802 Project Summary

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Introduction

This paper summarizes the consulting that was done for our assigned STAT 802 group. For more information on the experiment, the data, or any other files used in this paper see our Github page which can be found at https://github.com/maksudatoma/Stat-802-Project. The coding languages used in the paper are R and SAS. The corresponding code can be found in *Appendix A - R Code* and *Appendix B - SAS Code* respectively.

Initial Meetings

The first meeting with our clients was on September 13th. We discussed their project and what kind of data they were going to be looking at. They detailed to us their project, which is looking at the levels of Salmonella in beef jerky at different inoculations and thicknesses. Prior to the meeting they sent us what their variables would be, which gave us a good idea of what might be the best experimental design. The group informed us they were avoiding a completely randomized design (CRD) at the request of their professor. With that in mind, we suggested other possible models.

Later, after receiving feedback from Dr. Howard and several PhD students within the statistics department, we suggested adding a time component to the experiment as well as creating multiple batches to replicate each treatment combination. This lead to us suggested a mixed model for the analysis approach.

In both the initial meeting and the follow-up session the clients were more than happy to implement our suggestions. In the end the experiment involved two thickness levels (one-fourth and one-eighth of an inch), two inoculation methods (dry and wet), and five evenly spaced time points were measurements were taken (weeks 1-5) creating twenty entries per batch. The exact number of batches would not be known until after the power analysis, found in the *Power Analysis* section. We provided the client an example dataset we created to give them a better idea of what the end product may look like. This dataset had five batches.

Study Objectives and Proposed Model

The clients were most interested in the effect of the thickness levels, the inoculation method, and their interaction had on the Salmonella levels. In the final model we included the week effect and subsequent interactions as well. These variables are the fixed effects in the proposed mixed model.

The other variable included in the experiment is the batch number. This is a repeated measure and is therefore treated as a random variable. As mentioned above, the exact number of batches needed was unknown prior to the power analysis, but five was used as a starting value.

The model can be written in the form

$$Y_{ijkl} = \mu + \alpha_i + \beta_j + \tau_k + (\alpha\beta)_{ij} + (\alpha\tau)_{ik} + (\beta\tau)_{jk} + (\alpha\beta\tau)_{ijk} + u_l + e_{ijkl}$$

Here, Y_{ijkl} is the Salmonella level and μ is the overall mean. The fixed effects are represented by α_i for the effect of the ith inoculation method, β_j for the effect of the jth thickness level, and τ_k for the effect of the kth week. The interaction effect of the ith inoculation method and the jth thickness level is represented by $(\alpha\beta)_{ij}$, with the other two-way interactions following this form. The three-way interaction between all fixed effects is represented as $(\alpha\beta\tau)_{ijk}$. The random effect for batches is represented by u_l, which we assume are distributed as $u_l \sim N(0, \sigma_u^2)$. Lastly, the residuals are represented by e_{ijkl}, which we assume can be distributed as $e_{ijkl} \sim N(0, \sigma^2)$.

NEED TO ADD IN INFO ON COVARIANCE STRUCTURE

We reached out to the client later on in the process to determine what contrasts they were most interested in testing. They expressed they wanted to see the difference between the two levels of the inoculation method, the two levels of the thickness, and the orthogonal contrasts these variable. This resulted in six contrasts being tested.

Power Analysis

To determine the necessary number of batches needed to increase the likelihood of detecting a true treatment effect, we performed a power analysis. To do this, probable treatment mean estimates across all five weeks and variance estimates were needed. The clients provided these metrics from Brown et al. (2024). We then used these metrics to create a dataset with five batches where the response variable was identical across the batches. This dataset was then evaluated to determine the power. The results of the power analysis are shown below.

Obs	Label	NumDF	DenDF	FValue	ProbF	Effect	ncparm	alpha	fcrit	power
1	Dry vs Wet	1	76	9.23	0.0033		9.226	0.05	3.96676	0.85058
2	1/4 vs 1/8 inches	1	76	103.28	<.0001		103.276	0.05	3.96676	1.00000
3	Dry vs Wet at 1/4 Inches	1	76	5.70	0.0195		5.695	0.05	3.96676	0.65406
4	Dry vs Wet at 1/8 Inches	1	76	44.65	<.0001		44.651	0.05	3.96676	1.00000
5	1/4 vs 1/8 inches for Dry inoculation	1	76	137.36	<.0001		137.364	0.05	3.96676	1.00000
6	1/4 vs 1/8 inches for Wet inoculation	1	76	7.03	0.0097		7.031	0.05	3.96676	0.74475
7		1	76	9.23	0.0033	Inoculation_Method	9.226	0.05	3.96676	0.85058
8		1	76	103.28	<.0001	Thickness	103.276	0.05	3.96676	1.00000
9		1	76	41.12	<.0001	Inoculatio*Thickness	41.120	0.05	3.96676	0.99999
10		4	76	7.82	<.0001	Week	31.280	0.05	2.49205	0.99659
11		4	76	13.77	<.0001	Inoculation_Met*Week	55.092	0.05	2.49205	1.00000
12		4	76	20.78	<.0001	Thickness*Week	83.132	0.05	2.49205	1.00000
13		4	76	4.04	0.0050	Inocula*Thickne*Week	16.162	0.05	2.49205	0.89525

Figure 1: Results of power analysis.

The first six rows of the table correspond to the contrasts the clients were interested in testing, while the bottom seven rows are measuring the fixed effects of the model. Many of the terms have a very high power. Specifically the fixed effects were all high enough for both the clients and ourselves to feel comfortable using five batches. Two of the orthogonal contrasts, *Dry vs Wet at 1/4 Inches* and *1/4 vs 1/8 inches for Wet inoculation* did have lower power scores, but after talking with both the clients and Dr. Howard about them, we felt comfortable proceeding.

Simulating Data

After finding the necessary number of batches, which was five, we proceeded with simulating the data. The estimated treatment means and variances provided by the client were used in the simulation as well. We then reviews the simulated dataset for major issues, such as negative response values, and reran the power analysis on the new data set to ensure everything was working properly. After finding no problems with the dataset, we sent it to your clients.

