



MONASH University

Advances in Artificial Intelligence for Data Visualization

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Table of contents

Copyright notice	iv
Abstract	v
Declaration	vi
Acknowledgements	ix
1 Introduction	1
1.1 Quarto	1
1.2 Data	1
1.3 Figures	2
1.4 Results from analyses	3
1.5 Tables	3
2 A Plot is Worth a Thousand Tests: Assessing Residual Diagnostics with the Lineup Protocol	4
2.1 Introduction	4
2.2 Background	6
2.3 Calculation of Statistical Significance and Test Power	11
2.4 Experimental Design	13
2.5 Results	18
3 Limitations and Practicality	27
4 Conclusions	29
5 Automated assessment of residual plots with computer vision models	31
5.1 Introduction	31
Bibliography	35
Appendices	40
A Appendix to “A Plot is Worth a Thousand Tests: Assessing Residual Diagnostics with the Lineup Protocol”	40
A.1 Additional Details of Testing Procedures	40
A.2 Additional Details of Experimental Setup	48
A.3 Analysis of Results Relative to Data Collection Process	57

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Abstract

The abstract should outline the main approach and findings of the thesis and must not be more than 500 words.

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The contribution in `?@sec-litreview` of this thesis was presented in the International Symposium on Nonsense held in Dublin, Ireland, in July 2022.

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This thesis is written using Quarto with `renv` (`renv?`) to create a reproducible environment. All materials (including the data sets and source files) required to reproduce this document can be found at the Github repository github.com/SusanSu/thesis.

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Thesis chap- ter	Publication title	Status	Nature and % of student contribution	Nature and % of coauthors' contribution	Coauthors are Monash students
2	The life cycle of Mongolian crickets	Submitted	Concept and data analysis, writing first draft: 60%	Shu Xu, input into manuscript: 25%; Eddie Betts, input into manuscript: 15%	Shu Xu: No; Eddie Betts: Yes

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Acknowledgements

I would like to thank my pet goldfish for ...

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project; non-routine technical work; analysis and interpretation of research data; drafting significant parts of the work or critically revising it so as to contribute to the interpretation.

Chapter 1

Introduction

This is where you introduce the main ideas of your thesis, and an overview of the context and background.

In a PhD, Chapter 2 would normally contain a literature review. Typically, Chapters 3–5 would contain your own contributions. Think of each of these as potential papers to be submitted to journals. Finally, Chapter 6 provides some concluding remarks, discussion, ideas for future research, and so on. Appendixes can contain additional material that don't fit into any chapters, but that you want to put on record. For example, additional tables, output, etc.

1.1 Quarto

In this template, the rest of the chapter shows how to use quarto. The big advantage of using quarto is that it allows you to include your R or Python code directly into your thesis, to ensure there are no errors in copying and pasting, and that everything is reproducible. It also helps you stay better organized.

For details on using Quarto, see <http://quarto.org>.

1.2 Data

Included in this template is a file called `sales.csv`. This contains quarterly data on Sales and Advertising budget for a small company over the period 1981–2005. It also contains the GDP (gross domestic product) over the same period. All series have been adjusted for inflation. We can load in this data set using the following code:

```

sales <- readr::read_csv(here::here("data/sales.csv")) |>
  rename(Quarter = `...1`) |>
  mutate(
    Quarter = as.Date(paste0("01-", Quarter), "%d-%b-%y"),
    Quarter = yearquarter(Quarter)
  ) |>
  as_tsibble(index = Quarter)

```

Any data you use in your thesis can go into the `data` directory. The data should be in exactly the format you obtained it. Do no editing or manipulation of the data prior to including it in the `data` directory. Any data munging should be scripted and form part of your thesis files (possibly hidden in the output).

1.3 Figures

Figure 1.1 shows time plots of the data we just loaded. Notice how figure captions and references work. Chunk names can be used as figure labels with `fig-` prefixed. Never manually type figure numbers, as they can change when you add or delete figures. This way, the figure numbering is always correct.

