

COMPARING PERFORMANCE OF ANOVA TO POISSON AND NEGATIVE BINOMIAL
REGRESSION WHEN APPLIED TO COUNT DATA

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NEGATIVE BINOMIAL REGRESSION WHEN APPLIED TO COUNT
DATA

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State University's regulations and meets the accepted standards for the degree of

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ABSTRACT

Analysis of Variance (ANOVA) is the easiest and most widely used model nowadays in statistics. ANOVA however requires a set of assumptions for the model to be a valid choice and for the inferences to be accurate. Among many, ANOVA assumes the data in question is normally distributed and homogenous. However, data from most disciplines does not meet the assumption of normality and/or equal variance. Regrettably, researchers do not always check whether the assumptions are met, and if these assumptions are violated, inferences might well be wrong.

We conducted a simulation study to compare the performance of standard ANOVA to Poisson and Negative Binomial models when applied to counts data. We considered different combination of sample sizes and underlying distributions. In this simulation study, we first assessed Type I error for each model involved. We then compared power as well as the quality of the estimated parameters across the models.

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DEDICATION

To my parents, brothers and sisters, my wife and son for their unconditional love and support.

To my grandfather, Babourema DRAME, for believing in me and his continued unconditional support and love.

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LIST OF ABBREVIATIONS

NB.....Negative Binomial

Var.....Variance

LIST OF SYMBOLS

- μ Population mean.
- $\hat{\mu}$ Estimated sample mean.
- σ Population standard deviation.

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CHAPTER 1. INTRODUCTION

Linear Models analyses will provide accurate inferences only when the data meet certain assumptions (i.e., independence, normality of the residuals, homoscedasticity). Regrettably, researchers do not always verify whether the assumptions are met or not, and if these assumptions are violated, inferences might well be wrong. Data that violate model assumptions can produce incorrect standard errors and p values, and statistical programs do not inform the user when the reported p values are not to be trusted (Atkins & Gallop, 2007).

The normal distribution is the easiest distribution to work with in order to gain an understanding about statistics. In real life distributions are often skewed. Skewness, in statistics, is the degree of distortion from the symmetrical bell curve, or normal distribution, in a set of data. Skewness can be negative, positive or zero. A normal distribution has a skew of zero, while a log-normal distribution, for example, would exhibit some degree of right-skew. Depending on the degree of skewness many statistical techniques don't work resulting for example in a violation of type I error. As a result, researchers often invoke the central limit theorem or use different transformation techniques to make inferences on the data. However, transformations are limited and could result in type I error inflation. The generalized linear models are suitable alternatives. They are more flexible and consider data that have error distribution models other than a normal distribution.

More often, when assumptions are not perfectly met, researchers simply invoke the central limit theorem (CLT) to justify the use of specific statistical method that requires normal distribution. The CLT establishes that as the sample size increases, the sampling distribution of the mean tends toward a normal distribution regardless of the shape of the original distribution in the sample. However, it is rarely clear how big a sample size is big enough to assure that the

CLT protects against Type I errors, and Wilcox (2016), in his introduction to robust estimation and hypothesis tests, and other researchers have convincingly demonstrated that power to detect true effects plummets as assumptions are violated.

Another common remedy is to seek a transformation of the outcome variable that leads to normally distributed residuals (Atkins & Gallop, 2007). Common transformations include the square root, natural log, and inverse transformations (Cohen et al., 2003). Yet transformations are not without issues. First, it is common to find a large proportion of the data stacked at zero, often referred to as the zero-inflated distribution problem. No transformation can spread out a stack of zeros. Second, transforming the outcome fundamentally alters the structure of the residuals, and it is possible to transform the residuals to normality while concurrently violating a different assumption, such as unequal variances. Finally, the other issue with using transformations is that they require thinking in the transformed scale – often researchers do not think in the transformed scale so they back-transform for interpretations which can be misleading or possibly incorrect because the inferences are valid in the transformed scale.

There are many different fields of study that use count data in research including but not limited to sports medicine, animal science, pharmaceuticals, telecommunication, radar processing, econometrics, microbiology and psychology.

Historically the Poisson distribution has been the preferred method to analyze skewed event data. For most researchers count data are better modeled by the Poisson distribution than by the normal distribution. In that the Poisson distribution recognizes the nonnegative integer character of count data and the relative rarity of events during any one period of observation, it does a better job of modeling the nonlinear nature of count level data than the normal distribution (Winkelmann, 2003).

The Poisson distribution may be the benchmark model for count data, but its restrictive assumptions make it impractical in most research studies. First, the Poisson distribution assumes independence in the sense that it is grounded in a memoryless process in which past events do not influence future events (Cameron & Trivedi, 1998). Second, the Poisson distribution assumes that change in the dependent variable is fully modeled by the independent variables in one's regression equation, a process known as population homogeneity (Cameron & Trivedi, 1998). This assumption is rarely satisfied because unobserved heterogeneity is common in most data. Under such circumstances, the negative binomial distribution, a variant of the Poisson distribution, may be more appropriate because it has a second parameter that enables modeling some of this heterogeneity.

As we mentioned earlier, the ANOVA method is commonly used and widely understood by many researchers in medical, microbiological, pharmaceutical and various other fields that frequently deal with count data. Given the concern of using ANOVA to model skewed data although the main assumptions are violated, we are interested in comparing the performance of the traditional one-way ANOVA to Poisson regression and Negative Binomial regression. Most importantly how do the Type I error, power and parameter estimates compare across these three methods when applied to a count data? Essentially, we are interested in how robust ANOVA is when its assumptions are violated such as seen with count data.

The core of this study will be carried out in two phases. In the first phase we will conduct a Type I error estimation using Monte Carlo Simulation in SAS. We will simulate samples from Normal, Poisson and Negative Binomial distributions with varying sample sizes. For each combination of underlying distribution and sample size, we will fit each of the models (Normal, Log-Normal, Poisson and Negative Binomial) and obtain the Type I error. In this process each

model will be fitted to samples where its underlying assumptions are met and to others where its underlying assumptions are violated. The process just described was conducted for distribution with small mean (in our study we chose $\mu=5$ for small mean) and repeated for distributions with large mean ($\mu=20$).

After checking the capability of the models to control Type I error rate, we will then pursue a power comparison in phase 2. The process in phase 2 is pretty much similar to that conducted in phase 1. We will again sample each distribution with varying sample size. We will again fit each model to the simulated data and calculate the corresponding power across several samples.

Additionally, the two phases as described above were carried out under a Two-Treatment scenario. Initially we performed our analysis assuming the treatments have small means ($\mu_1=\mu_2=5$). We replicated the process a second time assuming a large mean ($\mu_1=\mu_2=20$) and obtained our estimated Type I error and Power. We will briefly explore the three-case scenario however that is not the focus of our study. Moreover, we will also apply the two phases described above to real data and see how the results compare to the simulation outcome.

We then attempt to answer the following research questions:

- How do Type I error, Power and Parameter Estimates compare across ANOVA, Poisson regression and Negative Binomial regression when applied to a count data?
- Does the sample size impact the quality of the results obtained?

In the following section, we will first describe more in depth the background of count data methods (Poisson and Negative Binomial), the use of Monte Carlo Simulation and SAS programming to estimate and test the simulated results, as well as past research. Second, we will discuss the methodology and simulation study approach. We will then present the results from

the simulations, along with some discussion on these results. Following the results, we will elaborate on the importance of the results and provide an example using real data. The last section of this paper will consist of the summation and the overall thoughts and findings of this simulation study.

CHAPTER 2. LITERATURE REVIEW

In this chapter, we will review some of the historical literature associated with our paper. First, we will review the use of ANOVA to model counts data, some common transformation used and their limits. Then we will review the generalized linear models as the ideal models for count data. More specifically we will review the use of Poisson and negative binomial regression to model count data. Finally, we will sum it up with review regarding the best model for count data.

ANOVA for Skewed Data

ANOVA was first introduced by Ronald Fisher through a manure trial on potato in 1923. In the following years, ANOVA became institutionalized as the central feature of what is commonly accepted as standard statistical analysis for experimental research data (Stroup, 2015).

To produce correct inferences on data, the Analysis of Variance (ANOVA) method relies essentially on three assumptions, namely: independent observations, normally distributed data and homogeneity of variance. However, in reality data with non-normal distribution are common in most research areas. In contrast to the normal distribution, the variance of Poisson and Negative Binomial distributions depends on the mean. As a result, whenever the normality assumption is violated, most likely the assumption of homogeneity of variance is also violated (Stroup, 2015).

When assumptions are violated one remedy commonly used by researchers is to invoke the central limit theorem. Regardless of the distribution of the data, the central limit theorem provides assurance that the sampling distribution of means could be assumed to be near normal (Stroup, 2015). Therefore, when faced with skewed data, we can ignore the problem and proceed

as if the data were normally distributed (Johnson & Wichern, 1998). This is by far the most common practice.

However, there are problems with invoking the central limit theorem with count data (Wilcox 2016). When assumptions are violated the resulting estimates may not be meaningful; this could result in a relationship not being discovered (i.e., Type II error) or misunderstanding of nonexistent relationship (i.e., Type I error) (Sturman, 1999).

Another common remedy used by researchers is to seek a transformation of the outcome that leads to normally distributed residuals. Usual transformations consist of square root, natural log and inverse transformations (Cohen et al., 2003). Although many of us have been exposed to data transformation, few researchers appear to use them or report data cleaning of any kind (Osborne, 2008b). Box-Cox is another transformation method used to for skewed data. It takes the idea of having a range of power transformations available to improve the efficacy of normalizing and variance equalizing for both positively and negatively skewed variables (Osborne, 2010).

Osborne (2010) showed that although transformations can easily normalize data, normalizing the data can have a dramatic impact on effect sizes in analyses. Data transformations can introduce complexity into substantive interpretation of the results (as they change the nature of the variable) (Osborne, 2010).

As an alternative to ignore normality issues with count data, researchers have come up with the generalized linear model. Generalized linear model techniques include among others, Poisson and Negative Binomial regression that we will introduce below.

Poisson Regression for Counts

Poisson regression is the natural stochastic model for data in which the dependent variable is a discrete count (Cameron & Trivedi, 1999). Count variables are integers, can never be negative and tend to be positively skewed. Whereas ANOVA assumes a normally distributed data which is symmetric and extends from negative to positive infinity, therefore ANOVA is not a good fit for these type of data (Atkins & Gallop, 2007).

Sturman (1999) and Lee (1986) agreed that the Poisson model is particularly attractive for modeling count data because the model has been extended into the regression framework, it presents a simple structure and can be easily estimated. Few critical characteristics of the Poisson distribution (see Long, 1997 pp.218-219; Atkins & Gallop, 2007) are as follows:

- The Poisson distribution is a probability distribution for positive integers.
- The shape of the distribution is strongly controlled by its mean. If the mean is close to zero, the distribution is strongly positively skewed and as the mean increases the distribution approximates a normal distribution.
- Unlike the normal distribution, the variance of a Poisson is equal to its mean.

As Sturman (1999) pointed out, the simplicity of the model is the result of some limiting assumptions violation of which may have great impact on the reliability of and efficiency of the model estimates. For instance, the equality of the mean and variance is not always the case in reality. Many times, real data do not share this property and the variance exceeds the mean known as overdispersion (Atkins & Gallop, 2007). Another important assumption that is not always satisfied is the independence of each occurrence from the number of previous occurrences and the expected number of occurrences is identical for every member of the sample.

Overdispersion may occur in count data due to unobserved heterogeneity. In this case the counts are viewed as being generated from a Poisson process, but the researcher is unable to correctly specify the rate parameter of this process (Cameron & Trivedi, 1999). This issue leads to the widely used negative binomial model that we will discuss below.

Negative Binomial Regression for Counts

Although the assumption of equality of mean and variance has been addressed by the overdispersed Poisson regression model, characteristics of count data may produce further violations of assumptions which may yield flaws in both Poisson and overdispersed Poisson (Sturman, 1999). The Negative Binomial regression model is a direct extension to the Poisson models' that allows for overdispersion (Atkins & Gallop, 2007). Unlike the Poisson model in which the dispersion parameter connecting the mean and the variance is fixed at one, the Negative Binomial model is simply a Poisson regression that estimates the dispersion parameter and allows for independent specification of the mean and variance (Atkins & Gallop, 1999). The variances are the only difference between the Poisson and the Negative Binomial therefore they tend to yield similar regression coefficients, but their standard errors can be different. Overdispersed variables have a larger standard deviation from Negative Binomial relative to Poisson and according to Atkins and Gallop (1999) the larger standard deviation from Negative Binomial is more appropriate. Thus, the probability value in Poisson regression are somewhat low with narrowed confidence interval in the presence of overdispersion.

In 1986 a study conducted by Cameron and Trivedi compared results from analyzing count data for Ordinary Least Squares (OLS) method, Poisson and Negative Binomial regression among others. At a 0.05 significance level the OLS model revealed four statistically significant coefficient out of twelve independent variables. The Poisson model however revealed five others

statistically significant coefficients in addition to the four from OLS whereas the Negative Binomial model came up with the same four detected by the OLS and two by the Poisson model plus one more statistically significant coefficient that neither the OLS nor the Poisson model detected. Cameron and Trivedi (1986) in their conclusion recommended a sequential modeling strategy.

Hausman et Al. (1984) conducted a similar study that focused on developing and adapting models of counts for panel data in which different predictions were obtained from the different models discussed above. Both of these studies referred to above demonstrate a useful alternative modeling strategy. However, they do not clarify on the meaning of statistically significant coefficient as well as the implication of the approaches discussed. Therefore, a more explicit comparison of modeling techniques to demonstrate the implications of various models for research using count data model is needed (Sturman, 1999).

CHAPTER 3. METHODOLOGY

In this chapter we will describe the data generation process and the method used to conduct this study.

Data Simulation Overview

The main purpose of this simulation study is to test the robustness of ANOVA, Poisson and Negative Binomial regression due to misspecification. We will be estimating Type I error, Power and parameter estimates (means) when the underlying distribution assumptions are met. We will then repeat the process by violating the underlying distribution assumptions and obtain the corresponding estimated Type I error, Power and the parameter estimates.

We simulated data from 10,000 samples with two treatments each with varying size but having equal means. By definition, Type I error is estimated by counting the number of times the null hypothesis was incorrectly rejected and dividing it by 10,000. Three main data-generating distributions using SAS are considered namely, Normal, Poisson and Negative Binomial.

We will consider different scenarios while simulating the data for our study. We will look at two main scenarios. First, we will simulate data from Normal, Poisson and Negative Binomial regression with a small mean. We chose here the level for the small mean as μ equals to 5. Then for the second scenario, we will set the value for the large mean at μ equal to 20. For each level of μ and for each underlying distribution, we considered varying level of sampling efforts. For our study, we are exploring two treatment groups with equal size levels from 5, 10, 15 and 20.

During our initial trial, the negative binomial regression model exhibited some convergence issues. We isolated the samples that were not converging for further investigation. For instance, Table 1 below shows data generated from the normal distribution when the mean is equal to 20 and variance equal to 20.

For all approaches used to fit the data, the estimated Type I error are very close to the theoretical 0.05 value and therefore, even if our model is not normal, it is not affecting the Type I errors. However, we noticed few samples failed to converge. Out of 10,000 samples only 63 did not converge. It might require a thorough investigation to understand what specific feature of these samples prevented them from converging. Since the percentage of the sample is somewhat less than 1% as shown in the table below, we therefore will ignore them for the rest of this study as this appears to have minimal impact on the results.

Table 1. Type I rejection rate for all fitted models

| Models | Normal Distribution | | |
|-------------------|---------------------|-------|-------|
| | ProbF (Pr>F) | | |
| | Reject | DNR | Total |
| Normal | 487 | 9513 | 10000 |
| Log-Normal | 410 | 9590 | 10000 |
| Poisson | 423 | 9577 | 10000 |
| Negative Binomial | 461 | 9476 | 9937 |
| Total | 1781 | 38156 | 39937 |

Simulation Parameters

Below we provide in detail the list of parameters used for our simulation in this study and their definitions:

- a) Sample: The number of samples for each underlying distribution; 10000 samples were used in this study.
- b) N(i): Sample size for treatment i population.
- c) Lambda(i): Poisson parameter for treatment i population.
- d) Mu(i): The mean of the normal distribution for treatment i population.

- e) $S(i)$: The variance of the normal distribution for treatment i population. Conventionally s represents the standard deviation but, in our study, we used it as variance.
- f) $P(i)$: The p parameter of the Negative Binomial distribution for treatment i population.
- g) $K(i)$: the k parameter of the Negative Binomial distribution for treatment i population.

The selection of the underlying parameters came from a dataset that originally inspired this study. The data set was from a microbiology thesis study with count response variable.

Type I Error Assessment

In a comparative power analysis, it is important to ensure that each model involved has controlled Type I error. Power comparisons between two models exhibiting different Type I error rates could most likely lead to an incorrect model selection being more powerful. There is strong correlation between Type I error rate and power such that a slight deviation in Type I error can significantly impact the power.

For our study, we simulated 10,000 samples of two treatments each of size n from the same underlying distribution. We then fit the models to each sample and count the number of times the null hypothesis for the test below was rejected:

$$H_0: \mu_1 = \mu_2$$

$$H_a: \mu_1 \neq \mu_2$$

The Type I error is obtained for each underlying distribution by dividing the total count of null hypothesis that was rejected by 10,000 (number of simulated samples). For a significance level of $\alpha=0.05$, we obtained the Type I error for each combination of underlying distributions and sampling efforts.

Power Comparison

We conducted power comparisons to check if certain models perform better than other under various conditions. For the power comparisons we considered three effect sizes: 0.5σ , 1σ and 2σ . By 1σ effect size we refer to the mean difference between a pair of treatments is equal to its standard deviation. For example, suppose that we have mean $\mu_1=20$ and variance $\sigma_1^2=25$ for treatment 1; a 1σ effect size will correspond to mean $\mu_2 = (\mu_1 - \sigma) = (20 - \sqrt{25}) = 15$ and variance $\sigma_2^2=25$ for treatment 2 such that $\mu_1 - \mu_2 = \sigma = \sqrt{25} = 5$. In general, as the effect sizes increase it becomes easier to detect any difference in means; namely, the power of the test increases as well.

Regarding the two-population scenarios in our study, we obtained the estimated power of the test by simulating observation from two treatments from the same underlying distributions (Normal, Poisson and Negative Binomial) and then fit each model (Normal, Poisson and Negative Binomial regression) to the simulated observations keeping count of the number of times the null hypothesis of the test below is rejected:

$$H_0: \mu_1 = \mu_2$$

$$H_a: \mu_1 \neq \mu_2$$

The power is defined as the probability of rejecting the null hypothesis when in fact it is false. Simulating our observations from two populations with different means and setting the null hypothesis as defined above makes the null hypothesis false. Taking the number of times each of the models correctly detect the difference in the two treatments (rejecting H_0 since there are in fact different and dividing it by 10,000 will give us our estimated powers). This process was repeated for each combination of underlying distribution and effect size. As we mentioned earlier, our expectation is that the powers will increase as the effect size becomes larger.

Parameter Estimates

After estimating the Type I errors for each situation, we further our research by estimating the parameters of the model. We are interested in how well each model estimates the parameters.

Essentially, we would like to see how accurately each of the models estimates the means. The estimates obtained will be compared to the actual means. Here we are mimicking methods described by Stroup (2012) in his book in Table 11.1, page 340. We suspect that each fitted model will perform relatively well in terms of the Type I error. However, if one wants to actually estimate the means, the model that is used might make a difference.

In the two-treatment case the model used might not be as impactful in estimating the means since there are only two treatments (two means) to compare; they are either equivalent or different. It will be then of interest to consider expanding to three treatments (three means) case. This is where the estimated parameters may be important when it comes to deciding which model is the best to use. For instance, if we have more than two treatments (means) we can then look closely to detect which treatment (mean) is different from the others. Such a study is generally complex with a high variability in the data.

In this research we conducted a small simulation study for three populations. We estimated Type I error and power as well as the means of the models. This is not however the focus of our study but could serve as a basis for potential future research in that direction. We will focus more on the two treatments scenarios in this research.

Simulation Study Outline

We provide below a synopsis of this simulation study in detail:

- 1) Type I error assessment with two treatments: $\mu_1 = \mu_2$
 - a) Three underlying distributions: Normal, Poisson and Negative Binomial.
 - b) Four levels of sampling effort: $n=5$, $n=10$, $n=15$ and $n=20$ for each combination of treatments and underlying distribution.
 - c) Fitted models: ANOVA, ANOVA on log transformation, Poisson and Negative Binomial Regression.
 - d) Simulation was conducted taking 10,000 samples for each combination of parameters defined above.
- 2) Type I error assessment with three treatments: $\mu_1 = \mu_2 = \mu_3$.
 - a) Three underlying distributions: Normal, Poisson and Negative Binomial.
 - b) Four levels of sampling effort: $n=5$, $n=10$, $n=15$ and $n=20$ for each combination of treatments and underlying distribution.
 - c) Fitted models: ANOVA, Log Normal Transformation, Poisson and Negative Binomial Regression.
 - d) Simulation was conducted taken 10,000 samples for each combination of parameters defined above.
- 3) Power comparison with two treatments: $\mu_1 \neq \mu_2$
 - a) Three underlying distributions: Normal, Poisson and Negative Binomial.
 - b) Four levels of sampling effort: $n=5$, $n=10$, $n=15$ and $n=20$ for each combination of treatments and underlying distribution.

- c) Fitted models: ANOVA, ANOVA on Transformation, Poisson and Negative Binomial Regression.
 - d) We considered three effect sizes: 0.5σ , 1σ and 2σ .
 - e) Simulation was conducted taking 10,000 samples for each combination of parameters defined above.
- 4) Power comparison with three treatments: $\mu_1 = \mu_2 = \mu_3$.
- a) Three underlying distributions: Normal, Poisson and Negative Binomial.
 - b) Four levels of sampling effort: $n=5$, $n=10$, $n=15$ and $n=20$ for each combination of treatments and underlying distribution.
 - c) Fitted models: ANOVA, ANOVA on Transformation, Poisson and Negative Binomial Regression.
 - d) We considered two effect sizes: 0.5σ and 1σ between the smallest and largest mean.
 - e) Simulation was conducted taking 10,000 samples for each combination of parameters defined above.
- a) Parameters estimates: The same parameters are estimated in case where we considered Type I error (equal means) and Power (means differ)
- a. Estimated means of the samples: we take the total mean of each treatment and divide by 10,000.
 - b. Standard deviation of the estimated means over all simulated samples.
 - c. Standard Error of the simulated samples means based on the assumed model.
 - d. Average mean differences
 - e. Standard deviation of the mean differences

- f. Standards Error of the mean differences based on the assumed model.

SAS Code

The SAS code used for this simulation study is provided in Appendix (). We provided the SAS code for the simulation from one underlying distribution since to get the others we just changed the underlying distribution to the desired distribution and everything else remains the same.

CHAPTER 4. RESULTS

In this chapter, we will discuss the results obtained from the Type I error assessment as well as for the power comparison for each underlying distribution we considered in the case of two populations scenarios.

Type I Error Assessment for Two-Treatments: $\mu_1 = \mu_2$

As defined in the methodology section, the Type I error is the probability of rejecting the null hypothesis when it is in fact true. In our study we set our alpha level at $\alpha=0.05$ and expect our estimated Type I error to be approximately 0.05.

For our simulation study, we estimated Type 1 errors based on two random samples from underlying distributions using three different models. Samples sizes from both populations were assumed to be equal and different samples sizes were used. Type I errors were estimated when the means were both 5 and then when the means were both 20.

For our simulation study we considered, for different combinations of underlying distribution and sampling efforts two main populations. First, we set the mean of the underlying distribution to be equal to 5 (that we referred to as small mean) with variance 5 and then estimated the Type I error for different combinations of underlying distribution, models and sampling efforts. And we repeated the process just described and set the mean to be equal to 20 with variance 20.

Regarding the Negative Binomial distribution, we solved for p and k accordingly which are the parameters used in SAS for generating the data. It is important to note that since the Negative binomial deal specifically with overdispersion, we increased the variance from 5 to 7.5 for the small means and from 20 to 25 for the large means.

Table 2 below displays the estimated Type I errors when sampling from Normal distributions with both means equal to 5. The results suggest that, for all combinations of sampling efforts and fitted models (Normal, Log-Normal, Poisson and Negative Binomial), Type I error is being maintained near the stated rate of $\alpha=0.05$ with the exception of Log-Normal which is conservative when $n=5$. Likewise, as shown in Tables 3 and 4, the results obtained when the data are from Poisson and Negative Binomial with mean 5, Type I error is maintained near the stated value of 0.05 for all combinations of sampling efforts and fitted models (Normal, Log-Normal, Poisson and Negative Binomial).

Table 2. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = 5$

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 4.87 | 4.00 | 4.26 | 4.46 |
| $n_1 = n_2 = 10$ | 5.35 | 4.42 | 5.00 | 5.91 |
| $n_1 = n_2 = 15$ | 4.85 | 4.50 | 4.71 | 5.77 |
| $n_1 = n_2 = 20$ | 4.67 | 4.30 | 4.57 | 5.79 |

Table 3. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = 5$

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 5.40 | 4.86 | 4.92 | 5.27 |
| $n_1 = n_2 = 10$ | 5.04 | 4.39 | 4.83 | 5.38 |
| $n_1 = n_2 = 15$ | 4.94 | 4.27 | 4.72 | 5.20 |
| $n_1 = n_2 = 20$ | 5.06 | 4.63 | 4.95 | 4.95 |

Table 4. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = 5$

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 4.93 | 4.20 | 4.43 | 4.69 |
| $n_1 = n_2 = 10$ | 4.85 | 4.34 | 4.70 | 4.98 |
| $n_1 = n_2 = 15$ | 5.18 | 4.45 | 5.00 | 5.21 |
| $n_1 = n_2 = 20$ | 5.22 | 4.75 | 5.20 | 5.32 |

Tables 5, 6 and 7 contain results when data are taken from Normal, Poisson and Negative Binomial distributions respectively with mean 20. Across all levels of sampling efforts (5, 10, 15 and 20), the fitted models seem to perform very well. We can see that Type I error is controlled around the stated alpha value of 0.05.

