hw-lect 10-1

Show that in the ANOVA decomposition, the "cross-term" between the 2^{nd} and 3^{rd} terms is zero. I.e. show that

$$\sum_{i,j} (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})(Y_{ij} - \bar{Y}_{i\cdot} - \bar{Y}_{\cdot j} + \bar{Y}_{\cdot\cdot}) = 0$$

Hint: This requires only 2 or 3 lines of algebra; and don't forget that $\sum_j (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot}) = 0$.

$$= \sum_{i,j} (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot}) Y_{ij} - \sum_{i,j} (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})(\bar{Y}_{i\cdot}) - \sum_{i,j}^{a,b} (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})\bar{Y}_{\cdot j} + \sum_{i,j}^{a,b} (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})\bar{Y}_{\cdot\cdot}$$

$$= \cancel{\sum_j (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})\underbrace{\left(\sum_i Y_{ij}\right)}_{a\bar{Y}_{\cdot j}}} - \underbrace{\left(\sum_j \bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot}\right)}_{0}\underbrace{\left(\sum_i \bar{Y}_{i\cdot}\right)}_{a\bar{Y}_{\cdot\cdot}} - \cancel{a\sum_j (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})\bar{Y}_{\cdot j}} + a\bar{Y}_{\cdot\cdot}\underbrace{\sum_j^{b} (\bar{Y}_{\cdot j} - \bar{Y}_{\cdot\cdot})}_{0}$$

$$= 0$$

hw-lect10-2

For the model $Y_{ij} = \mu + \alpha_i + \beta_j + \epsilon_{ij}$, $i = 1 \dots a$, $j = 1, \dots, b$,
show that $E[MS_{Tr}] = \sigma_\epsilon^2 + \frac{b}{a-1} \sum_i^a (\alpha_i - \bar{\alpha}_.)^2$

Hint: As always, use the model asap, so that you can use results that we have proven already. For example, you may use, without proof, that $E[(\bar{\epsilon}_{i.} - \bar{\epsilon}_{..})^2] = \frac{1}{b}(1 - \frac{1}{a})\sigma_\epsilon^2$

$Y_{ij} = \mu + \alpha_i + \beta_j + \epsilon_{ij}$ $\qquad SS_{Tr} = b \sum_i^a (\bar{Y}_{i.} - \bar{Y}_{..})^2$

$\bar{Y}_{i.} = \mu + \alpha_i + \bar{\beta}_. + \bar{\epsilon}_{i.} \rightarrow \bar{Y}_{..} = \mu + \bar{\alpha}_. + \bar{\beta}_. + \bar{\epsilon}_{..}$ use the model asap!

$$E[SS_{Tr}] = b \sum_i^a E[(\bar{Y}_{i.} - \bar{Y}_{..})^2] = b \sum_i^a E[(\cancel{\mu} + \alpha_i + \cancel{\bar{\beta}_.} + \bar{\epsilon}_{i.} - \cancel{\mu} - \bar{\alpha}_. - \cancel{\bar{\beta}_.} - \bar{\epsilon}_{..})^2]$$

$$= b \sum_i^a E[((\alpha_i - \bar{\alpha}_.) + (\bar{\epsilon}_{i.} - \bar{\epsilon}_{..}))^2]$$

$$= b \sum_i^a \left((\alpha_i - \bar{\alpha})^2 + 2(\alpha_i - \bar{\alpha}_.) \underbrace{E[\bar{\epsilon}_{i.} - \bar{\epsilon}_{..}]}_{} + E[(\bar{\epsilon}_{i.} - \bar{\epsilon}_{..})^2] \right)$$

$E[\bar{\epsilon}_{i.}] - E[\bar{\epsilon}_{..}]$, $\;= 0$, $\;= 0$

$$= b \sum_i^a \left((\alpha_i - \bar{\alpha})^2 + \underbrace{E[(\bar{\epsilon}_{i.} - \bar{\epsilon}_{..})^2]}_{\frac{1}{b}(1-\frac{1}{a})\sigma_\epsilon^2} \right)$$

from past hw.

