```
(hu-lest 13-1)
              Consider The following LSD: \begin{pmatrix} 111 & 122 & 133 \\ 221 & 232 & 213 \\ 331 & 312 & 323 \end{pmatrix}
                                                                                                                                                                                                                                                                        is zivo.
a) Use $ (\frac{1}{2}, -\frac{1}{2}, -\frac{1}{2}, \] =0 to show That The cross-term $\frac{1}{2} (\frac{1}{2}, -\frac{1}{2}, \) (\frac{1}{2}, -\frac{1}{2}, \)
           = (Yin-You) (Y-j. -You) =
              = (\overline{Y}_{1...} - \overline{Y}_{...}) (\overline{Y}_{.1.} - \overline{Y}_{...}) + (\overline{Y}_{1...} - \overline{Y}_{...}) (\overline{Y}_{.2.} - \overline{Y}_{...}) + (\overline{Y}_{1...} - \overline{Y}_{n.}) (\overline{Y}_{.3.} - \overline{Y}_{...})
                       (Y1., -Y--,) [(7.1, -Y--,) + (Y.2, -Y--,) + (Y.3, -Y--,)]
                                                                                         5 (Y.j.-Y...) = OF FYI, proof, below
              Similarly for The 2nd and 3rd vows. = 0.
b) Now, to illustrate The importance of LSD, /111 132
               consider The following non-LSD. It's hard (331 312
             to show generally that something is not zero; but provide some argument for why The above cross-term is not zero.
               = (\(\frac{7}{1}\), -\(\frac{7}{1}\), -\(\frac{7}\), -\(\frac{7}{1}\), -\(\frac{7}\), -\(\frac{7}\), -\(\frac{7}\), -\(\frac{7}\), -\(\frac{7}\), -\(\frac{7}\), -\(\frac{7}\)
               blue terms = (1.1.-Tim) = (Tim-Tim) = 0, but The rest don't group
               into anything That involves si(Yi... Y...) = or se (Yi... -Y...) = or ste.
                シ(イ), ーイ…) = シャーシャー = ラティンーコットー ライル = カイル = カイル = カイル = カイル = ローラ
```



Consider the world  $Y_{ij} = \mu + \tau_i + R_j + (Y)_{ij} + E_{ij}$ .

As I explained in class,  $Y_{ij}$ , simply does not have enough of to estimate everything. But let's try any way | Recall That we begin by taking derivatives of  $SSE = \sum_{ij} (Y_{ij} - \mu - \tau_i - \beta_j - Y_{ij})^2$ , with respect to  $\mu$ ,  $\tau_i$ ,  $\beta_j$ ,  $Y_{ij}$ , and setting the verilts to zero at  $\hat{\mu}$ ,  $\hat{\tau}_i$ ,  $\hat{\beta}_j$ ,  $\hat{y}_{ij}$ . Show that the deriv. w.v.t.  $Y_{ij}$  leads to an equation which implies  $\hat{E}_{ij} = Y_{ij} - \hat{Y}_{ij} = 0$ .

Yij = M+Tit bj + Vij + Eij

SSE = 2 (40 - M-70- B) - 800)2

 $\frac{2}{\delta \delta ij} = \frac{1}{1} - \hat{\mu} - \hat{\tau}_i - \hat{\beta}_j - \delta i_j = 0 \implies e_{ij} = 0 \implies \text{MSE} = 0$   $\tilde{\epsilon}_{ij} \text{ (or } e_{ij})$   $\text{Can't estimate } \sigma_{\epsilon}^2 \text{ with MSE}$ 

Just compare The above with what happens if There is a ke index;

Yigo= M+Ti+ hj+ dij + Eigo

SSE = = ( Yish - M - Ti - K; - Yi; )2

 $\frac{\partial}{\partial x_{ij}}\Big|_{\Lambda} = \underbrace{\sum_{k} (Y_{ijk} - \widehat{\mu} - \widehat{\gamma}_{i} - \widehat{\beta}_{i} - \widehat{\gamma}_{i}, \widehat{\gamma}_{i})}_{e_{ijk}} \Rightarrow \underbrace{e_{ij}}_{e_{ijk}} = 0$ 

This time we can estimate of because MSE + 0.

