

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 if 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	x_2	$x_1 x_2$
0	0	0
0	1	0
1	0	0
1	1	1

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x_1	x_2	$x_1 x_2$
0	0	0
0	1	0
1	0	0
1	1	1

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

x_1	x_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.

$$\begin{aligned}y &= \beta_1 x_1 + \beta_2(x_1)x_2 + \epsilon \\&= \beta_1 x_1 + (\beta_2 + \beta_{12}x_1)x_2 + \epsilon \\&= \beta_1 x_1 + \beta_2 x_2 + \beta_{12}x_1 x_2 + \epsilon\end{aligned}$$

Interactions with lm

Recall the data frame from our blood pressure clinical trial:

```
## # A tibble: 6 x 3
##   BPchange treated male
##   <dbl> <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       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      
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```

A shortcut for adding interactions and main effects

```
##
```

```
## Call:
```

```
## lm(formula = y ~ x1 * x2 * x3)
```

```
##
```

```
## Residuals:
```

```
##
```

	1	2	3	4	5	6
##	0.053936	0.121901	-0.188750	-0.081015	0.261358	0.292505

```
##
```

	8	9	10
##	-0.326646	-0.078732	-0.052560

```
##
```

```
## Coefficients:
```

```
##
```

	Estimate	Std. Error	t value	Pr(> t)
--	----------	------------	---------	----------

## (Intercept)	-4.729	30.580	-0.155	0.891
----------------	--------	--------	--------	-------

## x1	17.778	95.430	0.186	0.869
-------	--------	--------	-------	-------

## x2	9.121	46.268	0.197	0.862
-------	-------	--------	-------	-------

## x3	6.258	34.767	0.180	0.874
-------	-------	--------	-------	-------

## x1:x2	-28.809	143.813	-0.200	0.860
----------	---------	---------	--------	-------

## x1:x3	-21.140	110.656	-0.191	0.866
----------	---------	---------	--------	-------

## x2:x3	-11.096	53.031	-0.209	0.854
----------	---------	--------	--------	-------

## x1:x2:x3	32.847	163.304	0.201	0.859
-------------	--------	---------	-------	-------

```
##
```

How many interactions are there?

term	x_1	x_2	x_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
$\beta_{12} x_1 x_2$	1	1	0
$\beta_{13} x_1 x_3$	1	0	1
$\beta_{23} x_2 x_3$	0	1	1
$\beta_{123} x_1 x_2 x_3$	1	1	1

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$\beta_{123} x_1 x_2 x_3$	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.