The models (Normal, Log-Normal, Poisson and Negative Binomial) all controlled Type I error very well regardless of whether the data was taken from Normal, Poisson or Negative Binomial distribution for both small means (mean =5) and large means (mean=20).

Table 5. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = 20$

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 4.87 | 4.51 | 4.62 | 4.73 |
| $n_1 = n_2 = 10$ | 5.35 | 5.19 | 5.24 | 5.58 |
| $n_1 = n_2 = 15$ | 4.85 | 4.76 | 4.75 | 5.21 |
| $n_1 = n_2 = 20$ | 4.67 | 4.51 | 4.64 | 5.11 |

Table 6. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = 20$

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 5.07 | 4.97 | 4.93 | 5.09 |
| $n_1 = n_2 = 10$ | 5.09 | 5.11 | 5.03 | 5.33 |
| $n_1 = n_2 = 15$ | 4.92 | 4.89 | 4.89 | 5.15 |
| $n_1 = n_2 = 20$ | 4.96 | 4.93 | 5.01 | 5.23 |

Table 7. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = 20$

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 4.94 | 4.70 | 4.66 | 4.87 |
| $n_1 = n_2 = 10$ | 5.01 | 4.84 | 5.05 | 5.15 |
| $n_1 = n_2 = 15$ | 4.86 | 4.71 | 4.84 | 5.00 |
| $n_1 = n_2 = 20$ | 4.91 | 4.95 | 4.94 | 5.01 |

Type I Error Assessment for Three-Treatments: $\mu_1 = \mu_2 = \mu_3$

As we mentioned earlier in our methodology section, we ran a simulation for the three treatments case for when all means were equal to 20 (large means case).

Clearly from Tables 8, 9 and 10, we can confidently say that the Type I error is maintained for each combination of sampling effort and underlying distribution. The Type I errors are all within ± 0.01 of the stated alpha level of 5%. These results are what we actually expected to see. The model used may make more of a difference when estimating the parameter (mean)

Table 8. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = \mu_3 = 20$

| Sampling Efforts | Fitted Models | | | |
|------------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = n_3 = 5$ | 4.82 | 4.61 | 4.51 | 4.56 |
| $n_1 = n_2 = n_3 = 10$ | 5.12 | 4.88 | 4.79 | 5.00 |
| $n_1 = n_2 = n_3 = 15$ | 5.12 | 4.81 | 5.01 | 5.19 |
| $n_1 = n_2 = n_3 = 20$ | 4.81 | 4.43 | 4.73 | 4.75 |

Table 8 above gives us the Type I errors when sampling from Normal distribution with mean 20. When we fit the models (Normal, Log-Normal, Poisson and Negative Binomial) to the normal data, Type I error is controlled near the stated alpha level of 0.05 across all sampling efforts for each model.

Table 9. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = \mu_3$

| Sampling Efforts | Fitted Models | | | |
|------------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = n_3 = 5$ | 4.86 | 4.74 | 4.71 | 4.84 |
| $n_1 = n_2 = n_3 = 10$ | 4.95 | 4.89 | 4.87 | 5.18 |
| $n_1 = n_2 = n_3 = 15$ | 5.03 | 5.10 | 5.03 | 5.22 |
| $n_1 = n_2 = n_3 = 20$ | 4.89 | 7.93 | 4.84 | 5.21 |

The same results are obtained when sampling the data are from Poisson and Negative Binomial distribution. As shown in Table 9 and table 10, Type I error is controlled. For each combination of fitted models and sampling efforts, the Type I errors are all approximately 0.05, the stated alpha value.

Table 10. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = \mu_3$

| Sampling Efforts | Fitted Models | | | |
|------------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = n_3 = 5$ | 5.10 | 4.73 | 4.85 | 5.03 |
| $n_1 = n_2 = n_3 = 10$ | 5.09 | 5.10 | 5.06 | 5.27 |
| $n_1 = n_2 = n_3 = 15$ | 4.44 | 4.49 | 4.44 | 4.57 |
| $n_1 = n_2 = n_3 = 20$ | 5.01 | 5.02 | 4.97 | 5.12 |

The results obtained from the Type I error assessment for each combination of sampling efforts and underlying distributions, suggests that all the models fitted (Normal, Log-Normal, Poisson and Negative Binomial) control the Type I errors. Therefore, each of the above models are valid candidate to test the null hypothesis that the means are equal using count data. We will next discuss the results from the power comparison and parameters estimates quality to decide whether a particular model is preferred over the rest.

Power Comparison for Two-Treatments $\mu_1 \neq \mu_2$

- Effect size: Half sigma (0.5σ)

For two-treatment normal samples with a half sigma effect size, we can see from Table 11 and Figure 1 that the Normal model yielded higher powers to the Poisson and Negative Binomial models across all sampling sizes when the data are actually from a normal distribution. The Negative Binomial model has the second highest powers followed by the Poisson and Log-Normal. Log-Normal has the lowest power among the four models.

The results could be explained by the fact that Poisson and Negative Binomial are more designed to handle count data and it makes sense that the Normal model has higher power when the data are normally distributed. Also, since the data are actually normal, the log transformation actually causes the distribution to become asymmetric and less consistent with the ANOVA assumption.

Table 11. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$
(Effect size=0.5 σ , $\mu = 5$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 10.57 | 7.90 | 8.60 | 9.17 |
| $n_1 = n_2 = 10$ | 18.25 | 14.18 | 15.36 | 16.65 |
| $n_1 = n_2 = 15$ | 27.17 | 20.87 | 23.03 | 24.99 |
| $n_1 = n_2 = 20$ | 33.33 | 25.22 | 28.33 | 30.38 |

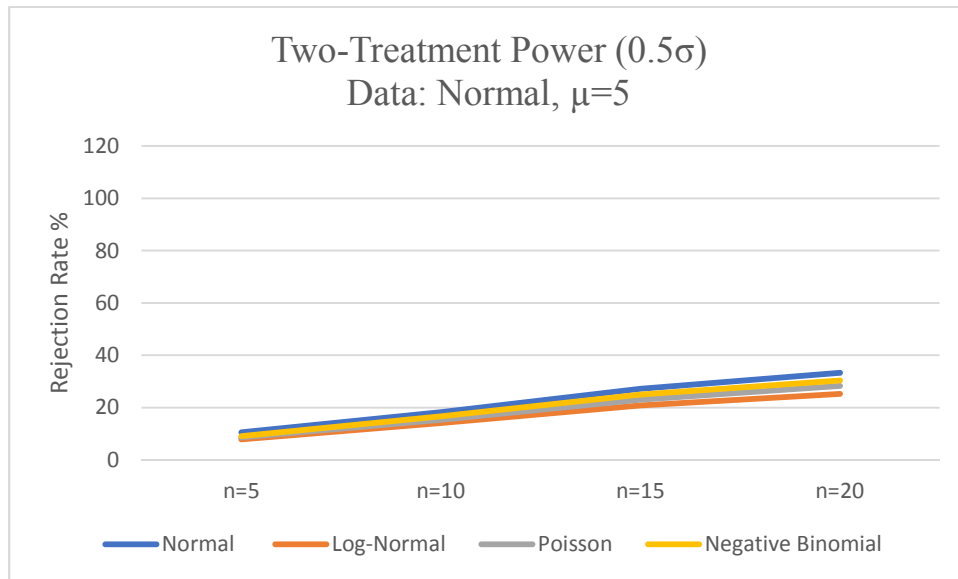


Figure 1. Normal Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$
(Effect size=0.5 σ , $\mu = 5$)

The results obtained in Table 12 below are estimated powers comparison from our fitted models when the data are sampled from a Poisson distribution with mean 5 and a half sigma effect size.

The three models, Normal, Poisson and Negative Binomial, yielded approximately the same powers. This is true throughout all sample sizes.

This is illustrated in Figure 2. Clearly, we can see that all the lines (except Log-Normal with the smallest power among the three) are almost indistinguishable.

Table 12. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size=0.5 σ , $\mu = 5$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 11.7 | 9.91 | 11.00 | 11.53 |
| $n_1 = n_2 = 10$ | 20.10 | 17.22 | 19.83 | 20.70 |
| $n_1 = n_2 = 15$ | 28.60 | 24.49 | 28.18 | 29.40 |
| $n_1 = n_2 = 20$ | 37.98 | 32.35 | 37.61 | 38.59 |

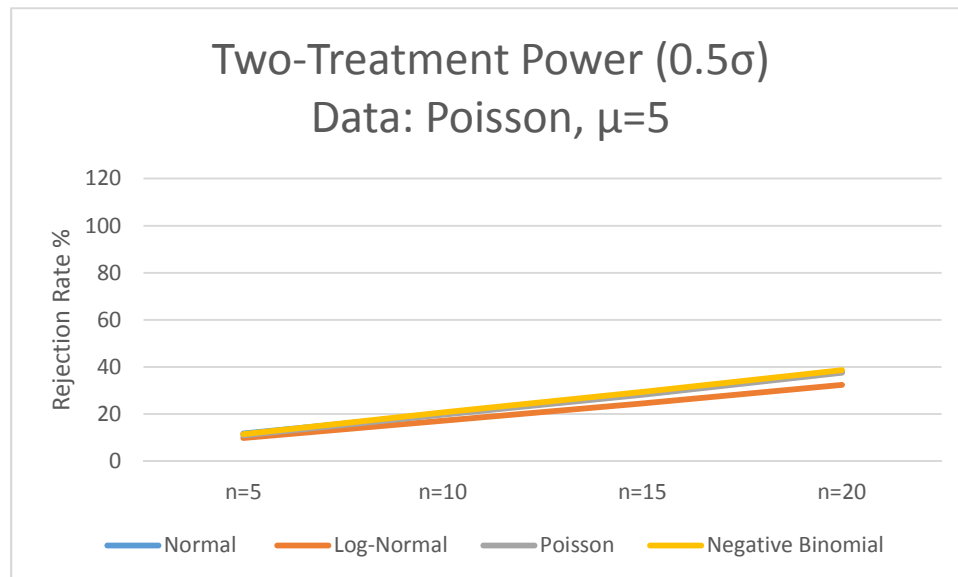


Figure 2. Poisson Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size=0.5 σ , $\mu = 5$)

Unlike the Poisson data, From Table 13 and Figure 3 below we can see that when sampling from Negative Binomial, all four models closely estimated powers for $n=10$. However, when $n=5$ the Normal model displays a slightly higher power. The Poisson and Negative Binomial models yielded close estimated powers whereas Log-Normal has the smallest power among the four models. For $n \geq 15$, Log-Normal has the highest powers, followed by the Normal model. Poisson and Negative Binomial models still have the close powers but smaller powers than the normal and log-normal models.

Table 13. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 0.5σ , $\mu = 5$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 12.39 | 9.74 | 10.90 | 11.73 |
| $n_1 = n_2 = 10$ | 18.93 | 19.07 | 17.84 | 18.30 |
| $n_1 = n_2 = 15$ | 28.27 | 30.88 | 27.12 | 27.14 |
| $n_1 = n_2 = 20$ | 35.08 | 40.68 | 33.73 | 33.74 |

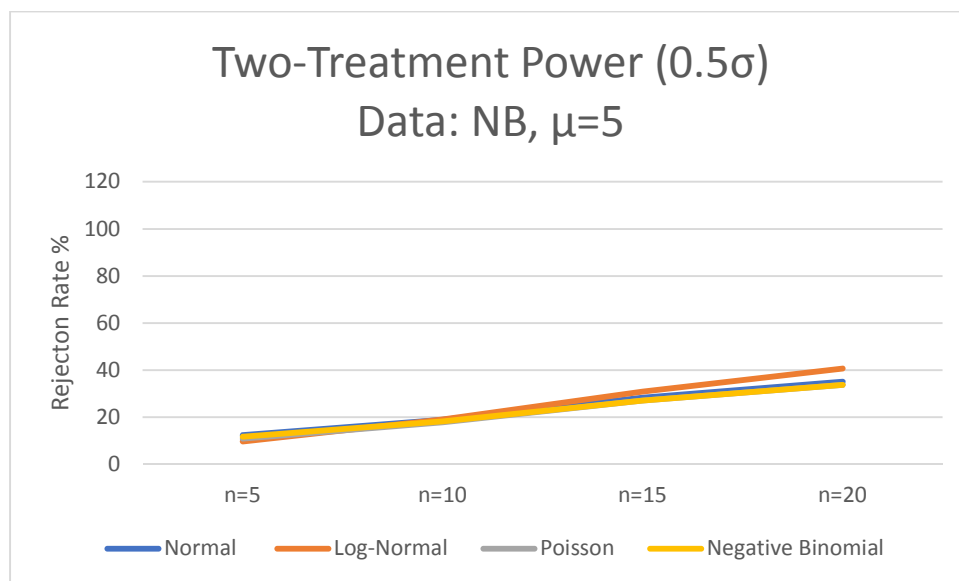


Figure 3. NB Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 0.5σ , $\mu = 5$)

The data from Tables 14, 15 and 16 are from Normal, Poisson and Negative Binomial samples with initial mean 20 respectively. The results obtained from the powers comparison as

shown in these tables below reveal no major differences in power across the sampling efforts for each model fitted to each data.

When samples are taken from population with larger mean ($\mu=20$ in our case) the models have comparable power across sampling efforts. And this well illustrated in Figures 4, 5 and 6.

Table 14. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 0.5σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 10.56 | 9.74 | 10.04 | 10.04 |
| $n_1 = n_2 = 10$ | 18.14 | 17.38 | 17.96 | 18.29 |
| $n_1 = n_2 = 15$ | 27.10 | 26.25 | 26.73 | 27.45 |
| $n_1 = n_2 = 20$ | 33.27 | 32.06 | 33.01 | 33.63 |

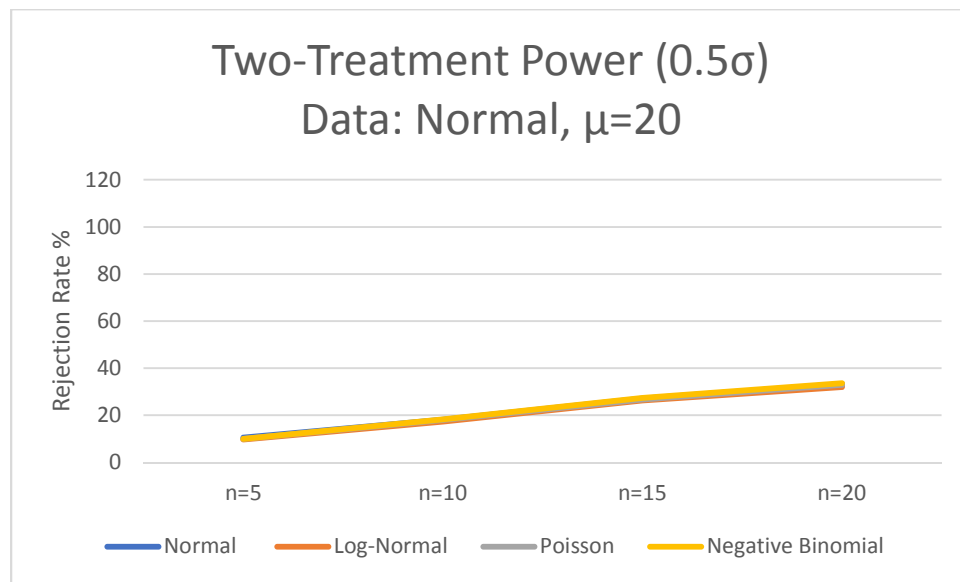


Figure 4. Normal Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 0.5σ , $\mu = 20$)

Table 15. Poisson Samples Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$
(Effect size=0.5 σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 11.46 | 11.19 | 11.28 | 11.33 |
| $n_1 = n_2 = 10$ | 20.28 | 20.08 | 20.15 | 20.39 |
| $n_1 = n_2 = 15$ | 27.11 | 26.58 | 27.04 | 27.77 |
| $n_1 = n_2 = 20$ | 34.84 | 34.30 | 34.77 | 35.62 |

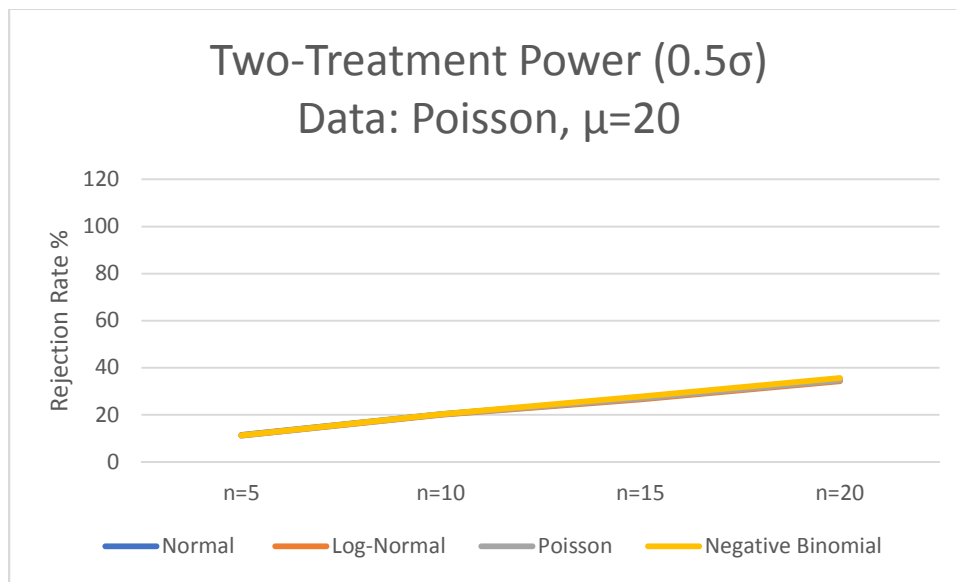


Figure 5. Poisson Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$
(Effect size=0.5 σ , $\mu = 20$)

Table 16. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size=0.5 σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 11.02 | 10.61 | 10.63 | 10.72 |
| $n_1 = n_2 = 10$ | 18.57 | 18.66 | 18.41 | 18.65 |
| $n_1 = n_2 = 15$ | 26.22 | 26.35 | 26.01 | 26.23 |
| $n_1 = n_2 = 20$ | 35.18 | 35.87 | 34.72 | 35.00 |

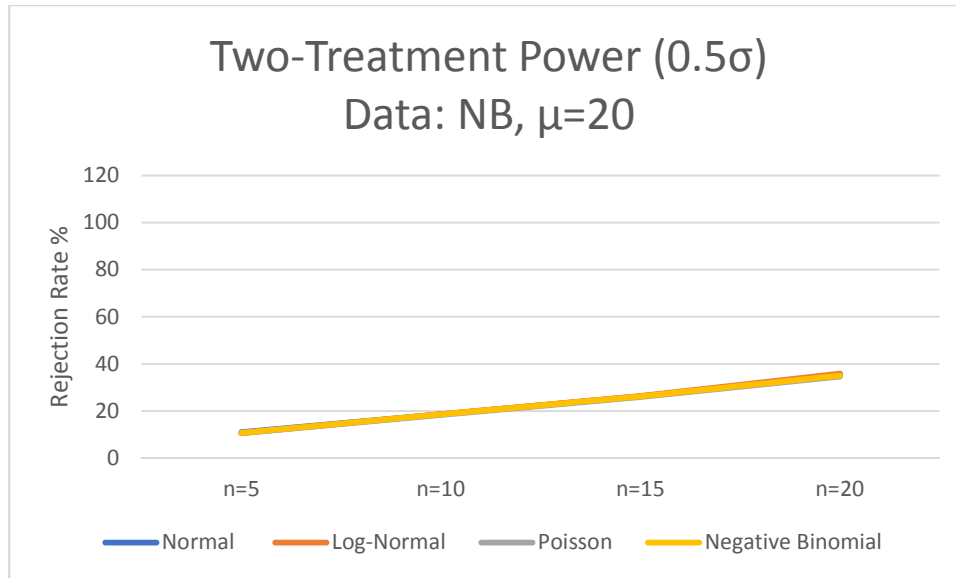


Figure 6. NB Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size=0.5 σ , $\mu = 20$)

- Effect size: One sigma (1σ)

When sampling from a Normal distribution with mean 5 and 1 sigma effect size, the Poisson and Negative Binomial models have comparable powers. However, both Poisson and Negative Binomial were outperformed by the Normal model across sampling efforts. The power comparison plot of the 1σ effect size for Normal, Log-Normal, Poisson and Negative Binomial models applied to Normal samples can be found in Figure 7.

Table 17. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu = 5$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 29.00 | 19.67 | 20.68 | 21.75 |
| $n_1 = n_2 = 10$ | 55.80 | 39.52 | 43.22 | 44.71 |
| $n_1 = n_2 = 15$ | 75.66 | 57.60 | 63.06 | 64.37 |
| $n_1 = n_2 = 20$ | 86.55 | 68.18 | 75.80 | 76.91 |

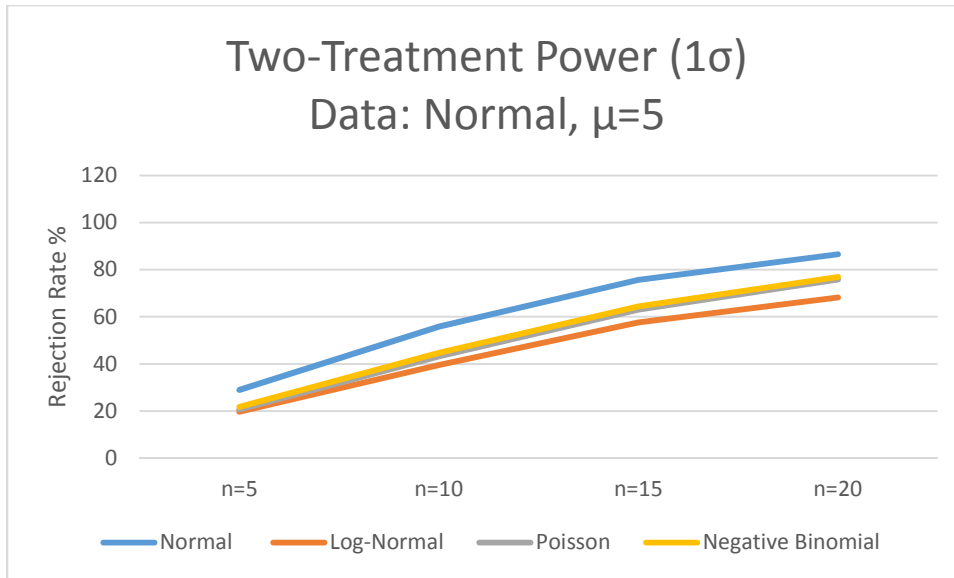


Figure 7. Normal Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu=5$)

The results from power comparison of the 1σ effect size for Normal, Log-Normal, Poisson and Negative Binomial models applied to Poisson samples with mean 5 are presented in Table 18 below. As we can see in the table and Figure 8, all three models Normal, Poisson and Negative Binomial yielded comparable powers with Log-Normal having the lowest powers. From this result we can say that count data with less variability will yield approximately the same powers for Normal, Poisson and Negative Binomial model.

Table 18. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu = 5$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 34.71 | 28.07 | 32.44 | 33.50 |
| $n_1 = n_2 = 10$ | 67.56 | 59.00 | 66.91 | 68.10 |
| $n_1 = n_2 = 15$ | 85.25 | 76.59 | 84.97 | 85.25 |
| $n_1 = n_2 = 20$ | 94.05 | 86.63 | 93.99 | 94.11 |

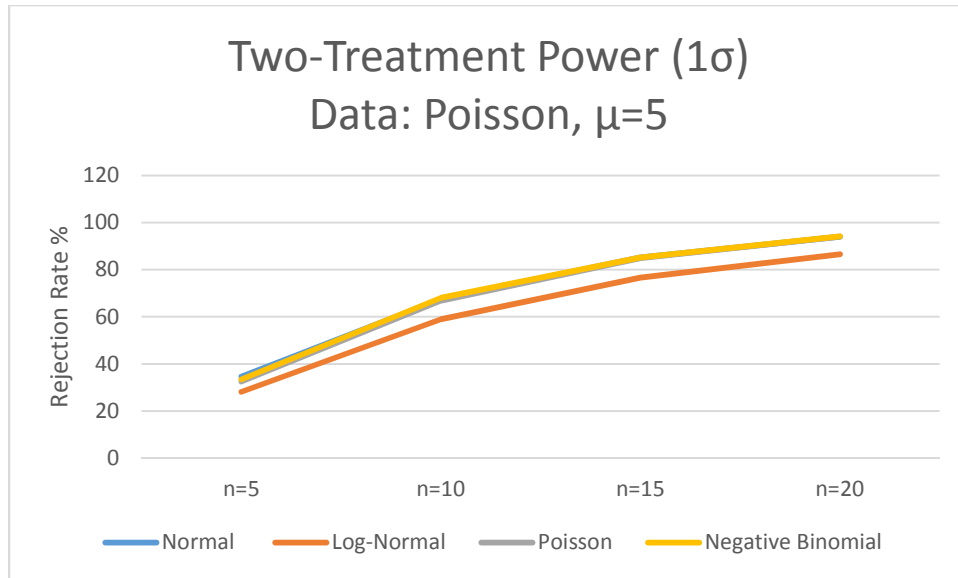


Figure 8. Poisson Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu=5$)

Unlike the Poisson data, the data from negative binomial have a larger variability. As we can see in Table 19 and Figure 9, the Normal model outperformed both the Poisson and Negative Binomial. The Poisson and Negative Binomial models still yielded comparable powers.