## (hw-let13-3)

For The full (interactive) model light = M+xi+ Bj+ (xB) ij+ Eigh, show that

- a) The sample mean (over i,j, h) of The predictions is equal to The Sample mean ( " " ) of The observations.
- b) The sample mean ( .. ., ) of The vesiduals is zero.
- c) The sample covariance between predictions and residuals, is zero.

defined as I & ( Îiîk - Î...) ( eiîk - E...)

d), e) same as a, b > but for veduced (additive) model.

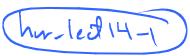
Note/Hint: All of The above as habout sample stats. They are not ashing about E[], V[] or COV[,]. So, just use The parameter estimates we have derived in The lecture, and simplify.

- a)  $\widehat{Y}_{ii} = \frac{1}{nab} \underbrace{\hat{y}_{ijk}}_{ijk} = \frac{1}{nab} \underbrace{\hat{y}_{ijk}}_{ijk} \underbrace{\hat{y}_{ij}}_{ijk} = \underbrace{\hat{y}_{ii}}_{ijk} \underbrace{\hat{y}_{ij}}_{ijk} = \underbrace{\hat{y}_{ii}}_{ijk} \underbrace{\hat{y}_{ij}}_{ijk} = \underbrace{\hat{y}_{ii}}_{ijk} \underbrace{\hat{y}_{ijk}}_{ijk} = \underbrace{\hat{y}_{ii}}_{ijk} \underbrace{\hat{y}_{ii}}_{ijk} = \underbrace{\hat{y}_{ii}}_{ijk} = \underbrace{\hat{y}_{ii}}_{ijk} =$
- b) P. + & eish = tob ish ( Yish Yish) = tob ish (Yish Yish)

$$= \frac{1}{nab} \left( \frac{2}{ijk} \frac{1}{kijk} - \frac{2}{ij} \frac{1}{kij} \cdot \frac{2}{kij} \cdot \frac{1}{n} \right) = 0$$

$$= \frac{1}{nab} \frac{1}{\sqrt{n}} \frac{1}{n} \frac{1}{$$

= \frac{1}{200} \left( \hat{\frac{1}{100}} \hat{\frac{1}{100}} \left( \frac{1}{100} \hat{\frac{1}{100}} \left( \frac{1}{100} \hat{\frac{1}{100}} \right) \left( \frac{1}{100} \hat{\frac{1}{100}} \hat{\frac{1}{100}} \right) \left( \frac{1}{100} \hat{\fra



Consider The model  $\forall ijk = \mu + di + (dis)ij + Eijk$ . j=1-ba) Write The Least-Squares equations (from  $\partial/\partial\mu$ , ...)

SSE = & (Yijh - M-xi-(xA)i) 2 an Them.

3/ = 5 ((ijh - M- x; - (xB); ) = 0 -> Y... - M - x, - (xB) = 0

Dai: 5 (Yin -μ- αi - (κβ)i)=0 → Yin -μ-αi - (κβ)i = 0 II

(4ijh-M- xi- (4B)ij) =0 -> Yij. -M-xi- (4B)ij =0.

b) How many indop, equations are There in part a)?

(I) = 1 equ. 5 (I) = (I).

1. It a-1 + ab - (a-1) -1 = ab indep. equations.

C) Fiven That The model has 1+ a+ ab params, will The following Gonstraints be sufficient?  $\alpha_i = 0$  (Bi. = 0) Explain.

