

TABLE 21.3 Design (Recipe) Matrix								
Test	1	2	3	4	5	6	7	Overrun (%)
1	—	—	—	+	+	+	—	115
2	+	—	—	—	—	+	+	81
3	—	+	—	—	+	—	+	110
4	+	+	—	+	—	—	—	69
5	—	—	+	+	—	—	+	174
6	+	—	+	—	+	—	—	99
7	—	+	+	—	—	+	—	80
8	+	+	+	+	+	+	+	63

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Full fold-over

TABLE 21.5 Design Matrix for the Mirror Image Design								
Test	1	2	3	4	5	6	7	Overrun (%)
9	+	+	+	—	—	—	+	84
10	—	+	+	+	+	—	—	69
11	+	—	+	+	—	+	—	56
12	—	—	+	—	+	+	+	161
13	+	+	—	—	+	+	—	56
14	—	+	—	+	—	+	+	40
15	+	—	—	+	+	—	+	92
16	—	—	—	—	—	—	—	208

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9:30 AM

Section 1

MANE 6313

Subsection 1

Week 11, Module D

Student Learning Outcome

- Select an appropriate experimental design with one or more factors,
- Select an appropriate model with one or more factors,
- Evaluate statistical analyses of experimental designs,
- Assess the model adequacy of any experimental design, and
- Interpret model results.

Module Learning Outcome

Describe sequential analysis and full fold-over design.

Sequential Experimentation

- This is particularly applicable for resolution III experiments
- Conduct another fraction based upon information gained in the initial model
- A fold-over design can be either a full fold-over or fold-over on an effect

Example Problem

- Taken from Devore, Chang~~x~~ and Sutherland
- 2^{7-4} resolution III design
- Generators are 4=12, 5=13, 6=23 and 7=123 (DCS uses numbers instead of letters)

123
A B C

D = AB

E = AC

F = BC

G = ABC

TABLE 21.1 Variables Under Study Together with Their Low and High Settings*

Variable	Ingredient	Level (weight %)	
		Low (−)	High (+)
1	Soybean emulsion: 9.3% soybean solids	1.67	5.00
2	Vegetable fat: hydrogenated coconut oil	10.00	20.00
3	Carbohydrates: corn syrup solids	0.00	5.00
4	Emulsifiers: mono- and di-glycerides	0.17	0.50
5	Primary stabilizer: hydroxypropyl methyl cellulose	0.00	0.50
6	Secondary stabilizer: microcrystalline cellulose	0.00	0.25
7	Salt: sodium chloride	0.00	0.10

*Amount of sucrose kept constant at 7%; water added to balance to 100%.

Example Problem - Design Matrix

TABLE 21.3 Design (Recipe) Matrix 

<i>Test</i>	<i>1</i>	<i>2</i>	<i>3</i>	<i>4</i>	<i>5</i>	<i>6</i>	<i>7</i>	<i>Overrun (%)</i>
1	—	—	—	+	+	+	—	115
2	+	—	—	—	—	+	+	81
3	—	+	—	—	+	—	+	110
4	+	+	—	+	—	—	—	69
5	—	—	+	+	—	—	+	174
6	+	—	+	—	+	—	—	99
7	—	+	+	—	—	+	—	80
8	+	+	+	+	+	+	+	63

Figure 2: Design Matrix for Example Problem

Design using R

```

81+ ```{r}
82 library(FrF2)
83 sequential.df <- FrF2(nFactors=7,nruns=8,gen=c("AB","AC","BC","ABC"),randomize=FALSE)
84 summary(sequential.df)
85+ ```

```

The R Studio interface displays the R Console with the executed code. The Environment pane shows two data frames: 'data.frame' (2 x 7) and 'data.frame' (8 x 7). The 'data.frame' (8 x 7) is expanded to show the following table:

	A <fctr>	B <fctr>	C <fctr>	D <fctr>	E <fctr>	F <fctr>	G <fctr>
1	-1	-1	-1	1	1	1	-1
2	1	-1	-1	-1	-1	1	1
3	-1	1	-1	-1	1	-1	1
4	1	1	-1	1	-1	-1	-1
5	-1	-1	1	1	-1	-1	1
6	1	-1	1	-1	1	-1	-1
7	-1	1	1	-1	-1	1	-1
8	1	1	1	1	1	1	1

