Advanced Statistical Modeling

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R version 3.6.3
Package: HH
Title: Statistical Analysis and Data Display: Heiberger and Holland
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Required Packages: "HH"
#install.packages("HH")

Data Details

Can we prevent or retard the spread of fire by selecting a specific chemical, panel, and sample combination?

A chemist compared the abilities of three chemicals used on four different types of plywood panels to retard the spread of fire. Each chemical was sprayed on each type of plywood. Two pieces were cut from each panel and the time was measured for each piece to be completely consumed by a standard flame. Therefore, each experiment has two samples, S1 and S2.

A thorough analysis was completed leading to a recommendation of which chemical, (C1, C2, or C3) to use under the various types of plywood.

Our goal is to recommend which chemical is most effective to prevent or retard the spread of fire. Time was measured for each piece to be completely consumed by a standard flame; therefore, higher measurements of time are desired.

ANOVA models to consider

THREE WAY ANOVA WITH NO INTERACTION TERM

```
retard.aov.noint <- aov(Time ~ Chemical + Panel + Sample, data=retard)

retard.aov.noint

## Call:
##    aov(formula = Time ~ Chemical + Panel + Sample, data = retard)
##
## Terms:
##                   Chemical    Panel   Sample Residuals
## Sum of Squares  93.63083 14.42333  0.28167  37.73750
## Deg. of Freedom       2       3       1       17
##
## Residual standard error: 1.489917
## Estimated effects may be unbalanced

anova(retard.aov.noint)
```

```
## Analysis of Variance Table
##
## Response: Time
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Chemical   2 93.631  46.815 21.0894 2.485e-05 ***
## Panel      3 14.423   4.808  2.1658    0.1296
## Sample     1  0.282   0.282  0.1269    0.7261
## Residuals 17 37.738   2.220
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

THREE WAY ANOVA WITH ONLY 2 INTERACTION TERMS

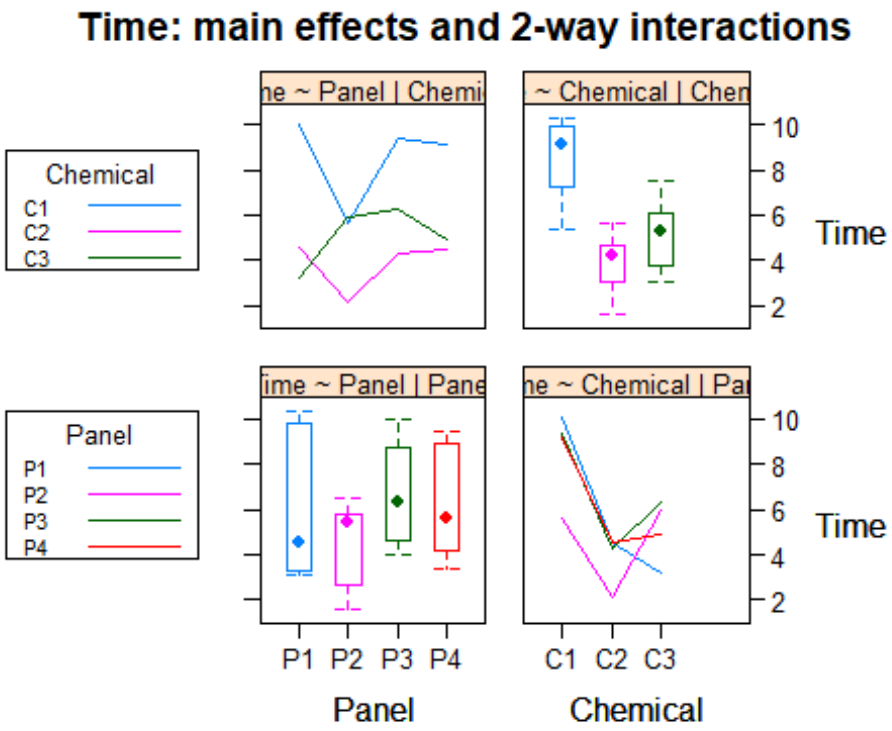
```
retardf.aov <- aov(Time ~
        (Chemical + Panel + Sample)^2,
        data=retard)
summary(retardf.aov)

##                Df Sum Sq Mean Sq F value   Pr(>F)
## Chemical        2  93.63   46.82  89.480 3.41e-05 ***
## Panel           3  14.42    4.81   9.189  0.01162 *
## Sample          1   0.28    0.28   0.538  0.49078
## Chemical:Panel  6  29.11    4.85   9.273  0.00793 **
## Chemical:Sample 2   1.44    0.72   1.377  0.32199
## Panel:Sample    3   4.05    1.35   2.579  0.14916
## Residuals       6   3.14    0.52
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Two Way ANOVA WITH 1 INTERACTION TERM

```
retard1.aov <- aov(Time ~
        (Chemical + Panel)^2,
        data=retard)

summary(retard1.aov)

##               Df Sum Sq Mean Sq F value  Pr(>F)
## Chemical       2  93.63   46.82  63.051 4.3e-07 ***
## Panel          3  14.42    4.81   6.475 0.00745 **
## Chemical:Panel 6  29.11    4.85   6.534 0.00297 **
## Residuals     12   8.91    0.74
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Interaction Plot

```
interaction2wt(Time ~ Panel + Chemical,
           data=retard,
  par.strip.text=list(cex=.8))
```



With simple effects

