Supporting information for
Analysis of statistical interactions in factorial experiments

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Abstract

This manuscript provides some supporting information to the article **Analysis of statistical interactions in factorial experiments** (Kitsche and Schaarschmidt, 2014). It presents the application of the `iacontrast()` and `plotcontrast()` function in the `statint` package to generate a labelled product type interaction contrast matrix for a detailed analysis of statistical interactions in the two-way layout. Furthermore, the analysis of statistical interactions of some selected data sets from the agronomy and crop sciences are demonstrated in case studies.

Contents

The package `statint()` is currently uploaded at `https://github.com/AKitsche/statint`. To install directly from github, the package `devtools` is needed (available on CRAN):

```r
install.packages("devtools")
library(devtools)
install_github(username = "AKitsche", repo = "statint")
library(statint)
```

1 Usage of iacontrast() function

The function `iacontrast()` generates a labelled interaction contrast matrix for the anaylsis of statistical interactions in two-way layouts. The user has to commit the two factor variables `fa` and `fb` and the types of the two one-way contrasts `typea` and `typeb`. Alternatively, the user can apply a-priori defined one-way contrast matrices `cma` and `cmb`.

The output is a list with two elements: i) `fab` a new factor generated by all pair-wise combinations of the levels of the two factors from the two-way layout, ii)`cmab` a labelled interaction contrast matrix.

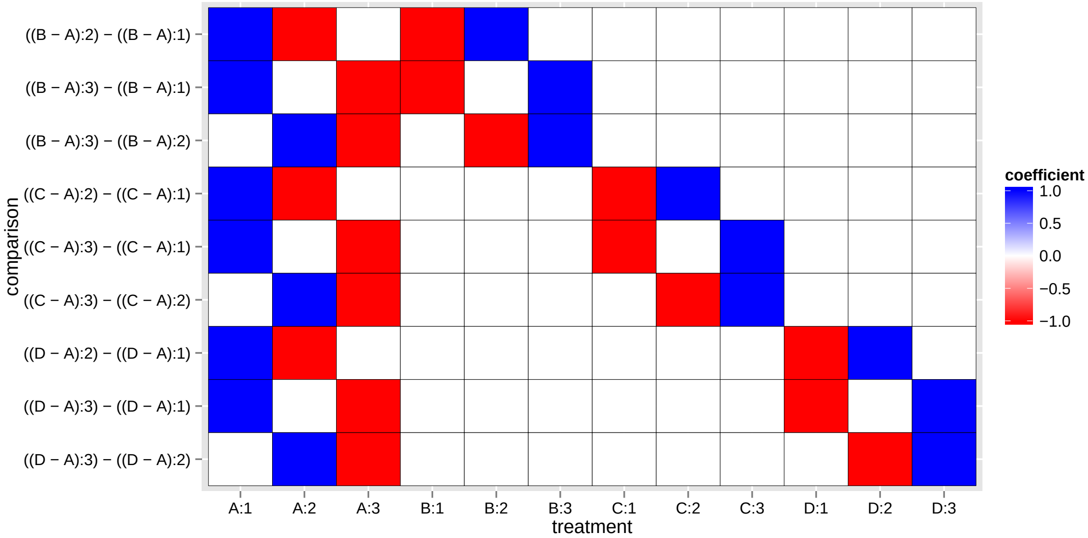
In the following the interaction contrast matrix is generated using the Dunnett type contrast (comparisons to a control) for the first factor and the Tukey type contrast (all pair-wise comparisons) for the second factor in a 4-by-3 layout.

```r
# generating factor variables
fa <- factor(rep(rep(LETTERS[1:4], rep(3, 4)), each = 3))
fb <- factor(rep(rep(c(1, 2, 3), rep(3, 3)), times = 4))
library(statint)
iacontrast(fa = fa, fb = fb, typea = "Dunnett", typeb = "Tukey")
```

	A:1	A:2	A:3	B:1	B:2	B:3	C:1	C:2	C:3	D:1	D:2	D:3
((B - A):2) - ((B - A):1)	1	-1	0	-1	1	0	0	0	0	0	0	0
((B - A):3) - ((B - A):1)	1	0	-1	-1	0	1	0	0	0	0	0	0
((B - A):3) - ((B - A):2)	0	1	-1	0	-1	1	0	0	0	0	0	0
((C - A):2) - ((C - A):1)	1	-1	0	0	0	0	-1	1	0	0	0	0
((C - A):3) - ((C - A):1)	1	0	-1	0	0	0	-1	0	1	0	0	0
((C - A):3) - ((C - A):2)	0	1	-1	0	0	0	0	-1	1	0	0	0
((D - A):2) - ((D - A):1)	1	-1	0	0	0	0	0	0	0	-1	1	0
((D - A):3) - ((D - A):1)	1	0	-1	0	0	0	0	0	0	-1	0	1
((D - A):3) - ((D - A):2)	0	1	-1	0	0	0	0	0	0	0	-1	1