$$= b \sum_i (\alpha_i - \bar{\alpha})^2 + \underbrace{b\,a\,\frac{1}{b}\left(1 - \frac{1}{a}\right)}_{(a-1)} \sigma_\epsilon^2 = b \sum_i (\alpha_i - \bar{\alpha})^2 + (a-1)\sigma_\epsilon^2.$$

$$\therefore E[MS_{Tr}] = E\left[\frac{SS_{Tr}}{a-1}\right] = \sigma_\epsilon^2 + \frac{b}{a-1} \sum_i (\alpha_i - \bar{\alpha})^2$$

hw-lect10-3

```
# In problem 4.3,
# In an RCBD design with one treatment and one block factor, we know how to test
# the treatment effect (and the block effect). The tests are based on an F-test,
# where F is MS_treatment/MSE (or MS_block/MSE). However, I have also mentioned that
# those tests are equivalent to another set of F tests which are based on the SSE's
# obtained from a full model and two reduced models. Let's confirm !

# For the data in problem 4.3, do the following (all by R):
#
# a) Write code to produce the anova table for the full model.
# Record/save the value of SSE.
# Also, save the F-ratios for the treatment and block effects in the full anova
table.
#
# b) Write code to develop the reduced model that excludes the treatment factor.
# Record/save the value of SSE.
#
# c) Write code to develop the reduced model that excludes the block factor.
# Record/save the value of SSE.
#
# d) Show that by computing the appropriate ratios of SSE in parts a, b, and c,
# you can compute the same F ratios you saved in the anova table of the full model
# in part a.

 y.matrix = matrix(c(                        # rows = treatment, col = block
   73, 68, 74, 71, 67,
   73, 67, 75, 72, 70,
   75, 68, 78, 73, 68,
   73, 71, 75, 75, 69), nrow=4,byrow=T)
 y = t(y.matrix)
 y = as.vector(y)

  a = 4
  b = 5
  A = as.factor(rep(c(1:a),each=b))
  B = as.factor(rep(c(1:b),a))

# a)

  lm.1 = lm(y ~ A + B)
  temp = summary.aov(lm.1)
  temp
  SSE_mu_tau_beta = temp[[1]][3,2]

#              Df Sum Sq Mean Sq F value   Pr(>F)
# A             3  12.95    4.32   2.376    0.121
# B             4 157.00   39.25  21.606 2.06e-05 ***
# Residuals    12  21.80    1.82
```

```
# b)

  lm.reducedB = lm(y ~ B )
  tempB = summary.aov(lm.reducedB)
  tempB
  SSE_mu_beta = tempB[[1]][2,2]

#             Df Sum Sq Mean Sq F value   Pr(>F)
# B            4 157.00   39.25   16.94 1.95e-05 ***
# Residuals   15  34.75    2.32

# c)

  lm.reducedA = lm(y ~ A )
  tempA = summary.aov(lm.reducedA)
  tempA
  SSE_mu_tau = tempA[[1]][2,2]

#             Df Sum Sq Mean Sq F value Pr(>F)
# A            3  12.95   4.317   0.386  0.764
# Residuals   16 178.80  11.175

# d)

  FA_numer = (SSE_mu_beta - SSE_mu_tau_beta) / (a-1)
  FA_denom = SSE_mu_tau_beta/((a-1)*(b-1))
  FA = FA_numer/FA_denom                                 # 2.376147 = in part a

  FB_numer = (SSE_mu_tau - SSE_mu_tau_beta) / (b-1)
  FB_denom = SSE_mu_tau_beta/((a-1)*(b-1))
  FB = FB_numer/FB_denom                                 # 21.6055 = in part a

# Although I did not ask you to do this, you can see that the p-values are
# the same too:

  pf(FA, df1=a-1, df2=(a-1)*(b-1), 0, lower.tail = FALSE)  # 0.1211445 = in part a
  pf(FB, df1=b-1, df2=(a-1)*(b-1), 0, lower.tail = FALSE)  # 2.059181e-05 = in part a
```