Table 19. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu = 5$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 36.82 | 35.67 | 29.27 | 31.9 |
| $n_1 = n_2 = 10$ | 60.92 | 73.13 | 54.92 | 53.87 |
| $n_1 = n_2 = 15$ | 75.77 | 90.36 | 70.87 | 69.43 |
| $n_1 = n_2 = 20$ | 85.77 | 96.56 | 82.34 | 80.87 |

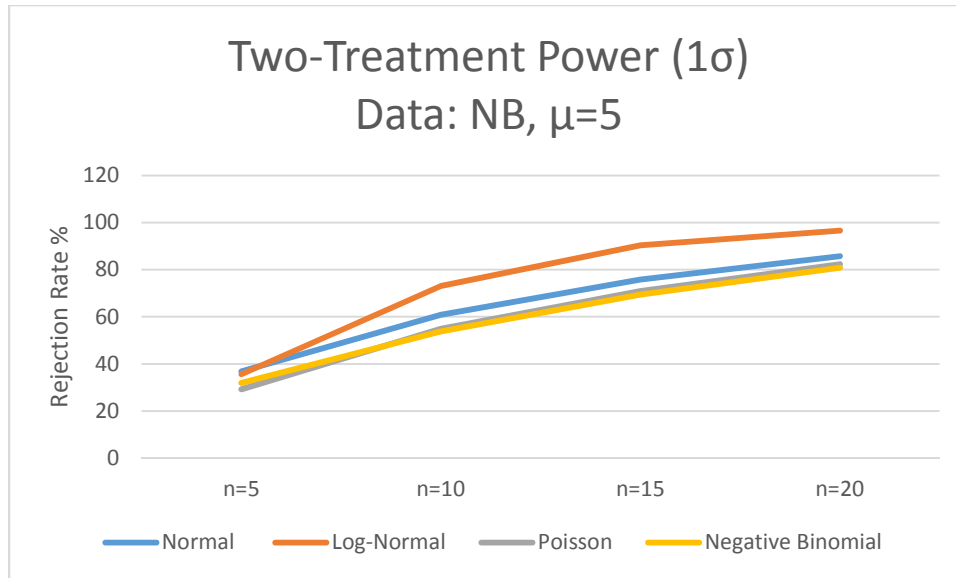


Figure 9. NB Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size=1 σ , $\mu = 5$)

The power comparison results of the 1 σ effect size for Normal, Log-Normal, Poisson and Negative Binomial models applied to Normal, Poisson and Negative Binomial with mean 20 are given in Tables 20, 21 and 22, respectively. For all combination of underlying distributions, fitted model and sampling effort, the powers seem to be similar between the models.

For larger sampling distribution mean, all models display comparable powers and this is well illustrated in Figures 10, 11 and 12.

Table 20. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size=1 σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 28.93 | 26.95 | 27.59 | 27.69 |
| $n_1 = n_2 = 10$ | 55.75 | 53.54 | 54.96 | 55.19 |
| $n_1 = n_2 = 15$ | 75.61 | 73.75 | 75.16 | 75.38 |
| $n_1 = n_2 = 20$ | 86.42 | 84.84 | 86.12 | 86.32 |

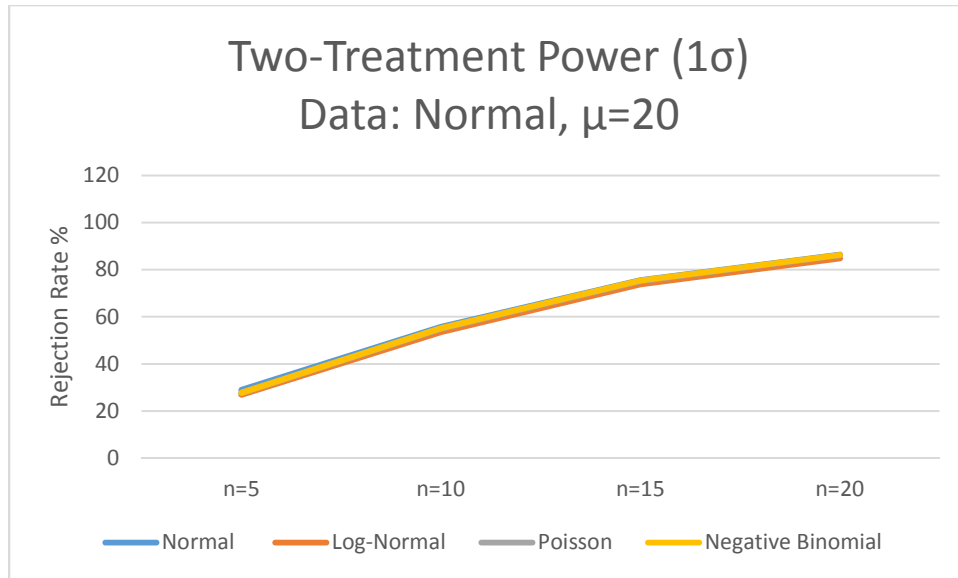


Figure 10. Normal Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu = 20$)

Table 21. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu = 5$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 31.33 | 30.16 | 30.77 | 31.14 |
| $n_1 = n_2 = 10$ | 61.29 | 60.69 | 61.26 | 61.83 |
| $n_1 = n_2 = 15$ | 80.06 | 79.11 | 80.01 | 80.35 |
| $n_1 = n_2 = 20$ | 90.08 | 89.37 | 90.09 | 90.26 |

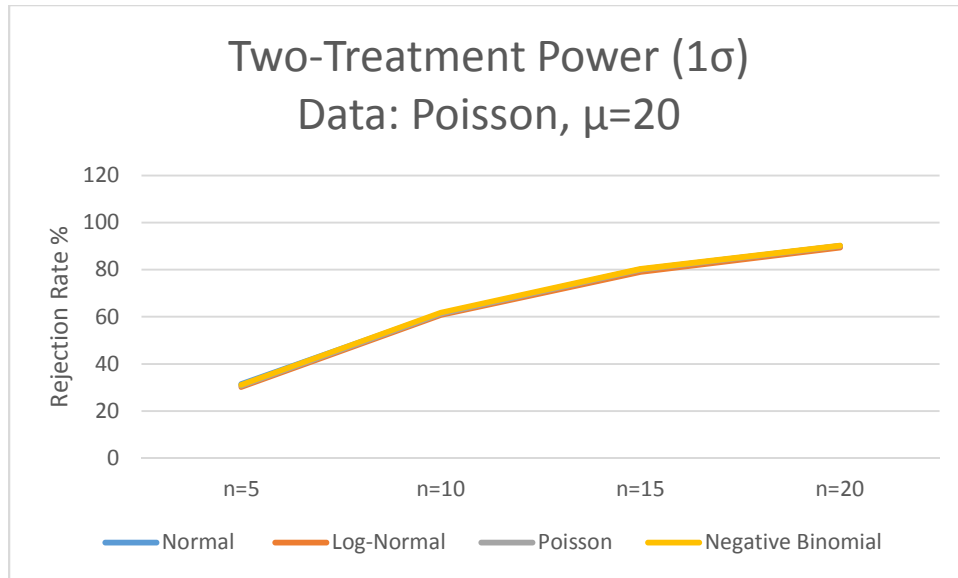


Figure 11. Poisson Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu = 20$)

Table 22. NB Samples - Rejection Rates (%) for Fitted models when $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 29.10 | 28.10 | 28.09 | 28.19 |
| $n_1 = n_2 = 10$ | 56.29 | 56.94 | 55.06 | 55.08 |
| $n_1 = n_2 = 15$ | 75.18 | 76.9 | 74.52 | 74.37 |
| $n_1 = n_2 = 20$ | 86.58 | 88.14 | 86.07 | 86.04 |

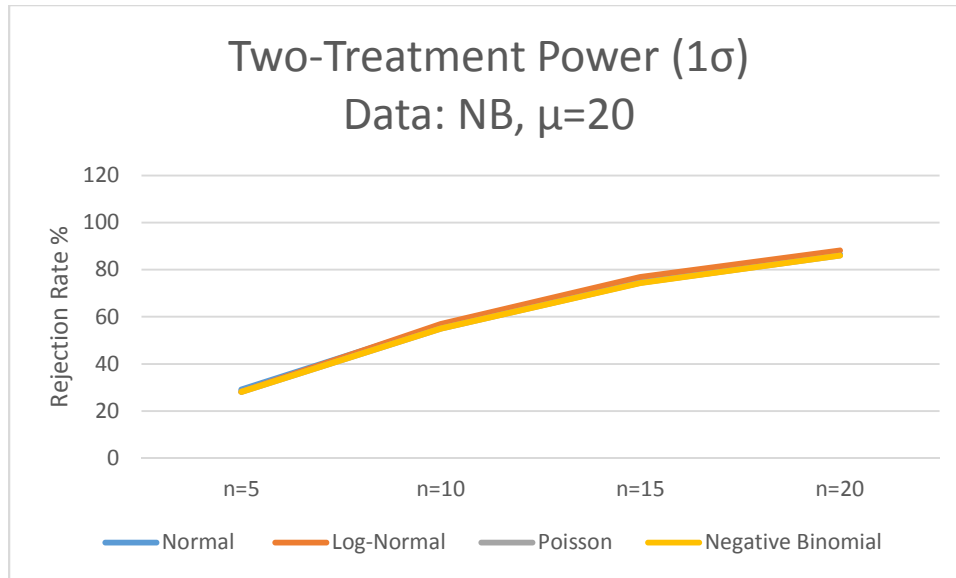


Figure 12. NB Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 1σ , $\mu = 20$)

- Effect size: Two sigma (2σ)

When sampling from Normal distribution with mean 5 and 2 sigma effect size, all three models (Normal, Poisson and Negative Binomial) have comparable powers for large sample size equal to 20. For small samples ($n \leq 15$), the Normal model performed better. The Poisson and Negative Binomial models yielded similar powers. The power comparison plot of the 2σ effect size for Normal, Log-Normal, Poisson and Negative Binomial models applied to Normal samples can be found in Figure 13.

Table 23. Normal samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 5$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 78.89 | 48.30 | 39.08 | 40.41 |
| $n_1 = n_2 = 10$ | 98.56 | 78.24 | 78.48 | 79.82 |
| $n_1 = n_2 = 15$ | 99.97 | 91.90 | 94.45 | 94.85 |
| $n_1 = n_2 = 20$ | 100.00 | 96.82 | 98.92 | 98.97 |

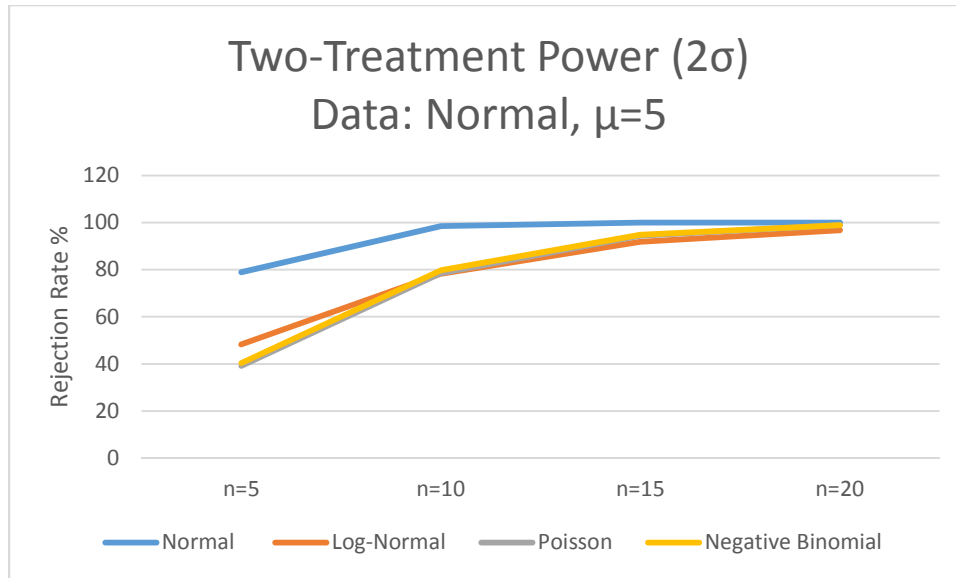


Figure 13. Normal Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 5$)

When sampling from Poisson distribution with 2 sigma effect size and mean 5, Normal, Log-Normal, Negative Binomial models yielded comparable powers for small sample sizes ($n=5$). The power for Poisson model however seems to be slightly lower than the other three when the sample size is small ($n=5$). As the sample size increases, all four models exhibit similar powers. The power comparison plot of the 2σ effect size for Normal, Log-Normal, Poisson and Negative Binomial models applied to Poisson samples can be found in Figure 14.

Table 24. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 5$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 97.34 | 96.62 | 88.48 | 95.52 |
| $n_1 = n_2 = 10$ | 100.00 | 99.99 | 99.42 | 99.86 |
| $n_1 = n_2 = 15$ | 100.00 | 100.00 | 99.95 | 99.97 |
| $n_1 = n_2 = 20$ | 100.00 | 100.00 | 100.00 | 100.00 |

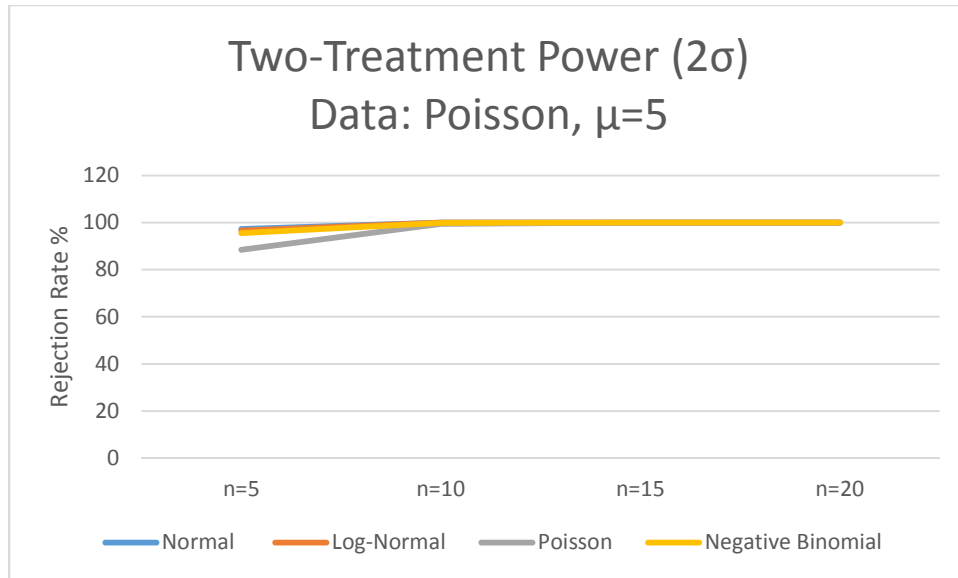


Figure 14. Poisson Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 5$)

Tables 25, 26 and 27 gives us the power comparison for Normal, Log-Normal, Poisson and Negative Binomial when sampling from Normal, Poisson and Negative Binomial distributions respectively for a large sample mean ($\mu = 20$) and 2 sigma effect size.

As shown in the tables below, all four models yielded comparable powers across all sample sizes and underlying distributions. The power comparison plot of the 2σ effect size for Normal, Log-Normal, Poisson and Negative Binomial models applied to Normal, Poisson and Negative Binomial samples can be found in Figure 15, 16 and 17 below, respectively.

Table 25. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 78.94 | 71.49 | 75.9 | 75.28 |
| $n_1 = n_2 = 10$ | 98.57 | 97.18 | 98.29 | 98.28 |
| $n_1 = n_2 = 15$ | 99.97 | 99.81 | 99.97 | 99.97 |
| $n_1 = n_2 = 20$ | 100.00 | 100.00 | 100.00 | 100.00 |

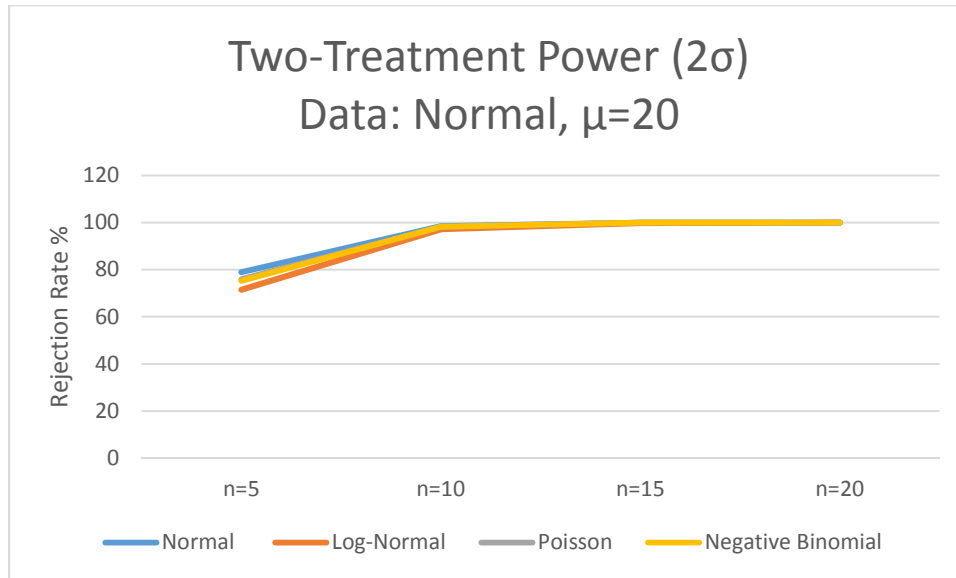


Figure 15. Normal Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 20$)

Table 26. Poisson Samples - Rejection Rates (%) for Fitted models when $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 89.01 | 87.87 | 88.95 | 89.3 |
| $n_1 = n_2 = 10$ | 99.74 | 99.69 | 99.74 | 99.73 |
| $n_1 = n_2 = 15$ | 100.00 | 99.98 | 100.00 | 100.00 |
| $n_1 = n_2 = 20$ | 100.00 | 100.00 | 100.00 | 100.00 |

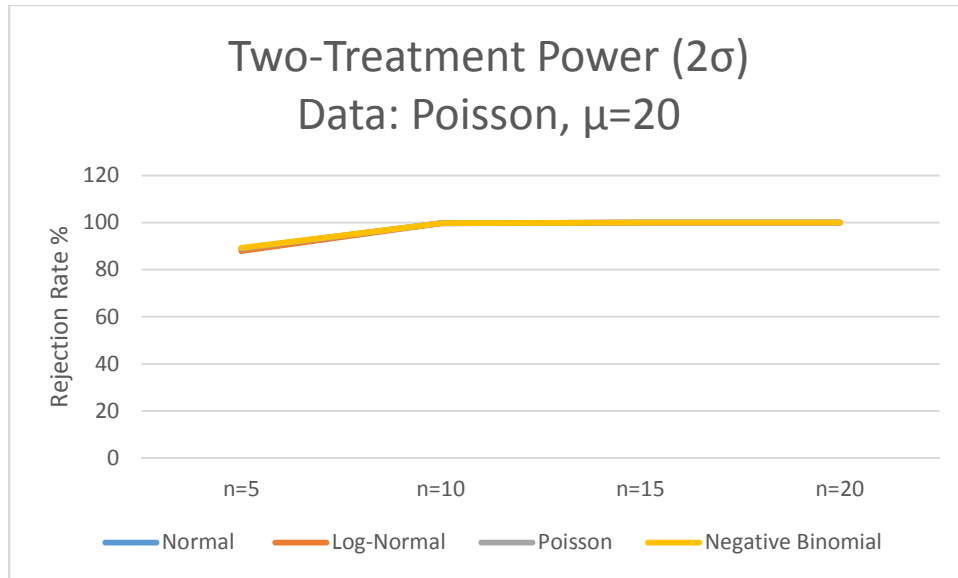


Figure 16. Poisson Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 20$)

Table 27. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = 5$ | 77.6 | 73.69 | 73.75 | 72.84 |
| $n_1 = n_2 = 10$ | 97.96 | 98.14 | 97.32 | 96.86 |
| $n_1 = n_2 = 15$ | 99.91 | 99.96 | 99.89 | 99.85 |
| $n_1 = n_2 = 20$ | 99.99 | 100.00 | 99.98 | 99.98 |

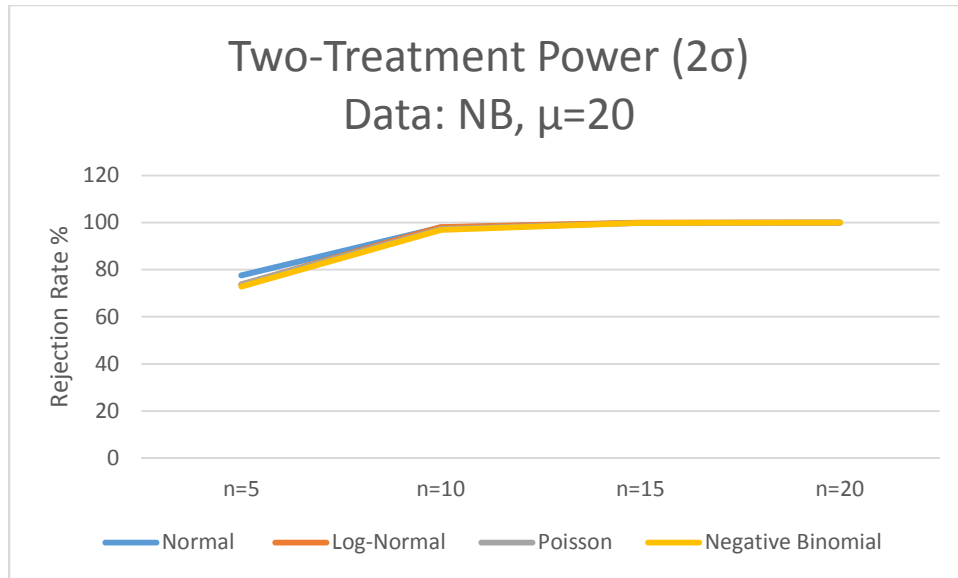


Figure 17. NB Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2$ (Effect size= 2σ , $\mu = 20$)

Power Comparison for Three-Treatment $\mu_1 \neq \mu_2 \neq \mu_3$

For the three-treatment power comparison, the three means are all different and sorted from smallest to largest. Unlike the Two-Treatment scenarios, we only considered two effect sizes: 0.5σ and 1σ . However, the effect size between the smallest and largest mean is twice the effect size between the middle and the other two means.

The setup is as follow: $\mu_1 < \mu_2 < \mu_3$. An 0.5σ effect size means $\mu_1 - \mu_2 = \mu_2 - \mu_3 = 0.5\sigma$ but $\mu_1 - \mu_3 = 1\sigma$. Likewise a 1σ effect size means $\mu_1 - \mu_2 = \mu_2 - \mu_3 = 1\sigma$ but $\mu_1 - \mu_3 = 2\sigma$.

- Effect size: Half sigma (0.5σ)

For the three-treatment case we only sampled from distributions with initial large mean ($\mu=20$). In the 0.5σ effect size, when applied observations from normal distributions, all four models have comparable powers.

Tables 28, 29, 30 and Figures 18, 19 and 20 gives us the results obtained from the power comparison in the half sigma effect size scenario for Three-Treatment for all combinations of underlying distributions, fitted models and sampling efforts.

Table 28. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size= 0.5σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = n_3 = 5$ | 21.64 | 20.31 | 20.51 | 20.81 |
| $n_1 = n_2 = n_3 = 10$ | 45.69 | 43.28 | 44.76 | 45.08 |
| $n_1 = n_2 = n_3 = 15$ | 64.65 | 62.52 | 64.16 | 64.38 |
| $n_1 = n_2 = n_3 = 20$ | 79.26 | 76.84 | 78.98 | 79.02 |

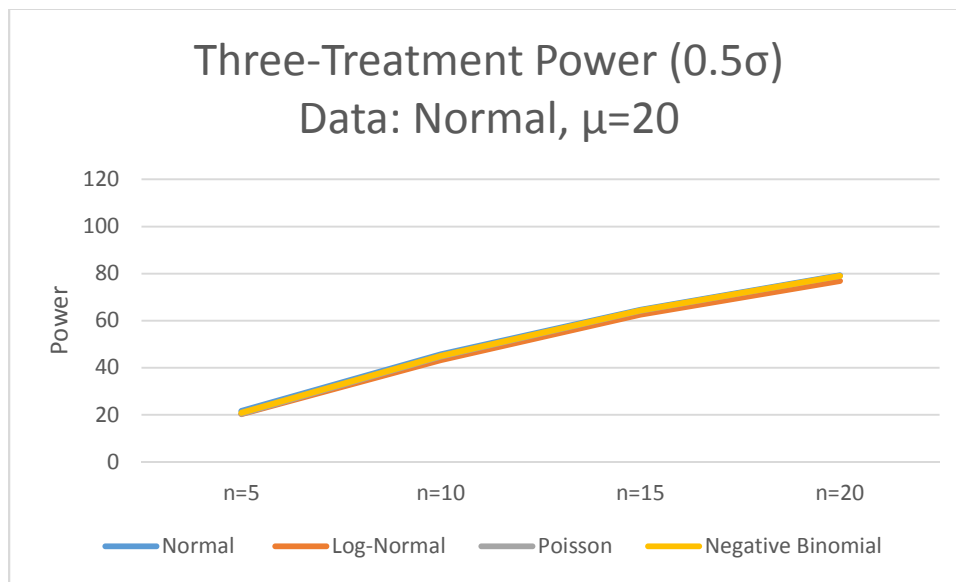


Figure 18. Normal Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size= 0.5σ , $\mu = 20$)

Table 29. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size= 0.5σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = n_3 = 5$ | 21.77 | 21.11 | 21.31 | 21.58 |
| $n_1 = n_2 = n_3 = 10$ | 46.15 | 45.21 | 45.77 | 46.22 |
| $n_1 = n_2 = n_3 = 15$ | 66.51 | 65.03 | 66.30 | 66.93 |
| $n_1 = n_2 = n_3 = 20$ | 79.40 | 78.48 | 79.46 | 79.86 |

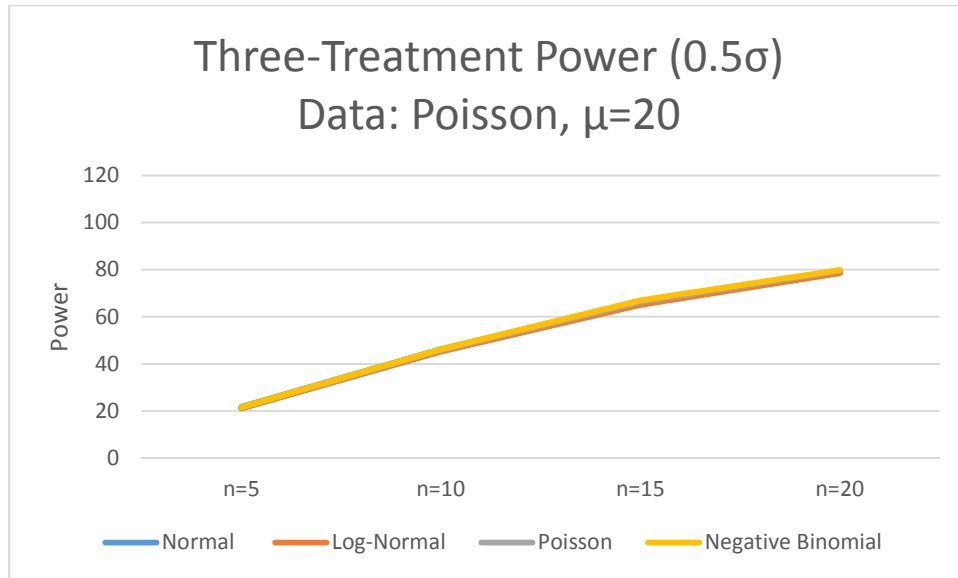


Figure 19. Poisson Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size=0.5 σ , $\mu = 20$)

Table 30. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size=0.5 σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = n_3 = 5$ | 21.95 | 21.77 | 21.36 | 21.65 |
| $n_1 = n_2 = n_3 = 10$ | 46.44 | 46.72 | 45.64 | 45.89 |
| $n_1 = n_2 = n_3 = 15$ | 65.66 | 66.73 | 65.04 | 65.32 |
| $n_1 = n_2 = n_3 = 20$ | 79.38 | 80.59 | 78.84 | 78.95 |

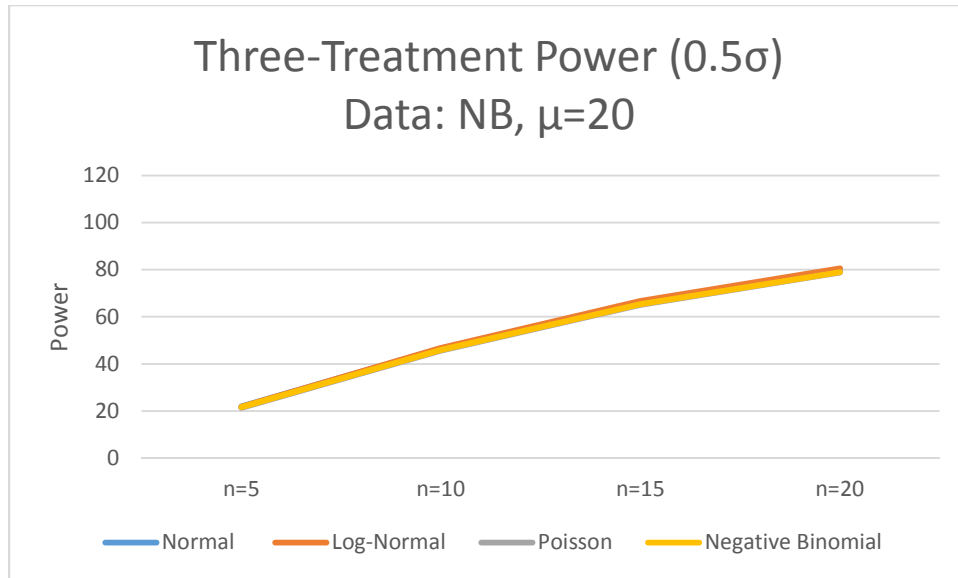


Figure 20. NB Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size=0.5 σ , $\mu = 20$)

- Effect size: One sigma (1 σ)

When samples are taken from Normal and Negative Binomial distribution, for small sizes (n=5) all four models seem to have comparable powers as shown in Tables 31, 32 and Figures 21, 22. The Normal model performed slightly better than the other three. However, when sampling from Poisson distributions, all four models performed equivalently across sampling efforts.

