Coding Categorical Data

Data Analysis for Psychology in R 2

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Weeks Learning Objectives

1. Interpret the output from a model using dummy coding.
2. Interpret the output from a model using sum-to-zero coding.
3. Create specific contrast matrices to test specific effects.
4. Understand the distinction between orthogonal and non-orthogonal contrasts.

Topics for today

- Last time we looked at the F-test in one-way designs and linear models
- This time we are going to consider contrasts and β coefficients

Looking beneath the F-test

- The F-test gives us an overall test of the model, or the difference between two models.
  - And we saw we can apply this to seeing the overall effect of a categorical variable with 2+ levels.
- But we may want to know something more specific.
  - Differences between specific groups or sets of groups.
- In such cases we talk about...
  - contrasts & planned comparisons
  - *post-hoc test (not for today)*
- So how do we approach these from the linear model perspective?

Contrasts and Planned comparisons

- Sometimes we want to make comparisons between pairs of things.
  - Treatment A vs Treatment B
  - Treatment A vs (Treatment B & Treatment C) etc.
- Such comparisons can be...
  - Specified a priori (confirmatory)
  - For all possible comparisons (exploratory)
- We achieve these comparisons via assigning weights to groups.
- May sound complicated, but we have already seen this practice in action this year

Dummy coding (reference group)

- Create k-1 dummy variables/contrasts
    - where k is the number of levels of the categorical predictor.
- Assign reference group 0 on all dummies.
- Assign 1 to the focal group for a particular dummy.
- Enter the dummies into the linear model and they code the difference in means between the focal group/level and the reference.

`Hospital` & `Treatment` data

- **Condition 1**: `Treatment` (Levels: TreatA, TreatB, TreatC).
- **Condition 2**: `Hospital` (Levels: Hosp1, Hosp2).
- Total sample n = 180 (30 patients in each of 6 groups).
  - Between person design.
- **Outcome**: Subjective well-being (`SWB`)
  - An average of multiple raters (the patient, a member of their family, and a friend).
  - SWB score ranged from 0 to 20.

The data

```
hosp_tbl <- read_csv("hospital.csv", col_types = "dff")
hosp_tbl %>%
  slice(1:10)
```

```
## # A tibble: 10 x 3
##      SWB Treatment Hospital
##    <dbl> <fct>     <fct>
##  1   6.2 TreatA    Hosp1
##  2  15.9 TreatA    Hosp1
##  3   7.2 TreatA    Hosp1
##  4  11.3 TreatA    Hosp1
##  5  11.2 TreatA    Hosp1
##  6   9   TreatA    Hosp1
##  7  14.5 TreatA    Hosp1
##  8   7.3 TreatA    Hosp1
##  9  13.7 TreatA    Hosp1
## 10  12.6 TreatA    Hosp1
```

Why do we need a reference group?

- Consider our example.
- We have three groups each given a specific Treatment A, B or C
- We want a model that represents our data (observations), but all we "know" is what group an observation belongs to. So;

$$y_{ij} = \mu_i + \epsilon_{ij}$$

- Where
  - y_{ij} are the individual observations
  - μ_i is the mean of group i and
  - ϵ_{ij} is the individual deviation from that mean.

Why do we need a reference group?

- An alternative way to present this idea looks much more like our linear model:

$$y_{ij} = \beta_0 + \underbrace{(\mu_i - \beta_0)}_{\beta_i} + \epsilon_{ij}$$

- Where
    - y_{ij} are the individual observations
    - β_0 is an estimate of reference/overall average
    - μ_i is the mean of group i
    - β_1 is the difference between the reference and the mean of group i, and
    - ϵ_{ij} is the individual deviation from that mean.

Why do we need a reference group?

