

Complete factorial designs

Session 6

MATH 80667A: Experimental Design and Statistical Methods
for Quantitative Research in Management
HEC Montréal

Outline

Unbalanced designs

Multifactorial designs

Unbalanced designs

Premise

So far, we have exclusively considered balanced samples

balanced = same number of observational units in each subgroup

Most experiments (even planned) end up with unequal sample sizes.

Noninformative drop-out

Unbalanced samples may be due to many causes, including randomization (need not balance) and loss-to-follow up (dropout)

If dropout is random, not a problem

- Example of Baumann, Seifert-Kessel, Jones (1992):

Because of illness and transfer to another school, incomplete data were obtained for one subject each from the TA and DRTA group

Problematic drop-out or exclusion

If loss of units due to treatment or underlying conditions, problematic!

Rosensaal (2021) rebuking a study on the effectiveness of hydrochloriquine as treatment for Covid19 and reviewing allocation:

Of these 26, six were excluded (and incorrectly labelled as lost to follow-up): three were transferred to the ICU, one died, and two terminated treatment or were discharged

Sick people excluded from the treatment group! then claim it is better.

Worst: "The index [treatment] group and control group were drawn from different centres."

Why seek balance?

Two main reasons

1. Power considerations: with equal variance in each group, balanced samples gives the best allocation
2. Simplicity of interpretation and calculations: the interpretation of the F test in a linear regression is unambiguous

Finding power in balance

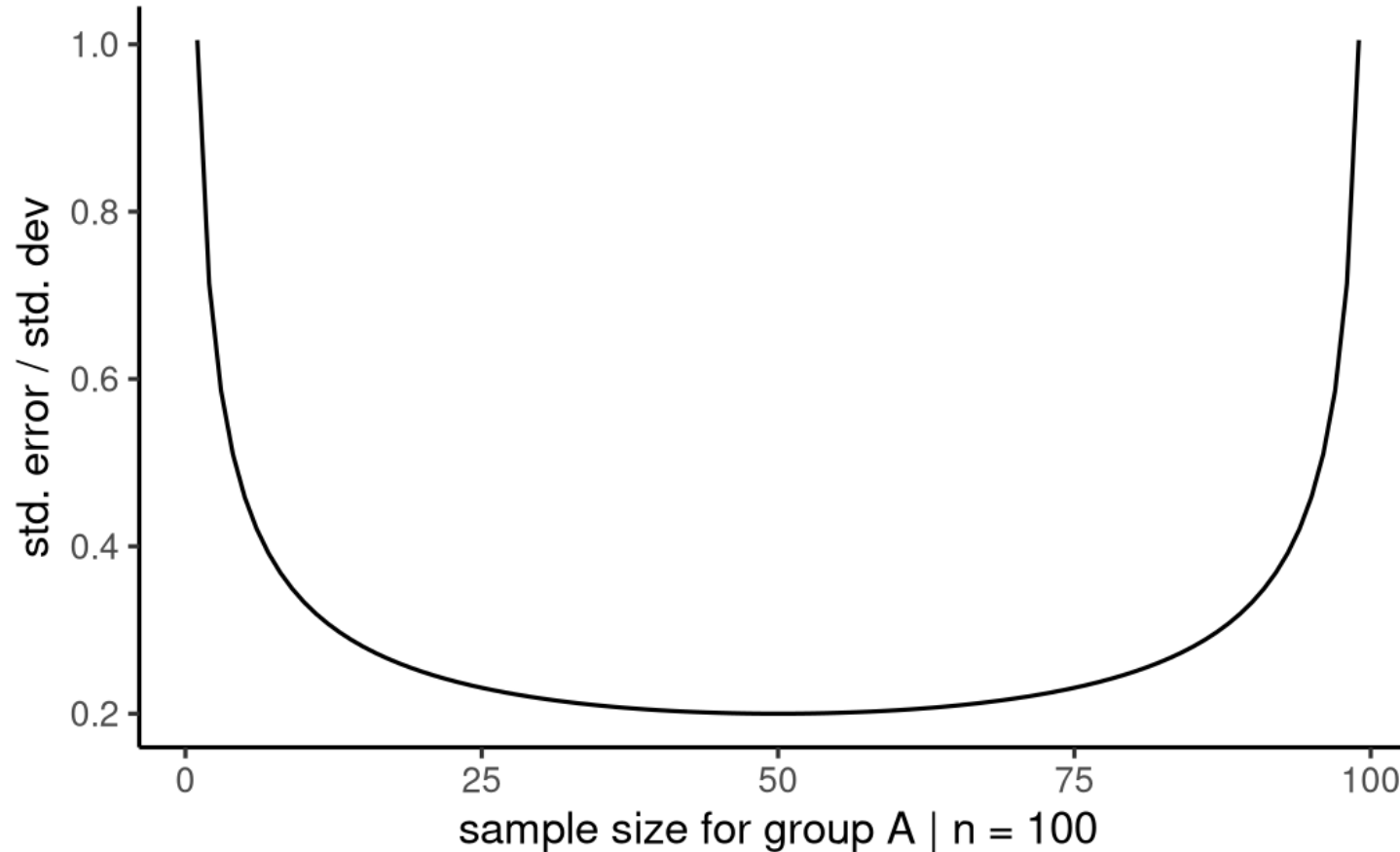
Consider a t-test for assessing the difference between treatments A and B with equal variability