hw-lect 11-1

In problem 4.3,
a) perform anova to compute a p-value from an F test of whether the 4 chemicals have an effect on strength, treating the data as if they were collected in a CRD. by hand
b) Repeat part a, but with an RCBD, with Bolts as the block factor. by hand.
c) Produce two residual plots: residuals versus y_hat, and residuals vs. y, (just to see why the latter is not recommended), for the residuals from the CRD design.
d) Repeat part c, but for RCBD.
e) Make qq plots for the CRD and RCBD residuals. Comment

```
 y = matrix(c(                    # rows = treatment, col = block
73, 68, 74, 71, 67,
73, 67, 75, 72, 70,
75, 68, 78, 73, 68,
73, 71, 75, 75, 69), nrow=4,byrow=T)

# a) CRD
 a = 4
 n = 5
 N = n*a
 means = apply(y,1,mean)      #  70.6 71.4 72.4 72.6
 vars = apply(y,1,var)        #  9.3  9.3 19.3  6.8   Note: unequal vars!
 grand.mean = mean(means)
 SS_treatment = n*sum((means - grand.mean)^2)
 SS_E = (n-1)*sum(vars)
 MS_treatment = SS_treatment/(a-1)                # 4.316667
 MS_E = SS_E/(N-a)                                # 11.175
 F_obs = MS_treatment/MS_E                        # 0.3862789
 pf(F_obs, df1=a-1, df2=N-a, 0, lower.tail = FALSE)   # 0.764377

 # Cannot reject H0 (that all 4 tau's are zero) in favor of H1.

# b) RCBD
 a = 4
 b = 5
 row.means = apply(y,1,mean)      #  70.6 71.4 72.4 72.6
 col.means = apply(y,2,mean)      #  73.50 68.50 75.50 72.75 68.50
 SS_treatment = b*sum((row.means - grand.mean)^2)
 SS_block = a*sum((col.means - grand.mean)^2)
 resid2 = (t(t(y - row.means) - col.means + grand.mean))      # Note t( t() )
 SS_E = sum( resid2^2 )
 MS_treatment = SS_treatment/(a-1)                     # 4.316667
 MS_block = SS_block/(b-1)                             # 39.25
 MS_E = SS_E/((a-1)*(b-1))                             # 1.816667
 F_obs = MS_treatment/MS_E                             # 2.376147
 pf(F_obs, df1=a-1, df2=(a-1)*(b-1), 0, lower.tail = FALSE)   # 0.1211445

 # Cannot reject H0 (that all 4 tau's are zero) in favor of H1.
```

```
# The conclusion to part a is this: assuming the design is CRD
# (when we know it's not), and applying an anova F-test, does NOT
# allow us to find the treatment effect.
# part b tells us that doing an F test that acknowledges
# the existing RCBD design is still not capable of finding the
# treatement effect, but it does have a lower p-value.

# c) residual for CRD

  resid.crd = y - row.means

  # residuals vs. y_hat:
  plot(rep(row.means,5), resid.crd, xlab="y_hat", ylab="residual")
  abline(h=0)

  # residuals vs. y: (not recommended)
  plot(as.vector(y), resid.crd, xlab="y", ylab="residual")
  abline(h=0)

  # The residual plots look adequate, except for the 2nd one
  # which is why it is not recommended.

# d) residual for RCBD

  resid.rcbd = t(t(y - row.means) - col.means + grand.mean)

  plot(rep(row.means,5), as.vector(resid.rcbd), xlab="row.means",ylab="residual")
  abline(h=0)

  plot(as.vector(y), as.vector(resid.rcbd), xlab="row.means", ylab="residual")
  abline(h=0)

  # This time both residual plots look adequate.

# e) qq plots fo CRD and RCBD

  qqnorm(resid.crd)          # consistent with normal
  qqnorm(resid.rcbd)         # consistent with normal.
```

hw_lect11-2

Consider The following data from an LSD :

Above, we proved That

$$\sum_{ijk}' Y_{i\cdot\cdot} = 3Y_{\cdot\cdot\cdot} \quad \left(\sum_{ijk}' Y_{i\cdot\cdot} = p\,Y_{\cdot\cdot\cdot} \right)$$

more generally.