Yes- 1 + a additional equs,

is how many we need.

d) write The df for each of The SS terms in The ANOVA decomp,

SST= SSA+SSAB + SSE

abn-1 a-1 ab-a abn-ab



```
# For the data in problem 5.28 in book
# a) Produce the ANOVA Table for the full model (By hand).
# b) Make a gaplot of the residuals, and the residuals plots (vs. predicted,
# versus factor1, versus factor2, and versus factor3). By R.
# c) The plots in part b call for data transformation (of y). Try log(y) and sqrt(y)
# to see if the results are improved, but do not turn in these results. Instead
# let y --> y^{1.7}, and then repeat parts a and b.
# Hint in all of the above, use the formulas on page 185-186 in book.
# You may also need to make a 3d-array in R; if so, you can do it this way:
# t = numeric(a); tt = matrix(nrow=b,ncol=c); 3d-array = outer(t,tt)
 library(AlgDesign)
 a = 2
                # levels of Booster
                # levels of Washings
 b = 2
 c = 2
                # levels of Formulation
                # replications (Here, no need to block)
 n = 2
 design = gen.factorial(c(a,b,c,n), varNames=c("A", "B", "C", "R"), factors="all")
 attach(design)
 y = c(6,6,3,4, 10,11,10,9,
                               # 1st replicate,
     5,5,2,1, 9,11,9,10) # second replicate
 cbind(A,B,C,R,y)
                             # Check.
 # Compute the conditional means:
                           # formulas on p 185 use sums (not means)
 y.... = sum(y)
 yi... = c(sum(y[A==1]), sum(y[A==2]))
 y.i.. = c(sum(y[B==1]), sum(y[B==2]))
 y..k. = c(sum(y[C==1]), sum(y[C==2]))
   yij.. = matrix(nrow=a,ncol=b)
   for(i in 1:a){
   for(j in 1:b){
   yij..[i,j] = sum(y[A==i \& B==j])
   yi.k. = matrix(nrow=a,ncol=c)
   for(i in 1:a){
   for(j in 1:c){
   yi.k.[i,j] = sum(y[A==i \& C==j])
   y.jk. = matrix(nrow=b,ncol=c)
   for(i in 1:b){
   for(j in 1:c){
   y.jk.[i,j] = sum(y[B==i \& C==j])
     t = numeric(a); tt = matrix(nrow=b,ncol=c); yijk. = outer(t,tt)
     for(i in 1:a){
     for(j in 1:b){
     for(k in 1:c){
     yijk.[i,j,k] = sum(y[A==i \& B==j \& C==k])
     }}}
```



```
# Get ready for ANOVA table:
dfA = (a-1)
dfB = (b-1)
dfC = (c-1)
dfAB = (a-1)*(b-1)
dfAC = (a-1)*(c-1)
dfBC = (b-1)*(c-1)
dfABC = (a-1)*(b-1)*(c-1)
dfE = a*b*c*(n-1)
SST = sum(y^2) - y....^2/(a*b*c*n)
SSA = sum(yi...^2)/(b*c*n) - y....^2/(a*b*c*n)
SSB = sum(y.j..^2)/(a*c*n) - y....^2/(a*b*c*n)
SSC = sum(y..k.^2)/(a*b*n) - y....^2/(a*b*c*n)
 temp = 0
 for(i in 1:a){
 for(j in 1:b){
 temp = temp + yij..[i,j]^2
 SSAB = temp/(c*n) - y....^2/(a*b*c*n) - SSA - SSB
 temp = 0
 for(i in 1:a){
 for(j in 1:c){
 temp = temp + yi.k.[i,j]^2
 SSAC = temp/(b*n) - y....^2/(a*b*c*n) - SSA - SSC
 temp = 0
 for(i in 1:b){
 for(j in 1:c){
 temp = temp + y.jk.[i,j]^2
 SSBC = temp/(a*n) - y....^2/(a*b*c*n) - SSB - SSC
 temp = 0
 for(i in 1:a){
 for(j in 1:b){
 for(k in 1:c){
