

# **Ecotoxicology is not normal.**

**How the use of proper statistical models can increase statistical power in  
ecotoxicological experiments.**

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## **Abstract**

Ecotoxicologists are often confronted with data that is inherently not normally distributed. To achieve the assumptions of normality and homoscedasticity has been a standard procedure to either transform the data or use non-parametric methods if this fails. Here, we argue that using appropriate models, namely Generalised Linear Models (GLM), can enhance statistical power.

We present examples of ecotoxicological studies illustrating the differences and advantages of GLM. Using simulations of two common data types (counts and discrete proportions), we show that GLMs provide a gain in statistical power compared to the analysis of transformed data or using non-parametric methods. Moreover GLMs provide a gain in interpretability of results.

GLMs should become a standard method in ecotoxicology to analyse data that is inherently not normally distributed.

# 1 Introduction

In environmental risk assessments (ERA) statistical tests play an important role to evaluate the effects of pesticides. Despite criticism (e.g. Landis and Chapman (2011)) statistics like the No Observed Effect Concentration (NOEC) are still regularly used to report results experiments (Jager, 2012). A critical issue of reporting a NOEC is the statistical power in the underlying experiments, i.e. the ability to detect an effect.

Ecotoxicologists perform various kinds of experiments yielding to different types of data, potentially with very low samples sizes. Examples are: animal counts in mesocosm experiments (positive, integer valued, discrete data), proportions of surviving animals (discrete, bonded between 0 and 1) or biomass in growth experiments (strictly positive data).

Such data are usually analysed by using methods assuming normal distributed data, although these types are inherently not normally distributed (Wang and Riffel, 2011). In order to approximate the normality and variance homogeneity assumptions data is usually transformed. It is advised that survival data can be transformed using an arcsine square root transformation (Newman, 2012; OECD, 2006). For count data from mesocosm experiments a  $\log(Ax + 1)$  transformation is usually usually, where the constant  $A$  is either chosen arbitrarily or following the recommendation of van den Brink et al. (2000):  $Ax$  to be 2 for the lowest abundance value ( $x$ ) greater than zero. Note, that there has been little evaluation and advice for the practitioners which transformations to use. If the transformed data does not meet the normality assumptions, usually non-parametric tests are applied (Wang and Riffel, 2011).

Generalized linear models (GLM) are a third possibility to analyse such not normally distributed data (Nelder and Wedderburn, 1972). GLMs can handle various types of data distributions, e.g. Poisson or negative binomial (for count data) or binomial (for discrete proportions); the normal distribution being a special case of GLMs. Despite that GLMs were available more than 40 years now, ecotoxicologists do not regularly make use of them.

Recently studies concluded that data transformations should be avoided and GLMs be used as they have better statistical properties (*Do not log-transform count data*, (O'Hara and Kotze, 2010); *The arcsine is asinine*, (Warton and Hui, 2011)). Especially in the light of low sample sizes, which are common in ecotoxicological studies (Sanderson, 2002; Szöcs et al., 2015), differences between statistical methods may be apparent.

We first give two motivating examples showing that different methods may lead to different conclusions. Then we compare three types of statistical methods (transformation and normality assumption, GLM, non-parametric tests) using simulations.

## 2 Motivating examples

### 2.1 Count data

Brock et al. (2014) provides a typical example data from a mesocosm study of mayfly larvae counts on artificial substrate samplers at one sampling day (Figure 1). 18 mesocosms have been sampled, with 6 treatments (Control,  $n = 4$ ; 0.1 mg/L, 0.3mg/L, 1mg/l, 3mg/L,  $n = 3$ ; 10 mg/L,  $n = 2$ ). We will use this data to demonstrate the differences between transformations, different GLMs and a non-parametric approach. A full exemplary analysis of this data using R (R Core Team, 2014) can be found in the supplement.

#### 2.1.1 The linear model

To fit the standard linear model, we first transform the counts following van den Brink et al. (2000) (eqn. 1):

$$\begin{aligned} y_i^T &= \log(Ay_i + 1) \\ A &= 2 / \min(y) \quad , \text{ for } y > 0 \end{aligned} \tag{1}$$

, where  $y_i$  is the measured abundance,  $y_i^T$  the transformed abundance and  $A = 2 / 11 = 0.182$ . We fit the well known linear model:

$$\begin{aligned} y_i^T &\sim N(\mu_i, \sigma^2) \\ y_i^T &= \alpha + \beta x_i \\ \text{var}(y_i^T) &= \sigma^2 \end{aligned} \tag{2}$$

This model assumes a normal distributed response with constant variance ( $\sigma^2$ ). Note, that we it parametrised as contrast ( $\beta x_i$ ) to the control group ( $\alpha$ ) so that the parameters ( $\beta$ ) are directly interpretable as changes from the control group (eqn. 2).