- We can write this equation more generally as:

$$\mu_i = \beta_0 + \beta_i$$

- or for the specific groups (in our case 3):

$$\mu_{treatmentA} = \beta_0 + \beta_{1A}$$

$$\mu_{treatmentB} = \beta_0 + \beta_{2B}$$

$$\mu_{treatmentC} = \beta_0 + \beta_{3C}$$

- **The problem**: we have four parameters (β_0 , β_{1A} , β_{2B} , β_{3C}) to model three group means ($\mu_{TreatmentA}$, $\mu_{TreatmentB}$, $\mu_{TreatmentC}$)
- We are trying to estimate too much with too little.
    - This is referred to as under-identification.
    - We need to estimate at least 1 parameter less

Constraints fix identification

- Consider dummy coding.
- Suppose we make Treatment A the reference. Then,

$$\mu_{treatmentA} = \beta_0$$

$$\mu_{treatmentB} = \beta_0 + \beta_{2B}$$

$$\mu_{treatmentC} = \beta_0 + \beta_{3C}$$

- Fixed!
- We now only have three parameters (β_0 , β_{2B} , β_{3C}) for the three group means ($\mu_{TreatmentA}$, $\mu_{TreatmentB}$, $\mu_{TreatmentC}$).

Group Means

```
hosp_tbl %>%
  select(1:2) %>%
  group_by(Treatment) %>%
  summarise(
    mean = round(mean(SWB),3),
    sd = round(sd(SWB),1),
    N = n()
  )
```

```
## # A tibble: 3 x 4
##   Treatment  mean    sd     N
##   <fct>     <dbl> <dbl> <int>
## 1 TreatA     9.33   2.9    60
## 2 TreatB    11.3    2.5    60
## 3 TreatC     9.04   2      60
```

Dummy (reference) model

```
summary(lm(SWB ~ Treatment, data = hosp_tbl))
```

```
## 
## Call:
## lm(formula = SWB ~ Treatment, data = hosp_tbl)
## 
## Residuals:
##    Min     1Q Median     3Q    Max 
## -5.373 -1.987 -0.300  1.838  7.173 
## 
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)    
## (Intercept)       9.3267     0.3242  28.770  < 2e-16 ***
## TreatmentTreatB   1.9467     0.4585   4.246 3.51e-05 ***
## TreatmentTreatC  -0.2850     0.4585  -0.622    0.535    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.511 on 177 degrees of freedom
## Multiple R-squared:  0.1369,	Adjusted R-squared:  0.1271 
## F-statistic: 14.04 on 2 and 177 DF,  p-value: 2.196e-06
```

Dummy (reference) model

```
##     (Intercept) TreatmentTreatB TreatmentTreatC 
##           9.327           1.947          -0.285 
```

- Recall the equations for the group means:

$$\mu_{treatmentA} = \beta_0$$

$$\mu_{treatmentB} = \beta_0 + \beta_1$$

$$\mu_{treatmentC} = \beta_0 + \beta_2$$

Treatment	mean
TreatA	9.327
TreatB	11.273
TreatC	9.042

Time for a break

Take a little time to look back over dummy coding to make sure you feel happy with the key principles