$$t = \frac{\text{estimated difference}}{\text{estimated variability}} = \frac{(\hat{\mu}_A - \hat{\mu}_B) - 0}{\text{se}(\hat{\mu}_A - \hat{\mu}_B)}.$$

The standard error of the average difference is

$$\sqrt{\frac{\text{variance}_A}{\text{nb of obs. in } A} + \frac{\text{variance}_B}{\text{nb of obs. in } B}} = \sqrt{\frac{\sigma^2}{n_A} + \frac{\sigma^2}{n_B}}$$

Optimal allocation of resources



The allocation of $n = n_A + n_B$ units that minimizes the std error is $n_A = n_B = n/2$.

Example: tempting fate

We consider data from Multi Lab 2, a replication study that examined Risen and Gilovich (2008) who

explored the belief that tempting fate increases bad outcomes. They tested whether people judge the likelihood of a negative outcome to be higher when they have imagined themselves [...] tempting fate [...] (by not reading before class) or not [tempting] fate (by coming to class prepared). Participants then estimated how likely it was that [they] would be called on by the professor (scale from 1, not at all likely, to 10, extremely likely).

The replication data gathered in 37 different labs focuses on a 2 by 2 factorial design with gender (male vs female) and condition (prepared vs unprepared) administered to undergraduates.

Load data

Check balance

Marginal means

- We consider a 2 by 2 factorial design.
- The response is `likelihod`
- The experimental factors are `condition` and `gender`
- Two data sets: `RS_unb` for the full data, `RS_bal` for the artificially balanced one.

Load data

Check balance

Marginal means

```
summary_stats <-  
  RS_unb |>  
  group_by(condition) |>  
  summarize(nobs = n(),  
            mean = mean(likelihood))
```

Summary statistics

condition	nobs	mean
unprepared	2192	4.606
prepared	2241	4.060

Load data

Check balance

Marginal means

```
# Enforce sum-to-zero parametrization
options(contrasts = rep("contr.sum", 2))
# Anova is a linear model, fit using 'lm
# 'aov' only for *balanced data*
model <- lm(
  likelihood ~ gender * condition,
  data = RS_unb)
library(emmeans)
emm <- emmeans(model,
  specs = "condition")
```

Marginal means for condition

condition	emmean	SE
unprepared	4.504	0.0540
prepared	4.022	0.0535

Note unequal standard errors.

Explaining the discrepancies

Estimated marginal means are based on equiweighted groups:

$$\hat{\mu} = \frac{1}{4}(\hat{\mu}_{11} + \hat{\mu}_{12} + \hat{\mu}_{21} + \hat{\mu}_{22})$$

where $\hat{\mu}_{ij} = n_{ij}^{-1} \sum_{r=1}^{n_{ij}} y_{ijr}$.

The sample mean is the sum of observations divided by the sample size.

The two coincide when $n_{11} = \dots = n_{22}$.

Why equal weight?

- The ANOVA and contrast analyses, in the case of unequal sample sizes, are generally based on marginal means (same weight for each subgroup).
- This choice is justified because research questions generally concern comparisons of means across experimental groups.