```
interaction2wt(data=retard, Time ~
          Panel + Chemical,
        simple=TRUE,
        simple.scale=list(Chemical=.3,
                  Panel=.3),
        xlim=c(.5, 3.5),
        between=list(x=.5, y=.5))
```

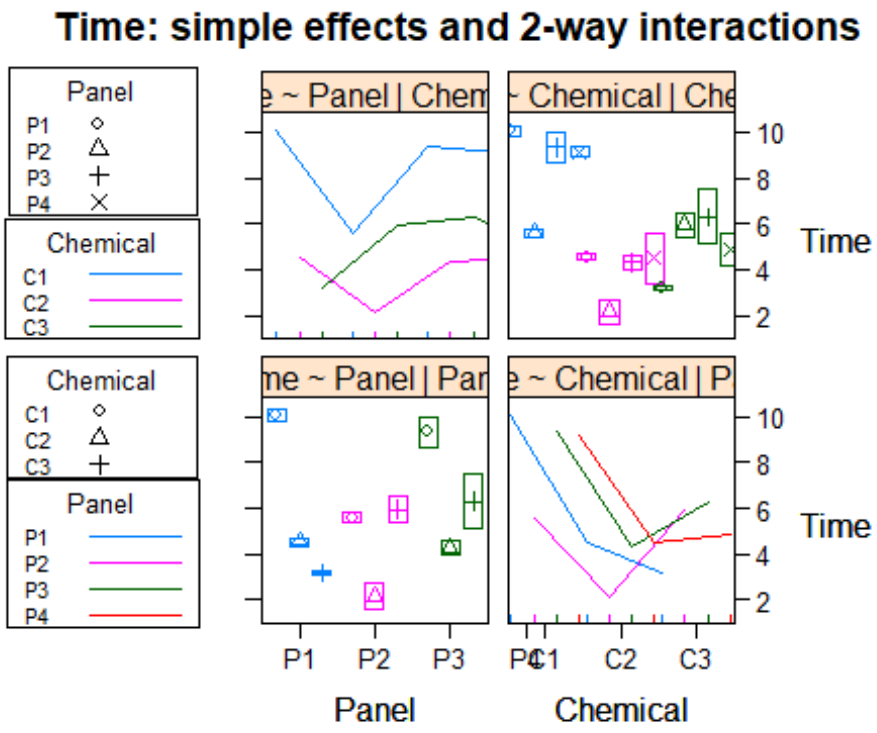


Table of means

```
model.tables(retard1.aov, "means")

## Tables of means
## Grand mean
##
## 5.833333
##
##  Chemical
## Chemical
##    C1    C2    C3
## 8.538 3.875 5.088
##
##  Panel
## Panel
##    P1    P2    P3    P4
## 5.933 4.567 6.650 6.183
##
##  Chemical:Panel
##         Panel
## Chemical P1    P2    P3    P4
##       C1 10.05  5.60  9.35  9.15
##       C2  4.55  2.15  4.30  4.50
##       C3  3.20  5.95  6.30  4.90
```

Separate ANOVA for each chemical level

```
retard.aov.3c <- sapply(levels(
 retard$Chemical),
 function(i) aov(Time ~ Panel, data = retard,
    subset=(Chemical==i)),
    simplify=FALSE)

print(lapply(retard.aov.3c, anova))
```

```
## $C1
## Analysis of Variance Table
##
## Response: Time
##          Df Sum Sq Mean Sq F value   Pr(>F)
## Panel     3 23.904  7.9679  27.125 0.004051 **
## Residuals  4  1.175  0.2937
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $C2
## Analysis of Variance Table
##
## Response: Time
##          Df Sum Sq Mean Sq F value Pr(>F)
## Panel     3  8.005  2.6683  3.2841 0.1404
## Residuals  4  3.250  0.8125
##
## $C3
## Analysis of Variance Table
##
## Response: Time
##          Df Sum Sq Mean Sq F value Pr(>F)
## Panel     3 11.624  3.8746  3.4556 0.1311
## Residuals  4  4.485  1.1212
```

ADDITIONAL, NOT NECESSARY

```
#Chemical_ONE-WAY ANOVA
#retard.aov.chemical.time <- aov(Time ~ Chemical, data = retard)
#anova(retard.aov.chemical.time)

#Chemical_MMC
#retard.aov.chemical.time.mmc <- mmc(retard.aov.chemical.time,
                #linfct = mcp(
                  #Chemical = "Tukey"))
#retard.aov.chemical.time.mmc

#mmcplot(retard.aov.chemical.time.mmc, style = "both")
```

Separate ANOVA for each panel level

```
retard.aov.4p <- sapply(levels(
 retard$Panel),
 function(i) aov(Time ~ Chemical, data = retard,
    subset=(Panel==i)),
    simplify=FALSE)

print(lapply(retard.aov.4p, anova))
```

```
## $P1
## Analysis of Variance Table
##
## Response: Time
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Chemical   2 52.663 26.3317  415.76 0.0002155 ***
## Residuals  3  0.190  0.0633
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $P2
## Analysis of Variance Table
##
## Response: Time
##           Df Sum Sq Mean Sq F value  Pr(>F)
## Chemical   2 17.643  8.8217  20.515 0.01778 *
## Residuals  3  1.290  0.4300
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $P3
## Analysis of Variance Table
##
## Response: Time
##           Df Sum Sq Mean Sq F value Pr(>F)
## Chemical   2 25.870 12.9350  9.9373 0.0475 *
## Residuals  3  3.905  1.3017
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $P4
## Analysis of Variance Table
##
## Response: Time
##           Df Sum Sq Mean Sq F value Pr(>F)
## Chemical   2 26.563  13.282  11.303 0.0401 *
## Residuals  3  3.525   1.175
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ADDITIONAL, NOT NECESSARY

```
#Panel_ONE-WAY ANOVA
#retard.aov.panel.time <- aov(Time ~ Panel, data = retard)
#anova(retard.aov.panel.time)

#Panel_MMC
#retard.aov.panel.time.mmc <- mmc(retard.aov.panel.time,
                #linfct = mcp(
                  #Panel = "Tukey"))
#retard.aov.panel.time.mmc

#mmcplot(retard.aov.panel.time.mmc, style = "both")
```