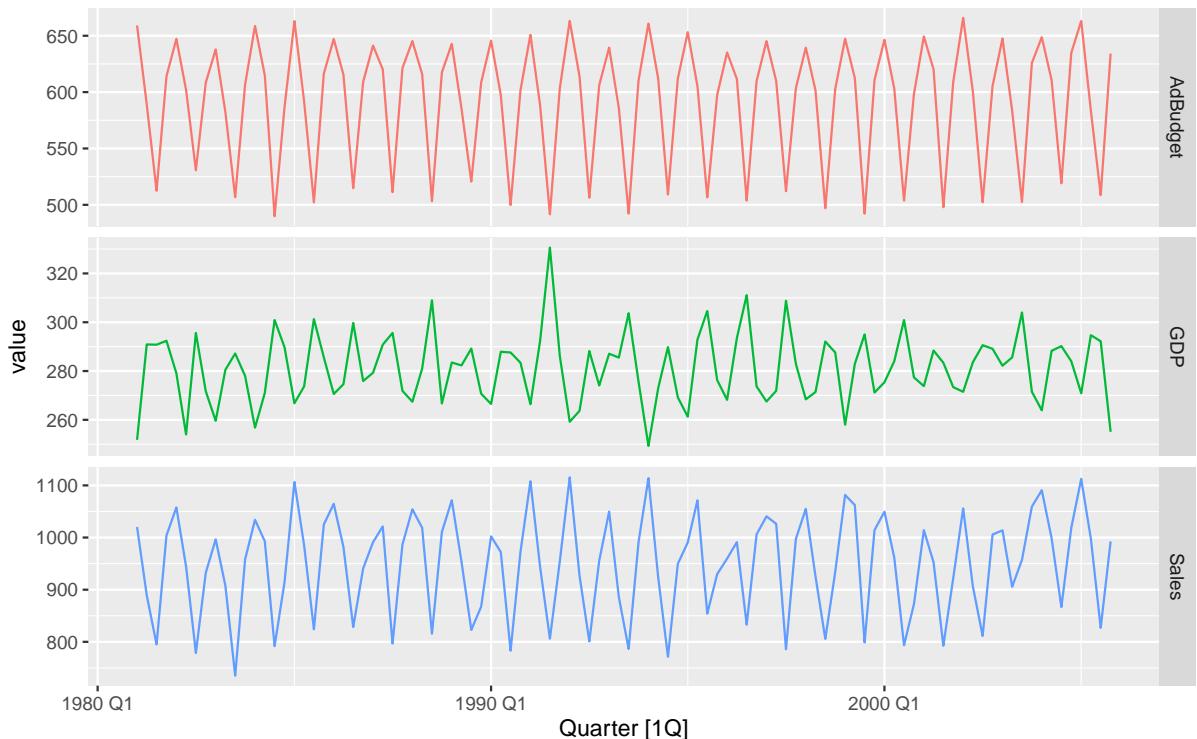


Figure 1.1: Quarterly sales, advertising and GDP data.

1.4 Results from analyses

We can fit a regression model to the sales data.

If y_t denotes the sales in quarter t , x_t denotes the corresponding advertising budget and z_t denotes the GDP, then the resulting model is:

$$y_t = \beta x_t + \gamma z_t + \varepsilon_t \quad (1.1)$$

where $\hat{\beta} = 1.85$, and $\hat{\gamma} = 1.04$. We can reference this equation using Equation 1.1.

1.5 Tables

We can also make a nice summary table of the coefficients, as shown in Table 1.1

Table 1.1: Coefficients from the fitted model.

Coefficient	Estimate	P value
(Intercept)	-438.98	0.02
GDP	1.04	0.02
AdBudget	1.85	0.00

Again, notice the use of labels and references to automatically generate table numbers.

Chapter 2

A Plot is Worth a Thousand Tests: Assessing Residual Diagnostics with the Lineup Protocol

Regression experts consistently recommend plotting residuals for model diagnosis, despite the availability of many numerical hypothesis test procedures designed to use residuals to assess problems with a model fit. Here we provide evidence for why this is good advice using data from a visual inference experiment. We show how conventional tests are too sensitive, which means that too often the conclusion would be that the model fit is inadequate. The experiment uses the lineup protocol which puts a residual plot in the context of null plots. This helps generate reliable and consistent reading of residual plots for better model diagnosis. It can also help in an obverse situation where a conventional test would fail to detect a problem with a model due to contaminated data. The lineup protocol also detects a range of departures from good residuals simultaneously. Supplemental materials for the article are available online.

2.1 Introduction

“Since all models are wrong the scientist must be alert to what is importantly wrong.”
(Box 1976)

Diagnosing a model is an important part of building an appropriate model. In linear regression analysis, studying the residuals from a model fit is a common diagnostic activity. Residuals summarise what is not captured by the model, and thus provide the capacity to identify what might be wrong.

We can assess residuals in multiple ways. To examine the univariate distribution, residuals may be plotted as a histogram or normal probability plot. Using the classical normal linear regression model as an example, if the distribution is symmetric and unimodal, we would consider it to be well-behaved. However, if the distribution is skewed, bimodal, multimodal, or contains outliers, there would be cause for concern. We can also inspect the distribution by conducting a goodness-of-fit test, such as the Shapiro-Wilk normality test (Shapiro and Wilk 1965).

Scatterplots of residuals against the fitted values, and each of the explanatory variables, are commonly used to scrutinize their relationships. If there are any visually discoverable associations, the model is potentially inadequate or incorrectly specified. We can also potentially discover patterns not directly connected to a linear model assumption from these residual plots, such as the discreteness or skewness of the fitted values, and outliers. To read residual plots, one looks for noticeable departures from the model such as non-linear pattern or heteroskedasticity. A non-linear pattern would suggest that the model needs to have some additional non-linear terms. Heteroskedasticity suggests that the error is dependent on the predictors, and hence violates the independence assumption. Statistical tests were developed to provide objective assessment, for example, of non-linear patterns (e.g. Ramsey 1969), and heteroskedasticity (e.g. Breusch and Pagan 1979).

The common wisdom of experts is that plotting the residuals is indispensable for diagnosing model fits (Cook and Weisberg 1982; Draper and Smith 1998; Montgomery et al. 1982). The lack of empirical evidence for the ubiquitous advice is *curious*, and is what this article tackles.

