A case study on cumulative logit models with low frequency and mixed effects

by

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#### Abstract

Data with ordinal responses may be encountered in many research fields, such as social, medical, agriculture or financial sciences. In this paper, we present a case study on cumulative logit models with low frequency and mixed effects and discuss some strengths and limitations of the current methodology. Two plant pathologists requested our statistical advice to fit a cumulative logit mixed model seeking for the effect of six commercial products on the control of a seed and seedling disease in soybeans *in vitro*. In their attempt to estimate the model parameters using a generalized linear mixed model approach with PROC GLIMMIX, the model failed to converge. Three alternative approaches to solve the problem were examined: 1) stratifying the data searching for the random effect; 2) assuming the random effect would be small and reducing the model to a fixed model; and 3) combining the original categories of the response variable to a lower number of categories. In addition, we conducted a power analysis to evaluate the required sample size to detect treatment differences. The results of all the proposed solutions were similar. Collapsing categories for a cumulative/proportional odds model has little effect on estimation. The sample size used in the case study is enough to detect a large shift of frequencies between categories, but not for moderated changes. Moreover, we do not have enough information to estimate a random effect. Even when it is present, the results regarding the fixed factors: pathogen, evaluation day, and treatment effects are the same as the obtained by the fixed model alternatives. All six products had a significant effect in slowing the effect of the pathogen, but the effects vary between pathogen species and assessment timing or date.

# **Table of Contents**

List of Figures
List of Tables
Acknowledgements xi
Chapter 1 - Introduction
1.1 Experimental Design and Data Collection
1.2 Data Description
Chapter 2 - Generalized Linear Mixed Models Methods for Multinomial Data 11
2.1 An Overview of Multinomial Data
2.1.1 Multinomial Distribution11
2.1.2 Multinomial Models
2.1.2.1 Models Using Cumulative Logits 12
2.2 Estimation with Generalized Linear Mixed Models14
2.2.1 Laplace Approximation in PROC GLIMMIX
Chapter 3 - Data Analysis
3.1 The Statistical Model
3.2 Data Analysis and Model Fitting
3.3 Results
3.3.1 Two-way cumulative logit mixed model
3.3.1.1 The odds ratios on the first evaluation
3.3.1.2 The odds ratios on <i>P. ultimum</i>
3.3.2 Three-way cumulative logit fixed model
3.3.3 Two-way cumulative logit fixed model
3.3.3.1 The odds ratios on the first evaluation
3.3.3.2 The odds ratio on <i>P. ultimum</i>
3.3.4 Excluding Control Treatment
3.3.5 Collapsing over Categories of the Response Variable
Chapter 4 - Power Analysis
4.1 Power Calculations
4.2 Power Results

Chapter 5 - Conclusion	49
References	53
Appendix A - Power Analysis Plots	55
Appendix B - SAS Code Data Analysis	66
Appendix C - SAS Code Power Analysis	145

# List of Figures

Figure 1.1 Plan plot of the study design and treatment structure
Figure 1.2 The observed counts for each category of the disease severity of each pathogen
(column) by each day (row)
Figure 1.3 Interaction plots of empirical probabilities $(n_{ij}/N_i)$ where $n_{ij}$ is number of observed
counts in jth category of the disease severity for ith treatment group and $N_i$ is the total
number of seeds for each treatment group of each treatment show interactions between
Pathogen (color) and Day (symbol) effects per treatment
Figure 1.4 Interaction plots of empirical probabilities $(n_{ij}/N_i)$ where $n_{ij}$ is number of observed
counts in jth category of the disease severity for Control group and $N_i$ is the total number of
seeds for Control group show interactions between Pathogen (color) and Day (symbol)
effects9
Figure 4.1 Power to detect a difference between Control and Experiment 1 (defined in Table
4.1). Simulation average power is marked (dotted line). Three combinations of petri dish
and seeds per dish sample sizes (columns) were simulated a thousand times. Power was
calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows)
Figure 4.2 Power to detect a difference between Experiments 2 and 6 (defined in Table 4.1).
Simulation average power is marked (dotted line). Three combinations of petri dish and
seeds per dish sample sizes (columns) were simulated a thousand times. Power was
calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows)
Figure 4.3 Power to detect a difference between Experiments 1 and 3 (defined in Table 4.1).
Simulation average power is marked (dotted line). Three combinations of petri dish and
seeds per dish sample sizes (columns) were simulated a thousand times. Power was
calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows)
Figure A.1 Power to detect a difference between Control and Experiment 1 (defined in Table
4.1). Simulation average power is marked (dotted line). Three combinations of petri dish
and seeds per dish sample sizes (columns) were simulated a thousand times. Power was
calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows)
Figure A.2 Power to detect a difference between Control and Experiment 2 (defined in Table
4.1). Simulation average power is marked (dotted line). Three combinations of petri dish

- Figure A.17 Power to detect a difference between Experiments 3 and 5 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and

## List of Tables

Table 3.1 Petri dish random effect estimate for fitting cumulative logit model with mixed effects
separately by each Day
Table 3.2 Petri dish random effect estimate for fitting cumulative logit model with mixed effect
separately by each Pathogen
Table 3.3 ANOVA shell for the three-way cumulative logit fixed model
Table 3.4 Odds ratios for <i>P. aphanidermatum</i> at the first evaluation of the mixed model
Table 3.5 Odds ratios for <i>P. irregulare</i> on the first evaluation of the mixed model
Table 3.6 Odds ratios for <i>P. ultimum</i> on the first evaluation of the mixed model
Table 3.7 Odds ratios for the first evaluation of mixed model for <i>P. ultimum</i>
Table 3.8 Odds ratios for the second evaluation of mixed model for <i>P. ultimum</i> 27
Table 3.9 Type III test of fixed effects model with the control treatment as the reference level. 28
Table 3.10 Type III test of fixed effects model with the MnPhi 200 treatment as the reference
level
Table 3.11 Odds ratios for the first evaluation at <i>P. aphanidermatum</i> of fixed model 29
Table 3.12 Odds ratios for the first evaluation at <i>P. irregulare</i> of fixed model
Table 3.13 Odds ratios for the first evaluation at <i>P. ultimum</i> of fixed model
Table 3.14 Odds ratios for the second evaluation at <i>P. aphanidermatum</i> of fixed model
Table 3.15 Odds ratios for the second evaluation at <i>P. irregulare</i> of fixed model
Table 3.16 Odds ratios for the second evaluation at <i>P. ultimum</i> of fixed model
Table 3.17 Odds ratios for <i>P. aphanidermatum</i> on the first evaluation of fixed model
Table 3.18 Odds ratios for P. irregulare on the first evaluation of fixed model
Table 3.19 Odds ratios for P. ultimum on the first evaluation of fixed model.       35
Table 3.20 Odds ratios for the first evaluation of fixed model for <i>P. ultimum</i>
Table 3.21 Odds ratios for the second evaluation of fixed model for <i>P. ultimum</i>
Table 3.22 Odds ratios for the first evaluation at <i>P. aphanidermatum</i> of fixed model excluding
the Control treatment
Table 3.23 Odds ratios for the first evaluation at <i>P. irregulare</i> of fixed model excluding the
Control treatment

Table 3.24 Odds ratios for the first evaluation at <i>P. ultimum</i> of fixed model excluding the Control
treatment
Table 3.25 Odds ratios for the second evaluation at <i>P. aphanidermatum</i> of fixed model excluding
the Control treatment
Table 3.26 Odds ratios for the second evaluation at <i>P. irregulare</i> of fixed model excluding the
Control treatment
Table 3.27 Odds ratios for the second evaluation at <i>P. ultimum</i> of fixed model excluding the
Control treatment
Table 4.1 Theoretical probabilities for the power analysis for multinomial responses
Table 4.2 Simulation average power for comparisons between treatments of different sample
sizes and different models, "Ctrl" and "Exp" refer to control and experimental treatment,
respectively

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## **Chapter 1 - Introduction**

Categorical data analysis is a broad topic in statistics and is encountered in many research fields, such as social, medical, agricultural or financial sciences. John & Sons (2013) defined "A categorical variable has a measurement scale consisting of a set of categories." Ordinal responses are a common type of categorical data in which the variable of interest has a natural ordering. For instance, in sensory analysis, outcomes may be used to denote different levels of preference: "excellent", "very good", "good", "neutral", "poor", and "very poor" (Snell, 1964). Surveys to address issues of public health measure frequency of certain symptoms or behaviors in categorical scales: "not at all", "several days", "more than half the days", "nearly every day" (National Health and Nutrition Examination Survey, 2016).

In this report, we discuss some of the strengths and limitations of current statistical methodologies to model ordered categorical data. In particular, cumulative logit mixed models to analyze experimental data with ordinal responses and low frequencies. To demonstrate the current statistical approach, we analyzed a real dataset as a case study. Two plant pathologists one from the School of Agronomy, Buenos Aires University, Argentina; and the other at Northwest Missouri State University conducted an experiment to evaluate the effect of three agrochemicals in the development of *Pythium* damping off: a seed and seedling disease of soybean caused primarily by several species of the oomycete pathogen *Pythium* spp.. Damping-off is characterized as the weakening or killing of seeds and seedlings (Kirkpatrick, et al. 2006). Thus, the response variable in the experiment was an ordinal rating with six categories, where 0 = "healthy seed (germinated)", 1 = "geminated with a small necrosis" and so on, up to 5 = "dead seed (non-germinated)" (Jiang, et al. 2012).

The researchers attempted to fit a cumulative logit mixed model using GLIMMIX procedure of SAS® to determine the effect of six treatments (three products at two application rates) in protecting soybean seeds from infection by three *Pythium* species: *P. aphanideramatum*, *P. irregulare*, and *P. ultimum*. Disease rating assessments were carried out at 5 and 21 days after inoculation. In their attempts to fit the cumulative logit model using PROC GLIMMIX, the model failed to converge so they requested our statistical expertise to help. This report describes the process that led us to the answer to their question by fitting a cumulative logit mixed model and discussing the strengths and limitations of such modeling strategy to analyze ordinal categorical data. Although SAS® GLIMMIX procedure enables estimation of model parameters for multinomial data, it may encounter several issues, especially those related to sample size and particularities of the observed data. In the present study, strong assumptions and compromises were made to obtain a response to the question of what product works best on controlling *Pythium* damping off.

The rest of this chapter presents the details of the experimental design and the data collection methodology. Chapter 2 introduces the statistical theory behind the modeling approaches and the methods used for estimation. On chapter 3, we present and discuss the results of the analysis. On chapter 4, we justify some of the compromises and assumptions needed to obtain answers by way of power calculations and a simulation experiment. Finally, the conclusion of this study is presented in chapter 5.

#### **1.1 Experimental Design and Data Collection**

Data provided by Drs. Carmona and Perez-Hernandez were used in this study. Details of the experiments are mentioned elsewhere (Carmona et. al., 2017). Briefly, seeds of the soybean cultivar NIDERA A5009RG, which is glyphosate-tolerant and susceptible to *Pythium* spp., were

2

surface-sterilized and treated with either a product or a control. Two hundred grams of seeds for each treatment were used in the experiment and they were sterilized with 1% sodium hypochlorite for 1 minute before receiving the treatment, and then rinsed in sterile water twice. Three species among a collection of *Pythium* isolates, i.e. specimens, that were previously recovered from soybean soils in different surveys in the province of Buenos Aires, Argentina were randomly selected such that one isolate of each *Pythium* species: *P. aphanidermatum*, *P. irregulare, and P. ultimum* were grown on potato dextrose agar (PDA; Merck). Before using these isolates, they were kept at 20°C for seven days in darkness. There were six different combinations of products such that the experiment had seven treatments levels including the control (seeds treated with water only).

Two commercial phosphite-based products, traded as foliar fertilizers were provided by Spraytec Fertilizers, LDTA; and the other, the fungicide Maxim widely used as a protectant soybean seed treatment for *Pythium*, was provided by Syngenta. Phosphite-based products were applied at the standard commercial rate and double this rate, whereas the fungicide rate was what the manufacturer recommended. The seven treatments from hereafter are MnPhi 200, MnPhi 400, Kphi 200, Kphi 400, MnPhi 200 + Maxim and Maxim 100. In a 500 ml Erlenmeyer flask plus 2% of sterile water, a slurry of each treatment was assigned to 200 g of seeds and similarly, untreated seeds were treated with disinfected distilled water. A 25 ml of PDA (one 6-mm diameter mycelial disc) was taken from 7-days stored cultures of the *Pythium* species to the center of 9-cm plastic petri dish. Next, from each treatment including the control treatment, five seeds were randomly assigned and placed at about 4-cm from the mycelial disc in a petri dish. All petri dishes were arranged on a bench in darkness at 24°C+/-0.2°C. There were ten petri dishes per treatment and pathogen combination. Five days later, each seed was evaluated to

3

determine the seeds' germination and necrosis in the radicle. The severity of the disease was rated at six levels: 0 = "Healthy seed, germinated", 1 = "Germinated but with tip of radicle showing necrosis", 2 = "Germinated seed with tip of radicle showing necrosis to a greater extent", 3 = "Germinated seed with advanced necrosis and with less overall growth", 4 = "Germinated seed, but radicle completely dead", and 5 = "Dead seed". This severity scale is a modified version of the one proposed by Jiang et al. (2012). After that, the severity of the disease on each seed was reevaluated on day twenty-first (Carmona et al, 2017).

We have mentioned that the researchers were interested in determining the effectiveness of the formulations to control the disease *in vitro*. According to their experiment description, the response variable (disease severity) was measured on an ordered scale with six categories. The treatments were applied to groups of seeds, but the pathogen inoculation was done at petri dish level, so the smallest experimental units were the petri dishes. We considered them as random effects because they represent a sample of the population of all petri dishes. In contrast, the disease was rated for each seed so they are the observational units. The researchers were interested in *Pythium* in general, but also in whether the effect may vary between isolates. In particular, differences between the three selected species of *Pythium* (*P. aphanidermatum*, *P. irregulare, and P. ultimum*), thus we consider the pathogen species as a fixed effect. Finally, disease severity on seeds was evaluated at five and twenty-one days after inoculation. We considered these as repeated measures and conceptualized the study design with the plan plot in figure 1.1.



Figure 1.1 Plan plot of the study design and treatment structure.

### **1.2 Data Description**

According to the experiment described in the previous section, we have a three-way

factorial treatment structure with repeated measurement on days five and twenty-one. The three-

fixed effect factors are the seven treatments, the two evaluations and the three Pythium species.

The random effect is the ten petri dishes per treatment pathogen combination that should be treated as the experimental units. In figure 1.2, we display the frequency distribution of the disease severity by *Pythium* species at each evaluation timing.



# Figure 1.2 The observed counts for each category of the disease severity of each pathogen (column) by each day (row).

As shown in figure 1.2, germinated seeds (severity 0) had the lowest frequency in all *Pythium* species except for the first evaluation of *P. aphanidermatum*. It is also shown that the first and second levels of disease severity had zero counts in the second evaluation of *P. irregulare* and *P. ultimum*. It appears that there tends to be less germination in these groups.

Overall, we notice that at the second evaluation, all seeds tend to be in worst shape, i.e., higher categories are observed, for all *Pythium* species and the third pathogen *P. aphanidermatum* seems to be less resistant to the products than the other two. Seeds infected with it have a higher frequency of germination in both evaluations. Furthermore, we notice that for all species and both evaluations, some categories of disease severity have very small counts. In the following plots (figures 1.3 and 1.4), we present the interaction between the three species and the two evaluations in each treatment for the observed counts.



Figure 1.3 Interaction plots of empirical probabilities  $(n_{ij}/N_i)$  where  $n_{ij}$  is number of observed counts in jth category of the disease severity for ith treatment group and  $N_i$  is the total number of seeds for each treatment group of each treatment show interactions between Pathogen (color) and Day (symbol) effects per treatment.



Figure 1.4 Interaction plots of empirical probabilities  $(n_{ij}/N_i)$  where  $n_{ij}$  is number of observed counts in jth category of the disease severity for Control group and  $N_i$  is the total number of seeds for Control group show interactions between Pathogen (color) and Day (symbol) effects.

From observing figure 1.3, it is evident that across treatments, the distribution of the frequencies by disease severity is not constant for each pathogen species; and the change from day 5 to day 21 also depends on the infecting species. In conclusion, the treatment effect varies depending on the *Pythium* isolate and when the evaluation was made. For example, for treatment MnPhi 200, the empirical probabilities of the severity levels for *P. irregulare* pathogen are not the same for the two different evaluations. Also, we can see that the effect of *P. irregulare* at Day 5 for category 1 is different across treatments and similar conclusions can be made for the rest of treatments and species. Moreover, in figure 1.4 for the Control treatment (untreated seeds), clearly dead seeds have the highest empirical probability for all three *Pythium* species in the two evaluations. Seeds with *P. irregulare* pathogen seem to have some natural resistance.

Thus, we believe that there might be a significant interaction between pathogen, treatment and day effects on the probabilities of each disease severity level.

From the experimental structure, it is evident that a multinomial generalized mixed model is necessary here. Moreover, the preliminary data exploration indicates that interaction effects need to be considered to account for the differential effects shown in figures 1.3 and 1.4.

# Chapter 2 - Generalized Linear Mixed Models Methods for Multinomial Data

#### 2.1 An Overview of Multinomial Data

According to John & Sons (2013), a categorical variable measures a phenomenon as a result of a set of categories, or possible outcomes. Moreover, categorical variables that have a natural ordering, such as disease rating ("asymptomatic", "mild symptoms", "moderate symptoms", "severe symptoms") or opinion rating ("strongly agree", "agree", "neither agree nor disagree", "disagree", "strongly disagree"), are called ordinal variables. In contrast, variables with unordered scales, such as eye color, or animal species, are called nominal. Here we focus our discussion on models for ordinal response variable. Categorical variables with two possible outcomes, also known as binary outcomes, are called binomial data in statistical terminology because they are assumed to follow a binomial distribution. Moreover, categorical variables with more than two possible outcomes are called multinomial data for a similar reason.

#### **2.1.1 Multinomial Distribution**

Formally, multinomial variables are defined as data resulting from N independent trials; each trial has more than two possible outcomes. Let *J* denote the number of possible outcomes, or response categories on these trials and define  $\mathbf{Y} = (y_1, y_2, \dots, y_J)$ , where  $y_j =$  number of trials with outcome "*j*". Thus, **Y** is the observed counts in *J* different categories after *N* trials or the observed counts of *J* different values for some categorical variable. If the probability of observing each of the categories stays constant for the *N* trials, then **Y** is said to follow a multinomial distribution. Define the probabilities of the observed outcome from each category to be as { $\pi_1, \pi_2, \dots, \pi_J$ }, where  $\sum_{j=1}^J \pi_j = 1$ . Then, the multinomial probability mass function is:

$$f(n_1, n_2, \dots n_J) = \frac{N!}{n_1! n_{2!} \dots n_{J!}} \pi_1^{n_1} \pi_2^{n_2} \cdots \pi_J^{n_J},$$
(2.1)

which refers to the probability that exactly  $n_1$  observations fall in category 1,  $n_2$  observations fall in category 2, ..., and  $n_j$  observations fall in category *J*, where  $\sum_{j=1}^{J} n_j = N$ . Any count  $n_j$  in any category *j* has a marginal distribution binomial with mean  $n\pi_j$  and variance  $n\pi_j$  (1- $\pi_j$ ), i.e., a probability of success  $\pi_i$  (Agresti, 2013).

#### **2.1.2 Multinomial Models**

For binary data, logistic regression is the most popular model and a generalization of this can be extended to multinomial data modeling. For ordinal multinomial data, the preferred model is the cumulative logit models also known as proportional odds models. Prior to generalized linear mixed models, ordinal categorical variables were often coded as numeric values and analyzed as an approximate normal data with normal distribution regardless of the normality assumption. This leads to two problems, what the right numeric code should be and what the interpretation of the average rating means. For example, if the numeric code of an ordinal response is 0, 1, ..., 5, what does an average rating 2.5 mean? We may propose many different ways to answer these questions; some of these answers could lead to very different conclusions about the relationship between predictors and our ordinal response. The models considered focus on  $\pi_j$ , the probabilities associated with each category rather than a possibly ambiguous numerical code (Stroup, 2013).

