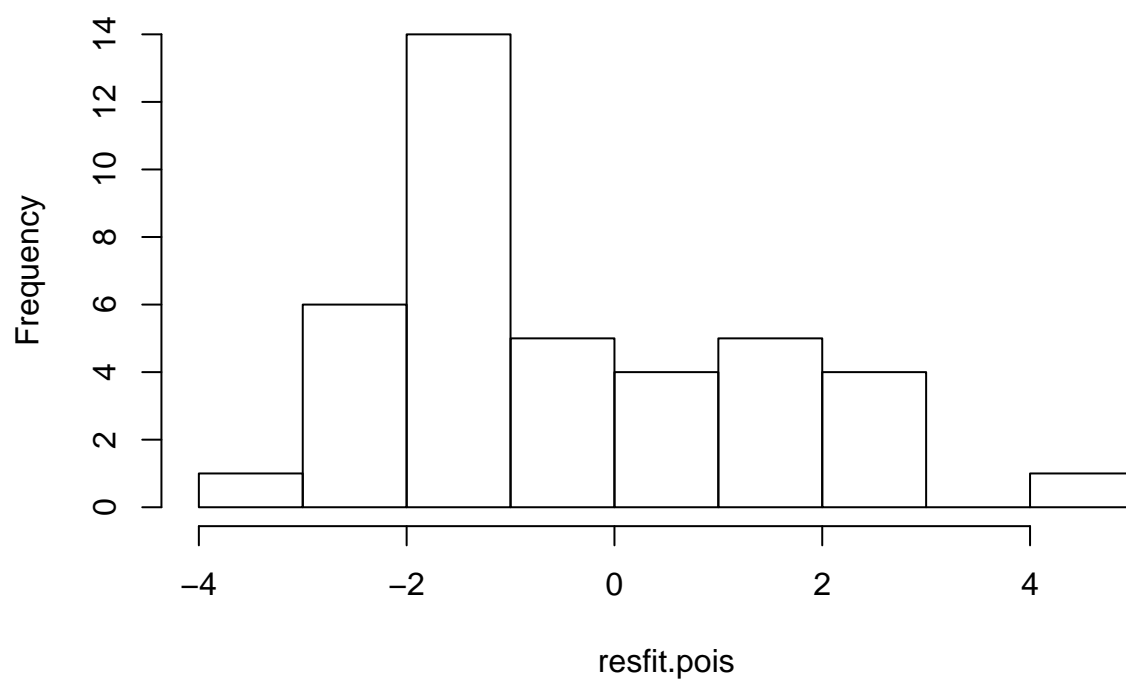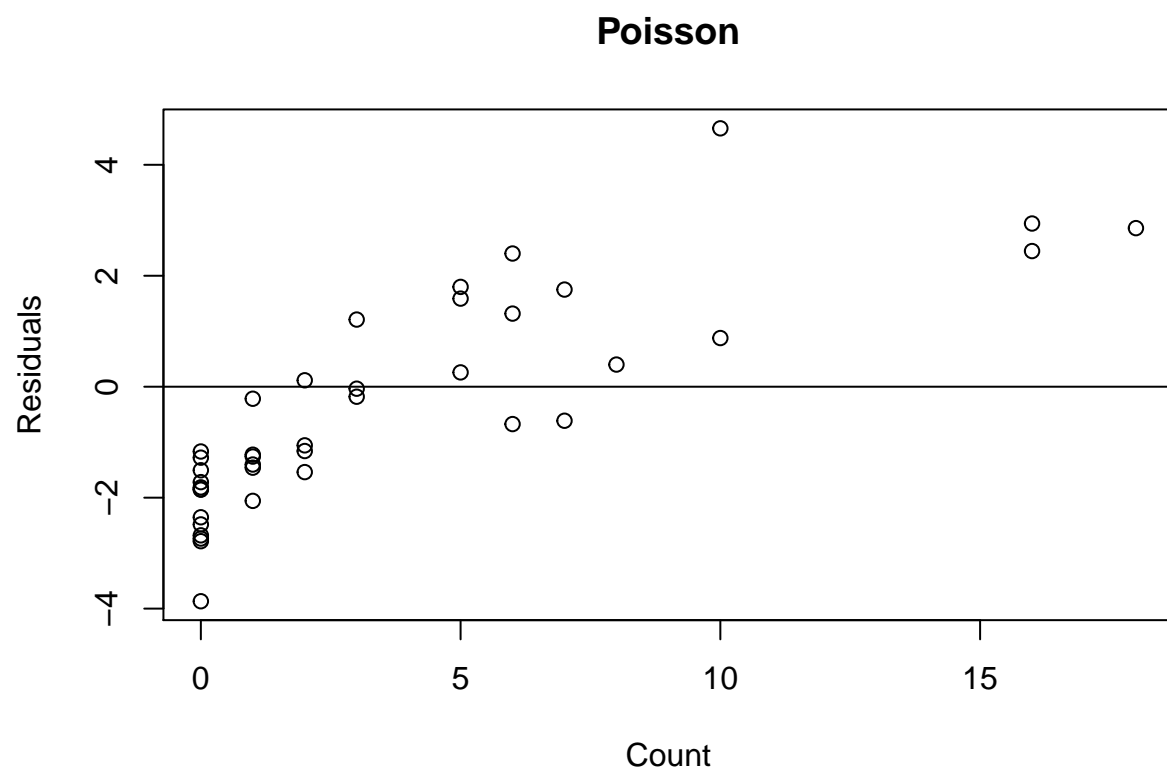

residuals(seed.obs.fit.pois)

Plot residuals from prediction