Additionally, relying solely on the subjective assessment of a single plot can be problematic. People will almost always see a pattern (see Kahneman 2011), so the question that really needs answering is whether any pattern perceived is consistent with randomness, or sampling variability, or noise. Correctly judging whether *no* pattern exists in a residual plot is a difficult task. Loy (2021) emphasizes that this is especially difficult to teach to new analysts and students, and advocates to the broader use of the lineup protocol (Buja et al. 2009a).

The lineup protocol places a data plot in a field of null plots, allowing for a comparison of patterns due purely by chance to what is perceived in the data plot. For residual analysis this is especially helpful for gauging whether there is *no* pattern. (Figure 2.1 shows an example of a lineup of residual plots.) In its strict use, one would insist that the data plot is not seen before seeing the lineup, so that the observer does not know which is the true plot. When used this way, it provides an objective test for data plots. Majumder et al. (2013a) validated that results from lineups assessed by human observers performed similarly to conventional tests. One would

not use a lineup when a conventional test exists and is adequate because it is more manually expensive to conduct. However, where no adequate conventional test exists, it is invaluable, as shown by Loy and Hofmann (2013). Here we use the lineup as a vehicle to rigorously explore why experts advise that residual plots are indispensable despite the prevalence of numerical tests.

The paper is structured as follows. Section 2.2 describes the background on the types of departures that one expects to detect, and outlines a formal statistical process for reading residual plots, called visual inference. Section 2.3 describes the calculation of the statistical significance and power of the test. Section 2.4 details the experimental design to compare the decisions made by formal hypothesis testing, and how humans would read diagnostic plots. The results are reported in Section 2.5. We conclude with a discussion of the presented work, and ideas for future directions.

2.2 Background

2.2.1 Departures from Good Residual Plots

Graphical summaries where residuals are plotted against fitted values, or other functions of the predictors (expected to be approximately orthogonal to the residuals) are considered to be the most important residual plots by Cook and Weisberg (1999). Figure 2.2A shows an example of an ideal residual plot where points are symmetrically distributed around the horizontal zero line (red), with no discernible patterns. There can be various types of departures from this ideal pattern. Non-linearity, heteroskedasticity and non-normality, shown in Figure 2.2B, Figure 2.2C, and Figure 2.2D, respectively, are three commonly checked departures.

Model misspecification occurs if functions of predictors that needed to accurately describe the relationship with the response are incorrectly specified. This includes instances where a higher-order polynomial term of a predictor is wrongfully omitted. Any non-linear pattern visible in the residual plot could be indicative of this problem. An example residual plot containing visual pattern of non-linearity is shown in Figure 2.2B. One can clearly observe the “S-shape” from the residual plot, which corresponds to the cubic term that should have been included in the model.

Heteroskedasticity refers to the presence of non-constant error variance in a regression model. It indicates that the distribution of residuals depends on the predictors, violating the independence assumption. This can be seen in a residual plot as an inconsistent spread of the residuals relative to the fitted values or predictors. An example is the “butterfly” shape shown in Figure 2.2C, or a “left-triangle” and “right-triangle” shape where the smallest variance occurs at one side of the