#### 2.1.2.1 Models Using Cumulative Logits

Proportional odds models are commonly used to model ordinal multinomial response with a linear predictor using a logit link function. The cumulative logit functions for generalized linear mixed models are as follows:

12

$$\begin{aligned} \eta_{1} = \log\left(\frac{\pi_{1}}{1-\pi_{1}}\right) &= \alpha_{1} + X\beta + Zb \\ \eta_{2} = \log\left(\frac{\pi_{1}+\pi_{2}}{1-(\pi_{1}+\pi_{2})}\right) &= \alpha_{2} + X\beta + Zb \end{aligned}$$

$$(2.2)$$

$$\vdots \\ \eta_{J-1} = \log\left(\frac{\pi_{1}+\pi_{2}+\dots+\pi_{J-1}}{1-(\pi_{1}+\pi_{2}+\dots+\pi_{J-1})}\right) = \alpha_{J-1} + X\beta + Zb, \end{aligned}$$

where j = 1, 2, ..., J, being the number of the response categories,  $\alpha_j$  is the intercept of the jth category,  $X\beta$  represents the linear predictor for the fixed effects and/or covariates/predictors coefficients; and Zb denotes the random part of the linear model with the vector b consisting of the random effects. Therefore, *J*-1 equations are needed for a multinomial distribution with *J* categories.

Alternatively, we can write the proportional odds model:

Logit 
$$P(Y \le j) = \text{Logit } \gamma_j = \log\left(\frac{\gamma_j}{1-\gamma_j}\right) = \alpha_j + X\beta + Zb$$
 (2.3)

where  $\gamma_j = P(Y \le j)$  is the probability that observation y falls in category j or lower,  $\gamma_1 \le \gamma_2 \le \dots \le \gamma_{J-1} \le \gamma_J \le 1$  and,  $\alpha_j + X\beta + Zb$  is the same as before.. The estimated probabilities are  $\widehat{\pi}_j = \widehat{\gamma}_j - \widehat{\gamma}_{j-1}$ , j=2, ..., J-1, and  $\widehat{\pi}_1 = \widehat{\gamma}_1$  where  $\widehat{\gamma}_J = 1$ .

We note that the intercept  $(\alpha_j)$  is the only parameter that changes between categories whereas the effects, fixed or random, stay the same on all response cumulative probabilities.

The sign of the fixed effect indicates the probability of the response of being in the lower categories or the higher ones. If the sign is positive, this indicates that as the level/value of a predictor increases, the response is more likely to fall in lower categories. On the other hand, if the sign is negative, it indicates that as the level/value of a predictor increases, the response is more likely to fall in higher categories.

The difference between any two treatments effects is the log odds ratio. Exponentiating this difference yields an estimate of the odds ratio (Stroup, 2013).

In categorical data models, odds ratio is commonly used as a measure of the association between a categorical response variable and predictors (Agresti, 2007). We will use two-by-two contingency tables to illustrate the concept. The odds of success can be defined as

$$Odds = \frac{\pi}{1-\pi},$$
(2.4)

where  $\pi$  is the probability of success, i.e., the probability that the desired outcome occurs. The higher the odds, the higher the chance of a successful outcome. If we have odds1 as odds of success in row 1 and odds2 as odds of success in row 2, where row 1 and row 2 represent categories of a predictor in the two-by-two contingency table, then the odds ratio is:

$$\Theta = \frac{\text{odds1}}{\text{odds2}} = \frac{\pi_1/(1-\pi_1)}{\pi_2/(1-\pi_2)}$$
(2.5)

For the interpretation of the odds ratio,  $\Theta = 1$ , this means that the two variables are independent and that  $\pi_1 = \pi_2$ . In contrast, if  $\Theta > 1$ , then the odds of success in row 1 are higher than in row 2. On the other hand, if  $\Theta < 1$ , then the odds of success in row 2 are higher than in row 1. The farther the odds ratio is from 1, the stronger the association between variables.

#### **2.2 Estimation with Generalized Linear Mixed Models**

In this section, we present a brief discussion about model parameter estimation with generalized linear mixed models. Generalized linear mixed models (GLMM) are considered general models encompassing other models that are GLMM special cases, namely, the linear models (LM), generalized linear models (GLM) and linear mixed models (LMM). The GLMM consists of the following components:

- Linear predictor: η = Xβ + Zb, where X is an N x p design matrix with p parameters in the linear predictor and N is the number of observations, β is a p x 1 vector of fixed effects model parameters and b is a vector of the random model effects.
- Link function:  $\eta = g(\mu|b)$ .
- Distribution: *b* ~N (0, *G*)
- Distribution or quasi-likelihood of the observations conditional on the random effects, y|b: E(y|b) = μ|b.

In GLMM, we need to estimate the parameters for the fixed effects  $\beta$ , any components of Var(*y*/*b*), *b* and the variance-covariance component *G*. A traditional maximum likelihood approach requires that the observations conditional on the random effect belong to the exponential family or have a quasi-likelihood. However, when maximizing the likelihood, further simplification of the marginal likelihood that involves the product of Gaussian and exponential family or quasi-likelihoods are not always possible. Therefore, we need some approximation instead of the direct maximization. This can be achieved using two approaches: 1) linearization: the pseudo-likelihood method; and 2) integral approximation: Laplace approximation and adaptive Gauss-Hermite quadrature (Stroup, 2013).

An advantage of using pseudo-likelihood (PL) is that the pseudo-likelihood assumes that the approximating function is close to the structure of the Gaussian log-likelihood so that we can use LMM estimating equations for the linear predictor effects and the covariance components. PL's estimating equations can be considered as the general estimating equations for all LM, GLM, LMM and GLMM. Additionally, PROC GLIMMIX by default uses RSPL a pseudolikelihood implemented with the restricted –or residual– maximum likelihood (REML) version for the covariance estimation, details can be found in Stroup, 2013 and SAS/STAT® 9.2 User's Guide. However, PL does not always work. Integral approximation is then used in situations that do not work with PL. Laplace and Quadrature approximations have the advantage that they focus on the actual likelihood where the statistics are well defined which is not true for pseudolikelihood. This only becomes an issue with non-Gaussian data (GLMM), which is our case. Thus, in this report we chose integral approximation. For quadrature approximation, increasing the number of quadrature points results in more accurate approximation. Quadrature approximation with a single point gives an identical result to Laplace approximation. In comparison to PL, Laplace has less bias for small samples. In addition, we have a small number of Bernoulli trials per units of observations of non-Gaussian data with mixed effects and repeated measures and Stroup 2013 suggests Laplace approximation for this type of cases. Thus, in this paper, we focus on Laplace approximation given that quadrature approximation is computationally more intensive.

In the following section, we present a short description of Laplace approximation used by the GLIMMIX procedure in SAS® software, which is the method and software used for next chapter's data analysis.

#### **2.2.1 Laplace Approximation in PROC GLIMMIX**

Let the marginal distribution of the data be

$$P(y) = \int p(y|\gamma, \beta, \Phi, \Theta) p(\gamma|\Theta^*) d\gamma$$
  
=  $\int \exp\{\log\{p(y|\gamma, \beta, \Phi, \Theta^*)\} + \log\{p(\gamma|\Theta^*)\}\} d\gamma$  (2.7)  
=  $\int \exp\{c_l f(y, \beta, \Theta, \gamma)\} d\gamma$ , where  $\beta$  is a vector of the fixed effects,  $\Theta$  is a vector of

covariance parameters that includes the G side parameters and  $\Phi$  a possible scale parameter and  $\theta^*$  is a vector of the G side parameter.

With large  $c_1$ , the Laplace approximation is

$$L\left(\beta,\theta,\hat{\gamma},y\right) = \left(\frac{2\pi}{c_l}\right)^{\frac{n_\gamma}{2}} \left|-f''(y,\beta,\theta,\hat{\gamma})\right|^{-\frac{1}{2}} e^{c_l f(y,\beta,\theta,\hat{\gamma})},\tag{2.8}$$

where  $n_{\gamma}$  is the number of elements in  $\gamma$  and f'' is the second derivative matrix

$$f''(y,\beta,\theta,\hat{\gamma}) = \frac{\partial^2 f(y,\beta,\theta,\gamma)}{\partial \gamma \partial \gamma} |_{\hat{\gamma}} \text{ and } \hat{\gamma} \text{ satisfies } \frac{\partial f(y,\beta,\theta,\gamma)}{\partial \gamma} = 0.$$

For Laplace parameter estimation, the objective function in GLIMMIX procedure is -2log{L ( $\beta$ ,  $\theta$ ,  $\hat{\gamma}$ , y)}. In GLIMMIX procedure, when processing the data by subject, as the number of subjects and observations per subject increases, the chance of having small sample bias of Laplace estimator decreases SAS® (SAS Institute Inc.).

## **Chapter 3 - Data Analysis**

In this chapter, we present the data analysis and results of the case study. Different approaches were followed to find the most appropriate model that accounted for the ordinal response and the required mixed effect. All models were fitted using GLIMMIX procedure in SAS®. We start in the next section by defining the GLMM that would represent the experiment and data collection best. However, we make evidence in the subsequent sections limitations caused by sample size and computational methodologies, forced us to adjust the model assumptions.

#### **3.1 The Statistical Model**

In chapter 1, we established that the objective of the experiment was to evaluate the effectiveness of some commercial products to control the disease development of specific species of *Pythium*. We have a response variable (disease severity) measured in an ordered scale with six categories, a treatment factor that was applied to groups of seeds and a pathogens factor that was applied at petri dish level. Petri dishes are the smallest experimental units and were assumed as random because we want to generalize our conclusions to the overall population of the petri dish. The observational units are the seeds. The pathogens factor is assumed fixed because Drs. Carmona and Perez-Hernandez were interested in making conclusions applicable to these three species of *Pythium (P. aphanidermatum, P. irregulare, and P. ultimum)* in specific first, and later generalize them if possible. Finally, seeds were evaluated on two different dates. We could have considered these as repeated measures, but with only two measurements and for simplicity, Time effect was modeled as a third fixed factor.

The number of seeds for each category of the response variable and each combination of treatment, pathogen and day is represented by:

 $Y_{ijkl}$  = number of seeds in the jth category of the disease rating, ith treatment, kth pathogen, lth day and mth petri dish where j=0, 1, ...5; i =1,2,...,7; k= 1,2,3; l= 1,2; m=1,2,...,10. The conditional distribution of the response variable (counts by disease severity) given the random effect (dish) is multinomial. Since our response variable is ordinal, we assumed a cumulative logit model with mixed effects, where the petri dish was represented by a random variable with normal distribution N(0,  $\sigma_D^2$ ). We defined the cumulative logit as

$$Logit(P(Y \le j)) = \prod_{j=1}^{\infty} \alpha_{j} + X\beta + Zb; \qquad (3.1)$$

where j=0,1,2,3,4 and the proportional odds model used as follows:

$$Logit(P(Y \le j)) = \prod_{ijklm} = \alpha_j + T_i + F_k + Day_l + Dish_m (T_i * F_k) + T_i F_k + T_i Day_l + F_k Day_l + T_i F_k Day_l$$

$$(3.2)$$

where  $\alpha$ j is the intercept for the jth link and T<sub>i</sub>, F<sub>k</sub>, Day<sub>l</sub> and Dish<sub>m</sub> denote the ith treatment, kth pathogen, lth day and mth petri dish effects respectively.

A 3-way factorial treatment structure with interaction was chosen based on the evidence of factor interactions detected during the exploratory data analysis. Furthermore, we set the reference category of treatment, pathogen and day as Control, P. ultimum, and Day 21, respectively. Petri dish<sub>m</sub> ~ iidN  $(0,\sigma_D^2)$  represents the petri dishes.

Although the model above seemed reasonable at the time, we soon discovered that SAS® PROC GLIMMIX could not fit the model. Next, we discuss the approach we took to understand the limitations of the data and the statistical models and how we were forced to make stronger assumptions to obtain some results.

#### **3.2 Data Analysis and Model Fitting**

In this section, we present the gradual processes that we followed to achieve the objective of this study. Once we discovered that we did not achieve convergence or reasonable estimates for the GLMM defined in the previous section, we looked for alternatives.

As we mentioned in chapter 1 that Drs. Carmona and Perez-Hernandez tried to fit a cumulative logit model in GLIMMIX using a response variable with six categories but encountered convergence problems. First, the researchers had labeled all petri dishes from one to ten for each combination of treatment and pathogen. Petri dishes are not blocks in this experiment, but different experimental units. We coded petri dishes as nested factor in both treatment and the pathogen factors to guarantee SAS® fitted the correct model. Secondly, as we discussed in section 2.2.1, GLIMMIX default method, Pseudo-likelihood approximation (PL) is not always applicable. PL does not approximate the likelihood properly for cases, like binomial or multinomial GLMMs with a small number of trials per unit of observation (Stroup, 2013). Thus, we used Laplace approximation since it is the method of choice with non-Gaussian GLMM data and repeated measures.

The severity of the disease was evaluated on two different days on the same petri dishes so that we consider these as repeated measures. To account for possibility of the correlation due to repeated measures with non-Gaussian data and Laplace approximation, we used the first order auto-regression model AR (1) but GLIMMIX couldn't estimate the random effects. Since the variability might differ between evaluations, we tried a heterogeneous first-order autoregressive structure ARH (1). Again, the variance components were not estimable by Laplace or other GLIMMIX methods. As we mentioned in section 3.1, with two time points, we decided to assume that the day effect was fixed and we kept only the petri dish effect as random. Thus, we fitted a three-way factorial treatment structure with mixed effects. When we tried to fit the model with Treatment, Pathogen, Day as fixed effects and Petri dish as a random effect, we obtained problematic results again. Even though GLIMMIX procedure convergence criterion was satisfied and we obtained estimates for the fixed effects, we found a zero estimate for the random effect (petri dish) with undetermined standard error. To capture the random effect of the petri dish closely, we fitted two-way cumulative logit model with mixed effects for each day and each pathogen separately using Laplace method in GLIMMX procedure and the results illustrated in tables 3.1 and 3.2.

	DAY 5	DAY 21		
Estimate	0.1644	0		
Standard Error	0.1208	•		

 Table 3.1 Petri dish random effect estimate for fitting cumulative logit model with mixed effects separately by each Day.

	P. aphanidermatum	P. irregulare	P. ultimum	
Estimate	0	0	0.1147	
Standard Error	0.07719		0.09726	

 Table 3.2 Petri dish random effect estimate for fitting cumulative logit model with mixed effect separately by each Pathogen.

Table 3.1 shows that when fitting the mixed model separating the data by Day, only the model for the first evaluation (Day 5) was estimable. The second measurement, day twenty-first has the same problem we had with the full mixed model. We could not obtain a valid estimate for the random effect. A similar situation occurred when trying separated fits for each of the pathogens (Table 3.2). We could not estimate the petri dish random effect on Irregulare. We present these results for day 5 and *P. ultimum* in the next section.

The model we defined in equations 3.1 and 3.2 assumes our response variable follows a multinomial with N=5 and six possible categories. Even with the ten replicates of the conditional distribution, five seeds per trial seemed small for a multinomial data with six categories, so we decided to fit a fixed effect model with 3-way factorial treatment structure removing the petri dish effect regardless of the random effect. Under this model, we observe fifty seeds per trial instead of five. In other words, by making the assumption that the effect of the petri dish is not significant. Our multinomial data moves from N=5 to N= 50. The ANOVA shell associated with this model is:

Source of Variation	DF	
Treatment	6	
Fungus	2	
Day	1	
Treatment* Fungus	12	
Day* Fungus	2	
Treatment* Day	6	
Treatment*Fungus*Day	12	
Error	2054	
Total	2095	

#### Table 3.3 ANOVA shell for the three-way cumulative logit fixed model.

In addition, we fitted two-way cumulative logit model with fixed effects for each day and each pathogen separately to compare the results with the previous two-way cumulative logit mixed model results. This comparison could provide insight into whether or not our results of three-way cumulative logit model with fixed effects can be reliable. If the smaller simpler models show little differences or gain from the inclusion of the random petri dish effect, then maybe  $\sigma_D^2$  is not significantly different than zero, even if we cannot prove it. The results are presented in the next section. Figure 1.4 shows another peculiarity of the data that we exploit in our pursuit of an estimable model. The Control treatment (untreated seeds) has very low variability. In the first evaluation, most seeds tend to be non-germinated which results in high frequency at categories 4 and 5, and zero frequencies in the remaining categories. Similar to what happens in logistic regression when only success or only failures are observed, we suspect some computational problems may arise from observing all values in only one category, or when estimated probabilities are very close to the boundaries of the parameter space. Moreover, figure 1.3 shows that treated seeds, regardless of the treatment, fairly much better than the control group. For these reasons, we tried estimating the models removing the control treatment from the analysis. Results are presented in section 3.3.4.

Finally, besides simplifying the linear model, we also tried reducing the number of parameters to estimate, since we have six categories of the response variable with low frequencies, we tried collapsing the categories of the response variable in two different ways and estimate the model from equations 3.1 and 3.2 in GLIMMIX but now with J = 3 categories as in Carmona, et. Al. 2017, and with J = 2 categories to reduce the problem to a more traditional logistic regression. These results will be discussed in section 3.3.5.

#### **3.3 Results**

First, we discuss the results of the two-way cumulative logit mixed model on the first evaluation of the severity of the disease and on *P.ultimum* in section 3.3.1. Then we present the results of the three-way cumulative logit fixed model in section 3.3.2. Additionally, we present the results of the two-way cumulative logit fixed model on the first evaluation of the severity of the disease and on *P. ultimum* in section 3.3.3.

#### 3.3.1 Two-way cumulative logit mixed model

When we fitted mixed model on the first evaluation, we found that the effect of each treatment was different for each pathogen which implies heterogeneous association relating the response probabilities to the linear predictor and we found that the interaction between treatment and pathogen is significant. We also conducted pairwise comparison tests using Bonferroni correction and obtained the estimated odds ratios to compare the differences for the effects of treatments at each pathogen in SAS as shown in the following tables. Also note that the odds ratios in the following tables are considered to compare treatments in the columns to treatments in the rows.

#### **3.3.1.1** The odds ratios on the first evaluation

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200
Kphi 200	-						
Kphi 400	0.2170	-					
Maxim 100	27.2739	125.65	-				
MnPhi 200 + Maxim	2.1718	10.0020	0.07960	-			
MnPhi 400	0.2185	1.0065	0.008010	0.1006	-		
Control	5130.38	23628	188.04	2362.31	23475	-	
MnPhi 200	0.2892	1.3319	0.01060	0.1332	1.3233	0.000056	-
Significant Not significant							

#### For *P. aphanidermatum*:

Table 3.4 Odds ratios for *P. aphanidermatum* at the first evaluation of the mixed model.
# For P. irregulare:

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200		
Kphi 200	-								
Kphi 400	0.1164	-							
Maxim 100	2.1286	18.2847	-						
MnPhi 200 + Maxim	0.1483	1.2737	0.06966	-					
MnPhi 400	0.01136	0.09760	0.005338	0.07663	-				
Control	26.4445	227.16	12.4233	178.34	2327.37	-			
MnPhi 200	0.01832	0.1574	0.008607	0.1236	1.6124	0.000693	-		
Significant Not significant									

Table 3.5	Odds ratios for P.	<i>irregulare</i> on	the first	evaluation of	of the mixed	model.
Fo	r P. ultimum:					

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200		
Kphi 200	-								
Kphi 400	1.0311	-							
Maxim 100	2.8171	2.7321	-						
MnPhi 200 + Maxim	0.3561	0.3454	0.1264	-					
MnPhi 400	0.1798	0.1744	0.06384	0.5049	-				
Control	1503.78	1458.41	533.80	4222.43	8362.13	-			
MnPhi 200	1.5314	1.4852	0.5436	4.2999	8.5155	0.001018	-		
	Significant Not significant								

Not significant

### Table 3.6 Odds ratios for *P. ultimum* on the first evaluation of the mixed model.

Some of the estimated odds ratios are significant and some are not. We can see all products are better than the Control treatment and all of them work better for *P. aphanidermatum* than the other species followed by *P. ultimum*. The best product of being resistant to *P*.

*aphanidermatum* are Kphi 400, MnPhi 400 and MnPhi 200 and the effect of them is the same since the odds ratio of these effects is not significant. For *P. ultimum*, the most effective products are MnPhi 400 and MnPhi 200 + Maxim and they have the same effect and most of the rest of the products have the same effect. For *P. irregulare*, the most resistant products are MnPhi 400 and MnPhi 200. Since the odds ratio of them is not significant, they have the same effect. Overall, the least effect on controlling all species is Maxim 100 when comparing with untreated seeds (Control). Also, the most resistant product to all pathogens seems to be MnPhi 400.