Table 31. Normal Samples Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size=1 σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = n_3 = 5$ | 70.25 | 65.36 | 67.74 | 67.81 |
| $n_1 = n_2 = n_3 = 10$ | 98.18 | 97.08 | 98.08 | 98.05 |
| $n_1 = n_2 = n_3 = 15$ | 99.88 | 99.73 | 99.87 | 99.88 |
| $n_1 = n_2 = n_3 = 20$ | 99.99 | 99.98 | 99.99 | 99.99 |

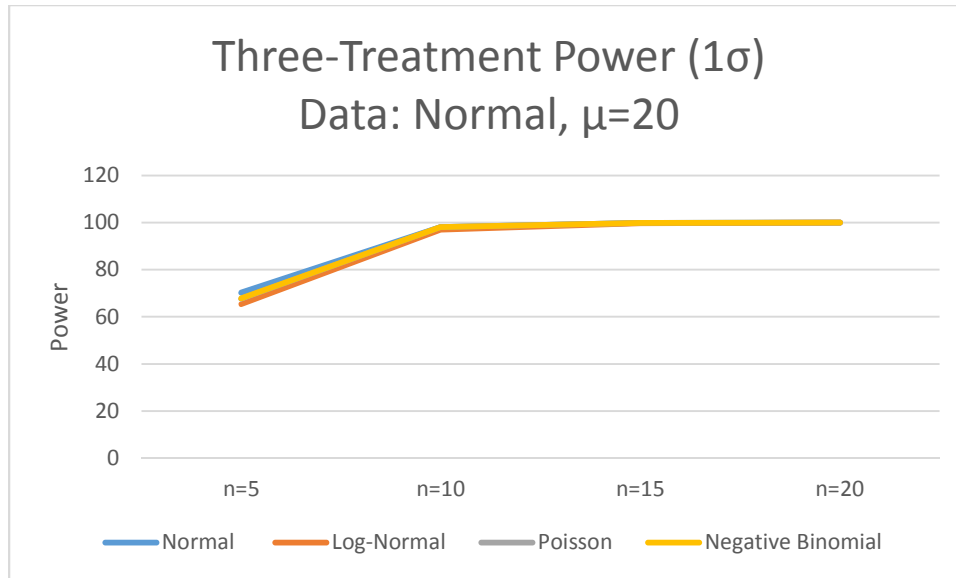


Figure 21. Normal Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size= 1σ , $\mu = 20$)

Table 32. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size= 1σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = n_3 = 5$ | 70.47 | 69.67 | 70.08 | 70.41 |
| $n_1 = n_2 = n_3 = 10$ | 97.46 | 97.08 | 97.47 | 97.48 |
| $n_1 = n_2 = n_3 = 15$ | 99.87 | 99.82 | 99.87 | 99.87 |
| $n_1 = n_2 = n_3 = 20$ | 99.99 | 99.99 | 99.99 | 99.99 |

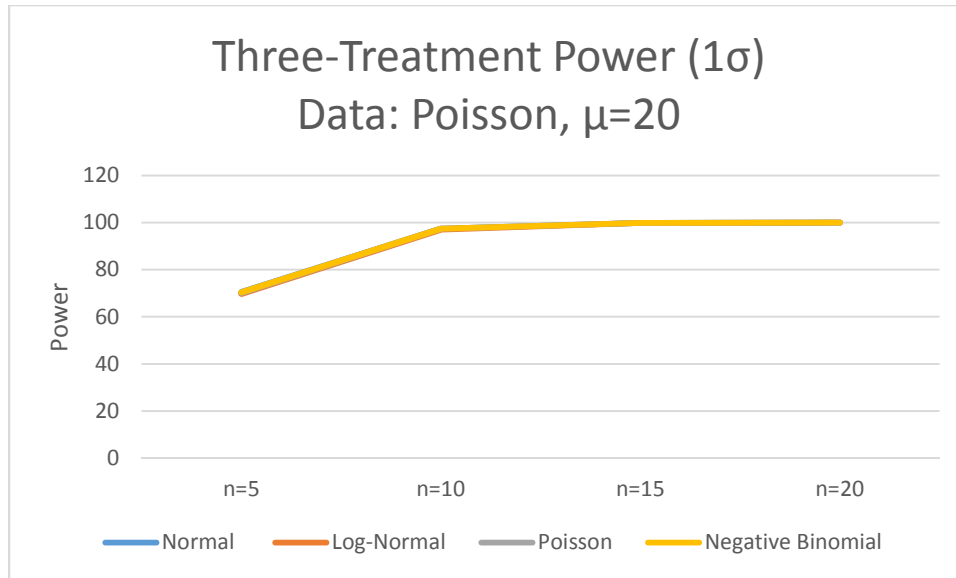


Figure 22. Poisson Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size= 1σ , $\mu = 20$)

Table 33. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size= 1σ , $\mu = 20$)

| Sampling Efforts | Fitted Models | | | |
|------------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1 = n_2 = n_3 = 5$ | 63.79 | 61.44 | 59.99 | 59.99 |
| $n_1 = n_2 = n_3 = 10$ | 96.22 | 96.83 | 95.51 | 95.19 |
| $n_1 = n_2 = n_3 = 15$ | 99.65 | 99.79 | 99.59 | 99.58 |
| $n_1 = n_2 = n_3 = 20$ | 99.99 | 100.00 | 99.99 | 99.99 |

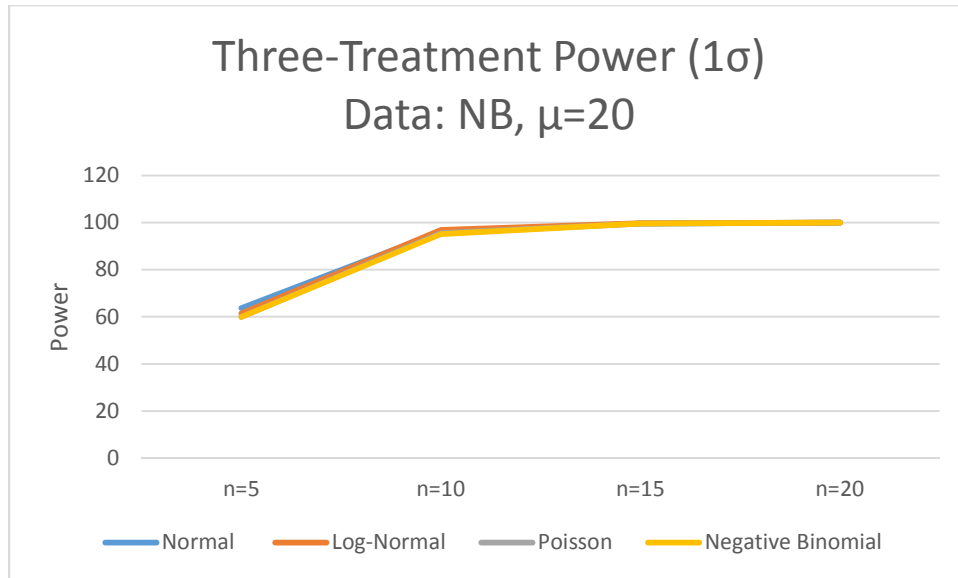


Figure 23. NB Samples - Rejection Rates (%) for various models $\mu_1 \neq \mu_2 \neq \mu_3$ (Effect size= 1σ , $\mu = 20$)

Parameters Estimates

After conducting the Type I error assessment and power comparison for the models (Normal, Log-Normal, Poisson and Negative Binomial), we also checked how well each model estimates the population means and the standard errors associated with those means. As shown previously, all four models reasonably controlled Type I error near the stated alpha value of 0.05. Likewise, all four models have comparable powers for each combination of underlying distribution, sample size and effect sizes.

Clearly, Type I error control is not an issue for any of these methods when applied to any of the underlying distributions therefore the quality of the parameters estimates becomes a deciding factor. We expect the estimates to be close to the parameter they are intended to estimate, and any substantial difference will imply poor performance of the model. The standard error of each estimate is based upon the model assumptions and is supposed to estimate the standard deviation of the estimator's sampling distribution.

For each simulated sample (we have 10,000), we fit a model (ANOVA, Poisson or NB) using the GLIMMIX procedure in SAS. We obtained the estimates (means) and corresponding standard error. The GLIMMIX procedure computes each means (LS-means) as $L\hat{\beta}$, where L is the coefficient matrix associated with the least squares mean and $\hat{\beta}$ is the estimate of the fixed-effects parameter vector. The approximate standard error for the LS-mean is computed as the square root of $L\widehat{Var}[\hat{\beta}]L'$ (SAS Institute Inc, 2019). The approximate variance matrix of the fixed-effects estimates depends on the estimation method. We then collect these standard errors and take the average (10,000 samples). Next, we considered the 10,000 estimates (means) as a new sampling distribution and computed the standard deviation of this new sample of size 10,000. According to Stroup, if we compare the standard deviation from the 10,000 simulated samples means to the average standard error of each estimate, we should see close agreement between these two. Again, if there is disparity between the two values this indicates poor performance of the model (Stroup 2013).

Two-Treatment $\mu_1 = \mu_2$

In each scenario, we checked for each sample the following:

- i. $H_0: \mu_1 = \mu_2$ Type I error rate.
- ii. $\hat{\mu}_1$ average estimated population 1 mean, average s.e. ($\hat{\mu}_1$) average population 1 standard error from the model assumptions, $sd(\hat{\mu}_1)$ standard error of estimated means based on population standard deviation of 10,000 samples means.
- iii. $\hat{\mu}_2$ average estimated population 2 mean, average s.e. ($\hat{\mu}_2$) average population 2 standard error from the model assumptions, $sd(\hat{\mu}_2)$ standard error of estimated means based on population standard deviation of 10,000 samples means.

iv. $\hat{\mu}_1 - \hat{\mu}_2$ average estimated mean difference, average s.e. $(\hat{\mu}_1 - \hat{\mu}_2)$, $sd(\hat{\mu}_1 - \hat{\mu}_2)$ based on standard deviation of 10,000 samples means.

we look for agreement between each the standard error from the fitted model and the standard deviation of the same estimator obtained from the 10,000 samples. A poor agreement between these two values will imply inadequate model performance.

- Population mean $\mu=5$

With the exception of Log-Normal, all three models (Normal, Poisson and Negative Binomial regression) yielded a good estimate of the means, very close to the theoretical value. Also, we can see from the tables below that the standard deviation and standard error of each treatment are very close. Likewise, the estimated standard error and standard deviation of the mean difference are almost the same. From Table 34 through Table 45, for all combination of underlying distributions, sample size and fitted model very we can see a close agreement between the standard error and standard deviation for each treatment as well as for the mean difference. These results are consistent with our expectation.

Table 34. Sampling from Normal Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 5.0162 | 4.62927 | 5.0841 | 5.0844 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 0.9707 | 1.06746 | 0.9484 | 0.9565 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.9971 | 1.1068 | 0.9677 | 0.9825 |
| Mean Trt2 ($\hat{\mu}_2$) | 5.0079 | 4.61472 | 5.0795 | 5.0773 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.9707 | 1.06097 | 0.948 | 0.9563 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.997 | 1.11548 | 0.969 | 0.985 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.008305 | 0.003703 | 0.000934 | 0.001501 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.3728 | 0.3429 | 0.2713 | 0.2743 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.4039 | 0.3787 | 0.2798 | 0.2888 |

Table 35. Sampling from Normal Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 4.9948 | 4.53753 | 5.0669 | 5.0646 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 0.6973 | 0.78442 | 0.6772 | 0.6803 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.7053 | 0.8061 | 0.6827 | 0.6997 |
| Mean Trt2 ($\hat{\mu}_2$) | 5.0174 | 4.55893 | 5.0898 | 5.0882 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.6973 | 0.78721 | 0.6786 | 0.6818 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.7141 | 0.81695 | 0.6897 | 0.7051 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.02261 | -0.0043 | -0.00445 | -0.00462 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.9861 | 0.2519 | 0.1914 | 0.1927 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.0076 | 0.2668 | 0.1957 | 0.2047 |

Table 36. Sampling from Normal Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|---------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 5.0115 | 4.52893 | 5.0811 | 5.0763 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 0.5719 | 0.65536 | 0.5554 | 0.5572 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.5777 | 0.67372 | 0.5591 | 0.5741 |
| Mean Trt2 ($\hat{\mu}_2$) | 4.51736 | 5.0746 | 5.0686 | 4.9991 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.5719 | 0.65364 | 0.5554 | 0.5572 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.5806 | 0.67628 | 0.5619 | 0.5773 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.01244 | 0.00271 | 0.001343 | 0.001588 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.8088 | 0.2091 | 0.1561 | 0.157 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.8188 | 0.2191 | 0.1579 | 0.1667 |

Table 37. Sampling from Normal Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 4.9966 | 4.50568 | 5.0704 | 5.0625 |
| Standard Error Trt1 s.e.($\hat{\mu}_1$) | 0.4969 | 0.57261 | 0.4818 | 0.4831 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.4969 | 0.58245 | 0.4833 | 0.4961 |
| Mean Trt2 ($\hat{\mu}_2$) | 5.0119 | 4.5148 | 5.0843 | 5.0768 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.4969 | 0.57349 | 0.4824 | 0.4837 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.503 | 0.58764 | 0.4842 | 0.499 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.01527 | -0.00186 | -0.00273 | -0.00278 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.7028 | 0.1826 | 0.1352 | 0.1359 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.7031 | 0.1885 | 0.1355 | 0.1436 |

Table 38. Sampling from Poisson Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 4.9936 | 4.52853 | 4.9936 | 4.9913 |
| Standard Error Trt1 s.e.($\hat{\mu}_1$) | 0.966 | 1.0378 | 0.9633 | 0.9676 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.0067 | 1.09901 | 1.0067 | 1.0165 |
| Mean Trt2 ($\hat{\mu}_2$) | 5.0001 | 4.53518 | 5.0001 | 4.9977 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.966 | 1.03975 | 0.9644 | 0.9687 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.0028 | 1.09084 | 1.0028 | 1.0128 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.00648 | -0.00186 | -0.00138 | -0.00138 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.3662 | 0.3392 | 0.2795 | 0.2811 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.428 | 0.3762 | 0.2959 | 0.3021 |

Table 39. Sampling from Poisson Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------|-------------------------------------------------------|----------|------------|----------|-------------------|
| n ₁ = n ₂ =10 | Mean Trt1 ($\hat{\mu}_1$) | 4.9945 | 4.45739 | 4.9945 | 4.9893 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 0.697 | 0.76621 | 0.6959 | 0.698 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.7113 | 0.80005 | 0.7113 | 0.7191 |
| | Mean Trt2 ($\hat{\mu}_2$) | 4.9987 | 4.46108 | 4.9987 | 4.9963 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.697 | 0.76852 | 0.6965 | 0.6991 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.6958 | 0.78369 | 0.6958 | 0.7051 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.00415 | -0.00153 | -0.00135 | -0.00191 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.9858 | 0.2501 | 0.1993 | 0.2003 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.9887 | 0.2631 | 0.2014 | 0.2069 |

Table 40. Sampling from Poisson Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------|-------------------------------------------------------|----------|------------|----------|-------------------|
| n ₁ = n ₂ =15 | Mean Trt1 ($\hat{\mu}_1$) | 5.009 | 4.44646 | 5.009 | 5.0033 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 0.5723 | 0.63894 | 0.5718 | 0.5732 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.5737 | 0.6522 | 0.5737 | 0.5803 |
| | Mean Trt2 ($\hat{\mu}_2$) | 5.0063 | 4.4451 | 5.0063 | 5.001 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.5723 | 0.6393 | 0.5717 | 0.5731 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.5723 | 0.65028 | 0.5723 | 0.5801 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.002727 | 0.00025 | 0.000535 | 0.000477 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.8093 | 0.2072 | 0.1627 | 0.1634 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.8101 | 0.2142 | 0.1635 | 0.1681 |

Table 41. Sampling from Poisson Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------|-------------------------------------------------------|----------|------------|----------|-------------------|
| n ₁ = n ₂ =20 | Mean Trt1 ($\hat{\mu}_1$) | 5.0047 | 4.42929 | 5.0047 | 4.9977 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 0.497 | 0.55782 | 0.4966 | 0.4974 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.5045 | 0.57506 | 0.5045 | 0.5112 |
| | Mean Trt2 ($\hat{\mu}_2$) | 5.0071 | 4.43515 | 5.0071 | 5.0009 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.497 | 0.55881 | 0.4968 | 0.4978 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.5008 | 0.56945 | 0.5008 | 0.5068 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.00243 | -0.00153 | -0.00057 | -0.00076 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.7028 | 0.1807 | 0.1411 | 0.1416 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.7079 | 0.1871 | 0.1424 | 0.1463 |

Table 42. Sampling from Negative Binomial Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------------------------|-------------------------------------------------------|---------|------------|----------|-------------------|
| n ₁ = n ₂ =5 | Mean Trt1 ($\hat{\mu}_1$) | 5.0106 | 4.31241 | 5.0106 | 5.0094 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.18 | 1.2662 | 1.1722 | 1.1786 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.2223 | 1.31511 | 1.2223 | 1.2283 |
| | Mean Trt2 ($\hat{\mu}_2$) | 5.0028 | 4.30393 | 5.0028 | 5.0043 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.18 | 1.26165 | 1.1708 | 1.1763 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.225 | 1.32104 | 1.225 | 1.2308 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.00772 | 0.002164 | 0.001817 | 0.00128 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.6687 | 0.4409 | 0.3407 | 0.341 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.7233 | 0.4861 | 0.3576 | 0.3616 |

Table 43. Sampling from Negative Binomial Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------|-------------------------------------------------------|----------|------------|----------|-------------------|
| n ₁ = n ₂ =10 | Mean Trt1 ($\hat{\mu}_1$) | 4.9972 | 4.1935 | 4.9972 | 4.9963 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 0.8515 | 0.93381 | 0.8478 | 0.85 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.8703 | 0.95973 | 0.8703 | 0.8745 |
| | Mean Trt2 ($\hat{\mu}_2$) | 5.0028 | 4.19088 | 5.0028 | 5.0021 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.8515 | 0.93111 | 0.8481 | 0.8503 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.873 | 0.96927 | 0.873 | 0.8758 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.00554 | 0.001303 | -0.00102 | -0.00112 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.2042 | 0.326 | 0.2434 | 0.2434 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.2362 | 0.3453 | 0.2518 | 0.2539 |

Table 44. Sampling from Negative Binomial Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------|-------------------------------------------------------|---------|------------|---------|-------------------|
| n ₁ = n ₂ =15 | Mean Trt1 ($\hat{\mu}_1$) | 4.9959 | 4.14646 | 4.9959 | 4.9939 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 0.6994 | 0.77532 | 0.6973 | 0.6983 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.708 | 0.79126 | 0.708 | 0.7097 |
| | Mean Trt2 ($\hat{\mu}_2$) | 4.9987 | 4.15531 | 4.9987 | 4.9988 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.6994 | 0.77612 | 0.6975 | 0.6986 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.7122 | 0.79884 | 0.7122 | 0.7132 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.0028 | -0.00166 | -0.0004 | -0.00084 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.9891 | 0.271 | 0.1993 | 0.1992 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.0065 | 0.2821 | 0.2035 | 0.2043 |

Table 45. Sampling from Negative Binomial Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 4.9902 | 4.12607 | 4.9902 | 4.9896 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 0.6074 | 0.67661 | 0.6052 | 0.6056 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.6103 | 0.69005 | 0.6103 | 0.612 |
| Mean Trt2 ($\hat{\mu}_2$) | 5.0128 | 4.14705 | 5.0128 | 5.0126 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.6074 | 0.68024 | 0.6067 | 0.6075 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.6153 | 0.69373 | 0.6153 | 0.6158 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.02265 | -0.00501 | -0.00445 | -0.00454 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.8589 | 0.2364 | 0.1726 | 0.1725 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.8695 | 0.2437 | 0.1754 | 0.1761 |

- Population mean $\mu=20$

We obtained similar results as that of the small mean ($\mu=5$). The estimated means from the fitted models for all combination of underlying distribution and sample size are very close to the theoretical value with the exception of the Log-Normal model. Moreover, we see a close agreement between the estimated standard errors and standard deviation for each combination of underlying distribution, sample size and fitted model as well as the mean difference. As Stroup mentioned, an agreement between the standard error and the standard deviation suggest the model is adequate for the data (Stroup, 2015).

Table 46 through Table 57 provide the parameter estimates for each combination of underlying distribution, sample size and fitted models.