Revisiting the F statistic

Statistical tests contrast competing **nested** models:

- an alternative (full) model
- a null model, which imposes restrictions (a simplification of the alternative models)

The numerator of the F -statistic compares the sum of square of a model with (given) main effect, etc. to a model without.

What is explained by condition?

Consider the 2×2 factorial design with factors A : gender and B : condition (prepared vs unprepared) without interaction.

What is the share of variability (sum of squares) explained by the experimental condition?

Comparing differences in sum of squares (1)

Consider a balanced sample

```
anova(lm(likelihood ~ 1, data = RS_bal),  
      lm(likelihood ~ condition, data = RS_bal))  
# When gender is present  
anova(lm(likelihood ~ gender, data = RS_bal),  
      lm(likelihood ~ gender + condition, data = RS_bal))
```

The difference in sum of squares is 141.86 in both cases.

Comparing differences in sum of squares (2)

Consider an unbalanced sample

```
anova(lm(likelihood ~ 1, data = RS_unb),  
      lm(likelihood ~ condition,  
          data = RS_unb))  
# When gender is present  
anova(lm(likelihood ~ gender, data = RS_unb),  
      lm(likelihood ~ gender + condition,  
          data = RS_unb))
```

The differences of sum of squares are respectively 330.95 and 332.34.

Orthogonality

Balanced designs yield orthogonal factors: the improvement in the goodness of fit (characterized by change in sum of squares) is the same regardless of other factors.

So effect of B and $B|A$ (read B given A) is the same.

- test for $B|A$ compares $SS(A, B) - SS(A)$
- for balanced design, $SS(A, B) = SS(A) + SS(B)$ (factorization).

We lose this property with unbalanced samples: there are distinct formulations of ANOVA.

Analysis of variance - Type I (sequential)

The default method in **R** with `anova` is the sequential decomposition: in the order of the variables A, B in the formula

- So F tests are for tests of effect of
 - A , based on $SS(A)$
 - $B | A$, based on $SS(A, B) - SS(A)$
 - $AB | A, B$ based on $SS(A, B, AB) - SS(A, B)$

Ordering matters

Since the order in which we list the variable is **arbitrary**, these F tests are not of interest.

Analysis of variance - Type II

Impact of

- $A | B$ based on $SS(A, B) - SS(B)$
- $B | A$ based on $SS(A, B) - SS(A)$
- $AB | A, B$ based on $SS(A, B, AB) - SS(A, B)$
- tests invalid if there is an interaction.
- In **R**, use `car::Anova(model, type = 2)`

Analysis of variance - Type III

Most commonly used approach

- Improvement due to $A | B, AB, B | A, AB$ and $AB | A, B$
- What is improved by adding a factor, interaction, etc. given the rest
- may require imposing equal mean for rows for $A | B, AB, etc.$
 - (**requires** sum-to-zero parametrization)
- valid in the presence of interaction
- but F -tests for main effects are not of interest
- In **R**, use `car::Anova(model, type = 3)`

ANOVA for unbalanced data

```
model <- lm(
  likelihood ~ condition * gender,
  data = RS_unb)
# Three distinct decompositions
anova(model) #type 1
car::Anova(model, type = 2)
car::Anova(model, type = 3)
```

ANOVA (type I)

	Df	Sum Sq	F value
gender	1	164.94	29.1
condition	1	332.34	58.7
gender:condition	1	36.55	6.5
Residuals	4429	25086.33	

ANOVA (type II)

	Df	Sum Sq	F value
gender	1	166.33	29.4
condition	1	332.34	58.7
gender:condition	1	36.55	6.5
Residuals	4429	25086.33	

ANOVA (type III)

	Df	Sum Sq	F value
gender	1	167.71	29.6
condition	1	227.88	40.2
gender:condition	1	36.55	6.5
Residuals	4429	25086.33	

ANOVA for balanced data

```
model2 <- lm(
  likelihood ~ condition * gender,
  data = RS_bal)
anova(model2) #type 1
car::Anova(model2, type = 2)
car::Anova(model2, type = 3)
# Same answer - orthogonal!
```

ANOVA (type I)

	Df	Sum Sq	F value
condition	1	141.86	24.1
gender	1	121.69	20.6
condition:gender	1	37.88	6.4
Residuals	2500	14733.84	