The function `plotcontrast()` plots a contrast matrix in a tile plane with rectangles. It requires a contrast matrix in which the rownames represent the names for the comparisons of interest and the colnames represent the levels of the factor of interest. Contrast coefficients with a negative sign are displayed in red, whereas contrast coefficients with a positive are displayed in blue.

```
IntContrastMat <- iacontrast(fa = fa, fb = fb, typea = "Dunnett", typeb = "Tukey")
plotcontrast(IntContrastMat$cmab)
```

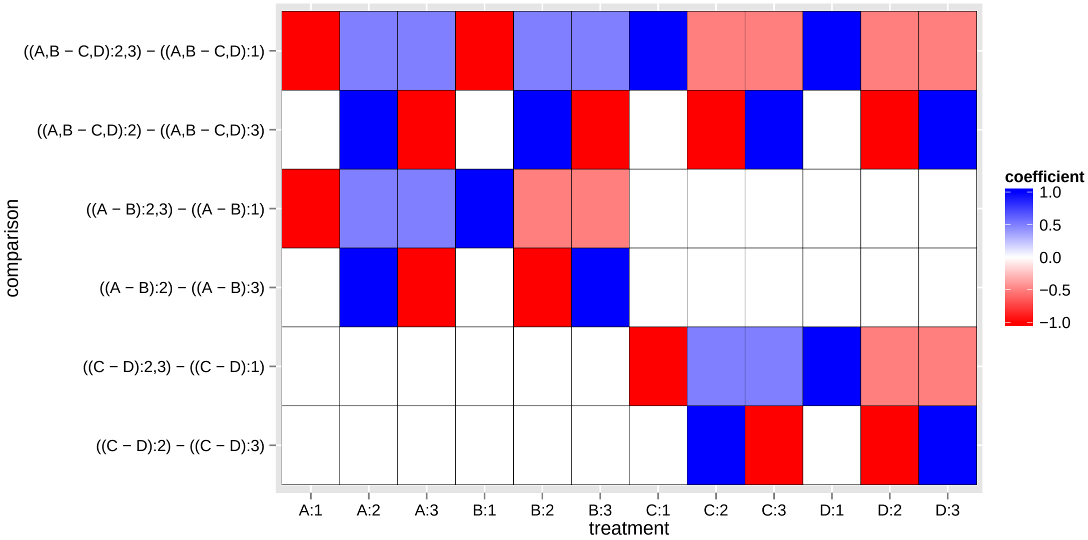


We next demonstrate the usage of prespecified user defined contrasts.

```
#generating user defined one-way contrast matrices
ContrastsA <- matrix(c(1 , 1, -1, -1,
                       1 ,-1,  0,  0,
                       0 , 0,  1, -1), nrow=3, byrow=TRUE)
ContrastsB <- matrix(c(-1, 0.5, 0.5,
                        0,   1,  -1), nrow=2, byrow=TRUE)
iacontrast(fa=fa, fb=fb, cma=ContrastsA, cmb=ContrastsB)
```

```
IntContrastMat <- iacontrast(fa = fa, fb = fb, cma = ContrastsA, cmb = ContrastsB)
plotcontrast(IntContrastMat$cmab)
```

	A:1	A:2	A:3	B:1	B:2	B:3	C:1	C:2	C:3	D:1	D:2	D:3
((A,B - C,D):2,3) - ((A,B - C,D):1)	-1.0	0.5	0.5	-1.0	0.5	0.5	1.0	-0.5	-0.5	1.0	-0.5	-0.5
((A,B - C,D):2) - ((A,B - C,D):3)	0.0	1.0	-1.0	0.0	1.0	-1.0	0.0	-1.0	1.0	0.0	-1.0	1.0
((A - B):2,3) - ((A - B):1)	-1.0	0.5	0.5	1.0	-0.5	-0.5	0.0	0.0	0.0	0.0	0.0	0.0
((A - B):2) - ((A - B):3)	0.0	1.0	-1.0	0.0	-1.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0
((C - D):2,3) - ((C - D):1)	0.0	0.0	0.0	0.0	0.0	0.0	-1.0	0.5	0.5	1.0	-0.5	-0.5
((C - D):2) - ((C - D):3)	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	-1.0	0.0	-1.0	1.0



