

Factorial Designs: Simple effects and pairwise tests

Data Analysis for Psychology in R 2

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Week's Learning Objectives

- Understand how to interpret simple effects for experimental designs
- Understand how to interpret exploratory pairwise analyses for factorial designs
- Know how to do both analyses using `emmeans()`

Just a little bit more of the hospital example

```
hosp_tbl <- read_csv("hospital.csv", col_types = "dff")  
m1 <- lm(SWB ~ Treatment + Hospital + Treatment*Hospital, data = hosp_tbl)  
anova(m1)
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: SWB
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)        
## Treatment      2  177.02   88.511  21.5597 4.315e-09 ***  
## Hospital       1    9.57    9.568   2.3306  0.1287        
## Treatment:Hospital  2 392.18 196.088 47.7635 < 2.2e-16 ***  
## Residuals     174 714.34    4.105        
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Our results

```
m1sum <- summary(m1)
round(m1sum$coefficients,2)
```

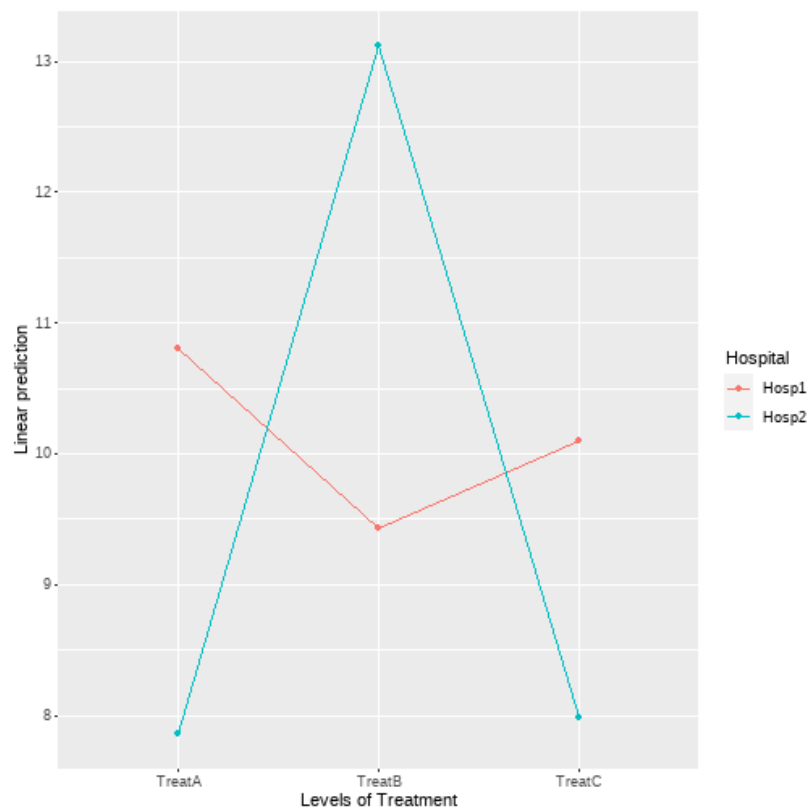
##	Estimate	Std. Error	t value	Pr(> t)
## (Intercept)	10.80	0.37	29.19	0.00
## TreatmentTreatB	-1.37	0.52	-2.62	0.01
## TreatmentTreatC	-0.70	0.52	-1.33	0.18
## HospitalHosp2	-2.95	0.52	-5.63	0.00
## TreatmentTreatB:HospitalHosp2	6.63	0.74	8.97	0.00
## TreatmentTreatC:HospitalHosp2	0.82	0.74	1.11	0.27

But where do we go next?

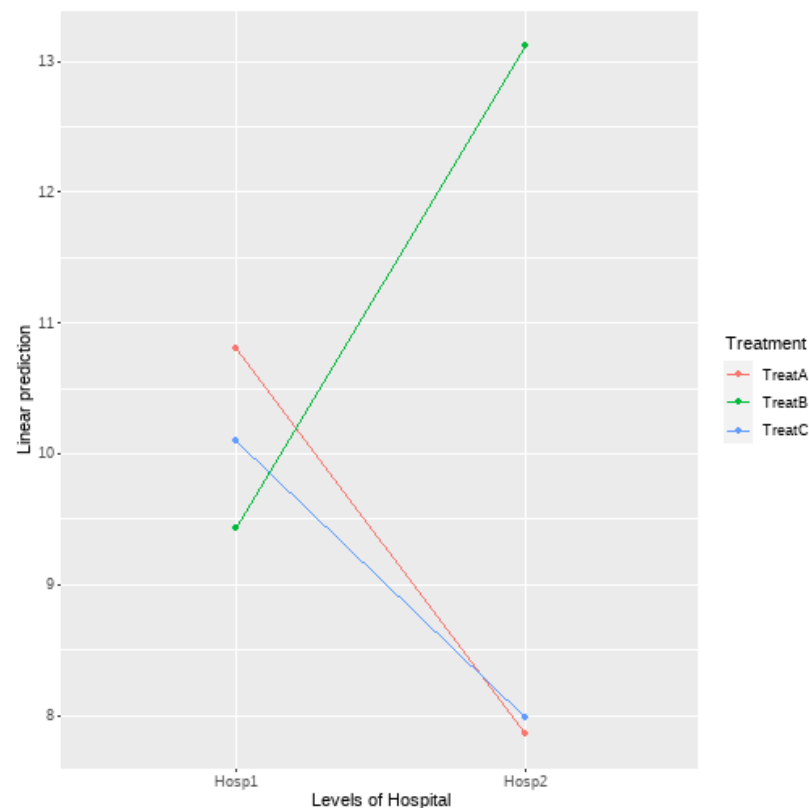
- It is typically a bad idea to focus on main effects in the presence of an interaction.
 - The interaction means the effect of the condition differs dependent on the interacting variable.
- So we need to understand more about the interaction
- We will use the `emmeans` package to explore this further:
 - We will start by looking at the visualizations
 - And then consider the simple effects

Visualizing the interaction

