MONASH University

Visual Inference and Experimental Design

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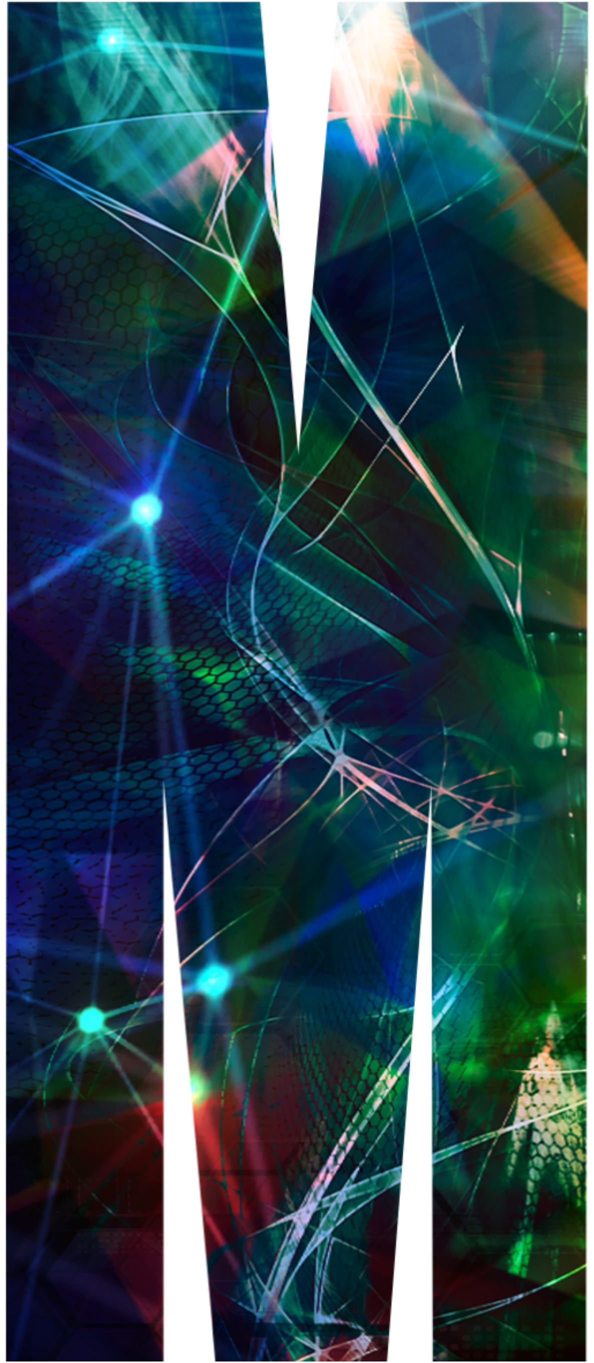

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Introduction to Visual Inference

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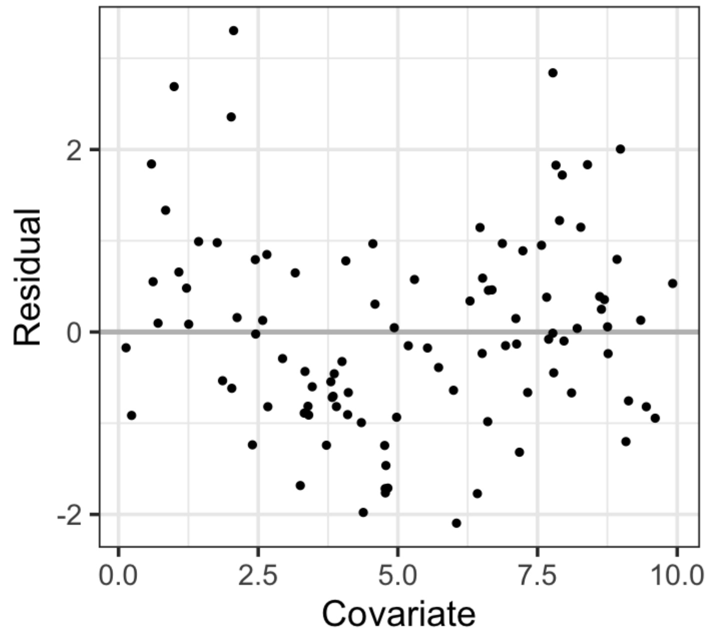
- Model diganostics are cruicial if inferences are to be made on the model
- A common model diagnostic is to look at residual plots and to search for any patterns
- If there is a pattern, it is indicative of a misspecified model
- **Do you see a pattern on the plot in the right?**