Data Analysis

Summary Statistics

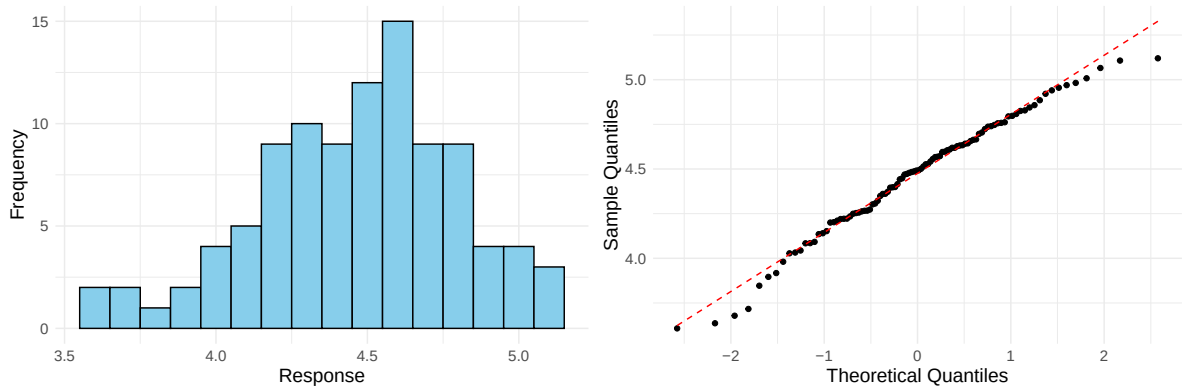
As part of the project, we analyzed the simulated dataset. Before fitting out model to the dataset, we first wanted to explore some of the variables. Figure 2 shows the mean values and standard deviations for each treatment combination. We can see the changes in mean values are small, so further exploration and analysis are needed.

Inoculation Method	Thickness	Week	Mean Response	SD Response	Count
Dry	1/4-inch	1	4.199	0.187	5
Dry	1/4-inch	2	4.137	0.163	5
Dry	1/4-inch	3	4.187	0.294	5
Dry	1/4-inch	4	4.306	0.272	5
Dry	1/4-inch	5	4.645	0.178	5
Dry	1/8-inch	1	4.801	0.173	5
Dry	1/8-inch	2	4.801	0.238	5
Dry	1/8-inch	3	4.596	0.235	5
Dry	1/8-inch	4	4.425	0.206	5
Dry	1/8-inch	5	4.876	0.177	5
Wet	1/4-inch	1	4.240	0.307	5
Wet	1/4-inch	2	4.523	0.236	5
Wet	1/4-inch	3	4.534	0.173	5
Wet	1/4-inch	4	4.357	0.421	5
Wet	1/4-inch	5	4.299	0.200	5
Wet	1/8-inch	1	4.697	0.181	5
Wet	1/8-inch	2	4.809	0.327	5
Wet	1/8-inch	3	4.530	0.215	5
Wet	1/8-inch	4	4.223	0.361	5
Wet	1/8-inch	5	4.151	0.295	5

Figure 2: Summary of response rariable across factors and weeks

Distribution of response variable

Before continuing our investigation into the relationships among the treatment variables, we want to look into the response variable (Salmonella levels). Specifically, we want to see how it is distributed. Figure 3 shows a histogram and Q-Q plot of the response variable in the left and right plots respectively. While the histogram shows a slight potential skew, this is not enough for us say the distribution is non-normal. Furthermore, the Q-Q plot indicates the response variable follows a relatively normal distribution.



(a) Histogram

(b) Q-Q plot

Figure 3: Plots to see the distribution of the response variable.

Exploring the Data

Now we will graphically look at how the different variables of the model impact the response variable. Figure 4 shows how the mean response variables we saw in Figure 2 change over time, while also controlling for thickness and inoculation method. Note the y-axis of plot does not start at the origin. We can see the mean values of samples that used a wet inoculation method (blue lines) tended decrease over time, while samples with the dry inoculation method (red lines) were more of a mixed bag but saw sharp increases between weeks four and five. The samples cut to 1/8 inches thick (dashed lines) were very similar for most weeks, but diverged near the end of the experiment, while samples cut to 1/4 inches thick (solid lines) did not seem as similar.

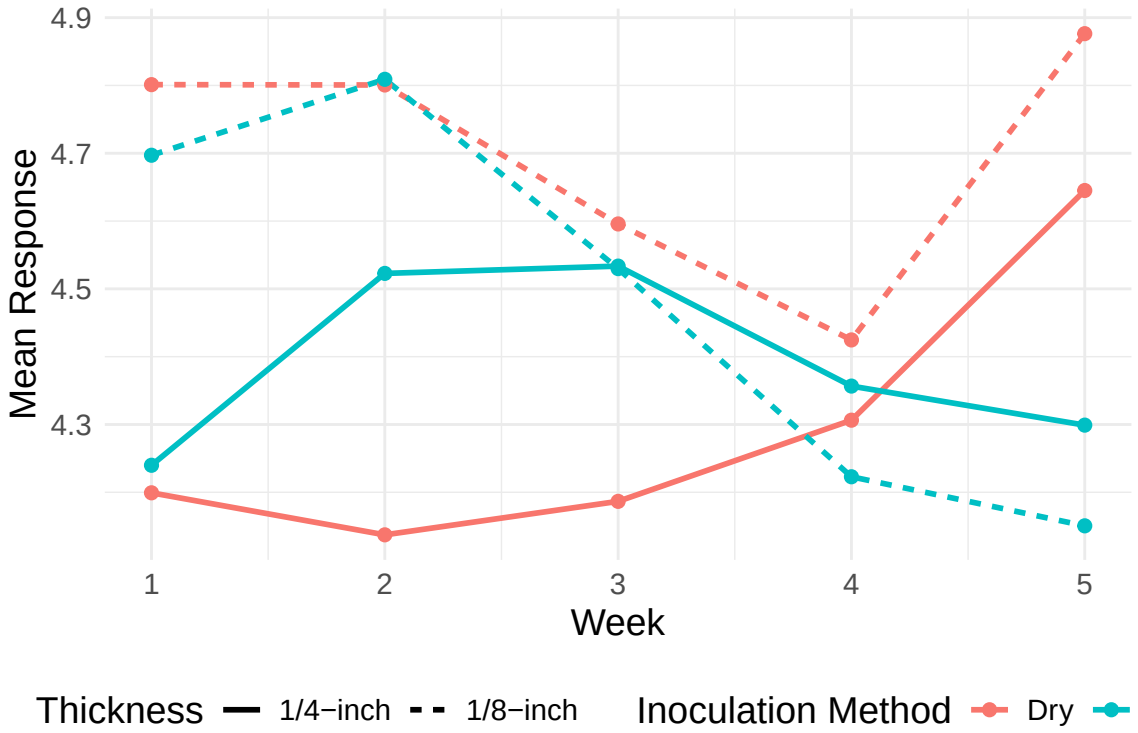


Figure 4: Line plot of response variable over time, controlling for thickness and inoculation method.