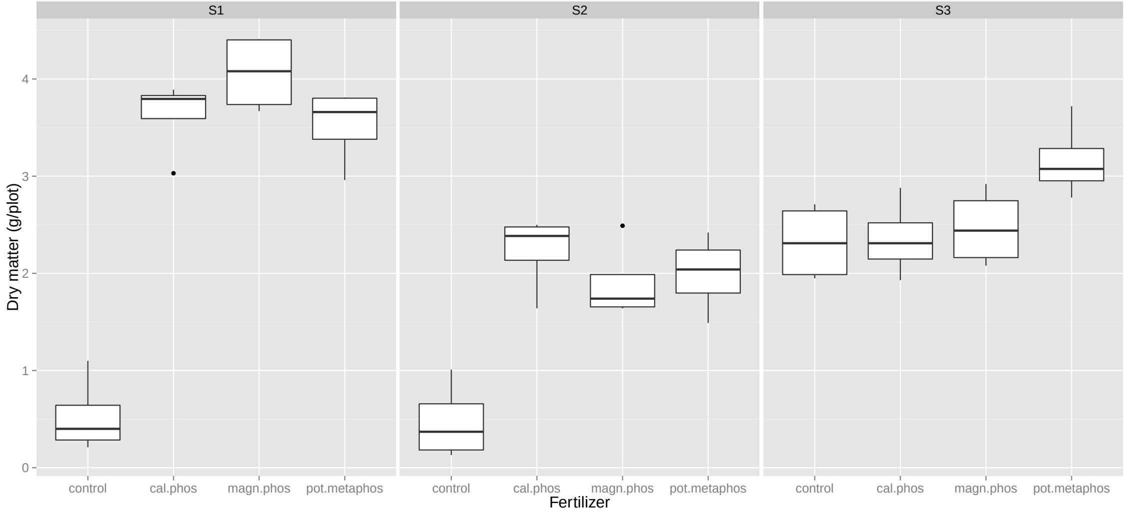


Figure 1: Boxplots of the dry matter based on each fertilizer-by-soil type combination.

2 Lettuce data set

The `lettuce` data set presents a simulated data set, inspired by the example presented in Bradu and Gabriel (1974). The example is an experiment conducted to analyse the effects of soil type and phosphate fertilizers on lettuce crops. The primary response variable was dry matter measured in grams per plot. Three different soil types, namely S1, S2 and S3, and four different levels of phosphate fertilization (including an untreated control) were investigated in a balanced, completely cross-classified treatment structure, laid out as completely randomized design with four replications per treatment combination.

```
data(lettuce)
str(lettuce)
#reorder Fertilizer levels
lettuce$Fertilizer <- factor(lettuce$Fertilizer,
        levels=c("control","cal.phos", "magn.phos","pot.metaphos"))
```

The factor fertilizer consists of an untreated control group and three different phosphorus fertilizers. The objective of including this factor is to estimate the increase in yield that results applying each of the fertilizers compared to the untreated control. The second factor, soil type, contains no further substructure, and interest is in comparing all three soil types among each other. The product type interaction contrasts allow to interpret to what extend the difference in yield between the three phosphate fertilizers compared to the control varies between the three soil types.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Fertilizer	3	26.41	8.80	55.00	0.0000
Soil	2	14.08	7.04	43.98	0.0000
Fertilizer:Soil	6	14.65	2.44	15.25	0.0000
Residuals	36	5.76	0.16		

Table 1: Two-way ANOVA of the Lettuce data set.

The interaction contrasts compare the differences of the fertilizer effects between the soil types, where the fertilizer effects of interest are restricted to the differences of each phosphorus fertilizer to the control group. To test the corresponding hypothesis fomulated by the interaction contrasts the function `glht()` in the package `multcomp` (Hothorn et al., 2008) is used. The corresponding multiplicity adjusted p-values and simutaneous confidence intervals are available using the functions `summary()` and `confint()`.

```
#define appropriate user defined contrast matrices
SoilMatrix <- matrix(c(1, -1, 0,
                       1,  0,-1,
                       0,  1,-1), nrow=3, byrow=TRUE)
FertMatrix <- matrix(c(1, -1, 0, 0,
                       1,  0,-1, 0,
                       1,  0, 0,-1),nrow=3, byrow=TRUE)
InteractionContrasts <- iacontrast(fa=lettuce$Fertilizer,
                                   fb=lettuce$Soil,
                                   cma=FertMatrix,
                                   cmb=SoilMatrix)
#assign the pseudo one-way factor (Fertilizer-by-Soil) to the data set
lettuce$FertSoil <- InteractionContrasts$fab
#fitting a cell means model using the pseudo one-way layout
CMM <- lm(Weight ~ FertSoil -1, data = lettuce)
#Multiple Comparisons
MultTest <- glht(model=CMM,
                 linfct = mcp(FertSoil=InteractionContrasts$cmab))
summary(MultTest)#calculating adjusted p-values
```

```
confint(MultTest)#calculating simultaneous confidence intervals
```

	Estimate	Std.Error	t value	Pr(>|t|)
((control - cal.phos):S1) - ((control - cal.phos):S2)	-1.34	0.40	-3.36	0.01
((control - cal.phos):S1) - ((control - cal.phos):S3)	-3.06	0.40	-7.65	0.00
((control - cal.phos):S2) - ((control - cal.phos):S3)	-1.72	0.40	-4.30	0.00
((control - magn.phos):S1) - ((control - magn.phos):S2)	-2.10	0.40	-5.25	0.00
((control - magn.phos):S1) - ((control - magn.phos):S3)	-3.38	0.40	-8.45	0.00
((control - magn.phos):S2) - ((control - magn.phos):S3)	-1.28	0.40	-3.21	0.02
((control - pot.metaphos):S1) - ((control - pot.metaphos):S2)	-1.47	0.40	-3.67	0.01
((control - pot.metaphos):S1) - ((control - pot.metaphos):S3)	-2.15	0.40	-5.38	0.00
((control - pot.metaphos):S2) - ((control - pot.metaphos):S3)	-0.69	0.40	-1.71	0.45

Table 2: Results for the lettuce data set analysed with user defined interaction contrasts. Estimate denote the estimate for the comparison of interest, the adjusted P-value, Lower and Upper the lower and upper bound of the two-sided 0.95 simultaneous confidence interval.

