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NEGATIVE BINOMIAL MODELING OF NEMATODE COUNT DATA YIELD MORE ACCURATE MEAN AND VARIANCE ESTIMATES

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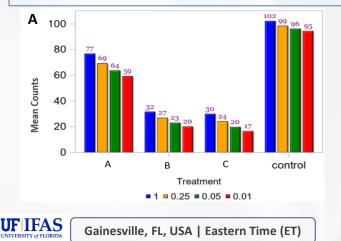
Introduction

Nematode count data are highly variable, nonnormal, discrete, and skewed. They often include valid '0' observations. Using classical statistical methods for counts can yield inaccurate mean and variance estimates.

Objective: Demonstrate that Negative binomial (NB) modeling is more suitable for analyzing nematode counts.

Methodology

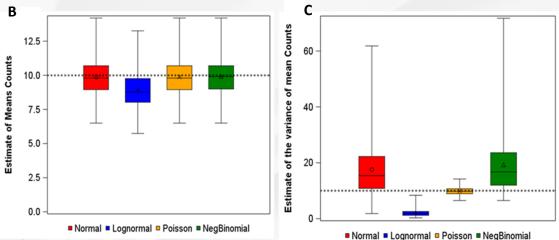
Simulations (500 times, N=10, Mean=10). Modeled using Normal, Lognormal, NB, and Poisson distributional assumptions in SAS 9.4 (PROC GLIMMIX)



Results

Fig. A: There is evidence that the added constants influence the mean counts. It is challenging to determine the best constant to use to yield an acceptable mean count.

Fig. B: Log-transformed means were underestimated compared with Negbinomial-modeled means. **Fig. C**: Negative binomial distributions explained the high natural variability seen with nematode counts.



Conclusion

- Generalized linear mixed models (GLMM) analysis of nematode counts with a NB distribution yield more accurate mean and variance estimates.
- We recommend a GLMM approach rather than force nematode count data into ANOVAconforming analysis using log transformation.
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