Lower Fractional Designs

BIOE 498/598 PJ

Spring 2022

Review

- ▶ A full factorial design with k factors requires 2^k runs.
- \triangleright 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)
 - ightharpoonup Compute the defining relation (I = ...) and confounding/alias structure.

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- Half-fractional factorials in action
- ► Today we define quarter- or eighth-factorial designs!

A large (2⁵) unreplicated study

```
tumor <- read.csv("TumorInhibition.csv")
head(tumor)</pre>
```

```
A B C D E inhibition run half pb
## 1 -1 -1 -1 -1
                       61
                           1
## 2 1 -1 -1 -1
                       53
                           2 1 0
                           3 1 1
## 3 -1 1 -1 -1 -1
                       63
## 4 1 1 -1 -1 -1
                       61
## 5 -1 -1 1 -1 -1
                     53
                           5 1 0
## 6 1 -1 1 -1 -1
                       56
                           6
```

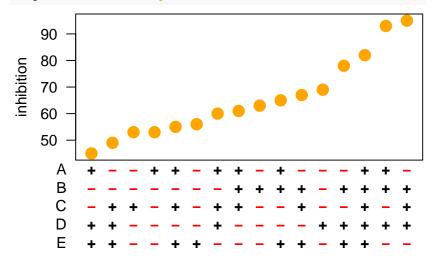
Let's pretend it was a 2^{5-1} half-fractional

```
half_tumor <- tumor[tumor$half==1, ]
half_tumor</pre>
```

```
##
      A B C D E inhibition run half pb
    1 -1 -1 -1 -1
                           53
                               2
                                       0
## 3 -1 1 -1 -1 -1
                           63
                               5
                                    1 0
## 5
    -1 -1 1 -1 -1
                           53
## 8
    1 1 1 -1 -1
                           61
                               8
                                       0
                                    1
## 9 -1 -1 -1 1 -1
                           69
## 12
     1 1 -1 1 -1
                           93
                              12
## 14
     1 -1 1 1 -1
                           60
                              14
## 15 -1 1
                           95
                              15
## 17 -1 -1 -1 1
                           56
                              17
                                       0
     1 1 -1 -1 1
                           65
                              20
                                       0
## 22 1 -1 1 -1 1
                           55
                              22
                                       0
## 23 -1 1
           1 -1 1
                           67
                              23
## 26 1 -1 -1 1
                           45
                              26
                                       0
## 27 -1 1 -1 1 1
                           78
                              27
                                       0
## 29 -1 -1 1 1 1
                           49
                              29
## 32 1 1 1
                           82
                              32
                                    1
                                       0
```

Step 2: Look at the data





Step 3: Fit a linear model

```
half_model <- lm(inhibition ~ A*B*C*D*E, data=half_tumor)</pre>
```

```
show_effects(half_model, scaling=2, show_effects(model, scaling=2, in8)r
                                            В
##
              20.5
                                 ##
                                                19.5
##
          D
              12.25
                                 ##
                                          B:D
                                                13.25
        B:D
              10.75
##
                                 ##
                                          D:E -11.
##
        D:E
            -9.5
                                 ##
                                            D 10.75
##
          Ε
              -6.25
                                 ##
                                            E
                                                -6.25
##
        C:E
               2.25
                                 ##
                                        A:C:E -2.5
##
          Α
              -2.
                                 ##
                                          C:D 2.125
##
        A:B
            1.5
                                          B:E
                                                 2.
                                 ##
##
        B:C
            1.5
                                 ##
                                        A:B:E
                                                -1.875
            1.25
                                        A:B:C 1.5
##
        A:E
                                 ##
##
        B:E
            1.25
                                 ##
                                      A:B:C:E
                                                 1.5
        A:D
                                        A:B:D
                                                 1.375
##
            -.75
                                 ##
##
        A:C
                .5
                                 ##
                                          A:B
                                                 1.375
        C:D
                .25
##
                                 ##
                                            Α
                                                -1.375
          C
                                        B:C:D
                                                 1.125
##
                                 ##
##
      A:B:C
              NA.
                                 ##
                                      A:C:D:E
                                                 1.
##
      A:B:D
              NA.
                                 ##
                                          A:D
                                                 -.875
##
      A:C:D
              NA.
                                 ##
                                          B:C
                                                  .875
```


0.5

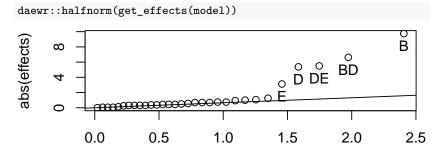
0.0

Half Normal scores

1.5

1.0

2.0



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$$A + BD + CE + ABCDE$$

$$B + AD + ABCE + CDE$$

$$C + ABCD + AE + BDE$$

$$D + AB + ACDE + BCE$$

$$E + ABDE + AC + BCD$$

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

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$$D = AB$$
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$$I = ABD = ACE = BCF$$

Eighth fractional design: 2^{6-3}

Factors A, B, C,
$$D = AB$$
, $E = AC$, $F = BC$
 $I = ABD = ACE = BCF$

Also, all combinations:

$$I^2 = I = (ABD)(ACE) = BCDE$$

 $I^2 = I = (ABD)(BCF) = ACDF$
 $I^2 = I = (ACE)(BCF) = ABEF$
 $I^3 = I = (ABD)(ACE)(BCF) = DEF$

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.)



A resolution R design has no $\emph{i}\text{-level}$ interaction aliased with effects lower than $R-\emph{i}.$

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.

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Resolution III

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

Resolution IV

- lacktriangle 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.

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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.

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$$I = ABCDF = ABCEG = DEFG$$
 resolution IV, aberration 1
 $I = ABCF = ADEG = BCDEFG$ resolution IV, aberration 2

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$$I = ABCDF = ABCEG = DEFG$$
 resolution IV, aberration 1
 $I = ABCF = ADEG = BCDEFG$ 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).

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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.