#### 3.3.1.2 The odds ratios on *P. ultimum*

In addition, as we mentioned in section 3.2 that we fitted cumulative logit model with mixed effect by each pathogen and we could estimate the random effect and obtained results at each evaluation on *P. ultimum* as the following tables:

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200
Kphi 200	-						
Kphi 400	1.0556	-					
Maxim 100	3.6299	3.4388	-				
MnPhi 200 + Maxim	0.3333	0.3157	0.09181	-			
MnPhi 400	0.1814	0.1718	0.04997	0.5442	-		
Control	14904	14120	4106.06	44724	82177	-	
MnPhi 200	1.7286	1.6377	0.4762	5.1871	9.5309	0.000116	-

#### For the first evaluation:

#### Table 3.7 Odds ratios for the first evaluation of mixed model for *P. ultimum*.

As we see in table 3.7 that all treatments are better than the control treatment for the first evaluation. Treatment Kphi 200, Kphi 400, Maxim 100, MnPhi 200 and MnPhi 200 + Maxim

have the same effect. Treatment MnPhi 400 seems to be the most effective treatment on the first evaluation since it has the highest odds ratio in comparison with untreated seeds and the results agrees with what we found in the previous section.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200	
Kphi 200	-							
Kphi 400	3.7983	-						
Maxim 100	7.9873	2.1029	-					
MnPhi 200 + Maxim	1.0350	0.2725	0.1296	-				
MnPhi 400	4.4428	1.1697	0.5562	4.2927	-			
Control	69411726	18274608	8690225	67066779	15623487	-		
MnPhi 200	1.7528	0.4615	0.2194	1.6936	0.3945	2.525E-8	-	
		Significant		Not significant				

#### For the second evaluation:

#### Table 3.8 Odds ratios for the second evaluation of mixed model for *P. ultimum*.

As we see in the second evaluation, all treatments seem to be ineffective with *P. ultimum* when comparing to untreated seeds. Clearly the treatment efficacy is affected by the time factor so that researchers may have to consider this point and apply treatments several times to keep the seeds safe.

#### 3.3.2 Three-way cumulative logit fixed model

Furthermore, we fitted cumulative logit model as 3-way factorial treatment structure with the fixed effects ignoring the petri dishes effect in GLIMMIX with the control treatment as the reference level. However, we didn't obtain the degrees of freedom for the ANOVA shell that we expected in the previous section as the following table:

Effect	Num DF	Den DF	F-value	P-value
Treatment	1	2054	0	1
Pathogen	2	2054	0	1
Day	1	2054	0	1
Treatment* Pathogen	2	2054	0	1
Day* Pathogen	2	2054	0	1
Treatment* Day	1	2054	0	1
Treatment*Pathogen*Day	4	2054	0	1

Table 3.9 Type III test of fixed effects model with the control treatment as the reference level.

As we see in table 3.9 GLIMMIX procedure with the control treatment as the reference level provides different degrees of freedom than table 3.3 for the effects, zeros for the F-values and ones for the p-values. This leads us to change the reference level to MnPhi 200 and consider this for all results in this chapter.

Now we fitted cumulative logit model as 3-way factorial treatment structure with the fixed effects and MnPhi 200 as the reference level. We found that the three-way interaction term is significant as shown in table 3.10.

Effect	Num DF	Den DF	F-value	P-value
Treatment	6	2054	59.68	<.0001
Pathogen	2	2054	0	0.9988
Day	1	2054	0.02	0.8888
Treatment* Pathogen	12	2054	13.86	<.0001
Day* Pathogen	2	2054	0	0.9993
Treatment* Day	6	2054	17.98	<.0001
Treatment*Pathogen*Day	12	2054	6.75	<.0001

# Table 3.10 Type III test of fixed effects model with the MnPhi 200 treatment as the reference level.

We also conducted pairwise comparison tests using Bonferroni correction and obtained

the estimated odds ratios to compare the differences for the effects of treatments at each

pathogen and each evaluation in SAS as shown in the following tables.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200		
Kphi 200	-								
Kphi 400	0.2358	-							
Maxim 100	62.1792	263.66	-						
MnPhi 200 + Maxim	2.1366	9.0595	0.03436	-					
MnPhi 400	0.2400	1.0178	0.003860	0.1123	-				
Control	43839	185888	705.04	20519	182643	-			
MnPhi 200	0.3134	1.3288	0.005040	0.1467	1.3056	7.148E-6	_		
Significant Not significant									

For the first evaluation at *P. aphanidermatum*:

Table 3.11 Odds ratios for the first evaluation at *P. aphanidermatum* of fixed model.

In this table, we can see that all treatments of seeds at the first evaluation are effective against *P. aphanidermatum*. The effect of treatments Kphi 400 and MnPhi 400 is the same and they seem to be the most effective treatments. The least effective treatment is Maxim 100. Also, if we compared this table results with the two-way factorial treatment structure results for mixed models of the first evaluation of seeds with *P. aphanidermatum*, we will see that they are in the same direction and have similar results.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200		
Kphi 200	-								
Kphi 400	0.08842	-							
Maxim 100	3.0970	35.0252	-						
MnPhi 200 + Maxim	0.1126	1.2731	0.03635	-					
MnPhi 400	0.009681	0.1095	0.003126	0.08600	-				
Control	169.59	1917.95	54.7592	1506.46	17517	-			
MnPhi 200	0.01513	0.1711	0.004884	0.1344	1.5624	0.000089	_		
Significant Not significant									

### For the first evaluation at *P. irregulare*:

#### Table 3.12 Odds ratios for the first evaluation at *P. irregulare* of fixed model.

For seeds that infected by *P. irregulare* at the first evaluation, treatments are effective too. The highest odds ratio when comparing to control treatment is MnPhi 400 followed by MnPhi 200 and the lowest is Maxim 100. Moreover, the overall results are similar to what we found in previous sections about *P. irregulare* at the first evaluation.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200		
Kphi 200	-								
Kphi 400	1.0436	-							
Maxim 100	3.2994	3.1617	-						
MnPhi 200 + Maxim	0.3484	0.3339	0.1056	-					
MnPhi 400	0.1742	0.1669	0.05279	0.4999	-				
Control	12590	12064	3815.66	36131	72279	-			
MnPhi 200	1.6706	1.6009	0.5063	4.7945	9.5913	0.000133	-		
Significant Not significant									

#### For the first evaluation at *P. ultimum*:

#### Table 3.13 Odds ratios for the first evaluation at *P. ultimum* of fixed model.

For *P. ultimum* at the first evaluation, all treatments have an effect that better than untreated seeds. Treatment that is the highest resistant to *P. ultimum* is MnPhi 400 and MnPhi 200 + Maxim and they have the same effect. Treatments Kphi 200, Kphi 400 and MnPhi 200 have the same effect. The minimum effect against *P. ultimum* is Maxim 100.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200
Kphi 200	-						
Kphi 400	3.2936	-					
Maxim 100	117.48	35.6706	-				
MnPhi 200 + Maxim	1.7921	0.5441	0.01525	-			
MnPhi 400	0.8523	0.2588	0.007255	0.4756	-		
Control	7.0396E8	2.1374E8	5991930	3.9281E8	8.2591E8	-	
MnPhi 200	0.6522	0.1980	0.005552	0.3639	0.7652	9.27E-10	-
		Significant		Not significant			

### For the second evaluation at *P. aphanidermatum*:

# Table 3.14 Odds ratios for the second evaluation at *P. aphanidermatum* of fixed model.

We can see that three-way factorial treatment structure fixed model for seeds that

infected by *P. aphanidermatum* shows that all treatments are ineffective after two weeks of being treated when comparing with untreated seeds (Control).

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200			
Kphi 200	-									
Kphi 400	0.7358	-								
Maxim 100	1.1050	1.5016	-							
MnPhi 200 + Maxim	0.7177	0.9753	0.6495	-						
MnPhi 400	1.0000	1.3590	0.9050	1.3934	-					
Control	13.3835	18.1882	12.1123	18.6487	13.3835	-				
MnPhi 200	0.4080	0.5545	0.3693	0.5685	0.4080	0.03049	-			
	Significant Not significant									

Tor the second evaluation at <i>i</i> . <i>n</i> egume.	For	the	second	evaluation	at P.	irregulare:
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Table 3.15 Odds ratios for the second evaluation at *P. irregulare* of fixed model.

At the second evaluation for seeds infected by *P. irregulare*, we found that all treatments are still effective when comparing with untreated seeds (Control) and all of them have the same effects.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200
Kphi 200	-						
Kphi 400	3.6422	-					
Maxim 100	7.6092	2.0892	-				
MnPhi 200 + Maxim	1.0347	0.2841	0.1360	-			
MnPhi 400	4.2624	1.1703	0.5602	4.1193	-		
Control	3.3762E8	92697380	44370244	3.2629E8	79209643	-	
MnPhi 200	1.7248	0.4736	0.2267	1.6669	0.4046	5.109E-9	-
		Significant			Not significant		

For the second evaluation at *P. ultimum*:

#### Table 3.16 Odds ratios for the second evaluation at *P. ultimum* of fixed model.

We can see that three-way logit fixed model for seeds that infected by *P. ultimum* shows that all treatments are ineffective when comparing with untreated seeds (Control) after two weeks of being treated which agrees with the mixed models with two-way factorial treatment structure results.

#### **3.3.3** Two-way cumulative logit fixed model

As we mentioned in section 3.2 that for our results of three-way cumulative logit fixed model to be reliable, we fitted two-way cumulative logit fixed model separately by each day and pathogen so that we can compare the results with the two-way mixed model for *P. ultimum* and at the first evaluation (Day 5). We also conducted pairwise comparison tests using Bonferroni correction and obtained the estimated odds ratios as shown in the following tables.

# **3.3.3.1** The odds ratios on the first evaluation

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200				
Kphi 200	-										
Kphi 400	0.2220	-									
Maxim 100	24.8440	111.93	-								
MnPhi 200 + Maxim	2.1288	9.5908	0.08569	-							
MnPhi 400	0.2262	1.0191	0.009105	0.1063	-						
Control	4185.47	18856	168.47	1966.10	18503	_					
MnPhi 200	0.2990	1.3470	0.01203	0.1405	1.3218	0.000071	-				
	Significant Not significant										

### For *P. aphanidermatum* pathogen:

Table 3.17 Odds ratios for P. aphanidermatum on the first evaluation of fixed model.For P. irregulare pathogen:

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200		
Kphi 200	-								
Kphi 400	0.1227	-							
Maxim 100	2.0844	16.9882	-						
MnPhi 200 + Maxim	0.1553	1.2656	0.07450	-					
MnPhi 400	0.01265	0.1031	0.006071	0.08149	-				
Control	23.8909	194.72	11.4619	153.86	1887.95	-			
MnPhi 200	0.02020	0.1646	0.009691	0.1301	1.5963	0.000845	-		
Significant Not significant									

 Table 3.18 Odds ratios for P. irregulare on the first evaluation of fixed model.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200	
Kphi 200	-							
Kphi 400	1.0174	-						
Maxim 100	2.7229	2.6764	-					
MnPhi 200 + Maxim	0.3711	0.3647	0.1363	-				
MnPhi 400	0.1853	0.1821	0.06804	0.4993	-			
Control	1276.80	1254.98	468.91	3440.84	6891.49	-		
MnPhi 200	1.5352	1.5089	0.5638	4.1371	8.2860	0.001202	-	
		Significant		Not significant				

#### For P. ultimum pathogen:

#### Table 3.19 Odds ratios for P. ultimum on the first evaluation of fixed model.

When comparing theses results of fixed effect model with the results of mixed model on the first evaluation, we can see that the odds ratios are very similar and the significance of the odds ratios is the same. Overall, the results of fixed models agree with mixed effect models results. This implies that the petri dishes random effect may not be significant.

#### 3.3.3.2 The odds ratio on *P. ultimum*

Now we present the results of fitting fixed effect for *P. ultimum* to compare it with mixed effect result.

#### For the first evaluation:

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200		
Kphi 200	-								
Kphi 400	1.0436	-							
Maxim 100	3.4922	3.3462	-						
MnPhi 200 + Maxim	0.3437	0.3293	0.09841	-					
MnPhi 400	0.1838	0.1761	0.05262	0.5347	-				
Control	12992	12449	3720.28	37804	70704	-			
MnPhi 200	1.7169	1.6451	0.4916	4.9958	9.3436	0.000132	-		
Significant Not significant									

# Table 3.20 Odds ratios for the first evaluation of fixed model for P. ultimum.For the second evaluation:

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	Control	MnPhi 200
Kphi 200	-						
Kphi 400	3.7207	-					
Maxim 100	7.7272	2.0768	-				
MnPhi 200 + Maxim	1.0339	0.2779	0.1338	-			
MnPhi 400	4.3511	1.1694	0.5631	4.2086	-		
Control	2.3361E8	62786509	30232447	2.2596E8	53690554	-	
MnPhi 200	1.7424	0.4683	0.2255	1.6853	0.4004	7.458E-9	-
		Significant		Not significant			

#### Table 3.21 Odds ratios for the second evaluation of fixed model for *P. ultimum*.

Overall, in the first evaluation of seeds contaminated with *P. ultimum*, all results agree with what we found with mixed models that all treatments are better than the control treatment for the first evaluation. The odds ratio comparing Maxim 100 to Kphi 200 became significant

with fixed models. Treatment Kphi 200, Kphi 400, MnPhi 200 and MnPhi 200 + Maxim have the same effect and treatment MnPhi 400 has the highest odds ratio in comparison with untreated seeds. Also for the second evaluation of the same seeds, all treatments seem to be ineffective when comparing to untreated seeds. Clearly the time factor has an effect on the treatments resistance to the isolates in the second evaluation.

#### **3.3.4 Excluding Control Treatment**

As we saw in figure 1.4, Control treatment (untreated seeds) does not have much variability. Most of seeds tend to be non-germinating which results in high frequency at category 4 and 5 and zeros frequencies in the remaining categories of the response variable making more noise in the data. Therefore, we excluded the Control treatment from the data and fitted 3-way logit mixed model and again we couldn't estimate the random effect of petri dish. Then we fitted 3-way logit fixed model and we obtained the following results.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	MnPhi 200
Kphi 200	-					
Kphi 400	0.06412	-				
Maxim 100	10.9627	43.1094	-			
MnPhi 200 + Maxim	0.6508	2.4797	0.005930	-		
MnPhi 400	0.06900	0.2837	0.000623	0.03119	-	
MnPhi 200	0.08977	0.3648	0.000814	0.04068	0.3787	-
		Significant			Not significant	

For the first evaluation at *P. aphanidermatum*:

 Table 3.22 Odds ratios for the first evaluation at *P. aphanidermatum* of fixed model excluding the Control treatment.

When comparing with results of the data including the Control treatment, the significance of the odds ratios hasn't changed but now the values of the odds ratios seem to be lower.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	MnPhi 200
Kphi 200	-					
Kphi 400	0.08724	-				
Maxim 100	3.1037	35.5755	-			
MnPhi 200 + Maxim	0.1112	1.2748	0.03583	-		
MnPhi 400	0.009357	0.1073	0.003015	0.08413	-	
MnPhi 200	0.01470	0.1685	0.004735	0.1321	1.5706	-
		Significant		Not significant		

For the first evaluation at *P. irregulare*:

# Table 3.23 Odds ratios for the first evaluation at *P. irregulare* of fixed model excluding the Control treatment.

For *P. irregulare* at the first evaluation, the results are very similar with and without the

control treatment.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	MnPhi 200
Kphi 200	-					
Kphi 400	1.0429	-				
Maxim 100	3.3183	3.1819	-			
MnPhi 200 + Maxim	0.3465	0.3323	0.1044	-		
MnPhi 400	0.1724	0.1654	0.05197	0.4977	-	
MnPhi 200	1.6748	1.6060	0.5047	4.8335	9.7122	-
		Significant	•		Not significant	

### For the first evaluation at *P. ultimum*:

# Table 3.24 Odds ratios for the first evaluation at *P. ultimum* of fixed model excluding the Control treatment.

For P. ultimum at the first evaluation, the results are very similar with and without the

control treatment.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	MnPhi 200
Kphi 200	-					
Kphi 400	3.2998	-				
Maxim 100	113.54	34.4091	-			
MnPhi 200 + Maxim	1.7939	0.5437	0.01580	-		
MnPhi 400	0.8519	0.2582	0.007502	0.4749	-	
MnPhi 200	0.6509	0.1973	0.005733	0.3628	0.7641	-
		Significant		Not significant		

For the second evaluation at *P. aphanidermatum*:

# Table 3.25 Odds ratios for the second evaluation at *P. aphanidermatum* of fixed model excluding the Control treatment.

For the second evaluation at *P. aphanidermatum*, the results are very similar with and

without the control treatment.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	MnPhi 200
Kphi 200	-					
Kphi 400	0.7361	-				
Maxim 100	1.1028	1.4982	-			
MnPhi 200 + Maxim	0.7180	0.9754	0.6510	-		
MnPhi 400	1.0000	1.3585	0.9068	1.3928	-	
MnPhi 200	0.4080	0.5542	0.3700	0.5682	0.4080	-
		Significant	•		Not significant	•

# For the second evaluation at *P. irregulare*:

Table 3.26 Odds ratios for the second evaluation at *P. irregulare* of fixed model excluding the Control treatment.

We can see that after excluding the Control treatment the results are almost the same.

	Kphi 200	Kphi 400	Maxim 100	MnPhi 200 + Maxim	MnPhi 400	MnPhi 200	
Kphi 200	-						
Kphi 400	3.6421	-					
Maxim 100	7.5579	2.0751	-				
MnPhi 200 + Maxim	1.0344	0.2840	0.1369	-			
MnPhi 400	4.2558	1.1685	0.5631	4.1141	-		
MnPhi 200	1.7258	0.4738	0.2283	1.6683	0.4055	-	
Significant				Not significant			

#### For the second evaluation at *P. ultimum*:

# Table 3.27 Odds ratios for the second evaluation at *P. ultimum* of fixed model excluding the Control treatment.

We can see that after excluding the Control treatment the results are almost the same.

#### **3.3.5** Collapsing over Categories of the Response Variable

As we mentioned in section 3.2, we collapsed the categories of the response variable to get larger frequencies. Instead of having six categories, we tried three categories and two categories of the response variable. For three categories, we collapsed categories 1, 2, and 3 as one category and 4 and 5 as another category so that overall, we have 0, 1 and 2 categories of the response variable where 0 = "germinated seeds", 1 = "less germination", and 2 = "almost nongerminated seeds". Then, we fitted proportional logit model with mixed effect as a three-way factorial treatment structure in GLIMMIX procedure in SAS using Laplace approximation. Unfortunately, we encountered the same problem that we could not estimate the petri dish effect. Next, we fitted proportional logit model with fixed effect as a three-way factorial treatment structure in GLIMMIX procedure in SAS and the Type III ANOVA table degrees of freedom were estimated incorrectly. Finally, we tried a binary response variable. We collapsed categories 0, 1, 2, and 3 as one category and 4 and 5 as another category so that overall, we have only two outcomes, 0 = "germinated or partly germinated seeds", and 1 = "almost non-germinated seeds". We fitted proportional logit model with mixed effect as a three-way factorial treatment structure in GLIMMIX procedure in SAS using Laplace approximation. Even though SAS did estimate the petri dish random effect, it gives Type III ANOVA table with wrong degrees of freedom. Additionally, we also fitted proportional logit model with fixed effect as a three-way factorial treatment structure in GLIMMIX procedure in SAS but we obtained the wrong Type III ANOVA table degrees of freedom.

# **Chapter 4 - Power Analysis**

In this chapter, we explain and present the results of the power analysis we conducted to evaluate the impact of our sample sizes in multinomial experiments similar to our case study. We used a modified version of the three steps procedure suggested by Stroup, 2013 to calculate GLMMs' power. The procedure consists of first, create an artificial dataset whose estimates would match the conditional expectations, i.e., probabilities, we expect to see and/or test. Then, fit a GLM or GLMM using GLIMMIX procedure in SAS®; and finally, use GLIMMIX's results to calculate the power. In the next section, we explain the procedure in detail and present our results.

#### **4.1 Power Calculations**

When Drs. Carmona and Perez-Hernandez designed their experiment, their main objective was to evaluate the effectiveness of several products to hinder the negative effect of pathogen infection on soybean seeds. Although they did not conduct a power analysis for determination of sample size in their experiment, they followed the "usual" design and sample size in their field. Conducting a power analysis should be encouraged in any circumstance, the rationality behind is beyond the scope of this project so we will focus our attention on our findings. For a detailed discussion on the importance of this step refer to Chapter 16, Stroup, 2013.