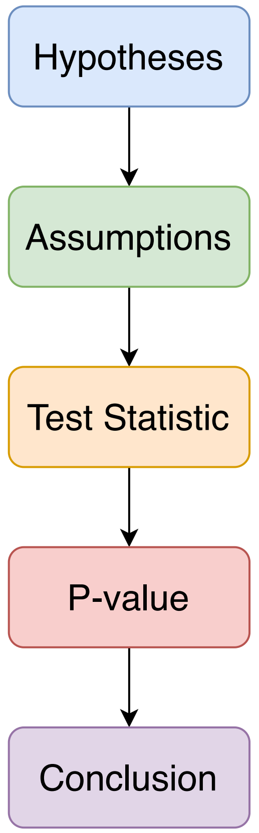
Residual plot



Assessing data plots Plots are also statistics

- In statistics, we are careful in assessing ***numerical* statistics** by taking into account its uncertainty
- BUT we are *quite informal in assessing plots*
- Data plots are also statistics
- ***Data plots ought to be treated with the same rigour as numerical statistics***

Frequentist framework



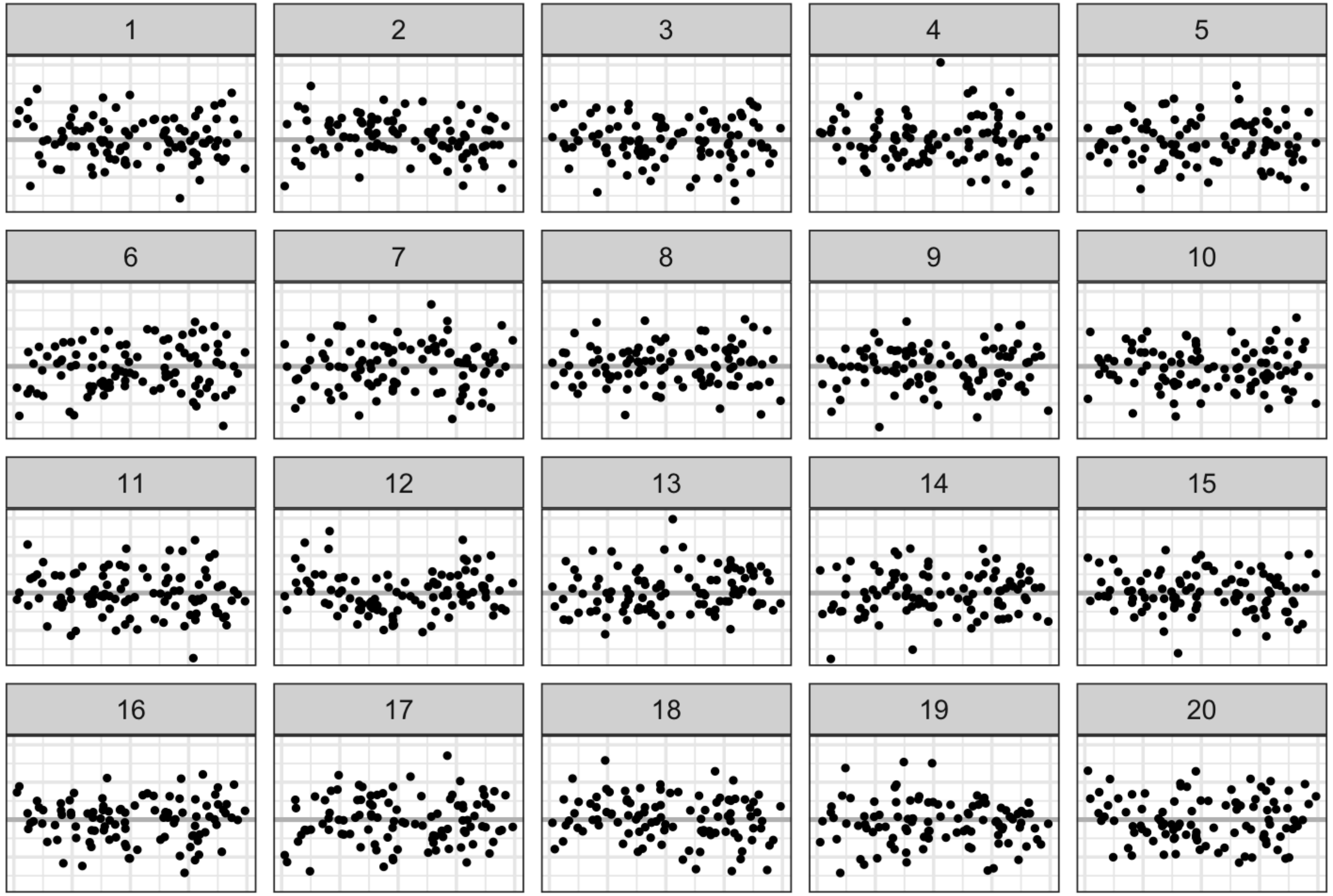
Assessing data plots Case study with residual plots Part 2