PROBLEM - ONLY 5 SAMPLES IN EACH BOX Since Figure 4 only considers the mean values of the response variables for each treatment combination, there is potential variability we have not shown. Figure 5 shows two boxplots to show how all observations differ over time. The left plot contains all samples cut to 1/4 inches thick, while the right plot contains the 1/8 inch thick samples. From the different sizes of boxes we can see the

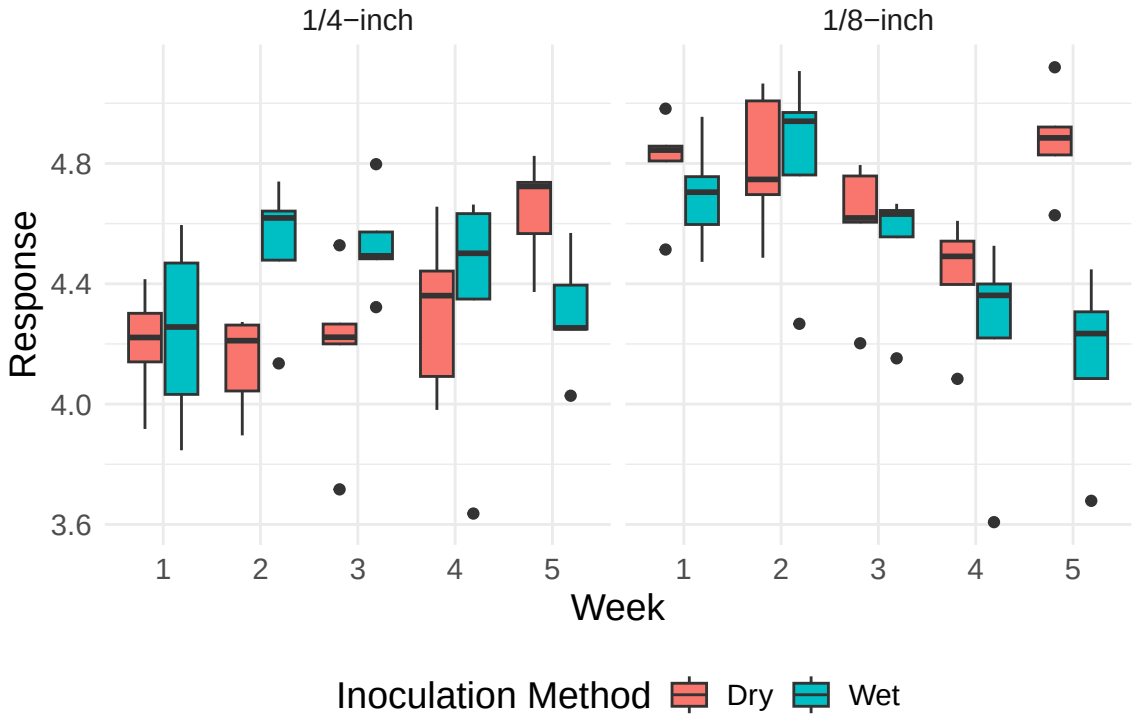
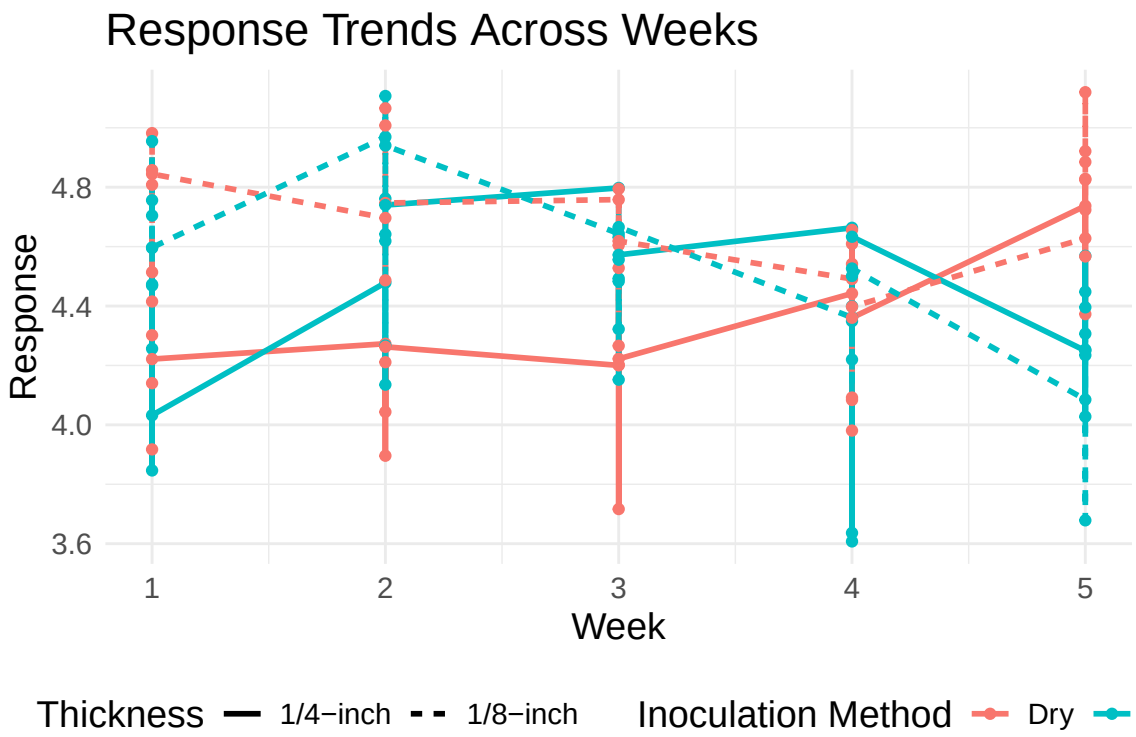
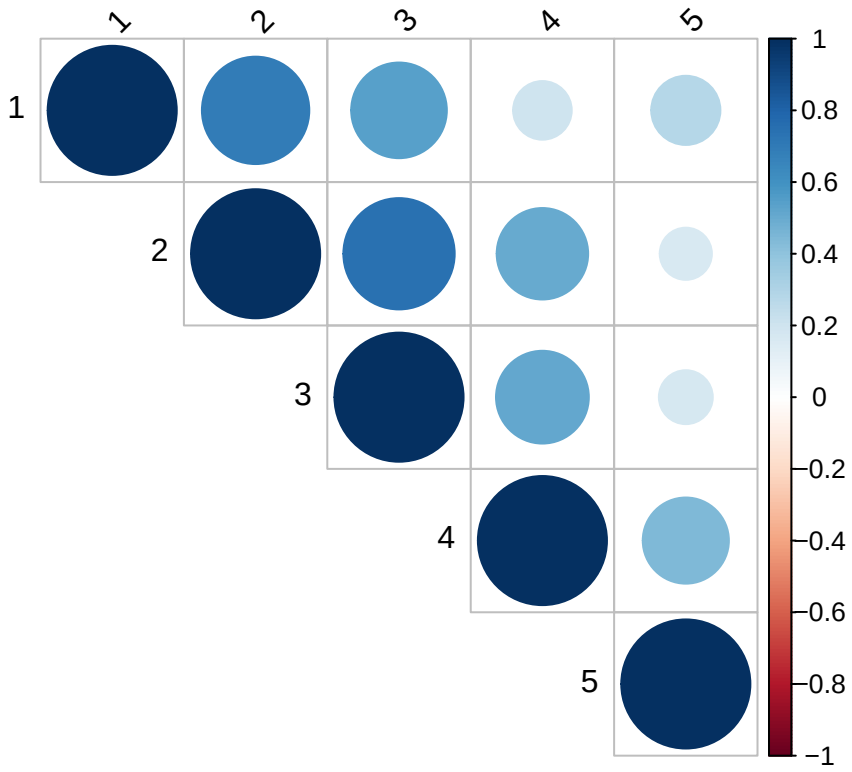