```
emmip(m1, Hospital ~ Treatment)
```



```
emmip(m1, Treatment ~ Hospital)
```



Simple Effects

- We noted previously that simple contrasts/effects consider the effect of one condition at a specific level of the other.
 - Is there an effect of **Hospital** for those receiving **Treatment A**? (and so on for all combinations)
 - Or, put another way, is there a difference in SWB between Hospitals 1 and 2 for people receiving Treatment A
- We also know an interaction is defined as the change in the effect of one variable given the value of another.
 - So here, value = a specific level.
 - So by considering the simple effects, we can identify at which levels of the interacting condition we see different effects.

Simple Effects with **emmeans**

```
m1_emm <- emmeans(m1, ~Treatment*Hospital)
m1_simple1 <- pairs(m1_emm, simple = "Hospital")
m1_simple1
```

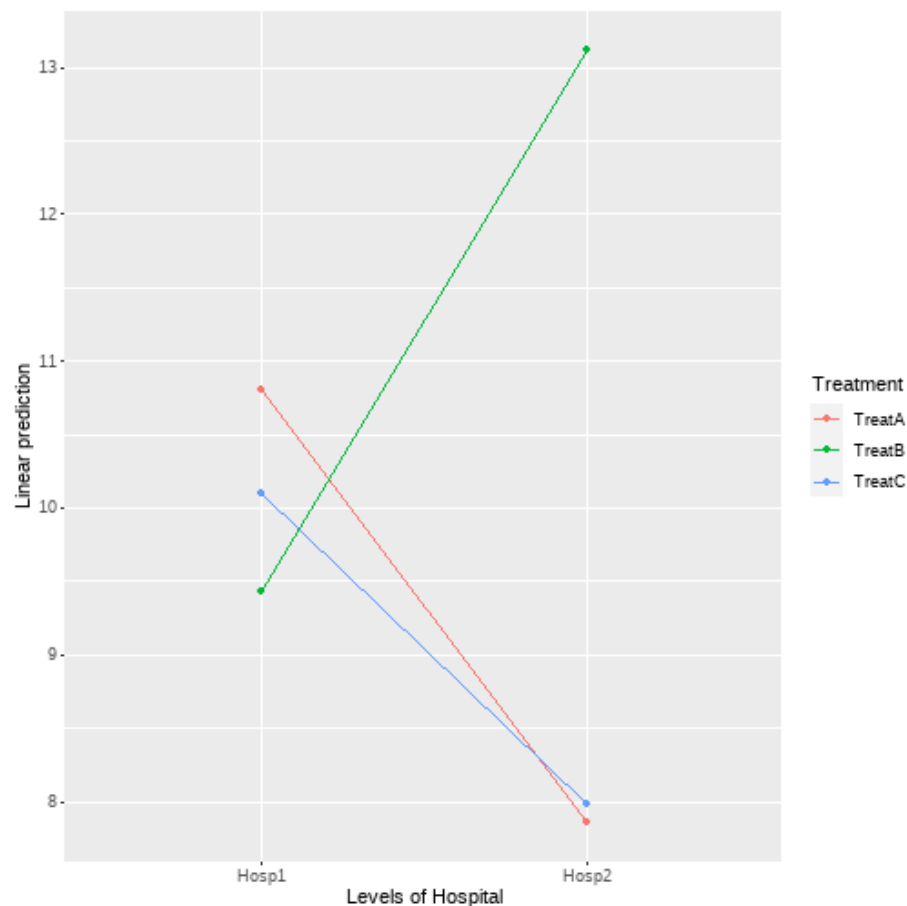
```
## Treatment = TreatA:
## contrast      estimate      SE  df t.ratio p.value
## Hosp1 - Hosp2      2.95 0.523 174   5.632  <.0001
##
## Treatment = TreatB:
## contrast      estimate      SE  df t.ratio p.value
## Hosp1 - Hosp2     -3.69 0.523 174  -7.047  <.0001
##
## Treatment = TreatC:
## contrast      estimate      SE  df t.ratio p.value
## Hosp1 - Hosp2      2.12 0.523 174   4.059  0.0001
```


Simple Effects with **emmeans**