8 rows

Figure 3: Base Design in R

R Design Details

```

81 {r}
82 library(FrF2)
83 sequential.df <- FrF2(nFactors=7,nruns=8,gen=c("AB","AC","BC","ABC"),randomize=FALSE)
84 summary(sequential.df)
85

```



Call:

```
FrF2(nFactors = 7, nruns = 8, gen = c("AB", "AC", "BC", "ABC"),
     randomize = FALSE)
```

Experimental design of type FrF2.generators
8 runs

Factor settings (scale ends):

Design generating information:

\$legend

[1] A=A B=B C=C D=D E=E F=F G=G

\$generators

[1] D=AB E=AC F=BC G=ABC ✓

Alias structure:

\$main

[1] A=BD=CE=FG B=AD=CF=EG C=AE=BF=DG D=AB=CG=EF E=AC=BG=DF F=AG=BC=DE G=AF=BE=CD

The design itself:

FrF2 Catalog Information

- Design is 7-4.1
- Design.info is shown below

```
$catlg.name
[1] "catlg"

$catlg.entry
Design: 7-4.1
      8 runs, 7 factors,
Resolution III
Generating columns: 3 5 6 7
WLP (3plus): 7 7 0 0 1, 0 clear 2fis

$aliased
$aliased$legend
[1] "A=A" "B=B" "C=C" "D=D" "E=E" "F=F" "G=G"

$aliased$main
[1] "A=BD=CE=FG" "B=AD=CF=EG" "C=AE=BF=DG" "D=AB=CG=EF" "E=AC=BG=DF" "F=AG=BC=DE" "G=AF=BE=CD"

$aliased$fi2
character(0)

$FrF2.version
[1] "2.2-3"

$replications
[1] 1

$repeat.only
[1] FALSE

$randomize
[1] TRUE
```

R: Response Variable

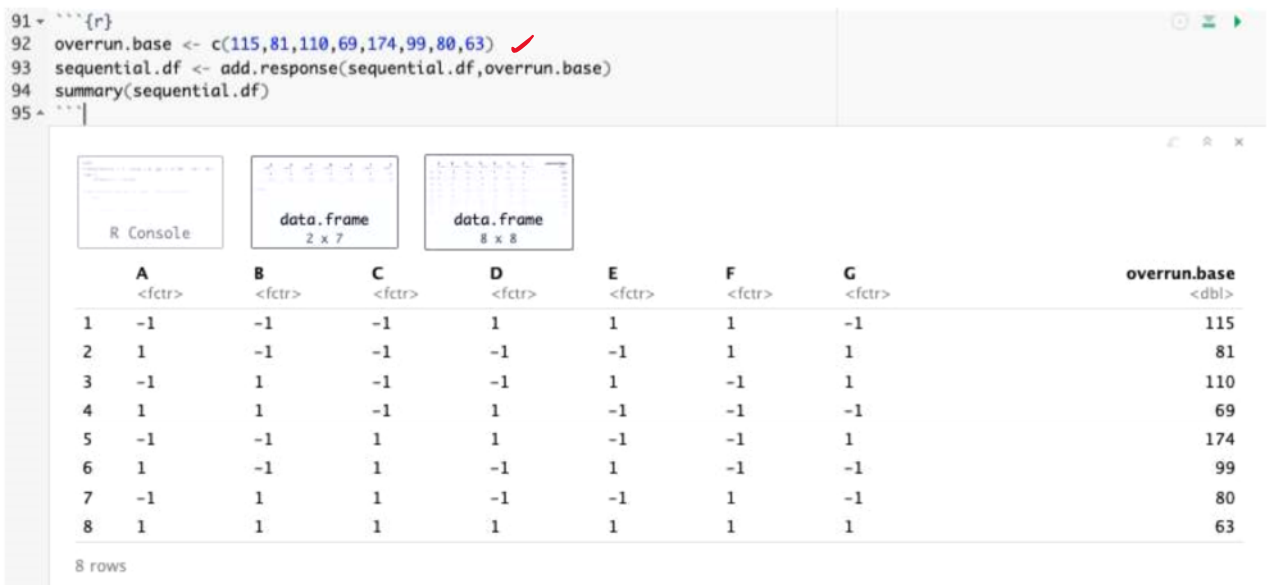
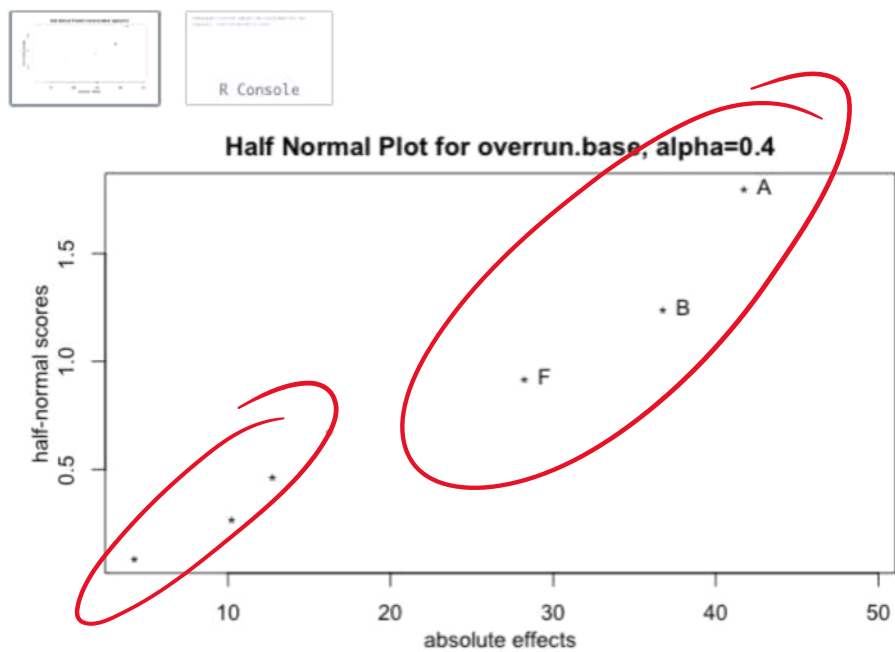