Figure 5: Boxplot of response variable over time, controlling for thickness and inoculation method.



Correlation Structure

	1	2	3	4	5
1	1.0000000	0.6918258	0.5490182	0.2060472	0.2870003
2	0.6918258	1.0000000	0.7435360	0.5019587	0.1631757
3	0.5490182	0.7435360	1.0000000	0.5166170	0.1741178
4	0.2060472	0.5019587	0.5166170	1.0000000	0.4450908
5	0.2870003	0.1631757	0.1741178	0.4450908	1.0000000



Model Comparison

The UN (Unstructured) model provides the best fit based on AIC and BIC, but it requires estimating many parameters. The ARH(1) model is a strong alternative, balancing simplicity with good fit, especially under BIC. The VC (Variance Components) and AR(1) models perform similarly under AICC, with AR(1) offering a simpler time correlation structure. BIC penalizes complexity more than AIC, favoring simpler models like ARH(1) over UN. Overall, UN is ideal for maximum flexibility, while AR(1) or ARH(1) are practical choices for computational efficiency and simplicity.

Mixed Model

1. RCBD

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: Response ~ Inoculation_Method * Thickness * Week + (1 | Batches)
   Data: data
```

Model	AIC	AICC	BIC
VC	-12.25	-12.09	-13.03
UN	-12.22	-3.58	-18.47
CS	-11.60	-11.29	-12.77
AR(1)	-12.86	-12.55	-14.03
ARH(1)	-12.56	-11.01	-15.30
ANTE(1)	-8.57	-5.39	-12.48
TOEP	-7.34	-6.19	-9.68

Figure 6: Model comparison table.

```
REML criterion at convergence: 7.3

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.65630 -0.66148  0.03765  0.64493  2.45790

Random effects:
 Groups   Name        Variance Std.Dev.
 Batches  (Intercept) 0.03574  0.1890
 Residual             0.04095  0.2024
Number of obs: 100, groups:  Batches, 5

Fixed effects:
                                            Estimate Std. Error       df
(Intercept)                                  3.97667    0.12711 17.26822
Inoculation_MethodWet                        0.42805    0.13423 88.00001
Thickness1/8-inch                            0.79075    0.13423 88.00001
Week                                         0.10608    0.02862 88.00001
Inoculation_MethodWet:Thickness1/8-inch     -0.20981    0.18983 88.00001
Inoculation_MethodWet:Week                  -0.11086    0.04047 88.00001
Thickness1/8-inch:Week                      -0.12864    0.04047 88.00001
Inoculation_MethodWet:Thickness1/8-inch:Week -0.03451    0.05724 88.00001
                                            t value Pr(>|t|)
(Intercept)                                  31.286  < 2e-16 ***
Inoculation_MethodWet                         3.189 0.001979 **
Thickness1/8-inch                             5.891  6.9e-08 ***
Week                                          3.707 0.000367 ***
Inoculation_MethodWet:Thickness1/8-inch      -1.105 0.272070
Inoculation_MethodWet:Week                   -2.739 0.007457 **
```

```
Thickness1/8-inch:Week                          -3.178 0.002044 **
Inoculation_MethodWet:Thickness1/8-inch:Week  -0.603 0.548158
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) Inc_MW Th1/8- Week   In_MW:T1/8- I_MW:W T1/8-:
Incltn_MthW -0.528
Thcknss1/8- -0.528  0.500
Week        -0.675  0.640  0.640
In_MW:T1/8-  0.373 -0.707 -0.707 -0.452
Incltn_MW:W  0.478 -0.905 -0.452 -0.707  0.640
Thckn1/8-:W  0.478 -0.452 -0.905 -0.707  0.640       0.500
I_MW:T1/8-: -0.338  0.640  0.640  0.500 -0.905      -0.707 -0.707

Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: Response ~ Inoculation_Method * Thickness * Week + (1 | Batches) +
    (1 | Batches:Week)
   Data: data

REML criterion at convergence: 4.8

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.23547 -0.54967  0.00388  0.63090  2.32784

Random effects:
 Groups       Name        Variance Std.Dev.
 Batches:Week (Intercept) 0.006513 0.0807
 Batches      (Intercept) 0.034715 0.1863
 Residual                 0.035326 0.1880
Number of obs: 100, groups:  Batches:Week, 25; Batches, 5