(k) (j) is The middle

$$Y_{ijk} = \begin{array}{c|ccc|c} & & & & \\ (i) & Y_{111} & Y_{122} & Y_{133} & Y_{1\cdot\cdot} \\ & Y_{221} & Y_{232} & Y_{213} & Y_{2\cdot\cdot} \\ & Y_{331} & Y_{312} & Y_{323} & Y_{3\cdot\cdot} \\ & Y_{\cdot\cdot1} & Y_{\cdot\cdot2} & Y_{\cdot\cdot3} & \end{array}$$

Similarly, it can be shown That

$$\sum_{ijk}' Y_{\cdot j\cdot} = \sum_{ijk}' Y_{\cdot\cdot k} = 3Y_{\cdot\cdot\cdot}$$

Here, Show That $\sum_{ijk}' Y_{ijk} = \sum_{i} Y_{i\cdot\cdot}$

unrestricted restricted

and $\sum_{ijk}' Y_{ijk} = \sum_{k} Y_{\cdot\cdot k}$

sum over 9 elements in LS

$$\begin{aligned} \sum_{ijk}' Y_{ijk} &= Y_{111} + Y_{122} + Y_{133} = Y_{1\cdot\cdot} \\ &+ Y_{221} + Y_{232} + Y_{213} = +\, Y_{2\cdot\cdot} \\ &+ Y_{331} + Y_{312} + Y_{323} = +\, Y_{3\cdot\cdot} \end{aligned} \quad \Rightarrow \quad \underline{\sum_{ijk}' Y_{ijk} = \sum_{i}^{3} Y_{i\cdot\cdot}}$$

restricted.

$$\begin{array}{ccc} \| & \| & \| \\ Y_{\cdot\cdot1} & Y_{\cdot\cdot2} & Y_{\cdot\cdot3} \end{array} \Rightarrow \underline{\sum_{ijk}' Y_{ijk} = \sum_{k=1}^{3} Y_{\cdot\cdot k}}$$

FYI: Similarly, $\sum_{ijk}' Y_{ijk} = \sum_{j} Y_{\cdot j\cdot}$. So, $Y_{\cdot\cdot\cdot} = \sum_i Y_{i\cdot\cdot}$

$$= \sum_j Y_{\cdot j\cdot}$$

$$= \sum_k Y_{\cdot\cdot k}$$

---

hw_lect11-3 Quite generally, show That

$$\bar{Y}_{\cdot\cdot\cdot} = \frac{1}{p^2} \sum_{ijk}' \bar{Y}_{i\cdot\cdot} .$$

$$\bar{Y}_{\cdot\cdot\cdot} = \frac{1}{p^2} \underbrace{Y_{\cdot\cdot\cdot} = \frac{1}{p^2} \frac{1}{p} \sum_{ijk}' Y_{i\cdot\cdot}}_{\text{statement of prev. problem}} = \frac{1}{p^2} \sum_{ijk}' \underbrace{\frac{1}{p} Y_{i\cdot\cdot} = \frac{1}{p^2} \sum_{ijk}' \bar{Y}_{i\cdot\cdot}}_{\text{defn.}}$$

hw-lect 11-4

To estimate the params of the LSD model, we are supposed to differentiate SSE w.r.t. μ, α_i, τ_j, β_k, and set the result to $\emptyset$.

$$SSE = \sum_{ijk}{}' \epsilon_{ijk} = \sum_{ijk}{}' \left(Y_{ijk} - \mu - \alpha_i - \tau_j - \beta_k \right)^2$$

Because of the restricted sum, we can't quite differentiate this.