to test for assumptions (seed detection models)

Negative binomial

resfit.nb

Negative binomial

Count

Poisson

Poisson

Seed richness distribution

Empirical density

Cumulative distribution
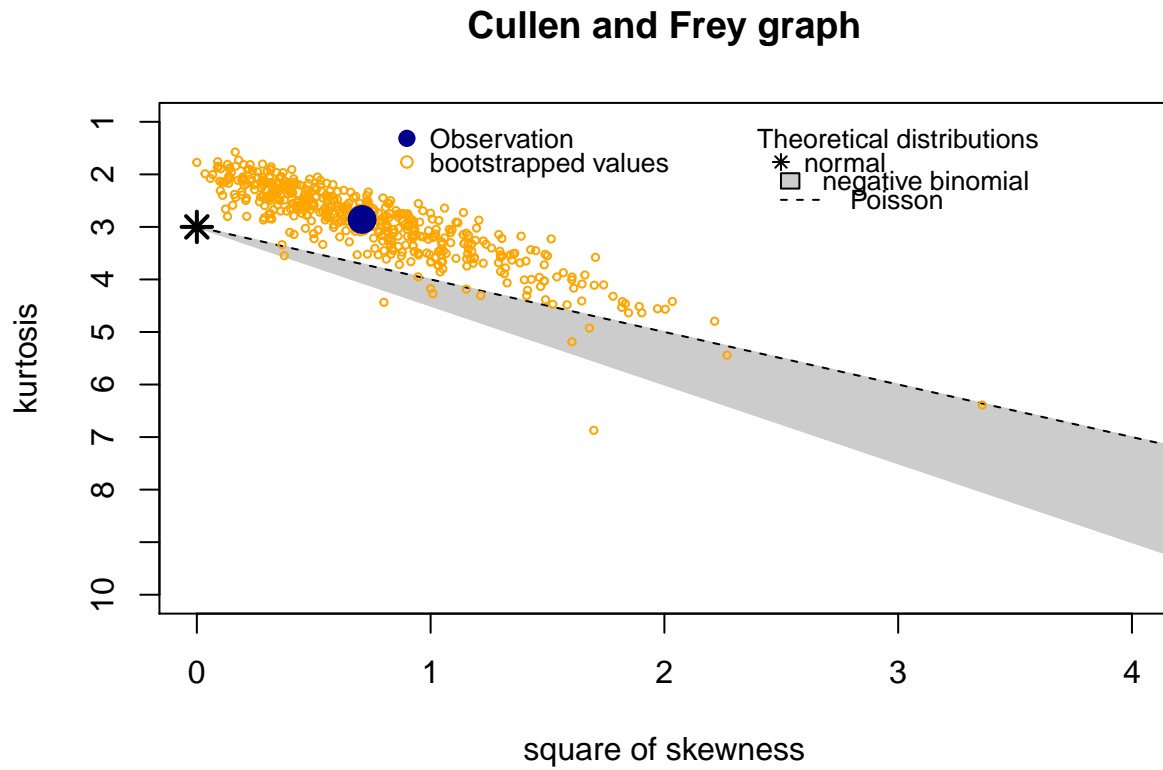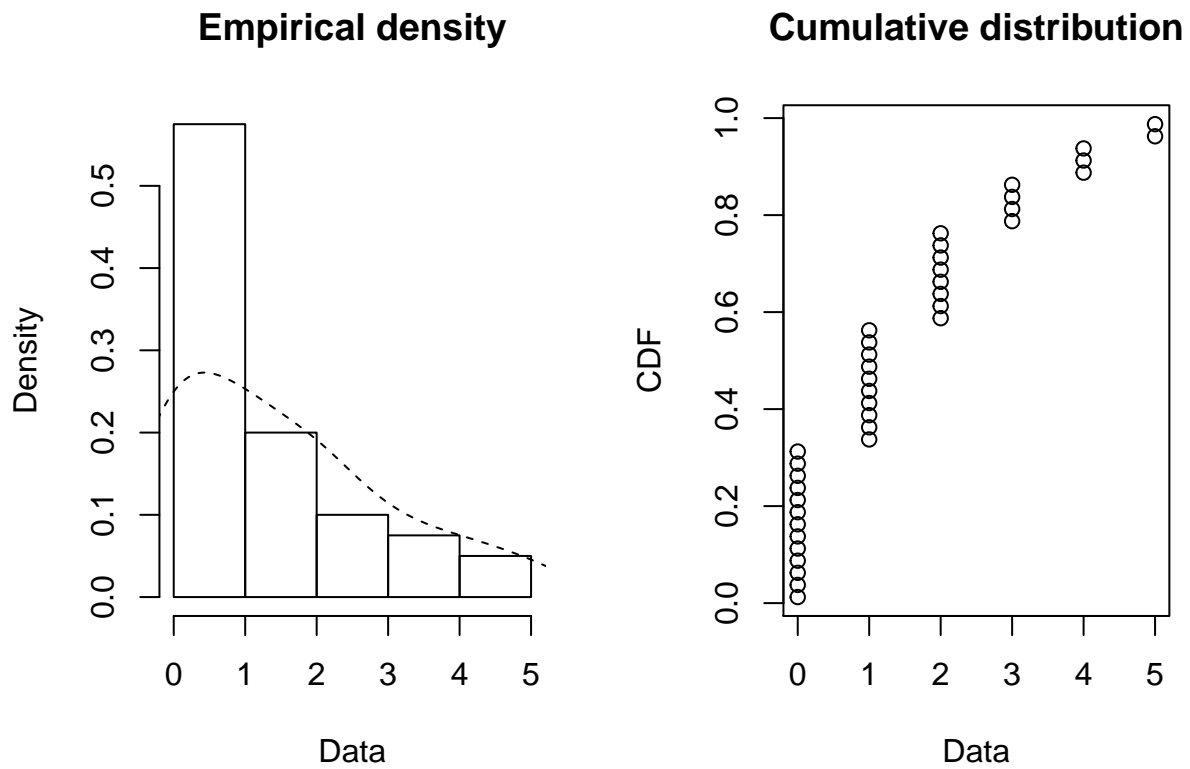

