

PSY 653 Module 3: Nested Designs

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Part 1: Demo of Nested ANOVAs

Load libraries

```
library(psych) # using for describe() function
library(tidyverse) # using for read_csv() function, so character variables still kept as characters
```

```
## Warning: package 'ggplot2' was built under R version 3.6.3
## Warning: package 'tibble' was built under R version 3.6.3
## Warning: package 'tidyr' was built under R version 3.6.3
## Warning: package 'dplyr' was built under R version 3.6.3
## Warning: package 'forcats' was built under R version 3.6.3
```

Read data

```
nested_demo<-read_csv(file="Nested_demo.csv")
```

Check how variables are read

```
str(nested_demo)

## tibble [114 x 4] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
## $ Y          : num [1:114] 5 4 3 5 4 3 6 5 4 6 ...
## $ Hospital   : chr [1:114] "H1" "H1" "H1" "H1" ...
## $ Drug       : chr [1:114] "D1" "D2" "D1" "D2" ...
## $ Condition  : chr [1:114] "C1" "C2" "C3" "C4" ...
## - attr(*, "spec")=
## .. cols(
## ..   Y = col_double(),
## ..   Hospital = col_character(),
## ..   Drug = col_character(),
## ..   Condition = col_character()
## .. )
```

Get variable descriptives

```
describe(nested_demo) #note: we get NaN because variables are factors (data includes letters)
```

```
## Warning in describe(nested_demo): NAs introduced by coercion
```

```
## Warning in describe(nested_demo): NAs introduced by coercion
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## Warning in FUN(newX[, i], ...): no non-missing arguments to min; returning Inf
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## Warning in FUN(newX[, i], ...): no non-missing arguments to min; returning Inf
## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf
## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf
## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf
##
##      vars    n mean   sd median trimmed  mad min  max range  skew kurtosis
## Y          1 114 8.75 2.91      9    8.79 2.97   3   15    12 -0.14   -0.71
## Hospital*   2 114  NaN  NA      NA      NaN  NA Inf -Inf -Inf    NA      NA
## Drug*       3 114  NaN  NA      NA      NaN  NA Inf -Inf -Inf    NA      NA
## Condition*  4 114  NaN  NA      NA      NaN  NA Inf -Inf -Inf    NA      NA
##
##      se
## Y      0.27
## Hospital*  NA
## Drug*      NA
## Condition*  NA
```

Calculate the mean values of Y by hospital, drug, and condition

```
# aggregate function here just shwows the values that we're comparing, but we're not saving these values
aggregate(nested_demo$Y, by=list(Hospital=nested_demo$Hospital), mean)
```

```
##   Hospital      x
## 1      H1 8.759259
## 2      H2 8.733333
```

```
aggregate(nested_demo$Y, by=list(Drug=nested_demo$Drug), mean)
```

```
##   Drug      x
## 1   D1 8.754386
## 2   D2 8.736842
```

```
aggregate(nested_demo$Y, by=list(Condition=nested_demo$Condition), mean)
```

```
##   Condition      x
## 1      C1 8.894737
## 2      C2 8.631579
## 3      C3 8.578947
## 4      C4 9.789474
## 5      C5 8.789474
## 6      C6 7.789474
```

5) Nested ANOVA in which Y is regressed on Hospital, Drug, Condition, and the

5a) Create ANOVA table that lists all of the factors and the df for each

Factors (i.e., effects we can test with this model)

Hospital

Drug

Condition within Drug Hospital * Drug Hospital * (Condition within Drug) Error

5b) Conduct a Hospital x Drug ANOVA, ignoring Condition

```
mod1 <- anova(lm(Y~Hospital + Drug + Hospital*Drug, data=nested_demo))
mod1
```

```
## Analysis of Variance Table
##
## Response: Y
##              Df Sum Sq Mean Sq F value Pr(>F)
## Hospital      1   0.02  0.0191  0.0022  0.9626
## Drug          1   0.01  0.0088  0.0010  0.9747
## Hospital:Drug  1   0.08  0.0764  0.0088  0.9254
## Residuals    110 953.52  8.6684
```

5c) Conduct separate ANOVA for effect of condition

```
mod2 <- anova(lm(Y~Drug/Condition + Hospital*(Drug/Condition), data=nested_demo))
mod2 # get same model output as for the full model
```

```
## Analysis of Variance Table
##
## Response: Y
##              Df Sum Sq Mean Sq F value Pr(>F)
## Drug          1   0.01  0.0088  0.0010  0.9751
## Hospital      1   0.02  0.0191  0.0021  0.9633
## Drug:Condition 4  39.30  9.8246  1.0970  0.3622
## Drug:Hospital  1   0.08  0.0764  0.0085  0.9266
## Drug:Condition:Hospital 4  0.75  0.1884  0.0210  0.9991
## Residuals    102 913.47  8.9556
```