3 Bush beans data set

This example was published in Petersen (1985, p. 154). The data used within the `statint` package are simulated according to those in Petersen (1985). A detailed description of the data set is given in Petersen (1985) and Kitsche and Schaarschmidt (2014).

We first analyse the data using a two-way ANOVA while including the block effect as fixed effect.

```
# fitting a linear model and calculate an ANOVA
anova(lm(Yield ~ Variety * Spacing + Block, data = beans))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Variety	3	1332.56	444.19	34.22	0.0000
Spacing	2	72.67	36.33	2.80	0.0754
Block	3	341.90	113.97	8.78	0.0002
Variety:Spacing	6	871.00	145.17	11.18	0.0000
Residuals	33	428.35	12.98		

Table 3: Two-way ANOVA table of the bush beans data set

Kitsche and Schaarschmidt (2014) described an alternative ANOVA that is also meaningful for this example, where the hierarchical structure between the growth type and the varieties within the growth type is taken into account. The resulting three-factorial ANOVA is given below.

```
beans$Type[beans$Variety == "LittleGem" | beans$Variety  == "RedLake"] <- "erect"
beans$Type[beans$Variety == "BigGreen"  | beans$Variety  == "NewEra" ] <- "bushy"
anova(lm(Yield ~ Block +
                 Type +
                 Spacing +
                 Type:Spacing +
                 Type:Variety +
                 Type:Variety:Spacing, data=beans))
```

Fore a detailed analysis of the variety-by-spacing interaction we generate the appropriate one-way contrasts according to Table 9 and 10 in Kitsche and Schaarschmidt (2014). Afterwards, the corresponding product-type interaction contrast matrix (see

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Block	3	341.90	113.97	8.78	0.0002
Type	1	105.02	105.02	8.09	0.0076
Spacing	2	72.67	36.33	2.80	0.0754
Type:Spacing	2	748.17	374.08	28.82	0.0000
Type:Variety	2	1227.54	613.77	47.28	0.0000
Type:Spacing:Variety	4	122.83	30.71	2.37	0.0730
Residuals	33	428.35	12.98		

Table 4: ANOVA table of the bush beans data set that takes the hierarchical structure between the growth type and the varieties within the growth type into account.

Table 11 in Kitsche and Schaarschmidt (2014)) is generated using the `iacontrast()` function.

```
VarMat   <- matrix(c(0.5,  0.5, -0.5, -0.5,
                       1,   -1,    0,    0,
                       0,    0,    1,   -1), nrow=3, byrow=TRUE)
SpaceMat <- matrix(c(1, -1,  0,
                     1,  0, -1,
                     0,  1, -1), nrow=3, byrow=TRUE)
InteractionMat <- iacontrast(fa=beans$Variety, fb=beans$Spacing,
                             cma=VarMat, cmb=SpaceMat)
```

The hypotheses formulated in terms of the generated interaction contrasts are further tested using the `glht()` function in the package `multcomp` (Hothorn et al., 2008). The corresponding multiplicity adjusted p-values and simutaneous confidence intervals are available using the functions `summary()` and `confint()`.

```
#generating a new factor for the cell means
beans$VarSpace <- InteractionMat$fab
#fitting a cell means model with the new factor
CMM <- lm(Yield ~ VarSpace + Block -1, data = beans)
#Multiple Comparisons
library(multcomp)
MultTest <- glht(model=CMM,
                 linfct = mcp(VarSpace=InteractionMat$cmab))
summary(MultTest)#calculating adjusted p-values
confint(MultTest)#calculating simultaneous confidence intervals
```

As an alternative analysis of the spacing-by-variety interaction the spacing factor could also be suggested as quantitative. In this case the comparison among regression slopes between varieties can be set up. Again it is assumed that interest is in the comparisons of the regression slopes between the different growth types and in comparisons of the varieties within the different growth types.

For illustrative purposes we fit a linear mixed model assuming the Block as random factor. This results in a parameter vector of the fixed effects with four (variety specific) intercepts and four slopes.

