# Project\_analysis\_V2.R

#### dylanloader

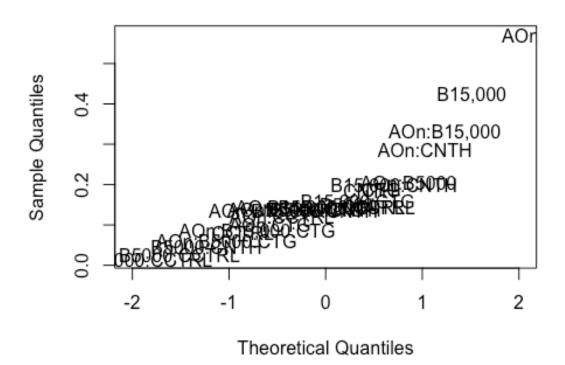
Sat Apr 8 13:45:43 2017

```
# Statistics 368 project analysis.
# Set required libraries.
library(MASS)
library(Rcmdr)
## Warning: package 'Rcmdr' was built under R version 3.3.2
## Loading required package: splines
## Loading required package: RcmdrMisc
## Loading required package: car
## Warning: package 'car' was built under R version 3.3.2
## Loading required package: sandwich
## The Commander GUI is launched only in interactive sessions
library(plyr)
# randomization done before running data for ordering.
# In our case randomization within each block is fine.
# So we set a block and randomize the order within it.
set.seed(9012)
treatment_selections <- c('tg4_fin','tg4_no_fin','nth1_fin','nth1_no_fin',</pre>
                          'as_fin','as_no_fin','no_treat','just_fin')
block1_order <- sample(treatment_selections)</pre>
block2 order <- sample(treatment selections)</pre>
block3 order <- sample(treatment selections)</pre>
block1_order
## [1] "tg4 no fin" "as fin"
                                                  "nth1_fin"
                                                                "as no fin"
                                   "no treat"
## [6] "nth1 no fin" "just fin"
                                   "tg4 fin"
block2_order
## [1] "nth1_no_fin" "tg4_no_fin"
                                   "no_treat"
                                                  "as_no_fin"
                                                                "as fin"
                    "nth1_fin"
## [6] "just_fin"
                                   "tg4_fin"
block3 order
## [1] "nth1 fin"
                    "tg4_no_fin"
                                   "as_fin"
                                                  "just_fin"
                                                                "no treat"
## [6] "nth1_no_fin" "as_no_fin"
                                   "tg4_fin"
```

```
#Data Entry from CSV.
###################
No_treat_B1 = 0.6840
No treat B2 = 0.8514
No\_treat\_B3 = 0.8805
just_fin_B1 = 0.6765
just fin B2 = 0.6133
just_fin_B3 = 0.6843
tg4 fin B1 = 0.6087
tg4 fin B2 = 0.6133
tg4 fin B3 = 0.7173
tg4_no_fin_B1 = 0.6450
tg4 no fin B2 = 1.042
tg4_no_fin_B3 = 1.5018
nth1_fin_B1 = 0.6450
nth1 fin B2 = 0.7051
nth1 fin B3 = 0.6690
nth1 no fin B1 = 0.6738
nth1 no fin B2 = 0.7035
nth1_no_fin_B3 = 0.8517
as fin B1 = 0.6444
as_fin_B2 = 0.5364
as fin B3 = 0.6100
as no fin B1 = 0.7159
as no fin B2 = 0.8324
as_{no}_{fin_{B3}} = 1.1386
# Create ordered blocks
block_1 <- c(tg4_no_fin_B1,as_fin_B1,No_treat_B1,nth1_fin_B1,as_no_fin_B1,
             nth1_no_fin_B1, just_fin_B1, tg4_fin_B1)
block 2 <- c(nth1 no fin B2, tg4 no fin B2, No treat B2, as no fin B2, as fin B2,
             just_fin_B2,nth1_fin_B2,tg4_fin_B2)
block_3 <- c(nth1_fin_B3,tg4_no_fin_B3,as_fin_B3,just_fin_B3,No_treat_B3,</pre>
             nth1 no fin B3,as no fin B3,tg4 fin B3)
# Begin analysis
# First we need to build the data frame
blocks \leftarrow c(1,1,1,1,1,1,2,2,2,2,2,3,3,3,3,3,3,3)
length(blocks)
## [1] 18
measures < c(0.6765,0.6840,0.6444,0.7159,0.6450,0.6738,0.6087,0.6450,
              0.6133,0.8514,0.5364,0.8324,0.7051,0.7035,0.6133,1.042,
              0.6843,0.8805,0.6100,1.1386,0.6690,0.8517,0.7173,1.5018)
# Try transformation
power measures <- (measures)^(-2)</pre>
```

```
#Asin does not work for numbers over 1 produces NaNs
#asin measures <- asin(measures)</pre>
fin_factors \leftarrow c((rep(c('On', 'Off'), each = 1, times = 12)))
fin_factorz <- as.factor(fin_factors)</pre>
# Legend for Pastes:
#paste_factors <- c(1,1,2,2,3,3,4,4,</pre>
                     1, 1, 2, 2, 3, 3, 4, 4,
                      1,1,2,2,3,3,4,4)
paste_factors <- c(rep(c('CTRL','AS','NTH','TG'), each = 2, times = 3))</pre>
paste_factorz <- as.factor(paste_factors)</pre>
block factors \langle c(rep(c('5000','10,000','15,000')), each = 8, times = 1))
block factorz <- as.factor(block factors)</pre>
data_frame <- data.frame(measures, power_measures,</pre>
paste_factorz,block_factorz,
                           fin factorz)
# Start ANOVA here
# Begin with residual analysis
A <- fin factorz
B <- block_factorz</pre>
C <- paste_factorz</pre>
complete model <- lm(measures \sim ((A+B+C)^3))
#complete_model
# we wish to test with a half normal plot the factors of interest.
complete model.effects = abs(complete model$effects[-1])
qq <- qqnorm(complete model.effects, type="n")</pre>
text(qq$x, qq$y, labels = names(complete_model.effects))
```

