factorial design multiple factors interaction

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Ammonium

$H_o : \alpha_i = 0$ Ho:αi=0

$H_a : \alpha_i \neq 0$ Ha:αi≠0

StirRate

$H_o : \beta_j = 0$ Ho:βj=0

$H_a : \beta_j \neq 0$ Ha:βj≠0

Temperature

$H\ o : \gamma_k = 0$ H o:γk=0
$H\ a : \gamma_k \neq 0$ H a:γk≠0

$H\ o : \alpha\beta_{ij} = 0$ H o:αβij=0 $H\ a : \alpha\beta_{ij} \neq 0$ H a:αβij≠0

$H\ o : \alpha\gamma_{ik} = 0$ H o:αγik=0 $H\ a : \alpha\gamma_{ik} \neq 0$ H a:αγik≠0

$H\ o : \beta\gamma_{jk} = 0$ H o:βγjk=0 $H\ a : \beta\gamma_{jk} \neq 0$ H a:βγjk≠0

$H\ o : \alpha\beta\gamma_{ijk} = 0$ H o:αβγijk=0 $H\ a : \alpha\beta\gamma_{ijk} \neq 0$ H a:αβγijk≠0

Model Equation

$Y_{ijkl} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \alpha\gamma_{ik} + \beta\gamma_{jk} + \alpha\beta\gamma_{ijk} + \epsilon_{ijkl}$ Yijkl=μ+αi+βj+αβij+αγik+βγjk+αβγijk+ϵijkl

We start testing hypothesis of the highest model interraction

```
dat<-read.csv("https://raw.githubusercontent.com/tmatis12/datafiles/main/PowderProduction.csv")
library(GAD)
```

```
## Loading required package: matrixStats
```

```
## Loading required package: R.methodsS3
```

```
## R.methodsS3 v1.8.1 (2020-08-26 16:20:06 UTC) successfully loaded. See ?R.methodsS3 for help.
```

```
dat$Ammonium<-as.fixed(dat$Ammonium)
dat$StirRate<-as.fixed(dat$StirRate)
dat$Temperature<-as.fixed(dat$Temperature)
model<-lm(Density~Ammonium*StirRate*Temperature, data = dat)
gad(model)
```

```
## Analysis of Variance Table
##
## Response: Density
##                               Df Sum Sq Mean Sq F value   Pr(>F)
## Ammonium                       1 44.389  44.389 11.1803 0.010175 *
## StirRate                       1 70.686  70.686 17.8037 0.002918 **
## Temperature                    1  0.328   0.328  0.0826 0.781170
## Ammonium:StirRate              1 28.117  28.117  7.0817 0.028754 *
## Ammonium:Temperature           1  0.022   0.022  0.0055 0.942808
## StirRate:Temperature           1 10.128  10.128  2.5510 0.148890
## Ammonium:StirRate:Temperature  1  1.519   1.519  0.3826 0.553412
## Residual                       8 31.762   3.970
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From the result, values of “Prob > F” less than 0.0500 indicate model terms are significant, in this case, Ammonium:StirRate:Temperature is insignificant, hence we fail to reject Ho

Model Equation

$Y_{ijkl} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \alpha\gamma_{ik} + \beta\gamma_{jk} + \epsilon_{ijkl}$ Yijkl=μ+αi+βj+αβij+αγik+βγjk+ϵijkl

```
model1<-lm(Density~Ammonium+StirRate+Temperature+Ammonium*StirRate+Temperature*Ammonium+StirRate*T
emperature, data = dat)
gad(model1)
```

```
## Analysis of Variance Table
##
## Response: Density
##                      Df Sum Sq Mean Sq F value   Pr(>F)
## Ammonium              1 44.389  44.389 12.0037 0.007109 **
## StirRate              1 70.686  70.686 19.1150 0.001792 **
## Temperature           1  0.328   0.328  0.0886 0.772681
## Ammonium:StirRate     1 28.117  28.117  7.6033 0.022206 *
## Ammonium:Temperature  1  0.022   0.022  0.0059 0.940538
## StirRate:Temperature  1 10.128  10.128  2.7389 0.132317
## Residual              9 33.281   3.698
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From the result, values of “Prob > F” less than 0.0500 indicate model terms are significant, in this case, StirRate:Temperature, Ammonium:Temperature are insignificant, hence we fail to reject Ho This model terms will be dropped