```
data(beans)
str(beans)
beans$Variety <-factor(beans$Variety, levels=c("BigGreen",
                                               "NewEra",
                                               "LittleGem",
                                               "RedLake"))
beans$Spacing <- as.numeric(beans$Spacing)
library(nlme)
fm1 <- lme(Yield ~ Variety+Variety:Spacing-1, data=beans,
                                              random= ~ 1|Block)
#Generating user defined contrasts for the comparisons of the
#regression slopes from the eight dimensional parameter vector
Contrasts_Slopes <- matrix(c(0 , 0, 0, 0, 0.5, 0.5,-0.5,-0.5,
                             0 , 0, 0, 0, 1  ,  -1,   0,   0,
                             0 , 0, 0, 0, 0  ,   0,   1,  -1),
                           byrow=TRUE,
                           nrow=3)
row.names(Contrasts_Slopes) <- c("Bushy-Tall",
                                 "Big Green-New Era",
                                 "Little Gem-Red Lake")
#testing the user defined comparisons of regression slopes
#using the glht() function
MultTest <- glht(fm1, linfct = Contrasts_Slopes)
summary(MultTest)
```

	Estimate	Std.Error	t value	Pr(>|t|)
Bushy-Tall	0.48	0.06	7.92	0.00
Big Green-New Era	0.22	0.09	2.55	0.03
Little Gem-Red Lake	0.17	0.09	1.96	0.14

Table 5: Results for the bush beans data set analysed with user defined contrasts of slopes for the linear regression on spacing. Estimate denote the estimate for the comparison of interest, the adjusted P-value, Lower and Upper the lower and upper bound of the two-sided 0.95 simultaneous confidence interval.

4 Ethylene data set

This data set results from an experiment to analyse the effect of the ethylene receptor blocker MCP for improvement of postharvest characteristics of *Pelargonium zonale* hybrids. A detailed description of the experiment is given in Kitsche and Schaarschmidt (2014).

```
data(ethylen)
str(ethylen)
#reordering the factor levels
ethylen$Cult  <- factor(ethylen$Cult,
                        levels=c(1,2,3),
                        labels=c("cultivar 1","cultivar 2","cultivar 3"))
ethylen$Treatment  <- factor(ethylen$Treatment,
                             levels=c("control","water","prod1","prod2","prod3"))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Cult	2	53.22	26.61	16.00	0.0000
Eth	1	98.85	98.85	59.43	0.0000
Treatment	4	156.05	39.01	23.46	0.0000
Cult:Eth	2	0.37	0.19	0.11	0.8938
Cult:Treatment	8	3.05	0.38	0.23	0.9840
Eth:Treatment	4	35.65	8.91	5.36	0.0009
Cult:Eth:Treatment	8	28.73	3.59	2.16	0.0436
Residuals	60	99.80	1.66		

Table 6: Three-way ANOVA table of the ethylene blocking data set.

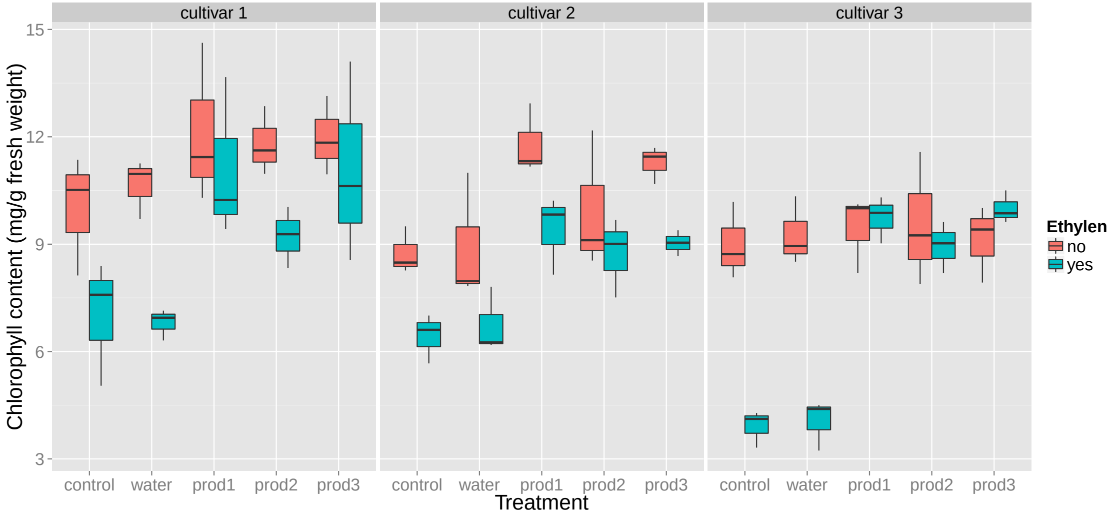


Figure 2: Boxplots of the chlorophyll content after eight days based on each ethylene-by-treatment-by-cultivar combination.