Figure 6: Response Variable for Example Problem

Half-normal Plot

```
97 > {r}  
98 library(FrF2)  
99 DanielPlot(sequential.df, response="overrun.base", half=TRUE, alpha=0.4)  
100 >
```



Interpreting Half-Normal Plot Results

- Factors A, B, and F alone are responsible for large effect estimates
- From aliasing scheme of A, BD and/or CE and/or FG could be responsible for large effect estimate for A (with or without A being large),
- From aliasing scheme of B, AD and/or DF and/or EG could be responsible for large effect estimate for B (with or without B being large),
- From aliasing scheme of F, AG and/or BC and/or DE could be responsible for large effect estimate for F (with or without F being large)
- **No clear pattern**

Full Fold-over

- Full fold-over occurs when you change all the signs in the design matrix; run another fraction
- A full fold-over will break the alias links between the main effects and two-factor interactions
 - Two-factor interactions may (still) be aliased with each other

TABLE 21.5 Design Matrix for the Mirror Image Design

Test	1	2	3	4	5	6	7	Overrun (%)
9	+	+	+	-	-	-	+	84
10	-	+	+	+	+	-	-	69
11	+	-	+	+	-	+	-	56
12	-	-	+	-	+	+	+	161
13	+	+	-	-	+	+	-	56
14	-	+	-	+	-	+	+	40
15	+	-	-	+	+	-	+	92
16	-	-	-	-	-	-	-	208

Figure 8: DCS Full Fold-Over

Full Fold-Over in R

```

102 > {r}
103 sequential.full <- fold.design(sequential.df,columns="full",randomize=FALSE)
104 summary(sequential.full)
105 ^

```

R Console

data.frame
2 x 8

data.frame
16 x 9

Multi-step-call:

[[1]]

```
FrF2(nFactors = 7, nruns = 8, gen = c("AB", "AC", "BC", "ABC"),
    randomize = FALSE)
```

\$fold

[1] full

Experimental design of type FrF2.generators.folded

16 runs

Factor settings (scale ends):

Responses:

[1] overrun.base

Design generating information:

\$legend

[1] A=A B=B C=C D=fold E=D F=E G=F H=G

Alias structure:

\$fi2

[1] AB=CH=-DE=FG AC=BH=-DF=EG AD=-BE=-CF=-GH AE=-BD=CG=FH AF=BG=-CD=EH AG=BF=CE=-DH

Full Fold-over Design



Figure 10: Full fold-Over in R

Full Fold-over Design, part 2

```

102 > ```{r}
103 sequential.full <- fold.design(sequential.df,columns="full",randomize=FALSE)
104 summary(sequential.full)
105 <

```



A <fctr>	B <fctr>	C <fctr>	fold <fctr>	D <fctr>	E <fctr>	F <fctr>	G <fctr>	overrun.base <dbl>
1	-1	1	mirror	1	-1	1	-1	NA
-1	-1	1	mirror	-1	1	1	1	NA
1	1	-1	mirror	-1	1	1	-1	NA
-1	1	-1	mirror	1	-1	1	1	NA
1	-1	-1	mirror	1	1	-1	1	NA
-1	-1	-1	mirror	-1	-1	-1	-1	NA

11-16 of 16 rows

Previous 1 **2** Next

Figure 11: Full Fold-Over Design, Part 2

Fold-over Design with Response

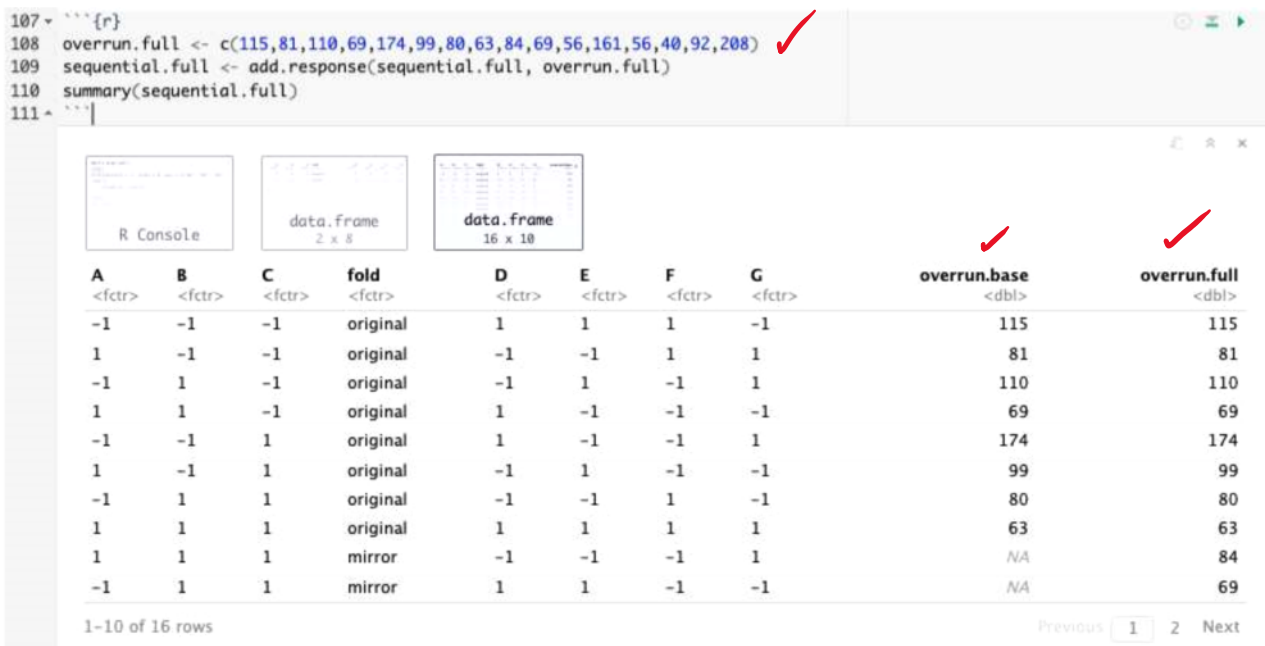


Figure 12: Response Variable for Full Fold-over

Half-Normal Plot for Fold-over

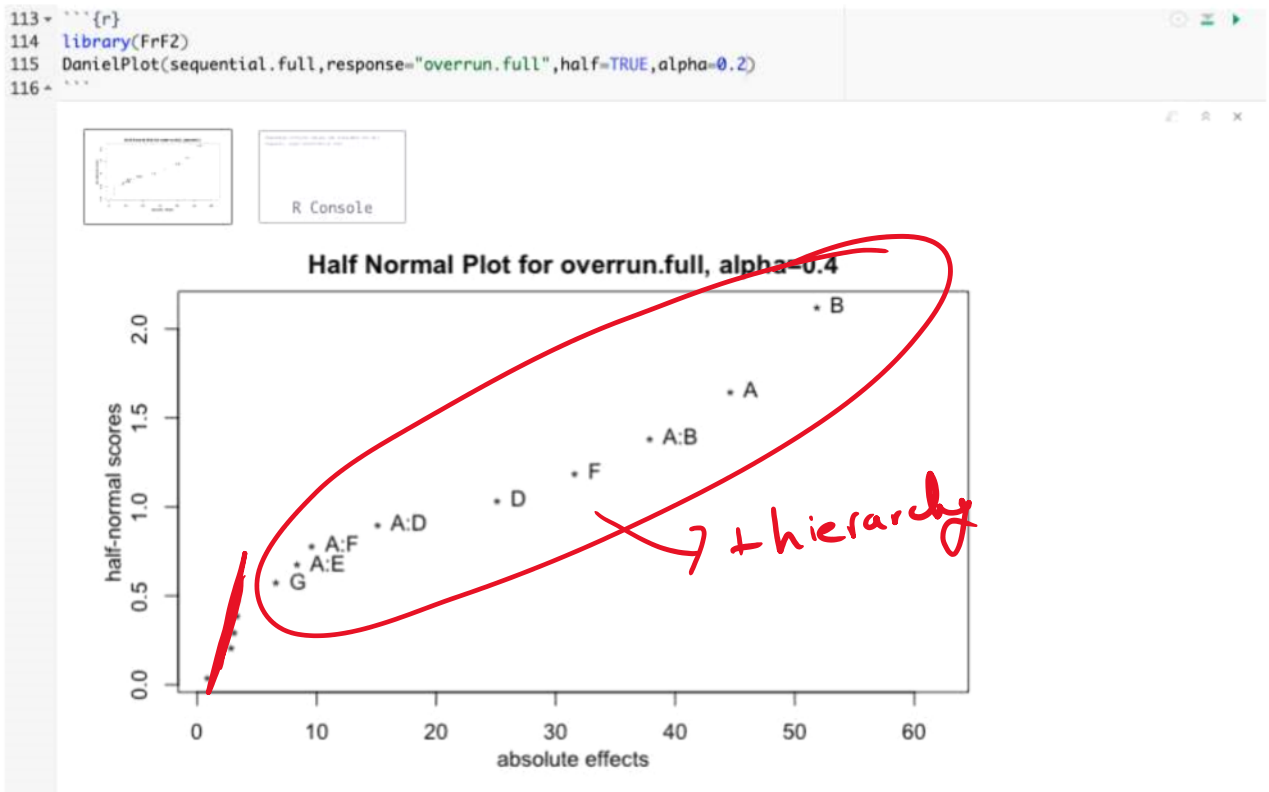


Figure 13: Half Normal Plot for Full fold-over Design

Interpretation of Half Normal Plot

- All main effects are not aliased with other main effects or two factor interactions (A, B, F, D, G)
- From aliasing scheme for AB, CH and/or -DE and/or FG (with or without AB being large)
- From aliasing scheme for AD, -BE and/or -DF and/or -Gh (with or without AD being large)
- From aliasing scheme for AE, -DB and/or CG and/or FH (with or without AE being large)

Initial Model

```

118 > {r}
119 full.model1 <- aov(overrun.full~A+B+A:B+D+F+A:D+A:F+A:E+E+G,data=sequential.full)
120 summary(full.model1)
121 >

```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
A	1	7966	7966	295.431	1.22e-05	***
B	1	10764	10764	399.223	5.80e-06	***
D	1	2525	2525	93.651	0.00020	***
F	1	4001	4001	148.375	6.59e-05	***
E	1	46	46	1.690	0.25032	
G	1	176	176	6.511	0.03116	.
A:B	1	5738	5738	212.816	2.73e-05	***
A:D	1	915	915	33.938	0.00211	**
A:F	1	371	371	13.744	0.01389	*
A:E	1	281	281	10.406	0.02332	*
Residuals	5	135	27			

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Aliasing in Initial Model

```
123 > ""{r}  
124 aliases(full,model1)  
125 > ""  
[1] no aliasing in the model
```