Mean Minus Mean Comparison (MMC) Analysis

```
#CHEMICAL



retard.aov.3c <- sapply(levels(
 retard$Chemical),
 function(i) aov(Time ~ Panel, data = retard,
    subset=(Chemical==i)),
    simplify=FALSE)

print(lapply(retard.aov.3c, anova))

## $C1
## Analysis of Variance Table
##
## Response: Time
##          Df Sum Sq Mean Sq F value   Pr(>F)
## Panel     3 23.904  7.9679  27.125 0.004051 **
## Residuals  4  1.175  0.2937
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $C2
## Analysis of Variance Table
##
## Response: Time
##          Df Sum Sq Mean Sq F value Pr(>F)
## Panel     3  8.005  2.6683  3.2841 0.1404
## Residuals  4  3.250  0.8125
##
## $C3
## Analysis of Variance Table
##
## Response: Time
##          Df Sum Sq Mean Sq F value Pr(>F)
```

```
## Panel      3 11.624  3.8746  3.4556 0.1311
## Residuals  4  4.485  1.1212
```

Adjustments needed for Multiple Comparisons

```
ResidMS <- function(x)
  summary(x)[[1]]["Residuals","Mean Sq"]

ResidMSAvg <- ResidMS(retardf.aov)
ResidMSAvg

## [1] 0.5231944

crit.val <- qtukey(p = 0.95, nmeans = 3,
                   df = 12, nranges = 3)/sqrt(2)
crit.val

## [1] 3.23371
```

Multiple Comparison Results by CHEMICAL

```
retard.mmc.3c <- sapply(
  retard.aov.3c, simplify = FALSE,
  function(x) mmc(x,
                  calpha = crit.val
                  * sqrt(ResidMSAvg/ResidMS(x))))
retard.mmc.3c

## $C1
## Tukey contrasts
## Fit: aov(formula = Time ~ Panel, data = retard, subset = (Chemical == i))
## Estimated Quantile = 4.315625
## 95% family-wise confidence level
## $mca
##       estimate    stderr     lower    upper height
## P1-P3     0.70 0.5419871 -1.639013 3.039013  9.700
## P1-P4     0.90 0.5419871 -1.439013 3.239013  9.600
## P3-P4     0.20 0.5419871 -2.139013 2.539013  9.250
## P1-P2     4.45 0.5419871  2.110987 6.789013  7.825
## P3-P2     3.75 0.5419871  1.410987 6.089013  7.475
## P4-P2     3.55 0.5419871  1.210987 5.889013  7.375
## $none
##    estimate    stderr    lower     upper height
## P1    10.05 0.3832427 8.396068 11.703932  10.05
## P3     9.35 0.3832427 7.696068 11.003932   9.35
## P4     9.15 0.3832427 7.496068 10.803932   9.15
## P2     5.60 0.3832427 3.946068  7.253932   5.60
##
## $C2
```

```
## Tukey contrasts
## Fit: aov(formula = Time ~ Panel, data = retard, subset = (Chemical == i))
## Estimated Quantile = 2.594902
## 95% family-wise confidence level
## $mca
##      estimate    stderr      lower    upper height
## P1-P4     0.05 0.9013878 -2.28901309 2.389013  4.525
## P1-P3     0.25 0.9013878 -2.08901309 2.589013  4.425
## P4-P3     0.20 0.9013878 -2.13901309 2.539013  4.400
## P1-P2     2.40 0.9013878  0.06098691 4.739013  3.350
## P4-P2     2.35 0.9013878  0.01098691 4.689013  3.325
## P3-P2     2.15 0.9013878 -0.18901309 4.489013  3.225
## $none
##    estimate    stderr    lower    upper height
## P1     4.55 0.6373774 2.896068 6.203932   4.55
## P4     4.50 0.6373774 2.846068 6.153932   4.50
## P3     4.30 0.6373774 2.646068 5.953932   4.30
## P2     2.15 0.6373774 0.496068 3.803932   2.15
##
## $C3
## Tukey contrasts
## Fit: aov(formula = Time ~ Panel, data = retard, subset = (Chemical == i))
## Estimated Quantile = 2.208927
## 95% family-wise confidence level
## $mca
##      estimate   stderr     lower    upper height
## P3-P2     0.35 1.058891 -1.9890131 2.689013  6.125
## P3-P4     1.40 1.058891 -0.9390131 3.739013  5.600
## P2-P4     1.05 1.058891 -1.2890131 3.389013  5.425
## P3-P1     3.10 1.058891  0.7609869 5.439013  4.750
## P2-P1     2.75 1.058891  0.4109869 5.089013  4.575
## P4-P1     1.70 1.058891 -0.6390131 4.039013  4.050
## $none
##    estimate   stderr    lower    upper height
## P3     6.30 0.748749 4.646068 7.953932   6.30
## P2     5.95 0.748749 4.296068 7.603932   5.95
## P4     4.90 0.748749 3.246068 6.553932   4.90
## P1     3.20 0.748749 1.546068 4.853932   3.20
```