The following one-way contrast matrices are used to analyse the ethylene-by-treatment interaction.

```
#definition of appropriate contrasts
#1. contrast for the different ethylen treatments
ContrMat_Ethylen <- matrix(c(1, -1), nrow=1, byrow=FALSE)
#2. contrasts for the Treatment factor
ContrMat_Treatment <- matrix(c(1/2, 1/2,-1/3,-1/3,-1/3,
                                 0,   0,   1,  -1,   0,
                                 0,   0,   1,   0,  -1,
                                 0,   0,   0,   1,  -1),
                             nrow=4, byrow=TRUE)
```

Since there is also a significant cultivar-by-treatment-by-ethylene interaction, the interaction contrast matrix has to be defined manually by using the Kronecker product.

```
ContrMat_Cult <- matrix(c(1/3,1/3,1/3),
                        nrow=1)
#interaction contrast matrix
```

```
InteractionContrasts<- kronecker(ContrMat_Cult,
                       kronecker(ContrMat_Treatment, ContrMat_Ethylen))
#fitting the appropriate cell means model
ethylen$CultTreatEth <- with(ethylen, Cult:Treatment:Eth)
CMM <- lm(Chloro8 ~ CultTreatEth-1, data=ethylen)
library(multcomp)
MultTest <- glht(CMM, linfct=mcp(CultTreatEth=InteractionContrasts))
summary(MultTest)
confint(MultTest)
```

For illustrative purposes we additionally demonstrate the analysis of the cultivar-by-treatment-by ethylene interaction. Therefore we consider that all pairwise comparisons of the cultivars are of interest.

```
CultMatrix <- matrix(c(1, -1, 0,
                       1,  0,-1,
                       0,  1,-1), nrow=3, byrow=TRUE)
InteractionContrasts<- kronecker(CultMatrix,
                       kronecker(ContrMat_Treatment, ContrMat_Ethylen))
MultTest <- glht(CMM, linfct=mcp(CultTreatEth=InteractionContrasts))
summary(MultTest)
confint(MultTest)
```

	Estimate	Std.Error	t value	Pr(>|t|)
Ethylene (control - Product)Cult1-Cult2	1.62	1.36	1.19	0.86
Ethylene (Prod1 - Prod2)Cult1-Cult2	-2.78	2.11	-1.32	0.79
Ethylene (Prod1 - Prod3)Cult1-Cult2	-0.04	2.11	-0.02	1.00
Ethylene (Prod2 - Prod3)Cult1-Cult2	2.75	2.11	1.30	0.80
Ethylene (control - Product)Cult1-Cult3	-3.42	1.36	-2.51	0.13
Ethylene (Prod1 - Prod2)Cult1-Cult3	-0.66	2.11	-0.31	1.00
Ethylene (Prod1 - Prod3)Cult1-Cult3	-0.45	2.11	-0.22	1.00
Ethylene (Prod2 - Prod3)Cult1-Cult3	0.21	2.11	0.10	1.00
Ethylene (control - Product)Cult2-Cult3	-5.04	1.36	-3.71	0.00
Ethylene (Prod1 - Prod2)Cult2-Cult3	2.12	2.11	1.01	0.93
Ethylene (Prod1 - Prod3)Cult2-Cult3	-0.42	2.11	-0.20	1.00
Ethylene (Prod2 - Prod3)Cult2-Cult3	-2.54	2.11	-1.20	0.86

Table 7: Results for the three-way interaction analysis of the ethylene blocking data set. Estimate denote the estimate for the comparison of interest, the adjusted P-value, Lower and Upper the lower and upper bound of the two-sided 0.95 simultaneous confidence interval.

5 Water deficiency data set

This data set was part of an experiment conducted at the Woody Plant and Propagation Physiology Section in the Institute of Horticultural Production Systems at the Leibniz Universität Hannover in 2013. The goal of the experiment was to investigate a potential differing response among nine varieties of starch potato (*Solanum tuberosum*) on water deficiency stress. The following nine varieties of starch potato were selected for cultivation: A, B, C, D, E, F, G, H and I. Each variety was cultivated under four different water conditions: standard control medium, 0.1M, 0.2M and 0.3M sorbitol medium. An increasing sorbitol concentration was used to induce an increasing water deficiency stress on the plants. For each treatment by variety combination 6 replicates were investigated. The trial was planned in a completely cross-classified treatment structure, in a completely randomized design. A total number of 13 objects were discarded from the analysis because of infection diseases. For each experimental unit the fresh weight of the shoot was measured. To achieve approximately equal variances over the factor levels of the response variable a log transformation was performed.

```
library(statint)
data(potato)
str(potato)
potato$treatment <- factor(potato$treatment,
                           levels=c("control","0.1","0.2","0.3"))
```

The researcher was interested in selecting those varieties with a different response on water deficiency in contrast to the general water deficiency response. Additionally, interest was in determining on which level of water deficiency stress those potential deviations occur.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
treatment	3	57.02	19.01	356.98	0.0000
genotype	8	40.96	5.12	96.16	0.0000
treatment:genotype	24	2.93	0.12	2.30	0.0012
Residuals	167	8.89	0.05		