```
m1_simple2 <- pairs(m1_emm, simple = "Treatment")  
m1_simple2
```

```
## Hospital = Hosp1:  
##   contrast      estimate      SE   df t.ratio p.value  
##   TreatA - TreatB      1.370 0.523 174    2.619  0.0259  
##   TreatA - TreatC      0.697 0.523 174    1.332  0.3796  
##   TreatB - TreatC     -0.673 0.523 174   -1.287  0.4044  
##  
## Hospital = Hosp2:  
##   contrast      estimate      SE   df t.ratio p.value  
##   TreatA - TreatB     -5.263 0.523 174  -10.061  <.0001  
##   TreatA - TreatC     -0.127 0.523 174   -0.242  0.9682  
##   TreatB - TreatC      5.137 0.523 174    9.819  <.0001  
##  
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Simple effects with plots



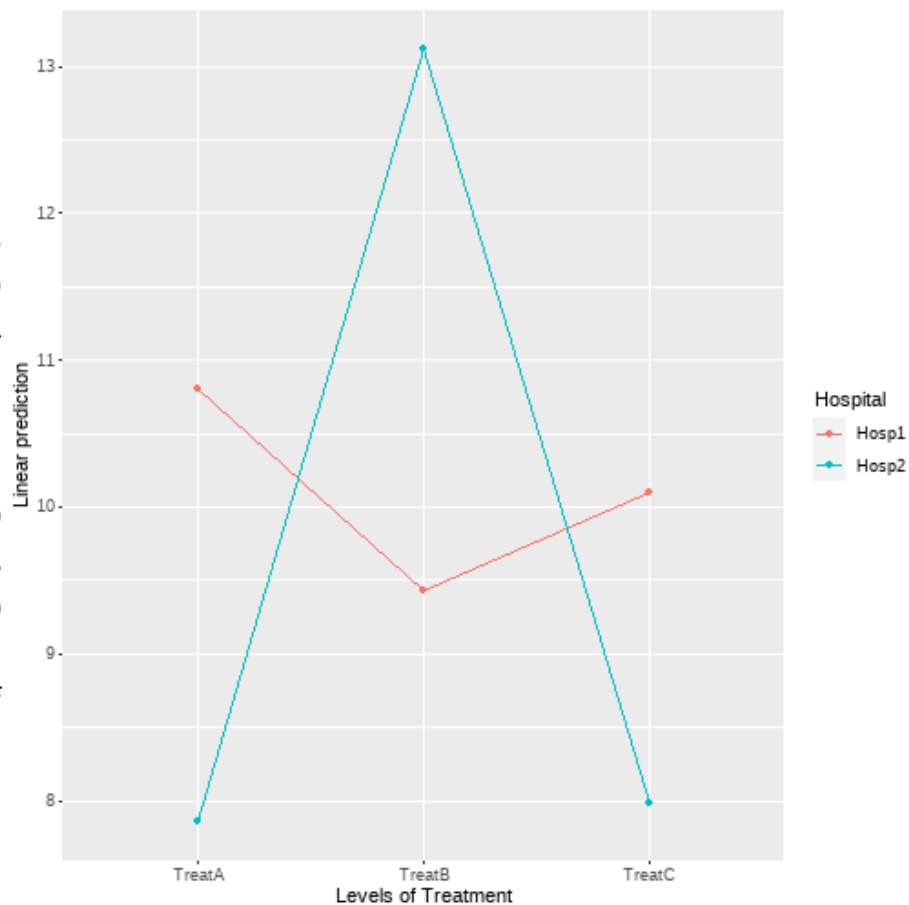
```
m1_simple1
```

```
## Treatment = TreatA:
## contrast      estimate      SE  df t.ratio p.value
## Hosp1 - Hosp2      2.95 0.523 174   5.632  <.0001
##
## Treatment = TreatB:
## contrast      estimate      SE  df t.ratio p.value
## Hosp1 - Hosp2     -3.69 0.523 174  -7.047  <.0001
##
## Treatment = TreatC:
## contrast      estimate      SE  df t.ratio p.value
## Hosp1 - Hosp2      2.12 0.523 174   4.059  0.0001
```