# Normal Q-Q Plot



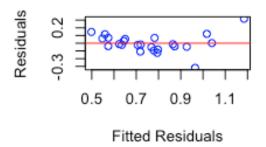
```
# From the half normal plot we see FF is the most significant and
# several block factors are also significant which is to be expected
# aand block interactions are not of interest at this time. We are more
# interested in fin and pase interaction which there is some evidence of.
# set the model that with the factor combinations of interest.
full_model <- lm(measures ~ block_factorz + paste_factorz + fin_factorz +</pre>
paste factorz*fin factorz)
#Residual analysis for full model.
# Residuals for Power model
par(mfrow=c(2,2))
plot(full_model$fitted,full_model$resid, col="blue",xlab= 'Fitted Residuals',
    ylab = 'Residuals', main = 'Fitted Residuals vs. Residuals')
abline(h=0, col="red")
plot(c(block_factorz), full_model$resid, xlab="Blocks",col="blue",
    ylab = 'Residuals', main = 'Block Factor Residual Plot')
abline(h=0, col="red")
plot(c(paste_factorz), full_model$resid, xlab="Paste",col="blue",
    ylab = 'Residuals', main = 'Paste Factor Residual Plot')
abline(h=0, col="red")
plot(c(fin factorz), full model$resid, xlab="Fin", col="blue",
```

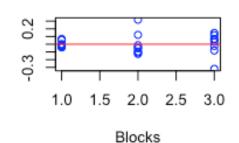
```
ylab = 'Residuals', main = 'Fin Factor Residual Plot')
abline(h=0, col="red")
```

