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## STAT 461: Project

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## GATHERING DATA

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The following table outlines the factors that were considered, their levels, and how they are associated. Originally tray position was not considered as a factor, however, when putting the trays into the oven, only one tray would fit on the top rack so the difference in top and bottom racks was added after the fact.

Factor	Levels	Fixed?	Nested/Crossed
Butter (b)	Melted (M), Creamed (C)	Fixed	Crossed with Dough & Tray
Dough Temp (d)	Refrigerated (R), NOT Refrigerated (N)	Fixed	Crossed with Butter & Tray
Tray Position (t)	Top (T), Bottom (B)	Fixed	Crossed with Butter & Dough

Using the possible combinations of butter and dough temperature, R was used draw 2 samples for position assignment for each tray. The following is the output from this procedure.

```
1 > tray1
2 [1] "CN" "CN" "MR" "CN" "MR" "CR" "CR" "MR" "MN" "MN" "CR" "MN"
3 > tray2
4 [1] "CN" "CN" "CR" "CR" "MR" "MN" "CN" "MN" "MR" "MR" "MN" "CR"
```

Listing 1: Randomized Tray Locations

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## DATA PLOTS

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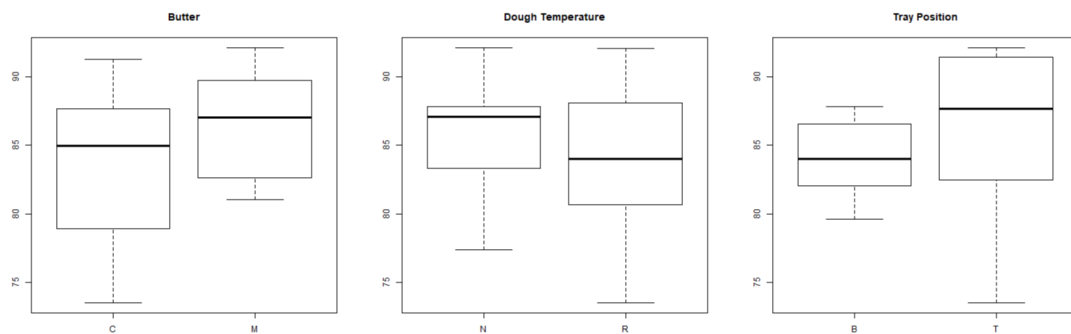