a) First, write out the Σ' in SSE for the specific LSD $\longrightarrow$

$\xrightarrow{(k)}$ (j) is the middle

$$Y_{ijk} = (i)\downarrow \begin{pmatrix} Y_{111} & Y_{122} & Y_{133} \\ Y_{221} & Y_{232} & Y_{213} \\ Y_{331} & Y_{312} & Y_{323} \end{pmatrix}$$

$$\begin{aligned} SSE = & (Y_{111} - \mu - \alpha_1 - \tau_1 - \beta_1)^2 + (Y_{122} - \mu - \alpha_1 - \tau_2 - \beta_2)^2 + (Y_{133} - \mu - \alpha_1 - \tau_3 - \beta_3)^2 \\ & (Y_{221} - \mu - \alpha_2 - \tau_2 - \beta_1)^2 + (Y_{232} - \mu - \alpha_2 - \tau_3 - \beta_2)^2 + (Y_{213} - \mu - \alpha_2 - \tau_1 - \beta_3)^2 \\ & (Y_{331} - \mu - \alpha_3 - \tau_3 - \beta_1)^2 + (Y_{312} - \mu - \alpha_3 - \tau_1 - \beta_2)^2 + (Y_{323} - \mu - \alpha_3 - \tau_2 - \beta_3)^2 \end{aligned}$$

b) Find $\partial / \partial \alpha_1 \Big|_{\hat{\mu}, \hat{\alpha}, \hat{\beta}, \hat{\tau}} = 0$

$$\frac{\partial SSE}{\partial \tau_1} : (Y_{111} - \mu - \alpha_1 - \tau_1 - \beta_1) + (Y_{213} - \mu - \alpha_2 - \tau_1 - \beta_3) + (Y_{312} - \mu - \alpha_3 - \tau_1 - \beta_2)$$

$$(Y_{111} + Y_{213} + Y_{312}) - 3\mu - (\alpha_1 + \alpha_2 + \alpha_3) - 3\tau_1 - (\beta_1 + \beta_2 + \beta_3) = 0.$$

$$\sum_{ijk}{}' Y_{.1.} - 3\hat{\mu} - 3\hat{\tau}_1 - \hat{\alpha}_. - \hat{\beta}_. = 0.$$

hw-lect12-1

Show that SS_{row} as defined by $\sum_{ijk}' (\bar{Y}_{i..} - \bar{Y}_{...})^2$ is equal to $\frac{1}{p}\sum_i^p Y_{i..}^2 - \frac{1}{p^2} Y_{...}^2$. You may use the specific LS shown ↓

$$\begin{pmatrix} Y_{111} & Y_{122} & Y_{133} \\ Y_{221} & Y_{232} & Y_{213} \\ Y_{331} & Y_{312} & Y_{323} \end{pmatrix}$$

$$SS_{row} = \sum_{ijk}' (\bar{Y}_{i..} - \bar{Y}_{...})^2 = \frac{1}{p}\sum_{i=1}^p Y_{i..}^2 - \frac{1}{p^2} Y_{...}^2$$

$$\left.\begin{aligned} = &(\bar{Y}_{1..} - \bar{Y}_{...})^2 + (\bar{Y}_{1..} - \bar{Y}_{...})^2 + (\bar{Y}_{1..} - \bar{Y}_{...})^2 \\ &+ (\bar{Y}_{2..} - \bar{Y}_{...})^2 + Y_{2..} \qquad Y_{2..} \\ &+ Y_{3..} \qquad + Y_{3..} \qquad Y_{3..} \end{aligned}\right\} = 3\sum_{i=1}^3 (\bar{Y}_{i..} - \bar{Y}_{...})^2$$

$$= 3\sum_i^3 (\bar{Y}_{i..}^2 + \bar{Y}_{...}^2 - 2\bar{Y}_{...}\bar{Y}_{i..}) = 3\left[\sum_i^3 \bar{Y}_{i..}^2 + 3\bar{Y}_{...}^2 - 2\bar{Y}_{...}\underbrace{\sum_{i=1}^3 \bar{Y}_{i..}}\right]$$