The following power calculations are not valid in the sense that they were done after the experiment. However, we were very curious about the consequences of the sample size selections on our results and lack of fit in the case of the random effect. Stroup 2013 suggests a three steps procedure to conduct a power analysis for a GLMM. Step one construct a data set with the same number of observations per block/treatment combination as the proposal

42

experiment structure and sample size, and use E(Y/b), i.e. the expected data mean given the random effects, as your observed values. The chosen means should reflect the differences that we want to evaluate. For instance, in a binomial model we may assume the control probability of success in 0.20 and want to compute the power of detecting an increment of 0.10. Therefore, we will create an exemplary data set with 20% of ones (successes) in our control group and 30% of ones in treatment one. Step two consists of fitting the model with SAS® PROG GLIMMIX including estimation of all the comparisons of interest, such as pairwise contrast:  $\tau_i - \tau_{t'}$ ,  $i \neq i'$ , keeping the covariance components constant, i.e. SAS should not estimate the variance parameter(s). We must set them according to our knowledge about the process. For each estimable function of interest, GLIMMIX computes approximate *F*-statistic. Step three use the estimated *F* values and degrees of freedom to obtain the critical value and the non-centrality parameter under the proposed design, best-guess covariance components and expected/important treatment effect. Then, the power to detect each comparison of interest is calculated as the area to the right of the critical value under the noncentral *F*.

For creating our exemplary datasets given our conclusion about factor interactions from chapter 3, we removed the Pathogen and Day factors and assumed that the results would be equivalent to fit each Pathogen\*Day combination separately. Thus, we defined seven treatments with different theoretical or expected probabilities of observing each of the six categories (0-5). The probabilities are listed in Table 4.1. Watchful of technical and logistical limitations, we tried only three designs: 10 petri dishes, 5 seeds per dish (like our case study); 10 petri dishes, 10 seeds per dish; and 20 petri dishes, 5 seeds per dish. At this point, we had to deviate from Stroup, 2013 because E(Y/b) resulted fractional, i.e. we only had 5 or 10 seeds to divide into six categories. Instead of creating one exemplary data, we generate 1,000 sets drawing the observed

43

	1010 4.1.					
		Powe	r Calculation	S		
	Theoretical Probabilities per Category					
Treatment	0	1	2	3	4	5
Control	0	0	0	0	0.05	0.95
Exp 1	0.3	0.5	0.2	0	0	0
Exp 2	0.1	0.3	0.1	0.1	0.1	0.3
Exp 3	0.15	0.8	0.05	0	0	0
Exp 4	0.05	0.45	0.45	0.05	0	0
Exp 5	0	0	0	0.1	0.75	0.15
Exp 6	0	0	0.1	0.75	0.15	0

counts from a multinomial with N= number of seeds per dish, and probabilities  $\pi_0, \pi_1, \pi_2, ..., \pi_5$  according to Table 4.1.

 Table 4.1 Theoretical probabilities for the power analysis for multinomial responses.

For step two, we fitted a fixed effects model (assuming the dish effect is zero) and two mixed effects models one setting  $\sigma_D^2$ =0.1 and another with  $\sigma_D^2$ =0.01, where  $\sigma_D^2$  represents the dish effect variance from equation 3.2. In all cases we used the same significance level from the case study, set to 0.238% for Bonferroni's adjustment for multiple comparisons. In the next section, we present our findings. The SAS code used for the simulation and the power calculations is included in Appendix C.

#### **4.2 Power Results**

In table 4.2, we present the average estimated power to detect a difference between two hypothetical expected means. As evident from the obtained results, we have good power to detect most of the potential difference with the exception of some comparisons with experimental treatment 2 and one extreme case, experiment 1 vs. 3. This treatment comparison scored almost no power (equal to significance level) to be detected, when in reality their probabilities are not very close.

	10 Petri Dishes,			10 Petri Dishes,		20 Petri Dishes,			
	5 Seeds per dish		10 Seeds per dish		5 Seeds per dish				
Contrast	Fixed	Mixed		Fixed	Mixed		Fixed	Mixed	
		$\sigma_D^2 = 0.1$	$\sigma_D^2 = 0.01$	TIXEU	$\sigma_D^2 = 0.1$	$\sigma_D^2 = 0.01$	Tixeu	$\sigma_D^2 = 0.1$	$\sigma_D^2 = 0.01$
Ctrl vs. Exp 1	0.912	0.912	0.912	0.993	0.993	0.993	0.990	0.990	0.990
Ctrl vs. Exp 2	0.908	0.906	0.906	0.993	0.993	0.993	0.990	0.990	0.990
Ctrl vs. Exp 3	0.912	0.912	0.912	0.993	0.993	0.993	0.990	0.990	0.990
Ctrl vs. Exp 4	0.912	0.912	0.912	0.993	0.993	0.993	0.990	0.990	0.990
Ctrl vs. Exp 5	0.898	0.893	0.892	0.993	0.992	0.992	0.990	0.990	0.990
Ctrl vs. Exp 6	0.912	0.912	0.912	0.993	0.993	0.993	0.990	0.990	0.990
Exp 1 vs. Exp 2	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Exp 1 vs. Exp 3	0.027	0.025	0.022	0.030	0.027	0.021	0.029	0.028	0.024
Exp 1 vs. Exp 4	0.763	0.733	0.694	0.974	0.964	0.933	0.974	0.970	0.959
Exp 1 vs. Exp 5	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Exp 1 vs. Exp 6	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Exp 2 vs. Exp 3	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Exp 2 vs. Exp 4	0.998	0.998	0.997	1.000	1.000	1.000	1.000	1.000	1.000
Exp 2 vs. Exp 5	0.284	0.267	0.255	0.472	0.443	0.397	0.483	0.471	0.456
Exp 2 vs. Exp 6	0.510	0.486	0.454	0.764	0.736	0.675	0.770	0.758	0.727
Exp 3 vs. Exp 4	0.772	0.738	0.691	0.982	0.972	0.938	0.983	0.980	0.968
Exp 3 vs. Exp 5	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Exp 3 vs. Exp 6	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Exp 4 vs. Exp 5	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
Exp 4 vs. Exp 6	1.000	1.000	0.999	1.000	1.000	1.000	1.000	1.000	1.000
Exp 5 vs. Exp 6	0.989	0.984	0.973	1.000	1.000	1.000	1.000	1.000	1.000

Table 4.2 Simulation average power for comparisons between treatments of different sample sizes and different models, "Ctrl" and "Exp" refer to control and experimental treatment, respectively.

The average may not reflect the variability of the power obtained in each of the 1000

simulations. Figures 4.1, 4.2 and 4.3 display the distribution of the estimated power by simulation for some comparisons to illustrate three situations that can happen. The rest of the plots are included in Appendix A. Figure 4.1 shows that comparing control against the experiments, experiment 1 in this case, will give a power of one even with the smallest sample size. However, sometimes we get a small value that is associated with simulating an exemplary data that produces a false negative. Figure 4.2 shows experiment 2 against 6, for this case the

power is low in general, but may be fixed by increasing the sample size. Lastly, figure 4.3 is the extreme case of experiment 1 against 3, whose power starts very low (significance level) and does not improve regardless the sample size increments.



Figure 4.1 Power to detect a difference between Control and Experiment 1 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure 4.2 Power to detect a difference between Experiments 2 and 6 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure 4.3 Power to detect a difference between Experiments 1 and 3 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).

So far, we have found evidence that the sample size is enough to detect large shifts in the probabilities per category, but will not be able to detect subtle differences. We can also conclude that across all simulation results we did not detect a significant gain or loss from including the variance component. In other words, we found that making the petri dish a random effect would not change the power results.

One open question left for future research is how many observations are needed to estimate  $\sigma_D^2$  properly. We left it for future work together with alternative methods to modeling the data such as Bayesian or Bootstrap approaches.

# **Chapter 5 - Conclusion**

On this report, we illustrated the statistical approach to analyze ordered categorical data with low frequencies using real data. Our case study originated in an experimental design set up; therefore, we focused on generalized linear mixed models, more specifically in the cumulative logit or proportional odds mixed model. Laplace approximation was the recommended technique in the literature for our case study. This is not the default estimation technique in PROC GLIMMIX. Users of the software should be aware that they must evaluate which estimation technique works best for their case before running any analysis.

During the modeling process explained in detail in chapter 3, we encountered two recurrent problems. The first one involved the estimation of the covariance parameters. Whenever we tried to estimate some types of random effect, repeated measurement or random petri dish effect, we frequently faced lack of convergence or singular variance-covariance matrix. Given the magnitude of the estimated random petri dish effect on the few occasions that it was obtained, it is likely that its true value is close to zero. We believe that the lack of estimation was caused in part by this fact. The small sample size contribution to the problem might have been partial, but most likely it made the estimation in the boundary of the parameter's space harder.

The second of our recurrent problems was the incorrect calculation of degrees of freedom on the ANOVA tables. This one is perhaps the most concerning from the practitioner's point of view. The miscalculation happened regardless of model complexity, with or without random effects, and even for the binomial case logistic regression. Sometimes it was easy to detect because it came with p-values equal to 1, others it was hidden in plain sight. It is likely a computational problem rather than a statistical one. However, it made the rest of the results produced GLIMMIX unusable, not knowing how far the consequences of the error causing the degrees of freedom miscalculation go.

In spite of the fact that we could not estimate the parameters of the statistically correct model or test if the petri dish random effect has a significant effect formally, we believe our findings are sound and we could answer the scientific question about the potential effects of commercial products in the control of the pathogen induced disease being studied, when evaluated at a six categories severity scale. The main conclusion of the case study being analyzed is that regardless of the model, GLM or GLMM, the data always produced the same results with regards of the treatment effects. Furthermore, excluding the Control treatment did not affect the obtained results or improved the estimation. There is a significant interaction between Treatment, Pathogen and Day factors. Thus, treatment comparisons should be made for each Pathogen\*Day combination separately. All types of effect models (fixed or mixed) agree that for soybean seeds inoculated with *P. aphanidermatum*, the treatments that offer the most potential to reduce the disease's severity on the first evaluation are MnPhi 400 and Kphi 400 when comparing to untreated seeds. They have the same efficacy as MnPhi 200 and Kphi 400 while the least resistance is provided by Maxim 100. Moreover, for seeds inoculated with *P. irregulare* on the first evaluation the most protection was shown by MnPhi 400, followed by Kphi 400 while the lowest protection was displayed by Maxim 100. In addition, for seeds contaminated with P. ultimum at the first evaluation, the best product resulted to be MnPhi 400 and MnPhi 200 + Maxim both having similar effects, while the least effective product is Maxim 100. On the other hand, after two weeks with *P. ultimum* and *P. aphanidermatum*, all treatments seem to be ineffective which implies that the six treatments age against *P. ultimum* and *P. aphanidermatum* in less than two weeks. For P. irregulare, all treatments offer some protection against dampingoff and work with the same efficacy. We also found that overall MnPhi 400 seems to be the best product against all three pathogens while Maxim 100 is the least effective. All products efficacy is less than two weeks for *P. ultimum* and *P. aphanidermatum* while all of them offer some resistance after two weeks when comparing to Control treatment with *P. irregulare* but there is no difference between treatments

Five seeds might not be enough with a multinomial data with six categories to estimate a random effect from the petri dish. We try collapsing categories, but GLIMMIX produced strange and unexpected degrees of freedom for this data set. Although it seems that we are gaining information by reducing the number of possible outcomes, the cumulative logit model we used only estimates one additional parameter per category, the intercepts in equation 2.2. We conducted a power analysis to study the effects of sample sizes and designs similar to our case study, where technical limitations and finite resources make it impossible to observe a very large sample.

The power analysis detailed in chapter 4 used a modified version of the three process suggested by Stroup 2013. We tested three sample sizes 10 petri dishes, 5 seeds per dish; 10 petri dishes, 10 seeds per dish; and 20 petri dishes, 5 seeds per dish. We kept the 6 category levels for the response variable and the seven treatments. Given our conclusion about factor interactions from chapter 3, we removed the Pathogen and Day factors and assumed that the results would be equivalent to fit each Pathogen\*Day combination separately. Data was simulated accordingly some hypothetical differences between categories and treatment effects listed in table 4.1. Results are presented in table 4.2 and graphically in both chapter 4 and appendix A. Accordingly with our power analysis, we can conclude that 10 petri dishes, 5 seeds per dish seem to be enough observations to detect large shifts in the frequencies per category, but not to identify

51

moderate movements. Regarding the impact of these findings on our case study's conclusions, it is important to point out that although we found that most products did effectively slow the pathogen infection, the sample size is potentially too small to detect more subtle differences. Thus, products that look equally effective in this experiment may be indeed much more different in their potential to control *Pythium* damping-off in soybean. The results of this study suggest that similar experiments to the one herein described would need to increase the sample size or modify the experiment structure to be able to detect treatment effects, thereby measure the potential effect of the petri dish.

The results of the study encourage testing of alternative approaches to modeling the low frequency data, for example, Bayesian Hierarchical Models or a Bootstrap approach, which could lead to more sound conclusions. Another aspect to consider in this situation is the exploration of how many observations are needed to estimate  $\sigma_D^2$  properly and whether or not the physical limitations would make the task impractical.

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# **Appendix A - Power Analysis Plots**

The figures present here display the estimated power to detect the difference between two hypothetical expected means. We plot the computed power for each of the 1000 simulated data sets for three combinations of petri dish and seeds per dish sample sizes, and using either a fixed model or a mixed model with variance 0.01, or 0.1. The fixed model assumed the petri dish effect was zero. The mixed model assumed the petri dish effect was random and followed a Gaussian distribution with variance 0.01 or 0.1. The simulation and computational details are presented in Chapter 4. The SAS code used for the simulation can be found in Appendix C.



Figure A.1 Power to detect a difference between Control and Experiment 1 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.2 Power to detect a difference between Control and Experiment 2 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.3 Power to detect a difference between Control and Experiment 3 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.4 Power to detect a difference between Control and Experiment 4 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.5 Power to detect a difference between Control and Experiment 5 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.6 Power to detect a difference between Control and Experiment 6 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.7 Power to detect a difference between Experiments 1 and 2 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.8 Power to detect a difference between Experiments 1 and 3 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.9 Power to detect a difference between Experiments 1 and 4 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.10 Power to detect a difference between Experiments 1 and 5 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.11 Power to detect a difference between Experiments 1 and 6 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).


Figure A.12 Power to detect a difference between Experiments 2 and 3 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.13 Power to detect a difference between Experiments 2 and 4 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.14 Power to detect a difference between Experiments 2 and 5 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.15 Power to detect a difference between Experiments 2 and 6 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.16 Power to detect a difference between Experiments 3 and 4 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.17 Power to detect a difference between Experiments 3 and 5 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.18 Power to detect a difference between Experiments 3 and 6 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.19 Power to detect a difference between Experiments 4 and 5 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.20 Power to detect a difference between Experiments 4 and 6 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).



Figure A.21 Power to detect a difference between Experiments 5 and 6 (defined in Table 4.1). Simulation average power is marked (dotted line). Three combinations of petri dish and seeds per dish sample sizes (columns) were simulated a thousand times. Power was calculated under fixed model or a mixed model with variances 0.01 or 0.1 (rows).

## **Appendix B - SAS Code Data Analysis**

/\* We refer to the Control treatment here as Testigo\*/ /\* EXP and Odds ratio options give the same results in Estimate statement \*/ PROC TABULATE DATA=allpredictors; CLASS treatment Day Fungus Dish Severity; TABLE Fungus\*Treatment\*Dish, Day\*Severity; RUN; proc glimmix data=allpredictors method = laplace; class treatment Day Severity Fungus Dish; model Severity=Treatment|Day|Fungus / solution ; random Dish(Treatment Fungus); run; proc sort data=allpredictors out=allpredictorsDay; by day; run; title 'Interaction Effects Mixed Model by Day'; proc glimmix data=allpredictorsDay method=Laplace; by Day; class treatment Day Severity Fungus Dish; model Severity=Treatment Fungus Treatment\*Fungus / solution oddsratio; random intercept / subject=dish(treatment Fungus); run; data Day5; set allpredictors; if Day=5; run; proc sort data=day5; by Fungus;run; data Day21; set allpredictors; if Day=21; run; proc sort data=day21; by Fungus;run;

```
proc glimmix data=Day5 method=Laplace;
by Fungus;
class treatment Severity Fungus Dish;
model Severity=Treatment / solution oddsratio;
random intercept / subject=dish(treatment);
run:
title 'Interaction Effects Mixed Model Day21 by Fungus';
proc glimmix data=Day21 method=Laplace;
by Fungus;
class treatment Severity Fungus Dish;
model Severity=Treatment / solution oddsratio;
random intercept / subject=dish(treatment);
run:
proc sort data=allpredictors out=allpredictorsFUNGUS; by Fungus; run;
proc glimmix data=allpredictorsFungus method=Laplace;
by Fungus;
class treatment Day Severity Fungus Dish;
model Severity=Treatment Day Treatment*Day / solution oddsratio;
random intercept / subject=dish(treatment);
run;
data Apha;
set allpredictors;
if Fungus='Apha';
run;
proc sort data=Apha; by day; run;
data Ultimun;
set allpredictors;
if Fungus='U';
run;
proc sort data=Ultimun; by day; run;
data Irregulare;
```

set allpredictors; if Fungus='I'; run; proc sort data=Irregulare; by day; run; proc glimmix data=Apha method=Laplace; by Day; class treatment Severity Fungus Dish; model Severity=Treatment / solution oddsratio; random intercept / subject=dish(treatment); run; proc glimmix data=Ultimun method=Laplace; by Day; class treatment Severity Fungus Dish; model Severity=Treatment / solution oddsratio; random intercept / subject=dish(treatment); run; proc glimmix data=Irregulare method=Laplace; by Day; class treatment Severity Fungus Dish; model Severity=Treatment / solution oddsratio; random intercept / subject=dish(treatment); run; data allNoTestigo; set allpredictors; if treatment="Testigo" then delete; run: proc glimmix data=allNoTestigo method = laplace; class treatment Day Severity Fungus Dish; model Severity=Treatment|Day|Fungus / solution; random Dish(Treatment Fungus); run;

data MnPhi200ToZMnPhi200; set allpredictors; if treatment="MnPhi 200" then treatment="ZMnPhi 200"; run; proc sort data=MnPhi200ToZMnPhi200 out=allpredictorsDay; by day; run; proc glimmix data=allpredictorsDay method=Laplace; by Day; class treatment Day Severity Fungus Dish; model Severity=Treatment Fungus Treatment\*Fungus / solution oddsratio ; random intercept / subject=dish(treatment Fungus); ESTIMATE 'Kphi 200 vs. Kphi 400 at Aphanidermatum' Treatment 1 -1 0 0 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs Maxim 100 at Aphanidermatum' Treatment 1 0 -1 0 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Aphanidermatum' Treatment 1 0 0 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs MnPhi 400 at Aphanidermatum' Treatment 1 0 0 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs Testigo at Aphanidermatum' Treatment 1 0 0 0 0 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Aphanidermatum' Treatment 1 0 0 0 0 0 -1 alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs Maxim 100 at Aphanidermatum' Treatment 0 1 -1 0 0 0 0 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Aphanidermatum' Treatment 0 1 0 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs MnPhi 400 at Aphanidermatum' Treatment 0 1 0 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs Testigo at Aphanidermatum' Treatment 0 1 0 0 0 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Aphanidermatum' Treatment 0 1 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Aphanidermatum' Treatment 0 0 1 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs MnPhi 400 at Aphanidermatum' Treatment 0 0 1 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs Testigo at Aphanidermatum' Treatment 0 0 1 0 0 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Aphanidermatum' Treatment 0 0 1 0 0 0 -1 Treatment\*Fungus 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Aphanidermatum' Treatment 0 0 0 1 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Aphanidermatum' Treatment 0 0 0 1 0 -1 0 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Aphanidermatum' Treatment 0 0 0 1 0 0 - 1

```
Treatment*Fungus 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo at Aphanidermatum' Treatment 0 0 0 0 1 -1 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Aphanidermatum' Treatment 0 0 0 0 1 0 -1
                /oddsratio alpha=0.00238 cl;
ESTIMATE 'Testigo vs ZMnPhi 200 at Aphanidermatum' Treatment 0 0 0 0 0 1 -1
                /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Kphi 400 at Irregular' Treatment 1 -1 0 0 0 0 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Maxim 100 at Irregular' Treatment 1 0 -1 0 0 0 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at at Irregular' Treatment 1 0 0 -1 0 0 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 400 at Irregular' Treatment 1 0 0 0 -1 0 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Testigo at Irregular' Treatment 1 0 0 0 0 -1 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Irregular' Treatment 1 0 0 0 0 0 -1
```

alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Maxim 100 at Irregular' Treatment 0 1 -1 0 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Irregular' Treatment 0 1 0 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs MnPhi 400 at Irregular' Treatment 0 1 0 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs Testigo at Irregular' Treatment 0 1 0 0 0 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Irregular' Treatment 0 1 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Irregular' Treatment 0 0 1 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs MnPhi 400 at Irregular' Treatment 0 0 1 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs Testigo at Irregular' Treatment 0 0 1 0 0 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Irregular' Treatment 0 0 1 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Irregular' Treatment 0 0 0 1 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Irregular' Treatment 0 0 0 1 0 -1 0

/oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Irregular' Treatment 0 0 0 1 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 400 vs Testigo at Irregular' Treatment 0 0 0 0 1 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Irregular' Treatment 0 0 0 0 1 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Testigo vs ZMnPhi 200 at Irregular' Treatment 0 0 0 0 0 1 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs. Kphi 400 at Ultimun' Treatment 1 -1 0 0 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs Maxim 100 at Ultimun' Treatment 1 0 -1 0 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Ultimun' Treatment 1 0 0 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs MnPhi 400 at Ultimun' Treatment 1 0 0 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs Testigo at Ultimun' Treatment 1 0 0 0 0 -1 0 Treatment\*Fungus 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Ultimun' Treatment 1 0 0 0 0 0 -1

Treatment*Fungus 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Maxim 100 at Ultimun' Treatment 0 1 -1 0 0 0 0
Treatment*Fungus 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Ultimun' Treatment 0 1 0 -1 0 0 0
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/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 400 at Ultimun' Treatment 0 1 0 0 -1 0 0
Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Testigo at Ultimun' Treatment 0 1 0 0 0 -1 0
Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Ultimun' Treatment 0 1 0 0 0 0 -1
Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Ultimun' Treatment 0 0 1 -1 0 0 0
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ESTIMATE 'Maxim 100 vs Testigo at Ultimun' Treatment 0 0 1 0 0 -1 0
Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0 0
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ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Ultimun' Treatment 0 0 1 0 0 0 -1
Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Ultimun' Treatment 0 0 0 1 -1 0 0

```
/oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Ultimun' Treatment 0 0 0 1 0 -1 0
                   Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Ultimun' Treatment 0 0 0 1 0 0 -1
                   /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo at Ultimun' Treatment 0 0 0 0 1 -1 0
                   /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Ultimun' Treatment 0 0 0 0 1 0 -1
                   /oddsratio alpha=0.00238 cl;
ESTIMATE 'Testigo vs ZMnPhi 200 at Ultimun' Treatment 0 0 0 0 0 1 -1
                   /oddsratio alpha=0.00238 cl;
run:
proc sort data=MnPhi200ToZMnPhi200 out=allpredictorsFUNGUS; by Fungus; run;
proc glimmix data=allpredictorsFungus method=Laplace;
by Fungus;
class treatment Day Severity Fungus Dish;
model Severity=Treatment Day Treatment*Day / solution oddsratio;
random intercept / subject=dish(treatment);
ESTIMATE 'Kphi 200 vs. Kphi 400 at Day5' Treatment 1 -1 0 0 0 0 0
                   Treatment*Day 1 0 -1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 /oddsratio alpha=0.00238
cl:
ESTIMATE 'Kphi 200 vs Maxim 100 at Day5' Treatment 1 0 -1 0 0 0 0
                   cl:
```

```
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Day5' Treatment 1 0 0 -1 0 0 0
```

ESTIMATE 'Maxim 100 vs Testigo at Day5' Treatment 0 0 1 0 0 -1 0
Treatment*Day 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Day5' Treatment 0 0 1 0 0 0 -1
Treatment*Day 0 0 0 0 1 0 0 0 0 0 0 -1 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Day5' Treatment 0 0 0 1 -1 0 0
Treatment*Day 0 0 0 0 0 0 1 0 -1 0 0 0 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Day5' Treatment 0 0 0 1 0 -1 0
Treatment*Day 0 0 0 0 0 0 1 0 0 0 -1 0 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Day5' Treatment 0 0 0 1 0 0 -1
Treatment*Day 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'MnPhi 400 vs Testigo at Day5' Treatment 0 0 0 0 1 -1 0
Treatment*Day 0 0 0 0 0 0 0 0 1 0 -1 0 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Day5' Treatment 0 0 0 0 1 0 -1
Treatment*Day 0 0 0 0 0 0 0 0 1 0 0 0 -1 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Testigo vs ZMnPhi 200 at Day5' Treatment 0 0 0 0 0 1 -1
Treatment*Day 0 0 0 0 0 0 0 0 0 1 0 -1 0 /oddsratio
alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs. Kphi 400 at Day21' Treatment 1 -1 0 0 0 0 0
Treatment*Day 0 1 0 -1 0 0 0 0 0 0 0 0 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Kphi 200 vs Maxim 100 at Day21' Treatment 1 0 -1 0 0 0 0
Treatment*Day 0 1 0 0 0 -1 0 0 0 0 0 0 0 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Day21' Treatment 1 0 0 -1 0 0 0

ESTIMATE 'Maxim 100 vs Testigo at Day21' Treatment 0 0 1 0 0 -1 0 Treatment\*Day 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Day21' Treatment 0 0 1 0 0 0 -1 Treatment\*Day 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl: ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Day21' Treatment 0 0 0 1 -1 0 0 Treatment\*Day 0 0 0 0 0 0 0 1 0 -1 0 0 0 0 /oddsratio alpha=0.00238 cl: ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Day21' Treatment 0 0 0 1 0 -1 0 Treatment\*Day 0 0 0 0 0 0 0 1 0 0 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Day21' Treatment 0 0 0 1 0 0 -1 Treatment\*Day 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 400 vs Testigo at Day21' Treatment 0 0 0 0 1 -1 0 Treatment\*Day 0 0 0 0 0 0 0 0 0 1 0 -1 0 0 /oddsratio alpha=0.00238 cl: ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Day21' Treatment 0 0 0 0 1 0 -1 Treatment\*Day 0 0 0 0 0 0 0 0 0 0 1 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Testigo vs ZMnPhi 200 at Day21' Treatment 0 0 0 0 0 1 -1 Treatment\*Day 0 0 0 0 0 0 0 0 0 0 0 1 0 -1 /oddsratio alpha=0.00238 cl; run; proc sort data=MnPhi200ToZMnPhi200 out=allpredictorsDay; by day; run; title 'Fixed effect model BY DAY': proc glimmix data=allpredictorsDay method=Laplace; by Day; class treatment Day Severity Fungus Dish; model Severity=Treatment Fungus Treatment\*Fungus / solution oddsratio;

ESTIMATE 'Kphi 200 vs. Kphi 400 at Aphanidermatum' Treatment 1 -1 0 0 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs Maxim 100 at Aphanidermatum' Treatment 1 0 -1 0 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Aphanidermatum' Treatment 1 0 0 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs MnPhi 400 at Aphanidermatum' Treatment 1 0 0 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs Testigo at Aphanidermatum' Treatment 1 0 0 0 0 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Aphanidermatum' Treatment 1 0 0 0 0 0 -1 alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs Maxim 100 at Aphanidermatum' Treatment 0 1 -1 0 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Aphanidermatum' Treatment 0 1 0 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs MnPhi 400 at Aphanidermatum' Treatment 0 1 0 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs Testigo at Aphanidermatum' Treatment 0 1 0 0 0 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Aphanidermatum' Treatment 0 1 0 0 0 0 -1

```
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Aphanidermatum' Treatment 0 0 1 -1 0 0 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 400 at Aphanidermatum' Treatment 0 0 1 0 -1 0 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs Testigo at Aphanidermatum' Treatment 0 0 1 0 0 -1 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Aphanidermatum' Treatment 0 0 1 0 0 0 -1
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Aphanidermatum' Treatment 0 0 0 1 -1 0 0
                 alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Aphanidermatum' Treatment 0 0 0 1 0 -1 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Aphanidermatum' Treatment 0 0 0 1 0 0 -
1
                 Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo at Aphanidermatum' Treatment 0 0 0 0 1 -1 0
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Aphanidermatum' Treatment 0 0 0 0 1 0 -1
                 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Testigo vs ZMnPhi 200 at Aphanidermatum' Treatment 0 0 0 0 0 1 -1
```

Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Kphi 400 at Irregular' Treatment 1 -1 0 0 0 0 0
Treatment*Fungus 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Maxim 100 at Irregular' Treatment 1 0 -1 0 0 0 0
Treatment*Fungus 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Irregular' Treatment 1 0 0 -1 0 0 0
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 -1 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 400 at Irregular' Treatment 1 0 0 0 -1 0 0
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 -1 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Testigo at Irregular' Treatment 1 0 0 0 0 -1 0
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Irregular' Treatment 1 0 0 0 0 0 -1
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Maxim 100 at Irregular' Treatment 0 1 -1 0 0 0 0
Treatment*Fungus 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Irregular' Treatment 0 1 0 -1 0 0 0
Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 400 at Irregular' Treatment 0 1 0 0 -1 0 0
Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Testigo at Irregular' Treatment 0 1 0 0 0 -1 0

/oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Irregular' Treatment 0 1 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Irregular' Treatment 0 0 1 -1 0 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs MnPhi 400 at Irregular' Treatment 0 0 1 0 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs Testigo at Irregular' Treatment 0 0 1 0 0 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Irregular' Treatment 0 0 1 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Irregular' Treatment 0 0 0 1 -1 0 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Irregular' Treatment 0 0 0 1 0 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Irregular' Treatment 0 0 0 1 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 400 vs Testigo at Irregular' Treatment 0 0 0 0 1 -1 0 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Irregular' Treatment 0 0 0 0 1 0 -1

Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 -1 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Testigo vs ZMnPhi 200 at Irregular' Treatment 0 0 0 0 0 1 -1
Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Kphi 400 at Ultimun' Treatment 1 -1 0 0 0 0 0
Treatment*Fungus 0 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Maxim 100 at Ultimun' Treatment 1 0 -1 0 0 0 0
Treatment*Fungus 0 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Ultimun' Treatment 1 0 0 -1 0 0 0
Treatment*Fungus 0 0 1 0 0 0 0 0 0 0 0 -1 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 400 at Ultimun' Treatment 1 0 0 0 -1 0 0
Treatment*Fungus 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Testigo at Ultimun' Treatment 1 0 0 0 0 -1 0
Treatment*Fungus 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Ultimun' Treatment 1 0 0 0 0 0 -1
Treatment*Fungus 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Maxim 100 at Ultimun' Treatment 0 1 -1 0 0 0 0
Treatment*Fungus 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Ultimun' Treatment 0 1 0 -1 0 0 0
Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 400 at Ultimun' Treatment 0 1 0 0 -1 0 0

Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Testigo at Ultimun' Treatment 0 1 0 0 0 -1 0
Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Ultimun' Treatment 0 1 0 0 0 0 -1
Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Ultimun' Treatment 0 0 1 -1 0 0 0
Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 400 at Ultimun' Treatment 0 0 1 0 -1 0 0
Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs Testigo at Ultimun' Treatment 0 0 1 0 0 -1 0
Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Ultimun' Treatment 0 0 1 0 0 0 -1
Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Ultimun' Treatment 0 0 0 1 -1 0 0
Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Ultimun' Treatment 0 0 0 1 0 -1 0
Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Ultimun' Treatment 0 0 0 1 0 0 -1
Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo at Ultimun' Treatment 0 0 0 0 1 -1 0

```
Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Ultimun' Treatment 0 0 0 0 1 0 -1
                         Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Testigo vs ZMnPhi 200 at Ultimun' Treatment 0 0 0 0 0 1 -1
                         /oddsratio alpha=0.00238 cl;
run;
proc sort data=MnPhi200ToZMnPhi200 out=allpredictorsFUNGUS; by Fungus; run;
proc glimmix data=allpredictorsFungus method=Laplace;
by Fungus;
class treatment Day Severity Fungus Dish;
model Severity=Treatment Day Treatment*Day / solution oddsratio;
ESTIMATE 'Kphi 200 vs. Kphi 400 at Day5' Treatment 1 -1 0 0 0 0 0
                         Treatment*Day 1 0 -1 0 0 0 0 0 0 0 0 0 0 0 0 0 /oddsratio alpha=0.00238
cl:
ESTIMATE 'Kphi 200 vs Maxim 100 at Day5' Treatment 1 0 -1 0 0 0 0
                         Treatment*Day 1 0 0 0 -1 0 0 0 0 0 0 0 0 0 0 0 0/oddsratio alpha=0.00238
cl;
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Day5' Treatment 1 0 0 -1 0 0 0
                         Treatment*Day 1 0 0 0 0 0 -1 0 0 0 0 0 0 0 0 0/oddsratio alpha=0.00238
cl;
ESTIMATE 'Kphi 200 vs MnPhi 400 at Day5' Treatment 1 0 0 0 -1 0 0
                         Treatment*Day 1 0 0 0 0 0 0 0 -1 0 0 0 0 0 0 /oddsratio alpha=0.00238
cl:
ESTIMATE 'Kphi 200 vs Testigo at Day5' Treatment 1 0 0 0 0 -1 0
                         Treatment*Day 1 0 0 0 0 0 0 0 0 0 -1 0 0 0/oddsratio alpha=0.00238
cl;
ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Day5' Treatment 1 0 0 0 0 0 -1
```

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86
```

Treatment*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Maxim 100 at Day21' Treatment 0 1 -1 0 0 0 0
Treatment*Day 0 0 0 1 0 -1 0 0 0 0 0 0 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Day21' Treatment 0 1 0 -1 0 0 0
Treatment*Day 0 0 0 1 0 0 0 -1 0 0 0 0 0 0 /oddsratio
alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 400 at Day21' Treatment 0 1 0 0 -1 0 0
Treatment*Day 0 0 0 1 0 0 0 0 0 -1 0 0 0 0 /oddsratio
alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Testigo at Day21' Treatment 0 1 0 0 0 -1 0
Treatment*Day 0 0 0 1 0 0 0 0 0 0 0 -1 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Day21' Treatment 0 1 0 0 0 0 -1
Treatment*Day 0 0 0 1 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Day21' Treatment 0 0 1 -1 0 0 0
Treatment*Day 0 0 0 0 0 1 0 -1 0 0 0 0 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Maxim 100 vs MnPhi 400 at Day21' Treatment 0 0 1 0 -1 0 0
Treatment*Day 0 0 0 0 0 1 0 0 0 -1 0 0 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Maxim 100 vs Testigo at Day21' Treatment 0 0 1 0 0 -1 0
Treatment*Day 0 0 0 0 0 1 0 0 0 0 -1 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Day21' Treatment 0 0 1 0 0 0 -1
Treatment*Day 0 0 0 0 1 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238
cl;
ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Dav21' Treatment 0 0 0 1 -1 0 0
Treatment*Day 0 0 0 0 0 0 0 1 0 -1 0 0 0 0 /oddsratio alpha=0.00238
cl;

```
ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Day21' Treatment 0 0 0 1 0 -1 0
                       Treatment*Day 0 0 0 0 0 0 0 1 0 0 0 -1 0 0 /oddsratio alpha=0.00238
cl;
ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Day21' Treatment 0 0 0 1 0 0 -1
                       Treatment*Day 0 0 0 0 0 0 0 1 0 0 0 0 -1 /oddsratio
alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo at Day21' Treatment 0 0 0 0 1 -1 0
                       Treatment*Day 0 0 0 0 0 0 0 0 0 1 0 -1 0 0 /oddsratio alpha=0.00238
cl:
ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Day21' Treatment 0 0 0 0 1 0 -1
                       Treatment*Day 0 0 0 0 0 0 0 0 0 0 1 0 0 0 -1 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Testigo vs ZMnPhi 200 at Day21' Treatment 0 0 0 0 0 1 -1
                       Treatment*Day 0 0 0 0 0 0 0 0 0 0 0 1 0 -1 /oddsratio alpha=0.00238
cl:
run;
proc glimmix data=MnPhi200ToZMnPhi200 method = laplace;
class treatment Day Severity Fungus Dish;
model Severity=Treatment|Day|Fungus / solution ;
ESTIMATE 'Kphi 200 vs Kphi 400 at Aphanidermatum at Day 5' Treatment 1 -1 0 0 0 0 0
                   Treatment*Day 1 0 -1 0 0 0 0 0 0 0 0 0 0 0 0
                       Treatment*Fungus*Day 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Max 100 at Aphanidermatum at Day 5' Treatment 1 0 -1 0 0 0 0
                   Treatment*Day 1 0 0 0 -1 0 0 0 0 0 0 0 0 0 0
                       Treatment*Fungus*Day 1000000000000-1 /oddsratio
alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Aphanidermatum at Day 5' Treatment 1 0 0 -
1
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Treatment\*Fungus 1 0 0 0 0 0 0 0 0 -1

Treatment\*Day 1 0 0 0 0 0 -1

## Treatment\*Fungus\*Day 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs MnPhi 400 at Aphanidermatum at Day 5' Treatment 1 0 0 0 -1

Treatment\*Fungus 1 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 1 0 0 0 0 0 0 0 -1

-1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs at Testigo at Day 5' Treatment 1 0 0 0 0 -1

Treatment\*Fungus 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 1 0 0 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs at ZMnPhi 200 at Day 5' Treatment 1 0 0 0 0 0 -1

Treatment\*Day 1 0 0 0 0 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Max 100 at Aphanidermatum at Day 5' Treatment 0 1 -1 0 0 0 0

Treatment\*Fungus 000100-1

Treatment\*Day 0 0 1 0 -1

Treatment\*Fungus\*Day 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio

alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Aphanidermatum at Day 5' Treatment 0 1 0 - 1 0 0 0

Treatment\*Fungus 0 0 0 1 0 0 0 0 0 -1

Treatment\*Day 0 0 1 0 0 0 -1

Treatment\*Fungus\*Day 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 400 at Aphanidermatum at Day 5' Treatment 0 1 0 0 -1 0 0

```
Treatment*Fungus 0 0 0 1 0 0 0 0 0 0 0 0 -1
```

Treatment\*Day 0 0 1 0 0 0 0 0 -1

## 

-1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Testigo at Aphanidermatum at Day 5' Treatment 0 1 0 0 0 -1 0

Treatment\*Fungus 0 0 0 1 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 0 0 1 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Aphanidermatum at Day 5' Treatment 0 1 0 0 0 0 -1 Treatment\*Fungus 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 0 0 1 0 0 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Aphanidermatum at Day 5' Treatment 0 0 1 -1 0 0 0

Treatment\*Day 0 0 0 0 1 0 -1

Treatment\*Fungus\*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 400 at Aphanidermatum at Day 5' Treatment 0 0 1 0 -1 0 0

Treatment\*Day 0 0 0 0 1 0 0 0 -1

-1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs Testigo at Aphanidermatum at Day 5' Treatment 0 0 1 0 0 -1 0

Treatment\*Day 0 0 0 0 1 0 0 0 0 0 -1

0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Aphanidermatum at Day 5' Treatment 0 0 1 0 0 0 -1