Table 8: Two-way ANOVA table of the water defciency data set

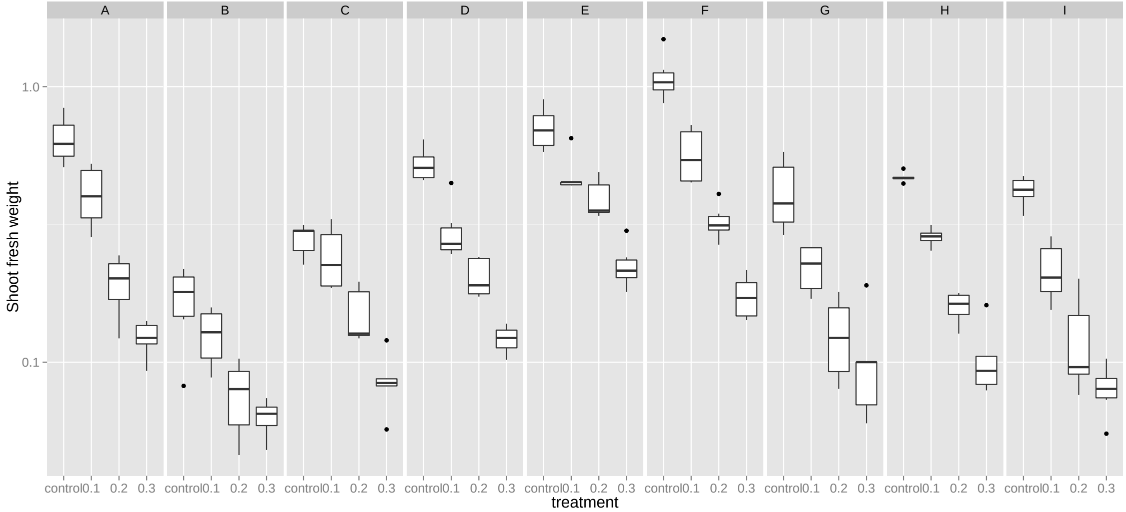


Figure 3: Boxplots of the shoot fresh weight based on each variety-by-stress combination.

```
InteractionContrasts <- iacontrast(fa=potato$treatment,
                                   fb=potato$genotype,
                                    typea="Dunnett", typeb="GrandMean")
potato$GenTreat <- InteractionContrasts$fab
CellMeansModel <- lm(log(shoot) ~ GenTreat-1, data=potato)
#conducting user defined multiple comparisons
MultTest <- glht(model=CellMeansModel,
                 linfct = mcp(GenTreat=InteractionContrasts$cmab))
summary(MultTest)#calculating adjusted p-values
ConfInt <- confint(MultTest)#calculating simultaneous confidence intervals
```

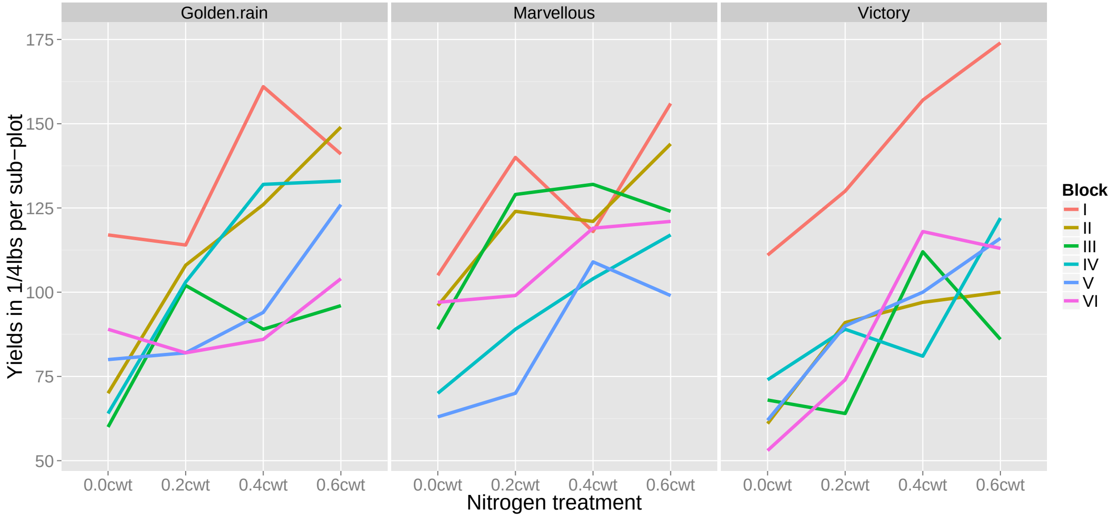


Figure 4: Interaction plot of the oats field trial.