Figure 1: Individual Factor Effects on Cookie Size

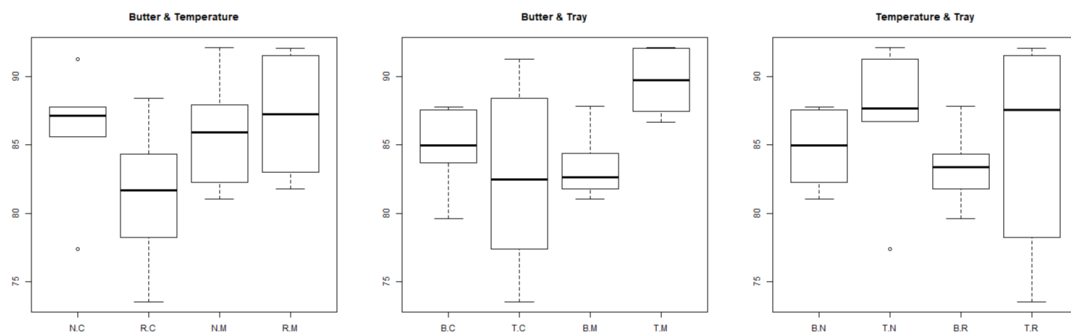


Figure 2: Pairwise Factor Effects on Cookie Size

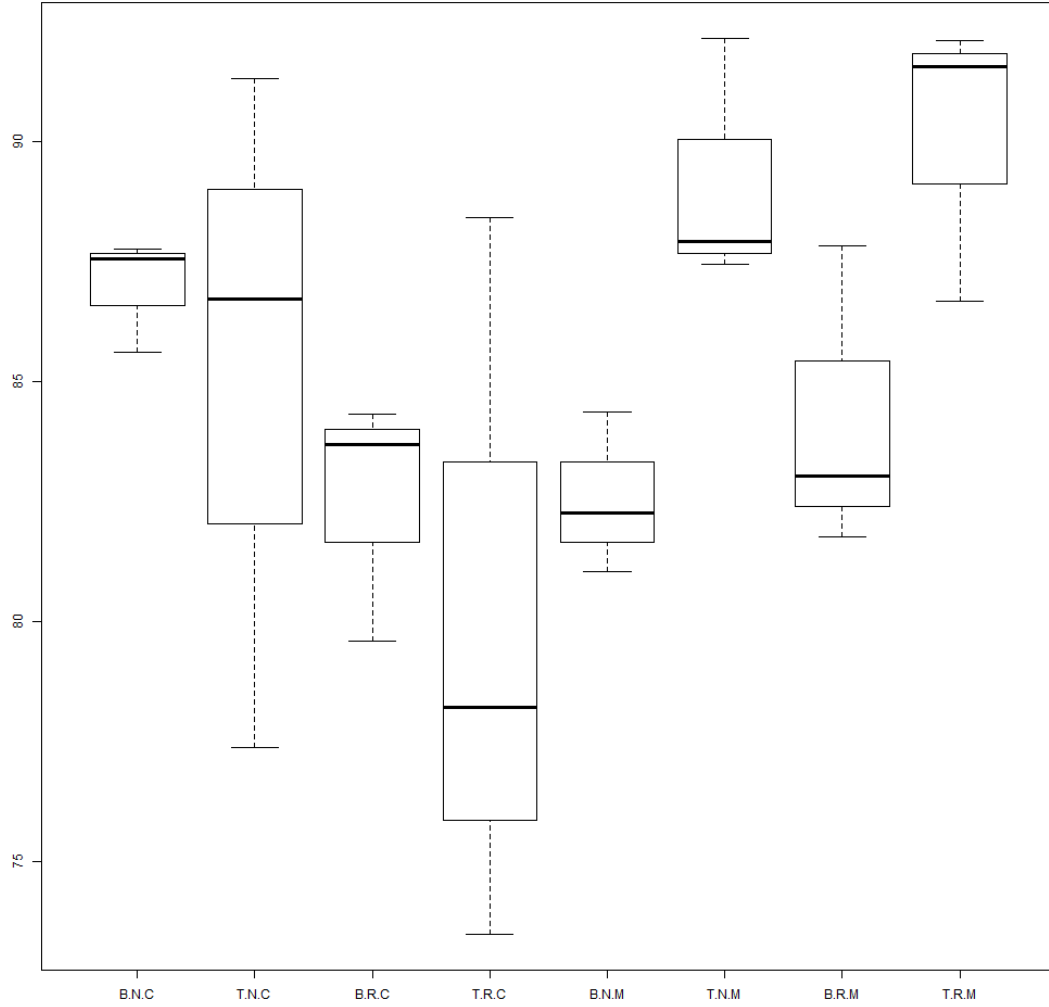


Figure 3: Full Factor Effects on Cookie Size

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## MODEL

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Using the full model with all interactions, we can obtain the following model:

$$Y_{b,d,t,c} = \alpha_b + \beta_d + \gamma_t + (\alpha\beta)_{b,d} + (\alpha\gamma)_{b,t} + (\beta\gamma)_{d,t} + \epsilon_{b,d,t,c}$$

$$\epsilon_{b,d,t,c} \sim N(0, \sigma^2)$$

If one were to only examine the main effects, the ME model is as follows:

$$Y_{b,d,t,c} = \alpha_b + \beta_d + \gamma_t + \epsilon_{b,d,t,c}$$

$$\epsilon_{b,d,t,c} \sim N(0, \sigma^2)$$

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## R ANALYSIS

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Looking at the ANOVA table for the full model, we can see that the only truly significant factor is the interaction between the type of butter used and the tray position. The chilled dough and butter type interaction is significant if we relax our alpha value to 0.1.

```

1 > cookieFullModel = aov(size ~ tray + chilled + butter + tray:chilled + tray:butter +
  chilled:butter, data=cookies)
2 > anova(cookieFullModel)
3 Analysis of Variance Table
4
5 Response: size
6      Df Sum Sq Mean Sq F value    Pr(>F)
7 tray      1  25.133   25.133   1.4696  0.24198
8 chilled    1  18.131   18.131   1.0602  0.31760
9 butter     1  48.621   48.621   2.8431  0.11003
10 tray:chilled 1    0.680    0.680   0.0398  0.84430
11 tray:butter  1 106.597  106.597   6.2332  0.02311 *
12 chilled:butter 1  55.085   55.085   3.2211  0.09050 .
13 Residuals   17 290.726   17.102
14 ---
15 Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Listing 2: Full Model ANOVA Table

For robustness, examining the full model yields the same result that the individual factors are not enough to result in a difference in the size of the cookies.