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Treatment*Fungus 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 0 0
                Treatment*Day 0 0 0 0 1 0 0 0 0 0 0 -1
                0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Aphanidermatum at Day 5' Treatment 0 0 0
1 -1 0 0
                Treatment*Day 0 0 0 0 0 0 1 0 -1
                -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Aphanidermatum at Day 5' Treatment 0 0 0 1 0
-10
                Treatment*Day 0 0 0 0 0 0 1 0 0 0 -1
                0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Aphanidermatum at Day 5' Treatment 0 0
0100-1
                Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0
                Treatment*Day 0 0 0 0 0 0 1 0 0 0 0 0 -1
                0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo at Aphanidermatum at Day 5' Treatment 0 0 0 0 1 -1 0
                Treatment*Day 0 0 0 0 0 0 0 0 1 0 -1
                1 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Aphanidermatum at Day 5' Treatment 0 0 0 0 1 0 -1
                Treatment*Day 0 0 0 0 0 0 0 0 0 1 0 0 0 -1
```

Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
1 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Testigo vs ZMnPhi 200 at Aphanidermatum at Day 5' Treatment 0 0 0 0 0 1 -1
Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Treatment*Day 0 0 0 0 0 0 0 0 0 0 1 0 -1
Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 1 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Kphi 400 at Irregular at Day 5' Treatment 1 -1 0 0 0 0 0
Treatment*Fungus 0 1 0 0 -1
Treatment*Day 1 0 -1
Treatment*Fungus*Day 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238
cl;
ESTIMATE 'Kphi 200 vs Maxim 100 at Irregular at Day 5' Treatment 1 0 -1 0 0 0 0
Treatment*Fungus 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0 0 0 0 0
Treatment*Day 1 0 0 0 -1
Treatment*Fungus*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio
alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at at Irregular at Day 5' Treatment 1 0 0 -1 0 0 0
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 -1 0 0 0 0 0 0 0 0
Treatment*Day 1 0 0 0 0 0 -1
Treatment*Fungus*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 400 at Irregular at Day 5' Treatment 1 0 0 0 -1 0 0
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 -1 0 0 0 0
Treatment*Day 1 0 0 0 0 0 0 0 -1
Treatment*Fungus*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Testigo at Irregular at Day 5' Treatment 1 0 0 0 0 -1 0
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Treatment*Day 1 0 0 0 0 0 0 0 0 0 -1

000000-1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Irregular at Day 5' Treatment 1 0 0 0 0 0 -1 Treatment\*Day 1 0 0 0 0 0 0 0 0 0 0 0 -1 0000000000000-1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs Maxim 100 at Irregular at Day 5' Treatment 0 1 -1 0 0 0 0 Treatment\*Day 0 0 1 0 -1 Treatment\*Fungus\*Day 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Irregular at Day 5' Treatment 0 1 0 -1 0 0 0 Treatment\*Day 0 0 1 0 0 0 -1 Treatment\*Fungus\*Day 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs MnPhi 400 at Irregular at Day 5' Treatment 0 1 0 0 -1 0 0 Treatment\*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 -1 Treatment\*Day 0 0 1 0 0 0 0 0 -1 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs Testigo at Irregular at Day 5' Treatment 0 1 0 0 0 -1 0 Treatment\*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 -1 Treatment\*Day 0 0 1 0 0 0 0 0 0 0 -1 000000-1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Irregular at Day 5' Treatment 0 1 0 0 0 0 -1 Treatment\*Day 0 0 1 0 0 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

Treatment\*Fungus\*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

Treatment\*Day 0 0 0 0 1 0 0 0 -1

0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs Testigo at Irregular at Day 5' Treatment 0 0 1 0 0 -1 0

Treatment\*Day 0 0 0 0 1 0 0 0 0 0 -1

0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Irregular at Day 5' Treatment 0 0 1 0 0 0 -1

Treatment\*Day 0 0 0 0 1 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

0 -1 /oddsratio alpha=0.00238 cl;
0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Irregular at Day 5' Treatment 0 0 0 1 0 0 - 1

Treatment\*Day 0 0 0 0 0 0 1 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 400 vs Testigo at Irregular at Day 5' Treatment 0 0 0 0 1 -1 0

Treatment\*Day 0 0 0 0 0 0 0 0 1 0 -1

0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Irregular at Day 5' Treatment 0 0 0 0 1 0 -1

Treatment\*Day 0 0 0 0 0 0 0 0 0 1 0 0 0 -1

0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Testigo vs ZMnPhi 200 at Irregular at Day 5' Treatment 0 0 0 0 0 1 -1

Treatment\*Day 0 0 0 0 0 0 0 0 0 0 1 0 -1

0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs. Kphi 400 at Ultimun at Day5' Treatment 1 -1 0 0 0 0 0

Treatment\*Day 1 0 -1

Treatment\*Fungus\*Day 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238

cl;

```
Treatment*Fungus*Day 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio
alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Ultimun at Day5' Treatment 1 0 0 -1 0 0 0
               Treatment*Day 1 0 0 0 0 0 -1
                /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 400 at Ultimun at Day5' Treatment 1 0 0 0 -1 0 0
               Treatment*Day 1 0 0 0 0 0 0 0 -1
               0.0 - 1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Testigo at Ultimun at Day5' Treatment 1 0 0 0 0 -1 0
               Treatment*Day 1 0 0 0 0 0 0 0 0 0 -1
               0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Ultimun at Day5' Treatment 1 0 0 0 0 0 -1
             Treatment*Day 1 0 0 0 0 0 0 0 0 0 0 0 -1
               000000000000000-1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Maxim 100 at Ultimun at Day5' Treatment 0 1 -1 0 0 0 0
               Treatment*Day 0010-1
                Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio
alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Ultimun at Day5' Treatment 0 1 0 -1 0 0 0
               Treatment*Day 001000-1
```

Treatment*Fungus*Day 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 400 at Ultimun at Day5' Treatment 0 1 0 0 -1 0 0
Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 -1 0 0 0 0
Treatment*Day 0010000-1
Treatment*Fungus*Day 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Testigo at Ultimun at Day5' Treatment 0 1 0 0 0 -1 0
Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
Treatment*Day 001000000-1
Treatment*Fungus*Day 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Ultimun at Day5' Treatment 0 1 0 0 0 0 -1
Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Treatment*Day 00100000000-1
Treatment*Fungus*Day 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Ultimun at Day5' Treatment 0 0 1 -1 0 0 0
Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0
Treatment*Day 000010-1
Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 -1
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 400 at Ultimun at Day5' Treatment 0 0 1 0 -1 0 0
Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0
Treatment*Day 00001000-1
Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs Testigo at Ultimun at Day5' Treatment 0 0 1 0 0 -1 0
Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0 0
Treatment*Day 000010000-1

0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Ultimun at Day5' Treatment 0 0 1 0 0 0 -1

Treatment\*Day 00001000000-1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Ultimun at Day5' Treatment 0 0 0 1 0 -1 0

Treatment\*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0

Treatment\*Day 0000001000-1

0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

Treatment\*Day 000000100000-1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 400 vs Testigo at Ultimun at Day5' Treatment 0 0 0 0 1 -1 0

Treatment\*Day 0000000010-1

0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Ultimun at Day5' Treatment 0 0 0 0 1 0 -1

Treatment\*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1

Treatment\*Day 0000000001000-1

0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Testigo vs ZMnPhi 200 at Ultimun at Day5' Treatment 0 0 0 0 0 1 -1

Treatment\*Day 0000000000010-1

0 0 0 0 0 0 0 1 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

Treatment\*Day 0 1 0 -1

Treatment\*Fungus\*Day 0 0 0 1 0 0 0 0 0 -1 /oddsratio

alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Max 100 at Aphanidermatum at Day 21' Treatment 1 0 -1 0 0 0 0

Treatment\*Fungus 1 0 0 0 0 0 -1

Treatment\*Day 0 1 0 0 0 -1

Treatment\*Fungus\*Day 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio

alpha=0.00238 cl;

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ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Aphanidermatum at Day 21' Treatment 1 0 0 -1
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Treatment\*Fungus 1 0 0 0 0 0 0 0 0 -1 Treatment\*Day 0 1 0 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs MnPhi 400 at Aphanidermatum at Day 21' Treatment 1 0 0 0 -1

Treatment\*Fungus 1 0 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 0 1 0 0 0 0 0 0 0 -1

ESTIMATE 'Kphi 200 vs at Testigo at Aphanidermatum at Day 21' Treatment 1 0 0 0 0 -1

Treatment\*Fungus 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 0 1 0 0 0 0 0 0 0 0 0 -1

 $0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ -1$  /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs at ZMnPhi 200 at Aphanidermatum Day 21' Treatment 1 0 0 0 0 0 -1

Treatment\*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Max 100 at Aphanidermatum at Day 21' Treatment 0 1 -1 0 0 0 0 Treatment\*Fungus 0 0 0 1 0 0 -1

Treatment\*Day 0 0 0 1 0 -1

Treatment\*Fungus\*Day 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio

alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Aphanidermatum at Day 21' Treatment 0 1 0

-1000

Treatment\*Fungus 0 0 0 1 0 0 0 0 0 -1

Treatment\*Day 0001000-1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 400 at Aphanidermatum at Day 21' Treatment 0 1 0 0 -1 0 0

Treatment\*Fungus 0 0 0 1 0 0 0 0 0 0 0 -1

Treatment\*Day 0 0 0 1 0 0 0 0 0 -1

0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Testigo at Aphanidermatum at Day 21' Treatment 0 1 0 0 0 -1 0

Treatment\*Fungus 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 0 0 0 1 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Aphanidermatum at Day 21' Treatment 0 1 0 0 0 0 -1

Treatment\*Day 0 0 0 1 0 0 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Aphanidermatum at Day 21' Treatment 0 0 1 -1 0 0 0

Treatment\*Fungus\*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 400 at Aphanidermatum at Day 21' Treatment 0 0 1 0 -1 0 0

Treatment\*Day 0 0 0 0 0 1 0 0 0 -1

0 0 0 -1 /oddsratio alpha=0.00238 cl;

Treatment\*Day 0 0 0 0 0 1 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Aphanidermatum at Day 21' Treatment 0 0 1 0 0 0 - 1

Treatment\*Day 0 0 0 0 0 1 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Aphanidermatum at Day 21' Treatment 0 0 0 1 -1 0 0

Treatment\*Day 0 0 0 0 0 0 0 1 0 -1

0 0 0 -1/oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Aphanidermatum at Day 21' Treatment 0 0 0 1 0 -1 0

0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Aphanidermatum at Day 21' Treatment 0 0 0 1 0 0 -1

Treatment\*Day 0 0 0 0 0 0 0 1 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 400 vs Testigo at Aphanidermatum at Day 21' Treatment 0 0 0 0 1 -1 0

Treatment\*Day 0 0 0 0 0 0 0 0 0 1 0 -1

0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Aphanidermatum at Day 21' Treatment 0 0 0 0 1 0 - 1

Treatment\*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 Treatment\*Day 0 0 0 0 0 0 0 0 0 1 0 0 0 -1

0 0 0 1 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Testigo vs ZMnPhi 200 at Aphanidermatum at Day 21' Treatment 0 0 0 0 0 1 -1

Treatment\*Day 0 0 0 0 0 0 0 0 0 0 0 1 0 -1

000000000100000-1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Kphi 400 at Irregular at Day 21' Treatment 1 -1 0 0 0 0 0

Treatment\*Fungus 0 1 0 0 -1

Treatment\*Day 0 1 0 -1

Tre	atment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio
alpha=0.00238 cl;	
ESTIMATE 'Kphi 200 vs Max	xim 100 at Irregular at Day 21' Treatment 1 0 -1 0 0 0 0
Tre	atment*Fungus 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0 0 0 0 0
Tre	atment*Day 0 1 0 0 0 -1
Tre	atment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio
alpha=0.00238 cl;	
ESTIMATE 'Kphi 200 vs Mnl	Phi 200 + Maxim at at Irregular at Day 21' Treatment 1 0 0 -1 0 0
0	
Tre	atment*Fungus 0 1 0 0 0 0 0 0 0 0 -1 0 0 0 0 0 0 0 0
Tre	atment*Day 0 1 0 0 0 0 0 -1
Tre	atment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;	
ESTIMATE 'Kphi 200 vs Mnl	Phi 400 at Irregular at Day 21' Treatment 1 0 0 0 -1 0 0
Tre	atment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 -1 0 0 0 0
Tre	eatment*Day 0 1 0 0 0 0 0 0 0 0 -1
Tre	eatment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 -1 /oddsratio alpha=0.0	00238 cl;
ESTIMATE 'Kphi 200 vs Test	tigo at Irregular at Day 21' Treatment 1 0 0 0 0 -1 0
Tre	atment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 0 0 0 0
Tre	eatment*Day 0 1 0 0 0 0 0 0 0 0 0 0 -1
Tre	eatment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0000000000-1 /oddsrati	o alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs ZM	nPhi 200 at Irregular at Day 21' Treatment 1 0 0 0 0 0 -1
Treatme	nt*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Treatme	nt*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 -1
Tre	atment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
00000000000000000000	1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Max	xim 100 at Irregular at Day 21' Treatment 0 1 -1 0 0 0 0
Tre	atment*Fungus 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 0 0
Tre	atment*Day 0 0 0 1 0 -1

```
Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio
```

alpha=0.00238 cl;

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 400 at Irregular at Day 21' Treatment 0 1 0 0 -1 0 0

Treatment\*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 -1

Treatment\*Day 0 0 0 1 0 0 0 0 0 -1

0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Testigo at Irregular at Day 21' Treatment 0 1 0 0 0 -1 0

Treatment\*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 0 0 0 1 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Irregular at Day 21' Treatment 0 1 0 0 0 0 -1

Treatment\*Day 0 0 0 1 0 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Irregular at Day 21' Treatment 0 0 1 -1 0 0 0

0

/oddsratio alpha=0.00238 cl;

```
0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs Testigo at Irregular at Day 21' Treatment 0 0 1 0 0 -1 0
               Treatment*Day 0 0 0 0 0 1 0 0 0 0 -1
               0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Irregular at Day 21' Treatment 0 0 1 0 0 0 -1
               Treatment*Day 0 0 0 0 0 1 0 0 0 0 0 0 -1
               0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Irregular at Day 21' Treatment 0 0 0 1 -1 0
0
             Treatment*Day 0 0 0 0 0 0 0 1 0 -1
               0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Irregular at Day 21' Treatment 0 0 0 1 0 -1 0
               Treatment*Day 0 0 0 0 0 0 0 1 0 0 0 -1
               0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Irregular at Day 21' Treatment 0 0 0 1 0 0
-1
               Treatment*Day 0 0 0 0 0 0 0 1 0 0 0 0 0 -1
               0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo at Irregular at 21' Treatment 0 0 0 0 1 -1 0
```

Treatment\*Day 0 0 0 0 0 0 0 0 0 1 0 -1

0 0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Irregular at Day 21' Treatment 0 0 0 0 1 0 -1

Treatment\*Day 0 0 0 0 0 0 0 0 0 1 0 0 0 -1

0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Testigo vs ZMnPhi 200 at Irregular at Day 21' Treatment 0 0 0 0 0 1 -1

Treatment\*Day 0 0 0 0 0 0 0 0 0 0 0 0 1 0 -1

0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

alpha=0.00238 cl;

Treatment\*Day 0 1 0 0 0 -1

Treatment\*Fungus\*Day 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio

alpha=0.00238 cl;

Treatment\*Day 0 1 0 0 0 0 0 -1

1 /oddsratio alpha=0.00238 cl;

0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Testigo at Ultimun at Day 21' Treatment 1 0 0 0 0 -1 0

Treatment\*Day 0 1 0 0 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Ultimun at Day 21' Treatment 1 0 0 0 0 0 -1

Treatment\*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 -1

ESTIMATE 'Kphi 400 vs Maxim 100 at Ultimun at Day 21' Treatment 0 1 -1 0 0 0 0

Treatment\*Day 00010-1

alpha=0.00238 cl;

1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 400 at Ultimun at Day 21' Treatment 0 1 0 0 -1 0 0

Treatment\*Day 000100000-1

0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Testigo at Ultimun at Day 21' Treatment 0 1 0 0 0 -1 0

Treatment\*Day 0001000000-1

0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs ZMnPhi 200 at Ultimun at Day 21' Treatment 0 1 0 0 0 0 -1

Treatment\*Day 000100000000-1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Ultimun at Day 21' Treatment 0 0 1 -1 0 0 0

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 400 at Ultimun at Day 21' Treatment 0 0 1 0 -1 0 0

Treatment\*Day 000001000-1

0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs Testigo at Ultimun at Day 21' Treatment 0 0 1 0 0 -1 0

Treatment\*Fungus 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 -1 0 0 0

Treatment\*Day 00000100000-1

0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Ultimun at Day 21' Treatment 0 0 1 0 0 0 -1

Treatment\*Day 000001000000-1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Ultimun at Day 21' Treatment 0 0 0 1 0 -1 0 Treatment\*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 Treatment\*Day 00000001000-1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Ultimun at Day 21' Treatment 0 0 0 1 0 0 -1 Treatment\*Day 000000100000-1 ESTIMATE 'MnPhi 400 vs Testigo at Ultimun at Day 21' Treatment 0 0 0 0 1 -1 0 Treatment\*Day 00000000010-1 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Ultimun at Day 21' Treatment 0 0 0 0 1 0 -1 Treatment\*Day 000000000000000-1 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; ESTIMATE 'Testigo vs ZMnPhi 200 at Ultimun at Day 21' Treatment 0 0 0 0 0 1 -1 Treatment\*Day 00000000000010-1 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl; run;

```
data allNoTestigo;
set allpredictors;
if treatment="Testigo" then delete;
if treatment="MnPhi 200" then treatment="ZMnPhi200";
run;
proc glimmix data=allNoTestigo method=laplace;
class treatment Day Severity Fungus Dish;
model Severity=Treatment|Day|Fungus / solution ;
random Dish(treatment Fungus);
run;
proc glimmix data=allNoTestigo method = laplace;
class treatment Day Severity Fungus Dish;
model Severity=Treatment|Day|Fungus / solution ;
run;
```

## data MnPhi200ToZMnPhi200;