- **Hypotheses**: $H_0: e_i \sim NID(0, \sigma^2)$ vs. $H_1:$ not H_0
- **Assumptions**: σ^2 is known and is equal to maximum likelihood estimate
- **Test statistic**: Residual plot
- **P-value**: ???
- We can use the approach by Buja et al. (2009):
  1. Strip away context from data plot so there is no bias
  2. Generate the null data under H_0
  3. Create $k-1$ "null plots" by using visual encoding choice as data plot but using the null data
  4. Embed the data plot in a random position within the lineup of null plots
  5. Ask m observers which plot is the most different in the lineup and let X be the # of observers who detected the data plot
  6. Assuming observers are independent and equal visual ability, $X \sim B(m, 1/k)$.
  7. And the P-value (or "see-value") is given as $P(X \geq x)$.

Buja, Andreas, Dianne Cook, Heike Hofmann, Michael Lawrence, Eun-Kyung Lee, Deborah F. Swayne, and Hadley Wickham. 2009. "Statistical Inference for Exploratory Data Analysis and Model Diagnostics." Philosophical Transactions. Series A, Mathematical, Physical, and Engineering Sciences 367 (1906): 4361–83.

Assessing data plots An example lineup

Which plot looks the most different to you?



- The data generating process is

$$y = 1 + 2x + sin(x) + e$$

  where $e \sim N(0, 1)$
- The fitted model is

$$y = \beta_0 + \beta_1 x + e$$

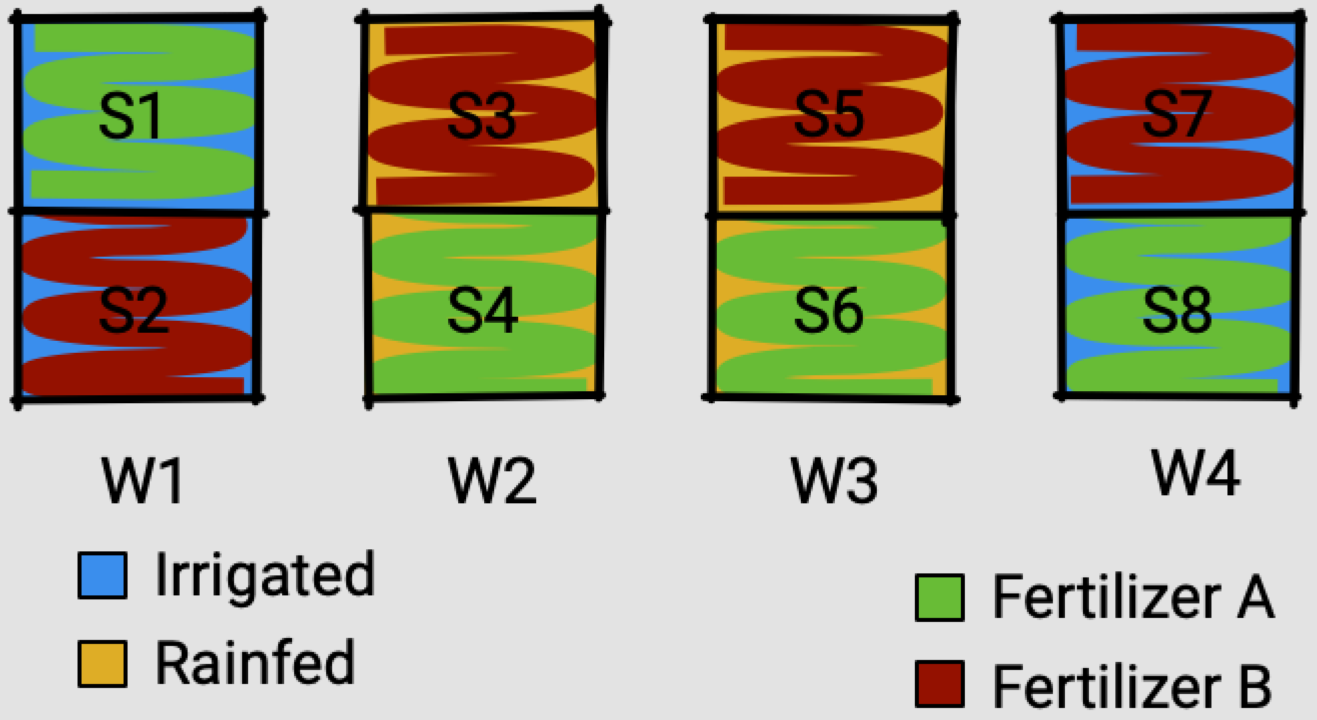
  where $e \sim N(0, \sigma^2)$
- The position of the data plot is 12

