

Ch-07_08 R Codes

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Textbook: Montgomery, D. C. (2012). *Design and analysis of experiments*, 8th Edition. John Wiley & Sons.
Online handouts: https://github.com/PingYangChen/ANOVA_Course_R_Code

7.21

By the defining contrast, to confound eight blocks with $ABCD$, ACE and $ABEF$, let

$$\begin{aligned}L_1 &= x_1 + x_2 + x_3 + x_4 \\L_2 &= x_1 + x_3 + x_5 \\L_3 &= x_1 + x_2 + x_5 + x_6\end{aligned}$$

```
designMat <- data.frame(
  A = rep(0:1, 32),
  B = rep(rep(0:1, each = 2), 16),
  C = rep(rep(0:1, each = 4), 8),
  D = rep(rep(0:1, each = 8), 4),
  E = rep(rep(0:1, each = 16), 2),
  F = rep(0:1, each = 32)
)
#print(head(designMat, 6))

letterMat <- sapply(1:ncol(designMat), function(j) {
  ifelse(designMat[,j] == 1, letters[j], ""))
})
#print(head(letterMat, 6))

effectNames <- sapply(1:nrow(letterMat), function(i) {
  ifelse(all(letterMat[i,] == ""), "(1)", paste0(letterMat[i,], collapse = "")))
})
rownames(designMat) <- effectNames
print(head(designMat, 6))

##      A B C D E F
## (1)  0 0 0 0 0 0
## a    1 0 0 0 0 0
## b    0 1 0 0 0 0
## ab   1 1 0 0 0 0
## c    0 0 1 0 0 0
## ac   1 0 1 0 0 0
```

Compute the linear combinations $L_1(i)$, $L_2(i)$ and $L_3(i)$, and take (mod 2) for each of them, $i = 1, 2, \dots, 64$.

```
attach(designMat)
assignBlock <- data.frame(
  L1 = (A + B + C + D) %% 2,
  L2 = (A + C + E) %% 2,
  L3 = (A + B + E + F) %% 2
)
detach(designMat)
```

Get the block IDs for each run.

```
blockId <- as.matrix(assignBlock) %*% c(2^2, 2, 1) + 1
```

Present the runs in each block.

```
result <- matrix("", 8, 8)
for (i in 1:8) {
  result[,i] <- effectNames[which(blockId == i)]
}
colnames(result) <- sprintf("Block %d", 1:8)
print(data.frame(result))
```

```
##   Block.1 Block.2 Block.3 Block.4 Block.5 Block.6 Block.7 Block.8
## 1    (1)      ac     ab     bc     abc      b      c      a
## 2    abcd     bd     cd     ad      d     acd     abd     bcd
## 3    bce     abe     ace      e     ae     ce     be     abce
## 4    ade     cde     bde  abcde    bcde    abde    acde     de
## 5    acf      f     bcf     abf      bf     abcf      af      cf
## 6    bdf  abcdf     adf     cdf    acdf      df     bcdf     abdf
## 7    abef    bcef      ef    acef     cef     aef    abcef     bef
## 8    cdef    adef  abcdef     bdef    abdef    bcdef      def    acdef
```

The other effects confounded with blocks:

$$\begin{aligned}(ABCD)(ACE) &= A^2BC^2DE = BDE \\ (ABCD)(ABEF) &= A^2B^2CDEF = CDEF \\ (ACE)(ABEF) &= A^2BCE^2F = BCF \\ (ABCD)(BCF) &= AB^2C^2DF = ADF\end{aligned}$$

8.11

2^{5-2} fractional factorial design with defining relation

$$I = ACE \text{ and } I = BDE$$

1. generate the 2^3 full factorial design

```

lvl <- c(-1, 1)
FF3 <- data.frame(
  A = rep(lvl, 4),
  B = rep(rep(lvl, each = 2), 2),
  C = rep(lvl, each = 4)
)
print(FF3)