Residuals

#### Fitted Residuals vs. Residual

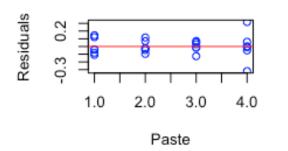
#### **Block Factor Residual Plot**

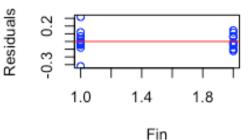




## Paste Factor Residual Plot

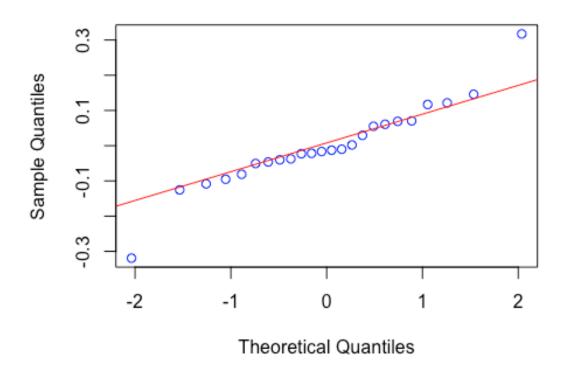
## Fin Factor Residual Plot



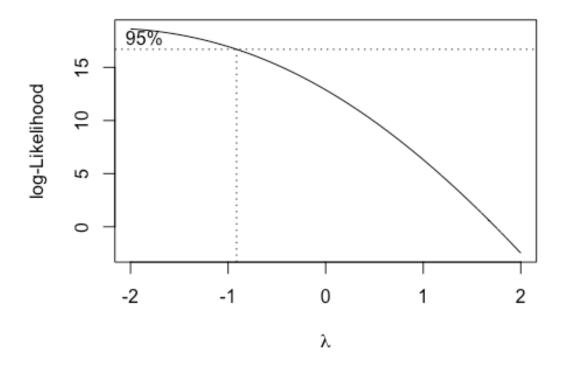


```
par(mfrow = c(1,1))
qqnorm(full_model$resid,col="blue", main = 'Normal Q-Q Plot')
qqline(full model$resid, col=2)
```

# Normal Q-Q Plot



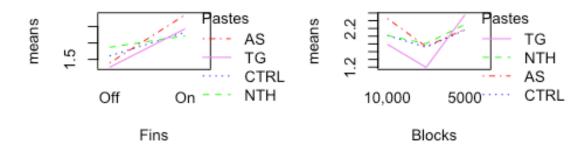
```
# From the fitted values vs residuals we can see an almost parabolic relation
# this suggests that the data should under go transformation
# Since the measures are positive we may use the MLE based Box Cox
# transform to find an asymptotically optimal alpha for the transformation
# of response measures
bc <-boxcox(full_model)</pre>
```



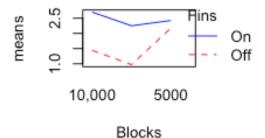
```
alpha <- bc$x[which.max(bc$y)]</pre>
alpha
## [1] -2
# Finding an alpha of -2 from the B.C transform suggests that
# the optimal model is a reciprocal square.
# we define the adjust the measures with the aforementioned transform
# and set a power model.
power_model <- lm(power_measures ~ block_factorz + paste_factorz +</pre>
fin_factorz + paste_factorz*fin_factorz)
######################################
# Interaction plots
par(mfrow=c(2,2),mar=c(4.5,4.5,4.5,4.5))
colors <- c('red','blue','green','violet')</pre>
interaction.plot(factor(fin_factorz), trace.factor =
paste_factorz,power_measures,
                 xlab = 'Fins',trace.label = 'Pastes', ylab = 'means',col =
colors, main = 'Fin-Paste Interaction Plot')
interaction.plot(factor(block factorz), trace.factor =
```

#### Fin-Paste Interaction Plot

#### Block-Paste Interaction Plot



#### Block-Fin Interaction Plot

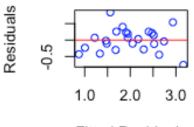


```
# Residuals for Power model
par(mfrow=c(2,2))
plot(power_model$fitted,power_model$resid, col="blue", xlab= 'Fitted
Residuals',
    ylab = 'Residuals', main = 'Fitted Residuals vs. Residuals')
abline(h=0, col="red")
plot(c(block_factorz), power_model$resid, xlab="Blocks",col="blue",
    ylab = 'Residuals', main = 'Block Factor Residual Plot')
abline(h=0, col="red")
plot(c(paste_factorz), power_model$resid, xlab="Pastes", col="blue",
    ylab = 'Residuals', main = 'Paste Factor Residual Plot')
abline(h=0, col="red")
plot(c(fin_factorz), power_model$resid, xlab="Fin", col="blue",
```

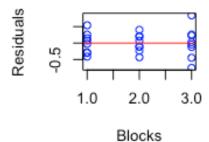
```
ylab = 'Residuals', main = 'Fin Factor Residual Plot')
abline(h=0, col="red")
```

### Fitted Residuals vs. Residuals

## **Block Factor Residual Plot**

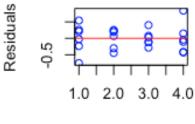




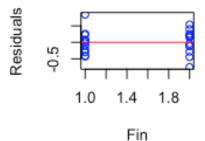


## Paste Factor Residual Plot

## Fin Factor Residual Plot

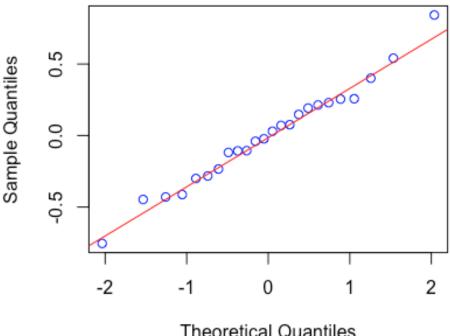






```
par(mfrow = c(1,1))
qqnorm(power_model$resid,col="blue", main = 'Normal Q-Q Plot')
qqline(power_model$resid, col=2)
```