#### 2.1.2 Generalized Linear Models

GLMs are the extension of the normal model, by allowing other distributions of the response variable. Instead of transforming the response variable the counts could be directly modelled by a Poisson distribution:

$$\begin{aligned}
y_i &\sim P(\lambda_i) \\
\log(\lambda_i) &= \mu_i \\
\mu_i &= \alpha + \beta x_i \\
\text{var}(y_i) &= \lambda_i
\end{aligned} \tag{3}$$

Again, this model is parametrised as contrast to the control group. The response variable is linked via a log-function to the predictors, i.a. to avoid negative fitted values (eqn. 3). The Poisson distribution assumes that the mean and the variance are equal - a assumption that is rarely met with ecological data which is typically characterized by greater variance (overdispersion). To overcome this problem a quasi-Poisson distribution could be used which introduces an additional overdispersion parameter ( $\Theta$ ) (eqn. 4).

$$\begin{aligned}
y_i &\sim P(\lambda_i, \Theta) \\
\text{var}(y_i) &= \Theta \lambda_i
\end{aligned} \tag{4}$$

Another possibility to deal with overdispersion is to use a negative binomial distribution (eqn. 5).

$$\begin{aligned}
y_i &\sim NB(\lambda, \kappa) \\
\text{var}(y_i) &= \lambda_i + \kappa \lambda_i^2
\end{aligned} \tag{5}$$

In both cases the parametrisation and link function is the same as in the Poission GLM (eqn. 3). Note, that the quasi-Poisson model assumes a linear mean-variance relationship (eqn. 4), whereas the negative binomial model a quadratic relationship (eqn. 5). The above described models are most commonly used in ecology (Ver Hoef and Boveng, 2007), although other distributions for count data are possible, like the negative binomial model with a linear mean variance relationship (also known as NB1) or the poisson inverse gaussian model (Hilbe, 2014).

### 2.1.3 Hypothesis testing

On this data, we could test different hypotheses like (i) if is there any effect of the treatment or (ii) test single parameters (treatments) to determine the LOEC. We used, following general

recommendations (Bolker et al., 2009), F-tests for the normal and quasi-Poisson models and Likelihood-Ratio (LR) tests for Poisson and negative binomial models to test if there is any treatment related effect. To assess the LOEC we used Dunnett contrasts with one-sided Wald t tests (normal and quasi-poisson) and one-sided Wald Z tests (Poisson and negative binomial).

#### 2.1.4 Results

The Poisson model showed considerable overdispersion and did not fit to the data. Therefore, inferences are not valid and we do not further discuss it's results. The normal ( $F = 2.57$ ,  $p = 0.084$ ) and quasi-Poisson model ( $F = 2.90$ ,  $p = 0.061$ ) did not indicate any treatment related effects. Whereas the LR test of the negative binomial model indicated a treatment related effect ( $LR = 13.99$ ,  $p = 0.016$ ).

see supplement

All methods resulted in similar predicted values, except the normal model predicting always lower abundances (Figure 1). 95% Confidence intervals (CI) where most narrow for the negative binomial model and widest for quasi-Poisson - especially at lower estimated abundances. Accordingly, the determined LOECs differed (Normal and quasi-Poisson: 3 mg/L, negative binomial: 0.3 mg/L).

Brock et al. (2014) assumed normality after data transformation and reported a LOEC of 0.3 mg/L for this data. The reason for this difference may be twofold: (Brock et al., 2014) used a  $\log(2y + 1)$  transformation, whereas we used a  $\log(0.182y + 1)$  transformation (van den Brink et al., 2000). Moreover, we applied a one-sided Dunnett test, as the toxic response in a mesocosm experiment may be either decreasing or increasing (due to biological interactions). Brock et al. (2014) used a one-sided Williams test, which is known to have larger power if the assumptions are met (Jaki and Hothorn, 2013). This example demonstrates that the choice of the statistical model and procedure might have tremendous impact on ecotoxicological inferences, especially when sample sizes are low.

## 2.2 Binomial data

Weber et al. (1989) provides fathead minnow *Pimephales promelas* larval survival data after sodium pentachlorophenol (NaPCP) exposure. This data was also exemplary analysed in Newman (2012). At six NaPCP concentrations (0, 32, 64, 128, 256, 512  $\mu\text{g/L}$ ) with 4 replications ten fish were exposed and proportions of total number alive at the end reported.