The Grammar of Experimental Designs

Classical split-plot design

CONTEXT

Study of **two irrigation methods** and **two fertilizer brands** on the yields of a crop.



The *grammar of experimental design* with edibble

```r
library(edibble)
start_design("split-plot")
```

MAIN POINTS

- Initialises an object with a special class
- It doesn't really contain much at this stage

OUTPUT

```
## split-plot
```

The *grammar of experimental design* with `edibble`

```r
library(edibble)
start_design("split-plot") %>%
  set_units(wholeplot = 4)
```

MAIN POINTS

- Now we specify that there are 4 wholeplots
- The object holds the *intermediate construct* of an experimental design

OUTPUT

```
## split-plot
## └─wholeplot (4 levels)
```

The *grammar of experimental design* with `edibble`

```r
library(edibble)
start_design("split-plot") %>%
  set_units(wholeplot = 4) %>%
  set_units(subplot = nested_in(wholeplot, 2))
```

MAIN POINTS

- Then we specify that there are 2 subplots for each wholeplot
- The name of the units are not restricted to "wholeplot" and "subplot"; the user can use *any* name

OUTPUT

```
## split-plot
## └─wholeplot (4 levels)
##   └─subplot (8 levels)
```

The *grammar of experimental design* with `edibble`

```r
library(edibble)
start_design("split-plot") %>%
  set_units(wholeplot = 4,
            subplot = nested_in(wholeplot, 2))
```

MAIN POINTS

- We can combine the "set_units"

OUTPUT

```
## split-plot
## └─wholeplot (4 levels)
##   └─subplot (8 levels)
```

The *grammar of experimental design* with `edibble`

```r
library(edibble)
start_design("split-plot") %>%
  set_units(wholeplot = 4,
            subplot = nested_in(wholeplot, 2)) %>%
  set_trts(water = c("irrigated", "rainfed"),
           fertilizer = c("A", "B"))
```

MAIN POINTS

- We now set the treatments
- There are 2 treatment factors (water and fertilizer) with 2 levels each

OUTPUT

```
## split-plot
## ├─wholeplot (4 levels)
## │  └─subplot (8 levels)
## ├─water (2 levels)
## └─fertilizer (2 levels)
```

The *grammar of experimental design* with `edibble`

```r
library(edibble)
start_design("split-plot") %>%
  set_trts(water = c("irrigated", "rainfed"),
           fertilizer = c("A", "B")) %>%
  set_units(wholeplot = 4,
            subplot = nested_in(wholeplot, 2))
```

MAIN POINTS

- You can set the treatment before the units

OUTPUT

```
## split-plot
## ├─water (2 levels)
## ├─fertilizer (2 levels)
## └─wholeplot (4 levels)
##   └─subplot (8 levels)
```

The *grammar of experimental design* with edibble

```r
library(edibble)
start_design("split-plot") %>%
  set_trts(water = c("irrigated", "rainfed")) %>%
  set_units(wholeplot = 4) %>%
  set_trts(fertilizer = c("A", "B")) %>%
  set_units(subplot = nested_in(wholeplot, 2))
```

MAIN POINTS

- Or mix it as you like (although subplot needs to appear after wholeplot)
- The edibble system tries to support a natural order to define the experimental structure

OUTPUT

```
## split-plot
## ├─water (2 levels)
## ├─wholeplot (4 levels)
## │  └─subplot (8 levels)
## └─fertilizer (2 levels)
```

The *grammar of experimental design* with `edibble`

```r
library(edibble)
start_design("split-plot") %>%
  set_units(wholeplot = 4,
            subplot = nested_in(wholeplot, 2)) %>%
  set_trts(water = c("irrigated", "rainfed"),
           fertilizer = c("A", "B")) %>%
  allocate_trts(water ~ wholeplot,
                fertilizer ~ subplot)
```