ANOVA (type II)

	Df	Sum Sq	F value
condition	1	141.86	24.1
gender	1	121.69	20.6
condition:gender	1	37.88	6.4
Residuals	2500	14733.84	

ANOVA (type III)

	Df	Sum Sq	F value
condition	1	141.86	24.1
gender	1	121.69	20.6
condition:gender	1	37.88	6.4
Residuals	2500	14733.84	

Recap

- If each observation has the same variability, a balanced sample maximizes power.
- Balanced designs have interesting properties:
 - estimated marginal means coincide with (sub)samples averages
 - the tests of effects are unambiguous
 - for unbalanced samples, we work with marginal means and type 3 ANOVA
 - if empty cells (no one assigned to a combination of treatment), cannot estimate corresponding coefficients (typically higher order interactions)

Practice

From the OSC psychology replication

People can be influenced by the prior consideration of a numerical anchor when forming numerical judgments. [...] The anchor provides an initial starting point from which estimates are adjusted, and a large body of research demonstrates that adjustment is usually insufficient, leading estimates to be biased towards the initial anchor.

Replication of Study 4a of Janiszewski & Uy (2008, Psychological Science) by J. Chandler

Multifactorial designs

Beyond two factors

We can consider multiple factors A, B, C, \dots with respectively n_a, n_b, n_c, \dots levels and with n_r replications for each.

The total number of treatment combinations is

$$n_a \times n_b \times n_c \times \dots$$

Curse of dimensionality

Full three-way ANOVA model

Each cell of the cube is allowed to have a different mean

$$Y_{ijk r} = \mu_{ijk} + \varepsilon_{ijk r}$$

response cell mean error

with $\varepsilon_{ijk r}$ are independent error term for

- row i
- column j
- depth k
- replication r

Parametrization of a three-way ANOVA model

With the **sum-to-zero** parametrization with factors A , B and C , write the response as

$$\begin{aligned} \underset{\text{theoretical average}}{E(Y_{ijk})} &= \underset{\text{global mean}}{\mu} \\ &+ \underset{\text{main effects}}{\alpha_i + \beta_j + \gamma_k} \\ &+ \underset{\text{two-way interactions}}{(\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk}} \\ &+ \underset{\text{three-way interaction}}{(\alpha\beta\gamma)_{ijk}} \end{aligned}$$



global mean, row, column and depth main effects



row/col, row/depth and col/depth interactions and three-way interaction.

Example of three-way design

Petty, Cacioppo and Heesacker (1981). Effects of rhetorical questions on persuasion: A cognitive response analysis. *Journal of Personality and Social Psychology*.