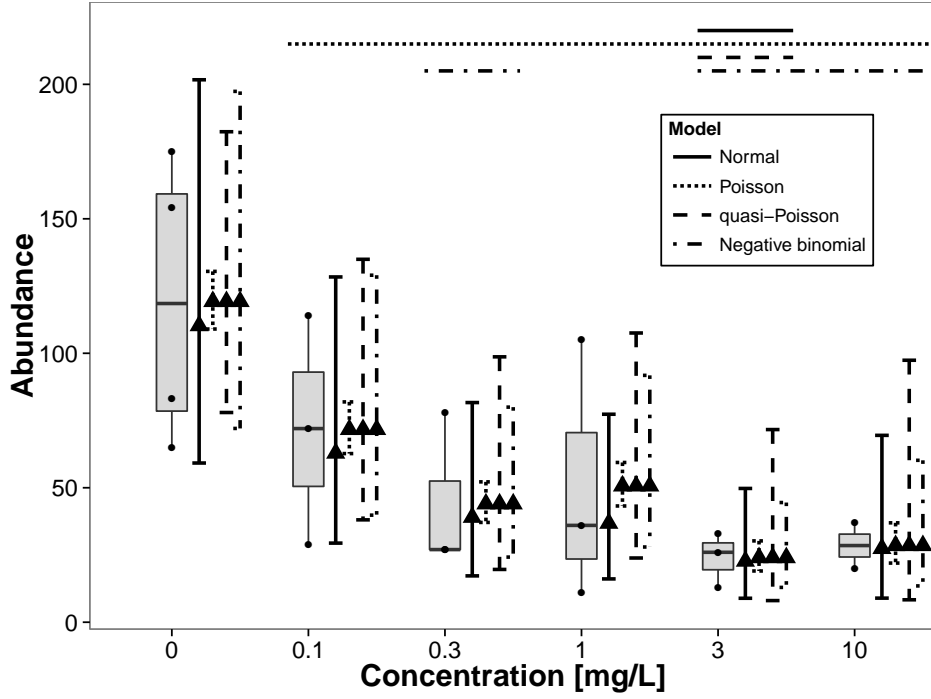


Figure 1: Data from Brock et al. (2014) (boxes + black points) and estimates + 95% Wald Z or t Confidence intervals from the fitted models (vertical lines). Bars above indicate treatments statistically significant different from the control group (Dunnett contrasts).

### 2.2.1 The linear model after transformation

To accommodate the assumption for the standard linear model the EPA suggests a special arcsine square root transformation (eqn. 6) for such kind of data (EPA, 2002):

$$y_i^T = \begin{cases} \arcsin(1) - \arcsin(\sqrt{\frac{1}{4N}}) & , \text{ if } y_i = 1 \\ \arcsin(\sqrt{\frac{1}{4N}}) & , \text{ if } y_i = 0 \\ \arcsin(\sqrt{y_i}) & , \text{ otherwise} \end{cases} \quad (6)$$

, where  $y_i^T$  are the transformed proportions and  $N$  is the number of exposed animals. The transformed proportions are then analysed using the standard linear model (eqn. 2). Note, that the parameters of this are not directly interpretable due to the transformation applied.

### 2.2.2 Generalized Linear Models

Data of type  $x$  out of  $n$  are typically modelled by a binomial distribution with parameters  $N$  and  $\pi$ :

$$\begin{aligned}
y_i &\sim \text{Bin}(N, \pi_i) \\
\text{logit}(\pi_i) &= \alpha + \beta x_i \\
\text{var}(y_i) &= \pi_i(1 - \pi_i)/N
\end{aligned} \tag{7}$$

, with  $N$  = number of exposed animals and  $\pi$  is the probability of survival. The variance of the binomial distribution is a quadratic function of the mean (eqn. 7). The parameters  $\beta$  of this model are directly interpretable as changes in log odds compared to the control group.

We used F-test for the normal and LR test for binomial GLM to determine a general treatment effect. LOEC was assessed using one-sided Dunnett contrasts.

### 2.2.3 Results

For this dataset, both methods yielded to same ecotoxicological inferences: The global tests of both methods indicated a strong effect of NaPCP on larval survival (linear model:  $F = 13.31$ ,  $p < 0.001$ ; GLM:  $LR = 64.79$ ,  $p < 0.001$ ). Moreover, both methods identified the highest concentration (512  $\mu\text{g/L}$ ) as LOEC.