Table 46. Sampling from Normal Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------------------------|-------------------------------------------------------|---------|------------|----------|-------------------|
| n ₁ = n ₂ =5 | Mean Trt1 ($\hat{\mu}_1$) | 20.0324 | 19.6111 | 20.0324 | 20.0219 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.9415 | 1.99795 | 1.945 | 1.9496 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.9942 | 2.06365 | 1.9942 | 2.0053 |
| | Mean Trt2 ($\hat{\mu}_2$) | 20.0158 | 19.5864 | 20.0158 | 20.0028 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.9415 | 1.99472 | 1.944 | 1.9491 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.9941 | 2.06606 | 1.9941 | 2.0041 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.01661 | 0.001256 | 0.000815 | 0.000936 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 2.7456 | 0.1454 | 0.1385 | 0.139 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 2.8079 | 0.1506 | 0.1418 | 0.1435 |

Table 47. Sampling from Normal Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------|-------------------------------------------------------|----------|------------|---------|-------------------|
| n ₁ = n ₂ =10 | Mean Trt1 ($\hat{\mu}_1$) | 19.9895 | 19.5103 | 19.9897 | 19.9757 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.3946 | 1.44477 | 1.3949 | 1.3967 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.4106 | 1.47113 | 1.4102 | 1.4202 |
| | Mean Trt2 ($\hat{\mu}_2$) | 20.0347 | 19.5516 | 20.0347 | 20.0216 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.3946 | 1.44778 | 1.3964 | 1.3984 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.4283 | 1.48807 | 1.4283 | 1.4378 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.04523 | -0.00206 | -0.0022 | -0.00225 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.9723 | 0.1052 | 0.09904 | 0.09929 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 2.0152 | 0.1083 | 0.1013 | 0.1028 |

Table 48. Sampling from Normal Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|---------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.023 | 19.5267 | 20.0232 | 20.0094 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1439 | 1.19077 | 1.1448 | 1.1462 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.1555 | 1.21015 | 1.1554 | 1.1672 |
| Mean Trt2 ($\hat{\mu}_2$) | 19.9981 | 19.4963 | 19.9986 | 19.9803 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1439 | 1.18892 | 1.1441 | 1.1453 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1613 | 1.21484 | 1.1612 | 1.1711 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.02488 | 0.001577 | 0.001247 | 0.00147 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.6177 | 0.08654 | 0.08111 | 0.08128 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.6375 | 0.08837 | 0.08215 | 0.08385 |

Table 49. Sampling from Normal Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 19.9933 | 19.4847 | 19.9935 | 19.9778 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 0.9939 | 1.03523 | 0.9938 | 0.9946 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.9938 | 1.03829 | 0.9933 | 1.0017 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.0238 | 19.5133 | 20.024 | 20.01 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.9939 | 1.03656 | 0.9945 | 0.9953 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.0061 | 1.05665 | 1.0061 | 1.0155 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.03055 | -0.00142 | -0.0015 | -0.00158 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.4055 | 0.07533 | 0.07042 | 0.07053 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.4062 | 0.07593 | 0.07053 | 0.07201 |

Table 50. Sampling from Poisson Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------------------------|-------------------------------------------------------|---------|------------|----------|-------------------|
| n ₁ = n ₂ =5 | Mean Trt1 ($\hat{\mu}_1$) | 20.0202 | 19.6164 | 20.0202 | 20.0132 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.9279 | 1.95106 | 1.9283 | 1.9318 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 2.0119 | 2.03323 | 2.0119 | 2.021 |
| | Mean Trt2 ($\hat{\mu}_2$) | 19.9725 | 19.5615 | 19.9725 | 19.962 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.9279 | 1.94531 | 1.9262 | 1.9292 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.9714 | 1.99733 | 1.9714 | 1.9795 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.04772 | 0.002656 | 0.002214 | 0.002385 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 2.7265 | 0.1414 | 0.1371 | 0.1374 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 2.8239 | 0.1476 | 0.1425 | 0.1437 |

Table 51. Sampling from Poisson Distribution with Two-Treatment $\mu_1 = \mu_2$

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------|-------------------------------------------------------|---------|------------|----------|-------------------|
| n ₁ = n ₂ =10 | Mean Trt1 ($\hat{\mu}_1$) | 20.0067 | 19.5409 | 20.0067 | 19.9924 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.3936 | 1.41139 | 1.3936 | 1.3951 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.4166 | 1.43645 | 1.4166 | 1.4255 |
| | Mean Trt2 ($\hat{\mu}_2$) | 19.9789 | 19.5179 | 19.9789 | 19.9656 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.3936 | 1.40997 | 1.3928 | 1.394 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.3991 | 1.41954 | 1.3991 | 1.4085 |
| | Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.0278 | 0.001115 | 0.001333 | 0.001284 |
| | Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.9708 | 0.1025 | 0.09883 | 0.09902 |
| | Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.996 | 0.1041 | 0.1002 | 0.1015 |

Table 52. Sampling from Poisson Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|---------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 19.9969 | 19.5171 | 19.9969 | 19.9802 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1427 | 1.15733 | 1.1425 | 1.1434 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.1542 | 1.16989 | 1.1542 | 1.1616 |
| Mean Trt2 ($\hat{\mu}_2$) | 19.9838 | 19.5039 | 19.9838 | 19.9681 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1427 | 1.15672 | 1.1422 | 1.1432 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.161 | 1.17451 | 1.161 | 1.1683 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.01309 | 0.000695 | 0.000678 | 0.000633 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.616 | 0.08403 | 0.08097 | 0.08112 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.6356 | 0.0851 | 0.08203 | 0.08309 |

Table 53. Sampling from Poisson Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 19.994 | 19.5048 | 19.994 | 19.9791 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 0.9935 | 1.00614 | 0.9933 | 0.9938 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.0123 | 1.02792 | 1.0123 | 1.0173 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.0015 | 19.5112 | 20.0015 | 19.9878 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.9935 | 1.00655 | 0.9935 | 0.9941 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.0067 | 1.0211 | 1.0067 | 1.0139 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.00748 | -0.00035 | -0.00039 | -0.00045 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.405 | 0.07306 | 0.07035 | 0.07045 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.4201 | 0.07415 | 0.07121 | 0.07215 |

Table 54. Sampling from Negative Binomial Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|---------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.0191 | 19.5077 | 20.0191 | 20.0133 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 2.1668 | 2.1848 | 2.1645 | 2.1685 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 2.2331 | 2.25504 | 2.2331 | 2.2394 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.0022 | 19.4871 | 20.0022 | 19.9949 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 2.1668 | 2.18292 | 2.1638 | 2.1677 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 2.2526 | 2.26811 | 2.2526 | 2.2584 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | 0.01686 | 0.00116 | 0.000975 | 0.001053 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 3.0643 | 0.1594 | 0.1539 | 0.1542 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 3.1754 | 0.1658 | 0.1598 | 0.1607 |

Table 55. Sampling from Negative Binomial Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 19.9875 | 19.4074 | 19.9875 | 19.9768 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.56 | 1.57386 | 1.5585 | 1.5601 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.5972 | 1.6123 | 1.5972 | 1.6018 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.0053 | 19.4256 | 20.0053 | 19.9978 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.56 | 1.57538 | 1.5591 | 1.5607 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.573 | 1.58618 | 1.573 | 1.5779 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.01783 | -0.00106 | -0.001 | -0.00116 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 2.2062 | 0.1151 | 0.1106 | 0.1107 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 2.2407 | 0.1169 | 0.1124 | 0.1131 |

Table 56. Sampling from Negative Binomial Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 19.9877 | 19.3892 | 19.9877 | 19.9822 |
| Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.2792 | 1.2913 | 1.2783 | 1.2791 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.2934 | 1.30708 | 1.2934 | 1.2972 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.0152 | 19.4122 | 20.0152 | 20.0052 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.2792 | 1.29267 | 1.279 | 1.2798 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.2917 | 1.30497 | 1.2917 | 1.2953 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.02745 | -0.00119 | -0.00138 | -0.00116 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.8091 | 0.09439 | 0.09059 | 0.09067 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.8123 | 0.09477 | 0.09087 | 0.09139 |

Table 57. Sampling from Negative Binomial Distribution with Two-Treatment $\mu_1 = \mu_2$

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------------------|----------|------------|----------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.0018 | 19.3883 | 20.0018 | 19.9953 |
| Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.1117 | 1.12295 | 1.1113 | 1.1118 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.1121 | 1.12719 | 1.1121 | 1.1157 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.0037 | 19.3917 | 20.0037 | 19.9977 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1117 | 1.1233 | 1.1114 | 1.112 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.124 | 1.13488 | 1.124 | 1.1269 |
| Mean Difference ($\hat{\mu}_1 - \hat{\mu}_2$) | -0.00185 | -0.00015 | -0.00006 | -0.00009 |
| Mean Diff Stderr s.e. ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.5722 | 0.08205 | 0.0787 | 0.07875 |
| Mean Diff SD sd ($\hat{\mu}_1 - \hat{\mu}_2$) | 1.581 | 0.08271 | 0.07917 | 0.07958 |

Research Questions

In this section we will review the research questions proposed in the introduction of our study:

- How do Type I error, Power and Parameter Estimates compare across ANOVA, Poisson and Negative Binomial when applied to a count data?
- How does the sample size impact the quality of the results obtained?

In the Two-Treatment scenario, Type I error is well controlled by all models when sampling from Normal, Poisson or Negative binomial distribution across all sampling efforts for both small and large means (5 or 20). We did not see any significance difference among the models when applied to count data (Poisson or negative Binomial). In other words, fitting count data with ANOVA or using models specific to count such as Poisson or Negative Binomial makes no difference in terms of controlling the Type I error since they all performed reasonably well with rates close to the stated alpha value of 5%. This result is what we expected to see. Most researchers are comfortable using ANOVA. Although count data do not always meet the assumption of normality and/or equal variance, our research suggests that there is no appreciable difference fitting the data with ANOVA or using models specific to count data such as Poisson and/or Negative binomial. In either case, Type I error is controlled near the stated alpha rate of 0.05.

Similarly, regarding the power of Poisson and Negative Binomial models compared to standard ANOVA when applied to count data (Poisson or Negative Binomial), the three models exhibit comparable powers for all sample sizes and distribution means (5 or 20). However, when the models are applied to Normal data with small means, ANOVA outperformed both Poisson and Negative Binomial. Moreover, ANOVA had a higher power when the data was from Negative Binomial Distribution in the case of small means.

The Power comparison results suggest that ANOVA, Poisson and Negative Binomial will perform similarly when applied to count data. However, if the data are a little over-dispersed with small mean (5 in our study) ANOVA displayed higher power compared to Poisson and Negative Binomial models. But when the mean is large enough then the powers obtained are comparable and the models are equally appropriate.

Thus far, we have seen that type I error is equally well controlled by ANOVA, Poisson and Negative Binomial when applied to count data. Also, the three models have comparable power with the exception of ANOVA performing slight better on over-dispersed data with small mean. Clearly, Type I error and power are not an issue for any of these models (ANOVA, Poisson or Negative Binomial) when applied to any of the underlying distributions. Therefore, the quality of the estimates obtained from each fitted model becomes of a differentiation factor of interest.

According to Stroup (2013), the standard error of each estimate is expected to estimate the standard deviation of the estimator's sampling distribution. Any significant disparity between these two values is an indication of a poor performance from the model (Stroup 2013). In our study as shown previously, for all combination of underlying distribution and fitted model, there is no significant difference between the standard error and the standard deviation as Stroup described it. Again, all three models (ANOVA, Poisson and Negative Binomial) performed comparably well when the underlying distribution assumption was met or violated (recall that the underlying distributions are Normal, Poisson and Negative Binomial distributions).

CHAPTER 5. CONCLUSION

Most researchers nowadays are more comfortable fitting ANOVA, understanding and interpreting its results. It has become so popular that within some disciplines it is common that folks simply fit ANOVA without first ensuring the underlying assumptions of the distribution are met. This could lead to biased results with unknown consequences.

Data are not always normal and homogeneous. In fact, count data are very common in many research studies. We designed this simulation study to compare the performance of ANOVA, Poisson and Negative Binomial when applied to count data. We looked at how well each model controlled the Type I errors and Power. We explored the following research questions:

- How do Type I error, Power and Parameter Estimates compare across ANOVA, Poisson and Negative Binomial when applied to count data?
- Does the sample size have an impact on the quality of the results obtained?

We compared these three models (ANOVA, Poisson and Negative Binomial) in the case of two-population samples with equal sample sizes. We simulated our two-population samples from three underlying distributions namely: Normal, Poisson and Negative Binomial. For each underlying distribution, we considered different sample sizes (5, 10, 15, 20) and different sample means (5 and 20).

For two samples case with equal sample sizes, our results suggest that for each combination of underlying distribution, fitted model and sample size, Types I error is controlled near the stated alpha value of 0.05 for both small mean (mean=5) and large mean (mean=20). In other words, all three models, namely: ANOVA Poisson and Negative Binomial (NB) controlled Type I error in the event where the data was normal and when it was skewed (from Poisson or

NB). Also, the sample size seems to have no impact on the type I error. Likewise, all three models had a comparable power performance for each combination of underlying distribution, fitted model and sample size.

Reviewing our research questions, for the combination of underlying distribution, fitted model and sample sizes we considered, all three models (ANOVA, Poisson and NB) controlled reasonably well the Type I error near the stated alpha level of 0.05. The sample size, as shown in this study, has no impact on the Type I error control.

In addition, all three models exhibited comparable power performance for each design scenario. The power performance however improved as the sample size increases. It is important to point out that the results obtained from small sample mean (5) are similar to that obtained from large sample mean (20).

Furthermore, we have proven that all three models yield a good estimate of the model parameters. We particularly compared the standard error of the estimates to the standard deviation of the estimate's sampling distribution which according to Stroup should be similar. Our simulation shows not significant difference between these two measures.

From all the evidences shown above, there appear to be no appreciable difference between ANOVA, Poisson or Negative Binomial on count data for small samples or large samples. Recall that in this research we focused more on the two-population samples scenario with equal sample size. These results are not necessarily true in the case of three-population samples and/or an unbalanced samples scenario. We did run some few simulations to check for any eventually difference in the models that could serve as a motive for future research in that direction.

Future Research

This simulation study could be replicated by exploring three-population samples and unbalanced samples scenarios. We did run a preliminary simulation for both three-population samples and unbalanced samples. The results of this simulation are given in appendix A. The simulation results for the three-population scenarios reveal a potential issue for small sample size when we fit ANOVA to Poisson or Negative Binomial distribution in the case of 1σ effect size. This scenario could be expanded by simulating three samples with different sample sizes (for example $n_1=5$, $n_2=10$, $n_3=15$). Moreover, we could also consider scenarios where the sample have different variance.

We also checked how well the three models control Type I error in the case of two-population scenario with unbalanced sample sizes. Interestingly Type I error is well controlled near the stated alpha value of 0.05 for each combination of underlying distribution, fitted model and sample sizes (unbalanced sample sizes). The simulation results can be found in appendix B and C.

This simulation results could serve as basis for future researcher interesting in understanding how ANOVA would perform in different design scenarios compared to Poisson and Negative Binomial when the underlying distribution is skewed (specifically count data).

CHAPTER 6. CASE STUDY

The Figure 24 below is the distribution of root branches in canola plants obtained from a study conducted by Yayra Domfeh (Domfeh, 2015) as part of the fulfillment of the requirement for her master's degree. We are specifically interested in the count of the number of root branches in canola plants exposed to different isolates of a growth promoting rhizobacterium. We will conduct appropriate test to compare the number of root branches in treatment 1 versus treatment 2.

The experiment consists of two treatments groups with an equal number of 21 isolate (plants/strains). In the first treatment, isolates are treated with NaCL (salt) and in the second treatment there is no NaCl. In this experiment we are interested in the growth of root branches within each treatment group.

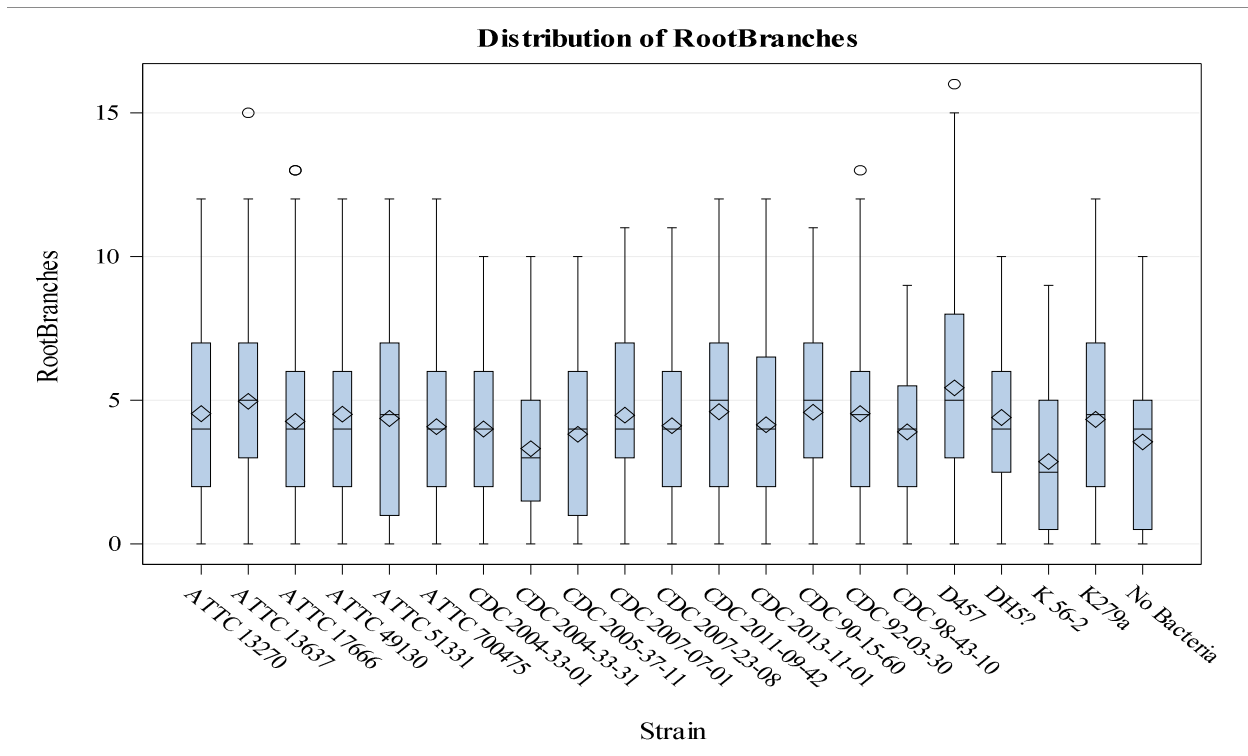


Figure 24. Fragment of data from microbiology thesis.

The original analysis yielded results shown below using simple ANOVA. They most likely violated several assumptions but almost certainly the assumption of normality since the data are discrete. We are now interested in fitting the data using Poisson and Negative Binomial regression for comparison purposes. Since our study suggested no significant difference, comparing the results obtained from the ANOVA to that of Poisson and Negative Binomial regression when applied to a real data will help us reinforce our theoretical findings.

ANOVA Results

Clearly, this data is a count data (number of root branches) with skewed distribution. One of the generalized linear models would be more appropriate to use to fit data. However, in the initial study, simple ANOVA was used and the results are given below.

From the ANOVA test in Table 58 and Figure 25 below, the probability obtained for the difference of the two treatments groups is <0.0001 which is less than 0.05. We reject the null hypothesis and conclude that there is enough evidence to prove that the means of the two treatments are different.

As illustrated by Figure 25 below, the two means exhibit different bar color which indicates they are different.

In conclusion, we can derive from the ANOVA test that the isolates treated with salt yielded different number of branches compared to those without salt.

Table 58. ANOVA Test Results

| NaCl | RootBranches LSMEAN | H0:LSMean1=LSMean2 |
|------|------------------------|--------------------|
| | | Pr > t |
| 0 | 5.05714286 | <.0001 |
| 1 | 3.40158730 | |

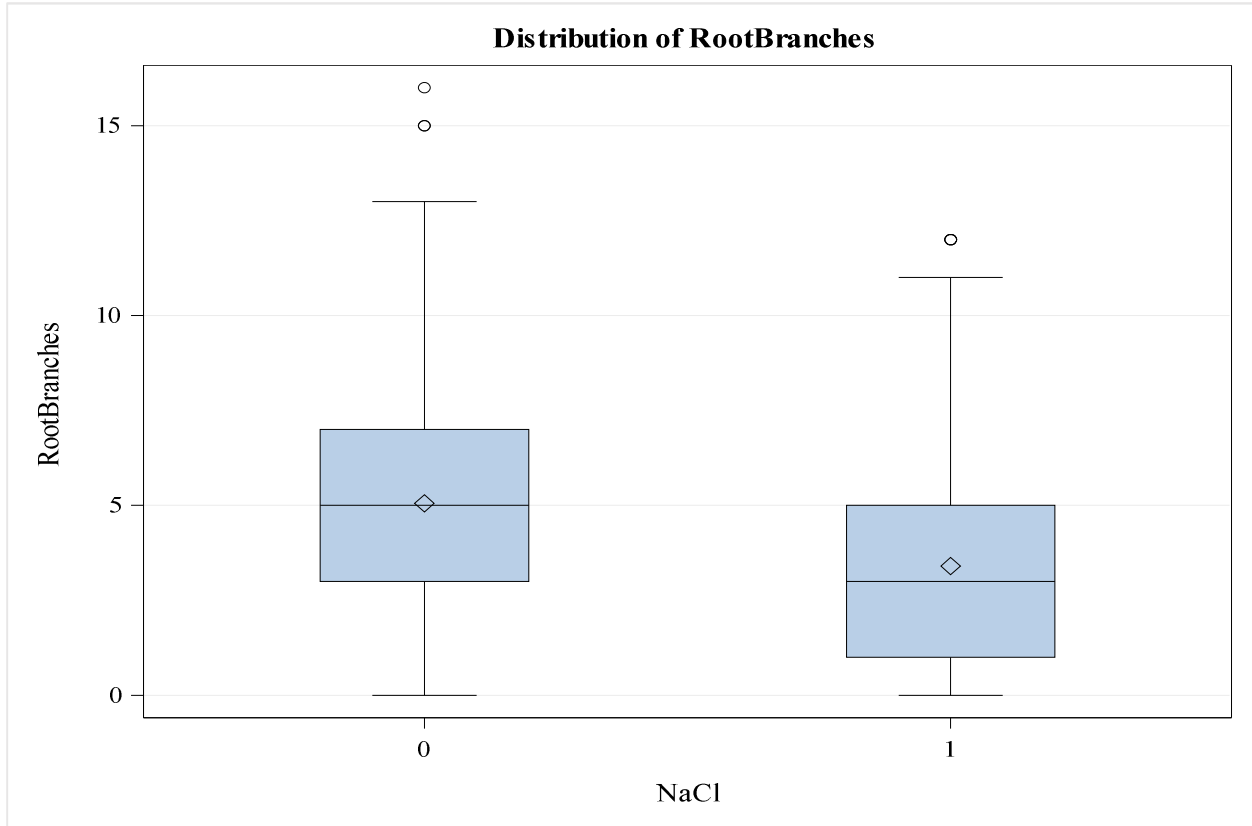


Figure 25. Distribution of Root Branches.

Table 59. Bonferroni (Dunn) t Tests for Root Branches

| | |
|--------------------------------|----------|
| Alpha | 0.05 |
| Error Degrees of Freedom | 1218 |
| Error Mean Square | 7.737247 |
| Critical Value of t | 1.96191 |
| Minimum Significant Difference | 0.3075 |

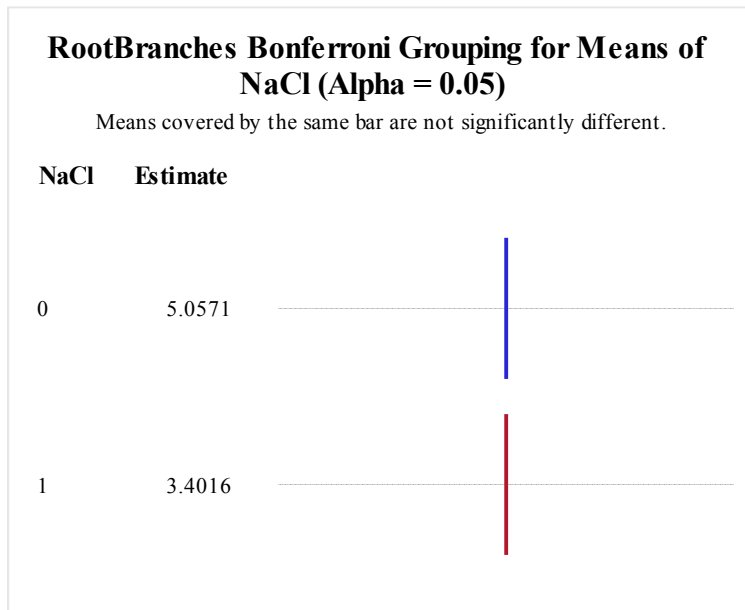


Figure 26. Root Branches Bonferroni Grouping for Means of NaCL ($\alpha=0.05$).

Poisson Results

Now we fit the same data using Poisson regression. As shown in Tables 60 and 61 below, the two treatments means have different letters: A for treatment without salt and B for treatment with salt. This means that the two means are not the same.

Note that the estimates are expressed in log scale. That is why we observe lower value from the ANOVA means

Table 60. Poisson Test Results

| NaCl | Estimate | Standard Error | DF | t Value | Pr > t | Mean | Standard Error Mean |
|------|----------|----------------|------|---------|---------|--------|---------------------|
| 0 | 1.6045 | 0.02485 | 1218 | 64.57 | <.0001 | 4.9754 | 0.1236 |
| 1 | 1.2129 | 0.03008 | 1218 | 40.32 | <.0001 | 3.3633 | 0.1012 |

Table 61. Root Branches Bonferroni Grouping for Means of NaCL ($\alpha=0.05$).

| NaCl | Estimate | |
|------|----------|---|
| 0 | 1.6045 | A |
| 1 | 1.2129 | B |

Negative Binomial Results

The results from the negative binomial regression when applied to the same data also suggest that the two treatments have different means. As we can see in Table 63 below, the probability obtained from comparing the difference is <0.0001 which is less than 0.05. The null hypothesis of equal means is rejected and there is strong evidence in favor of a difference in mean not null.

As we saw in the Poisson model, the estimates from the binomial model are also expressed in the log scale. This result is also backed up by the graphical representation of the test below.

Table 62. NaCL Least Squares Means.

| NaCl | Estimate | Standard Error | DF | t Value | Pr > t | Mean | Standard Error Mean |
|------|----------|----------------|------|---------|---------|--------|---------------------|
| 0 | 1.6045 | 0.02629 | 1218 | 61.04 | <.0001 | 4.9754 | 0.1308 |
| 1 | 1.2129 | 0.02889 | 1218 | 41.98 | <.0001 | 3.3633 | 0.09718 |

Table 63. Negative Binomial results.

| Differences of NaCl Least Squares Means | | | | | | |
|-----------------------------------------|-------|----------|----------------|------|---------|---------|
| NaCl | _NaCl | Estimate | Standard Error | DF | t Value | Pr > t |
| 0 | 1 | 0.3916 | 0.03906 | 1218 | 10.02 | <.0001 |

All three models fitted above namely: ANOVA, Poisson and Negative Binomial, converged to the same results. All three rejected the hypothesis of equal mean and supported that the mean of isolates treated with salt is different from that isolate without salt.

These results are consistent without research findings and serve as a support for our simulation study. We can then conclude that it appears to make no difference using ANOVA, Poisson or Negative Binomial in the case of two treatments groups with balanced and count data.