Fixed effects:
                                            Estimate Std. Error       df
(Intercept)                                  3.97667    0.12707 17.18690
Inoculation_MethodWet                        0.42805    0.12467 68.99732
Thickness1/8-inch                            0.79075    0.12467 68.99732
Week                                         0.10608    0.02893 77.57730
Inoculation_MethodWet:Thickness1/8-inch     -0.20981    0.17631 68.99732
Inoculation_MethodWet:Week                  -0.11086    0.03759 68.99732
```

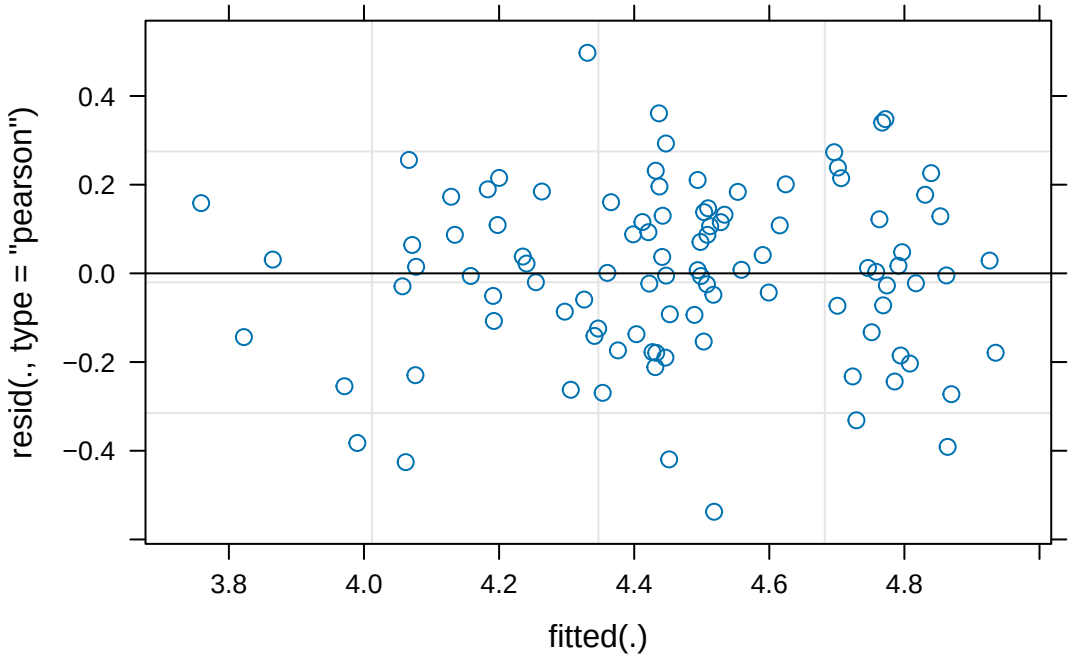
```
Thickness1/8-inch:Week                          -0.12864    0.03759 68.99732
Inoculation_MethodWet:Thickness1/8-inch:Week -0.03451    0.05316 68.99732
                                                t value Pr(>|t|)
(Intercept)                                      31.294  < 2e-16 ***
Inoculation_MethodWet                             3.433 0.001012 **
Thickness1/8-inch                                 6.343 2.02e-08 ***
Week                                              3.667 0.000447 ***
Inoculation_MethodWet:Thickness1/8-inch          -1.190 0.238128
Inoculation_MethodWet:Week                       -2.949 0.004347 **
Thickness1/8-inch:Week                           -3.422 0.001049 **
Inoculation_MethodWet:Thickness1/8-inch:Week  -0.649 0.518440
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) Inc_MW Th1/8- Week   In_MW:T1/8- I_MW:W T1/8-:
Incltn_MthW -0.491
Thcknss1/8- -0.491  0.500
Week        -0.683  0.588  0.588
In_MW:T1/8-  0.347 -0.707 -0.707 -0.416
Incltn_MW:W  0.444 -0.905 -0.452 -0.650  0.640
Thckn1/8-:W  0.444 -0.452 -0.905 -0.650  0.640       0.500
I_MW:T1/8-: -0.314  0.640  0.640  0.459 -0.905      -0.707 -0.707
```

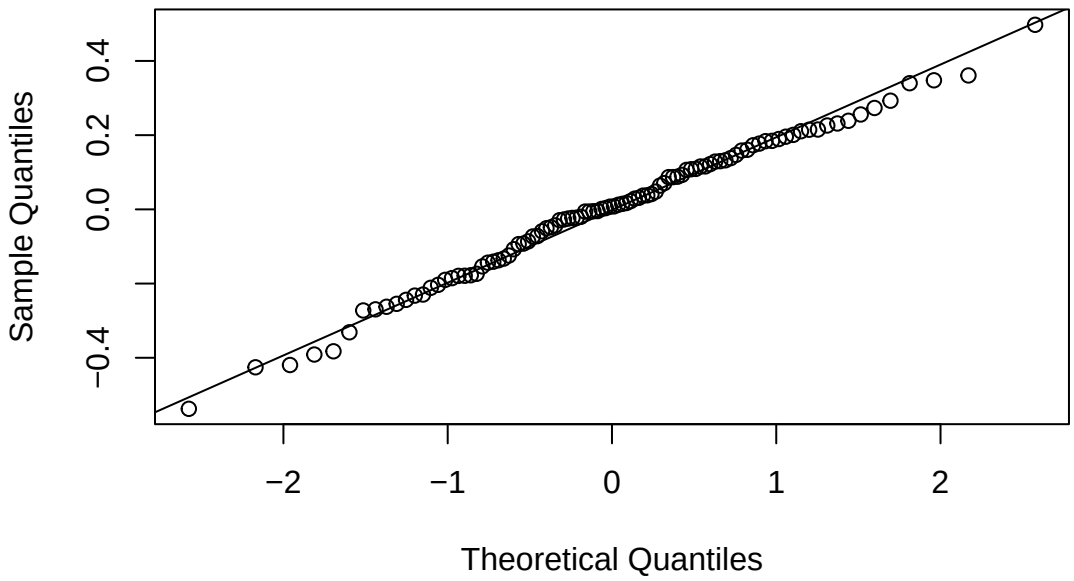
3. Weeks differs across Batches

```
Linear mixed model fit by REML. t-tests use Satterthwaite's method [
lmerModLmerTest]
Formula: Response ~ Inoculation_Method * Thickness * Week + (1 | Batches) +
    (1 | Batches:Week)
   Data: data

REML criterion at convergence: 4.8

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.23547 -0.54967  0.00388  0.63090  2.32784