The coefficients of the binomial model are directly interpretable as change in the odds ratio: Compared to the control group, the odds in the highest treatment are reduced by a factor of  $e^{-3.675} = 0.025$ . Such a direct interpretation of parameters is not possible with the transformed data (Table 1).

Table 1: Estimated parameters and 95% Confidence Intervals for the binomial data example.

Asterisks indicate LOEC as determined using one-sided Dunnett tests.

Parameter	Model			
	LM		GLM	
Control ( $\alpha$ )	1.331	(1.180, 1.481)	2.994	(1.523, 4.366)
32 $\mu\text{g/L}$	-0.147	(-0.360, 0.066)	-1.21	(2.876, 0.456)
64 $\mu\text{g/L}$	0.041	(0.172, 0.254)	0.719	(-1.723, 3.161)
128 $\mu\text{g/L}$	-0.076	(0.289, 0.137)	-0.747	(-2.505, 1.010)
256 $\mu\text{g/L}$	-0.221	(-0.434, -0.008)	-1.708	(-3.312, -0.104)
512 $\mu\text{g/L}$	-0.727	(-0.941, -0.514)*	-3.675	(-5.244, -2.107)*

## 3 Simulations

We used simulations to compare the methods described above to analyse count and binomial data. Methods were compared in terms of Type I error (maintain a significance level of 0.05 when there is no effect) and power (detect an effect when it is present). We fitted the models and tested hypotheses on the simulated data as described in the motivating example.

All simulations were done in R (Version 3.1.2) (R Core Team, 2014) on a 64-bit Linux machine with 8 GB and 2.2 GHz. Source code for the simulations is available online at <https://github.com/EDiLD/usetheglm>.

### 3.1 Count data

#### 3.1.1 Methods

We simulated count data that mimics count data encountered in mesocosm experiments, with five treatments (T1 - T5) and one control group (C). Counts were drawn from a negative binomial distribution with slight over dispersion (dispersion parameter for all treatments:  $\kappa = 0.25$ ). We simulated datasets with different number of replicates ( $N = \{3, 6, 9\}$ ) and different abundances in control treatments ( $\mu_C = \{2, 4, 8, 16, 32, 64, 128\}$ ). For power estimation mean abundance in treatments T2 - T5 was reduced to half of control and T1 ( $\mu_{T2} = \dots = \mu_{T5} = 0.5 \mu_C = 0.5 \mu_{T1}$ ), resulting to a theoretical LOEC at T2. For Type I error estimation mean abundance was kept equal between all groups.

For each combination we generated 100 datasets. We fitted a linear model after log ( $Ax + 1$ ) transformation ( $LM$ ), negative binomial GLM ( $GLM_{nb}$ ) and quasi-Poisson GLM ( $GLM_{qp}$ ) to this datasets. We tested a general treatment effect using F tests ( $LM$  and  $GLM_{qp}$ ) and LR tests ( $GLM_{nb}$ ). Additionally, we applied parametric bootstrap to assess the LR in the negative binomial model ( $GLM_{pb}$ ) and used a Kruskal-Wallis test on untransformed data as non-parametric method. To assess the performance in detecting the LOEC (T2 in our simulation design) we used a one-sided Dunnett test for all models and a one-sided pairwise Wilcoxon test as non-parametric method.

#### 3.1.2 Results

For small sample sizes ( $n = 3, 6$ ) and low abundances ( $\mu_C = 2, 4$ ) many of the negative binomial models ( $GLM_{nb}$  and  $GLM_{pb}$ ) did not converge to a solution (convergence rate <80% of the simulations, see supplement). For this simulation design (reduction in abundance by 50%) a sample size of  $n = 9$  was needed to achieve a power greater than 80%.  $GLM_{nb}$  showed

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an increased Type I error at low sample sizes for the test of treatment effect. However, this decreased with increasing sample sizes (Figure 2, bottom). Using parametric bootstrap ( $GLM_{pb}$ ) resulted to an appropriate Type 1 error level for the negative binomial model.  $LM$ ,  $GLM_{qp}$  maintained also an appropriate Type I error. The Kruskal-Wallis test showed least power, with low Type I error at small sample sizes. All GLM showed greater power than  $LM$  or the Kruskal test.  $GLM_{qp}$  showed up to 17% greater power compared to  $LM$ .