 temp = temp + yijk.[i,j,k]^2
 SSABC = temp/n - y....^2/(a*b*c*n) - SSA - SSB - SSC - SSAB - SSAC - SSBC
 SSE = SST - SSA - SSB - SSC - SSAB - SSAC - SSBC - SSABC
MSA = SSA/dfA
MSB = SSB/dfB
MSC = SSC/dfC
MSAB = SSAB/dfAB
MSAC = SSAC/dfAC
MSBC = SSBC/dfBC
MSABC = SSABC/dfABC
MSE = SSE/dfE
```

```
FA = MSA/MSE
 FB = MSB/MSE
 FC = MSC/MSE
 FAB = MSAB/MSE
 FAC = MSAC/MSE
 FBC = MSBC/MSE
 FABC = MSABC/MSE
 pvA = pf(FA,dfA,dfE,lower.tail=F)
 pvB = pf(FB,dfB,dfE,lower.tail=F)
 pvC = pf(FC,dfC,dfE,lower.tail=F)
 pvAB = pf(FAB,dfAB,dfE,lower.tail=F)
 pvAC = pf(FAC,dfAC,dfE,lower.tail=F)
 pvBC = pf(FBC,dfBC,dfE,lower.tail=F)
 pvABC = pf(FABC,dfABC,dfE,lower.tail=F)
 table = rbind(
    cbind(dfA,dfB,dfC,dfAB,dfAC,dfBC,dfABC,dfE),
    cbind(SSA,SSB,SSC,SSAB,SSAC,SSBC,SSABC,SSE),
    cbind(MSA,MSB,MSC,MSAB,MSAC,MSBC,MSABC,MSE),
    cbind(FA,FB,FC,FAB,FAC,FBC,FABC,-99),
                                                # -99 as a place holder.
    cbind(pvA,pvB,pvC,pvAB,pvAC,pvBC,pvABC,-99)
 t(table)
# A
      1 0.5625 0.5625 0.6000 4.608560e-01
      1 14.0625 14.0625 15.0000 4.721383e-03
# C
      1 138.0625 138.0625 147.2667 1.968149e-06
      1 0.5625 0.5625 0.6000 4.608560e-01
# AB
       1 0.5625 0.5625 0.6000 4.608560e-01
# AC
      1 5.0625 5.0625 5.4000 4.863085e-02
# BC
# ABC 1 0.5625 0.5625 0.6000 4.608560e-01
      8 7.5000 0.9375 -99.0000 -9.900000e+01
# All of the above agrees with R says:
 Im.1 = Im(y \sim A*B*C)
 summary.aov(lm.1)
        Df Sum Sq Mean Sq F value Pr(>F)
#
# A
         1 0.56 0.56 0.6 0.46086
         1 14.06 14.06 15.0 0.00472 **
# B
         1 138.06 138.06 147.3 1.97e-06 ***
# C
# A:B
          1 0.56 0.56 0.6 0.46086
          1 0.56 0.56
# A:C
                          0.6 0.46086
          1 5.06 5.06
                          5.4 0.04863 *
# B:C
           1 0.56 0.56
# A:B:C
                          0.6 0.46086
# Residuals 8 7.50 0.94
```

```
# b)
 Im.1 = Im( y \sim A*B*C)
                                    # full model
 summary.aov(lm.1)
                                     # View with suspicision, because of
 yhat = predict(lm.1)
                                   # the following plots don't look good.
 par(mfrow=c(3,2),mar=c(2,2,2,2))
 qqnorm(Im.1$resid)
 plot(yhat, lm.1$resid); abline(h=0)
 plot(as.numeric(A),lm.1$resid); abline(h=0) # w/o as.numeric() you'll get boxplots.
 plot(as.numeric(B),lm.1$resid); abline(h=0)
 plot(as.numeric(C),lm.1$resid); abline(h=0)
# All of these look bad. The ganorm plot is not straight, and the residual plots
# all show non-constant variances. The recommended thing to do is transform data.
# Some standard transformations and sgrt and log, certainly when y is positive:
 Im.1 = Im( sqrt(y) \sim A*B*C)
                                     # sqrt transform
\# \text{Im.1} = \text{Im}(\text{log(y)} \sim \text{A*B*C})