$$\frac{1}{3}\sum_i^3 Y_{i..} = \frac{1}{3} Y_{...}$$

like before! $3\bar{Y}_{...}$

$$= 3\left[\sum_i \bar{Y}_{i..}^2 + 3\bar{Y}_{...}^2 - 6\bar{Y}_{...}^2\right]$$

$$= 3\left[\sum_i \bar{Y}_{i..}^2 - 3\bar{Y}_{...}^2\right]$$

$$= 3\left[\sum_i \left(\frac{1}{3} Y_{i..}\right)^2 - 3\left(\frac{1}{9} Y_{...}\right)^2\right]$$

$$= \frac{1}{3}\sum_i Y_{i..}^2 - \frac{1}{9} Y_{...}^2$$

hw-lect 12-2

```
# For the data in problem 4.22, perform the appropriate ANOVA analysis; report SSA,
SSB, SSC, SST, SSE, the F ratios, and the corresponding p-values a) by hand, b) by R.
   rm(list=ls(all=TRUE))
   na = 5
   nb = 5
   nc = 5
   p =  na

   y.m = matrix(nrow=na,ncol=nb)      # rows = factor, col = replicates
   y.m[1,]=c(8,7,1,7,3)
   y.m[2,]=c(11,2,7,3,8)
   y.m[3,]=c(4,9,10,1,5)
   y.m[4,]=c(6,8,6,6,10)
   y.m[5,]=c(4,2,3,8,8)
   y = as.vector(t(y.m))
   A = as.factor(c(rep(1:na,each=nb)))            # row-var = Batch (block)
   B = as.factor(rep(c(1:nb),na))                 # col-var = Day (block)
   C = as.factor(c( 1,2,4,3,5,                    # ingredient
                    3,5,1,4,2,
                    2,1,3,5,4,
                    4,3,5,2,1,
                    5,4,2,1,3 ))

   cbind(A,B,C,y)     # you can confirm that the data in R is same as in problem.

   y... = sum(y)
   yi.. = c(sum(y[A==1]), sum(y[A==2]), sum(y[A==3]), sum(y[A==4]), sum(y[A==5]))
   y.j. = c(sum(y[B==1]), sum(y[B==2]), sum(y[B==3]), sum(y[B==4]), sum(y[B==5]))
   y..k = c(sum(y[C==1]), sum(y[C==2]), sum(y[C==3]), sum(y[C==4]), sum(y[C==5]))

   SSA = sum((yi..)^2)/p - (y...)^2/p^2
   SSB = sum((y.j.)^2)/p - (y...)^2/p^2
   SSC = sum((y..k)^2)/p - (y...)^2/p^2
   SST = sum(y^2) - (y...)^2/p^2
   SSE = SST - (SSA + SSB + SSC)
```

```
    MSA = SSA/(p-1)
    MSB = SSB/(p-1)
    MSC = SSC/(p-1)
    MSE = SSE/((p-2)*(p-1))

    FA = MSA/MSE
    FB = MSB/MSE
    FC = MSC/MSE

    pf(FA,p-1,(p-2)*(p-1),lower.tail=F)    # 0.3476182
    pf(FB,p-1,(p-2)*(p-1),lower.tail=F)    # 0.4550143
    pf(FC,p-1,(p-2)*(p-1),lower.tail=F)    # 0.0004876512

# By R

    lm.1 = lm(y ~ A + B + C)
    summary.aov(lm.1)

#              Df Sum Sq Mean Sq F value   Pr(>F)
# A             4  15.44    3.86   1.235 0.347618
# B             4  12.24    3.06   0.979 0.455014
# C             4 141.44   35.36  11.309 0.000488 ***
# Residuals    12  37.52    3.13

# All the values in the table are the same as those computed by hand, above.

# The conclusion of the study is that there is no evidence that A and B have an
effect,
# but C (the ingredient) does. Technically, we should look at residual plots to
# check all the assumptions.
```

hw-lect 12-3

There are only four, 4x4, different, standard LSs:

I

$$\begin{matrix} A & B & C & D \\ B & A & D & C \\ C & D & B & A \\ D & C & A & B \end{matrix}$$

II

$$\begin{matrix} A & B & C & D \\ B & A & D & C \\ C & D & A & B \\ D & C & B & A \end{matrix}$$

III

$$\begin{matrix} A & B & C & D \\ B & C & D & A \\ C & D & A & B \\ D & A & B & C \end{matrix}$$

IV

$$\begin{matrix} A & B & C & D \\ B & D & A & C \\ C & A & D & B \\ D & C & B & A \end{matrix}$$

The colors are intended to give you a sense of how I generated them. You don't have to do it for this hw.