Random effects:
 Groups       Name        Variance Std.Dev.
 Batches:Week (Intercept) 0.006513 0.0807
 Batches      (Intercept) 0.034715 0.1863
 Residual                 0.035326 0.1880
```

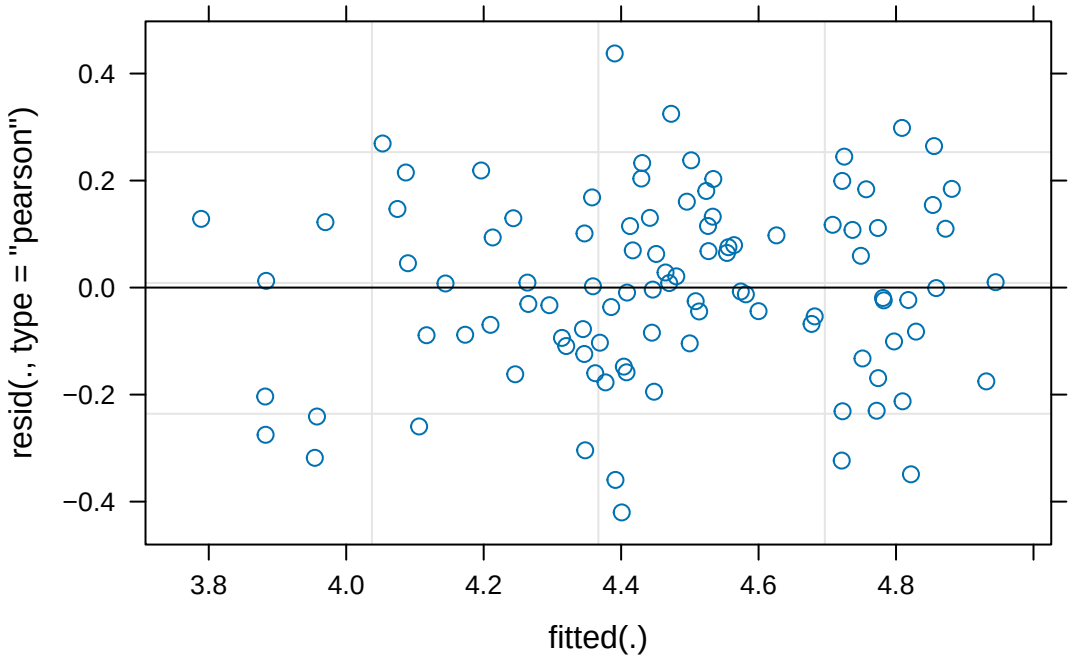
```
Number of obs: 100, groups:  Batches:Week, 25; Batches, 5

Fixed effects:
                                            Estimate Std. Error       df
(Intercept)                                  3.97667    0.12707 17.18690
Inoculation_MethodWet                        0.42805    0.12467 68.99732
Thickness1/8-inch                            0.79075    0.12467 68.99732
Week                                         0.10608    0.02893 77.57730
Inoculation_MethodWet:Thickness1/8-inch     -0.20981    0.17631 68.99732
Inoculation_MethodWet:Week                  -0.11086    0.03759 68.99732
Thickness1/8-inch:Week                      -0.12864    0.03759 68.99732
Inoculation_MethodWet:Thickness1/8-inch:Week -0.03451    0.05316 68.99732
                                            t value Pr(>|t|)
(Intercept)                                  31.294  < 2e-16 ***
Inoculation_MethodWet                         3.433 0.001012 **
Thickness1/8-inch                             6.343 2.02e-08 ***
Week                                          3.667 0.000447 ***
Inoculation_MethodWet:Thickness1/8-inch      -1.190 0.238128
Inoculation_MethodWet:Week                   -2.949 0.004347 **
Thickness1/8-inch:Week                       -3.422 0.001049 **
Inoculation_MethodWet:Thickness1/8-inch:Week  -0.649 0.518440
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
            (Intr) Inc_MW Th1/8- Week   In_MW:T1/8- I_MW:W T1/8-:
Incltn_MthW -0.491
Thcknss1/8- -0.491  0.500
Week        -0.683  0.588  0.588
In_MW:T1/8-  0.347 -0.707 -0.707 -0.416
Incltn_MW:W  0.444 -0.905 -0.452 -0.650  0.640
Thckn1/8-:W  0.444 -0.452 -0.905 -0.650  0.640       0.500
I_MW:T1/8-: -0.314  0.640  0.640  0.459 -0.905      -0.707 -0.707
```

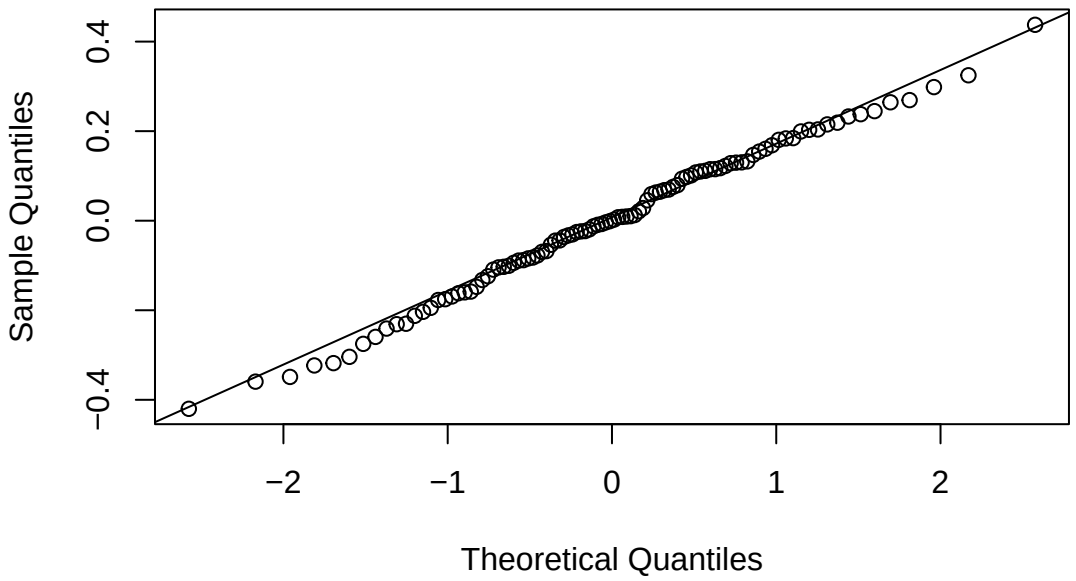
Model Diagnozition






```
Type III Analysis of Variance Table with Satterthwaite's method
                                  Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
Inoculation_Method                0.47465 0.47465     1    88 11.5906    0.0010
Thickness                         2.13808 2.13808     1    88 52.2103 1.714e-10
Week                              0.09943 0.09943     1    88  2.4280    0.1228
Inoculation_Method:Thickness      0.05002 0.05002     1    88  1.2215    0.2721
Inoculation_Method:Week           0.82064 0.82064     1    88 20.0393 2.264e-05
Thickness:Week                    1.06420 1.06420     1    88 25.9870 1.950e-06
Inoculation_Method:Thickness:Week 0.01488 0.01488     1    88  0.3634    0.5482

Inoculation_Method                **
Thickness                         ***
Week
Inoculation_Method:Thickness
Inoculation_Method:Week           ***
Thickness:Week                    ***
Inoculation_Method:Thickness:Week
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


resid(., type = "pearson")
0.4
0.2
0.0
−0.2
−0.4
3.8
4.0
4.2
4.4
4.6
4.8
fitted(.)