Simple effects with plots

```
m1_simple2
```

```
## Hospital = Hosp1:  
## contrast      estimate      SE   df t.ratio p.valu  
## TreatA - TreatB    1.370 0.523 174    2.619  0.025  
## TreatA - TreatC    0.697 0.523 174    1.332  0.379  
## TreatB - TreatC   -0.673 0.523 174   -1.287  0.404  
##  
## Hospital = Hosp2:  
## contrast      estimate      SE   df t.ratio p.valu  
## TreatA - TreatB   -5.263 0.523 174  -10.061 <.000  
## TreatA - TreatC   -0.127 0.523 174   -0.242  0.968  
## TreatB - TreatC    5.137 0.523 174    9.819 <.000  
##  
## P value adjustment: tukey method for comparing a f
```



Time for a break

Welcome Back!

One more step in exploration

Pairwise comparisons

- So far we have been discussing tests which move from the very general to the specific:
 - Overall model F
 - Incremental F/ F per condition
 - Contrasts and codes
 - Simple effects
- But we have one more layer that more closely aligns to looking at the β coefficients, namely a fully exploratory pairwise analysis.

Pairwise comparisons

- As the name suggests, pairwise comparisons compare all levels of a given predictor variable with all levels of the other.

```
pairs_res <- pairs(m1_emm)
```

Pairwise comparisons

```
## contrast estimate SE df t.ratio p.value
## TreatA Hosp1 - TreatB Hosp1 1.370 0.523 174 2.619 0.0982
## TreatA Hosp1 - TreatC Hosp1 0.697 0.523 174 1.332 0.7670
## TreatA Hosp1 - TreatA Hosp2 2.947 0.523 174 5.632 <.0001
## TreatA Hosp1 - TreatB Hosp2 -2.317 0.523 174 -4.428 0.0002
## TreatA Hosp1 - TreatC Hosp2 2.820 0.523 174 5.390 <.0001
## TreatB Hosp1 - TreatC Hosp1 -0.673 0.523 174 -1.287 0.7918
## TreatB Hosp1 - TreatA Hosp2 1.577 0.523 174 3.014 0.0346
## TreatB Hosp1 - TreatB Hosp2 -3.687 0.523 174 -7.047 <.0001
## TreatB Hosp1 - TreatC Hosp2 1.450 0.523 174 2.772 0.0670
## TreatC Hosp1 - TreatA Hosp2 2.250 0.523 174 4.301 0.0004
## TreatC Hosp1 - TreatB Hosp2 -3.013 0.523 174 -5.760 <.0001
## TreatC Hosp1 - TreatC Hosp2 2.123 0.523 174 4.059 0.0010
## TreatA Hosp2 - TreatB Hosp2 -5.263 0.523 174 -10.061 <.0001
## TreatA Hosp2 - TreatC Hosp2 -0.127 0.523 174 -0.242 0.9999
## TreatB Hosp2 - TreatC Hosp2 5.137 0.523 174 9.819 <.0001
##
## P value adjustment: tukey method for comparing a family of 6 estimates
```


Why do pairwise comparisons?

- Sometimes we do not have a concrete hypothesis to test.
- Sometimes we do, but the exploratory analysis is still useful information for the field.
- Pairwise comparisons throws up a statistical issue, namely the problem of multiple comparisons.
 - When we do lots and lots of tests, the chances of Type I error (false-positives) increase.
- We will move on to how we can adjust our inferences to deal with this next week, along with a quick revisit of assumption checks.

Summary

- This week we have looked at:
 - Probing and understanding interactions via simple effects.
 - Estimation of pairwise tests
 - Both of the above using `emmeans()`
- This completes the new learning related to analysing experimental designs.

Thanks for listening!