```

1 > cookieMainModel = aov(size ~ tray + chilled + butter, data=cookies)
2 > anova(cookieMainModel)
3 Analysis of Variance Table
4
5 Response: size
6      Df Sum Sq Mean Sq F value    Pr(>F)
7 tray      1  25.13   25.133   1.1094  0.3048
8 chilled    1  18.13   18.131   0.8003  0.3816
9 butter     1  48.62   48.621   2.1462  0.1585
10 Residuals 20 453.09   22.654
11 ---
12 Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Listing 3: Main Effects Model ANOVA Table

Moving to check our normality assumptions, the below Q-Q and Residual vs Fitted Plots. The residual vs fitted plot shows relatively constant variance and there is nothing significantly out of place in the Q-Q plot to indicate that our normality assumptions are violated. The tails are both a bit skewed but the majority of the data is within a reasonable variance. Performing a log and square-root transformation on the data yielded minimal change in the normality plots, so the unaltered model was used.

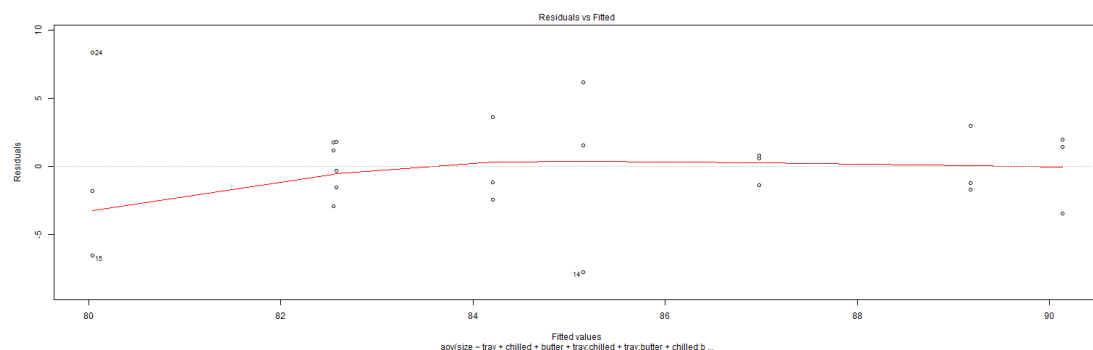


Figure 4: Residual vs Fitted Plot for Full Model

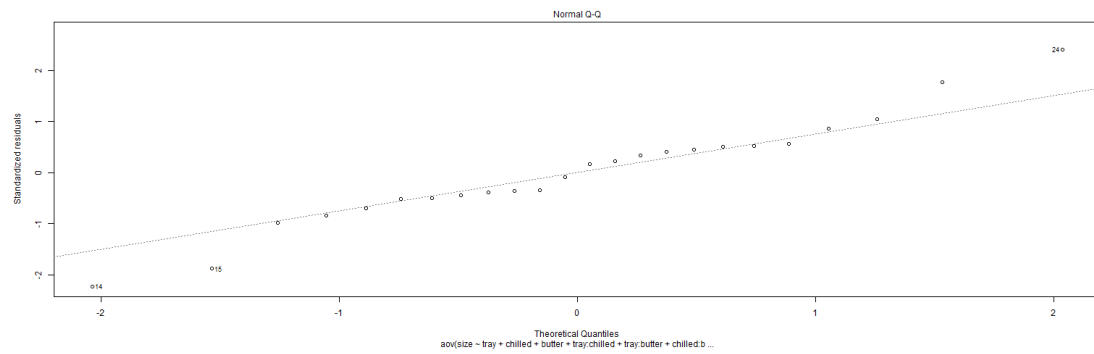


Figure 5: Q-Q Plot for Full Model

Finally, because the only significant terms are interaction terms, an interaction plot was created for the two interaction pairs. These plots are below:

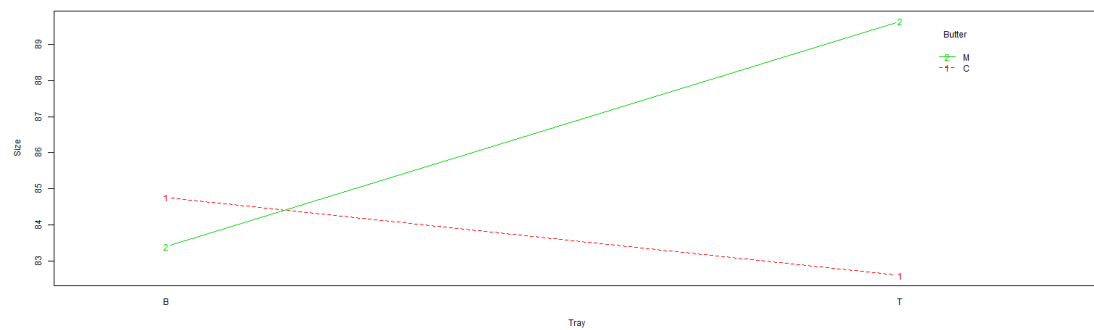


Figure 6: (Tray Position:Butter Type) Interaction Plot

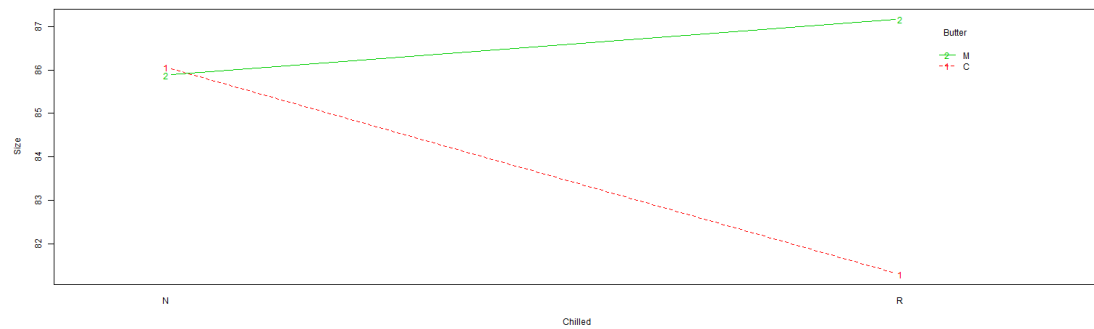


Figure 7: (Dough Temperature:Butter Type) Interaction Plot

## DATA APPENDIX

Size (mm)	Butter	Dough Temperature	Tray Position
85.61	C	N	B
87.56	C	N	B
83.03	M	R	B
87.78	C	N	B
81.78	M	R	B
83.70	C	R	B
84.32	C	R	B
87.83	M	R	B
82.28	M	N	B
81.06	M	N	B
79.60	C	R	B
84.38	M	N	B
91.32	C	N	T
77.38	C	N	T
73.49	C	R	T
78.23	C	R	T
86.69	M	R	T
87.93	M	N	T
86.72	C	N	T
87.45	M	N	T
91.57	M	R	T
92.12	M	R	T
92.17	M	N	T
88.42	C	R	T