## Normal Q-Q Plot



Theoretical Quantiles

```
bartlett.test(anova(power model))
##
  Bartlett test of homogeneity of variances
##
##
## data: anova(power model)
## Bartlett's K-squared = 25.81, df = 4, p-value = 3.457e-05
# Barlett's test for homoscedasticity is not rubust against deviations from
normality so we should try
# levenes test which is robust against violations to the normality
assumption.
leveneTest(power_measures, group = block_factorz)
## Levene's Test for Homogeneity of Variance (center = median)
        Df F value Pr(>F)
##
## group 2 4.3174 0.02688 *
##
         21
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
# Heterogeneous variances (moderate rejection P=0.02688
leveneTest(power_measures, group = paste_factorz)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##
        Df F value Pr(>F)
## group 3 1.8518 0.1704
         20
##
# Homogeneous variances (Do not reject P=0.1704)
leveneTest(power_measures, group = fin_factorz)
## Levene's Test for Homogeneity of Variance (center = median)
        Df F value Pr(>F)
## group 1 2.1449 0.1572
##
         22
# Homogenous variances (Do not reject P=0.1572)
bartlett.test(anova(power_model))
##
##
   Bartlett test of homogeneity of variances
##
## data: anova(power model)
## Bartlett's K-squared = 25.81, df = 4, p-value = 3.457e-05
# still Barletts test suggests heteroscedasticity of variances
# this is most likely to do with the failure of homoscedasticity
# with the block facto
shapiro.test(power model$residuals)
##
##
   Shapiro-Wilk normality test
##
## data: power model$residuals
## W = 0.9866, p-value = 0.981
# This returns P=0.981 which suggests normality of the residuals.
#qqnorm(power model$residuals)
# Since the assumptions for the ANOVA model seem to be valid we can begin
analysis
anova(power_model)
## Analysis of Variance Table
##
## Response: power_measures
##
                             Df Sum Sq Mean Sq F value
                                                          Pr(>F)
                              2 1.9675 0.9838 4.8337 0.0253416 *
## block_factorz
## paste_factorz
                              3 0.2520 0.0840 0.4128 0.7464158
## fin factorz
                              1 5.1880 5.1880 25.4917 0.0001777 ***
## paste_factorz:fin_factorz 3 1.0964 0.3655 1.7958 0.1941700
## Residuals
                             14 2.8493 0.2035
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Here we can see both the paste factor and paste-fin interactions
# do not seem to be significant. So we remove the highest order term
# in this case Paste-fin interaction and run the ANOVA model again.
power_model_adj <- lm(power_measures ~ block_factorz + paste_factorz +</pre>
fin factorz)
anova(power_model_adj)
## Analysis of Variance Table
##
## Response: power measures
                 Df Sum Sq Mean Sq F value
                                              Pr(>F)
## block_factorz 2 1.9675 0.9838 4.2385 0.0321040 *
## paste factorz 3 0.2520 0.0840 0.3620 0.7812583
## fin factorz
                 1 5.1880 5.1880 22.3526 0.0001944 ***
## Residuals
                 17 3.9457 0.2321
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# Here we see that the paste factor is not significant so we remove this
# factor and run the adjusted anova again
power_model_final <- lm(power_measures ~ block_factorz + fin_factorz)</pre>
anova(power model final)
## Analysis of Variance Table
##
## Response: power_measures
                 Df Sum Sq Mean Sq F value
                                              Pr(>F)
## block_factorz 2 1.9675 0.9838 4.6871
                                             0.02141 *
                            5.1880 24.7183 7.334e-05 ***
## fin factorz
                  1 5.1880
## Residuals
                 20 4.1977 0.2099
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
# finally we find a model which only contains significant factors
# this suggests that both blocks and fins are significant.
# from the anova output we can suggest that the fin factor is the
# most important in determining the thermal conduction on the processor.
# we should now find where the differences occur using Tukey's HSD
final anova <- aov(power model final)</pre>
TukeyHSD(final_anova, 'fin_factorz')
     Tukey multiple comparisons of means
##
##
       95% family-wise confidence level
##
## Fit: aov(formula = power model final)
##
## $fin_factorz
               diff
##
                         lwr
                                 upr
                                        p adj
## On-Off 0.9298776 0.539735 1.32002 7.33e-05
```

