Lower Fractional Designs

BIOE 498/598 PJ

Spring 2021

Review

- A full factorial design with k factors requires 2^k runs.
- A half factorial design uses only 2^{k-1} runs.
  - Begin with a base design.
  - Set the remaining factor equal to an interaction (generator, $E = AB$)
  - Compute the defining relation ($I = \ldots$) and confounding/alias structure.

Review

- A full factorial design with k factors requires 2^k runs.
- A half factorial design uses only 2^{k-1} runs.
  - Begin with a base design.
  - Set the remaining factor equal to an interaction (generator, $E = AB$)
  - Compute the defining relation ($I = \ldots$) and confounding/alias structure.
- Today we define quarter- or eighth-factorial designs!

Quarter factorial (2^{k-2}) designs

Let's create a 2^{5-2} design (8 runs, factors $ABCDE$).

Quarter factorial (2^{k-2}) designs

Let's create a 2^{5-2} design (8 runs, factors $ABCDE$).

Start with a base 2^3 design (factors ABC).

Quarter factorial (2^{k-2}) designs

Let's create a 2^{5-2} design (8 runs, factors $ABCDE$).

Start with a base 2^3 design (factors ABC).

Define $D = AB$ and $E = AC$.

$$D^2 = I = ABD, \quad E^2 = I = ACE$$

Quarter factorial (2^{k-2}) designs

Let's create a 2^{5-2} design (8 runs, factors $ABCDE$).

Start with a base 2^3 design (factors ABC).

Define $D = AB$ and $E = AC$.

$$D^2 = I = ABD, \quad E^2 = I = ACE$$

Also, $I^2 = I = (ABD)(ACE) = BCDE$.

Quarter factorial (2^{k-2}) designs

Let's create a 2^{5-2} design (8 runs, factors $ABCDE$).

Start with a base 2^3 design (factors ABC).

Define $D = AB$ and $E = AC$.

$$D^2 = I = ABD, \quad E^2 = I = ACE$$

Also, $I^2 = I = (ABD)(ACE) = BCDE$.

Defining relation: $I = ABD = ACE = BCDE$

Confounding in our 2^{5-2} design

Defining relation: $I = ABD = ACE = BCDE$

$$A(I) = A(ABD) = A(ACE) = A(BCDE)$$

Confounding in our 2^{5-2} design

Defining relation: $I = ABD = ACE = BCDE$

$$A(I) = A(ABD) = A(ACE) = A(BCDE)$$

$$A + BD + CE + ABCDE$$

Confounding in our 2^{5-2} design

Defining relation: $I = ABD = ACE = BCDE$

$$A(I) = A(ABD) = A(ACE) = A(BCDE)$$

$$A + BD + CE + ABCDE$$

$$B + AD + ABCE + CDE$$

$$C + ABCD + AE + BDE$$

$$D + AB + ACDE + BCE$$

$$E + ABDE + AC + BCD$$

Confounding in our 2^{5-2} design

Defining relation: $I = ABD = ACE = BCDE$

$$A(I) = A(ABD) = A(ACE) = A(BCDE)$$

$$A + BD + CE + ABCDE$$

$$B + AD + ABCE + CDE$$

$$C + ABCD + AE + BDE$$

$$D + AB + ACDE + BCE$$

$$E + ABDE + AC + BCD$$

$$BC + ACD + ABE + DE$$

$$BE + ADE + ABC + CD$$

Eighth fractional design: 2^{6-3}

Factors A, B, C, $D = AB$, $E = AC$, $F = BC$

Eighth fractional design: 2^{6-3}

Factors A, B, C, $D = AB$, $E = AC$, $F = BC$

$$I = ABD = ACE = BCF$$

Eighth fractional design: 2^{6-3}

Factors A, B, C, $D = AB$, $E = AC$, $F = BC$

$$I = ABD = ACE = BCF$$

Also, all combinations:

$$\begin{aligned}
I^2 = I &= (ABD)(ACE) = BCDE \\
I^2 = I &= (ABD)(BCF) = ACDF \\
I^2 = I &= (ACE)(BCF) = ABEF \\
I^3 = I &= (ABD)(ACE)(BCF) = DEF
\end{aligned}$$

Defining relation:

$$I = ABD = ACE = BCF = BCDE = ACDF = ABEF = DEF$$

Which generator should I choose?

A generator's optimality is assessed with three criteria:

- **Resolution:** difference in the level of confounding.
- **Aberration:** the multiplicity of the worst confounding.
- **Clarity:** # of confounded main effects or two-way interactions.

Criterion #1: Design Resolution

The resolution of a fractional design is the length of the shortest word in the defining relation.

For the 2^{5-2} design generated by D=AB and E=AC, the definig relation is

$$I = ABD = ACE = BCDE$$

This is a Resolution III design. (Resolution is written with Roman numerals.)

Resolution measures the degree of confounding

A resolution R design has no i-level interaction aliased with effects lower than $R - i$.