```
set allpredictors;
if treatment="Testigo" then delete;
if treatment="MnPhi 200" then treatment="ZMnPhi 200";
```

run;

ESTIMATE 'Kphi 200 vs Max 100 at Aphanidermatum at Day 5'

Treatment\*Day 0 0 1 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 -1/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Aphanidermatum at Day 5'

Treatment 0 0 1 -1 0 0

Treatment\*Fungus 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0

Treatment\*Day 0 0 0 0 1 0 -1

Treatment\*Fungus\*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -

1/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 400 at Aphanidermatum at Day 5'

Treatment 0 0 1 0 -1 0

Treatment\*Fungus 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0 0

Treatment\*Day 0 0 0 0 1 0 0 0 -1

0 0 0 0 0 -1/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs Testigo at Aphanidermatum at Day 5'

Treatment 0 0 1 0 0 0

Treatment\*Day 0 0 0 0 1 0 0 0 0 0

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Aphanidermatum at Day 5'

Treatment 0 0 1 0 0 -1

Treatment\*Fungus 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0 0

Treatment\*Day 0 0 0 0 1 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 -1/oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Aphanidermatum at Day 5'

Treatment 0 0 0 1 -1 0

Treatment\*Fungus 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0

Treatment\*Day 0 0 0 0 0 0 1 0 -1

0 0 0 0 0 -1/oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Aphanidermatum at Day 5'

Treatment 0 0 0 1 0 0

Treatment\*Day 0 0 0 0 0 0 1 0 0 0

	$Treatment*Fungus*Day\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\$
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Aphanidermatum at Day 5'	
	Treatment 0 0 0 1 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0
	Treatment*Day 0 0 0 0 0 0 1 0 0 0 -1
	$Treatment*Fungus*Day\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\$
0 0 0 0 0 0 0 0 0 0 0 0 -1/oddsratio alp	ha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo	at Aphanidermatum at Day 5'
	Treatment 0 0 0 0 1 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 1 0
	$Treatment*Fungus*Day\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\$
0 0 0 0 0 1 0 0 0 0 0 0/oddsratio alpha	=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnPh	i 200 at Aphanidermatum at Day 5'
	Treatment 0 0 0 0 1 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 1 0 -1
	$Treatment*Fungus*Day\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\$
0 0 0 0 0 1 0 0 0 0 0 -1/oddsratio alp	ha=0.00238 cl;
ESTIMATE 'Testigo vs ZMnPhi 200 at Aphanidermatum at Day 5'	
	Treatment 0 0 0 0 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 0 0 -1
	$Treatment*Fungus*Day\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\$
0 0 0 0 0 0 0 0 0 0 0 0 -1/oddsratio alp	ha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Kphi 400	at Irregular at Day 5'
	Treatment 1 -1 0 0 0 0
	Treatment*Fungus 0 1 0 0 -1
	Treatment*Day 1 0 -1

	Treatment*Fungus*Day 0 1 0 0 0 0 0 -1/oddsratio
alpha=0.00238 cl;	
ESTIMATE 'Kphi 200 vs Maxim 10	00 at Irregular at Day 5'
	Treatment 1 0 -1 0 0 0
	Treatment*Fungus 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 1 0 0 0 -1
	Treatment*Fungus*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 -
1/oddsratio alpha=0.00238 cl;	
ESTIMATE 'Kphi 200 vs MnPhi 20	00 + Maxim at at Irregular at Day 5'
	Treatment 1 0 0 -1 0 0
	Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 -1 0 0 0 0 0 0 0
	Treatment*Day 1 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
-1/oddsratio alpha=0.00238 cl;	
ESTIMATE 'Kphi 200 vs MnPhi 40	00 at Irregular at Day 5'
	Treatment 1 0 0 0 -1 0
	Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 -1 0 0 0 0
	Treatment*Day 1 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 -1/oddsratio alpha=0.002	38 cl;
ESTIMATE 'Kphi 200 vs Testigo at	t Irregular at Day 5'
	Treatment 1 0 0 0 0 0
	Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 1 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Fungus*Day 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
/oddsr	atio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs ZI	MnPhi 200 at Irregular at Day 5'
	Treatment 1 0 0 0 0 -1
	Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 0

## Treatment\*Day 1 0 0 0 0 0 0 0 0 0 -1

00000000000000-1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Maxim 100 at Irregular at Day 5'

Treatment 0 1 -1 0 0 0

Treatment\*Fungus 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 0 0

Treatment\*Day 0 0 1 0 -1

Treatment\*Fungus\*Day 0 0 0 0 0 0 0 1 0 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 400 at Irregular at Day 5'

Treatment 0 1 0 0 -1 0

Treatment\*Fungus  $0\ 0\ 0\ 0\ 1\ 0\ 0\ 0\ 0\ 0\ 0\ -1$ 

Treatment\*Day 0 0 1 0 0 0 0 0 -1

00000-1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Testigo at Irregular at Day 5'

Treatment 0 1 0 0 0 0  $\!$ 

	Treatment*Day 0 0 1 0 0 0 0 0 0 0 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0
000000000000	
/odds	ratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs ZMnPhi	200 at Irregular at Day 5'
	Treatment 0 1 0 0 0 -1
	Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 0
	Treatment*Day 0 0 1 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 -1	
/odds	ratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi	200 + Maxim at Irregular at Day 5'
	Treatment 0 0 1 -1 0 0
	Treatment*Fungus 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
-1	
/odds	ratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi	400 at Irregular at Day 5'
	Treatment 0 0 1 0 -1 0
	Treatment*Fungus 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0
	Treatment*Day 0 0 0 0 1 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 -1	
/odds	ratio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 ve Testion	a at Irregular at Day 5'

	Treatment*Fungus 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 1 0 0 0 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
000000000000	
/oddsr	atio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs ZMnPh	ni 200 at Irregular at Day 5'
	Treatment 0 0 1 0 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0
	Treatment*Day 0 0 0 0 1 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1	
/oddsr	atio alpha=0.00238 cl;
ESTIMATE Maphi 200 - Marima	is Maphi 400 at Imagular at Day 5'
$\mathbf{ESTIMATE}  \mathbf{MIIFIII}  200 + \mathbf{MIAXIIII}  \mathbf{V}$	Tractment 0.0.0.1 1.0
	Treatment*Europy 0.00000000000000000000000000000000000
	Treatment*Dev 0.00000000000000000000000000000000000
	Treatment*Fungue*Dev 0.00000000000000000000000000000000000
10000 1	
100000-1	atio $alpha=0.00228 alc$
/oddsi	ano apria–0.00238 ci,
ESTIMATE 'MnPhi 200 + Maxim	vs Testigo at Irregular at Day 5'
	Treatment 0 0 0 1 0 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 1 0 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
$1 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ $	
/oddsr	atio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Irregular at Day 5'

	Treatment 0 0 0 1 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0
	Treatment*Day 0 0 0 0 0 0 1 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
100000000000-1	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo	at Irregular at Day 5'
	Treatment 0 0 0 0 1 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 1 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0000010000	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnPhi	200 at Irregular at Day 5'
	Treatment 0 0 0 0 1 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 1 0 0 0 0 0 -1	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Testigo vs ZMnPhi 200	0 at Irregular at Day 5'
	Treatment 0 0 0 0 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 -1	
/oddsra	atio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs. Kphi 400 at Ultimun at Day5'

Treatment 1 -1 0 0 0 0

Treatment\*Day 1 0 -1

Treatment\*Fungus\*Day 0 0 1 0 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Maxim 100 at Ultimun at Day5'

Treatment 1 0 -1 0 0 0 Treatment\*Fungus 0 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0 0 0 0 Treatment\*Day 1 0 0 0 -1 Treatment\*Fungus\*Day 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Ultimun at Day5'

0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs MnPhi 400 at Ultimun at Day5'

000000-1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Testigo at Ultimun at Day5'

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Ultimun at Day5'

Treatment 1 0 0 0 0 -1

Treatment\*Fungus 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 1 0 0 0 0 0 0 0 0 0 -1

000000000000000-1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Maxim 100 at Ultimun at Day5'

Treatment 0 1 -1 0 0 0 Treatment\*Fungus 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 Treatment\*Day 0 0 1 0 -1 Treatment\*Fungus\*Day 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Ultimun at Day5'

Treatment 0 1 0 -1 0 0 Treatment\*Fungus 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 Treatment\*Day 0 0 1 0 0 0 -1 Treatment\*Fungus\*Day 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0

0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 400 at Ultimun at Day5'

	Treatment 0 1 0 0 -1 0
	Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 -1 0 0 0
	Treatment*Day 0 0 1 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 -1	
/oddsr:	atio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Testigo at	t Ultimun at Day5'
	Treatment 0 1 0 0 0 0
	Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 1 0 0 0 0 0 0 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
000000000000	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs ZMnPhi 2	200 at Ultimun at Day5'
	Treatment 0 1 0 0 0 -1
	Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1
	Treatment*Day 0 0 1 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
000000000000000-1	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi	200 + Maxim at Ultimun at Day5'
	Treatment 0 0 1 -1 0 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 -1	

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 4	00 at Ultimun at Day5'
	Treatment 0 0 1 0 -1 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0
	Treatment*Day 0 0 0 0 1 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 -1	
/oddsra	tio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs Testigo a	at Ultimun at Day5'
	Treatment 0 0 1 0 0 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 1 0 0 0 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
/oddsra	tio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs ZMnPhi	200 at Ultimun at Day5'
	Treatment 0 0 1 0 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1
	Treatment*Day 0 0 0 0 1 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1	
/oddsra	tio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs	s MnPhi 400 at Ultimun at Day5'
	Treatment 0 0 0 1 -1 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0
	Treatment*Day 0 0 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 1 0 0 0 0 0 -1	
/oddsra	tio $alpha=0.00238$ cl:

/oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim	vs Testigo at Ultimun at Day5'
	Treatment 0 0 0 1 0 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 1 0 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
01000000000	
/oddsr	atio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim	vs ZMnPhi 200 at Ultimun at Day5'
	Treatment 0 0 0 1 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1
	Treatment*Day 0 0 0 0 0 0 0 1 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0100000000000-1	
/oddsr	atio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo	at Ultimun at Day5'
	Treatment 0 0 0 0 1 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 1 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0000001000	
/oddsr	atio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnPh	i 200 at Ultimun at Day5'
	Treatment 0 0 0 0 1 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1
	Treatment*Day 0 0 0 0 0 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
000000100000-1	

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Testigo vs ZMnPhi 200 at Ultimun at Day5'

Treatment 0 0 0 0 0 -1

Treatment\*Day 0 0 0 0 0 0 0 0 0 0 -1

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/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Kphi 400 at Aphanidermatum at Day 21'

ESTIMATE 'Kphi 200 vs Max 100 at Aphanidermatum at Day 21'

Treatment 1 0 -1 0 0 0 Treatment\*Fungus 1 0 0 0 0 0 -1 Treatment\*Day 0 1 0 0 0 -1 Treatment\*Fungus\*Day 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

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/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs MnPhi	400 at Aphanidermatum at Day 21'
	Treatment 1 0 0 0 -1
	Treatment*Fungus 1 0 0 0 0 0 0 0 0 0 0 0 -1
	Treatment*Day 0 1 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 -1	
/odd	sratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs at Testi	go at Day 21'
	Treatment 1 0 0 0 0
	Treatment*Fungus 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 1 0 0 0 0 0 0 0 0 0 0
	Treatment*Fungus*Day 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0	
/odd	sratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs at ZMn	Phi 200 at Day 21'
	Treatment 1 0 0 0 0 -1
	Treatment*Fungus 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1
	Treatment*Day 0 1 0 0 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0000000000000000-1	
/odd	sratio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Max 10	0 at Aphanidermatum at Day 21'
	Treatment 0 1 -1 0 0 0
	Treatment*Fungus 0 0 0 1 0 0 -1
	Treatment*Day 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 1 0 0 0 0 -1
/odd	sratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 20	0 + Maxim at Aphanidermatum at Day 21'	
	Treatment 0 1 0 -1 0 0	
	Treatment*Fungus 0 0 0 1 0 0 0 0 0 -1	
	Treatment*Day 0 0 0 1 0 0 0 -1	
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0	
0 0 -1		
/oddsratio alpha=0.00238 cl;		
ESTIMATE 'Kphi 400 vs MnPhi 40	00 at Aphanidermatum at Day 21'	
	Treatment 0 1 0 0 -1 0	
	Treatment*Fungus 0 0 0 1 0 0 0 0 0 0 0 0 0 -1	
	Treatment*Day 0 0 0 1 0 0 0 0 0 -1	
	$Treatment*Fungus*Day\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\ 0\$	
0 0 0 0 0 0 0 0 0 -1		
/oddsra	atio alpha=0.00238 cl;	
ESTIMATE 'Kphi 400 vs Testigo at Aphanidermatum at Day 21'		
	Treatment 0 1 0 0 0 0	
	Treatment*Fungus 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0	
	Treatment*Day 0 0 0 1 0 0 0 0 0 0 0	
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0	
0 0 0 0 0 0 0 0 0 0 0 0 0		
/oddsra	atio alpha=0.00238 cl;	
ESTIMATE 'Kphi 400 vs ZMnPhi 2	200 at Aphanidermatum at Day 21'	
	Treatment 0 1 0 0 0 -1	
	Treatment*Fungus 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1	
	Treatment*Day 0 0 0 1 0 0 0 0 0 0 0 0 -1	
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0	
00000000000000000-1		

/oddsratio	alpha=0.00238	cl;
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ESTIMATE 'Maxim 100 vs MnPhi	200 + Maxim at Aphanidermatum at Day 21'	
	Treatment 0 0 1 -1 0 0	
	Treatment*Fungus 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0	
	Treatment*Day 0 0 0 0 0 1 0 -1	
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
0 0 -1		
/oddsra	atio alpha=0.00238 cl;	
ESTIMATE 'Maxim 100 vs MnPhi 400 at Aphanidermatum at Day 21'		
	Treatment 0 0 1 0 -1 0	
	Treatment*Fungus 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0 0	
	Treatment*Day 0 0 0 0 0 1 0 0 0 -1	
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
0 0 0 0 0 0 0 0 0 -1		
/oddsra	atio alpha=0.00238 cl;	
ESTIMATE 'Maxim 100 vs Testigo at Aphanidermatum at Day 21'		
	Treatment 0 0 1 0 0 0	
	Treatment*Fungus 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	
	Treatment*Day 0 0 0 0 0 1 0 0 0 0	
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		
/oddsra	atio alpha=0.00238 cl;	
ESTIMATE 'Maxim 100 vs ZMnPh	i 200 at Aphanidermatum at Day 21'	
	Treatment 0 0 1 0 0 -1	
	Treatment*Fungus 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 -1 0 0	
	Treatment*Day 0 0 0 0 0 1 0 0 0 0 0 -1	

	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1	
/odd	lsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim	vs MnPhi 400 at Aphanidermatum at Day 21'
	Treatment 0 0 0 1 -1 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 1 0 0 0 0 0 -1	
/odd	sratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim	vs Testigo at Aphanidermatum at Day 21'
	Treatment 0 0 0 1 0 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 1 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
00100000000	
/odd	sratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim	vs ZMnPhi 200 at Aphanidermatum at Day 21'
	Treatment 0 0 0 1 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 1 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
00100000000000-1	
/odd	lsratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testig	go at Aphanidermatum at Day 21'
	Treatment 0 0 0 0 1 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

## Treatment\*Day 0 0 0 0 0 0 0 0 0 1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 400 vs ZMnPhi 200 at Aphanidermatum at Day 21'

Treatment 0 0 0 0 1 -1

Treatment\*Day 0 0 0 0 0 0 0 0 0 1 0 -1

0 0 0 0 0 0 0 0 1 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Testigo vs ZMnPhi 200 at Aphanidermatum at Day 21'

Treatment 0 0 0 0 0 -1

Treatment\*Day 0 0 0 0 0 0 0 0 0 0 0 0 -1

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Kphi 400 at Irregular at Day 21'

Treatment 1 -1 0 0 0 0

Treatment\*Fungus 0 1 0 0 -1

Treatment\*Day 0 1 0 -1

 $Treatment*Fungus*Day\ 0\ 0\ 0\ 0\ 1\ 0\ 0\ 0\ 0\ -1$ 

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Maxim 100 at Irregular at Day 21'

Treatment 1 0 -1 0 0 0
Treatment*Day 0 1 0 0 0 -1
Treatment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 -1
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at at Irregular at Day 21'
Treatment 1 0 0 -1 0 0
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 -1 0 0 0 0 0 0 0 0
Treatment*Day 0 1 0 0 0 0 0 -1
Treatment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 -1
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs MnPhi 400 at Irregular at Day 21'
Treatment 1 0 0 0 -1 0
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 0 0 0 0
Treatment*Day 0 1 0 0 0 0 0 0 0 -1
Treatment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 -1
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs Testigo at Irregular at Day 21'
Treatment 1 0 0 0 0 0
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Treatment*Day 0 1 0 0 0 0 0 0 0 0 0
Treatment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
/oddsratio alpha=0.00238 cl;
ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Irregular at Day 21'
Treatment 1 0 0 0 0 -1
Treatment*Fungus 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1 0

	Treatment*Day 0 1 0 0 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0
00000000000000000-1	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Maxim 10	00 at Irregular at Day 21'
	Treatment 0 1 -1 0 0 0
	Treatment*Fungus 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 20	0 + Maxim at Irregular at Day 21'
	Treatment 0 1 0 -1 0 0
	Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 1 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 -1	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs MnPhi 40	0 at Irregular at Day 21'
-	Treatment 0 1 0 0 -1 0
	Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 0 -1
	Treatment*Day 0 0 0 1 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0
000000000-1	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Testigo at	Irregular at Day 21'
- 0	Treatment 0 1 0 0 0 0
	Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0

	Treatment*Day 0 0 0 1 0 0 0 0 0 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0	
/oddsra	tio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs ZMnPhi 2	00 at Irregular at Day 21'
	Treatment 0 1 0 0 0 -1
	Treatment*Fungus 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 0
	Treatment*Day 0 0 0 1 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1	
/oddsra	tio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 2	200 + Maxim at Irregular at Day 21'
	Treatment 0 0 1 -1 0 0
	Treatment*Fungus 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 -1	
/oddsra	tio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 4	400 at Irregular at Day 21'
	Treatment 0 0 1 0 -1 0
	Treatment*Fungus 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0 0
	Treatment*Day 0 0 0 0 0 1 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
00000000-1	
/oddsra	tio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs Testigo	at Irregular at Day 21'
	Treatment 0 0 1 0 0 0

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/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs ZMnPhi 200 at Irregular at Day 21'

Treatment 0 0 1 0 0 -1

Treatment\*Fungus 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1 0

Treatment\*Day 0 0 0 0 0 1 0 0 0 0 -1

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/oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs MnPhi 400 at Irregular at Day 21'

Treatment 0 0 0 1 -1 0

Treatment\*Fungus 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0

Treatment\*Day 0 0 0 0 0 0 0 1 0 -1

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/oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs Testigo at Irregular at Day 21'

Treatment 0 0 0 1 0 0

Treatment\*Day 0 0 0 0 0 0 0 1 0 0

/oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim vs ZMnPhi 200 at Irregular at Day 21'

	Treatment 0 0 0 1 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0
	Treatment*Day 0 0 0 0 0 0 0 1 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0001000000000000-1	
/odds	aratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testig	o at Irregular at 21'
	Treatment 0 0 0 0 1 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 0 1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
00000000010	
/odds	pratio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnP	hi 200 at Irregular at Day 21'
	Treatment 0 0 0 0 1 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 1 0 0 0 0 -1	
/odds	aratio alpha=0.00238 cl;
ESTIMATE 'Testigo vs ZMnPhi 2	00 at Irregular at Day 21'
	Treatment 0 0 0 0 0 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
000000000000000000-1	
/odds	ratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Maxim 100 at Ultimun at Day 21'

Treatment 1 0 -1 0 0 0 Treatment\*Fungus 0 0 1 0 0 0 0 0 -1 0 0 0 0 0 0 0 0 0 Treatment\*Day 0 1 0 0 0 -1 Treatment\*Fungus\*Day 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs MnPhi 200 + Maxim at Ultimun at Day 21'

Treatment 1 0 0 -1 0 0 Treatment\*Fungus 0 0 1 0 0 0 0 0 0 0 0 -1 0 0 0 0 0 0 Treatment\*Day 0 1 0 0 0 0 0 -1 Treatment\*Fungus\*Day 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0

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/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs MnPhi 400 at Ultimun at Day 21'

Treatment 1 0 0 0 -1 0 Treatment\*Fungus 0 0 1 0 0 0 0 0 0 0 0 0 0 0 -1 0 0 0 Treatment\*Day 0 1 0 0 0 0 0 0 0 -1 Treatment\*Fungus\*Day 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0

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/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs Testigo at Ultimun at Day 21'

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 200 vs ZMnPhi 200 at Ultimun at Day 21'

Treatment 1 0 0 0 0 -1

Treatment\*Fungus 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1

Treatment\*Day 0 1 0 0 0 0 0 0 0 0 0 -1

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/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs Maxim 100 at Ultimun at Day 21'

Treatment 0 1 -1 0 0 0 Treatment\*Fungus 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0 0 0 0 Treatment\*Day 0 0 0 1 0 -1 Treatment\*Fungus\*Day 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 /oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 200 + Maxim at Ultimun at Day 21'

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/oddsratio alpha=0.00238 cl;

ESTIMATE 'Kphi 400 vs MnPhi 400 at Ultimun at Day 21'

	Treatment 0 1 0 0 -1 0
	Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 -1 0 0 0
	Treatment*Day 0 0 0 1 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0000000000-1	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs Testigo at	Ultimun at Day 21'
	Treatment 0 1 0 0 0 0
	Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 1 0 0 0 0 0 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Kphi 400 vs ZMnPhi 2	200 at Ultimun at Day 21'
	Treatment 0 1 0 0 0 -1
	Treatment*Fungus 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 -1
	Treatment*Day 0 0 0 1 0 0 0 0 0 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0000000000000000000-1	
/oddsra	atio alpha=0.00238 cl;
ESTIMATE 'Maxim 100 vs MnPhi 200 + Maxim at Ultimun at Day 21'	
	Treatment 0 0 1 -1 0 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 -1	

/oddsratio alpha=0.00238 cl;

ESTIMATE 'Maxim 100 vs MnPhi 400 at U	Iltimun at Day 21'
Treatm	ent 0 0 1 0 -1 0
Treatm	ent*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1 0 0 0
Treatm	ent*Day 0 0 0 0 0 1 0 0 0 -1
Treatm	ent*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 -1	
/oddsratio alph	a=0.00238 cl;
ESTIMATE 'Maxim 100 vs Testigo at Ultin	nun at Day 21'
Treatm	ent 0 0 1 0 0 0
Treatm	ent*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0
Treatm	ent*Day 0 0 0 0 0 1 0 0 0 0
Treatm	ent*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
/oddsratio alph	a=0.00238 cl;
ESTIMATE 'Maxim 100 vs ZMnPhi 200 at	Ultimun at Day 21'
Treatm	ent 0 0 1 0 0 -1
Treatm	ent*Fungus 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0 0 -1
Treatm	ent*Day 0 0 0 0 0 1 0 0 0 0 0 -1
Treatm	ent*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 -1	
/oddsratio alph	a=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim vs MnPh	i 400 at Ultimun at Day 21'
Treatm	ent 0 0 0 1 -1 0
Treatm	ent*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1 0 0 0
Treatm	ent*Day 0 0 0 0 0 0 0 1 0 -1
Treatm	ent*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 1 0 0 0 0 0 -1	
/oddsratio alph	a=0.00238 cl·

/oddsratio alpha=0.00238 cl;

ESTIMATE 'MnPhi 200 + Maxim	vs Testigo at Ultimun at Day 21'
	Treatment 0 0 0 1 0 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 1 0 0
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
00001000000	
/oddsr	atio alpha=0.00238 cl;
ESTIMATE 'MnPhi 200 + Maxim	vs ZMnPhi 200 at Ultimun at Day 21'
	Treatment 0 0 0 1 0 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 0 0 0 -1
	Treatment*Day 0 0 0 0 0 0 0 0 1 0 0 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
000010000000000000-1	
/oddsr	atio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs Testigo	at Ultimun at Day 21'
	Treatment 0 0 0 0 1 0
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
	Treatment*Day 0 0 0 0 0 0 0 0 0 0 1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
000000000001	
/oddsr	atio alpha=0.00238 cl;
ESTIMATE 'MnPhi 400 vs ZMnPh	i 200 at Ultimun at Day 21'
	Treatment 0 0 0 0 1 -1
	Treatment*Fungus 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 0 0 -1
	Treatment*Day 0 0 0 0 0 0 0 0 0 0 1 0 -1
	Treatment*Fungus*Day 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0000000000100000-1	

# /oddsratio alpha=0.00238 cl;

ESTIMATE 'Testigo vs ZMnPhi 200 at Ultimun at Day 21'

Treatment 0 0 0 0 0 -1

Treatment\*Day 0 0 0 0 0 0 0 0 0 0 0 -1

# 0000000000000000000-1

