LONGITUDINAL ANALYSIS: CONSOLIDATE AND EXPLAIN

WEEK 11 · OPTIONAL AFTER-CLASS REVIEW

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READ THE SAME CALF STUDY

Researchers assign Control or Enhanced feed to each of 32 calves, balancing the two diets within each of four rooms. They weigh each calf at weeks 0, 2, 4, 6 and 8. These invented records illustrate longitudinal data: measurements collected from the same animals over time.

```
library("dplyr")

library("lme4")
library("performance")
library("marginaleffects", warn.conflicts = FALSE)
library("ggplot2")
d <- readr::read_csv("data/calf-growth.csv")
d <- d |>
  mutate(
    diet = factor(diet, levels = c("Control", "Enhanced")),
    room = factor(room),
    calf = factor(calf),
    week = time_week
  )
head(d |> select("calf", "diet", "week", "weight_kg"), 3)
```

`week` counts weeks since researchers assigned the diets. They record week 0 before feeding starts.

READ THE SAME CALF STUDY

```
# A tibble: 3 × 4
  calf  diet     week weight_kg
  <fct> <fct>   <dbl>     <dbl>
1 C01   Control     0      47.9
2 C01   Control     2      58.6
3 C01   Control     4      65.8
```

CHOOSE WHAT TO REVIEW

Work	Minutes
Review this deck and recap	20
Revisit code and supplied extension	20–25
Revise project methods and result	20–30

Choose the steps that help with your Unit 12 draft for 25 November.

FIT THE CURVE DIRECTLY

```
curved <- lmer(
  weight_kg ~ diet * week + I(week^2) + room + (1 | calf),
  data = d,
  REML = TRUE
)
summary(curved)
```

Explain what changes when `I(week^2)` is added. Which parts of the model still connect repeated weights?

FIT THE CURVE DIRECTLY

```
Linear mixed model fit by REML ['lmerMod']
Formula: weight_kg ~ diet * week + I(week^2) + room + (1 | calf)
   Data: d

REML criterion at convergence: 725.7

Scaled residuals:
     Min       1Q   Median       3Q      Max
-2.27062 -0.60674  0.06788  0.62813  2.19214

Random effects:
 Groups   Name        Variance Std.Dev.
 calf     (Intercept) 29.084   5.393
 Residual              2.595   1.611
Number of obs: 160, groups:  calf, 32

Fixed effects:
                 Estimate Std. Error t value
(Intercept)      38.39388    2.17105  17.684
dietEnhanced      0.20787    1.95706   0.106
week              5.38766    0.16500  32.652
I(week^2)        -0.10708    0.01903  -5.628
roomR2            0.05862    2.72041   0.022
roomR3            2.40960    2.72041   0.886
roomR4            4.03347    2.72041   1.483
dietEnhanced:week 0.42749    0.09005   4.747
```

CHOOSE WEEKS AND ROOMS

Compare the diets at weeks 0, 4 and 8, giving each room equal weight.

```
grid <- tidyr::crossing(
  week = c(0, 4, 8),
  diet = d$diet,
  room = d$room
) |>
  mutate(calf = d$calf[1])
head(grid, 3)
```

```
# A tibble: 3 × 4
   week diet    room  calf
  <dbl> <fct>   <fct> <fct>
1     0 Control R1    C01
2     0 Control R2    C01
3     0 Control R3    C01
```

COMPARE THE THREE WEEKS

Use the same fitted curve. Leave out an existing calf's fitted difference with `re.form = NA` and compare Enhanced minus Control.

```
differences <- avg_comparisons(
  curved,
  newdata = grid,
  variables = list(diet = c("Control", "Enhanced")),
  by = "week",
  re.form = NA
)
differences
```

Researchers record week 0 before feeding starts. Which row describes chance starting differences, and which answers the eight-week feeding question?

COMPARE THE THREE WEEKS

```
 week Estimate Std. Error     z Pr(>|z|)   S  2.5 % 97.5 %
    0    0.208       1.96 0.106   0.9154 0.1 -3.628   4.04
    4    1.918       1.92 0.997   0.3188 1.6 -1.852   5.69
    8    3.628       1.96 1.854   0.0638 4.0 -0.208   7.46

Term: diet
Type: response
Comparison: Enhanced - Control
```

KEEP THE UNCERTAINTY TARGET CLEAR

The intervals concern differences in **expected weight**, in kg.

They do not describe individual future weights.

Our question weights rooms equally and averages over new calves under the model.

Even if errors at nearby visits have near-zero sample correlation, that does not prove a calf's remaining errors are unrelated.

USE CHECKS TO ASK BETTER QUESTIONS

```
check_singularity(curved)
```

```
[1] FALSE
```

```
check_normality(curved)
```

```
OK: residuals appear as normally distributed (p = 0.268).
```

Read the supplied visit-correlation extension in `reference/extension-output.txt`.

What assumption changed? Did the question or units change?

REVISE YOUR PROJECT

Write 150–200 words. Explain what researchers did to the animals or groups and what they measured. Give one useful estimate with its uncertainty, one model check, an alternative assumption worth comparing and a limitation.

Use this optional review to refine the same project draft you will bring on **25 November**.

Use `lme4`, `performance` and `marginaleffects` directly. Choose a model and comparison that fit your own study.