GRAPHIC

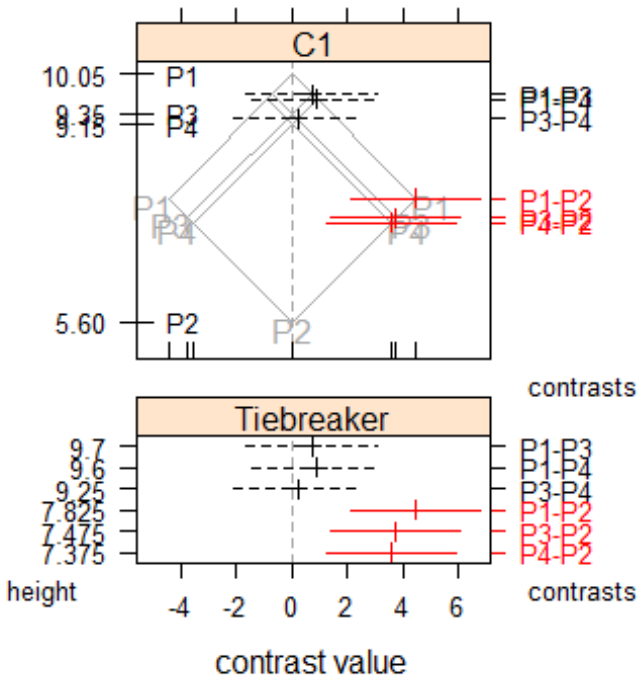
```
mmc3CB <- sapply(retard.mmc.3c,
            mmcplot, style="both",
            simplify=FALSE, axis.right=2,
            ylab.right=NULL, ylab=NULL)
```

mmc3CB

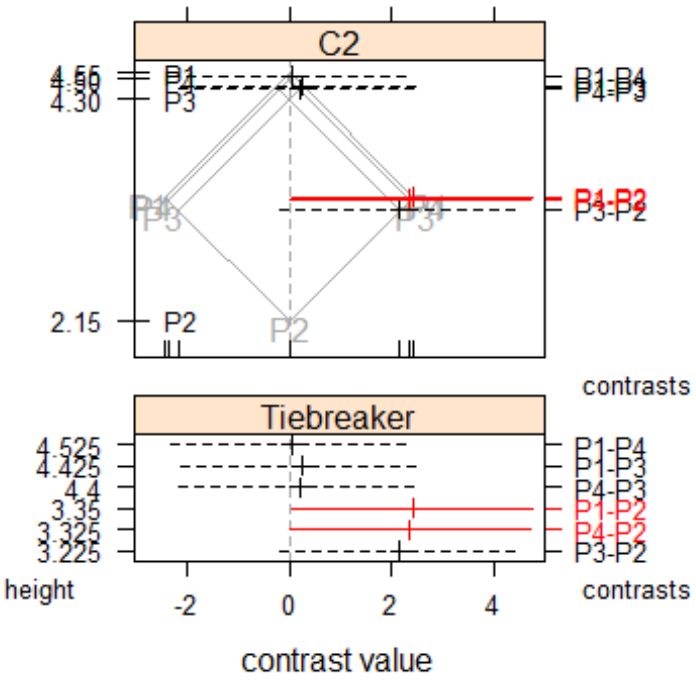
```
mmc3CB[[1]]$condlevels[[1]][1] <-
  names(mmc3CB)[1]
mmc3CB[[2]]$condlevels[[1]][1] <-
  names(mmc3CB)[2]
mmc3CB[[3]]$condlevels[[1]][1] <-
  names(mmc3CB)[3]
old.digits <- options(digits=4)
```

Prints each level of chemical individually

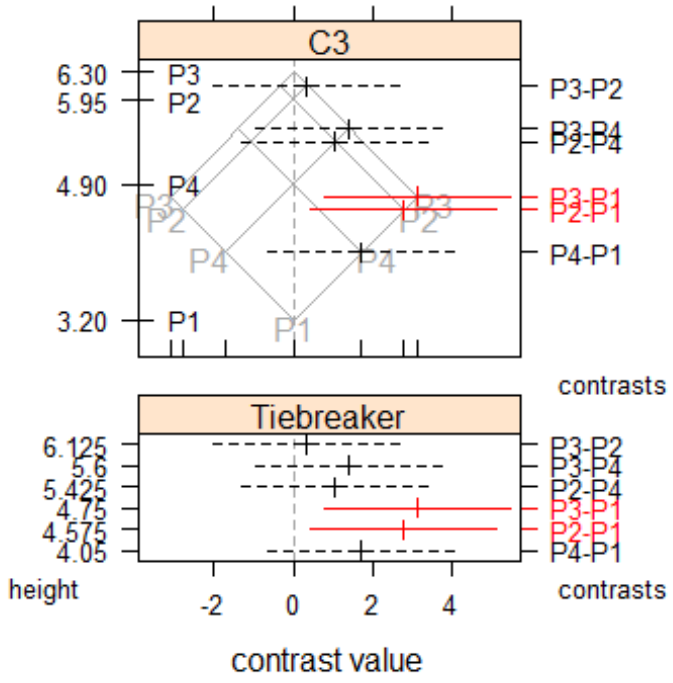
```
print(mmc3CB[[1]])
```




```
print(mmc3CB[[2]])
```




```
print(mmc3CB[[3]])
```