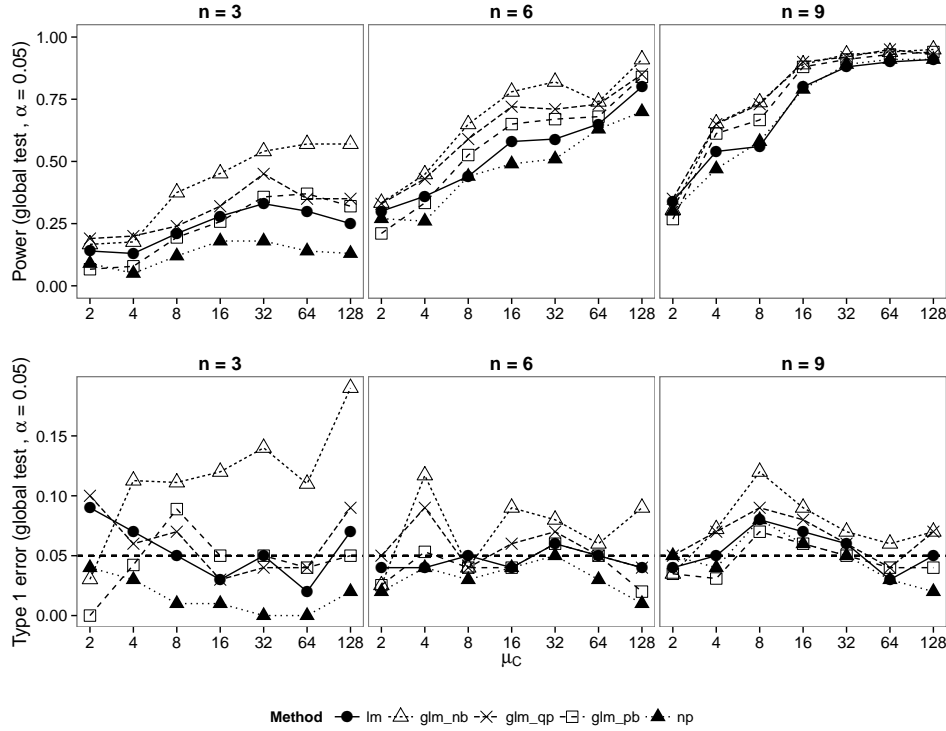


Figure 2: Simulation results for count data. Power (top) and Type I error (bottom) for the test of a treatment effect. Compared methods were: Linear model after log ( $Ax + 1$ ) transformation ( $lm$ ), negative binomial GLM with LRT ( $glm\_nb$ ), negative binomial GLM with parametric bootstrap ( $glm\_pb$ ), quasi-Poisson GLM ( $glm\_qp$ ) and Kruskal-Wallis test on untransformed data ( $np$ ). For  $n = 3$  and  $\mu_C = 2, 4$  less than 80% of  $glm\_nb$  and  $glm\_pb$  models did converge.

The inferences on parameters showed generally less power. For  $LM$  this reduction was up to 35% (Figures 2 and 3). At low sample sizes  $GLM_{nb}$  showed an increased Type 1 error and the pairwise Wilcoxon Test had no power at all to detect the correct LOEC.  $GLM_{qp}$  and  $LM$  yielded comparable Type 1 errors, with  $GLM_{qp}$  having up to 11% greater power (Figure 3, top).