Cullen and Frey graph

```
## summary statistics
## ------
## min:  0    max:  5
## median:   1
## mean:   1.5
## estimated sd:   1.484967
## estimated skewness:   0.840739
## estimated kurtosis:   2.857663
```

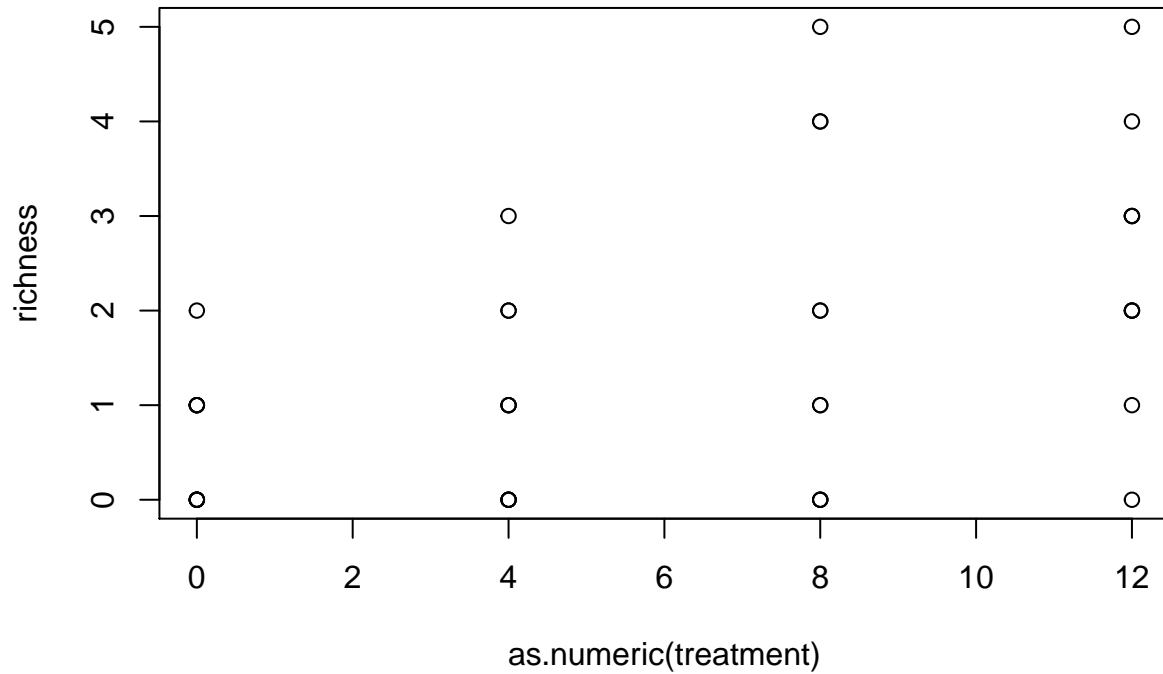# Negative binomial and poisson model fits for seed richness models

```r
# neg binom fit
seeds.rich.fit.nb <- glmer.nb(richness ~ treatment + (1 | sites),