Mean Minus Mean Comparison (MMC) Analysis

```
#PANEL



retard.aov.4p <- sapply(levels(
 retard$Panel),
 function(i) aov(Time ~ Chemical, data = retard,
    subset=(Panel==i)),
    simplify=FALSE)

print(lapply(retard.aov.4p, anova))
```

```
## $P1
## Analysis of Variance Table
##
## Response: Time
##           Df Sum Sq Mean Sq F value  Pr(>F)
## Chemical   2   52.7   26.33     416 0.00022 ***
## Residuals  3    0.2    0.06
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $P2
## Analysis of Variance Table
##
## Response: Time
##           Df Sum Sq Mean Sq F value Pr(>F)
## Chemical   2  17.64    8.82    20.5  0.018 *
## Residuals  3   1.29    0.43
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $P3
## Analysis of Variance Table
##
## Response: Time
##           Df Sum Sq Mean Sq F value Pr(>F)
## Chemical   2   25.9    12.9    9.94  0.047 *
## Residuals  3    3.9     1.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## $P4
## Analysis of Variance Table
##
## Response: Time
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## Chemical   2  26.56   13.28    11.3   0.04 *
## Residuals  3   3.52    1.17
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Adjustments needed for Multiple Comparisons

```
ResidMS <- function(x)
 summary(x)[[1]]["Residuals","Mean Sq"]

ResidMSAvg <- ResidMS(retardf.aov)
ResidMSAvg

## [1] 0.5232

crit.val <- qtukey(p = 0.95, nmeans = 3,
              df = 12, nranges = 3)/sqrt(2)
crit.val

## [1] 3.234
```

Multiple Comparison Results by PANEL

```
retard.mmc.4p <- sapply(
 retard.aov.4p, simplify = FALSE,
 function(x) mmc(x,
             calpha = crit.val
             * sqrt(ResidMSAvg/ResidMS(x))))
retard.mmc.4p

## $P1
## Tukey contrasts
## Fit: aov(formula = Time ~ Chemical, data = retard, subset = (Panel == i))
## Estimated Quantile = 9.294
## 95% family-wise confidence level
## $mca
##       estimate stderr  lower upper height
## C1-C2     5.50 0.2517  3.161 7.839  7.300
## C1-C3     6.85 0.2517  4.511 9.189  6.625
## C2-C3     1.35 0.2517 -0.989 3.689  3.875
## $none
##    estimate stderr lower  upper height
## C1    10.05  0.178 8.396 11.704  10.05
## C2     4.55  0.178 2.896  6.204   4.55
## C3     3.20  0.178 1.546  4.854   3.20
##
## $P2
## Tukey contrasts
## Fit: aov(formula = Time ~ Chemical, data = retard, subset = (Panel == i))
```