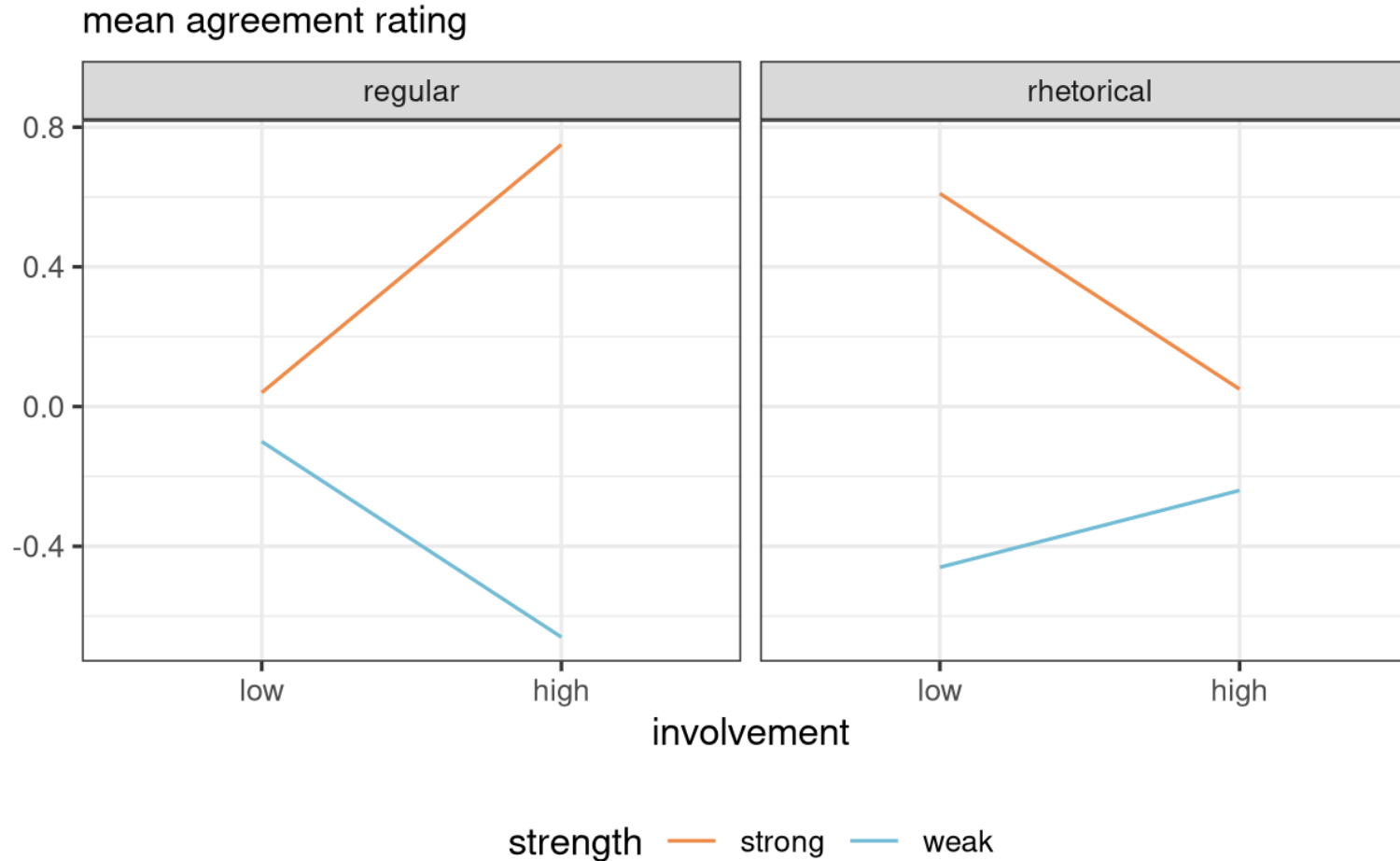
A $2 \times 2 \times 2$ factorial design with 8 treatments groups and $n = 160$ undergraduates.

Setup: should a comprehensive exam be administered to bachelor students in their final year?

- **Response** Likert scale on -5 (do not agree at all) to 5 (completely agree)
- **Factors**
- *A*: strength of the argument (*strong* or *weak*)
- *B*: involvement of students *low* (far away, in a long time) or *high* (next year, at their university)
- *C*: style of argument, either *regular form* or *rhetorical* (Don't you think?, ...)

Interaction plot

Interaction plot for a $2 \times 2 \times 2$ factorial design from Petty, Cacioppo and Heesacker (1981)



The microwave popcorn experiment

What is the best brand of microwave popcorn?

- **Factors**
- brand (two national, one local)
- power: 500W and 600W
- time: 4, 4.5 and 5 minutes
- **Response:** ~~weight, volume, number~~, percentage of popped kernels.
- Pilot study showed average of 70% overall popped kernels (10% standard dev), timing values reasonable
- Power calculation suggested at least $r = 4$ replicates, but researchers proceeded with $r = 2...$

ANOVA

QQ-plot

R code

Interaction plot

```
data(popcorn, package = 'hecedsm')  
# Fit model with three-way interaction  
model <- aov(percentage ~ brand*power*time,  
            data = popcorn)  
# ANOVA table - 'anova' is ONLY for balanced designs  
anova_table <- anova(model)  
# Quantile-quantile plot  
car::qqPlot(model)
```