Table of Collected Data

## CODE APPENDIX

```
1 #####
2 #### Setup
3 #####
4 ## Install and load libraries
5 # ipak function taken from: https://gist.github.com/stevenworthington/3178163
6 ipak = function(pkg) {
7   new.pkg = pkg[!(pkg %in% installed.packages()[, "Package"])]
8   if (length(new.pkg))
9     install.packages(new.pkg, dependencies = TRUE)
10  sapply(pkg, require, character.only = TRUE)
11 }
12 packages = c("ggplot2", "ggplotify", "reshape2", "gridExtra", "TSA", "astsa",
13             "orcutt", "nlme", "fGarch", "vars", "lsmeans", "multcompView",
14             "base2grob", "lme4", "lmerTest")
15 ipak(packages)
16
17 #####
18 #### Randomly assign 3 of each pair of treatments to spots on the tray
19 #####
20 options = c(rep("MR", 3), rep("MN", 3), rep("CR", 3), rep("CN", 3))
21 tray1 = sample(options)
22 tray2 = sample(options)
23 tray1
24 tray2
25
26 #####
27 ## Read in Data
28 #####
29 cookies=read.table("cookies.txt", header=TRUE)
30
31 #####
32 ## Plot Data in Boxplots
33 #####
34 plotWidth=512;
35 plotHeight=512;
36
37 #####
38 ## Individual Plots
39 #####
40
41 png("./figures/boxplots/boxplot-1-butter.png", width = plotWidth, height = plotHeight
42 )
43   boxplot(size ~ butter, data=cookies, main = "Butter")
44 dev.off()
45
46 png("./figures/boxplots/boxplot-1-chilled.png", width = plotWidth, height =
47   plotHeight)
48   boxplot(size ~ chilled, data=cookies, main = "Dough Temperature")
49 dev.off()
50
51 png("./figures/boxplots/boxplot-1-tray.png", width = plotWidth, height = plotHeight)
52   boxplot(size ~ tray, data=cookies, main = "Tray Position")
53 dev.off()
54
55 #####
56 ## Pair Plots
57 #####
58 png("./figures/boxplots/boxplot-2-butter-chilled.png", width = plotWidth, height =
59   plotHeight)
60   boxplot(size ~ chilled + butter, data=cookies, main = "Butter & Temperature")
61 dev.off()
62
63 png("./figures/boxplots/boxplot-2-butter-tray.png", width = plotWidth, height =
64   plotHeight)
```

```

61   boxplot(size ~ tray + butter, data=cookies, main = "Butter & Tray")
62 dev.off()
63
64 png("./figures/boxplots/boxplot-2-chilled-tray.png", width = plotWidth, height =
    plotHeight)
65   boxplot(size ~ tray + chilled, data=cookies, main = "Temperature & Tray")
66 dev.off()
67
68 #####
69 ## Full Plot
70 #####
71 png("./figures/boxplot-full.png", width = 2*plotWidth, height = 2*plotHeight)
72   boxplot(size ~ tray + chilled + butter, data=cookies)
73 dev.off()
74
75 #####
76 ## Compile Plots
77 #####
78 singleBoxplots = lapply(sprintf("./figures/boxplots/boxplot-1-%s.png", c("butter", "
    chilled", "tray")), png::readPNG)
79 singleBoxGrid = lapply(singleBoxplots, grid::rasterGrob)
80
81 doubleBoxPlots = lapply(sprintf("./figures/boxplots/boxplot-2-%s.png", c("butter-
    chilled", "butter-tray", "chilled-tray")), png::readPNG)
82 doubleBoxGrid = lapply(doubleBoxPlots, grid::rasterGrob)
83
84 png("./figures/boxplot-individuals.png", width = 3*plotWidth, height = plotHeight)
85   gridExtra::grid.arrange(ncol=3, grobs=singleBoxGrid)
86 dev.off()
87
88 png("./figures/boxplot-pairs.png", width = 3*plotWidth, height = plotHeight)
89   gridExtra::grid.arrange(ncol=3, grobs=doubleBoxGrid)
90 dev.off()
91
92 #####
93 ## Create Model
94 #####
95 cookieFullModel = aov(size ~ tray + chilled + butter + tray:chilled + tray:butter +
    chilled:butter, data=cookies)
96 anova(cookieFullModel)
97
98 cookieMainModel = aov(size ~ tray + chilled + butter, data=cookies)
99 anova(cookieMainModel)
100
101 #####
102 # Check Normality
103 #####
104 png("./figures/normality-residuals.png", width = 3*plotWidth, height = plotHeight)
105   plot(cookieFullModel, 1)
106 dev.off()
107
108 png("./figures/normality-qq.png", width = 3*plotWidth, height = plotHeight)
109   plot(cookieFullModel, 2)
110 dev.off()
111
112 #####
113 # Examine Interactions
114 #####
115 png("./figures/interaction-tray-butter.png", width = 3*plotWidth, height = plotHeight
    )
116   interaction.plot(x.factor = cookies$tray, trace.factor = cookies$butter,
117     response = cookies$size, type = "b", col = 2:3,
118     xlab = "Tray", ylab = "Size", trace.label = "Butter")
119 dev.off()
120

```



```
121 png("./figures/interaction-chilled-butter.png", width = 3*plotWidth, height =  
    plotHeight)  
122   interaction.plot(x.factor = cookies$chilled, trace.factor = cookies$butter,  
123     response = cookies$size, type = "b", col = 2:3,  
124     xlab = "Chilled", ylab = "Size", trace.label = "Butter")  
125 dev.off()
```