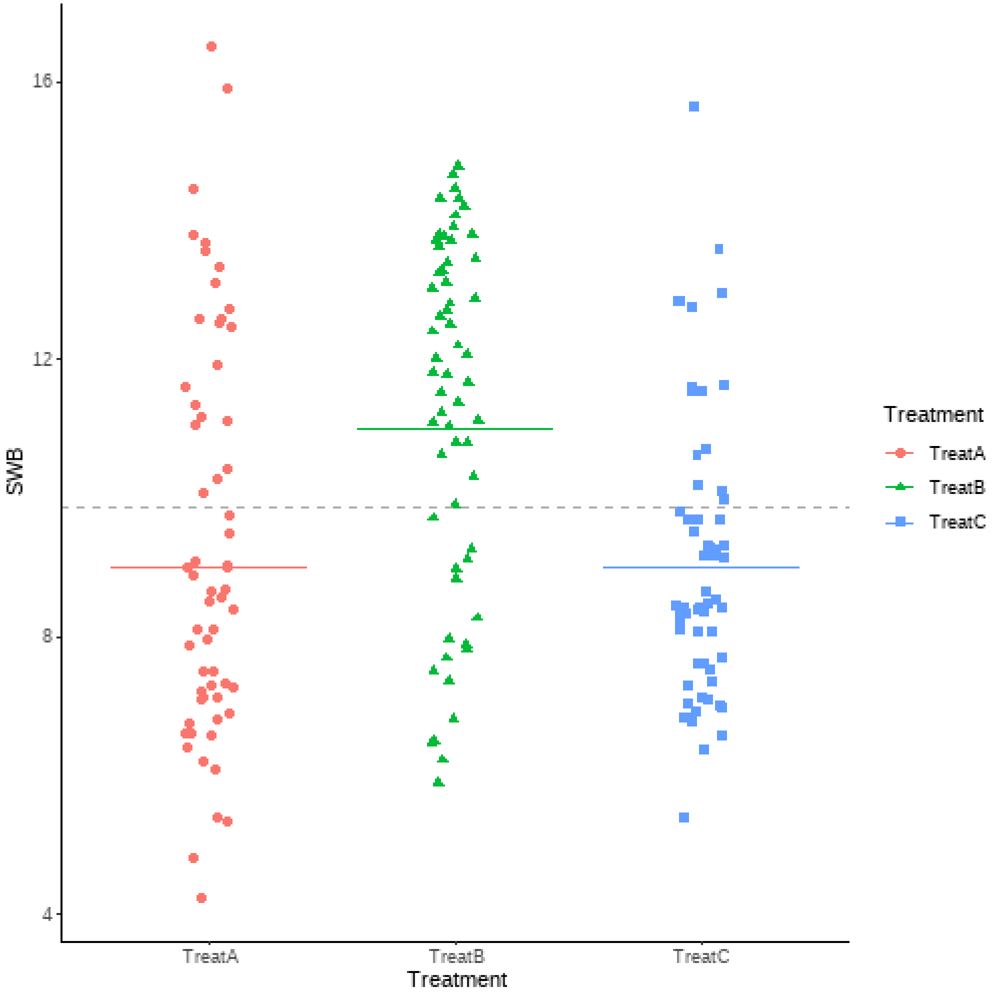
Welcome Back!

Now we are going to look at some other options to dummy coding

Why not always use dummy coding?

- We might not always want to compare against a reference group.
- We might want to compare to:
  - The overall or grand mean
  - Group 1 vs groups 2, 3, 4 combined
  - and on we go!
- Let's consider the example of the grand mean...

Effects coding (sum to zero coding)



Sum to zero constraint

- With dummy coding we had a reference group constraint, and the mean of that group was equal to the value of β_0, or

$$\mu_{reference} = \beta_0$$

- Alternately, we can apply what is referred to as the sum to zero constraint (again using example of three levels).

$$\beta_1 + \beta_2 + \beta_3 = 0$$

- This constraints leads to the following interpretations:
- β_0 is the grand mean (mean of all observations)

$$\beta_0 = \frac{\mu_1 + \mu_2 + \mu_3}{3}$$

- β_i are the differences between the coded group and the grand mean:

$$\beta_i = \mu_i - \mu$$

Sum to zero constraint

- Finally, we can get back to our group means from the coefficients as follows:

$$\mu_1 = \beta_0 + \beta_1$$

$$\mu_2 = \beta_0 + \beta_2$$

$$\mu_3 = \beta_0 - (\beta_1 + \beta_2)$$

OK, but how do we apply the constraint?

- Answer, in the same way as we did with dummy coding.
- We can create a set of sum to zero (sometimes called effect, or deviation) variables
  - Or the equivalent contrast matrix.
- For effect code variables we:
  - Create $k-1$ variables
  - For observations in the focal group, assign 1
  - For observations in the last group, assign -1
  - For all other groups assign 0