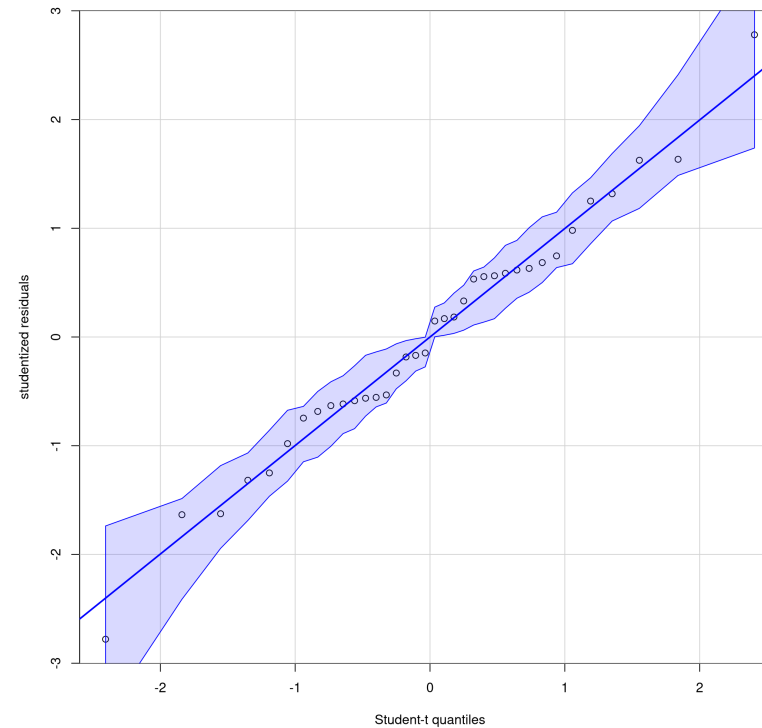
Model assumptions: plots and tests are meaningless with $(n_r=2)$ replications per group...

ANOVA

QQ-plot

R code

Interaction plot



All points fall roughly on a straight line.

ANOVA

QQ-plot

R code

Interaction plot

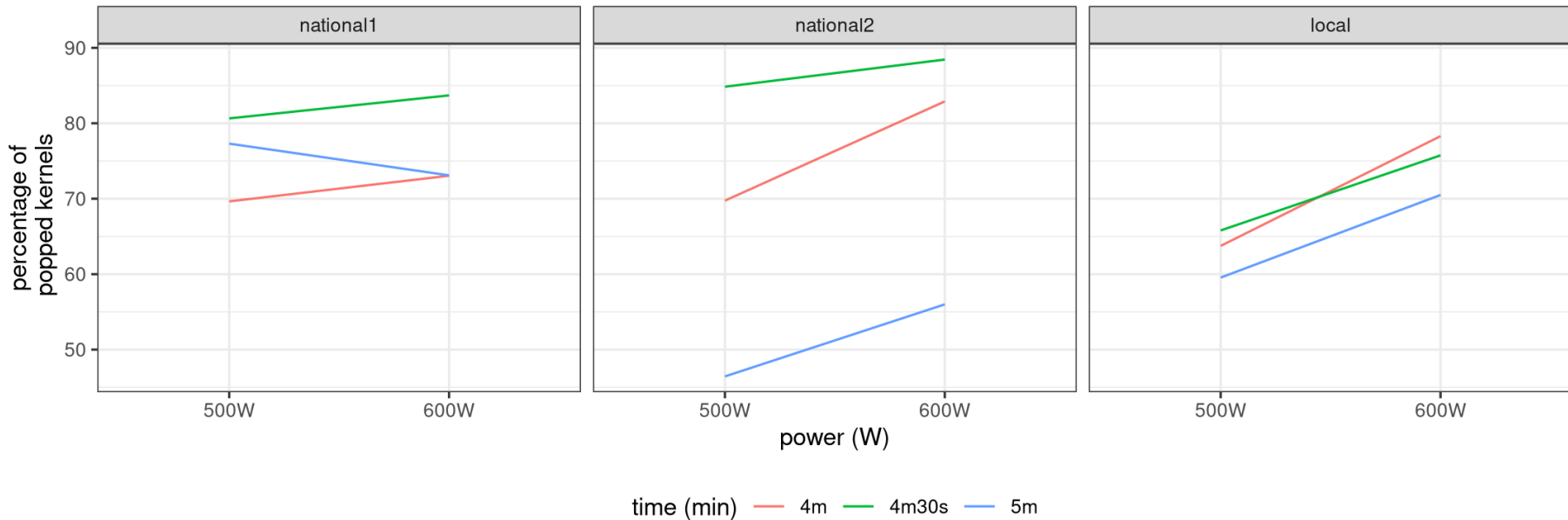
```
popcorn |>
  group_by(brand, time, power) |>
  summarize(meanp = mean(percentage)) |>
ggplot(mapping = aes(x = power,
                     y = meanp,
                     col = time,
                     group = time)) +
  geom_line() +
  facet_wrap(~brand)
```

ANOVA

QQ-plot

R code

Interaction plot



No evidence of three-way interaction (hard to tell with $r = 2$ replications).