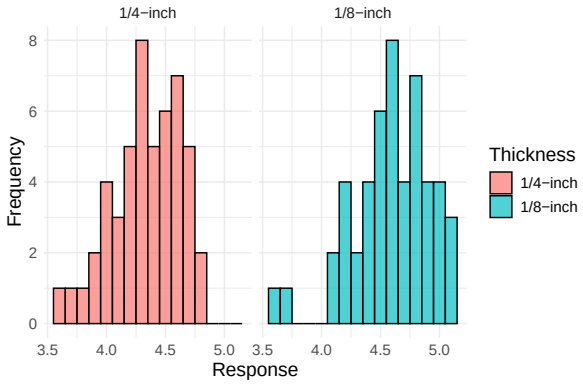

```
Type III Analysis of Variance Table with Satterthwaite's method
                                  Sum Sq Mean Sq NumDF  DenDF F value
Inoculation_Method                0.47465 0.47465     1 68.997 13.4365
Thickness                         2.13808 2.13808     1 68.997 60.5250
Week                              0.05722 0.05722     1 19.002  1.6199
Inoculation_Method:Thickness      0.05002 0.05002     1 68.997  1.4161
Inoculation_Method:Week           0.82064 0.82064     1 68.997 23.2306
Thickness:Week                    1.06420 1.06420     1 68.997 30.1256
Inoculation_Method:Thickness:Week 0.01488 0.01488     1 68.997  0.4213
                                     Pr(>F)
Inoculation_Method                0.0004807 ***
Thickness                         5.054e-11 ***
Week                              0.2184554
Inoculation_Method:Thickness      0.2381275
Inoculation_Method:Week           8.239e-06 ***
Thickness:Week                    6.287e-07 ***
Inoculation_Method:Thickness:Week 0.5184400
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Data: data
Models:
rcbd_model: Response ~ Inoculation_Method * Thickness * Week + (1 | Batches)
repeated_model: Response ~ Inoculation_Method * Thickness * Week + (1 | Batches) + (1 | Batch
repeated_slop_model: Response ~ Inoculation_Method * Thickness * Week + (1 | Batches) + (1 |
                    npar      AIC    BIC logLik deviance Chisq Df Pr(>Chisq)
rcbd_model            10  -9.5603 16.491 14.780  -29.560
repeated_model        11 -10.5583 18.099 16.279  -32.558 2.998  1    0.08337 .
repeated_slop_model   11 -10.5583 18.099 16.279  -32.558 0.000  0
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Post hoc test

```
$emmeans
 Inoculation_Method Thickness emmean     SE   df lower.CL upper.CL
 Dry                1/4-inch    4.29 0.0928 5.19     4.06     4.53
 Wet                1/4-inch    4.39 0.0928 5.19     4.15     4.63
 Dry                1/8-inch    4.70 0.0928 5.19     4.46     4.94
 Wet                1/8-inch    4.48 0.0928 5.19     4.25     4.72

Degrees-of-freedom method: kenward-roger
Confidence level used: 0.95

$contrasts
 contrast                          estimate     SE df t.ratio p.value
 (Dry 1/4-inch) - (Wet 1/4-inch)  -0.0955 0.0532 69  -1.796  0.2841
 (Dry 1/4-inch) - (Dry 1/8-inch)  -0.4048 0.0532 69  -7.615  <.0001
 (Dry 1/4-inch) - (Wet 1/8-inch)  -0.1870 0.0532 69  -3.517  0.0042
 (Wet 1/4-inch) - (Dry 1/8-inch)  -0.3094 0.0532 69  -5.819  <.0001
 (Wet 1/4-inch) - (Wet 1/8-inch)  -0.0915 0.0532 69  -1.721  0.3206
 (Dry 1/8-inch) - (Wet 1/8-inch)   0.2179 0.0532 69   4.098  0.0006

Degrees-of-freedom method: kenward-roger
P value adjustment: tukey method for comparing a family of 4 estimates
```

EXTRA PLOTS RYAN TOOK OUT - WE CAN PUT BACK IN LATER IF WE WANT



(a) 1/4 inch thickness

Figure 7: Histograms of response variable controlling for thickness.

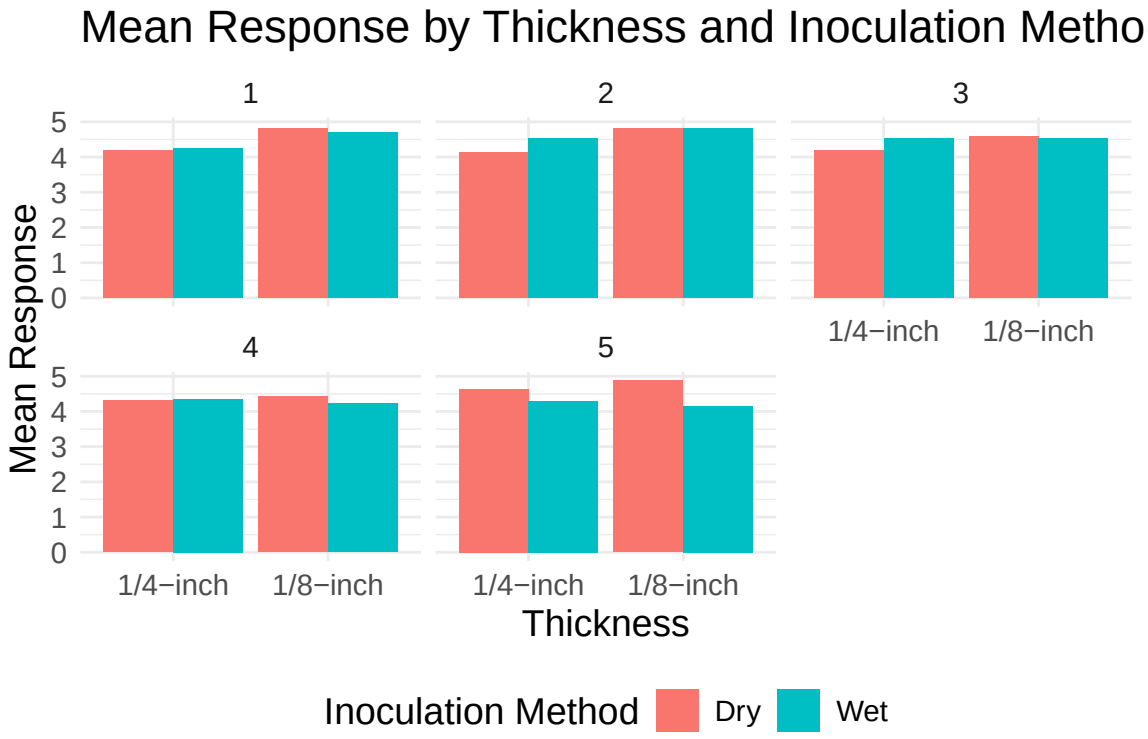


Figure 8: Barplot of response variable controlling for thickness and inoculation method.

Conclusion

Future Work

References

Brown, Jessica, Taylor Bannon, Chad AND Kowalcyk Havelaar Arie AND Carr, and Jason M. Scheffler. 2024. "Inactivation of Salmonella Enterica, Escherichia Coli O157:H7, and Campylobacter Jejuni in a Restructured Beef Jerky Developed for Production in Ethiopia." *Meat and Muscle Biology* 8 (April): 1–12. https://doi.org/10.22175/mmb.16091.

Appendix A - R Code

Appendix B - SAS Code

Power Analysis