```
/oddsratio alpha=0.00238 cl;
```

run;

# data MnPhi200ToZMnPhi200;

set allpredictors;

```
if treatment="MnPhi 200" then treatment="ZMnPhi 200";
```

run;

```
/* combined Severity 0 =A, 1+2+3=B, 4+5=C */
```

data LessCategories;

```
set MnPhi200ToZMnPhi200;
```

```
if severity <1 then smallsev='A';
```

```
else if severity <=3 then smallsev='B';
```

else smallsev='C';

run;

```
proc print data=lesscategories;
run;
```

proc glimmix data=LessCategories method=laplace; class treatment Day Severity smallsev Fungus Dish; model smallsev=Treatment|Day|Fungus / solution ; random Dish(Treatment Fungus) ; run;

```
/* combined Severity 0+1+2+3=A, 4+5=B */
data LessCategories;
set MnPhi200ToZMnPhi200;
if severity <=3 then smallsev='A';
else smallsev='B';
run:
proc print data=lesscategories;
run;
proc glimmix data=LessCategories method=laplace;
class treatment Day Severity smallsev Fungus Dish;
model smallsev=Treatment|Day|Fungus / solution ;
random Dish(Treatment Fungus);
run:
proc glimmix data=LessCategories method=laplace;
   class treatment Day smallsev fungus Dish;
   model smallsev=Treatment|Day|Fungus / solution dist=Binomial link=logit;
  random Dish(Treatment fungus);
run;
title 'Fixed model with 3 categories of Severity';
proc glimmix data=LessCategories method=laplace;
class treatment Day Severity smallsev Fungus Dish;
model smallsev=Treatment|Day|Fungus / solution ;
run;
title 'Fixed model with 2 categories of Severity';
proc glimmix data=LessCategories method=laplace;
class treatment Day Severity smallsev Fungus Dish;
model smallsev=Treatment|Day|Fungus / solution ;
```

```
run;
```

# **Appendix C - SAS Code Power Analysis**

/\* Power for Several Simulated Data Sets \*/

/\* THE MULTINOMIAL DRAWS MODIFIES

SAS Blog

Simulate from the multinomial distribution in the SAS DATA step By Rick Wicklin on The DO Loop, March 16, 2016 \*/

%let SampleSize = 10; /\* number of observations in MN sample \*/

% let N = 5; /\* number of trials in each MN draw \*/

% let categ = 6; /\* number of categories in each MN draw \*/

% let Ntreat = 7; /\* number of treatments \*/

```
%macro Simul(N_B=, seed=);
```

data MN;

call streaminit(&seed);

```
/* prob of drawing items */
array probs{&Ntreat, &categ} _temporary_ (0 0 0 0 0.05 0.95 0.3 0.5 0.2 0 0 0
0.1 0.1 0.1 0.1 0.3 0.3 0.15 0.8 0.05 0 0 0 0.05 0.45 0.45 0.05 0 0 0 0 0 0.1
0.75 0.15 0 0 0.1 0.75 0.15 0);
```

array x{&categ};

/\* counts for each item \*/

do trt=1 to &Ntreat;

do dish=1 to &SampleSize;

```
ItemsLeft=&N; /* how many items remain? */
cumProb=0; /* cumulative probability */
do i=1 to &categ-1;/* loop over k categories */
```

if ItemsLeft=0 or cumProb=1 then

do;

```
x[i]=0;
```

end;

else

do;

p=probs[trt, i] / (1 - cumProb);

if  $p \ge 1$  then

x[i]=ItemsLeft;

else if p < 1 then

do;

x[i]=rand("binomial", p, ItemsLeft);

/\* binomial draw \*/

end;

cumProb=cumProb + probs[trt, i]; /\* adjust prob of

next binomial draw \*/

ItemsLeft=ItemsLeft - x[i]; /\* decrement size by

selection \*/

end;

end;

x[&categ]=ItemsLeft; /\* remaining items go into last category \*/

output;

end;

end;

keep trt dish x:;

run;

proc transpose data=MN out=power1 name=raiting;

by trt dish;

var x:;

/\* Runs the first simulation outside the Loop to create the output DataSets \*/

```
proc glimmix data=power1 method=laplace;
        class trt raiting dish;
        freq col1;
        model raiting(order=data)=trt /dist=multinomial solution;
        *random intercept /subject=dish(trt) solution;
        *parms (0.01) / hold=1;
        contrast 'ctr v exp 1' trt 1 -1;
        contrast 'ctr v exp 2' trt 1 0 -1;
        contrast 'ctr v exp 3' trt 1 0 0 -1;
       contrast 'ctr v exp 4' trt 1000-1;
        contrast 'ctr v exp 5' trt 1 0 0 0 0 -1;
        contrast 'ctr v exp 6' trt 1 0 0 0 0 0 -1;
        contrast 'exp 1 v exp 2' trt 0 1 -1;
        contrast 'exp 1 v exp 3' trt 0 1 0 -1;
        contrast 'exp 1 v exp 4' trt 0 1 0 0 -1;
        contrast 'exp 1 v exp 5' trt 0 1 0 0 0 -1;
        contrast 'exp 1 v exp 6' trt 0 1 0 0 0 0 -1;
        contrast 'exp 2 v exp 3' trt 0 0 1 -1;
       contrast 'exp 2 v exp 4' trt 0 0 1 0 -1;
        contrast 'exp 2 v exp 5' trt 0 0 1 0 0 -1;
        contrast 'exp 2 v exp 6' trt 0 0 1 0 0 0 -1;
        contrast 'exp 3 v exp 4' trt 0 0 0 1 -1;
        contrast 'exp 3 v exp 5' trt 0 0 0 1 0 -1;
        contrast 'exp 3 v exp 6' trt 0 0 0 1 0 0 -1;
        contrast 'exp 4 v exp 5' trt 0 0 0 0 1 -1;
        contrast 'exp 4 v exp 6' trt 0 0 0 0 1 0 -1;
        contrast 'exp 5 v exp 6' trt 0 0 0 0 0 1 -1;
```

```
ods output tests3=F_overall contrasts=F_contrasts;
```

```
data powerFIXED;
```

```
set F_overall F_contrasts;
Simul=0;
```

# run;

proc glimmix data=power1 method=laplace;

```
class trt raiting dish;
freq col1;
model raiting(order=data)=trt /dist=multinomial solution;
random intercept /subject=dish(trt) solution;
parms (0.1) / hold=1;
contrast 'ctr v exp 1' trt 1 -1;
contrast 'ctr v exp 2' trt 1 0 -1;
contrast 'ctr v exp 3' trt 1 0 0 -1;
contrast 'ctr v exp 4' trt 1000-1;
contrast 'ctr v exp 5' trt 1 0 0 0 0 -1;
contrast 'ctr v exp 6' trt 1 0 0 0 0 0 -1;
contrast 'exp 1 v exp 2' trt 0 1 -1;
contrast 'exp 1 v exp 3' trt 0 1 0 -1;
contrast 'exp 1 v exp 4' trt 0 1 0 0 -1;
contrast 'exp 1 v exp 5' trt 0 1 0 0 0 -1;
contrast 'exp 1 v exp 6' trt 0 1 0 0 0 0 -1;
contrast 'exp 2 v exp 3' trt 0 0 1 -1;
contrast 'exp 2 v exp 4' trt 0 0 1 0 -1;
contrast 'exp 2 v exp 5' trt 0 0 1 0 0 -1;
contrast 'exp 2 v exp 6' trt 0 0 1 0 0 0 -1;
contrast 'exp 3 v exp 4' trt 0 0 0 1 -1;
contrast 'exp 3 v exp 5' trt 0 0 0 1 0 -1;
```

```
contrast 'exp 3 v exp 6' trt 0 0 0 1 0 0 -1;
contrast 'exp 4 v exp 5' trt 0 0 0 0 1 -1;
contrast 'exp 4 v exp 6' trt 0 0 0 0 1 0 -1;
contrast 'exp 5 v exp 6' trt 0 0 0 0 0 1 -1;
ods output tests3=F_overall contrasts=F_contrasts;
```

```
data powerMIXEDLARGE;
```

```
set F_overall F_contrasts;
simul=0;
```

run;

```
proc glimmix data=power1 method=laplace;
       class trt raiting dish;
       freq col1;
        model raiting(order=data)=trt /dist=multinomial solution;
        random intercept /subject=dish(trt) solution;
        parms (0.01) / hold=1;
       contrast 'ctr v exp 1' trt 1 -1;
       contrast 'ctr v exp 2' trt 1 0 -1;
       contrast 'ctr v exp 3' trt 1 0 0 -1;
       contrast 'ctr v exp 4' trt 1000-1;
       contrast 'ctr v exp 5' trt 1 0 0 0 0 -1;
       contrast 'ctr v exp 6' trt 1 0 0 0 0 0 -1;
       contrast 'exp 1 v exp 2' trt 0 1 -1;
       contrast 'exp 1 v exp 3' trt 0 1 0 -1;
       contrast 'exp 1 v exp 4' trt 0 1 0 0 -1;
        contrast 'exp 1 v exp 5' trt 0 1 0 0 0 -1;
        contrast 'exp 1 v exp 6' trt 0 1 0 0 0 0 -1;
        contrast 'exp 2 v exp 3' trt 0 0 1 -1;
        contrast 'exp 2 v exp 4' trt 0 0 1 0 -1;
```

run;

#### data powerMIXEDSMALL;

set F\_overall F\_contrasts; simul=0;

run;

%do b=1 %to &N\_B;

data MN;

call streaminit(&seed&b);

/\* prob of drawing items \*/ array probs{&Ntreat, &categ} \_temporary\_ (0 0 0 0 0.05 0.95 0.3 0.5 0.2

#### 0 0

 $0\ 0.1\ 0.1\ 0.1\ 0.1\ 0.3\ 0.3\ 0.15\ 0.8\ 0.05\ 0\ 0\ 0\ 0.05\ 0.45\ 0.45\ 0.05\ 0\ 0$ 

 $0 \ 0 \ 0$ 

0.1 0.75 0.15 0 0 0.1 0.75 0.15 0); array x{&categ};

/\* counts for each item \*/ do trt=1 to &Ntreat; do dish=1 to &SampleSize;

ItemsLeft=&N; /\* how many items remain? \*/

cumProb=0; /\* cumulative probability \*/

do i=1 to &categ-1; /\* loop over k categories \*/

if ItemsLeft=0 or cumProb=1 then

do;

x[i]=0;

end;

else

do;

p=probs[trt, i] / (1 - cumProb);

if  $p \ge 1$  then

x[i]=ItemsLeft;

else if p < 1 then

do;

x[i]=rand("binomial",

p, ItemsLeft); /\* binomial draw \*/

end;

cumProb=cumProb + probs[trt, i]; /\*

adjust prob of next binomial draw \*/

ItemsLeft=ItemsLeft - x[i]; /\*

decrement size by selection \*/

#### end;

end;

x[&categ]=ItemsLeft; /\* remaining items go into last

category \*/

output;

end;

end;

keep trt dish x:;

#### run;

var x:;

run;

proc glimmix data=power1 method=laplace;

class trt raiting dish; freq col1; model raiting(order=data)=trt /dist=multinomial solution; \*random intercept /subject=dish(trt) solution; \*parms (0.01) / hold=1; contrast 'ctr v exp 1' trt 1 -1; contrast 'ctr v exp 2' trt 1 0 -1; contrast 'ctr v exp 3' trt 1 0 0 -1; contrast 'ctr v exp 4' trt 1000-1; contrast 'ctr v exp 5' trt 1 0 0 0 0 -1; contrast 'ctr v exp 6' trt 1 0 0 0 0 0 -1; contrast 'exp 1 v exp 2' trt 0 1 -1; contrast 'exp 1 v exp 3' trt 0 1 0 -1; contrast 'exp 1 v exp 4' trt 0 1 0 0 -1; contrast 'exp 1 v exp 5' trt 0 1 0 0 0 -1; contrast 'exp 1 v exp 6' trt 0 1 0 0 0 0 -1; contrast 'exp 2 v exp 3' trt 0 0 1 -1; contrast 'exp 2 v exp 4' trt 0 0 1 0 -1; contrast 'exp 2 v exp 5' trt 0 0 1 0 0 -1; contrast 'exp 2 v exp 6' trt 0 0 1 0 0 0 -1; contrast 'exp 3 v exp 4' trt 0 0 0 1 -1; contrast 'exp 3 v exp 5' trt 0 0 0 1 0 -1;

```
contrast 'exp 3 v exp 6' trt 0 0 0 1 0 0 -1;
contrast 'exp 4 v exp 5' trt 0 0 0 0 1 -1;
contrast 'exp 4 v exp 6' trt 0 0 0 0 1 0 -1;
contrast 'exp 5 v exp 6' trt 0 0 0 0 0 1 -1;
ods output tests3=F_overall contrasts=F_contrasts;
```

data powerFIXED0;

set F\_overall F\_contrasts; Simul=&b;

run;

proc glimmix data=power1 method=laplace; class trt raiting dish; freq col1; model raiting(order=data)=trt /dist=multinomial solution; random intercept /subject=dish(trt) solution; parms (0.1) / hold=1; contrast 'ctr v exp 1' trt 1 -1; contrast 'ctr v exp 2' trt 1 0 -1; contrast 'ctr v exp 3' trt 1 0 0 -1; contrast 'ctr v exp 4' trt 1000-1; contrast 'ctr v exp 5' trt 1 0 0 0 0 -1; contrast 'ctr v exp 6' trt 1 0 0 0 0 0 -1; contrast 'exp 1 v exp 2' trt 0 1 -1; contrast 'exp 1 v exp 3' trt 0 1 0 -1; contrast 'exp 1 v exp 4' trt 0 1 0 0 -1; contrast 'exp 1 v exp 5' trt 0 1 0 0 0 -1; contrast 'exp 1 v exp 6' trt 0 1 0 0 0 0 -1; contrast 'exp 2 v exp 3' trt 0 0 1 -1; contrast 'exp 2 v exp 4' trt 0 0 1 0 -1;

run;

data powerMIXEDLARGE0;

set F\_overall F\_contrasts; simul=&b;

run;

proc glimmix data=power1 method=laplace; class trt raiting dish; freq col1; model raiting(order=data)=trt /dist=multinomial solution; random intercept /subject=dish(trt) solution; parms (0.01) / hold=1; contrast 'ctr v exp 1' trt 1 -1; contrast 'ctr v exp 2' trt 1 0 -1; contrast 'ctr v exp 2' trt 1 0 -1; contrast 'ctr v exp 3' trt 1 0 0 0 -1; contrast 'ctr v exp 4' trt 1 0 0 0 0 -1; contrast 'ctr v exp 5' trt 1 0 0 0 0 -1; contrast 'ctr v exp 6' trt 1 0 0 0 0 0 -1; contrast 'exp 1 v exp 2' trt 0 1 -1; contrast 'exp 1 v exp 3' trt 0 1 0 -1; contrast 'exp 1 v exp 4' trt 0 1 0 0 -1; contrast 'exp 1 v exp 5' trt 0 1 0 0 0 -1; contrast 'exp 1 v exp 6' trt 0 1 0 0 0 0 -1; contrast 'exp 2 v exp 3' trt 0 0 1 -1; contrast 'exp 2 v exp 4' trt 0 0 1 0 -1; contrast 'exp 2 v exp 5' trt 0 0 1 0 0 0 -1; contrast 'exp 2 v exp 6' trt 0 0 1 0 0 0 0 -1; contrast 'exp 3 v exp 4' trt 0 0 0 1 -1; contrast 'exp 3 v exp 5' trt 0 0 0 1 0 -1; contrast 'exp 3 v exp 5' trt 0 0 0 1 0 -1; contrast 'exp 3 v exp 5' trt 0 0 0 1 0 -1; contrast 'exp 4 v exp 5' trt 0 0 0 1 0 -1; contrast 'exp 4 v exp 5' trt 0 0 0 0 1 0 -1; contrast 'exp 5 v exp 6' trt 0 0 0 0 1 0 -1; contrast 'exp 5 v exp 6' trt 0 0 0 0 1 0 -1; contrast 'exp 5 v exp 6' trt 0 0 0 0 1 0 -1; contrast 'exp 5 v exp 6' trt 0 0 0 0 1 0 -1; contrast 'exp 5 v exp 6' trt 0 0 0 0 1 0 -1;

run;

data powerMIXEDSMALL0;

set F\_overall F\_contrasts; simul=&b;

run;

data powerFIXED;

set powerFIXED powerFIXED0;

run;

data powerMIXEDLARGE;

set powerMIXEDLARGE powerMIXEDLARGE0; run;

data powerMIXEDSMALL;

set powerMIXEDSMALL powerMIXEDSMALL0; run;

%end;

%mend;

%let SampleSize = 10; /\* number of observations in MN sample \*/
%let N = 5; /\* number of trials in each MN draw \*/
%let categ = 6;
%let Ntreat = 7;

%Simul(N\_B=1000, seed=36457);

libname fungus "/home/USERNAME"; /\*Setting the LIBNAME directory to Save the Results\*/

```
data fungus.powerFIXED&SampleSize&N;
```

```
set powerFIXED;
nc_parm=numdf*Fvalue;
alpha=0.00238;
F_Crit=Finv(1-alpha, numdf, dendf, 0);
Power_F=1-probF(F_crit, numdf, dendf, nc_parm);
```

run;

data fungus.powerMIXEDLARGE&SampleSize&N;

```
set powerMIXEDLARGE;
nc_parm=numdf*Fvalue;
alpha=0.00238;
F_Crit=Finv(1-alpha, numdf, dendf, 0);
Power_F=1-probF(F_crit, numdf, dendf, nc_parm);
```

run;

data fungus.powerMIXEDSMALL&SampleSize&N;

set powerMIXEDSMALL;

```
nc_parm=numdf*Fvalue;
alpha=0.00238;
F_Crit=Finv(1-alpha, numdf, dendf, 0);
Power_F=1-probF(F_crit, numdf, dendf, nc_parm);
```

%let SampleSize = 10; /\* number of observations in MN sample \*/
%let N = 10; /\* number of trials in each MN draw \*/
%let categ = 6;
%let Ntreat = 7;

```
%Simul(N_B=1000, seed=36457);
```

```
data fungus.powerFIXED&SampleSize&N;
set powerFIXED;
nc_parm=numdf*Fvalue;
alpha=0.00238;
F_Crit=Finv(1-alpha, numdf, dendf, 0);
Power_F=1-probF(F_crit, numdf, dendf, nc_parm);
```

run;

```
data fungus.powerMIXEDLARGE&SampleSize&N;
    set powerMIXEDLARGE;
    nc_parm=numdf*Fvalue;
    alpha=0.00238;
    F_Crit=Finv(1-alpha, numdf, dendf, 0);
    Power_F=1-probF(F_crit, numdf, dendf, nc_parm);
```

run;

data fungus.powerMIXEDSMALL&SampleSize&N;

```
set powerMIXEDSMALL;
nc_parm=numdf*Fvalue;
alpha=0.00238;
F_Crit=Finv(1-alpha, numdf, dendf, 0);
Power_F=1-probF(F_crit, numdf, dendf, nc_parm);
```

%let SampleSize = 20; /\* number of observations in MN sample \*/
%let N = 5; /\* number of trials in each MN draw \*/
%let categ = 6;
%let Ntreat = 7;

```
%Simul(N_B=1000, seed=36457);
```

```
data fungus.powerFIXED&SampleSize&N;
```

```
set powerFIXED;
nc_parm=numdf*Fvalue;
alpha=0.00238;
F_Crit=Finv(1-alpha, numdf, dendf, 0);
Power_F=1-probF(F_crit, numdf, dendf, nc_parm);
```

run;

```
data fungus.powerMIXEDLARGE&SampleSize&N;
```

```
set powerMIXEDLARGE;
nc_parm=numdf*Fvalue;
alpha=0.00238;
F_Crit=Finv(1-alpha, numdf, dendf, 0);
Power_F=1-probF(F_crit, numdf, dendf, nc_parm);
```

run;

data fungus.powerMIXEDSMALL&SampleSize&N;

set powerMIXEDSMALL; nc\_parm=numdf\*Fvalue; alpha=0.00238; F\_Crit=Finv(1-alpha, numdf, dendf, 0); Power\_F=1-probF(F\_crit, numdf, dendf, nc\_parm);

run;