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APPENDIX A. PARAMETERS ESTIMATES

Three-Treatment $\mu_1 = \mu_2 = \mu_3$: Normal Distribution

Sample distribution: Normal

Simulations: 10,000

$n_1 = n_2 = n_3$

$\mu_1 = \mu_2 = \mu_3 = 20$

Population mean $\mu = 20$

Table A1. Normal Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 5$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|---------------------------------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.0234 | 19.4822 | 20.0234 | 20.0148 |
| Mean Trt2 ($\hat{\mu}_2$) | 19.9834 | 19.4394 | 19.9842 | 19.9734 |
| Mean Trt3 ($\hat{\mu}_3$) | 20.0421 | 19.4968 | 20.0421 | 20.0355 |
| $n_1 = n_2 = n_3 = 5$ Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 2.1925 | 2.29964 | 2.1984 | 2.2047 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 2.1925 | 2.29442 | 2.1964 | 2.2021 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 2.1925 | 2.30108 | 2.1995 | 2.2067 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 2.2546 | 2.3679 | 2.2546 | 2.2642 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 2.2256 | 2.33702 | 2.2254 | 2.2343 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 2.2281 | 2.34311 | 2.2281 | 2.2409 |

Table A2. Normal Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 10$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|----------------------------------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.0119 | 19.4 | 20.0125 | 20.0055 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.0266 | 19.4145 | 20.027 | 20.0194 |
| Mean Trt3 ($\hat{\mu}_3$) | 19.997 | 19.3799 | 19.9983 | 19.9876 |
| $n_1 = n_2 = n_3 = 10$ Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.566 | 1.65391 | 1.5677 | 1.57 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.566 | 1.65552 | 1.5684 | 1.571 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.566 | 1.65248 | 1.5672 | 1.5694 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.5799 | 1.67664 | 1.5797 | 1.5889 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.581 | 1.67421 | 1.5807 | 1.5875 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.5871 | 1.6766 | 1.5853 | 1.5922 |

Table A3. Normal Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 15$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.0076 | 19.3685 | 20.0081 | 20.0027 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.013 | 19.3739 | 20.0146 | 20.009 |
| Mean Trt3 ($\hat{\mu}_3$) | 20.0034 | 19.3666 | 20.0039 | 19.9984 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.2836 | 1.36015 | 1.2846 | 1.2858 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.2836 | 1.36061 | 1.2848 | 1.2861 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.2836 | 1.36007 | 1.2844 | 1.2857 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.2995 | 1.37971 | 1.2992 | 1.3051 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.2996 | 1.38011 | 1.2988 | 1.3038 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.2908 | 1.37571 | 1.2904 | 1.2959 |

Table A4. Normal Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 20$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.0185 | 19.3677 | 20.0195 | 20.0142 |
| Mean Trt2 ($\hat{\mu}_2$) | 19.9872 | 19.3336 | 19.9881 | 19.982 |
| Mean Trt3 ($\hat{\mu}_3$) | 20.0115 | 19.3594 | 20.012 | 20.006 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1141 | 1.18408 | 1.1151 | 1.1159 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1141 | 1.18175 | 1.1142 | 1.1148 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.1141 | 1.18355 | 1.1149 | 1.1157 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.1181 | 1.18905 | 1.1171 | 1.1211 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1203 | 1.19676 | 1.1191 | 1.1229 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.116 | 1.18773 | 1.1157 | 1.1196 |

Three-Treatment $\mu_1 = \mu_2 = \mu_3$: Poisson Distribution

Sample distribution: Poisson

Simulations: 10,000

$n_1 = n_2 = n_3$

$\mu_1 = \mu_2 = \mu_3 = 20$

Population mean $\mu = 20$

Table A5. Poisson Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 5$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-----------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1 = n_2 = n_3 = 5$ | Mean Trt1 (μ_1) | 19.9365 | 19.5234 | 19.9365 | 19.9291 |
| | Mean Trt2 (μ_2) | 19.991 | 19.5771 | 19.991 | 19.98 |
| | Mean Trt3 (μ_3) | 20.013 | 19.6026 | 20.013 | 20.0063 |
| | Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.9599 | 1.98352 | 1.9563 | 1.9614 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.9599 | 1.98905 | 1.959 | 1.9636 |
| | Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.9599 | 1.99199 | 1.9602 | 1.9659 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.995 | 2.02056 | 1.995 | 2.0059 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 2.0046 | 2.02862 | 2.0046 | 2.0144 |
| | Standard Dev Trt3 sd ($\hat{\mu}_3$) | 2.0034 | 2.01924 | 2.0034 | 2.0177 |

Table A6. Poisson Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 10$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1 = n_2 = n_3 = 10$ | Mean Trt1 (μ_1) | 19.9931 | 19.5299 | 19.9931 | 19.979 |
| | Mean Trt2 (μ_2) | 20.0057 | 19.5427 | 20.0057 | 19.9897 |
| | Mean Trt3 (μ_3) | 20.0069 | 19.5413 | 20.0069 | 19.9913 |
| | Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.4011 | 1.4204 | 1.4001 | 1.4019 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.4011 | 1.42126 | 1.4005 | 1.4023 |
| | Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.4011 | 1.42128 | 1.4006 | 1.4025 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.417 | 1.43621 | 1.417 | 1.4272 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.4317 | 1.45127 | 1.4317 | 1.4409 |
| | Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.4175 | 1.43391 | 1.4175 | 1.4278 |

Table A7. Poisson Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 15$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1 = n_2 = n_3 = 15$ | Mean Trt1 (μ_1) | 19.9973 | 19.5167 | 19.9973 | 19.9844 |
| | Mean Trt2 (μ_2) | 20.0075 | 19.5262 | 20.0075 | 19.9941 |
| | Mean Trt3 (μ_3) | 20.0075 | 19.525 | 20.0075 | 19.9931 |
| | Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1482 | 1.16406 | 1.1477 | 1.1488 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1482 | 1.16449 | 1.148 | 1.149 |
| | Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.1482 | 1.16439 | 1.1479 | 1.1489 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.1543 | 1.16535 | 1.1543 | 1.1631 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1453 | 1.16165 | 1.1453 | 1.1545 |
| | Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.1672 | 1.18342 | 1.1672 | 1.1762 |

Table A8. Poisson Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 20$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1 = n_2 = n_3 = 20$ | Mean Trt1 (μ_1) | 20.0039 | 19.513 | 20.0039 | 19.9861 |
| | Mean Trt2 (μ_2) | 19.9993 | 19.5118 | 19.9993 | 19.9824 |
| | Mean Trt3 (μ_3) | 19.9953 | 19.507 | 19.9953 | 19.9791 |
| | Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 0.9945 | 1.00901 | 0.9944 | 0.9951 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.9945 | 1.00905 | 0.9943 | 0.9951 |
| | Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 0.9945 | 1.00865 | 0.9942 | 0.9949 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.0064 | 1.01986 | 1.0064 | 1.0147 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.0023 | 1.01506 | 1.0023 | 1.0111 |
| | Standard Dev Trt3 sd ($\hat{\mu}_3$) | 0.9946 | 1.01255 | 0.9946 | 1.0052 |

Three-Treatment $\mu_1 = \mu_2 = \mu_3$: Negative Binomial Distribution

Sample distribution: Negative Binomial

Simulations: 10,000

$n_1 = n_2 = n_3$

$\mu_1 = \mu_2 = \mu_3 = 20$

Population mean $\mu = 20$

Table A9. NB Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 5$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-----------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1 = n_2 = n_3 = 5$ | Mean Trt1 (μ_1) | 20.0158 | 19.5066 | 20.0158 | 20.0099 |
| | Mean Trt2 (μ_2) | 19.9692 | 19.4519 | 19.9692 | 19.9588 |
| | Mean Trt3 (μ_3) | 20.0397 | 19.527 | 20.0397 | 20.0336 |
| | Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 2.1893 | 2.21397 | 2.1852 | 2.1887 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 2.1893 | 2.20858 | 2.1829 | 2.1863 |
| | Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 2.1893 | 2.2177 | 2.1871 | 2.1916 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 2.2413 | 2.26088 | 2.2413 | 2.2489 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 2.2498 | 2.27023 | 2.2498 | 2.2581 |
| | Standard Dev Trt3 sd ($\hat{\mu}_3$) | 2.2488 | 2.25828 | 2.2488 | 2.2565 |

Table A10. NB Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 10$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1 = n_2 = n_3 = 10$ | Mean Trt1 (μ_1) | 19.9817 | 19.404 | 19.9817 | 19.9733 |
| | Mean Trt2 (μ_2) | 20.0176 | 19.4404 | 20.0176 | 20.0097 |
| | Mean Trt3 (μ_3) | 20.005 | 19.4239 | 20.005 | 19.9962 |
| | Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.5659 | 1.58208 | 1.5636 | 1.565 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.5659 | 1.58482 | 1.565 | 1.5665 |
| | Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.5659 | 1.58366 | 1.5645 | 1.566 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.5788 | 1.59691 | 1.5788 | 1.5836 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.5929 | 1.60552 | 1.5929 | 1.598 |
| | Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.5843 | 1.59868 | 1.5843 | 1.591 |

Table A11. NB Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 15$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1 = n_2 = n_3 = 15$ | Mean Trt1 (μ_1) | 19.9801 | 19.3776 | 19.9801 | 19.974 |
| | Mean Trt2 (μ_2) | 20.0168 | 19.4151 | 20.0168 | 20.0113 |
| | Mean Trt3 (μ_3) | 19.9943 | 19.3951 | 19.9943 | 19.9864 |
| | Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.2836 | 1.29667 | 1.2821 | 1.2829 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.2836 | 1.29934 | 1.2834 | 1.2844 |
| | Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.2836 | 1.29813 | 1.2827 | 1.2835 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.3079 | 1.32418 | 1.3079 | 1.312 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.2836 | 1.29682 | 1.2836 | 1.2861 |
| | Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.2834 | 1.29252 | 1.2834 | 1.2869 |

Table A12. NB Samples with Three-Treatment $\mu_1 = \mu_2 = \mu_3$ ($n_1 = n_2 = n_3 = 20$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1 = n_2 = n_3 = 20$ | Mean Trt1 (μ_1) | 19.9957 | 19.3856 | 19.9957 | 19.9916 |
| | Mean Trt2 (μ_2) | 19.9947 | 19.3845 | 19.9947 | 19.9884 |
| | Mean Trt3 (μ_3) | 19.9944 | 19.3773 | 19.9944 | 19.9885 |
| | Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1137 | 1.12666 | 1.1133 | 1.1137 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1137 | 1.12666 | 1.1132 | 1.1136 |
| | Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.1137 | 1.12619 | 1.1132 | 1.1136 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.1235 | 1.13618 | 1.1235 | 1.1272 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1103 | 1.12265 | 1.1103 | 1.113 |
| | Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.1098 | 1.122 | 1.1098 | 1.1131 |

Three-Treatment $\mu_1 \neq \mu_2 \neq \mu_3$: Normal Distribution

Sample distribution: Normal

Simulations: 10,000

$n_1 = n_2 = n_3$

$\mu_1 \neq \mu_2 \neq \mu_3$

Population mean $\mu=20$

Effect size 0.5σ

Table A13. Normal Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 0.5σ , $n_1 = n_2 = n_3 = 5$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 17.5234 | 16.8886 | 17.5264 | 17.5138 |
| Mean Trt2 (μ_2) | 19.9834 | 19.4394 | 19.9842 | 19.9774 |
| Mean Trt3 (μ_3) | 22.5421 | 22.0678 | 22.5421 | 22.5522 |
| Standard Error Trt1 s.e. (μ_1) | 2.1925 | 2.02198 | 2.0649 | 2.0521 |
| Standard Error Trt2 s.e. (μ_2) | 2.1925 | 2.34625 | 2.207 | 2.2142 |
| Standard Error Trt3 s.e. (μ_3) | 2.1925 | 2.6747 | 2.3455 | 2.3774 |
| Standard Dev Trt1 sd (μ_1) | 2.2546 | 2.41516 | 2.251 | 2.2512 |
| Standard Dev Trt2 sd (μ_2) | 2.2256 | 2.33702 | 2.2254 | 2.2317 |
| Standard Dev Trt3 sd (μ_3) | 2.2281 | 2.30947 | 2.2281 | 2.2418 |

Table A14. Normal Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 0.5σ , $n_1 = n_2 = n_3 = 10$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 17.5119 | 16.7949 | 17.5166 | 17.5035 |
| Mean Trt2 (μ_2) | 20.0266 | 19.4145 | 20.027 | 20.0203 |
| Mean Trt3 (μ_3) | 22.497 | 21.9603 | 22.4977 | 22.5086 |
| Standard Error Trt1 s.e. (μ_1) | 1.566 | 1.459 | 1.4731 | 1.461 |
| Standard Error Trt2 s.e. (μ_2) | 1.566 | 1.69426 | 1.5758 | 1.5796 |
| Standard Error Trt3 s.e. (μ_3) | 1.566 | 1.91961 | 1.6706 | 1.6919 |
| Standard Dev Trt1 sd (μ_1) | 1.5799 | 1.71012 | 1.5756 | 1.5751 |
| Standard Dev Trt2 sd (μ_2) | 1.581 | 1.67421 | 1.5807 | 1.5826 |
| Standard Dev Trt3 sd (μ_3) | 1.5871 | 1.65245 | 1.5861 | 1.597 |

Table A15. Normal Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size =0.5 σ , $n_1= n_2=n_3=15$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 17.5076 | 16.7522 | 17.5106 | 17.5016 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.013 | 19.3739 | 20.0146 | 20.009 |
| Mean Trt3 ($\hat{\mu}_3$) | 22.5034 | 21.9504 | 22.5035 | 22.515 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.2836 | 1.20332 | 1.2075 | 1.1968 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.2836 | 1.3965 | 1.2913 | 1.2939 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.2836 | 1.58475 | 1.3695 | 1.3873 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.2995 | 1.41901 | 1.2978 | 1.3005 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.2996 | 1.38011 | 1.2988 | 1.3006 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.2908 | 1.35142 | 1.2907 | 1.3009 |

Table A16. Normal Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size =0.5 σ , $n_1= n_2=n_3=20$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 17.5185 | 16.7533 | 17.5233 | 17.5157 |
| Mean Trt2 ($\hat{\mu}_2$) | 19.9872 | 19.3336 | 19.9881 | 19.984 |
| Mean Trt3 ($\hat{\mu}_3$) | 22.5115 | 21.9454 | 22.5116 | 22.5213 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1141 | 1.04729 | 1.0481 | 1.0382 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1141 | 1.21125 | 1.1195 | 1.1213 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.1141 | 1.37673 | 1.1883 | 1.2039 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.1181 | 1.2211 | 1.1161 | 1.1173 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1203 | 1.19676 | 1.1191 | 1.12 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.116 | 1.16625 | 1.116 | 1.124 |

Three-Treatment $\mu_1 \neq \mu_2 \neq \mu_3$: Poisson Distribution

Sample distribution: Poisson

Simulations: 10,000

$n_1 = n_2 = n_3$

$\mu_1 \neq \mu_2 \neq \mu_3$

Population mean $\mu=20$

Effect size 0.5σ

Table A17. Poisson Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size= 0.5σ , $n_1 = n_2 = n_3 = 5$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 17.7781 | 17.3652 | 17.7781 | 17.7622 |
| Mean Trt2 (μ_2) | 19.9639 | 19.5489 | 19.9639 | 19.9535 |
| Mean Trt3 (μ_3) | 22.2634 | 21.8537 | 22.2634 | 22.2693 |
| Standard Error Trt1 s.e. (μ_1) | 1.9607 | 1.76874 | 1.8471 | 1.8439 |
| Standard Error Trt2 s.e. (μ_2) | 1.9607 | 1.99259 | 1.9574 | 1.9602 |
| Standard Error Trt3 s.e. (μ_3) | 1.9607 | 2.23071 | 2.0679 | 2.0796 |
| Standard Dev Trt1 sd (μ_1) | 1.8796 | 1.90643 | 1.8796 | 1.8814 |
| Standard Dev Trt2 sd (μ_2) | 1.9792 | 2.00178 | 1.9792 | 1.9875 |
| Standard Dev Trt3 sd (μ_3) | 2.0935 | 2.11537 | 2.0935 | 2.1016 |

Table A18. Poisson Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size= 0.5σ , $n_1 = n_2 = n_3 = 10$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 17.7594 | 17.2959 | 17.7594 | 17.7412 |
| Mean Trt2 (μ_2) | 20.0108 | 19.5435 | 20.0108 | 20.0019 |
| Mean Trt3 (μ_3) | 22.2576 | 21.7916 | 22.2576 | 22.2597 |
| Standard Error Trt1 s.e. (μ_1) | 1.4039 | 1.26543 | 1.3219 | 1.3188 |
| Standard Error Trt2 s.e. (μ_2) | 1.4039 | 1.43034 | 1.4032 | 1.4044 |
| Standard Error Trt3 s.e. (μ_3) | 1.4039 | 1.59558 | 1.48 | 1.4864 |
| Standard Dev Trt1 sd (μ_1) | 1.3367 | 1.35708 | 1.3367 | 1.3373 |
| Standard Dev Trt2 sd (μ_2) | 1.4112 | 1.43133 | 1.4112 | 1.4143 |
| Standard Dev Trt3 sd (μ_3) | 1.501 | 1.5205 | 1.501 | 1.5095 |

Table A19. Poisson Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect siz =0.5 σ , $n_1= n_2=n_3=15$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 17.759 | 17.2758 | 17.759 | 17.7398 |
| Mean Trt2 ($\hat{\mu}_2$) | 19.9953 | 19.5156 | 19.9953 | 19.9854 |
| Mean Trt3 ($\hat{\mu}_3$) | 22.255 | 21.7741 | 22.255 | 22.2631 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1475 | 1.03496 | 1.0808 | 1.0779 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1475 | 1.16968 | 1.1469 | 1.1474 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.1475 | 1.30542 | 1.2101 | 1.2147 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.0957 | 1.11294 | 1.0957 | 1.0951 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1611 | 1.17909 | 1.1611 | 1.1665 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.2256 | 1.23957 | 1.2256 | 1.2324 |

Table A20. Poisson Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size=0.5 σ , $n_1= n_2=n_3=20$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 17.7639 | 17.271 | 17.7639 | 17.7441 |
| Mean Trt2 ($\hat{\mu}_2$) | 19.9782 | 19.4905 | 19.9782 | 19.97 |
| Mean Trt3 ($\hat{\mu}_3$) | 22.2454 | 21.7538 | 22.2454 | 22.2517 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 0.996 | 0.89915 | 0.9385 | 0.936 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.996 | 1.01504 | 0.9953 | 0.9957 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 0.996 | 1.13299 | 1.0503 | 1.0539 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.9437 | 0.95891 | 0.9437 | 0.943 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.9967 | 1.00922 | 0.9967 | 0.9998 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.0493 | 1.06352 | 1.0493 | 1.0596 |

Three-Treatment $\mu_1 \neq \mu_2 \neq \mu_3$: Negative Binomial Distribution

Sample distribution: NB

Simulations: 10,000

$n_1 = n_2 = n_3$

$\mu_1 \neq \mu_2 \neq \mu_3$

Population mean $\mu=20$

Effect size 0.5σ

Table A21. NB Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 0.5σ , $n_1 = n_2 = n_3 = 5$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|---------------------------------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 20.0109 | 19.4966 | 20.0109 | 20.0021 |
| Mean Trt2 (μ_2) | 17.4899 | 16.9002 | 17.4899 | 17.4749 |
| Mean Trt3 (μ_3) | 22.4627 | 22.0074 | 22.4627 | 22.4781 |
| $n_1 = n_2 = n_3 = 5$ Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 2.192 | 2.25529 | 2.2002 | 2.2047 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 2.192 | 1.95004 | 2.0566 | 2.0439 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 2.192 | 2.55027 | 2.3318 | 2.3572 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 2.2213 | 2.24268 | 2.2213 | 2.2259 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 2.224 | 2.24257 | 2.224 | 2.2224 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 2.2386 | 2.25699 | 2.2386 | 2.2444 |

Table A22. NB Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 0.5σ , $n_1 = n_2 = n_3 = 10$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|----------------------------------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 19.9904 | 19.4096 | 19.9904 | 19.9825 |
| Mean Trt2 (μ_2) | 17.4897 | 16.8277 | 17.4897 | 17.477 |
| Mean Trt3 (μ_3) | 22.5027 | 21.991 | 22.5027 | 22.5142 |
| $n_1 = n_2 = n_3 = 10$ Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.5657 | 1.61046 | 1.5719 | 1.5745 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.5657 | 1.39449 | 1.4702 | 1.4589 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.5657 | 1.82583 | 1.6678 | 1.6872 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.5851 | 1.60225 | 1.5851 | 1.5859 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.5939 | 1.60451 | 1.5939 | 1.5937 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.5786 | 1.59705 | 1.5786 | 1.5845 |

Table A23. NB Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 0.5σ , $n_1 = n_2 = n_3 = 15$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.0094 | 19.4066 | 20.0094 | 20.0051 |
| Mean Trt2 ($\hat{\mu}_2$) | 17.4946 | 16.8042 | 17.4946 | 17.4857 |
| Mean Trt3 ($\hat{\mu}_3$) | 22.5131 | 21.9819 | 22.5131 | 22.5231 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.2837 | 1.32282 | 1.2898 | 1.2919 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.2837 | 1.14416 | 1.2058 | 1.1953 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.2837 | 1.49905 | 1.3681 | 1.3843 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.3006 | 1.31642 | 1.3006 | 1.3024 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.2849 | 1.30102 | 1.2849 | 1.2847 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.28 | 1.29448 | 1.28 | 1.2848 |

Table A24. NB Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 0.5σ , $n_1 = n_2 = n_3 = 20$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.0135 | 19.3994 | 20.0135 | 20.0095 |
| Mean Trt2 ($\hat{\mu}_2$) | 17.4931 | 16.7896 | 17.4931 | 17.4864 |
| Mean Trt3 ($\hat{\mu}_3$) | 22.4992 | 21.9583 | 22.4992 | 22.5097 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1135 | 1.14853 | 1.1191 | 1.1209 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1135 | 0.99315 | 1.0462 | 1.0366 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.1135 | 1.30031 | 1.1866 | 1.2008 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.1205 | 1.1331 | 1.1205 | 1.1217 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1099 | 1.12272 | 1.1099 | 1.1116 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.1157 | 1.13217 | 1.1157 | 1.121 |

Three-Treatment $\mu_1 \neq \mu_2 \neq \mu_3$: Normal Distribution

Sample distribution: Normal

Simulations: 10,000

$n_1 = n_2 = n_3$

$\mu_1 \neq \mu_2 \neq \mu_3$

Population mean $\mu=20$

Effect size 1σ

Table A25. Normal Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1 = n_2 = n_3 = 5$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\mu\hat{1}$) | 15.0234 | 14.2776 | 15.0443 | 15.0269 |
| Mean Trt2 ($\mu\hat{2}$) | 19.9834 | 19.4394 | 19.9842 | 19.9691 |
| Mean Trt3 ($\mu\hat{3}$) | 25.0421 | 24.6208 | 25.0421 | 25.0915 |
| Standard Error Trt1 s.e. ($\mu\hat{1}$) | 2.1925 | 1.80585 | 1.939 | 1.9129 |
| Standard Error Trt2 s.e. ($\mu\hat{2}$) | 2.1925 | 2.51462 | 2.2384 | 2.2526 |
| Standard Error Trt3 s.e. ($\mu\hat{3}$) | 2.1925 | 3.2022 | 2.5083 | 2.5824 |
| Standard Dev Trt1 sd ($\mu\hat{1}$) | 2.2546 | 2.46861 | 2.2412 | 2.2519 |
| Standard Dev Trt2 sd ($\mu\hat{2}$) | 2.2256 | 2.33702 | 2.2254 | 2.2268 |
| Standard Dev Trt3 sd ($\mu\hat{3}$) | 2.2281 | 2.29044 | 2.2281 | 2.2589 |

Table A26. Normal Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1 = n_2 = n_3 = 10$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\mu\hat{1}$) | 15.0106 | 14.3365 | 15.0169 | 14.9886 |
| Mean Trt2 ($\mu\hat{2}$) | 20.0266 | 19.4145 | 20.027 | 20.0124 |
| Mean Trt3 ($\mu\hat{3}$) | 24.997 | 24.5197 | 24.997 | 25.0602 |
| Standard Error Trt1 s.e. ($\mu\hat{1}$) | 1.5129 | 1.24095 | 1.3258 | 1.3078 |
| Standard Error Trt2 s.e. ($\mu\hat{2}$) | 1.5129 | 1.6914 | 1.5318 | 1.5364 |
| Standard Error Trt3 s.e. ($\mu\hat{3}$) | 1.5129 | 2.14202 | 1.7121 | 1.7483 |
| Standard Dev Trt1 sd ($\mu\hat{1}$) | 1.4131 | 1.54212 | 1.4091 | 1.4234 |
| Standard Dev Trt2 sd ($\mu\hat{2}$) | 1.581 | 1.67421 | 1.5807 | 1.5856 |
| Standard Dev Trt3 sd ($\mu\hat{3}$) | 1.5871 | 1.64007 | 1.5871 | 1.6185 |

Table A27. Normal Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1 = n_2 = n_3 = 15$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|----------------------------------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 15.0076 | 14.1028 | 15.0267 | 14.9945 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.013 | 19.3739 | 20.0146 | 20.0073 |
| Mean Trt3 ($\hat{\mu}_3$) | 25.0034 | 24.513 | 25.0034 | 25.0593 |
| $n_1 = n_2 = n_3 = 15$ Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.2836 | 1.09013 | 1.1349 | 1.1156 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.2836 | 1.51242 | 1.3099 | 1.3181 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.2836 | 1.91733 | 1.4646 | 1.5082 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.2995 | 1.46864 | 1.2913 | 1.3048 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.2996 | 1.38011 | 1.2988 | 1.3012 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.2908 | 1.33751 | 1.2908 | 1.3161 |

Table A28. Normal Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1 = n_2 = n_3 = 20$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|----------------------------------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 15.0166 | 14.2943 | 15.0228 | 14.9893 |
| Mean Trt2 ($\hat{\mu}_2$) | 19.9872 | 19.3336 | 19.9881 | 19.9799 |
| Mean Trt3 ($\hat{\mu}_3$) | 25.0115 | 24.5094 | 25.0115 | 25.0715 |
| $n_1 = n_2 = n_3 = 20$ Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.0763 | 0.89311 | 0.9434 | 0.9298 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.0763 | 1.2123 | 1.0883 | 1.0913 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.0763 | 1.53971 | 1.2178 | 1.2434 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.0001 | 1.10343 | 0.9973 | 1.0069 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1203 | 1.19676 | 1.1191 | 1.1253 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.116 | 1.15419 | 1.116 | 1.1397 |

Table A29. Poisson Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1=n_2=n_3=5$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|---------------------------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 15.5415 | 15.1244 | 15.5415 | 15.5283 |
| Mean Trt2 (μ_2) | 19.9935 | 19.5828 | 19.9935 | 19.9858 |
| Mean Trt3 (μ_3) | 24.4719 | 24.0663 | 24.4719 | 24.4931 |
| $n_1=n_2=n_3=5$ Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.9555 | 1.55811 | 1.7238 | 1.7126 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.9555 | 2.02436 | 1.9565 | 1.9579 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.9555 | 2.49055 | 2.1649 | 2.1828 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.7595 | 1.78994 | 1.7595 | 1.7601 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 2.0127 | 2.04007 | 2.0127 | 2.0185 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 2.197 | 2.21836 | 2.197 | 2.2116 |