Model Equation

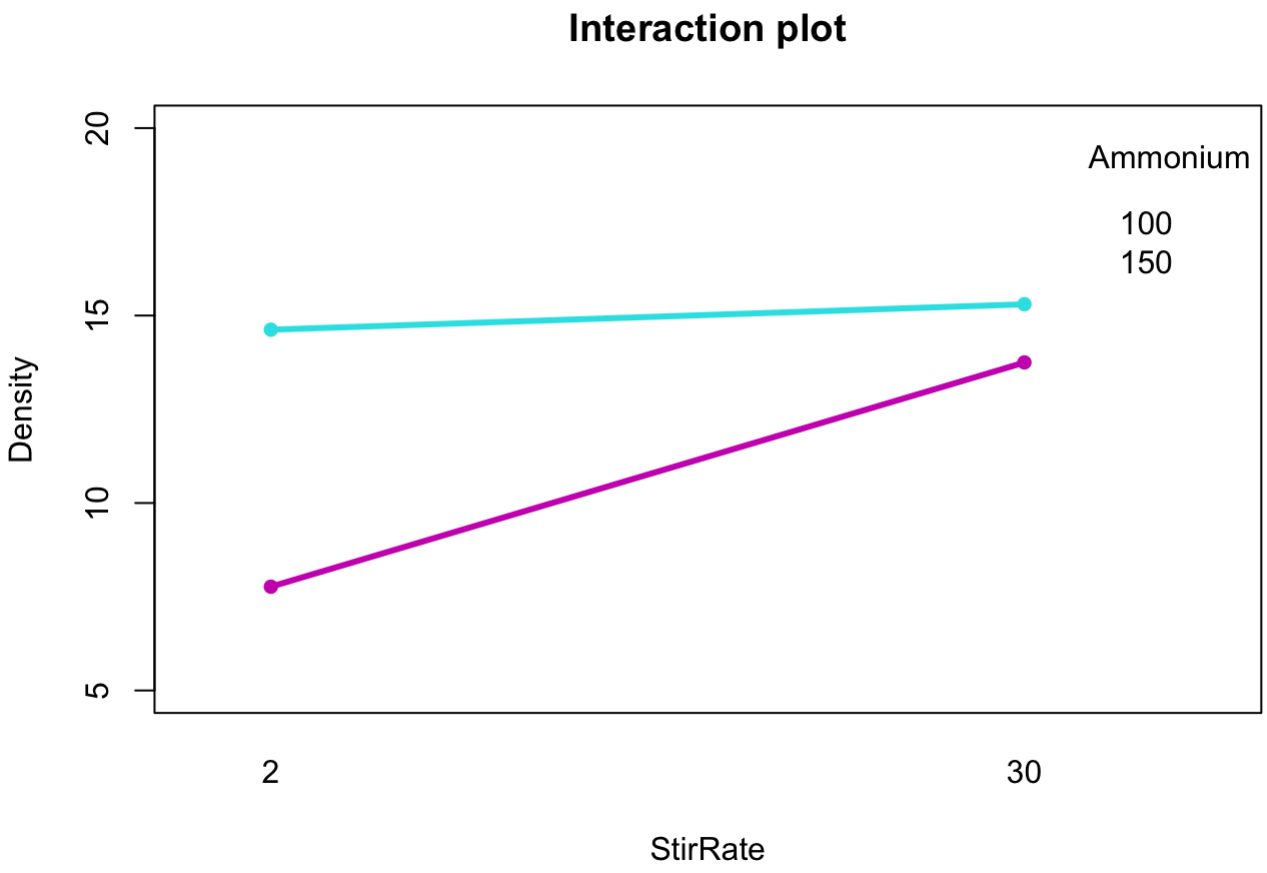
$Y_{ijkl} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \epsilon_{ijkl}$ Yijkl=μ+αi+βj+αβij+ϵijkl

```
model3<-lm(Density~Ammonium+StirRate+Temperature+Ammonium*StirRate, data = dat)
gad(model3)
```

```
## Analysis of Variance Table
##
## Response: Density
##                   Df Sum Sq Mean Sq F value   Pr(>F)
## Ammonium           1 44.389  44.389 11.2425 0.006443 **
## StirRate           1 70.686  70.686 17.9028 0.001410 **
## Temperature        1  0.328   0.328  0.0830 0.778613
## Ammonium:StirRate  1 28.117  28.117  7.1211 0.021851 *
## Residual          11 43.431   3.948
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From the result, values of “Prob > F” less than 0.0500 indicate model terms are significant, in this case, Ammonium:StirRate, Ammonium, StirRate are significant model terms, hence we reject Ho.

```
interaction.plot(dat$Ammonium, dat$StirRate, dat$Density, type = "o", main="Interaction plot",col=
5:7,ylab = "Density", xlab = "StirRate", trace.label = "Ammonium", lwd=3,lty = 1, ylim = c(5,20 ),
pch = c(16))
```




```
#interaction.plot(culture,time,response1,fun="mean",type = "b", col = 5:7,
#main ="Interraction Plot", ylab = "Virus response", xlab = "Culture medium",
#trace.label = "Time", lwd = 3, lty = 1, ylim = c(20,40), pch = c(4,2))
```