 summary.aov(lm.1)
 yhat = predict(lm.1)
 par(mfrow=c(3,2),mar=c(2,2,2,2))
 qqnorm(Im.1$resid)
 plot(yhat, lm.1$resid); abline(h=0)
 plot(as.numeric(A),lm.1$resid); abline(h=0)
 plot(as.numeric(B),lm.1$resid); abline(h=0)
 plot(as.numeric(C),lm.1$resid); abline(h=0)
# Both the sqrt and the log transform improve the qqplot a bit, but the
# residuals are still bad. Now you can try a weird transform:
 Im.1 = Im((y)^1.7 \sim A*B*C)
 summary.aov(lm.1)
 yhat = predict(lm.1)
 par(mfrow=c(3,2),mar=c(2,2,2,2))
 ggnorm(Im.1$resid)
 plot(yhat, lm.1$resid); abline(h=0)
 plot(as.numeric(A),lm.1$resid); abline(h=0)
 plot(as.numeric(B),lm.1$resid); abline(h=0)
 plot(as.numeric(C),lm.1$resid); abline(h=0)
# This one improves the residual plots, but now the applot looks bad.
# Note that the F tests do differ in terms of which factors are significant.
# For example, the non-transformed data and the sqrt and log transformed data
# all lead to BC being a significant interaction. But the 1.7 transformed data
# leads to a model in which BC is not significant.
# It's possible that there exists yet another transformation that improves
# both the applot and the residual plots, but for now this is good enough.
```

```
nu-led 14-3
# 5.23
 rm(list=ls(all=TRUE))
 library(AlgDesign)
 y.m = matrix(c(
     109, 110, 108, 110,
      110, 115, 109, 108,
     110, 110, 111, 114,
     112, 111, 109, 112,
     116, 112, 114, 120,
     114, 115, 119, 117), ncol=4, byrow=T)
 y = as.vector(t(y.m))
# By comparing the order of these y-values with the data given in the problem, you can see that the machine factor (A) is
changing fastest, then replication (R), and then the slowest changing factor is operator (B). So, we need
  design = gen.factorial(c(4,2,3),varNames=c("A","R","B"), factors="all")
  attach(design)
  cbind(A,R,B,y)
                       # compare and confirm with data in the problem.
  # If you don't include the Replication factor in the model, then you will be
  # solving problem 5.8, i.e., developing a full model involving A and B:
 lm.1 = lm(y \sim A*B)
  summary.aov(lm.1)
         Df Sum Sq Mean Sq F value Pr(>F)
# machine
              3 12.46 4.15 1.095 0.388753
# oper
            2 160.33 80.17 21.143 0.000117 ***
# machine:oper 6 44.67 7.44 1.963 0.150681
# Residuals 12 45.50 3.79
# But, here we want the replication to be a block factor. As far as R is concerned, you simply enter the R factor as a factor in
the model. R has no way of knowing whether a factor is a treatment factor or a block factor - that difference arises in the way
the experiment is performed, AND in the interpretation of the p-values in the anove table:
 lm.2 = lm(y \sim A*B + R)
 summary.aov(lm.2)
      Df Sum Sq Mean Sq F value Pr(>F)
         3 12.46 4.15 1.051 0.408659
A
         2 160.33 80.17 20.291 0.000204 ***
В
```