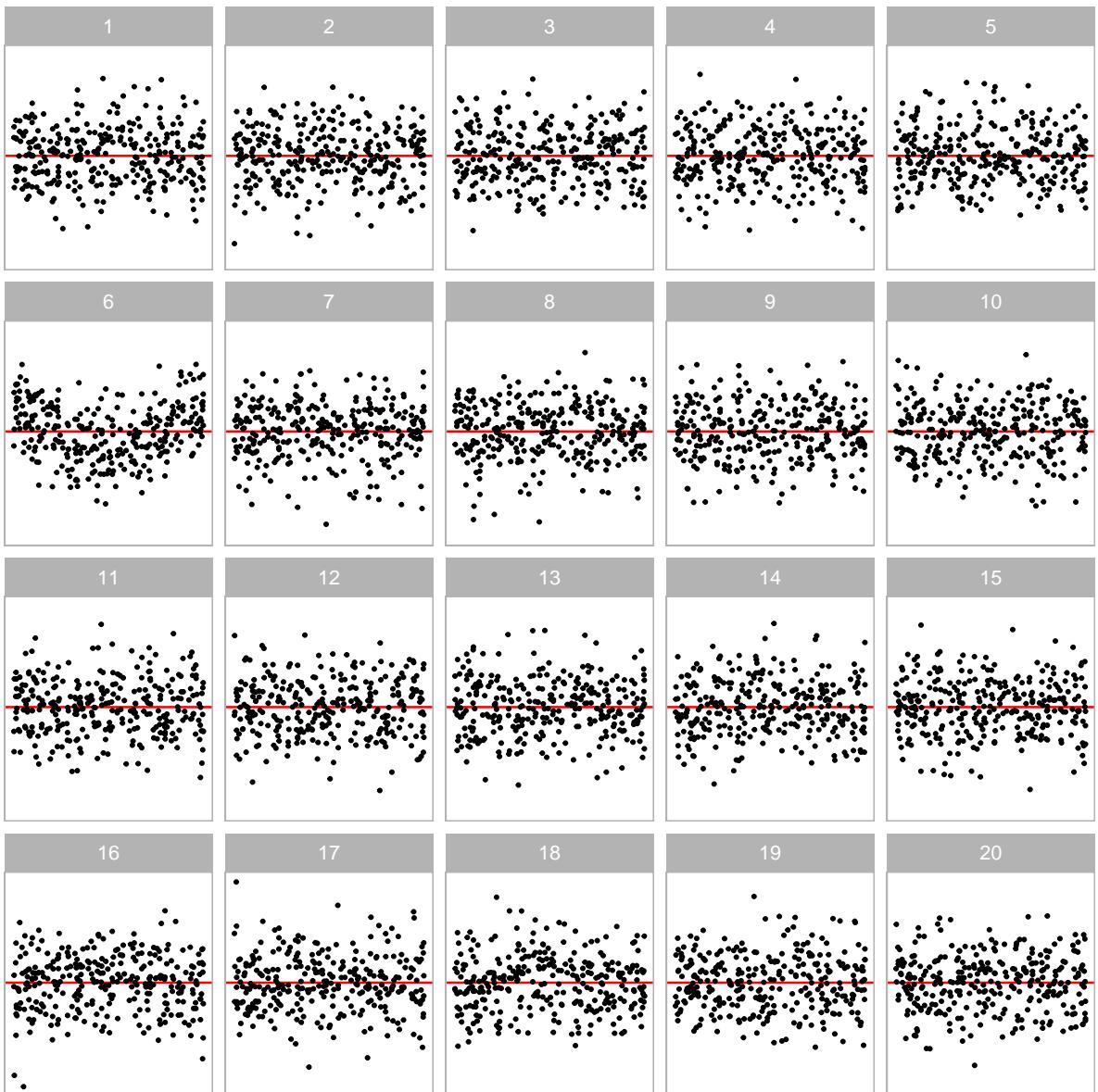


Figure 2.1: Visual testing is conducted using a lineup, as in the example here. The residual plot computed from the observed data is embedded among 19 null plots, where the residuals are simulated from a standard error model. Computing the p -value requires that the lineup be examined by a number of human judges, each asked to select the most different plot. A small p -value would result from a substantial number selecting the data plot (at position 6, exhibiting non-linearity).

horizontal axis.

Figure 2.2D shows a scatterplot where the residuals have a skewed distribution, as seen by the uneven vertical spread. Unlike non-linearity and heteroskedasticity, non-normality is usually detected with a different type of residual plot: a histogram or a normal probability plot. Because we focus on scatterplots, non-normality is not one of the departures examined in depth in this paper. (Loy et al. 2016 discuss related work on non-normality checking.)

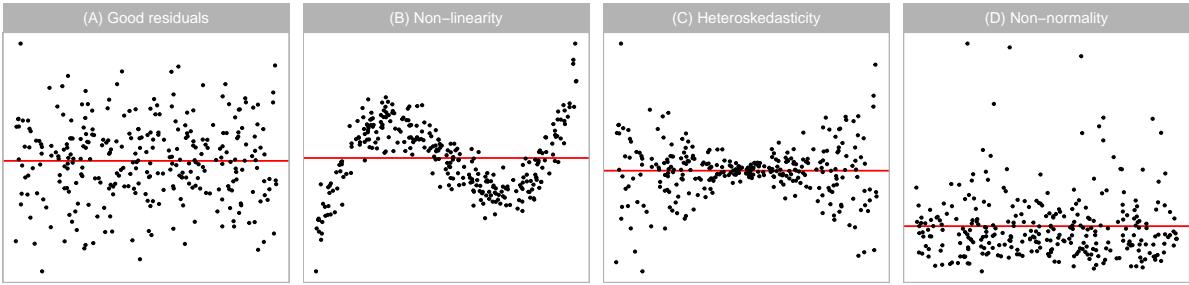


Figure 2.2: Example residual vs fitted value plots (horizontal line indicates 0): (A) classically good looking residuals, (B) non-linearity pattern indicates that the model has not captured a non-linear association, (C) heteroskedasticity indicating that variance around the fitted model is not uniform, and (D) non-normality where the residual distribution is not symmetric around 0. The latter pattern might best be assessed using a univariate plot of the residuals, but patterns B and C need to be assessed using a residual vs fitted value plot.

2.2.2 Conventionally Testing for Departures

Many different hypothesis tests are available to detect specific model defects. For example, the presence of heteroskedasticity can usually be tested by applying the White test (White 1980) or the Breusch-Pagan (BP) test (Breusch and Pagan 1979), which are both derived from the Lagrange multiplier test (Silvey 1959) principle that relies on the asymptotic properties of the null distribution. To test specific forms of non-linearity, one may apply the F-test as a model structural test to examine the significance of a specific polynomial and non-linear forms of the predictors, or the significance of proxy variables as in the Ramsey Regression Equation Specification Error Test (RESET) (Ramsey 1969). The Shapiro-Wilk (SW) normality test (Shapiro and Wilk 1965) is the most widely used test of non-normality included by many of the statistical software programs. The Jarque-Bera test (Jarque and Bera 1980) is also used to directly check whether the sample skewness and kurtosis match a normal distribution.

Table 2.1 displays the p -values from the RESET, BP and SW tests applied to the residual plots in Figure 2.2. The RESET test and BP test were computed using the `resettest` and `bptest` functions from the R package `lmtest`, respectively. The SW test was computed using the `shapiro.test` from the core R package `stats`.¹ The RESET test requires the selection of a power parameter. Ramsey (1969) recommends a power of four, which we adopted in our analysis.

