Linear Models: Interactions

BIOE 498/598 PJ

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What is an interaction?

Imagine we're modeling the response (y) from two input variables, x_1 and x_2 . The simplest model is

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What is there is another effect that depends on both x_1 and x_2 ? This is an **interaction** between x_1 and x_2 .

How do we model interactions?

We model the interaction of x_1 and x_2 using the product of these variables.

$$y = \beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_1 x_2 + \epsilon$$

The coefficient β_{12} is the effect size of the interaction.

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Why do we multiply x_1 and x_2 ? There are at least two ways to interpret this term.

The coded factor interpretation

Often we set up design matrices using **coded variables**. If we're testing the variable at two levels, we code the variable as "on/off" $(\{0,1\})$ or "low/high" $(\{-1,+1\})$.

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on/off \rightarrow interaction when both "on"

x_1	<i>x</i> ₂	x_1x_2
0	0	0
0	1	0
1	0	0
1	1	1

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x_1	<i>x</i> ₂	x_1x_2
0	0	0
0	1	0
1	0	0
1	1	1

high/low \rightarrow interaction when both "high" or both "low"

<i>x</i> ₁	<i>x</i> ₂	$x_1 x_2$
-1	-1	+1
-1	+1	-1
+1	-1	-1
+1	+1	+1

The augmented slope interpretation

We can also interpret the interaction as one variable changing the effect of the other variable.

$$y = \beta_1 x_1 + \beta_2(x_1)x_2 + \epsilon$$

= $\beta_1 x_1 + (\beta_2 + \beta_{12}x_1)x_2 + \epsilon$
= $\beta_1 x_1 + \beta_2 x_2 + \beta_{12}x_1x_2 + \epsilon$

Interactions with 1m

Recall the data frame from out blood pressure clinical trial:

```
## # A tibble: 6 x 3
## BPchange treated male
## <dbl> <lgl> <lgl> <lgl> <lgl>
## 1 -0.525 TRUE FALSE
## 2 4.17 TRUE FALSE
## 3 6.03 TRUE TRUE
## 4 -1.40 TRUE FALSE
## 5 0.493 TRUE FALSE
## 6 12.9 FALSE TRUE
```

Adding an interaction term to our model

```
##
## Call:
## lm(formula = BPchange ~ treated + male + treated:male, data =
##
## Residuals:
##
      Min
            1Q Median 3Q
                                  Max
## -20.465 -4.407 2.309 5.887 18.738
##
## Coefficients:
                     Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
                     12.319 7.895 1.560 0.145
## treatedTRUE
                     -10.090 9.116 -1.107 0.290
## maleTRUE
                 14.898 9.116 1.634 0.128
## treatedTRUE:maleTRUE 1.049 12.893 0.081 0.936
##
## Residual standard error: 11.17 on 12 degrees of freedom
## Multiple R-squared: 0.5606, Adjusted R-squared: 0.4507
## F-statistic: 5.102 on 3 and 12 DF, p-value: 0.01666
```

A shortcut for adding interactions and main effects

```
##
## Call:
## lm(formula = BPchange ~ treated * male, data = bp data)
##
## Residuals:
      Min
            10 Median
                             3Q
##
                                   Max
## -20.465 -4.407 2.309 5.887 18.738
##
## Coefficients:
                      Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
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A shortcut for adding interactions and main effects

```
## Call:
## lm(formula = y ~ x1 * x2 * x3)
##
  Residuals:
##
## -0.053712  0.130828  0.062348 -0.331228  0.004367
                                                0.059872
##
                           10
   0.184778 -0.123954 0.023741
##
##
## Coefficients:
             Estimate Std. Error t value Pr(>|t|)
##
## (Intercept)
             -11.02 9.52 -1.158
                                         0.367
## x1
                12.04 10.54 1.142 0.372
                17.03
                          17.79 0.957 0.440
## x2
## x3
                20.78
                          21.16 0.982
                                         0.430
## x1:x2
              -17.16
                     20.71 -0.828
                                         0.495
## x1:x3
              -20.57 23.86
                               -0.862
                                         0.479
## x2:x3
              -31.54 36.32
                                -0.868
                                         0.477
## x1:x2:x3
                30.02
                          42.31
                               0.710
                                         0.551
##
```

How many interactions are there?

term	x_1	x_2	<i>X</i> 3
β_0	0	0	0
$\beta_1 x_1$	1	0	0
$\beta_2 x_2$	0	1	0
$\beta_3 x_3$	0	0	1
$\beta_{12}x_1$	1	1	0
$\beta_{13}x_2$	1	0	1
$\beta_{23} x_2 x_3$	0	1	1
$\beta_{123}x_1x_2x_3$	1	1	1

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$\beta_{123}x_1x_2x_3$	1	1	1

A model with n factors has 2^n possible terms; 2^n-n-1 of these are interactions.

Hierarchical ordering to the rescue

Hierarchical Ordering principle

- Lower order effects are more likely to be important than higher order effects.
- ▶ Effects of the same order are equally likely to be important.

How many interactions are there?

n	intercept	main effects	TWI	higher-order
1	1	1	0	0
2	1	2	1	0
3	1	3	3	1
4	1	4	6	5
5	1	5	10	16
6	1	6	15	42
7	1	7	21	99
8	1	8	28	219
9	1	9	36	466
10	1	10	45	968

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2	1	2	1	0
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6	1	6	15	42
7	1	7	21	99
8	1	8	28	219
9	1	9	36	466
10	1	10	45	968

We will design experiments that focus on main effects and two-way interactions.

Hierarchical ordering to the rescue

Hierarchical Ordering Principle

- Lower-order effects are more likely to be important than higher-order effects.
- Effects of the same order are equally likely to be important.

If we neglect an important higher-order term, the effects can appear anywhere in our model!

We can design the experiment to constrain where higher-order effects appear.

Things to remember about interactions

- ▶ Interaction are modeled as the product of variables.
- ► The interaction effect is "above and beyond" the independent effects (synergy/super-additivity, antagonism/sub-additivity).
- ▶ Higher-order interactions are possible (e.g. $x_1x_2x_3$), but these are rare.
- Proper experiment design is needed when "ignoring" higher-order interactions.