# We can see that the operator factor (B) is still significant, and the machine factor (A) is not, just as in the unblocked/full model. This is consistent with the large p-value associated with the block factor, suggesting that there is no evidence for variability across blocks anyway (Although we remind ourselves that we should be cautious in interpretating this p-value).

R

A:B

Residuals 11 43.46 3.95

1 2.04 2.04 0.517 0.487209 6 44.67 7.44 1.884 0.171630 h-v-14-4)

```
# Consider the data from example 9.1. The design is a factorial involving 3 factors
# A, B, and C, each with 3 levels. Consider only the first replicate.
# a) Fit a model that includes at most 2-way interactions, and produce the
# ahova table. State your conclusions; which effects are significant, and
# which are not?
# b) Now consider only the portion of the data that would follow if we had
# followed a Latin Square Design, of the form
#
     1,2,3
# B (2,3,1)
                                  # Note B = row factor.
     3,1,2
# Develop an additive model, and and produce the anova table / State your
# conclusions; which effects are significant, and which are not?
# Are the conclusions in parts a and b consistent?
# c) For the LSD consider a non-additive model that includes A + B + C but
# also a single 2-way interaction term BC. Develop the model and produce
# the anova table. What comments can you make about this table?
  rm(list=ls(all=TRUE))
  library(AlgDesign)
                                       # for gen.factorial()
# a)
                                  # Number of factors.
  nf = 3
  p±3
                                  # Number of levels.
  design = gen.factorial(rep(p,nf), varNames=c("A","B","C"), factors="all")
  attach(design)
  y = c(-35,17,-39, -45,-65,-55, -40,20,15, # 1st replicate in Table 9.1
       110,55,90, -10,-55,-28, 80,110,110,
       4,-23,-30, -40,-64,-61, 31,-20,54)
  cbind(A,B,C,y)
                                       # Confirm with Table 9.1
  lm.1 = lm(y \sim A*B + A*C + B*C)
                                               \# same as A+B+C+ A*B+ A*C+ B*C
  summary.aov(lm.1)
            Df Sum Sq Mean Sq F value Pr(>F)
# A
             2 480
                      240
                               0.506 0.620709
# B
             2 36474
                      18237
                              38.481 7.86e-05 ***
                              33.375 0.000131 ***
# C
             2 31634
                      15817
# A:B
             4 3399
                               1.793 0.223418
                      850
             4 3729
                               1.967 0.192726
# A:C
                      932
             4 7626
                      1906
                               4.023 0.044649 *
# B:C
                      474
# Residuals 8 3791
# The (main) effects of B and C are statistically significant, but there is
\# n\phi evidence from this data that factor A has an effect on y. The interaction
# between B and C is also significant.
# This is not necessary for hw, but as a rule check the residual and qqplot:
  plot(lm.1$residuals, predict(lm.1)); abline(h=0) # Looks OK/random.
  qqnorm(lm.1$residuals)
                                                 # Looks straight/normal.
```

```
(2)
```

```
# b) This time, only A and B have a factorial design, and C follows the pattern in
# the given LSD with B (A) as row (col) factors. Note: if the LSD is read-in row-wise,
# then, A changes faster than B:
  design = gen.factorial(rep(p,2), varNames=c("A","B"), factors="all")
  attach(design)
  C = as.factor(c(1,2,3,
                  2,3,1,
                  3,1,2))
 y = c(-35,
              55, -30,
                              # Keep only the corresponding y's.
        -10, -64, -55,
         31, 20, 110)
                             # Confirm.
  cbind(A,B,C,y)
  lm.2 = lm(y \sim A + B + C)
  summary.aov(lm.2)
           Df Sum Sq Mean Sq F value Pr(>F)
            2 260
# A
                     130 0.591 0.6285
            2 14167 7083 32.181 0.0301 *
# B
# C
            2 10911 5455 24.785 0.0388 *
# Residuals 2 440
                     220
# The significant factors are B and C. This is the same conclusion that followed
\# from fitting the model with 2-way interactions. This is not guaranteed, but in
# this case, the two models agree.
# If you're wondering why we didn't include interactions in this model, see next part.
# Again, not necessary for hw, but check these plots:
  plot(lm.2$residuals, predict(lm.2)); abline(h=0) # OK
  qqnorm(lm.2$residuals)
# c)
  lm|.3 = lm(y \sim A + B + C + B:C)
  summary.aov(lm.3)
            Df Sum Sq Mean Sq
# A
             2 260
                     130
# B
             2 14167 7083
# C
             2 10911 5455
# B:C
             2 440
                     220
# This time, there is no SSE (or MSE) term, and so no tests can be performed.
# The same conclusion follows if you include A:C or A:B. This is happening
# because the LSD data simply does not have enough df to estimate all the
# parameters/effects. Of course, if we had replication, then we would have more
# df in the data; we are not doing that here because we have not completely
# learned how to do LSD with replication; maybe later. However, LSD designs
# do generally assume that the interactions are small, because in an LSD
# we cannot discriminate between a main effect (from A, B, or C), and an
# interaction (from AB, BC, AC). The effects one computes in LSD are some
# unknown linear combination of the true main effects and interaction effects.
# The inability do discriminate between two things already shows up in the
# amova tables above; note that SS(BC) in the LSD model with an interaction
# is equal to SSE of the factorial design, i.e., 440.
```