```
## Estimated Quantile = 3.567
## 95% family-wise confidence level
## $mca
##       estimate stderr  lower upper height
## C3-C1     0.35 0.6557 -1.989 2.689  5.775
## C3-C2     3.80 0.6557  1.461 6.139  4.050
## C1-C2     3.45 0.6557  1.111 5.789  3.875
## $none
##    estimate stderr  lower upper height
## C3     5.95 0.4637 4.2961 7.604   5.95
## C1     5.60 0.4637 3.9461 7.254   5.60
## C2     2.15 0.4637 0.4961 3.804   2.15
##
## $P3
## Tukey contrasts
## Fit: aov(formula = Time ~ Chemical, data = retard, subset = (Panel == i))
## Estimated Quantile = 2.05
## 95% family-wise confidence level
## $mca
##       estimate stderr  lower upper height
## C1-C3     3.05  1.141  0.711 5.389  7.825
## C1-C2     5.05  1.141  2.711 7.389  6.825
## C3-C2     2.00  1.141 -0.339 4.339  5.300
## $none
##    estimate stderr lower  upper height
## C1     9.35 0.8067 7.696 11.004   9.35
## C3     6.30 0.8067 4.646  7.954   6.30
## C2     4.30 0.8067 2.646  5.954   4.30
##
## $P4
## Tukey contrasts
## Fit: aov(formula = Time ~ Chemical, data = retard, subset = (Panel == i))
## Estimated Quantile = 2.158
## 95% family-wise confidence level
## $mca
##       estimate stderr  lower upper height
## C1-C3     4.25  1.084  1.911 6.589  7.025
## C1-C2     4.65  1.084  2.311 6.989  6.825
## C3-C2     0.40  1.084 -1.939 2.739  4.700
## $none
##    estimate stderr lower  upper height
## C1     9.15 0.7665 7.496 10.804   9.15
## C3     4.90 0.7665 3.246  6.554   4.90
## C2     4.50 0.7665 2.846  6.154   4.50
```

GRAPHIC

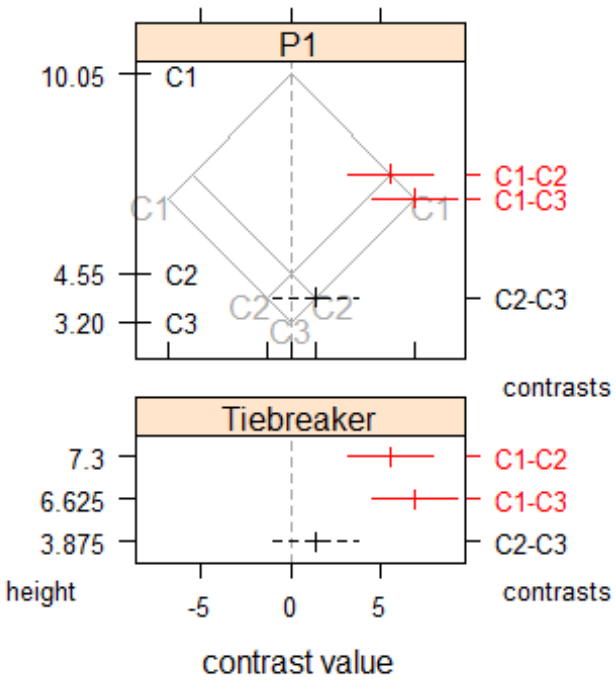
```
mmc4Pb <- sapply(retard.mmc.4p,
                 mmcplot, style="both",
                 simplify=FALSE, axis.right=2,
                 ylab.right=NULL, ylab=NULL)
```

mmc3CB

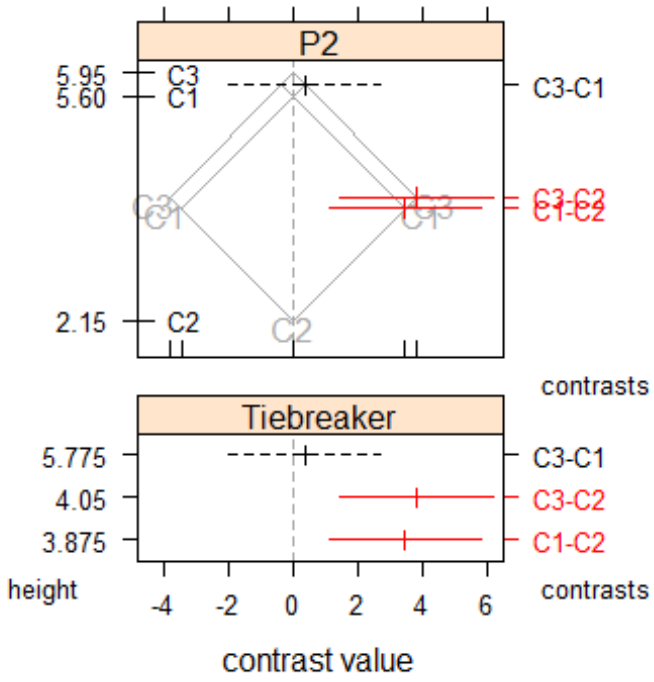
```
mmc4Pb[[1]]$condlevels[[1]][1] <-
  names(mmc4Pb)[1]
mmc4Pb[[2]]$condlevels[[1]][1] <-
  names(mmc4Pb)[2]
mmc4Pb[[3]]$condlevels[[1]][1] <-
  names(mmc4Pb)[3]
mmc4Pb[[4]]$condlevels[[1]][1] <-
  names(mmc4Pb)[4]
old.digits <- options(digits=4)
```

Prints each level of panel individually

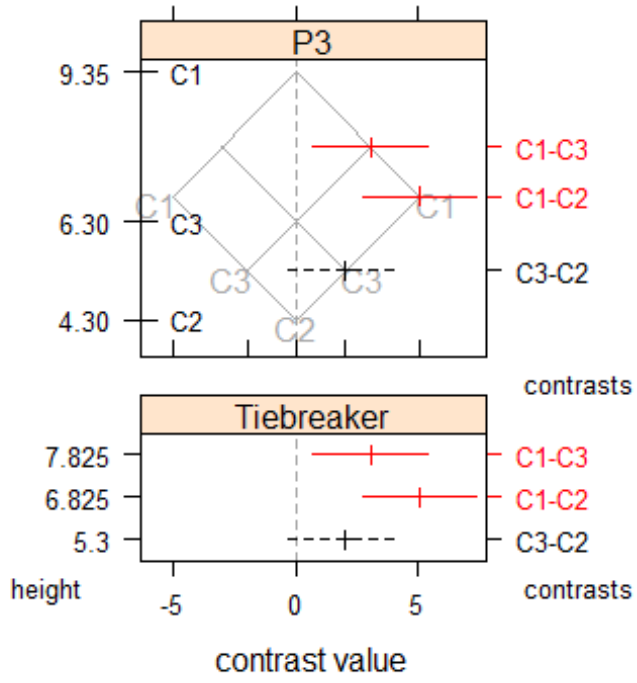
```
print(mmc4Pb[[1]])
```



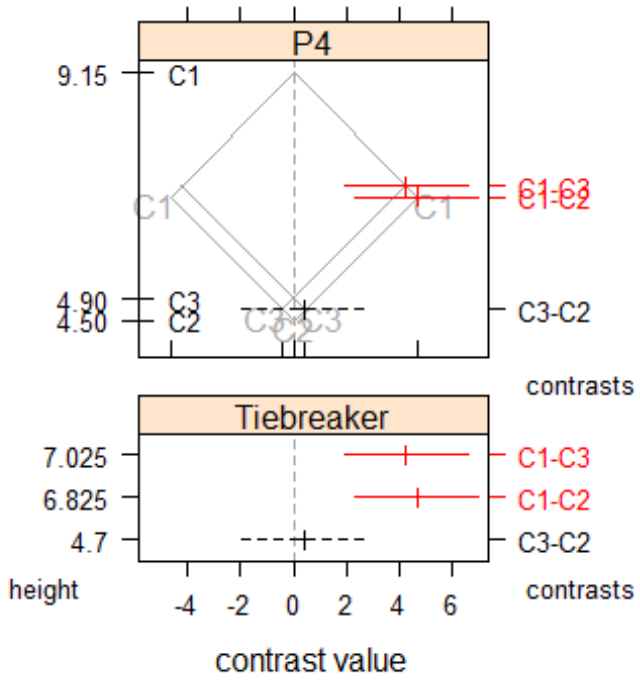

```
print(mmc4Pb[[2]])
```




```
print(mmc4Pb[[3]])
```




```
print(mmc4Pb[[4]])
```



Incorrect MMC

```
retard.mmc.3c <- sapply(
 retard.aov.3c, simplify = FALSE,
 function(x) mmc(x,
            calpha = crit.val
            * sqrt(ResidMSAvg/ResidMS(x))))
retard.mmc.3c