Analysis of variance table for balanced designs

terms	degrees of freedom
<i>A</i>	$n_a - 1$
<i>B</i>	$n_b - 1$
<i>C</i>	$n_c - 1$
<i>AB</i>	$(n_a - 1)(n_b - 1)$
<i>AC</i>	$(n_a - 1)(n_c - 1)$
<i>BC</i>	$(n_b - 1)(n_c - 1)$
<i>ABC</i>	$(n_a - 1)(n_b - 1)(n_c - 1)$
residual	$n_a n_b n_c (R - 1)$
total	$n_a n_b n_c n_r - 1$

Analysis of variance table for microwave-popcorn

	Degrees of freedom	Sum of squares	Mean square	F statistic	p-value
brand	2	331.10	165.55	1.89	0.180
power	1	455.11	455.11	5.19	0.035
time	2	1554.58	777.29	8.87	0.002
brand:power	2	196.04	98.02	1.12	0.349
brand:time	4	1433.86	358.46	4.09	0.016
power:time	2	47.71	23.85	0.27	0.765
brand:power:time	4	47.33	11.83	0.13	0.967
Residuals	18	1577.87	87.66		

Omitting terms in a factorial design

The more levels and factors, the more parameters to estimate (and replications needed)

- Costly to get enough observations / power
- The assumption of normality becomes more critical when $r = 2!$

It may be useful not to consider some interactions if they are known or (strongly) suspected not to be present

- If important interactions are omitted from the model, biased estimates/output!

Guidelines for the interpretation of effects

Start with the most complicated term (top down)

- If the three-way interaction ABC is significant:
 - don't interpret main effects or two-way interactions!
 - comparison is done cell by cell within each level
- If the ABC term isn't significant:
 - can marginalize and interpret lower order terms
 - back to a series of two-way ANOVAs

What contrasts are of interest?

- Can view a three-way ANOVA as a series of one-way ANOVA or two-way ANOVAs...

Depending on the goal, could compare for variable A

- marginal contrast ψ_A (averaging over B and C)
- marginal conditional contrast for particular subgroup: ψ_A within c_1
- contrast involving two variables: ψ_{AB}
- contrast differences between treatment at $\psi_A \times B$, averaging over C .
- etc.

See helper code and chapter 22 of Keppel & Wickens (2004) for a detailed example.

Effects and contrasts for microwave-popcorn

Following preplanned comparisons

- Which combo (brand, power, time) gives highest popping rate? (pairwise comparisons of all combos)
- Best brand overall (marginal means marginalizing over power and time, assuming no interaction)
- Effect of time and power on percentage of popped kernels
- pairwise comparison of time \times power
- main effect of power
- main effect of time

Preplanned comparisons using emmeans

Let A =brand, B =power, C =time

Compare difference between percentage of popped kernels for 4.5 versus 5 minutes, for brands 1 and 2

$$\mathcal{H}_0 : (\mu_{1.2} - \mu_{1.3}) - (\mu_{2.2} - \mu_{2.3}) = 0$$

```
library(emmeans)
# marginal means
emm_popcorn_AC <- emmeans(model,
                           specs = c("brand", "time"))
contrast_list <-
  list(
    brand12with4.5vs5min = c(0, 0, 0, 1, -1, 0, -1, 1, 0))
contrast(emm_popcorn_AC, # marginal mean (no time)
         method = contrast_list) # list of contrasts
```

Preplanned comparisons

Compare all three times (4, 4.5 and 5 minutes)

At level 99% with Tukey's HSD method

- Careful! Potentially misleading because there is a `brand * time` interaction present.

```
# List of variables to keep go in `specs`: keep only time  
emm_popcorn_C <- emmeans(model, specs = "time")  
pairs(emm_popcorn_C,  
      adjust = "tukey",  
      level = 0.99,  
      infer = TRUE)
```