For residual plots in Figure 2.2, we would expect the RESET test for non-linearity to reject residual plot B, the BP test for heteroskedasticity to reject the residual plot C, and the SW test for non-normality to reject residual plot D, which they all do and all tests also correctly fail to reject residual plot A. Interestingly, the BP and SW tests also reject the residual plots

¹Although we did not use it, it is useful to know that the R package `skedastic` (Farrar 2020) also contains a large collection of functions to test for heteroskedasticity.

Table 2.1: Statistical significance testing for departures from good residuals for plots in @fig-residual-plot-common-departures. Shown are the p -values calculated for the RESET, the BP and the SW tests. The good residual plot (A) is judged a good residual plot, as expected, by all tests. The non-linearity (B) is detected by all tests, as might be expected given the extreme structure.

Plot	Departures	RESET	BP	SW
A	None	0.779	0.133	0.728
B	Non-linearity	0.000	0.000	0.039
C	Heteroskedasticity	0.658	0.000	0.000
D	Non-normality	0.863	0.736	0.000

exhibiting structure that they were not designed for. Cook and Weisberg (1982) explain that most residual-based tests for a particular departure from the model assumptions are also sensitive to other types of departures. This could be considered a Type III error (Kimball 1957), where the null hypothesis of good residuals is correctly rejected but for the wrong reason. Also, some types of departure can have elements of other types of departure, for example, non-linearity can appear like heteroskedasticity. Additionally, other data problems such as outliers can trigger rejection (or not) of the null hypothesis (Cook and Weisberg 1999).

With large sample sizes, hypothesis tests may reject the null hypothesis when there is only a small effect. (A good discussion can be found in Kirk (1996).) While such rejections may be statistically correct, their sensitivity may render the results impractical. A key goal of residual plot diagnostics is to identify potential issues that could lead to incorrect conclusions or errors in subsequent analyses, but minor defects in the model are unlikely to have a significant impact and may be best disregarded for practical purposes. The experiment discussed in this paper specifically addresses this tension between statistical significance and practical significance.

2.2.3 Visual Test Procedure based on Lineups

The examination of data plots to infer signals or patterns (or lack thereof) is fraught with variation in the human ability to interpret and decode the information embedded in a graph (Cleveland and McGill 1984). In practice, over-interpretation of a single plot is common. For instance, Roy Chowdhury et al. (2015) described a published example where authors over-interpreted separation between gene groups from a two-dimensional projection of a linear discriminant analysis even when there were no differences in the expression levels between the gene groups.

One solution to over-interpretation is to examine the plot in the context of natural sampling variability assumed by the model, called the lineup protocol, as proposed in Buja et al. (2009b). Majumder et al. (2013b) showed that the lineup protocol is analogous to the null hypothesis significance testing framework. The protocol consists of m randomly placed plots, where one plot

is the data plot, and the remaining $m - 1$ plots, referred to as the *null plots*, are constructed using the same graphical procedure as the data plot but the data is replaced with null data that is generated in a manner consistent with the null hypothesis, H_0 . Then, an observer who has not seen the data plot is asked to point out the most different plot from the lineup. Under H_0 , it is expected that the data plot would have no distinguishable difference from the null plots, and the probability that the observer correctly picks the data plot is $1/m$. If one rejects H_0 as the observer correctly picks the data plot, then the Type I error of this test is $1/m$. This protocol requires a priori specification of H_0 (or at least a null data generating mechanism), much like the requirement of knowing the sampling distribution of the test statistic in null hypothesis significance testing framework.

Figure Figure 2.1 is an example of a lineup protocol. If the data plot at position 6 is identifiable, then it is evidence for the rejection of H_0 . In fact, the actual residual plot is obtained from a misspecified regression model with missing non-linear terms.

Data used in the $m - 1$ null plots needs to be simulated. In regression diagnostics, sampling data consistent with H_0 is equivalent to sampling data from the assumed model. As Buja et al. (2009b) suggested, H_0 is usually a composite hypothesis controlled by nuisance parameters. Since regression models can have various forms, there is no general solution to this problem, but it sometimes can be reduced to a so called “reference distribution” by applying one of the three methods: (i) sampling from a conditional distribution given a minimal sufficient statistic under H_0 , (ii) parametric bootstrap sampling with nuisance parameters estimated under H_0 , and (iii) Bayesian posterior predictive sampling. The conditional distribution given a minimal sufficient statistic is the best justified reference distribution among the three (Buja et al. 2009b). Under this method, the null residuals can essentially be simulated by independent drawing from a standard normal random distribution, then regressing the draws on the predictors, and then re-scaling it by the ratio of the residual sum of square in two regressions.

The effectiveness of lineup protocol for regression analysis has been validated by Majumder et al. (2013b) under relatively simple settings with up to two predictors. Their results suggest that visual tests are capable of testing the significance of a single predictor with a similar power to a t-test, though they express that in general it is unnecessary to use visual inference if there exists a corresponding conventional test, and they do not expect the visual test to perform equally well as the conventional test. In their third experiment, where the contamination of the data violate the assumptions of the conventional test, visual test outperforms the conventional test by a large margin. This supports the use of visual inference in situations where there are no

existing numerical testing procedures. Visual inference has also been integrated into diagnostics for hierarchical linear models where the lineup protocol is used to judge the assumptions of linearity, normality and constant error variance for both the level-1 and level-2 residuals (Loy and Hofmann 2013, 2014, 2015).