6 Oats Field Trial

In this section the analysis of statistical interaction in a split-plot field trial is demonstrated. The underlying methodoly is roughly described in Kitsche and Schaarschmidt (2014). Therefore, the `oats` dataset from the R add-on package `MASS` is used (Venables and Ripley, 2002). In this trial the yield of three different varieties of oats was investigated unter four levels of manurial treatment. For a detailed description we refer to the `MASS` package documentation of the data set.

```
library(nlme)
fit <- lme(Y ~ N + V + N:V, data = oats, random = ~1 | B/V)
anova(fit)
```

Although there is no evidence for an interaction in this trial, we further assume that interest is in the anylsis of the nitrogen-by-variety interaction for illustrative purposes.

```
InteractionContrasts <- iacontrast(fa=oats$N, fb=oats$V,
                                   typea = "Tukey", typeb = "Tukey",
                                   abbrevnames=list("minlength"=4))
oats$NV <- InteractionContrasts$fab
```

```r
#fitting the cell means model
CMM <- lme(Y ~ NV, data=oats, random=~1|B/V)
anova(CMM)
# In principle, there may be more appropriate denominator degrees
# of freedom here. For consistency with ANOVA we select 43
MultTest <- glht(CMM, mcp(NV = InteractionContrasts$cmab), df=43)
summary(MultTest)
confint(MultTest)
```

References

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	Estimate	Std.Error	t value	Pr(>|t|)
((0.1 - control):A) - ((0.1 - control):B,C,D,E,F,G,H,I)	0.00	0.13	0.03	1.00
((0.1 - control):B) - ((0.1 - control):A,C,D,E,F,G,H,I)	0.21	0.13	1.69	0.87
((0.1 - control):C) - ((0.1 - control):A,B,D,E,F,G,H,I)	0.32	0.14	2.36	0.36
((0.1 - control):D) - ((0.1 - control):A,B,C,E,F,G,H,I)	-0.09	0.13	-0.75	1.00
((0.1 - control):E) - ((0.1 - control):A,B,C,D,F,G,H,I)	0.09	0.13	0.72	1.00
((0.1 - control):F) - ((0.1 - control):A,B,C,D,E,G,H,I)	-0.18	0.13	-1.41	0.97
((0.1 - control):G) - ((0.1 - control):A,B,C,D,E,F,H,I)	-0.13	0.13	-1.05	1.00
((0.1 - control):H) - ((0.1 - control):A,B,C,D,E,F,G,I)	-0.02	0.14	-0.18	1.00
((0.1 - control):I) - ((0.1 - control):A,B,C,D,E,F,G,H)	-0.21	0.13	-1.64	0.90
((0.2 - control):A) - ((0.2 - control):B,C,D,E,F,G,H,I)	-0.22	0.13	-1.75	0.84
((0.2 - control):B) - ((0.2 - control):A,C,D,E,F,G,H,I)	0.22	0.13	1.73	0.85
((0.2 - control):C) - ((0.2 - control):A,B,D,E,F,G,H,I)	0.36	0.14	2.66	0.19
((0.2 - control):D) - ((0.2 - control):A,B,C,E,F,G,H,I)	0.05	0.13	0.38	1.00
((0.2 - control):E) - ((0.2 - control):A,B,C,D,F,G,H,I)	0.40	0.13	3.21	0.04
((0.2 - control):F) - ((0.2 - control):A,B,C,D,E,G,H,I)	-0.21	0.13	-1.66	0.89
((0.2 - control):G) - ((0.2 - control):A,B,C,D,E,F,H,I)	-0.20	0.13	-1.60	0.92
((0.2 - control):H) - ((0.2 - control):A,B,C,D,E,F,G,I)	-0.10	0.14	-0.70	1.00
((0.2 - control):I) - ((0.2 - control):A,B,C,D,E,F,G,H)	-0.31	0.13	-2.43	0.31
((0.3 - control):A) - ((0.3 - control):B,C,D,E,F,G,H,I)	-0.23	0.13	-1.82	0.79
((0.3 - control):B) - ((0.3 - control):A,C,D,E,F,G,H,I)	0.49	0.14	3.50	0.02
((0.3 - control):C) - ((0.3 - control):A,B,D,E,F,G,H,I)	0.24	0.14	1.72	0.85
((0.3 - control):D) - ((0.3 - control):A,B,C,E,F,G,H,I)	-0.03	0.13	-0.22	1.00
((0.3 - control):E) - ((0.3 - control):A,B,C,D,F,G,H,I)	0.28	0.13	2.22	0.47
((0.3 - control):F) - ((0.3 - control):A,B,C,D,E,G,H,I)	-0.40	0.13	-3.18	0.04
((0.3 - control):G) - ((0.3 - control):A,B,C,D,E,F,H,I)	-0.00	0.13	-0.00	1.00
((0.3 - control):H) - ((0.3 - control):A,B,C,D,E,F,G,I)	-0.11	0.14	-0.78	1.00
((0.3 - control):I) - ((0.3 - control):A,B,C,D,E,F,G,H)	-0.24	0.13	-1.88	0.75

Table 9: Results for the interaction analysis of the Water deficiency data set. Estimate denote the estimate for the comparison of interest, the adjusted P-value, Lower and Upper the lower and upper bound of the two-sided 0.95 simultaneous confidence interval

	numDF	denDF	F-value	p-value
(Intercept)	1	45.00	245.14	0.00
N	3	45.00	37.69	0.00
V	2	10.00	1.49	0.27
N:V	6	45.00	0.30	0.93

Table 10: ANOVA of the split-plot oats field trial.