5d) Conduct ANOVA on full nested model Full

This gives same output as the two models above combined

```
mod_full <- anova(lm(Y~Hospital + Drug + Drug/Condition + Hospital*Drug + Hospital*(Drug/Condition), data=nested_demo))
mod_full
```

```
## Analysis of Variance Table
##
## Response: Y
##              Df Sum Sq Mean Sq F value Pr(>F)
## Hospital      1   0.02  0.0191  0.0021  0.9633
## Drug          1   0.01  0.0088  0.0010  0.9751
## Drug:Condition 4  39.30  9.8246  1.0970  0.3622
## Hospital:Drug  1   0.08  0.0764  0.0085  0.9266
```

```
## Hospital:Drug:Condition    4    0.75  0.1884  0.0210 0.9991
## Residuals                  102 913.47  8.9556
```

```
# Syntax: / specifies within, and * specifies the interaction
```

```
# Drug not nested within hospital in this data, because the drugs are the same between the two hospital.
```

```
# Similarly, condition is not nested within hospital in this data, because the conditions are the same
```

```
# However, condition IS nested within drug, because the conditions are different between the two drugs.
```

Part 2: Try it Yourself

Factors (i.e., effects we can test with this model)

Hospital (df=1)

Drug within hospital (df=2; 1 for each hospital) Condition within drug within hospital (df=8; 2 for each drug in each hospital) Error (df = 114-11-1 = 102)

No interactions testable here, because the model is fully nested

Read data

```
nested_practice<-read_csv(file="Nested_practice.csv")
```

Get variable descriptives

```
psych::describe(nested_practice) #note: variables are characters (include text)
```

```
## Warning in psych::describe(nested_practice): NAs introduced by coercion
```

```
## Warning in psych::describe(nested_practice): NAs introduced by coercion
```

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## Warning in psych::describe(nested_practice): NAs introduced by coercion
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```
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```

```
## Warning in FUN(newX[, i], ...): no non-missing arguments to max; returning -Inf
```

```
##          vars    n mean    sd median trimmed  mad min  max range  skew kurtosis
## Y           1 114 8.75 2.91      9    8.79 2.97   3   15    12 -0.14    -0.71
## Hospital*   2 114  NaN   NA      NA      NaN   NA Inf -Inf -Inf    NA      NA
## Drug*       3 114  NaN   NA      NA      NaN   NA Inf -Inf -Inf    NA      NA
## Condition*  4 114  NaN   NA      NA      NaN   NA Inf -Inf -Inf    NA      NA
##           se
## Y          0.27
## Hospital*   NA
## Drug*       NA
## Condition*  NA
```

4

4a) ANOVA table of factors and df for each

Factors (i.e., effects we can test with this model)

Hospital (df=1)

Drug within hospital (df=2; 1 for each hospital) Condition within drug within hospital (df=8; 2 for each drug in each hospital) Error (df = 114-11-1 = 102)

No interactions testable here, because the model is fully nested

4b) Run one-way ANOVA for Hospital, ignoring Condition and Drug

```
mod4 <- anova(lm(Y ~ Hospital, data=nested_practice))
mod4
```

```
## Analysis of Variance Table
##
## Response: Y
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hospital    1   0.02  0.0191  0.0022 0.9623
## Residuals 112 953.60  8.5143
```

4c) Run one-way ANOVA for Drug (ignoring Condition) in Hospital 1, do the same thing in Hospital 2

```
mod5 <- anova(lm(Y ~ Hospital/Drug, data=nested_practice))
mod5
```

```
## Analysis of Variance Table
##
## Response: Y
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hospital      1   0.02  0.0191  0.0022 0.9626
## Hospital:Drug  2   0.09  0.0426  0.0049 0.9951
## Residuals    110 953.52  8.6684
```

4d) Run one-way ANOVA for Condition and plug results into the ANOVA table

```
mod6 <- anova(lm(Y ~ Hospital/Drug/Condition, data=nested_practice))
mod6
```

```
## Analysis of Variance Table
##
## Response: Y
##           Df Sum Sq Mean Sq F value Pr(>F)
## Hospital      1   0.02  0.0191  0.0021 0.9633
## Hospital:Drug  2   0.09  0.0426  0.0048 0.9953
## Hospital:Drug:Condition  8 40.05  5.0065  0.5590 0.8090
## Residuals    102 913.47  8.9556
```

4e) Run full nested ANOVA to test effect of Hospital, Drug, and Condition on Y

```
mod3 <- anova(lm(Y ~ Hospital + Hospital/Drug + Hospital/Drug/Condition, data=nested_practice))
mod3
```

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

```
##
```

```
## Response: Y
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## Hospital	1	0.02	0.0191	0.0021	0.9633
## Hospital:Drug	2	0.09	0.0426	0.0048	0.9953
## Hospital:Drug:Condition	8	40.05	5.0065	0.5590	0.8090
## Residuals	102	913.47	8.9556		

```
# drug is nested within hospital, condition is nested within drug, and both are nested within hospital
```