## hw/12/15-1

For Yigh = M+di+ Rj+ (&B)ij + Eijk, consider The main effect for A, for B, and The interaction effect, all written in Yates' notation. We showed That The product of the contrast constants for A and for B is equal to the contrast constant of the interaction effect. Show That The product of the main effect for A, and for B, does NOT give the interaction effect.

$$A = \frac{1}{2n} \left[ -(1) + a - b + ab \right] A \times B = \frac{1}{4n^2} \left[ (-(1) + ab) + (a - b) \right] \times \left[ (-(1) + ab) - (a - b) \right] \times \left[ (-(1) + ab) - (a - b) \right]$$

$$A \times B = \frac{1}{4n^2} \left[ (-(1) + ab)^2 - (a - b)^2 \right] + AB = \frac{1}{2n} \left[ +(1) - a - b + ab \right]$$

No squares.

## hurlet 15-2

- In a 2 design with The model \(\ii) = \( \ta + \ti \), \(\in \) = \( \ti \in \),

  a) Starting from either  $S_A = \sum_{i=1}^{2n} (V_i V_i)^2$  or  $V_i = V_i^2 V_i^2$ . Show that  $V_i = V_i =$
- b) Can SSE be written in terms of a (contrast)??
  provide some math/explanation.
- a)  $Yi\hat{j} = Y_{-} + (\overline{Y}_{i}, -\overline{Y}_{-}) + (Y_{i}, -\overline{Y}_{i})$ 
  - $SS_{A} = \sum_{i=1}^{a_{i}} (Y_{i}.-Y_{i})^{2} = n \sum_{i=1}^{a_{i}} (Y_{i}.-A_{i}Y_{i})^{2} = 1 \sum_{i=1}^{a_{i}} (Y_{i}.-A_{i}Y_{i})^{2}$   $= \frac{1}{n} \left[ \sum_{i=1}^{a_{i}} Y_{i}^{2}. \frac{2}{a_{i}} Y_{i}. + \frac{1}{a_{i}} Y_{i}^{2}. \sum_{i=1}^{a_{i}} \right]$
  - SSA = 1 & Yii 1 y 2 Con may start from here. 3.9, p.74
    - $=\frac{1}{n}\left[Y_{1.}^{2}+Y_{2.}^{2}-\frac{1}{2}\left(Y_{1.}+Y_{2.}\right)^{2}\right] \quad (\alpha=2)$
    - $= \frac{1}{2n} \left( Y_{1.}^{2} + Y_{2.}^{2} 2Y_{1.}Y_{2.} \right) = \frac{1}{2n} \left( Y_{2.} Y_{1.} \right)^{2} \xrightarrow{11} A$   $= \frac{1}{2n} \left[ a (1) \right]^{2} \xrightarrow{11} Y_{1.} \quad Y_{2.}$
    - =  $\frac{1}{2n} (Contrast_A)^2$  where  $contrast_A = -(1) + \alpha$

b) 
$$SS_{E} = \sum_{i}^{n} \sum_{j}^{n} \left( \chi_{i,j} - \overline{\chi}_{i,j} \right)^{2} = \sum_{i,j}^{n} \left( \chi_{i,j} - \overline{\chi}_{i,j} \right)^{2}$$

$$= \sum_{i,j}^{n} \chi_{i,j}^{2} - \sum_{i}^{n} \chi_{i,i}^{2} \geq \chi_{i,i}^{2} \leq \chi_{i,j}^{2} + \sum_{i}^{n} \chi_{i,i}^{2} \leq \chi_{i,i}^{2$$

The only contrasts are (1)-a and -(1)+a.

= cannot be written as (contrast)2

:- SSE cannot be written in terms of a (contrast)2.