Can you find another 4x4 LS (standard or not, different or not) that is orthogonal to the third one? Hint: set the first row of this matrix to $\alpha, \beta, \gamma, \delta$, and use these Latin letters in the remainder of the LS.

(3) By LS

(1) Can't be α (because LS), nor β ($B\beta$ already in GLSD)

So, either γ or δ

$$\begin{pmatrix} A & B & C & D \\ B & C & D & A \\ C & D & A & B \\ D & A & B & C \end{pmatrix} \begin{pmatrix} \alpha & \beta & \gamma & \delta \\ \gamma & \alpha & \bullet & \\ \delta & & & \\ \beta & & & \end{pmatrix} = \begin{pmatrix} A\alpha & B\beta & C\gamma & D\delta \\ B\gamma & C\alpha & D & A \\ C\delta & D & A & B \\ D\beta & A & B & C \end{pmatrix}$$

(2) Can be either β or δ; but $D\delta$ is already in the GLSD

(4) Can't be β (LS), nor γ ($C\gamma$ already in GLSD)
nor δ ($C\delta$ " " ")

(5) Can't be α or γ (LS)
Can't be β or δ ($D\beta$, $D\delta$ already in GLSD) $\Rightarrow$ STOP

$$\begin{pmatrix} \alpha & \beta & \gamma & \delta \\ \delta & \alpha & & \\ \beta & \bullet & & \\ \gamma & & & \end{pmatrix} = \begin{pmatrix} A\alpha & B\beta & C\gamma & D\delta \\ B\delta & C & D & A \\ C\beta & D & A & B \\ D\gamma & A & B & C \end{pmatrix}$$

(2) $C\gamma$ already in GLSD

(3) By LS

$D\gamma$ and $D\delta$ already in GLSD. $\Rightarrow$ STOP

$\therefore$ There is no LS orthog. to III.

(In fact, no 2 of these are orthogonal).

4.36

```
# 4.29 (7th ed.) = 4.36 (8th ed.)

 rm(list=ls(all=TRUE))

 p = 4

   y.m = matrix(nrow=p,ncol=p)
   y.m[1,]=c(11, 10, 14,  8)
   y.m[2,]=c(8,  12, 10, 12)
   y.m[3,]=c(9,  11, 7, 15)
   y.m[4,]=c(9, 8, 18, 6)

   y = as.vector(t(y.m))
   A = as.factor(c(rep(1:p,each=p)))        # row-factor (Order of Assembly).
   B = as.factor(c(3, 2, 4, 1,              # Greek factor (treatment)
                  2, 3, 1, 4,
                  1, 4, 2, 3,
                  4, 1, 3, 2))
   C = as.factor(rep(c(1:p),p))             # col-factor (Operator).

   D = as.factor(c(2, 3, 4, 1,
                  1, 4, 3, 2,
                  4, 1, 2, 3,
                  3, 2, 1, 4))             # Latin factor

   cbind(A,B,C,D,y)                         # Always, visually confirm data are correct.    summary.aov(lm(y~A+B+C+D))

#              Df Sum Sq Mean Sq F value Pr(>F)
# A             3    0.5    0.17   0.018  0.996
# B             3   95.5   31.83   3.473  0.167
# C             3   19.0    6.33   0.691  0.616
# D             3    7.5    2.50   0.273  0.843
# Residuals     3   27.5    9.17

# All the p-values are relatively large, and so there is no evidence from data
# that any of the 4 factors have an effect on the response. But, it's worth noting
# that all of the p-values are based on only 3 degrees of freedom. That's almost
# like having a sample of size 3 ! Would you trust the results of that data?!
```