Comparing coding matrices

Level	D1	D2
Treatment A	0	0
Treatment B	1	0
Treatment C	0	1

$$y_{ij} = \beta_0 + \beta_1 D_1 + \beta_2 D_2 + \epsilon_{ij}$$

Level	E1	E2
Treatment A	1	0
Treatment B	0	1
Treatment C	-1	-1

$$y_{ij} = \beta_0 + \beta_1 E_1 + \beta_2 E_2 + \epsilon_{ij}$$

Sum to zero/effects for group means

Level	E1	E2
Treatment A	1	0
Treatment B	0	1
Treatment C	-1	-1

$$\mu_1 = \beta_0 + \beta_1$$

$$\mu_2 = \beta_0 + \beta_2$$

$$\mu_3 = \beta_0 - (\beta_1 + \beta_2)$$

$$\mu_1 = \beta_0 + 1 * \beta_1 + 0 * \beta_2 = \beta_0 + \beta_1$$

$$\mu_2 = \beta_0 + 0 * \beta_1 + 1 * \beta_2 = \beta_0 + \beta_2$$

$$\mu_3 = \beta_0 - 1 * \beta_1 - 1 * \beta_2 = \beta_0 - \beta_1 - \beta_2$$

- Now we will look practically at the implementation and differences

Group Means

```r
hosp_tbl %>%
  select(1:2) %>%
  group_by(Treatment) %>%
  summarise(
    mean = round(mean(SWB),3),
    sd = round(sd(SWB),1),
    N = n()
  )
```

```
## # A tibble: 3 x 4
##   Treatment  mean    sd     N
##   <fct>     <dbl> <dbl> <int>
## 1 TreatA     9.33   2.9    60
## 2 TreatB    11.3    2.5    60
## 3 TreatC     9.04   2      60
```

Effects (sum to zero) model

- We need to change the contrast scheme from default.

```
contrasts(hosp_tbl$Treatment) <- contr.sum
contrasts(hosp_tbl$Treatment)
```

```
##        [,1] [,2]
## TreatA    1    0
## TreatB    0    1
## TreatC   -1   -1
```

Effects (sum to zero) model

```
summary(lm(SWB ~ Treatment, data = hosp_tbl))
```

```
##
## Call:
## lm(formula = SWB ~ Treatment, data = hosp_tbl)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.373 -1.987 -0.300  1.838  7.173
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   9.8806     0.1872  52.791  < 2e-16 ***
## Treatment1   -0.5539     0.2647  -2.093   0.0378 *
## Treatment2    1.3928     0.2647   5.262 4.09e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.511 on 177 degrees of freedom
## Multiple R-squared:  0.1369,    Adjusted R-squared:  0.1271
## F-statistic: 14.04 on 2 and 177 DF,  p-value: 2.196e-06
```

Effects (sum to zero) model

```
## (Intercept)  Treatment1  Treatment2
##       9.881      -0.554       1.393
```

- Coefficients from group means

$$\beta_0 = \frac{\mu_1 + \mu_2 + \mu_3}{3}$$

$$\beta_1 = \mu_1 - \mu$$

$$\beta_2 = \mu_2 - \mu$$

.pull-right[

Treatment	mean	Gmean
TreatA	9.327	9.881
TreatB	11.273	9.881
TreatC	9.042	9.881

Effects (sum to zero) model

```
## (Intercept)  Treatment1  Treatment2
##       9.881      -0.554       1.393
```

- Group means from coefficients:

$$\mu_1 = \beta_0 + \beta_1$$

$$\mu_2 = \beta_0 + \beta_2$$

$$\mu_3 = \beta_0 - (\beta_1 + \beta_2)$$

Treatment	mean	Gmean
TreatA	9.327	9.881
TreatB	11.273	9.881
TreatC	9.042	9.881

The wide world of contrasts

- We have now seen two examples of coding schemes (dummy and effect).
- There are **lots** of different coding schemes we can use for categorical variables to make different comparisons.
  - If you are interested, see the excellent resource on UCLA website
- **But always remember...**

The data is the same, the tested contrasts differ

- Run both models:

```
contrasts(hosp_tbl$Treatment) <- contr.treatment
m_dummy <- lm(SWB ~ Treatment, data = hosp_tbl)

# Change the contrasts and run again
contrasts(hosp_tbl$Treatment) <- contr.sum
m_zero <- lm(SWB ~ Treatment, data = hosp_tbl)
```

- Create a small data set:

```
treat <- tibble(Treatment = c("TreatA", "TreatB", "TreatC"))
```

The data is the same, the tested contrasts differ

- Add the predicted values from our models

```
treat %>%
  mutate(
    pred_dummy = predict(m_dummy, newdata = .),
    pred_zero = predict(m_zero, newdata = .)
  )
```

```
## # A tibble: 3 x 3
##   Treatment pred_dummy pred_zero
##   <chr>          <dbl>     <dbl>
## 1 TreatA          9.33      9.33
## 2 TreatB         11.3      11.3 
## 3 TreatC          9.04      9.04
```

- No matter what coding or contrasts we use, we are still modelling the group means!