Table A30. Poisson Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1=n_2=n_3=10$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|----------------------------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 15.5201 | 15.0512 | 15.5201 | 15.5019 |
| Mean Trt2 (μ_2) | 20.0027 | 19.5401 | 20.0027 | 19.993 |
| Mean Trt3 (μ_3) | 24.4693 | 24.0063 | 24.4693 | 24.5098 |
| $n_1=n_2=n_3=10$ Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.4016 | 1.11627 | 1.2344 | 1.2264 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.4016 | 1.45128 | 1.4015 | 1.4016 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.4016 | 1.78407 | 1.5503 | 1.5619 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.2497 | 1.27116 | 1.2497 | 1.2566 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.4266 | 1.44416 | 1.4266 | 1.4306 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.5739 | 1.5917 | 1.5739 | 1.5945 |

Table A31. Poisson Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1=n_2=n_3=15$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 15.542 | 15.0599 | 15.542 | 15.5177 |
| Mean Trt2 ($\hat{\mu}_2$) | 19.9701 | 19.4879 | 19.9701 | 19.9606 |
| Mean Trt3 ($\hat{\mu}_3$) | 24.4826 | 24.0051 | 24.4826 | 24.5305 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1468 | 0.91417 | 1.0106 | 1.0046 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1468 | 1.18382 | 1.1456 | 1.1458 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.1468 | 1.45918 | 1.2686 | 1.2779 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.0241 | 1.04191 | 1.0241 | 1.034 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1541 | 1.17247 | 1.1541 | 1.1577 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.2819 | 1.29718 | 1.2819 | 1.3015 |

Table A32. Poisson Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1=n_2=n_3=20$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 15.5271 | 15.0323 | 15.5271 | 15.4973 |
| Mean Trt2 ($\hat{\mu}_2$) | 20.0226 | 19.5308 | 20.0226 | 20.0132 |
| Mean Trt3 ($\hat{\mu}_3$) | 24.4739 | 23.988 | 24.4739 | 24.5297 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 0.9959 | 0.79379 | 0.8772 | 0.872 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.9959 | 1.03218 | 0.9962 | 0.9965 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 0.9959 | 1.26801 | 1.1014 | 1.1092 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 0.8878 | 0.90508 | 0.8878 | 0.8962 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.0041 | 1.01605 | 1.0041 | 1.0082 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.1077 | 1.12217 | 1.1077 | 1.1256 |

Table A33. NB Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1=n_2=n_3=5$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 19.9598 | 19.4419 | 19.9598 | 20.0014 |
| Mean Trt2 (μ_2) | 15.3325 | 14.6501 | 15.3325 | 15.3563 |
| Mean Trt3 (μ_3) | 10.5269 | 9.4654 | 10.5269 | 10.4932 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 2.2116 | 3.4601 | 2.601 | 2.7591 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 2.2116 | 2.59814 | 2.2781 | 2.3187 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 2.2116 | 1.63113 | 1.8864 | 1.8305 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 2.2299 | 2.24664 | 2.2299 | 2.2482 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 2.2827 | 2.29272 | 2.2827 | 2.2913 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 2.3122 | 2.32534 | 2.3122 | 2.3375 |

Table A34. NB Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1=n_2=n_3=10$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 (μ_1) | 19.9894 | 19.406 | 19.9894 | 20.0127 |
| Mean Trt2 (μ_2) | 14.9959 | 14.2236 | 14.9959 | 15.0086 |
| Mean Trt3 (μ_3) | 10.0214 | 8.8155 | 10.0214 | 10.0014 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.5628 | 2.5571 | 1.8684 | 2.012 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.5628 | 1.8702 | 1.6177 | 1.6504 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.5628 | 1.13694 | 1.3221 | 1.2697 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.6009 | 1.61486 | 1.6009 | 1.6087 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.5769 | 1.58961 | 1.5769 | 1.579 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.5753 | 1.6062 | 1.5753 | 1.5898 |

Table A35. NB Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1=n_2=n_3=15$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 20.0133 | 19.4106 | 20.0133 | 20.0249 |
| Mean Trt2 ($\hat{\mu}_2$) | 14.9918 | 14.1819 | 14.9918 | 14.9967 |
| Mean Trt3 ($\hat{\mu}_3$) | 10.0291 | 8.7683 | 10.0291 | 10.0225 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.2838 | 2.11086 | 1.5372 | 1.6637 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.2838 | 1.54038 | 1.3301 | 1.3578 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.2838 | 0.93919 | 1.0878 | 1.0402 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.2928 | 1.30627 | 1.2928 | 1.2967 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.2915 | 1.30711 | 1.2915 | 1.2914 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.2785 | 1.31488 | 1.2785 | 1.2833 |

Table A36. NB Samples with Three -Treatment $\mu_1 \neq \mu_2 \neq \mu_3$ (effect size = 1σ , $n_1=n_2=n_3=20$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|--------------------------------------------|---------|------------|---------|-------------------|
| Mean Trt1 ($\hat{\mu}_1$) | 19.9957 | 19.3842 | 19.9957 | 20.0007 |
| Mean Trt2 ($\hat{\mu}_2$) | 15.0175 | 14.1926 | 15.0175 | 15.0195 |
| Mean Trt3 ($\hat{\mu}_3$) | 9.9998 | 8.7135 | 9.9998 | 9.9969 |
| Standard Error Trt1 s.e. ($\hat{\mu}_1$) | 1.1131 | 1.8348 | 1.3344 | 1.448 |
| Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1131 | 1.34211 | 1.1562 | 1.1813 |
| Standard Error Trt3 s.e. ($\hat{\mu}_3$) | 1.1131 | 0.81508 | 0.9434 | 0.9 |
| Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.1109 | 1.12509 | 1.1109 | 1.1135 |
| Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.118 | 1.1326 | 1.118 | 1.1182 |
| Standard Dev Trt3 sd ($\hat{\mu}_3$) | 1.1227 | 1.14621 | 1.1227 | 1.1251 |

**APPENDIX B. TWO POPULATIONS UNBALANCED SAMPLES: TYPE I ERROR
RATE**

Two-Treatment $\mu_1 = \mu_2$: Normal Distribution

Table B1. Normal Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = 20$

| Sampling Efforts | Fitted Models | | | |
|-------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1=5$ $n_2=10$ | 5.31 | 5.07 | 5.27 | 5.37 |
| $n_1=10$ $n_2=15$ | 4.89 | 4.85 | 4.76 | 5.21 |
| $n_1=10$ $n_2=20$ | 5.04 | 4.89 | 4.9 | 5.25 |

Table B2. Poisson Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = 20$

| Sampling Efforts | Fitted Models | | | |
|-------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1=5$ $n_2=10$ | 5.05 | 4.78 | 4.95 | 5.16 |
| $n_1=10$ $n_2=15$ | 4.76 | 4.68 | 4.78 | 5.07 |
| $n_1=10$ $n_2=20$ | 4.82 | 4.78 | 4.8 | 4.99 |

Table B3. NB Samples - Rejection Rates (%) for Fitted models $\mu_1 = \mu_2 = 20$

| Sampling Efforts | Fitted Models | | | |
|-------------------|---------------|------------|---------|-------------------|
| | Normal | Log-Normal | Poisson | Negative Binomial |
| $n_1=5$ $n_2=10$ | 5.2 | 4.99 | 5.01 | 5.14 |
| $n_1=10$ $n_2=15$ | 4.78 | 4.79 | 4.78 | 5.01 |
| $n_1=10$ $n_2=20$ | 4.95 | 4.89 | 4.91 | 5 |

APPENDIX C. TWO POPULATIONS UNBALANCED SAMPLES: PARAMETERS

ESTIMATES

Two-Treatment $\mu_1 = \mu_2$: Normal Distribution

Table C1. Normal Samples with Two -Treatment $\mu_1 = \mu_2$ ($n_1= 5$ $n_2=10$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial | |
|--------------------------------------|--------------------------------------------|------------|---------|-------------------|---------|
| n ₁ =5 n ₂ =10 | Mean Trt1 ($\hat{\mu}_1$) | 20.0209 | 19.5967 | 20.0209 | 20.0224 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.9622 | 2.0335 | 1.9636 | 1.9678 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 2.0166 | 2.09038 | 2.0166 | 2.0357 |
| | Mean Trt2 ($\hat{\mu}_2$) | 20.0114 | 19.5296 | 20.0114 | 19.9944 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.9622 | 2.0335 | 1.9636 | 1.9678 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 2.0166 | 2.09038 | 2.0166 | 2.0357 |

Table C2. Normal Samples with Two -Treatment $\mu_1 = \mu_2$ ($n_1= 10$ $n_2=15$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial | |
|---------------------------------------|--------------------------------------------|------------|---------|-------------------|---------|
| n ₁ =10 n ₂ =15 | Mean Trt1 ($\hat{\mu}_1$) | 20.024 | 19.5431 | 20.024 | 20.0124 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.3992 | 1.45554 | 1.4004 | 1.4021 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.4138 | 1.47188 | 1.4138 | 1.4272 |
| | Mean Trt2 ($\hat{\mu}_2$) | 20.008 | 19.5075 | 20.0082 | 19.9881 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1425 | 1.1858 | 1.1431 | 1.1441 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.154 | 1.20977 | 1.1537 | 1.1609 |

Table C3. Normal Samples with Two -Treatment $\mu_1 = \mu_2$ ($n_1=10$ $n_2=20$)

| Criteria | Normal | Log-Normal | Poisson | Negative Binomial | |
|---------------------------------------|--------------------------------------------|------------|---------|-------------------|---------|
| n ₁ =10 n ₂ =20 | Mean Trt1 ($\hat{\mu}_1$) | 20.0106 | 19.5314 | 20.0108 | 20.001 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.401 | 1.45895 | 1.4013 | 1.403 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.4131 | 1.47569 | 1.4131 | 1.4321 |
| | Mean Trt2 ($\hat{\mu}_2$) | 20.0106 | 19.5013 | 20.0109 | 19.9903 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.9907 | 1.02991 | 0.9912 | 0.992 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.0062 | 1.0522 | 1.006 | 1.0102 |

Two-Treatment $\mu_1 = \mu_2$: Poisson Distribution

Table C4. Poisson Samples with Two -Treatment $\mu_1 = \mu_2$ ($n_1=5$ $n_2=10$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1=5$ $n_2=10$ | Mean Trt1 ($\hat{\mu}_1$) | 19.9689 | 19.5626 | 19.9689 | 19.9682 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.9615 | 1.98994 | 1.9598 | 1.9633 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 2.0086 | 2.02961 | 2.0086 | 2.0191 |
| | Mean Trt2 ($\hat{\mu}_2$) | 19.9692 | 19.5019 | 19.9692 | 19.9524 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.387 | 1.40191 | 1.3867 | 1.3882 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.4005 | 1.42056 | 1.4005 | 1.405 |

Table C5. Poisson Samples with Two -Treatment $\mu_1 = \mu_2$ ($n_1=10$ $n_2=15$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1=10$ $n_2=15$ | Mean Trt1 ($\hat{\mu}_1$) | 20.0131 | 19.5508 | 20.0132 | 19.9999 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.396 | 1.41438 | 1.3955 | 1.397 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.4184 | 1.43943 | 1.4184 | 1.428 |
| | Mean Trt2 ($\hat{\mu}_2$) | 20.0121 | 19.5337 | 20.0121 | 19.9937 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1398 | 1.15385 | 1.1397 | 1.1406 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1453 | 1.15993 | 1.1453 | 1.1518 |

Table C6. Poisson Samples with Two -Treatment $\mu_1 = \mu_2$ ($n_1=10$ $n_2=20$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1=10$ $n_2=20$ | Mean Trt1 ($\hat{\mu}_1$) | 20.0146 | 19.5514 | 20.0146 | 20.0055 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.4035 | 1.4229 | 1.4029 | 1.4045 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.4208 | 1.44007 | 1.4208 | 1.4321 |
| | Mean Trt2 ($\hat{\mu}_2$) | 20.0171 | 19.5256 | 20.0171 | 19.9987 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 0.9924 | 1.00466 | 0.9924 | 0.9931 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 0.9986 | 1.0126 | 0.9986 | 1.002 |

Two-Treatment $\mu_1 = \mu_2$: NB Distribution

Table C7. NB Samples with Two -Treatment $\mu_1 = \mu_2$ ($n_1=5$ $n_2=10$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1=5$ $n_2=10$ | Mean Trt1 ($\hat{\mu}_1$) | 20.0214 | 19.5066 | 20.0158 | 20.0214 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 2.1932 | 2.21865 | 2.19 | 2.1935 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 2.2413 | 2.26088 | 2.2413 | 2.2505 |
| | Mean Trt2 ($\hat{\mu}_2$) | 20.0044 | 19.4235 | 20.0044 | 19.9927 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.5508 | 1.56195 | 1.5497 | 1.5512 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.5942 | 1.6049 | 1.5942 | 1.5975 |

Table C8. NB Samples with Two -Treatment $\mu_1 = \mu_2$ ($n_1=10$ $n_2=15$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1=10$ $n_2=15$ | Mean Trt1 ($\hat{\mu}_1$) | 20.0066 | 19.4263 | 20.0066 | 19.9983 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.5645 | 1.58201 | 1.5638 | 1.5654 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.5894 | 1.60715 | 1.5894 | 1.5943 |
| | Mean Trt2 ($\hat{\mu}_2$) | 19.9882 | 19.3867 | 19.9882 | 19.9777 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.2774 | 1.28886 | 1.2766 | 1.2775 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.2919 | 1.30611 | 1.2919 | 1.2951 |

Table C9. NB Samples with Two -Treatment $\mu_1 = \mu_2$ ($n_1=10$ $n_2=20$)

| | Criteria | Normal | Log-Normal | Poisson | Negative Binomial |
|-------------------|--------------------------------------------|---------|------------|---------|-------------------|
| $n_1=10$ $n_2=20$ | Mean Trt1 ($\hat{\mu}_1$) | 19.9817 | 19.404 | 19.9817 | 19.9802 |
| | Standard Error Trt1 s.e.($\hat{\mu}_1$) | 1.5668 | 1.58278 | 1.5649 | 1.5662 |
| | Standard Dev Trt1 sd ($\hat{\mu}_1$) | 1.5788 | 1.59691 | 1.5788 | 1.5852 |
| | Mean Trt2 ($\hat{\mu}_2$) | 20.0113 | 19.3991 | 20.0113 | 20.0002 |
| | Standard Error Trt2 s.e. ($\hat{\mu}_2$) | 1.1079 | 1.11871 | 1.1078 | 1.1085 |
| | Standard Dev Trt2 sd ($\hat{\mu}_2$) | 1.1226 | 1.13408 | 1.1226 | 1.1241 |

APPENDIX D. SAS CODE

Normal Distribution

```
options mprint symbolgen formchar="|----+|----+|-\<>*";

title1 'Poisson Count Data Comparative Analyses - Traditional vs GLMM
Approach';

*****
*** The generate macro accepts 8 parameters as follows:          ***
***   Samples = # of sample runs to generate                    ***
***   N1 = sample size for treatment 1 population                ***
***   mu1 = Sample mean for treatment 1 population              ***
***   s1 = Sample variance for treatment 1 population           ***
***   N2 = sample size for treatment 2 population                ***
***   mu2 = Sample mean for treatment 2 population              ***
***   s2 = Sample variance for treatment 2 population           ***
***   seed0 = starting seed for simulation                       ***
*** The RAND function generates a random value from the specified ***
*** distribution (here Poisson with parameter Lambda).          ***
*****;
*** Wicklin ODS control macros ***;

%macro ODSOff(); *** Call prior to BY-group processing ***;
ods graphics off;
ods exclude all;
ods noresults;
%mend;

%macro ODSOn(); *** Call after BY-group processing ***;
ods graphics on;
ods exclude none;
ods results;
%mend;

libname norfive 'C:\Users\Ibrahim.Soumare\Desktop\MS_Full_code\Normal\n=5';

%macro generate(Samples, n1, mu1, s1, n2, mu2, s2, seed0);

data norfive.genNormal (keep=Sample Iter n1 mu1 s1 n2 mu2 s2 Trt Y logY);
  call streaminit(498455); *** Initialize with desired seed. ***;

  n1=&n1; mu1=&mu1; s1=&s1;
  n2=&n2; mu2=&mu2; s2=&s2;
  do Sample=1 to &Samples;
    do Iter=1 to &n1;
      Trt=1;
      Y=rand('Normal', &mu1, sqrt(&s1));
      if Y=0 then logY=log(Y+0.1);
      else logY=log(Y);
      output;
    end;
    do Iter=&n1+1 to &n1+&n2;
      Trt=2;
      Y=rand('Normal', &mu2, sqrt(&s2));
```

```

        if Y=0 then logY=log(Y+0.1);
        else logY=log(Y);
        output;
    end;
end;
run;

proc print data=norfive.genNormal(obs=100);
    title2 'Check Small Subset of Simulated Values';
run;

proc sort;
    by Sample Trt;
run;

*****
***** Traditional ANOVA Approach - Untransformed Y *****
*****;

%ODSOFF
ods output FitStatistics=norfive.NFitStats;
ods output ParameterEstimates=norfive.NParmEsts;
ods output Tests3=norfive.NFixed3;
ods output LSMeans=norfive.NLSMns;
ods output Diffs=norfive.NDiffsMns;

proc glimmix data=norfive.genNormal;
    by Sample;
    class Trt;
    model Y=Trt / solution;
* random _residual_;
    lsmeans Trt / diff;
    title2 'Traditional ANOVA Approach';
run;
%ODSON

*****
***** Traditional ANOVA Approach - Log Transformed Y *****
*****;

%ODSOFF
ods output FitStatistics=norfive.LNFitStats;
ods output ParameterEstimates=norfive.LNParmEsts;
ods output Tests3=norfive.LNFixed3;
ods output LSMeans=norfive.LNLSMns;
ods output Diffs=norfive.LNDiffsMns;

proc glimmix data=norfive.genNormal;
    by Sample;
    class Trt;
    model logY=Trt / solution;
* random _residual_;
    lsmeans Trt / diff;
    title2 'Traditional ANOVA Approach on Log Tranformed Y';
run;
%ODSON

```

```

*** This chunk may be used later if want to compare      *****;
*** parameter estimates from different approaches.      *****;
*** Back-transform lsmeans from model to data scale.    ***;
/*
data Orig_Scale_Mns;
  set LNLSMns;
  Lamda_Hat=exp(estimate);
  StdErrLamda=exp(estimate)*stderr;    *** delta rule ***;
  run;

proc print data=Orig_Scale_Mns;
  var Trt estimate stderr Lamda_Hat StdErrLamda;
  title2 'View Back-Transformed Results';
  run;
*/

*****
***** Generalized Linear Model Approach - Poisson Y *****
*****;

%ODSOFF
ods output FitStatistics=norfive.PFitStats;
ods output ParameterEstimates=norfive.PParmEsts;
ods output Tests3=norfive.PFixed3;
ods output LSMeans=norfive.PLSMns;
ods output Diffs=norfive.PDiffsMns;

proc glimmix data=norfive.genNormal;
  by Sample;
  class Trt;
  model Y=Trt / d=poisson solution ddfm=kr;
  random _residual_;
  lsmeans Trt / diff ilink;
  title2 'Generalized Linear Model Approach';
  run;
%ODSON

*****
***** Generalized Linear Model Approach - NB Y *****
*****;

%ODSOFF
ods output FitStatistics=norfive.NBFitStats;
ods output ParameterEstimates=norfive.NBParmEsts;
ods output Tests3=norfive.NBFixed3;
ods output LSMeans=norfive.NBLSMns;
ods output Diffs=norfive.NBDiffsMns;

proc glimmix data=norfive.genNormal method=rml initglm;
  by Sample;
  class Trt;
  model Y=Trt / d=NB solution ddfm=kr;
  nloptions tech=nrridg;
  random _residual_;
  lsmeans Trt / diff ilink;
  title2 'Generalized Linear Model Approach - Negative Binomial';

```

```

run;
%ODSON

%mend generate;

ods pdf file='Stroup_chk_Normal_5.pdf';

***** Generate parameters: *****
***** Samples, n1,  $\mu$ 1, s1, n2,  $\mu$ 2, s2, seed0 *****;
%*generate(10000, n1, mu1, s1, n2, mu, s2, 0); *** Type I Error Check ***;
%generate(10000, n1, mu1, s1, n2, mu, s2, 0);

/*
proc print data=NFixed3;
  title2 'Standard ANOVA - Effect Tests';
run;
proc print data=LNFixed3;
  title2 'Log-Transformed ANOVA - Effect Tests';
run;
proc print data=PFixed3;
  title2 'Poisson GLM - Effect Tests';
run;
*/

data norfive.AllFixed3;
  set norfive.NFixed3 (in=in1)
      norfive.LNFixed3 (in=in2)
      norfive.PFixed3 (in=in3)
      norfive.NBFixed3 (in=in4);
  if in1 then Approach=1;
  else if in2 then Approach=2;
  else if in3 then Approach=3;
  else if in4 then Approach=4;
run;

/*
proc print data=AllFixed3;
  title2 'All Effect Tests - Compare 3 Methods';
run;
*/

proc format;
  value sig 0-.05 = 'Reject'
           .05<-1 = 'DNR';
  value app 1='ANOVA'
           2='LogYAoV'
           3='Poisson'
           4='NegBin';
run;

*****
*****
***** Get Rejection Rates (Row 1 Table 11.1 Stroup) *****
*****
*****;

proc freq;
  tables Approach*ProbF / nopct nocol;

```

```

format Approach app. ProbF sig.;
title2 'Compare Rejection Rates Across Approaches';
run;

*****
*****
***** Get Trt Mean, SE Ests for Table 11.1 Stroup *****
***** Rows 5-10 *****
*****;
*** NORMAL ***;
data norfive.nlsmsns(rename=(Estimate=Norm_MnY StdErr=Norm_StdErr)
                    drop=Effect DF tValue Probt);
set norfive.nlsmsns;
run;

*** Log NORMAL ***;
data norfive.lnlsmsns(keep=Sample Trt BTLog_mnY BTLog_StdErr);
set norfive.lnlsmsns;
BTLog_mnY=exp(Estimate);
BTLog_StdErr=exp(Estimate)*StdErr;
run;

*** Poisson ***;
data norfive.plsmns(rename=(Mu=Pois_MnY StdErrMu=Pois_StdErr)
                   drop=Effect Estimate StdErr DF tValue Probt);
set norfive.plsmns;
run;

*** Negative Binomial ***;
data norfive.nblsmns(rename=(Mu=NegB_MnY StdErrMu=NegB_StdErr)
                    drop=Effect Estimate StdErr DF tValue Probt);
set norfive.nblsmns;
run;

data norfive.all_mns;
merge norfive.nlsmsns norfive.lnlsmsns norfive.plsmns norfive.nblsmns;
by sample trt;
run;
proc print data=norfive.all_mns(obs=100);
title2 'Check Mean Estimates for some Samples';
run;

proc sort data=norfive.all_mns;
by trt;
run;

*****
***** Get averages of estimated means by trt *****
*****;
proc means data=norfive.all_mns(drop=Sample) noprint;
by trt;
output out=norfive.all_lamb_mns(drop=_type_)
       mean=MnNorm_MnY MnBTLog_mnY MnPois_MnY MnNegB_MnY;
var Norm_MnY BTLog_mnY Pois_MnY NegB_MnY;
run;

```

```

proc print data=norfive.all_lamb_mns;
  run;

*****
***** Get averages of estimated SEs by trt *****
*****;
proc means data=norfive.all_mns(drop=Sample) noprint;
  by trt;
  output out=norfive.all_lamb_SEs(drop=_type_)
    mean=MnNorm_StdErr MnBTLog_StdErr MnPois_StdErr MnNegB_StdErr;
  var Norm_StdErr BTLog_StdErr Pois_StdErr NegB_StdErr;
  run;
proc print data=norfive.all_lamb_SEs;
  run;

*****
***** Get SEs of Observed Sampling Distribution by trt ***
*****;
proc means data=norfive.all_mns(drop=Sample) noprint;
  by trt;
  output out=norfive.all_lamb_SD (drop=_type_)
    std=SDNorm_MnY SDBTLog_mnY SDPois_MnY SDNegB_MnY;
  var Norm_MnY BTLog_mnY Pois_MnY NegB_MnY;
  run;
proc print data=norfive.all_lamb_SD;
  run;

*****
*****
***** Get Mean Diffs Ests for Table 11.1 Stroup *****
***** Rows 2-4 *****
*****
*****;
*** NORMAL ***;

data norfive.NDiffsMns (rename=(Estimate=NDiff_MnY StdErr=NDiff_StdErr)
  drop=Effect Trt _trt DF tValue Probt);
  set norfive.NDiffsMns;
  run;

data norfive.LNDiffsMns (rename=(Estimate=LNDiff_MnY StdErr=LNDiff_StdErr)
  drop=Effect Trt _trt DF tValue Probt);
  set norfive.LNDiffsMns;
  run;

data norfive.PDiffsMns (rename=(Estimate=PDiff_MnY StdErr=PDiff_StdErr)
  drop=Effect Trt _trt DF tValue Probt);
  set norfive.PDiffsMns;
  run;

data norfive.NBDiffsMns (rename=(Estimate=NBDiff_MnY StdErr=NBDiff_StdErr)
  drop=Effect Trt _trt DF tValue Probt);