2.3 Calculation of Statistical Significance and Test Power

2.3.1 What is Being Tested?

In diagnosing a model fit using the residuals, we are generally interested in testing whether “*the regression model is correctly specified*” (H_0) against the broad alternative “*the regression model is misspecified*” (H_a). However, it is practically impossible to test this broad H_0 with conventional tests, because they need specific structure causing the departure to be quantifiable in order to be computable. For example, the RESET test for detecting non-linear departures is formulated by fitting $y = \tau_0 + \sum_{i=1}^p \tau_i x_p + \gamma_1 \hat{y}^2 + \gamma_2 \hat{y}^3 + \gamma_3 \hat{y}^4 + u$, $u \sim N(0, \sigma_u^2)$ in order to test $H_0 : \gamma_1 = \gamma_2 = \gamma_3 = 0$ against $H_a : \gamma_1 \neq 0$ or $\gamma_2 \neq 0$ or $\gamma_3 \neq 0$. Similarly, the BP test is designed to specifically test $H_0 : \text{error variances are all equal}$ ($\zeta_i = 0$ for $i = 1, \dots, p$) versus the alternative $H_a : \text{that the error variances are a multiplicative function of one or more variables}$ (at least one $\zeta_i \neq 0$) from $e^2 = \zeta_0 + \sum_{i=1}^p \zeta_i x_i + u$, $u \sim N(0, \sigma_u^2)$.

While a battery of conventional tests for different types of departures could be applied, this is intrinsic to the lineup protocol. The lineup protocol operates as an omnibus test, able to detect a range of departures from good residuals in a single application.

2.3.2 Statistical Significance

In hypothesis testing, a p -value is defined as the probability of observing test results at least as extreme as the observed result assuming H_0 is true. Conventional hypothesis tests usually have an existing method to derive or compute the p -value based on the null distribution. The method to estimate a p -value for a visual test essentially follows the process detailed by VanderPlas et al. (2021). Details are given in Appendix A.1.

2.3.3 Power of the Tests

The power of a model misspecification test is the probability that H_0 is rejected given the regression model is misspecified in a specific way. It is an important indicator when one is concerned about whether model assumptions have been violated. In practice, one might be more interested in knowing how much the residuals deviate from the model assumptions, and whether

this deviation is of practical significance.

The power of a conventional hypothesis test is affected by both the true parameters $\boldsymbol{\theta}$ and the sample size n . These two can be quantified in terms of effect size E to measure the strength of the residual departures from the model assumptions. Details about the calculation of effect size are provided in Section 2.4.2 after the introduction of the simulation model used in our experiment. The theoretical power of a test is sometimes not a trivial solution, but it can be estimated if the data generating process is known. We use a predefined model to generate a large set of simulated data under different effect sizes, and record if the conventional test rejects H_0 . The probability of the conventional test rejects H_0 is then fitted by a logistic regression formulated as

$$Pr(\text{reject } H_0|H_1, E) = \Lambda \left(\log \left(\frac{0.05}{0.95} \right) + \beta_1 E \right), \quad (2.1)$$

where $\Lambda(\cdot)$ is the standard logistic function given as $\Lambda(z) = \exp(z)(1 + \exp(z))^{-1}$. The effect size E is the only predictor and the intercept is fixed to $\log(0.05/0.95)$ so that $\hat{Pr}(\text{reject } H_0|H_1, E = 0) = 0.05$, the desired significance level.

The power of a visual test on the other hand, may additionally depend on the ability of the particular participant, as the skill of each individual may affect the number of observers who identify the data plot from the lineup (Majumder et al. 2013b). To address this issue, Majumder et al. (2013b) models the probability of participant j correctly picking the data plot from lineup l using a mixed-effect logistic regression, with participants treated as random effects. Then, the estimated power of a visual test evaluated by a single participant is the predicted value obtained from the mixed effects model. However, this mixed effects model does not work with scenario where participants are asked to select one or more most different plots. In this scenario, having the probability of a participant j correctly picking the data plot from a lineup l is insufficient to determine the power of a visual test because it does not provide information about the number of selections made by the participant for the calculation of the p -value. Therefore, we directly estimate the probability of a lineup being rejected by assuming that individual skill has negligible effect on the variation of the power. This assumption essentially averages out the subject ability and helps to simplify the model structure, thereby obviating a costly large-scale experiment to estimate complex covariance matrices. The same model given in Equation Equation 2.1 is applied to model the power of a visual test.

To study various factors contributing to the power of both tests, the same logistic regression

model is fit on different subsets of the collated data grouped by levels of factors. These include the distribution of the fitted values, type of the simulation model and the shape of the residual departures.

2.4 Experimental Design

Our experiment was conducted over three data collection periods to investigate the difference between conventional hypothesis testing and visual inference in the application of linear regression diagnostics. Two types of departures, non-linearity and heteroskedasticity, were collected during data collection periods I and II. The data collection period III was designed primarily to measure human responses to null lineups so that the visual p -values can be estimated. Additional lineups for both non-linearity and heteroskedasticity, using uniform fitted value distributions, were included for additional data, and to avoid participant frustration of too many difficult tasks.