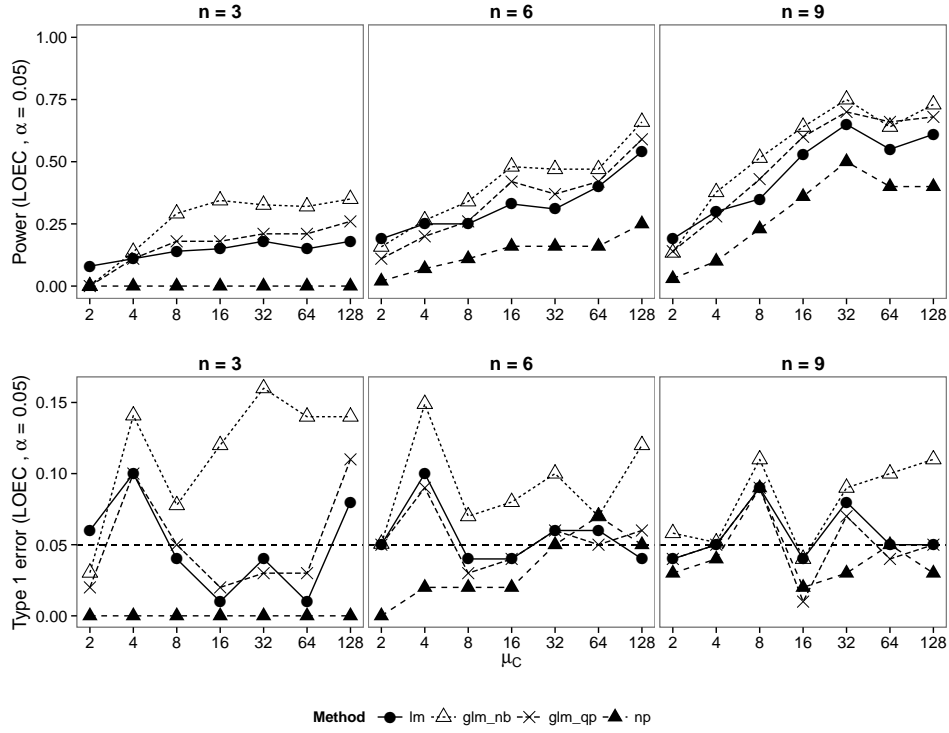


Figure 3: Simulation results for count data. Power (top) and Type I error (bottom) for determination of LOEC. Compared methods were: Linear model after log ( $Ax + 1$ ) transformation (lm), negative binomial GLM with LRT (glm\_nb), negative binomial GLM with parametric bootstrap (glm\_pb), quasi-Poisson GLM (glm\_qp) and pairwise Wilcoxon test on untransformed data (np). For  $n = 3$  and  $\mu_C = 2, 4$  less than 80% of glm\_nb and glm\_pb models did converge.

## 3.2 Binomial data

### 3.2.1 Methods

We simulated data from a design as described in the motivating example, with 5 treated (T1 - T5) and a control group (C). Proportions were drawn from a  $\text{Bin}(10, \pi)$  distribution, with varying probability of success ( $\pi = \{0.60, 0.65, 0.70, 0.75, 0.80, 0.85, 0.90, 0.95\}$ ) and varying number of replicates ( $N = \{3, 6, 9\}$ ). For Type I error estimation  $\pi$  was held constant between groups. For power estimation  $\pi$  in C and T1 was set to 0.95 and  $\pi$  in T2 - T5 varied between 0.6 and 0.95).

We simulated 250 datasets for each combination and analysed them using the linear model after arcsine transformation (LM), binomial GLM (GLM) and Kruskal-Wallis test. Moreover, we compared the methods ability to determine the LOEC (T2 in our simulation design) by

comparing inferences on model parameters and a pairwise Wilcoxon test.

### 3.2.2 Results

Binomial GLM showed greatest power for testing the treatment effect, while maintaining an appropriate Type I error level. This was especially apparent at low sample sizes ( $n = 3$ ), with up to 22% higher power. Kruskal-Wallis test had lowest power and a low Type I error rate. However, the difference between methods quickly vanished with increasing samples sizes (Figure 4).

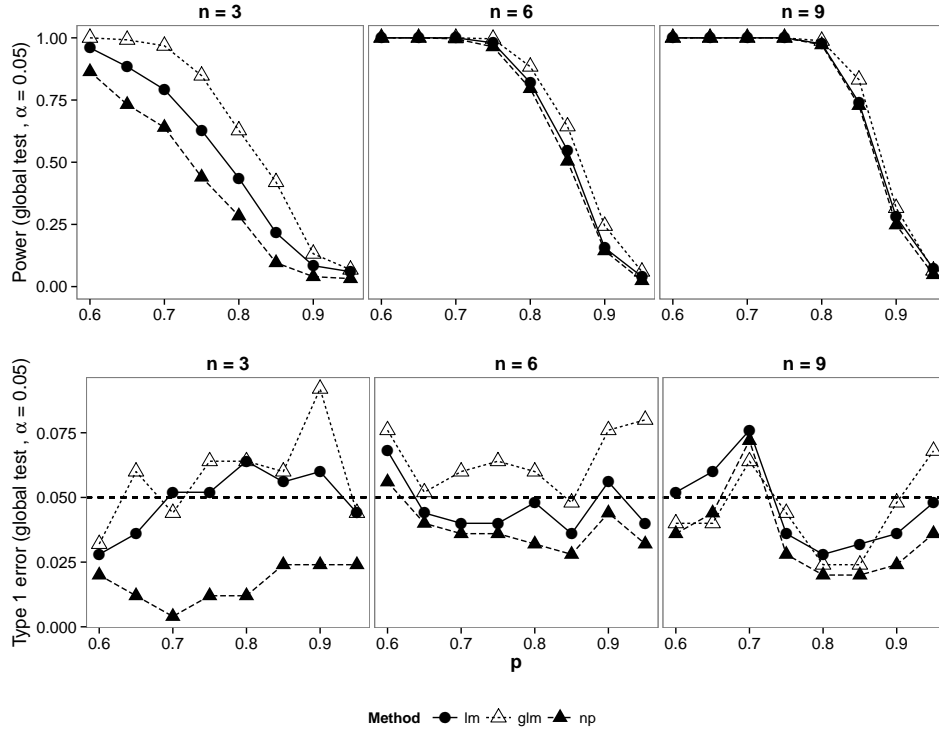


Figure 4: Simulation results for binomial data. Power (top) and Type I error (bottom) for the test of a treatment effect. Compared methods were: Linear model after arcsine square root transformation (lm), binomial GLM with LRT (glm) and Kruskal-Wallis test on untransformed data (np).