                              data = seed.rich) # iteration limit reached
```

```
## Warning in theta.ml(Y, mu, weights = object@resp$weights, limit = limit, :
## iteration limit reached
```
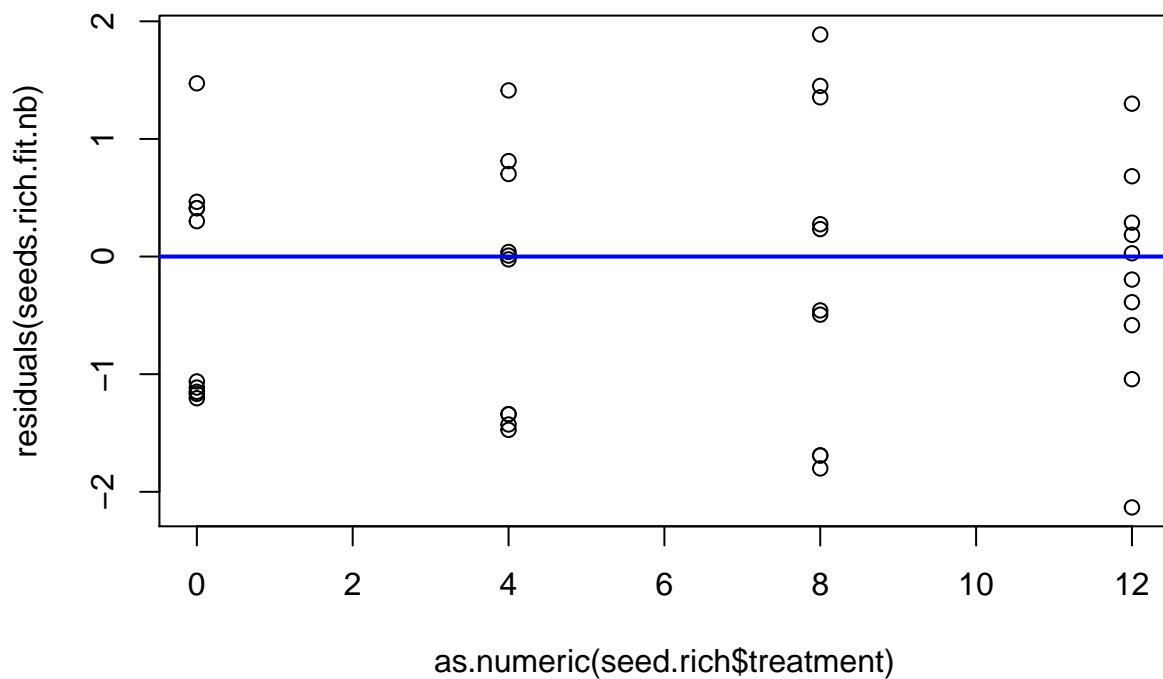
```r
# poisson fit
seeds.rich.fit.pois <- glmer(richness ~ treatment + (1 | sites),
                             data = seed.rich, family = poisson(link = "log"))
```
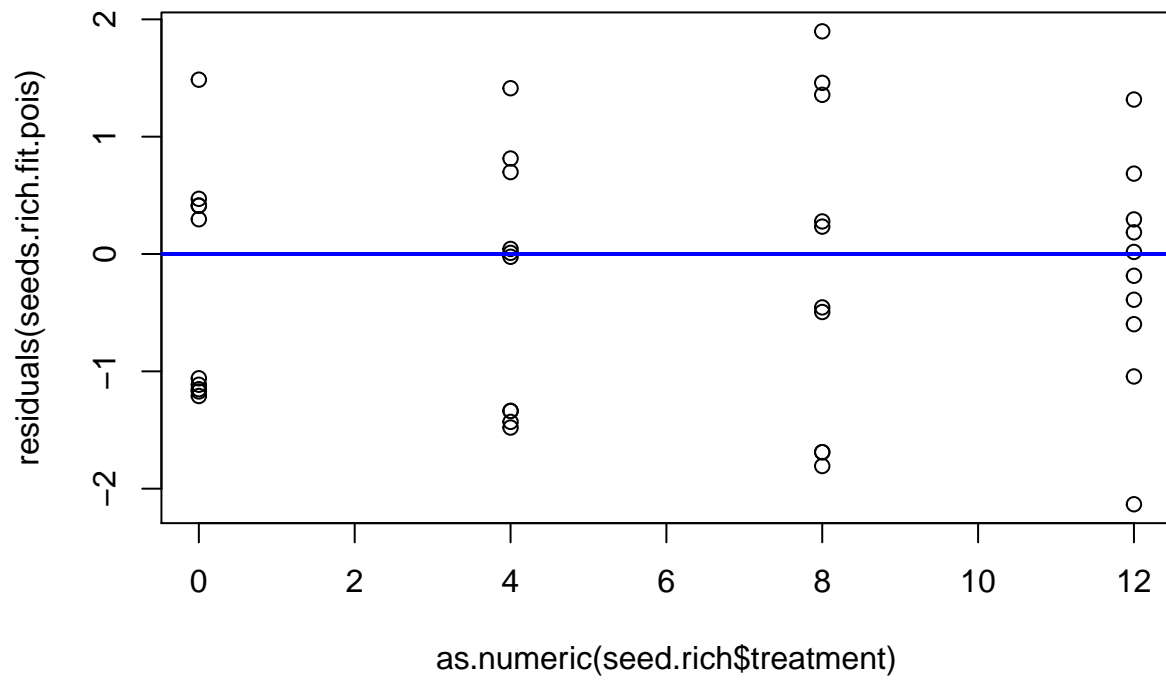