During the experiment, every participant recruited from the Prolific crowd-sourcing platform (Palan and Schitter 2018) was presented with a block of 20 lineups. A lineup consisted of a randomly placed data plot and 19 null plots, which were all residual plots drawn with raw residuals on the y-axis and fitted values on the x-axis. An additional horizontal red line was added at $y = 0$ as a visual reference. The data in the data plot was simulated from one of two models described in Section 2.4.1, while the data of the remaining 19 null plots were generated by the residual rotation technique discussed in Section 2.2.3.

In each lineup evaluation, the participant was asked to select one or more plots that are most different from others, provide a reason for their selections, and evaluate how different they think the selected plots are from others. If there is no noticeable difference between plots in a lineup, participants had the option to select zero plots without the need to provide a reason. During the process of recording the responses, a zero selection was considered to be equivalent to selecting all 20 plots. No participant was shown the same lineup twice. Information about preferred pronouns, age group, education, and previous experience in visual experiments were also collected. A participant’s submission was only included in the analysis if the data plot is identified for at least one attention check.

Overall, we collected 7974 evaluations on 1152 unique lineups performed by 443 participants. A summary of the factors used in the experiment can be found in Table 2.2. There were four levels of the non-linear structure, and three levels of heteroskedastic structure. The signal strength was controlled by error variance (σ) for the non-linear pattern, and by a ratio (b) parameter for the heteroskedasticity. Additionally, three levels of sample size (n) and four different fitted value

Table 2.2: Levels of the factors used in data collection periods I, II, and III.

Non-linearity		Heteroskedasticity		Common	
Poly Order (j)	SD (σ)	Shape (a)	Ratio (b)	Size (n)	Distribution of the fitted values
2	0.25	-1	0.25	50	Uniform
3	1.00	0	1.00	100	Normal
6	2.00	1	4.00	300	Skewed
18	4.00		16.00		Discrete
			64.00		

distributions were incorporated.

2.4.1 Simulating Departures from Good Residuals

2.4.1.1 Non-linearity and Heteroskedasticity

Data collection period I was designed to study the ability of participants to detect non-linearity departures from residual plots. The non-linearity departure was constructed by omitting a j th order Hermite polynomial (Hermite 1864; originally by Laplace 1820) term of the predictor from the simple linear regression equation. Four different values of $j = 2, 3, 6, 18$ were chosen so that distinct shapes of non-linearity were included in the residual plots. These include “U”, “S”, “M” and “triple-U” shape as shown in Figure 2.3. A greater value of j will result in a curve with more turning points. It is expected that the “U” shape will be the easiest to detect, and as the shape gets more complex it will be harder to perceive in a scatterplot, particularly when there is noise. Figure 2.4 shows the “U” shape for different amounts of noise (σ).

Data collection period II was similar to period I but focuses on heteroskedasticity departures. We generated the heteroskedasticity departures by setting the variance-covariance matrix of the error term as a function of the predictor, but fitted the data with the simple linear regression model, intentionally violated the constant variance assumption. Visual patterns of heteroskedasticity are simulated using three different shapes ($a = -1, 0, 1$) including “left-triangle”, “butterfly” and “right-triangle” shapes as displayed in Figure 2.5. Figure 2.6 shows the butterfly shape as the ratio parameter (b) is changed. More details about the simulation process are provided in Appendix A.2.

2.4.1.2 Factors Common to both Data Collection Periods

Fitted values are a function of the independent variables (or predictors), and the distribution of the observed values affects the distribution of the fitted values. Ideally, we would want the fitted values to have a uniform coverage across the range of observed values or have a

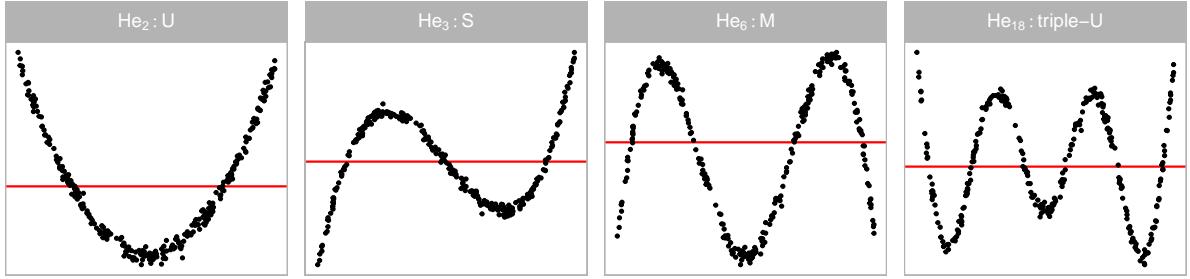


Figure 2.3: Polynomial forms generated for the residual plots used to assess detecting non-linearity. The four shapes are generated by varying the order of polynomial given by j in $He_j(\cdot)$.