(m- let 15-3)

We have sceen That for 2, The mo Il

i=1,2 j=1,2 Yijh= M+ x-+ B; + (x B); + Ei; h k=1,--;n

decomposition wherein SSA, defined as

can be written as In (ontrastA)2

It can be shown that SSAB, defined as

can be written in terms of  $\pm (\text{contrast } AB)^2$ . Here all you have to show is that the i=1, j=1 term in SSAB is equal to  $\pm (\text{contrast } AB)^2$ , ie. show = 1/11, -71., +7., 2 = 167 (contrast AB) 2.

$$=\frac{1}{n}\left[\left(y_{11},-\frac{1}{2}(y_{11},+y_{12},)-\frac{1}{2}(y_{11},+y_{21},)+\frac{1}{4}(y_{11},+y_{12},+y_{21},+y_{22},)\right]^{2}+\cdots\right]$$

$$=\frac{1}{n}\frac{1}{16}\left[11-b-a+ab\right]^{2}+\cdots$$

$$= \frac{1}{16n} \left[ (1) - a - b + ab \right]^{2} + \cdots$$

$$= \frac{1}{16n} \left[ \text{Contrast AB } \right]^{2} + \cdots$$

$$= \frac{1}{16n} \left[ \text{Contrast AB } \right]^{2} + \cdots$$

Chrolest 15-4

For the data in problem 6.5, a) Perform ANOVA By R.

rm(list=ls(all=TRUE))

a = sum(y[A==+1 & B==-1])

sum((y-predict(lm.1))^2)

```
nr = 4
                     # number replicates.
   y.m = matrix(
   c(18.2, 18.9, 12.9, 14.4,
     27.2, 24.0, 22.4, 22.5,
     15.9, 14.5, 15.1, 14.2,
     41.0, 43.9, 36.3, 39.9), nrow = 4, ncol= 4, byrow=T)
    y = as.vector(y.m)
    A = as.factor(rep(c(-1,+1,-1,+1),4))
     B = as.factor(rep(c(-1,-1,+1,+1),4))
     lm.1 = lm(y \sim A + B + A*B)
     summary.aov(lm.1)
         Df Sum Sq Mean Sq F value Pr(>F)
# A
           1 1107.2 1107.2 185.25 1.17e-08 ***
# B
           1 227.3 227.3 38.02 4.83e-05 ***
# A:B
           1 303.6 303.6 50.80 1.20e-05 ***
# Residuals 12 71.7 6.0
b) Recompute the 4 SS values in the anova table of part a, this time by hand, using the y-totals (1), a, b, ab, and the contrasts.
# Totals:
  one = sum(y[A==-1 \& B==-1])
                                           #(1) = 64.4
```

```
\# b = 59.7
  b = sum(y[A==-1 \& B==+1])
                                           \# ab = 161.1
  ab = sum(y[A==+1 \& B==+1])
# Contrasts:
  cont1 = (-one + a - b + ab)/nr
  cont2 = (-one - a + b + ab)/nr
  cont3 = (+one - a - b + ab)/nr
  cont1^2/(4/nr)
                                 #1107.226 = SS in printout above.
  cont2^2/(4/nr)
                                 # 227.2556
  cont3^2/(4/nr)
                                 # 303,6306
  # SSE can be computed either by subtraction from SST:
  sum((y - mean(y))^2) - (cont1^2/(4/nr) + cont2^2/(4/nr) + cont3^2/(4/nr))
  # or from its definition:
```

# a = 96.1

c) Under what conditions (bit size and cutting speed) would you operate this process? To answer that question, make comparative boxplots of y for each of the treatement combinations.

```
boxplot(y[A==-1 & B==-1],y[A==+1 & B==-1], ylim=c(10,50))
boxplot(y[A==-1 & B==+1],y[A==+1 & B==+1],add=T,col=2,boxwex=0.5)
```

The x axis refers to the 2 levels of A. And the 2 colors correspond to different levels of B. Two reduce vibration, it is clearly better to use A=-1 (smaller bit). As for the factor B (speed), given the big overlap between the boxplots corresponding to B=-1 and B=+1, when A=-1, as long as we use A=-1, B does not have have a significant effect on vibration.

d) How does the interaction term in the anova table manifest itself in the diagram of part c.

#71.7225

Imagine the same-colored boxplots are connected by a straight line. The big difference in the slope of the two lines (black and red), is consistent with the significant interaction term in the anova printout.

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