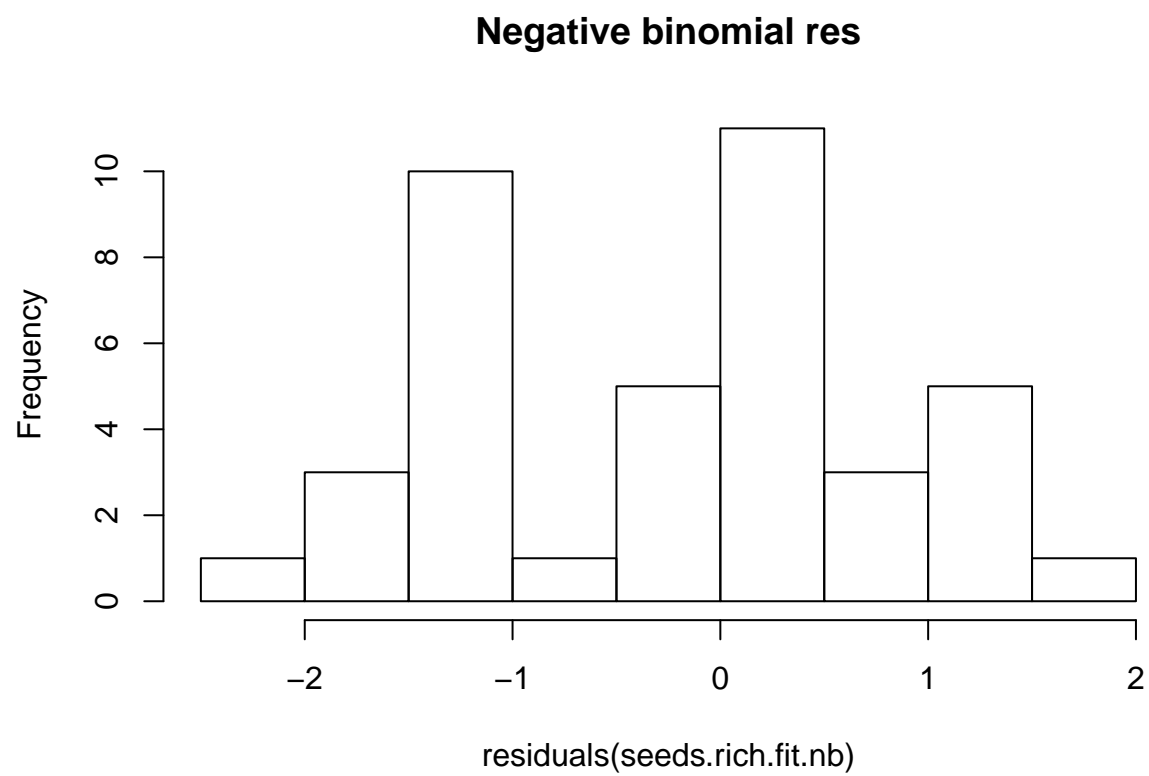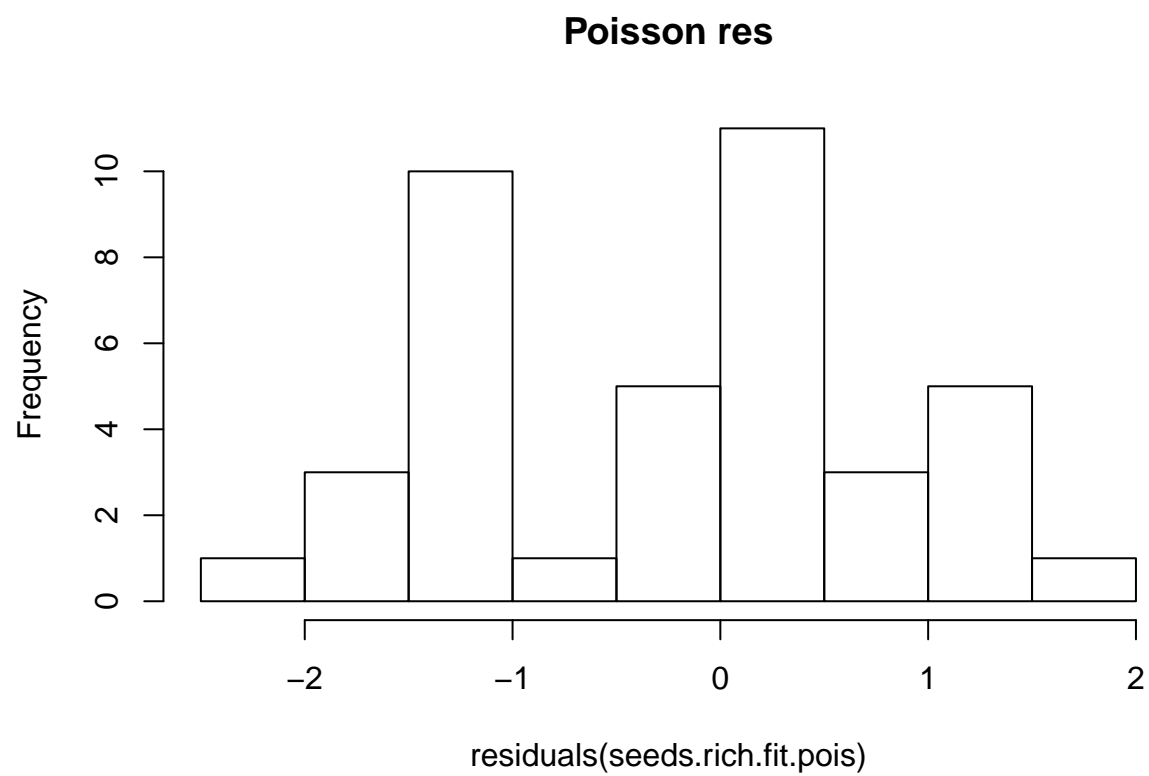Check some assumptions (seed richness models)

Seed richness by treatment

Negative binomial residuals by treatment

Poisson residuals by treatment

Negative binomial res

residuals(seeds.rich.fit.nb)

Poisson res

residuals(seeds.rich.fit.pois)

Plot residuals from prediction to test for assumptions (seed richness models)

Negative binomial

Negative binomial

Poisson

Poisson