```



```

set norfive.NBDiffsMns;
run;

data norfive.all_Diffmns;
merge norfive.NDiffsMns norfive.LNDiffsMns norfive.PDiffsMns
norfive.NBDiffsMns;
by sample;
run;
*****
***** Get averages of estimated meandiff all samples *****
*****;
proc means data=norfive.all_Diffmns(drop=Sample) noprint;
output out=norfive.all_diff_mns(drop=_type_)
mean=MnNDiff_MnY MnLnDiff_mnY MnPDiff_MnY MnNBDiff_MnY;
var NDiff_MnY LNDiff_MnY PDiff_MnY NBDiff_MnY;
run;
proc print data=norfive.all_diff_mns;
run;

*****
***** Get averages of estimated SEs by trt *****
*****;
proc means data=norfive.all_Diffmns(drop=Sample) noprint;
output out=norfive.all_diff_SEs(drop=_type_)
mean=MnNDiff_StdErr MnLnDiff_StdErr MnPDiff_StdErr
MnNBDiff_StdErr;
var NDiff_StdErr LNDiff_StdErr PDiff_StdErr NBDiff_StdErr;
run;
proc print data=norfive.all_diff_SEs;
run;

*****
***** Get SDs of Observed Sampling Distribution by trt ***
*****;
proc means data=norfive.all_Diffmns(drop=Sample) noprint;
output out=norfive.all_diff_SD(drop=_type_)
std=SDNDiff_MnY SDLNDiff_mnY SDPDiff_MnY SDNBDiff_MnY;
var NDiff_MnY LNDiff_MnY PDiff_MnY NBDiff_MnY;
run;
proc print data=norfive.all_diff_SD;
run;
ods pdf close;

```

Poisson Distribution

```
options mprint symbolgen formchar="|----|+|---+=|-\<>*";

title1 'Poisson Count Data Comparative Analyses - Traditional vs GLMM
Approach';

*****
*** The generate macro accepts 6 parameters as follows:          ***
***   Samples = # of sample runs to generate                    ***
***   N1 = sample size for treatment 1 population                ***
***   Lambda1 = Poisson parameter for treatment 1 population    ***
***   N2 = sample size for treatment 2 population                ***
***   Lambda2 = Poisson parameter for treatment 2 population    ***
***   seed0 = starting seed for simulation                       ***
*** The RAND function generates a random value from the specified ***
*** distribution (here Poisson with parameter Lambda).          ***
*****;
*** Wicklin ODS control macros ***;

%macro ODSoff(); *** Call prior to BY-group processing ***;
ods graphics off;
ods exclude all;
ods noresults;
%mend;

%macro ODSon(); *** Call after BY-group processing ***;
ods graphics on;
ods exclude none;
ods results;
%mend;

libname poisfive 'C:\Users\Ibrahim.Soumare\Desktop\MS_Full_code\Poisson\n=5';

%macro generate(Samples, N1, Lambda1, N2, Lambda2, seed0);

data poisfive.genPoi (keep=Sample Iter n1 n2 Trt Y logY);

    call streaminit(&seed0);  *** Initialize with desired seed. ***;

    n1=&N1;
    n2=&N2;
    do Sample=1 to &Samples;
        do Iter=1 to &N1;
            Trt=1;
            Y=rand('Poisson', &Lambda1);
            if Y=0 then logY=log(Y+0.1);
            else logY=log(Y);
            output;
        end;
        do Iter=&N1+1 to &N1+&N2;
            Trt=2;
            Y=rand('Poisson', &Lambda2);
            if Y=0 then logY=log(Y+0.1);
            else logY=log(Y);
            output;
        end;
    end;
endmacro;
```

```

        end;
    end;
run;

proc print data=poisfive.genPoi(obs=100);
    title2 'Check Small Subset of Simulated Values';
run;

proc sort;
    by Sample Trt;
run;

*** Run UNIVARIATE to check dist initially. ***;
*** If OK, then comment off. ***;
/*
proc univariate plot normal;
    Class Trt;
    var Y;
    histogram Y;
    title2 'Check Distribution of Simulated Data';
    title3 'All Samples Combined';
run;
*/

*****
***** Traditional ANOVA Approach - Untransformed Y *****
*****;

%ODSoff
ods output FitStatistics=poisfive.NFitStats;
ods output ParameterEstimates=poisfive.NParmEsts;
ods output Tests3=poisfive.NFixed3;
ods output LSMeans=poisfive.NLSMns;
ods output Diffs=poisfive.NDiffsMns;

proc glimmix data=poisfive.genPoi;
    by Sample;
    class Trt;
    model Y=Trt / solution;
* random _residual_;
    lsmeans Trt / diff;
    title2 'Traditional ANOVA Approach';
run;
%ODSON

*****
***** Traditional ANOVA Approach - Log Transformed Y *****
*****;

%ODSoff
ods output FitStatistics=poisfive.LNFitStats;
ods output ParameterEstimates=poisfive.LNParmEsts;
ods output Tests3=poisfive.LNFixed3;
ods output LSMeans=poisfive.LNLSMns;
ods output Diffs=poisfive.LNDiffsMns;

proc glimmix data=poisfive.genPoi;

```

```

by Sample;
class Trt;
model logY=Trt / solution;
* random _residual_;
lsmeans Trt / diff;
title2 'Traditional ANOVA Approach on Log Tranformed Y';
run;
%ODSON

*** This chunk may be used later if want to compare *****;
*** parameter estimates from different approaches. *****;
*** Back-transform lsmeans from model to data scale. ****;
/*
data Orig_Scale_Mns;
set LNLSMns;
Lamda_Hat=exp(estimate);
StdErrLamda=exp(estimate)*stderr;    *** delta rule ***;
run;

proc print data=Orig_Scale_Mns;
var Trt estimate stderr Lamda_Hat StdErrLamda;
title2 'View Back-Transformed Results';
run;
*/

*****
***** Generalized Linear Model Approach - Poisson Y *****
*****;

%ODSOFF
ods output FitStatistics=poisfive.PFitStats;
ods output ParameterEstimates=poisfive.PParmEsts;
ods output Tests3=poisfive.PFixed3;
ods output LSMeans=poisfive.PLSMns;
ods output Diffs=poisfive.PDiffsMns;

proc glimmix data=poisfive.genPoi;
by Sample;
class Trt;
model Y=Trt / d=poisson solution ddfm=kr;
random _residual_;
lsmeans Trt / diff ilink;
title2 'Generalized Linear Model Approach';
run;
%ODSON

*****
***** Generalized Linear Model Approach - NB Y *****
*****;

%ODSOFF
ods output FitStatistics=poisfive.NBFitStats;
ods output ParameterEstimates=poisfive.NBParmEsts;
ods output Tests3=poisfive.NBFixed3;
ods output LSMeans=poisfive.NBLSMns;
ods output Diffs=poisfive.NBDiffsMns;

```

```

proc glimmix data=poisfive.genPoi method=rml initglm;
  by Sample;
  class Trt;
  model Y=Trt / d=NB solution ddfm=kr;
  nloptions tech=nrridg;
  random _residual_;
  lsmeans Trt / diff ilink;
  title2 'Generalized Linear Model Approach - Negative Binomial';
run;
%ODSON

%mend generate;

ods pdf file='Stroup_chk_5.pdf';
***** Generate parameters: *****
***** Samples, N1, Lambda1, N2, Lambda2, seed0 *****;
%*generate(10000, N1, Lambda1, N2, Lambda2, 0); *** Type I Error Check ***;
%generate(10000, N1, Lambda1, N2, Lambda2, 0);

/*
proc print data=NFixed3;
  title2 'Standard ANOVA - Effect Tests';
run;
proc print data=LNFixed3;
  title2 'Log-Transformed ANOVA - Effect Tests';
run;
proc print data=PFixed3;
  title2 'Poisson GLM - Effect Tests';
run;
*/

data poisfive.AllFixed3;
  set poisfive.NFixed3 (in=in1)
      poisfive.LNFixed3 (in=in2)
      poisfive.PFixed3 (in=in3)
      poisfive.NBFixed3 (in=in4);
  if in1 then Approach=1;
  else if in2 then Approach=2;
  else if in3 then Approach=3;
  else if in4 then Approach=4;
run;

/*
proc print data=AllFixed3;
  title2 'All Effect Tests - Compare 3 Methods';
run;
*/

proc format;
  value sig 0-.05 = 'Reject'
           .05<-1 = 'DNR';
  value app 1='ANOVA'
           2='LogYAOV'
           3='Poisson'
           4='NegBin';
run;

```

```

*****
*****
***** Get Rejection Rates (Row 1 Table 11.1 Stroup) *****
*****
*****;
proc freq;
  tables Approach*ProbF / nopct nocol;
  format Approach app. ProbF sig.;
  title2 'Compare Rejection Rates Across Approaches';
run;

*****
*****
***** Get Trt Mean, SE Ests for Table 11.1 Stroup *****
*****
***** Rows 5-10 *****
*****
*****;
*** NORMAL ***;
data poisfive.nlsmns(rename=(Estimate=Norm_MnY StdErr=Norm_StdErr)
  drop=Effect DF tValue Probt);
  set poisfive.nlsmns;
run;

*** Log NORMAL ***;
data poisfive.lnlsmns(keep=Sample Trt BTLog_mnY BTLog_StdErr);
  set poisfive.nlsmns;
  BTLog_mnY=exp(Estimate);
  BTLog_StdErr=exp(Estimate)*StdErr;
run;

*** Poisson ***;
data poisfive.plsmns(rename=(Mu=Pois_MnY StdErrMu=Pois_StdErr)
  drop=Effect Estimate StdErr DF tValue Probt);
  set poisfive.nlsmns;
run;

*** Negative Binomial ***;
data poisfive.nblsmns(rename=(Mu=NegB_MnY StdErrMu=NegB_StdErr)
  drop=Effect Estimate StdErr DF tValue Probt);
  set poisfive.nlsmns;
run;

data poisfive.all_mns;
  merge poisfive.nlsmns poisfive.lnlsmns poisfive.plsmns poisfive.nblsmns;
  by sample trt;
run;
proc print data=poisfive.all_mns(obs=100);
  title2 'Check Mean Estimates for some Samples';
run;

proc sort data=poisfive.all_mns;
  by trt;
run;

*****
***** Get averages of estimated means by trt *****

```

```

*****;
proc means data=poisfive.all_mns(drop=Sample) noprint;
  by trt;
  output out=poisfive.all_lamb_mns(drop=_type_)
    mean=MnNorm_MnY MnBTLog_mnY MnPois_MnY MnNegB_MnY;
  var Norm_MnY BTLog_mnY Pois_MnY NegB_MnY;
run;
proc print data=poisfive.all_lamb_mns;
run;

*****
***** Get averages of estimated SEs by trt *****
*****;
proc means data=poisfive.all_mns(drop=Sample) noprint;
  by trt;
  output out=poisfive.all_lamb_SEs(drop=_type_)
    mean=MnNorm_StdErr MnBTLog_StdErr MnPois_StdErr MnNegB_StdErr;
  var Norm_StdErr BTLog_StdErr Pois_StdErr NegB_StdErr;
run;
proc print data=poisfive.all_lamb_SEs;
run;

*****
***** Get SEs of Observed Sampling Distribution by trt ***
*****;
proc means data=poisfive.all_mns(drop=Sample) noprint;
  by trt;
  output out=poisfive.all_lamb_SD(drop=_type_)
    std=SDNorm_MnY SDBTLog_mnY SDPois_MnY SDNegB_MnY;
  var Norm_MnY BTLog_mnY Pois_MnY NegB_MnY;
run;
proc print data=poisfive.all_lamb_SD;
run;

*****
***** Get Mean Diffs Ests for Table 11.1 Stroup *****
***** Rows 2-4 *****
*****;
*** NORMAL ***;

data poisfive.NDiffsMns (rename=(Estimate=NDiff_MnY StdErr=NDiff_StdErr)
  drop=Effect Trt _trt DF tValue Probt);
set poisfive.NDiffsMns;
run;

data poisfive.LNDiffsMns (rename=(Estimate=LNDiff_MnY StdErr=LNDiff_StdErr)
  drop=Effect Trt _trt DF tValue Probt);
set poisfive.LNDiffsMns;
run;

data poisfive.PDiffsMns (rename=(Estimate=PDiff_MnY StdErr=PDiff_StdErr)

```

```

                drop=Effect Trt _trt DF tValue Probt);
set poisfive.PDiffsMns;
run;

data poisfive.NBDiffsMns (rename=(Estimate=NBDiff_MnY StdErr=NBDiff_StdErr)
                drop=Effect Trt _trt DF tValue Probt);
set poisfive.NBDiffsMns;
run;

data poisfive.all_Diffmns;
merge poisfive.NDiffsMns poisfive.LNDiffsMns poisfive.PDiffsMns
poisfive.NBDiffsMns;
by sample;
run;
*****
***** Get averages of estimated meandiff all samples *****
*****;
proc means data=poisfive.all_Diffmns(drop=Sample) noprint;
output out=poisfive.all_diff_mns(drop=_type_)
        mean=MnNDiff_MnY MnLnDiff_mnY MnPDiff_MnY MnNBDiff_MnY;
var NDiff_MnY LNDiff_MnY PDiff_MnY NBDiff_MnY;
run;
proc print data=poisfive.all_diff_mns;
run;

*****
***** Get averages of estimated SEs by trt *****
*****;
proc means data=poisfive.all_Diffmns(drop=Sample) noprint;
output out=poisfive.all_diff_SEs(drop=_type_)
        mean=MnNDiff_StdErr MnLnDiff_StdErr MnPDiff_StdErr
MnNBDiff_StdErr;
var NDiff_StdErr LNDiff_StdErr PDiff_StdErr NBDiff_StdErr;
run;
proc print data=poisfive.all_diff_SEs;
run;

*****
***** Get SDs of Observed Sampling Distribution by trt ***
*****;
proc means data=poisfive.all_Diffmns(drop=Sample) noprint;
output out=poisfive.all_diff_SD (drop=_type_)
        std=SDNDiff_MnY SDLNDiff_mnY SDPDiff_MnY SDNBDiff_MnY;
var NDiff_MnY LNDiff_MnY PDiff_MnY NBDiff_MnY;
run;
proc print data=poisfive.all_diff_SD;
run;
ods pdf close;

```


Negative Binomial Distribution

```
options mprint symbolgen formchar="|----+|----+|-\<>*";

title1 'Poisson Count Data Comparative Analyses - Traditional vs GLMM
Approach';

*****
*** The generate macro accepts 8 parameters as follows:      ***
*** Samples = # of sample runs to generate                  ***
*** N1 = sample size for treatment 1 population              ***
*** p1 = NB proportion parameter for treatment 1 population ***
*** k1 = NB parameter for treatment 1 population            ***
*** N2 = sample size for treatment 2 population              ***
*** p2 = NB proportion parameter for treatment 2 population ***
*** k1 = NB parameter for treatment 2 population            ***
*** seed0 = starting seed for simulation                     ***
*** The RAND function generates a random value from the specified ***
*** distribution (here Poisson with parameter Lambda).       ***
*****;
*** Wicklin ODS control macros ***;

%macro ODSoff(); *** Call prior to BY-group processing ***;
ods graphics off;
ods exclude all;
ods noresults;
%mend;

%macro ODSon(); *** Call after BY-group processing ***;
ods graphics on;
ods exclude none;
ods results;
%mend;

libname NBfive 'C:\Users\Ibrahim.Soumare\Desktop\MS_Full_code\NB\n=5';

%macro generate(Samples, n1, p1, k1, n2, p2, k2, seed0);

data NBfive.genNB (keep=Sample Iter n1 p1 k1 n2 p2 k2 Trt Y logY);
  call streaminit(498455); *** Initialize with desired seed. ***;

  n1=&n1; p1=&p1; k1=&k1;
  n2=&n2; p2=&p2; k2=&k2;
  do Sample=1 to &Samples;
    do Iter=1 to &n1;
      Trt=1;
      Y=rand('NEGBinomial',&p1, &k1);
      if Y=0 then logY=log(Y+0.1);
      else logY=log(Y);
      output;
    end;
    do Iter=&n1+1 to &n1+&n2;
      Trt=2;
      Y=rand('NEGBinomial',&p2, &k2);
      if Y=0 then logY=log(Y+0.1);
      else logY=log(Y);
    end;
  end;
end;
```

```

        output;
    end;
end;
run;

proc print data=NBfive.genNB(obs=100);
    title2 'Check Small Subset of Simulated Values';
run;

proc sort;
    by Sample Trt;
run;

*** Run UNIVARIATE to check dist initially. ***;
*** If OK, then comment off. ***;
/*
proc univariate plot normal;
    Class Trt;
    var Y;
    histogram Y;
    title2 'Check Distribution of Simulated Data';
    title3 'All Samples Combined';
run;
*/

*****
***** Traditional ANOVA Approach - Untransformed Y *****
*****;

%ODSOFF
ods output FitStatistics=NBfive.NFitStats;
ods output ParameterEstimates=NBfive.NParmEsts;
ods output Tests3=NBfive.NFixed3;
ods output LSMeans=NBfive.NLSMns;
ods output Diffs=NBfive.NDiffsMns;

proc glimmix data=NBfive.genNB;
    by Sample;
    class Trt;
    model Y=Trt / solution;
* random _residual_;
    lsmeans Trt / diff;
    title2 'Traditional ANOVA Approach';
run;
%ODSON

*****
***** Traditional ANOVA Approach - Log Transformed Y *****
*****;

%ODSOFF
ods output FitStatistics=NBfive.LNFitStats;
ods output ParameterEstimates=NBfive.LNParmEsts;
ods output Tests3=NBfive.LNFixed3;
ods output LSMeans=NBfive.LNLSMns;
ods output Diffs=NBfive.LNDiffsMns;

```

```

proc glimmix data=NBfive.genNB;
  by Sample;
  class Trt;
  model logY=Trt / solution;
* random _residual_;
  lsmeans Trt / diff;
  title2 'Traditional ANOVA Approach on Log Tranformed Y';
run;
%ODSON

*** This chunk may be used later if want to compare      *****;
*** parameter estimates from different approaches.      *****;
*** Back-transform lsmeans from model to data scale.    ****;
/*
data Orig_Scale_Mns;
  set LNLSMns;
  Lamda_Hat=exp(estimate);
  StdErrLamda=exp(estimate)*stderr;      *** delta rule ***;
run;

proc print data=Orig_Scale_Mns;
  var Trt estimate stderr Lamda_Hat StdErrLamda;
  title2 'View Back-Transformed Results';
run;
*/

*****
***** Generalized Linear Model Approach - Poisson Y *****
*****;

%ODSOFF
ods output FitStatistics=NBfive.PFitStats;
ods output ParameterEstimates=NBfive.PParmEsts;
ods output Tests3=NBfive.PFixed3;
ods output LSMeans=NBfive.PLSMns;
ods output Diffs=NBfive.PDiffsMns;

proc glimmix data=NBfive.genNB;
  by Sample;
  class Trt;
  model Y=Trt / d=poisson solution ddfm=kr;
  random _residual_;
  lsmeans Trt / diff ilink;
  title2 'Generalized Linear Model Approach';
run;
%ODSON

*****
***** Generalized Linear Model Approach - NB Y *****
*****;

%ODSOFF
ods output FitStatistics=NBfive.NBFitStats;
ods output ParameterEstimates=NBfive.NBParmEsts;
ods output Tests3=NBfive.NBFixed3;
ods output LSMeans=NBfive.NBLSMns;
ods output Diffs=NBfive.NBDiffsMns;

```

```

proc glimmix data=NBfive.genNB method=rml initglm;
  by Sample;
  class Trt;
  model Y=Trt / d=NB solution ddfm=kr;
  nloptions tech=nrridg;
  random _residual_;
  lsmeans Trt / diff ilink;
  title2 'Generalized Linear Model Approach - Negative Binomial';
run;
%ODSON

%mend generate;

ods pdf file='Stroup_chk_NB_5.pdf';
***** Generate parameters: *****
***** Samples, n1, p1, k1, n2, p2, k2, seed0 *****;
%*generate(10000, 5, 2/3, 10, 5, 2/3, 10, 0); *** Type I Error Check ***;
%generate(10000, 5, 2/3, 10, 5, 2/3, 10, 0);

/* Simulated NB distribution mean=20 var=25*/

/*
proc print data=NFixed3;
  title2 'Standard ANOVA - Effect Tests';
run;
proc print data=LNFixed3;
  title2 'Log-Transformed ANOVA - Effect Tests';
run;
proc print data=PFixed3;
  title2 'Poisson GLM - Effect Tests';
run;
*/

data NBfive.AllFixed3;
  set NBfive.NFixed3 (in=in1)
      NBfive.LNFixed3 (in=in2)
      NBfive.PFixed3 (in=in3)
      NBfive.NBFixed3 (in=in4);
  if in1 then Approach=1;
  else if in2 then Approach=2;
  else if in3 then Approach=3;
  else if in4 then Approach=4;
run;

/*
proc print data=AllFixed3;
  title2 'All Effect Tests - Compare 3 Methods';
run;
*/

proc format;
  value sig 0-.05 = 'Reject'
           .05<-1 = 'DNR';
  value app 1='ANOVA'
           2='LogYAoV'
           3='Poisson'
           4='NegBin';

```

```

run;

*****
*****
***** Get Rejection Rates (Row 1 Table 11.1 Stroup) *****
*****
*****;

proc freq;
  tables Approach*ProbF / nopct nocol;
  format Approach app. ProbF sig.;
  title2 'Compare Rejection Rates Across Approaches';
run;

*****
*****
***** Get Trt Mean, SE Ests for Table 11.1 Stroup *****
*****
***** Rows 5-10 *****
*****
*****;

*** NORMAL ***;
data NBfive.nlsmsns(rename=(Estimate=Norm_MnY StdErr=Norm_StdErr)
  drop=Effect DF tValue Probt);
  set NBfive.nlsmsns;
run;

*** Log NORMAL ***;
data NBfive.lnlsmsns(keep=Sample Trt BTLog_mnY BTLog_StdErr);
  set NBfive.lnlsmsns;
  BTLog_mnY=exp(Estimate);
  BTLog_StdErr=exp(Estimate)*StdErr;
run;

*** Poisson ***;
data NBfive.plsmns(rename=(Mu=Pois_MnY StdErrMu=Pois_StdErr)
  drop=Effect Estimate StdErr DF tValue Probt);
  set NBfive.plsmns;
run;

*** Negative Binomial ***;
data NBfive.nblsmns(rename=(Mu=NegB_MnY StdErrMu=NegB_StdErr)
  drop=Effect Estimate StdErr DF tValue Probt);
  set NBfive.nblsmns;
run;

data NBfive.all_mns;
merge NBfive.nlsmsns NBfive.lnlsmsns NBfive.plsmns NBfive.nblsmns;
by sample trt;
run;
proc print data=NBfive.all_mns(obs=100);
  title2 'Check Mean Estimates for some Samples';
run;

proc sort data=NBfive.all_mns;
  by trt;
run;

```

```

*****
***** Get averages of estimated means by trt *****
*****;
proc means data=NBfive.all_mns(drop=Sample) noprint;
  by trt;
  output out=NBfive.all_lamb_mns(drop=_type_)
    mean=MnNorm_MnY MnBTLog_mnY MnPois_MnY MnNegB_MnY;
  var Norm_MnY BTLog_mnY Pois_MnY NegB_MnY;
run;
proc print data=NBfive.all_lamb_mns;
run;

*****
***** Get averages of estimated SEs by trt *****
*****;
proc means data=NBfive.all_mns(drop=Sample) noprint;
  by trt;
  output out=NBfive.all_lamb_SEs(drop=_type_)
    mean=MnNorm_StdErr MnBTLog_StdErr MnPois_StdErr MnNegB_StdErr;
  var Norm_StdErr BTLog_StdErr Pois_StdErr NegB_StdErr;
run;
proc print data=NBfive.all_lamb_SEs;
run;

*****
***** Get SEs of Observed Sampling Distribution by trt ***
*****;
proc means data=NBfive.all_mns(drop=Sample) noprint;
  by trt;
  output out=NBfive.all_lamb_SD(drop=_type_)
    std=SDNorm_MnY SDBTLog_mnY SDPois_MnY SDNegB_MnY;
  var Norm_MnY BTLog_mnY Pois_MnY NegB_MnY;
run;
proc print data=NBfive.all_lamb_SD;
run;

*****
***** Get Mean Diffs Ests for Table 11.1 Stroup *****
*****
***** Rows 2-4 *****
*****;
*** NORMAL ***;

data NBfive.NDiffsMns (rename=(Estimate=NDiff_MnY StdErr=NDiff_StdErr)
  drop=Effect Trt _trt DF tValue Probt);
set NBfive.NDiffsMns;
run;

data NBfive.LNDiffsMns (rename=(Estimate=LNDiff_MnY StdErr=LNDiff_StdErr)
  drop=Effect Trt _trt DF tValue Probt);
set NBfive.LNDiffsMns;
run;

```

```

data NBfive.PDiffsMns (rename=(Estimate=PDiff_MnY StdErr=PDiff_StdErr)
                    drop=Effect Trt _trt DF tValue Probt);
set NBfive.PDiffsMns;
run;

data NBfive.NBDiffsMns (rename=(Estimate=NBDiff_MnY StdErr=NBDiff_StdErr)
                    drop=Effect Trt _trt DF tValue Probt);
set NBfive.NBDiffsMns;
run;

data NBfive.all_Diffmns;
merge NBfive.NDiffsMns NBfive.LNDiffsMns NBfive.PDiffsMns
NBfive.NBDiffsMns;
by sample;
run;
*****
***** Get averages of estimated meandiff all samples *****
*****;
proc means data=NBfive.all_Diffmns(drop=Sample) noprint;
output out=NBfive.all_diff_mns(drop=_type_)
mean=MnNDiff_MnY MnLnDiff_mnY MnPDiff_MnY MnNBDiff_MnY;
var NDiff_MnY LNDiff_MnY PDiff_MnY NBDiff_MnY;
run;
proc print data=NBfive.all_diff_mns;
run;

*****
***** Get averages of estimated SEs by trt *****
*****;
proc means data=NBfive.all_Diffmns(drop=Sample) noprint;
output out=NBfive.all_diff_SEs(drop=_type_)
mean=MnNDiff_StdErr MnLnDiff_StdErr MnPDiff_StdErr
MnNBDiff_StdErr;
var NDiff_StdErr LNDiff_StdErr PDiff_StdErr NBDiff_StdErr;
run;
proc print data=NBfive.all_diff_SEs;
run;

*****
***** Get SDs of Observed Sampling Distribution by trt ***
*****;
proc means data=NBfive.all_Diffmns(drop=Sample) noprint;
output out=NBfive.all_diff_SD (drop=_type_)
std=SDNDiff_MnY SDLNDiff_mnY SDPDiff_MnY SDNBDiff_MnY;
var NDiff_MnY LNDiff_MnY PDiff_MnY NBDiff_MnY;
run;
proc print data=NBfive.all_diff_SD;
run;
ods pdf close;

```