```

```

##      A  B  C
## 1 -1 -1 -1
## 2  1 -1 -1
## 3 -1  1 -1
## 4  1  1 -1
## 5 -1 -1  1
## 6  1 -1  1
## 7 -1  1  1
## 8  1  1  1

```

2. add two columns D and E to form the 2^{5-2} by the defining relation

$$I = ACE \implies E = AC$$

$$I = BDE \implies D = BE \implies D = BAC$$

```

attach(FF3)
augmentFrF <- data.frame(
  D = A * B * C,
  E = A * C
)
detach(FF3)

FrF5_2 <- cbind(FF3, augmentFrF)
# Get letters of each effect
letterMat <- sapply(1:ncol(FrF5_2), function(j) {
  ifelse(FrF5_2[,j] == 1, letters[j], ""))
})
# Combine letters
effectNames <- sapply(1:nrow(letterMat), function(i) {
  ifelse(all(letterMat[i,] == ""), "(1)", paste0(letterMat[i,], collapse = "")))
})
rownames(FrF5_2) <- effectNames
print(FrF5_2)

```

```

##      A  B  C  D  E
## e    -1 -1 -1 -1  1
## ad   1 -1 -1  1 -1
## bde  -1  1 -1  1  1
## ab   1  1 -1 -1 -1
## cd   -1 -1  1  1 -1
## ace  1 -1  1 -1  1

```

```
## bc      -1  1  1 -1 -1
## abcde  1  1  1  1  1
```

Complete defining relation is

$$I = ACE = BDE = ABCD$$

All aliases are

$$\begin{aligned} A &= CE = BCD \quad AB = CD \\ B &= DE = ACD \quad AD = BC \\ C &= AE = ABD \quad AC = BD \\ D &= BE = ABC \\ E &= AC = BD \end{aligned}$$

Add column of the response variable.

```
y <- numeric(8)
y[effectNames == "e"]     <- 23.2
y[effectNames == "ad"]    <- 16.9
y[effectNames == "cd"]    <- 23.8
y[effectNames == "bde"]   <- 16.8
y[effectNames == "ab"]    <- 15.5
y[effectNames == "bc"]    <- 16.2
y[effectNames == "ace"]   <- 23.4
y[effectNames == "abcde"] <- 18.1
frfData <- cbind(FrF5_2, y = y)
```

The estimation of main effects are:

```
# Compute the model matrix of all effect terms without intercept
mmat5 <- model.matrix(~ A+B+C+D+E - 1, data = frfData)
# Calculate the effect sizes using the +/- signs of the model matrix
eff5 <- numeric(ncol(mmat5))
for (i in 1:ncol(mmat5)) {
  eff5[i] <- 2*mean(frfData$y*mmat5[,i])
}
names(eff5) <- colnames(mmat5)

## Factor Est.Effect
## 1      A     -1.525
## 2      B     -5.175
## 3      C      2.275
## 4      D     -0.675
## 5      E      2.275

# Half Normal Plot
halfqnorm <- function(input, tol = 0.5) {
  y <- sort(abs(input))
  nq <- qnorm(seq(0.5, 0.99, length = length(y)))
  plot(y, nq, yaxt = "n", pch = 15,
       xlab = "|Effects|", ylab = "Half Normal Probability")
```

```

title("Half Normal Plot")
# choose anchor point to draw a straight line
s <- min(which(diff(y)/diff(range(y)) > 1/(length(y)-1)))
abline(a = -y[1]*(nq[s]-nq[1])/(y[s]-y[1]), b = (nq[s]-nq[1])/(y[s]-y[1]))
axis(2, at = qnorm(seq(0.5, 0.9999, length = 5)),
     labels = round(seq(0, 1, length = 5),2))
loc <- sqrt((nq - (y - y[1])*(nq[s]-nq[1])/(y[s]-y[1]))^2) > tol
if (is.null(names(y))) {
  text(y[loc], nq[loc], order(abs(input))[loc], pos = 2)
} else {
  text(y[loc], nq[loc], names(abs(input))[order(abs(input))[loc]], pos = 2)
}
}