## $C1
## Tukey contrasts
## Fit: aov(formula = Time ~ Panel, data = retard, subset = (Chemical == i))
## Estimated Quantile = 4.316
## 95% family-wise confidence level
## $mca
##       estimate stderr  lower upper height
## P1-P3     0.70  0.542 -1.639 3.039  9.700
## P1-P4     0.90  0.542 -1.439 3.239  9.600
## P3-P4     0.20  0.542 -2.139 2.539  9.250
## P1-P2     4.45  0.542  2.111 6.789  7.825
## P3-P2     3.75  0.542  1.411 6.089  7.475
## P4-P2     3.55  0.542  1.211 5.889  7.375
## $none
##    estimate stderr lower  upper height
## P1    10.05 0.3832 8.396 11.704  10.05
## P3     9.35 0.3832 7.696 11.004   9.35
## P4     9.15 0.3832 7.496 10.804   9.15
```

```
## P2    5.60 0.3832 3.946  7.254   5.60
##
## $C2
## Tukey contrasts
## Fit: aov(formula = Time ~ Panel, data = retard, subset = (Chemical == i))
## Estimated Quantile = 2.595
## 95% family-wise confidence level
## $mca
##      estimate stderr    lower upper height
## P1-P4    0.05 0.9014 -2.28901 2.389  4.525
## P1-P3    0.25 0.9014 -2.08901 2.589  4.425
## P4-P3    0.20 0.9014 -2.13901 2.539  4.400
## P1-P2    2.40 0.9014  0.06099 4.739  3.350
## P4-P2    2.35 0.9014  0.01099 4.689  3.325
## P3-P2    2.15 0.9014 -0.18901 4.489  3.225
## $none
##    estimate stderr  lower upper height
## P1    4.55 0.6374 2.8961 6.204   4.55
## P4    4.50 0.6374 2.8461 6.154   4.50
## P3    4.30 0.6374 2.6461 5.954   4.30
## P2    2.15 0.6374 0.4961 3.804   2.15
##
## $C3
## Tukey contrasts
## Fit: aov(formula = Time ~ Panel, data = retard, subset = (Chemical == i))
## Estimated Quantile = 2.209
## 95% family-wise confidence level
## $mca
##      estimate stderr  lower upper height
## P3-P2    0.35  1.059 -1.989 2.689  6.125
## P3-P4    1.40  1.059 -0.939 3.739  5.600
## P2-P4    1.05  1.059 -1.289 3.389  5.425
## P3-P1    3.10  1.059  0.761 5.439  4.750
## P2-P1    2.75  1.059  0.411 5.089  4.575
## P4-P1    1.70  1.059 -0.639 4.039  4.050
## $none
##    estimate stderr lower upper height
## P3    6.30 0.7487 4.646 7.954   6.30
## P2    5.95 0.7487 4.296 7.604   5.95
## P4    4.90 0.7487 3.246 6.554   4.90
## P1    3.20 0.7487 1.546 4.854   3.20
```

Incorrect MMC CON'T

```
mmc3CB <- sapply(retard.mmc.3c,
            mmcplot, style="both",
            simplify=FALSE, axis.right=2,
            ylab.right=NULL, ylab=NULL)
```

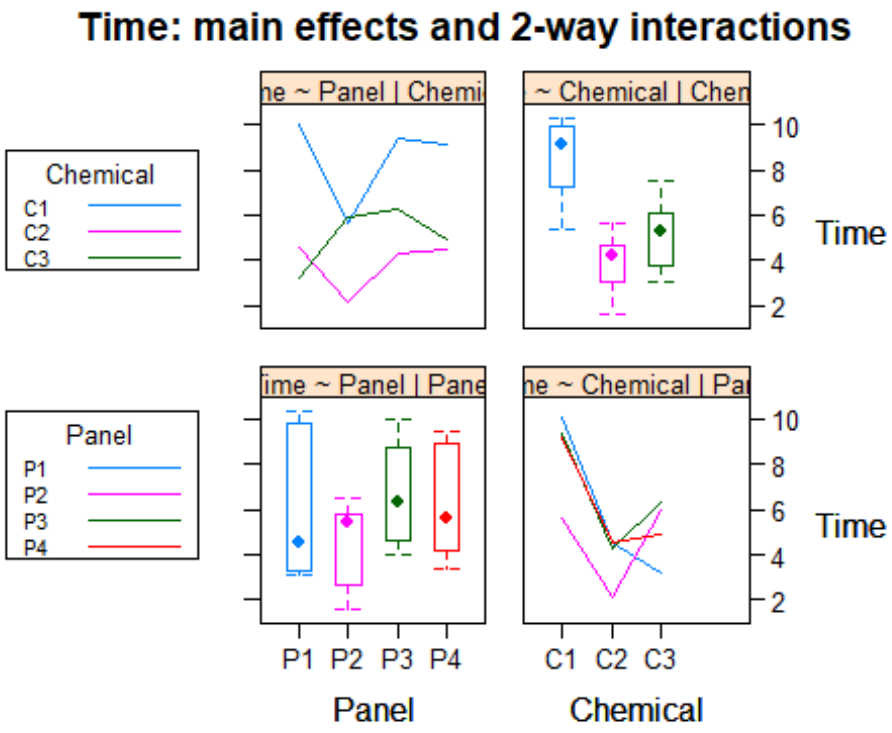
Three-way analysis of variance with two- and three-way interaction terms. Are these results useful?