Time for a break

Deep breaths and a cup of tea

Welcome Back!

But we can still do more...

Manual contrast testing

- We can structure a wide variety of contrasts so long as they can be written:

1. A as a linear combination of population means.
2. The associated coefficients (weights) sum to zero.

- So

$$H_0 : c_1\mu_1 + c_1\mu_2 + c_3\mu_3$$

- With

$$c_1 + c_2 + c_3 = 0$$

Manual contrast testing

- For both dummy and effects coding we have seen we assign values for the contrasts
  - Dummy = 0 and 1
  - Effects = 1, 0 and -1
- When we create our own contrasts, we have certain rules to follow in assigning values

Rules for assigning weights

- **Rule 1**: Weights are -1 ≤ x ≤ 1
- **Rule 2**: The group(s) in one chunk are given negative weights, the group(s) in the other get positive weights
- **Rule 3**: The sum of the weights of the comparison must be 0
- **Rule 4**: If a group is not involved in the comparison, weight is 0
- **Rule 5**: For a given comparison, weights assigned to group(s) are equal to 1 divided by the number of groups in that chunk.
- **Rule 7**: Restrict yourself to running k – 1 comparisons (where k = number of groups)
- **Rule 8**: Each contrast can only compare 2 chunks of variance
- **Rule 9**: Once a group singled out, it can't enter other contrasts

New example

- Suppose we were interested in the effect of various relationship statuses on an individuals subjective well-being (`swb`)
    - Keeping with a theme on our outcome.
- Our predictor is `status` which has 5 levels:
    - Married or Cival Partnership
    - Cohabiting relationship
    - Single
    - Widowed
    - Divorced
- Let's say we have data on 500 people.

Data

status	n	mean	sd
Cohab	100	11.44	4.22
Divorced	50	9.37	2.34
Married/CP	275	10.63	3.41
Single	50	8.06	2.19
Widowed	25	6.00	1.07

Applying rules

- Let's say we want to make two contrasts

1. Those who are currently or previously married or in a civil partnership vs not.
2. Those who are currently married or in a civial partnership vs those who have previously been.

group	contrast1	contrast2
Cohab	-0.50	0.0
Divorced	0.33	-0.5
Married/CP	0.33	1.0
Single	-0.50	0.0
Widowed	0.33	-0.5

`emmeans`

- We will use the package `emmeans` to test our contrasts
  - We will also be using this in the next few weeks to look at analysing experimental designs.
- **E**stimated
- **M**arginal
- **Means**
- Essentially this package provides us with a lot of tools to help us model contrasts and linear functions.

Orthogonal vs. Non-orthogonal Contrasts

- Orthogonal contrasts test independent sources of variation.
    - If we follow the rules above, we will have orthogonal contrasts.
- Non-orthogonal contrasts test non-independent sources of variation.
    - This presents some further statistical challenges in terms of making inferences.
    - We will come back to this discussion later in the course.

Rule 10: Checking if contrasts are orthogonal

- The sum of the products of the weights will = 0 for any pair of orthogonal comparisons

$$\sum c_{1j}c_{2j} = 0$$

From our example

```
contrasts %>%
  mutate(
    Orthogonal = contrast1*contrast2
  ) %>%
  kable(.) %>%
  kable_styling(., full_width = F)
```

group	contrast1	contrast2	Orthogonal
Cohab	-0.50	0.0	0.000
Divorced	0.33	-0.5	-0.165
Married/CP	0.33	1.0	0.330
Single	-0.50	0.0	0.000
Widowed	0.33	-0.5	-0.165

Summary of today

- We have considered different ways in which we can code categorical predictors.

- Take home:

    - Use of coding matrices allows us to compare groups (or levels) in lots of ways.
    - Our β's will represent differences in group means.
    - The scheme we use determines which group or combination of groups we are comparing.
    - **In all cases the underlying data is unchanged.**

- This makes coding schemes a very flexible tool for testing hypotheses.

Thanks for listening!