```
data rptm_means;
input Inoculation_Method $ Thickness $ @@;
do Week=1 to 5 by 1;
    input mu @@;
    output;
end;
datalines;
Dry 1/4 4.26 4.25 4.47 4.33 4.54
Dry 1/8 4.91 4.95 4.67 4.56 4.97
Wet 1/4 4.21 4.57 4.65 4.49 4.38
Wet 1/8 4.86 4.78 4.62 4.32 4.22
;

data rptm_design;
 set rptm_means;
 do Batches = 1 to 5; /* Creating 3 blocks (batches) */
  output;
 end;
run;

proc print data=rptm_design;
run;

/* Creating Model */

proc glimmix data=rptm_design;
    class Batches Inoculation_Method Thickness Week;
    model mu = Inoculation_Method|Thickness|Week;
    random intercept / subject=Batches;
    random Week / subject=Batches*Inoculation_Method*Thickness type=ar(1) residual;
    parms (.029)(0.017)(.028)/hold=1,2,3;  /* Provide 3 parameters for variance components */
    lsmeans Inoculation_Method*Thickness*Week / slicediff=Week cl;
    /* Define main effect contrasts */
    contrast 'Dry vs Wet'
        Inoculation_Method 1 -1;
    contrast '1/4 vs 1/8 inches'
        Thickness 1 -1;
```

```
    /* Define interaction contrasts */
   contrast 'Dry vs Wet at 1/4 Inches'
        Inoculation_Method 1 -1 Inoculation_Method*Thickness 1 0 -1 0;
    contrast 'Dry vs Wet at 1/8 Inches'
        Inoculation_Method 1 -1 Inoculation_Method*Thickness 0 1 0 -1;
    contrast '1/4 vs 1/8 inches for Dry inoculation'
        Thickness 1 -1 Inoculation_Method*Thickness 1 -1 0 0;
    contrast '1/4 vs 1/8 inches for Wet inoculation'
        Thickness 1 -1 Inoculation_Method*Thickness 0 0 1 -1;

    ods output contrasts=f_contrast tests3=f_anova;
run;

/*Power*/
data power;
    set f_contrast f_anova;
    ncparm = numdf * fvalue;
    alpha = 0.05;
    fcrit = finv(1-alpha, numdf, dendf, 0);
    power = 1 - probf(fcrit, numdf, dendf, ncparm);
run;

proc print data=power;
run;
```

Simulation

```
/* Step 1: Define AR(1) Covariance Structure in PROC IML */
proc iml;
    n = 20;                    /* Number of subjects per treatment, updated to 20 */
    mean = {0 0 0 0 0};        /* Mean for each week */
    T = 5;                     /* Number of repeated measures (weeks) */
    rho = 0.2;                 /* AR(1) correlation parameter */
    sigma2 = {0.29 0.29 0.29 0.29 0.29};      /* Variance for each week */

    /* Construct AR(1) covariance matrix */
    cov = j(T, T, 0);
    do i = 1 to T;
        do j = 1 to T;
            cov[i, j] = sqrt(sigma2[i] * sigma2[j]) * rho**abs(i - j);
```

```
        end;
    end;

    /* Print covariance matrix */
    print "Covariance Matrix:", cov;

    /* Generate simulated data using the covariance matrix */
    call randseed(12349);      /* Set random seed */
    x = randnormal(n, mean, cov); /* Simulate AR(1) correlated data */
    cname = {"t1", "t2", "t3", "t4", "t5"};

    /* Print the simulated data matrix directly */
    print "Simulated Data Matrix (x):", x;
    /* Print Sample mean */
    samplemean = x[:,];
    print samplemean n;

    /* Create dataset from simulated data */
    create inputdatacb from x[colname=cname];
    append from x;
close inputdatacb;
quit;

/* Step 2: Display the Simulated Data as a SAS Table */
proc print data=inputdatacb label;
    title "Simulated Data with AR(1) Covariance Structure";
run;

/* Step 3: Define Treatment Structure and Random Effects */
data rptm_simulation;
    retain Subject 0;
    keep Inoculation_Method Thickness Week Batches Response;

    array weeks[5] t1-t5;

    /* Define mean values for each combination of factors and week */
    if _n_ = 1 then do;
        array mean_values[4,2,5] _temporary_ (
            /* Dry, 1/4 inch */
            4.26, 4.25, 4.47, 4.33, 4.54,
            /* Dry, 1/8 inch */
            4.91, 4.95, 4.67, 4.56, 4.97,
```

```
            /* Wet, 1/4 inch */
            4.21, 4.57, 4.65, 4.49, 4.38,
            /* Wet, 1/8 inch */
            4.86, 4.78, 4.62, 4.32, 4.22
        );
    end;

    /* Simulation parameters */
    sigma_batch = sqrt(0.029); /* Batch variance */
    sigma_resid = sqrt(0.017); /* Residual variance */

    /* Loop through each combination of factors */
    do Batches = 1 to 5; /* Number of batches */
        batch_effect = rand("Normal", 0, sigma_batch); /* Random batch effect */

        do Inoculation_Method = "Dry", "Wet";
            do Thickness = "1/4-inch", "1/8-inch";
                Subject + 1;
                set inputdatacb;

                /* Generate response for each week with AR(1) structure */
                do Week = 1 to 5;
                    Mean_Value = mean_values[
                        (Inoculation_Method="Dry")*1 + (Inoculation_Method="Wet")*2,
                        (Thickness="1/4-inch")*1 + (Thickness="1/8-inch")*2,
                        Week
                    ];
                    Response = Mean_Value + batch_effect + weeks[Week];
                    output;
                end;
            end;
        end;
    end;
run;

/* Step 4: Display the Simulated Data in a Structured Format */
proc print data=rptm_simulation label;
    title "Simulated Data for 2x2 Factorial Design with Repeated Measures";
run;
```

Analysis

Appendix C - Additional SAS Output