```
## THREE WAY ANOVA WITH ONLY 2 INTERACTION TERMS

retardf.aov <- aov(Time ~
        (Chemical + Panel + Sample)^2,
        data=retard)
summary(retardf.aov)

##                Df Sum Sq Mean Sq F value  Pr(>F)
## Chemical        2   93.6    46.8   89.48 3.4e-05 ***
## Panel           3   14.4     4.8    9.19  0.0116 *
## Sample          1    0.3     0.3    0.54  0.4908
## Chemical:Panel  6   29.1     4.9    9.27  0.0079 **
## Chemical:Sample 2    1.4     0.7    1.38  0.3220
## Panel:Sample    3    4.0     1.3    2.58  0.1492
## Residuals       6    3.1     0.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## THREE WAY ANOVA WITH 3 INTERACTION TERMS
summary(aov(Time ~
        (Chemical + Panel + Sample)^3,
         data=retard))

##                    Df Sum Sq Mean Sq
## Chemical            2   93.6    46.8
## Panel               3   14.4     4.8
## Sample              1    0.3     0.3
## Chemical:Panel      6   29.1     4.9
## Chemical:Sample     2    1.4     0.7
## Panel:Sample        3    4.0     1.3
## Chemical:Panel:Sample  6    3.1     0.5
```

The results from the three-way analysis of variance with three-way interaction terms are not useful. The results are not useful in this case because the model is saturated, I believe, because there are 3 factors (chemical, panel, and sample) with levels of 3, 4, and 2 and DFs of 2, 3, and 1 and they require additional degrees of freedom. The interaction takes another 6 degrees of freedom. Summing those 6+3+2+6+1+3+2 = 23, and I only have 24 data. So, there are no degrees of freedom left in order for me to determine the residual variability, errors, or hypothesis testing, given the model will use at LEAST > 1 df.

Important Insights

```
interaction2wt(Time ~ Panel + Chemical,
           data=retard,
  par.strip.text=list(cex=.8))
```



OBSERVATION 1

BOX PLOT OF DIFFERENT PANELS: THE INNER QUARTILE RANGE AMONG THE PANELS ARE OVERLAPPING. HOWEVER, THE MEDIAN VALUE SEEMS TO BE LOWER WITH PANEL 1, 2, AND 3 AND HIGHER WITH PANEL 2 (TIME ~ PANEL | PANEL)

OBSERVATION 2

THERE ARE DIFFERENT DISTRIBUTIONS IN THE CHEMICALS, WHICH IS NOT SURPRISING, AS DIFFERENT CHEMICALS REQUIRE DIFFERENT TIMING. SOME CHEMICALS TAKE LONGER TO BURN, WHILE OTHERS DO NOT TAKE AS LONG TO BURN. CHEMICAL 1 SHOWS A LONGER BURN TIME COMPARED TO CHEMICAL 2 AND CHEMCIAL 3. (TIME ~ CHEMICAL | CHEMICAL)

OBSERVATION 3

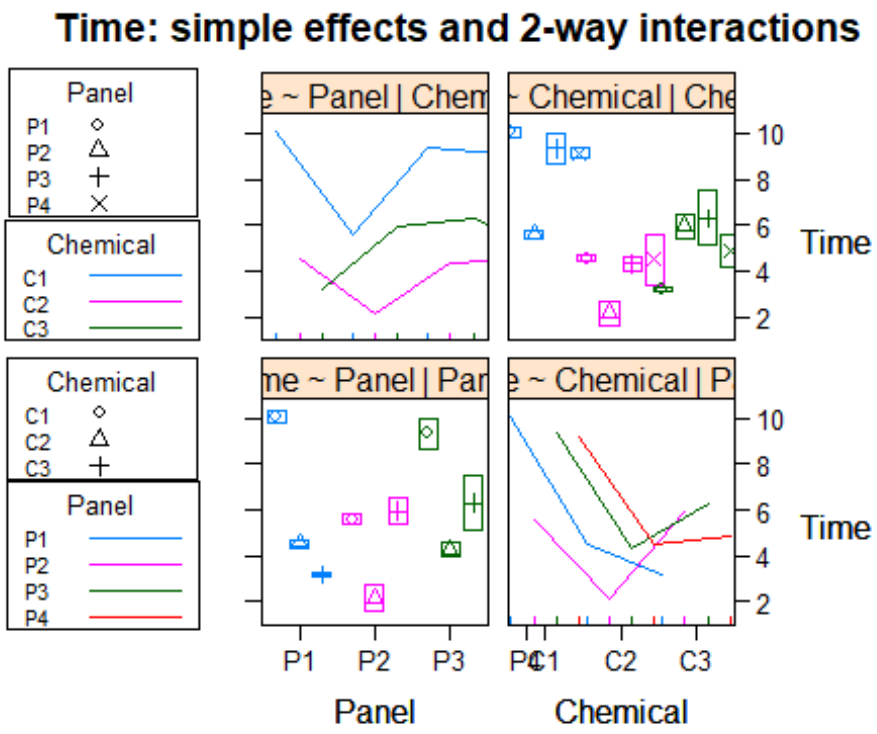
CHEMICAL 3 GOES AGAINST THE OVERALL TREND AS IT DIPS AND WAS TESTED FOR SIGNIFICANT INTERACTION. (TIME ~ PANEL | CHEMICAL)

OBSERVATION 4

CHEMICAL 1 SHOWS THE LARGEST TIME REGARDLESS OF THE PANELS. (TIME ~ CHEMICAL | PANEL)

```
interaction2wt(data=retard, Time ~
                 Panel + Chemical,
               simple=TRUE,
               simple.scale=list(Panel=.3,
                                 Chemical=.3),
```

```
        xlim=c(.5, 3.5),
        between=list(x=.5, y=.5))
```



Findings:

Chemical 1 has an average time significantly larger than chemical 2 or 3 for plywood types 1, 3, and 4. Chemical 1 should be used on these plywood types. Plywood 2 shows chemical 2 has significantly lower average times and should not be used on this plywood. For plywood 2, either chemical 1 or 3 should be used. No significant difference exists between these two chemicals.