```

- (d) From part (b), we have AB and AD are aliased with other effects. Suppose CD and BC are negligible, we can try include AB and AD solely into the main effect model. First, the estimated effects are

```

# Compute the model matrix of all effect terms without intercept
mmat_add2fi <- model.matrix(~ A + B + C + D + E + A:B + A:D - 1, data = frfData)
# Calculate the effect sizes using the +/- signs of the model matrix
eff_add2fi <- numeric(ncol(mmat_add2fi))
for (i in 1:ncol(mmat_add2fi)) {
  eff_add2fi[i] <- 2*mean(frfData$y*mmat_add2fi[,i])
}
names(eff_add2fi) <- colnames(mmat_add2fi)

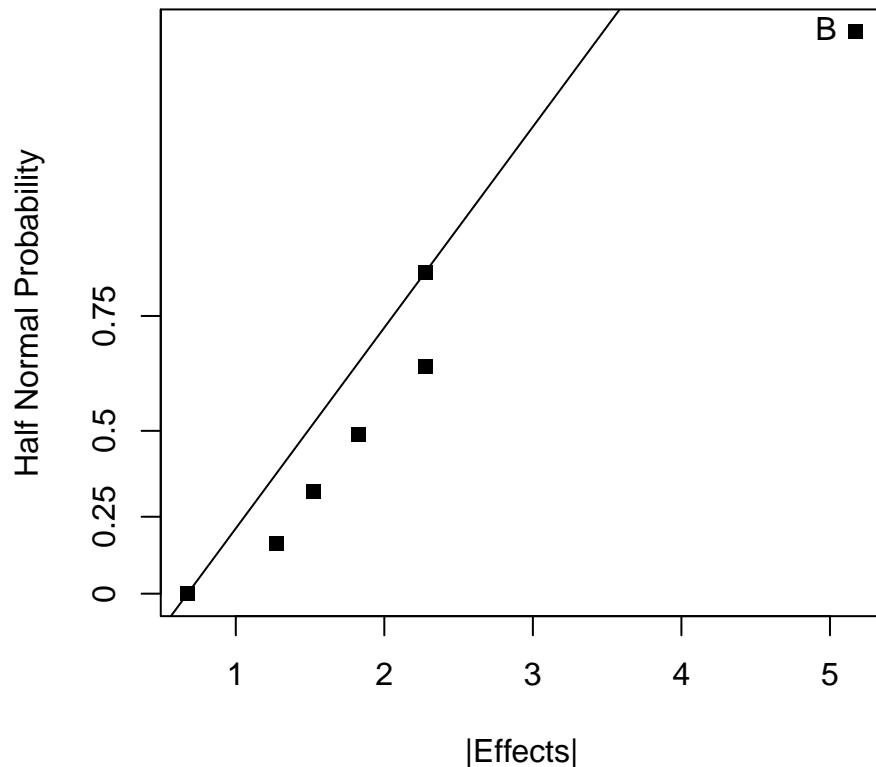
##   Factor Est.Effect
## 1      A    -1.525
## 2      B    -5.175
## 3      C     2.275
## 4      D    -0.675
## 5      E     2.275
## 6    A:B     1.825
## 7    A:D    -1.275

```

The half normal plot shows that only the effect of B is large indicating that AB and AD could be pooled as an estimate of error.

```
halfqqnorm(eff_add2fi)
```

Half Normal Plot



The final ANOVA result is

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## A           1   4.65   4.65   0.938 0.4349
## B           1  53.56  53.56  10.807 0.0814 .
## C           1  10.35  10.35   2.089 0.2853
## D           1   0.91   0.91   0.184 0.7098
## E           1  10.35  10.35   2.089 0.2853
## Residuals    2   9.91   4.96
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```