MAIN POINTS

- We then define the mapping of treatment to units
- The print output doesn't look any different

OUTPUT

```
## split-plot
## ├─wholeplot (4 levels)
## │ └─subplot (8 levels)
## ├─water (2 levels)
## └─fertilizer (2 levels)
```

The *grammar of experimental design* with `edibble`

```r
library(edibble)
start_design("split-plot") %>%
  set_units(wholeplot = 4,
            subplot = nested_in(wholeplot, 2)) %>%
  set_trts(water = c("irrigated", "rainfed"),
           fertilizer = c("A", "B")) %>%
  allocate_trts(water ~ wholeplot,
                fertilizer ~ subplot) %>%
  randomise_trts()
```

MAIN POINTS

- Then we randomise the treatment to units
- Again, the output doesn't look different

OUTPUT

```
## split-plot
## ├─wholeplot (4 levels)
## │ └─subplot (8 levels)
## ├─water (2 levels)
## └─fertilizer (2 levels)
```

The *grammar of experimental design* with edibble

```
library(edibble)
start_design("split-plot") %>%
  set_units(wholeplot = 4,
            subplot = nested_in(wholeplot, 2)) %>%
  set_trts(water = c("irrigated", "rainfed"),
           fertilizer = c("A", "B")) %>%
  allocate_trts(water ~ wholeplot,
                fertilizer ~ subplot) %>%
  randomise_trts() %>%
  serve_table()
```

MAIN POINTS

- Finally, we signal that we're done constructing the design
- The output gets converted to a data frame

OUTPUT

```
## # An edibble: 8 x 4
##    wholeplot   subplot     water f
##    <unit(4)> <unit(8)>   <trt(2)>
## 1 wholeplot1  subplot1 irrigated
## 2 wholeplot1  subplot2 irrigated
## 3 wholeplot2  subplot3 rainfed
## 4 wholeplot2  subplot4 rainfed
## 5 wholeplot3  subplot5 irrigated
## 6 wholeplot3  subplot6 irrigated
## 7 wholeplot4  subplot7 rainfed
## 8 wholeplot4  subplot8 rainfed
```

The *grammar of experimental design* with `edibble`

```r
library(edibble)
start_design("Modified allocation") %>%
  set_units(wholeplot = 4,
            subplot = nested_in(wholeplot, 2)) %>%
  set_trts(water = c("irrigated", "rainfed"),
           fertilizer = c("A", "B")) %>%
  allocate_trts(water:fertilizer ~ subplot) %>%
  randomise_trts() %>%
  serve_table()
```

MAIN POINTS

- Let's say we modify the treatment allocation
- The resulting design is what we call "randomised complete block design"

OUTPUT

```
## # An edibble: 8 x 4
##    wholeplot   subplot     water f
##    <unit(4)> <unit(8)>   <trt(2)>
## 1 wholeplot1  subplot1 irrigated
## 2 wholeplot1  subplot2 irrigated
## 3 wholeplot2  subplot3 rainfed
## 4 wholeplot2  subplot4 rainfed
## 5 wholeplot3  subplot5 rainfed
## 6 wholeplot3  subplot6 rainfed
## 7 wholeplot4  subplot7 irrigated
## 8 wholeplot4  subplot8 irrigated
```

Main contributions

MAIN POINTS

- The *grammar of experimental design* is a (programming language agnostic) framework that functionally maps the fundamental components of the experiment to an object oriented programming system to build and modify an experimental design
- The *edibble* R-package is an implementation of the grammar of experimental design in the R language
  </> https://github.com/emitanaka/edibble
- The approach is designed to be *human-friendly* and accommodate natural order of thinking for specifying experimental structure
- The approach also *promotes higher order thinking about experimental design*, e.g. the difference between a split-plot design and a randomised complete block design is pronounced in code
- Finally, the grammar makes each step modular... you can *easily extend* or *mix-and-match methods*

Summary

- **Adopting good computational practices** is important to me for transparency and reproducibility (e.g. version control, sharing code, open-source tools)
- **Visual inference** extends statistical inference to data visualisation
- I proactively work in **software development with human-centered design for the design of experiments**
- You can find these slides and *code* at:

emitanaka.org/slides-DARE-LOOP
https://github.com/emitanaka/slides-DARE-LOOP