Inference on parameters was not as powerful as inference on the general treatment effect. Contrary to the global test, LM showed highest power for small sample sizes, while maintaining a Type 1 error level of 0.05. GLM had less power and showed a low Type 1 error rate, especially with decreasing effect size. The pairwise Wilcoxon test had no power at all for  $n = 3$  and showed less power in the other simulation runs. Differences in power to detect a LOEC was only apparent at  $n = 3$  and vanished quickly with increasing sample sizes (Figure 5).

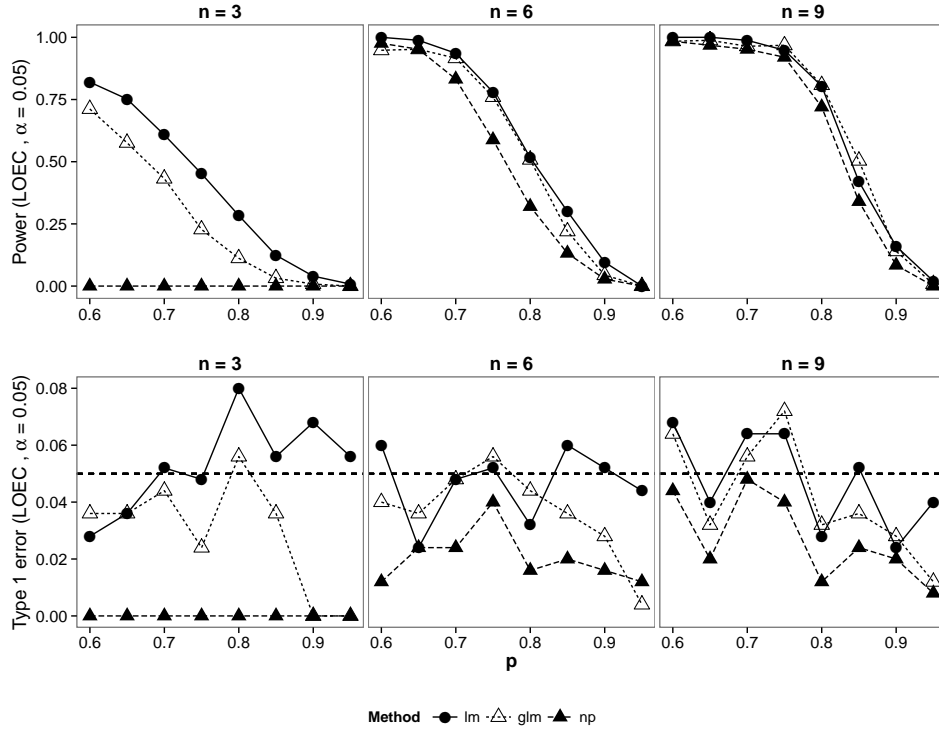


Figure 5: Simulation results for binomial data. Power (top) and Type I error (bottom) for determination of LOEC. Compared methods were: Linear model after arcsine square root transformation (lm), binomial GLM with LRT (glm) and a pairwise Wilcoxon test on untransformed data (np).

## 4 Discussion

Ecotoxicology experiments are often planned with small sample sizes due to practical constraints. For example, extremely low samples sizes ( $n < 5$ ) are common in mesocosm experiments (Sanderson, 2002; Szöcs et al., 2015). Statistical power is crucial for the determination of LOEC/NOEC values. Although, the use of LOEC/NOEC has been heavily criticized in the past (Landis and Chapman, 2011) they are still regularly used in ecotoxicology (Jager, 2012). Especially in mesocosm studies NOEC calculations are used in the majority of mesocosm experiments (Brock et al., 2014; EFSA PPR, 2013). To counteract the problems with low power Brock et al. (2014) proposed to take the Minimum Detectable Difference (MDD), a methods to assess statistical power *a posteriori*, for inference into account. Our results suggest that power in common mesocosm experiment is low. For common samples sizes and a reduction in abundance of 50% we found a unacceptably low power to detect any treatment related effect ( $< 50\%$  for methods with appropriate Type 1 error, Figure 2). Additionally, O'Hara and Kotze (2010) showed that using a log

transformation gave unreliable and biased parameter estimates. Statistical power to detect the correct LOEC was even worse, with power less than 30%. This suggests that NOEC reported from mesocosm experiments should be interpreted with caution. *A priory* power analyses can be performed easily using simulations, even for complex experimental designs (Johnson et al., 2014), and might further help to design, interpret and evaluate ecotoxicological studies.