Resolution measures the degree of confounding

A resolution R design has no i-level interaction aliased with effects lower than $R - i$.

Resolution III

- Main effects ($i = 1$) are confounded with secondary ($3 - 1 = 2$) interactions.

Resolution measures the degree of confounding

A resolution R design has no i-level interaction aliased with effects lower than $R - i$.

Resolution III

- Main effects ($i = 1$) are confounded with secondary ($3 - 1 = 2$) interactions.

Resolution IV

- Main effects ($i = 1$) are confounded with tertiary ($4 - 1 = 3$) interactions.
- TWIs ($i = 2$) are confounded with other TWIs ($4 - 2 = 2$).

Resolution and nested factorial designs

A design with resolution R contains a full factorial design for any subset of $k = R - 1$ factors.

Resolution and nested factorial designs

A design with resolution R contains a full factorial design for any subset of $k = R - 1$ factors.

If after the fractional experiments you drop to k factors you can re-analyze the data for all the interactions.

Criterion #2: Design Aberration

- **Resolution:** Length of the shortest word in the defining relation.
- **Aberration:** Number of words with length equal to the resolution.

Criterion #2: Design Aberration

- **Resolution:** Length of the shortest word in the defining relation.
- **Aberration:** Number of words with length equal to the resolution.

$I = ABCDF = ABCEG = DEFG$ resolution IV, aberration 1

$I = ABCF = ADEG = BCDEFG$ resolution IV, aberration 2

Criterion #2: Design Aberration

- **Resolution:** Length of the shortest word in the defining relation.
- **Aberration:** Number of words with length equal to the resolution.

$$I = ABCDF = ABCEG = DEFG \quad \text{resolution IV, aberration 1}$$

$$I = ABCF = ADEG = BCDEFG \quad \text{resolution IV, aberration 2}$$

We favor the design with the lower aberration. It will have fewer main effects confounded with low-order interactions.

Criterion #3: Clear Effects

A main effect or two-way interaction effect is **clear** if it is only confounded with higher order terms (three-way or higher).

Criterion #3: Clear Effects

A main effect or two-way interaction effect is **clear** if it is only confounded with higher order terms (three-way or higher).

Clear effects always lead to tradeoffs. For a 2^{6-2} design:

$I = ABCE = ABDF = CDEF$	6 main effects clear
$I = ABE = ACDF = BCDEF$	3 main effects + 6 TWIs clear

Overall design guidelines

1. Choose the highest **resolution** that fits your budget.
2. For that resolution, choose the **minimum aberration** design.
3. If you have particular effects that you know are signficant, try to choose a factor or generator that clears them.

Example: Biomass optimization of *P. variotii*

Table 6.5 *Factors and Levels for Biomass Experiment*

Label	Factors	Levels −	Levels +
A	Inhibitors (Furfural and Acetic Acid)	1.25g/L	7.8g/L
B	Rice Bran	10.0g/L	30.0g/L
C	Urea	0.0g/L	2.0g/L
D	Magnesium Sulfate	0.0g/L	1.5g/L
E	Ammonium Sulfate	0.0g/L	2.0g/L
F	Potassium Nitrate	0.0g/L	2.0g/L
G	Sodium Phosphate	0.0g/L	2.0g/L
H	Fermentation Time	72 hrs	96 hrs

Design: 2^{8-4}, 16 runs, no replicates

- Generators: $E = BCD$, $F = ACD$, $G = ABC$, $H = ABD$
- Resolution IV, minimum aberration
- All main effects clear
- TWI confounding:

$$CG + DH + AB + EF$$

$$AC + BG + DF + EH$$

$$CF + AD + EG + BH$$

$$CH + DG + AE + BF$$

$$CD + GH + AF + BE$$

$$BC + AG + DE + FH$$

$$CE + FG + AH + BD$$

Setting up the design with the FrF2 package

```
culture <- FrF2::FrF2(16,
                      generators=c("BCD","ACD","ABC","ABD"),
                      randomize=FALSE)
y <- c(5.75, 6.7, 11.12, 10.67, 4.92, 5.35, 2.81, 10.83,
       6.08, 7.27, 9.68, 4.2, 3.9, 3.78, 11.57, 7.39)
culture <- DoE.base::add.response(culture, y)
```

```
##     A  B  C  D  E  F  G  H     y
## 1  -1 -1 -1 -1 -1 -1 -1 -1  5.75
## 2   1 -1 -1 -1 -1  1  1  1  6.70
## 3  -1  1 -1 -1  1 -1  1  1 11.12
## 4   1  1 -1 -1  1  1 -1 -1 10.67
## 5  -1 -1  1 -1  1  1  1 -1  4.92
## 6   1 -1  1 -1  1 -1 -1  1  5.35
## 7  -1  1  1 -1 -1  1 -1  1  2.81
## 8   1  1  1 -1 -1 -1  1 -1 10.83
## 9  -1 -1 -1  1  1  1 -1  1  6.08
## 10  1 -1 -1  1  1 -1  1 -1  7.27
## 11 -1  1 -1  1 -1  1  1 -1  9.68
## 12  1  1 -1  1 -1 -1 -1  1  4.20
## 13 -1 -1  1  1 -1 -1  1  1  3.90
## 14  1 -1  1  1 -1  1 -1 -1  3.78
## 15 -1  1  1  1  1 -1 -1 -1 11.57
## 16  1  1  1  1  1  1  1  1  7.39
## class=design, type= FrF2.generators
```

```
##
## Call:
## lm.default(formula = y ~ (.)^2, data = culture)
##
## Residuals:
## ALL 16 residuals are 0: no residual degrees of freedom!
##
## Coefficients: (21 not defined because of singularities)
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  7.00125         NA      NA       NA
## A1           0.02250         NA      NA       NA
## B1           1.53250         NA      NA       NA
## C1          -0.68250         NA      NA       NA
## D1          -0.26750         NA      NA       NA
## E1           1.04500         NA      NA       NA
## F1          -0.49750         NA      NA       NA
## G1           0.72500         NA      NA       NA
## H1          -1.05750         NA      NA       NA
## A1:B1       -0.28375         NA      NA       NA
## A1:C1        0.49625         NA      NA       NA
## A1:D1       -1.09625         NA      NA       NA
## A1:E1       -0.39875         NA      NA       NA
## A1:F1        0.60875         NA      NA       NA
```

Aren't we short on degrees of freedom?

We only have 16 runs, so R estimates 1 intercept, 8 main effects, and 7 TWIs (AB through AH).

Not only do we have no DoF left for confidence intervals, we only estimated 7/28 TWIs!

Aren't we short on degrees of freedom?

We only have 16 runs, so R estimates 1 intercept, 8 main effects, and 7 TWIs (AB through AH).

Not only do we have no DoF left for confidence intervals, we only estimated 7/28 TWIs!

Or did we...

$$CG + DH + AB + EF$$

$$AC + BG + DF + EH$$

$$CF + AD + EG + BH$$

$$CH + DG + AE + BF$$

$$CD + GH + AF + BE$$

$$BC + AG + DE + FH$$

$$CE + FG + AH + BD$$

But we don't have DoF to estimate confidence intervals

True, but there's still something we can do.

- All factor levels are coded to units -1 and $+1$. Thus the effect sizes are directly comparable.
- We can assume the *practical significance* of an effect is proportional to its magnitude.

But we don't have DoF to estimate confidence intervals

True, but there's still something we can do.

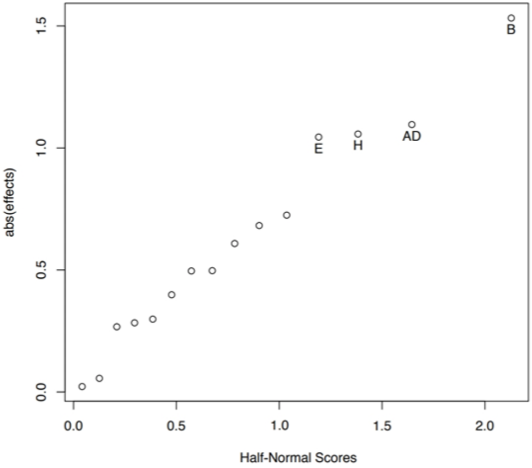
- All factor levels are coded to units -1 and $+1$. Thus the effect sizes are directly comparable.
- We can assume the *practical significance* of an effect is proportional to its magnitude.

We can also estimate statistical signficance.

- Assume that all the effect sizes in the model are normally distributed with mean zero.
- The z-score of the effect sizes can be compared with a standard normal to find a p-value.

Half-normal plot

Figure 6.5 *Half-Normal Plot of Effects from* 2^{8-4} Paecilomyces variotii *Culture Experiment*



$$CG + DH + AB + EF$$
$$AC + BG + DF + EH$$
$$CF + AD + EG + BH$$
$$CH + DG + AE + BF$$
$$CD + GH + AF + BE$$
$$BC + AG + DE + FH$$
$$CE + FG + AH + BD$$

Using half-normal plots

- Assumes the variables are coded so the effects sizes can be compared directly.
- Provides a ranked list of factors based on *practical significance*.
- Assuming normality of effect sizes allows estimation of *statistical significance* using z-scores.
- Great for screening designs; practically insignificant factors are dropped for a follow-up design with replicates or higher resolution.

Take-home problem

At the beginning of the lecture we described a 2^{5-2} design with generators $D = AB$ and $E = AC$. The defining relation was $I = ABD = ACE = BCDE$.

Problem: Construct a 2^{5-2} design using the generators $D = ABC$ and $E = AB$.

- Compute the defining relation for your design.
- What is the resolution and aberration? How does this compare to the design from the lecture?
- Compute the confounding relations for all five main effects.