Moreover, Brock et al. (2014) proposed that statistical power of mesocosm experiments can be increased by reducing sampling variability by better sampling and quantification methods. But they also caution to avoid depleting populations by increasing sampling efficiency. As we showed, using appropriate statistical methods (like GLMs) can enhance the power at no extra costs.

It has been advocated that, in the typical case of small sample sizes ( $n < 20$ ) and non-normal data, non-parametric tests perform better than parametric tests assuming normality (Wang and Riffel, 2011). In contrast our results showed that the often applied Kruskal test and pair-wise Wilcoxon test have equal or less power compared to tests assuming normality after data transformation. Moreover, GLMs always performed better than non-parametric tests. However, there might be more powerful non-parametric tests available (Konietschke et al., 2012) which we did not investigate. Non-parametric statistics are focused on testing, but not on estimation of effects. Additional to testing GLM allow the estimation and interpretation of effects that might not be statistically significant, but ecologically relevant. Therefore, we do not advise to generally use non-parametric tests for non-normal data, but instead try to fit GLMs.

At small sample sizes and low abundance a significant amount of negative binomial models did not converge. We used an iterative algorithm to fit these models (Venables and Ripley, 2002) and other methods directly assessing the Likelihood may perform better. Moreover, the Likelihood-Ratio test gave increased Type-I error for these models. It is well known that the LR statistic is unreliable for small sample sizes (Bolker et al., 2009; Wilks, 1938) and we found that parametric bootstrap provides a valuable alternative in such situations. At small samples sizes and / or low abundances it might be hard to decide which mean-variance relationship fits best. The quasi-Poisson models assumes a simpler, linear mean-variance relationship, which might explain why it performed best for our simulated data sets.

Binomial data is often collected in lab trials. where increasing sample size is easier to accomplish. We found notable differences in power to detect a treatment effect up to a sample size of 9. Similarly, Warton and Hui (2011) also found that GLM have higher power than arcsine transformed linear models. However, for deriving LOEC the normal model was only at low sample sizes more power full. At greater samples sizes greater then three we found no power differences

for detecting the correct LOEC. The interpretation of binomial GLMs is much simpler then for the arcsine transformed data, giving equal or higher power at sample sizes greater then three. Therefore, we recommend to use a binomial GLM instead of the arcsine transformation.

In the introduction we pointed out, that there is little advice how to choose from the plenty of possible transformations. How do GLMs simplify this problem? First of all, the distribution modelled should be chosen to give a statistically sound model. Proportions are bounded between 0 and 1 and could be modelled using a binomial distribution. Counts are positive discrete values and should be modelled with a discrete distribution. In a factorial design the mean-variance relationship can be easily checked with diagnostic plots. Moreover, it should be checked for overdispersion. Standard error will be underestimated and significance overestimated, if not accounted for (Figure 1). The model selection process can be guided by the data and diagnostic plots and, therefore, is much more sound then choosing between transformations.

Although, our simulations covered only simple experimental designs, these findings may also extend to more complex designs. Nested or repeated designs with non-normal data could be analysed using Generalized Linear Mixed Models (GLMM) and may have advantages with respect to power (Stroup, 2014). For community analyses *GLM for multivariate data* have been proposed as alternative to Principal Response Curves (PRC) and yielded to similar inferences, but better indication of responsive taxa (Szöcs et al., 2015; Warton et al., 2012).

## 5 Conclusions

Statistical hypothesis tests are commonly used in ecotoxicology to make inferences on pesticide effects. The choice how we treat, model and test the data can have massive impacts on the conclusions we draw from experiments, especially at extremely low sample sizes. We showed for two common data types in ecotoxicology, that using appropriate models yielded higher statistical power, than trying to meet the assumptions of normality and variance homogeneity using transformations. Therefore, we cannot recommend the current practice to either transform the data or use non-parametric approaches if data is not normally distributed, but instead use models fitting to the data. GLMs should become a standard method in ecotoxicology and guidelines need to be updated accordingly.

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