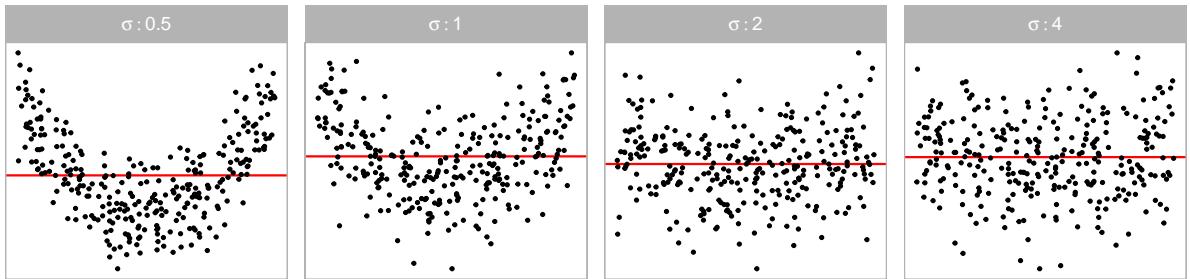


Figure 2.4: Examining the effect of σ on the signal strength in the non-linearity detection, for $n = 300$, uniform fitted value distribution and the “U” shape. As σ increases the signal strength decreases, to the point that the “U” is almost unrecognisable when $\sigma = 4$.

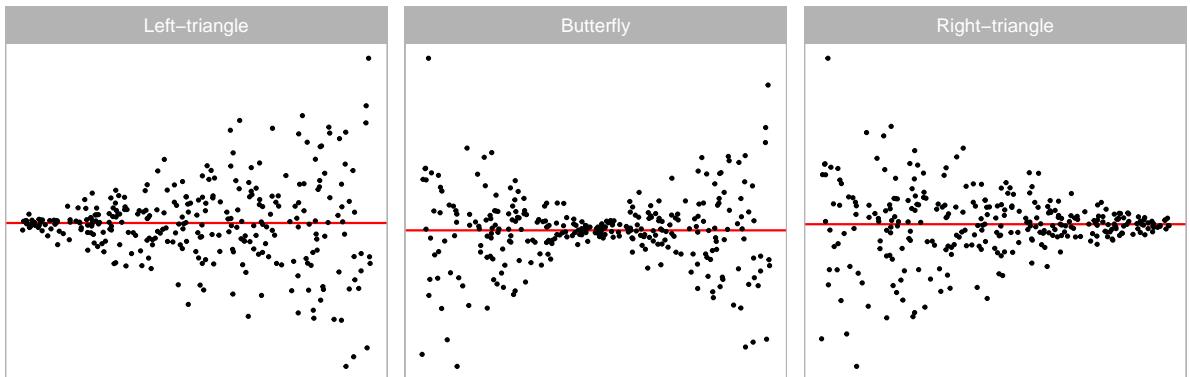


Figure 2.5: Heteroskedasticity forms used in the experiment. Three different shapes ($a = -1, 0, 1$) are used in the experiment to create “left-triangle”, “butterfly” and “right-triangle” shapes, respectively.

uniform distribution across all of the predictors. This is not always present in the collected data. Sometimes the fitted values are discrete because one or more predictors were measured discretely. It is also common to see a skewed distribution of fitted values if one or more of the predictors has a skewed distribution. This latter problem is usually corrected before modelling, using a variable transformation. Our simulation assess this by using four different distributions to represent fitted values, constructed by different sampling of the predictor, including $U(-1, 1)$ (uniform), $N(0, 0.3^2)$ (normal), $\text{lognormal}(0, 0.6^2)/3$ (skewed) and $U\{-1, 1\}$ (discrete).

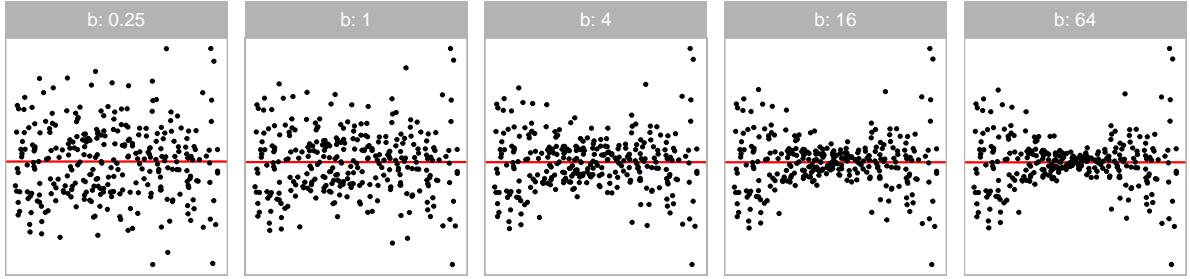


Figure 2.6: Five different values of b are used in heteroskedasticity simulation to control the strength of the signal. Larger values of b yield a bigger difference in variation, and thus stronger heteroskedasticity signal.

Figure 2.7 shows the non-linear pattern, a “U” shape, with the different fitted value distributions. We would expect that structure in residual plots would be easier to perceive when the fitted values are uniformly distributed.

Three different sample sizes were used in our experiment: $n = 50, 100, 300$. Figure 2.8 shows the non-linear “S” shape for different sample sizes. We expect signal strength to decline in the simulated data plots with smaller n . We chose 300 as the upper limit, because it is typically enough for structure to be visible in a scatterplot reliably. Beyond 300, the scatterplot should probably be used with transparency or replaced with a density or binned plot as scatterplots suffer from over-plotting.

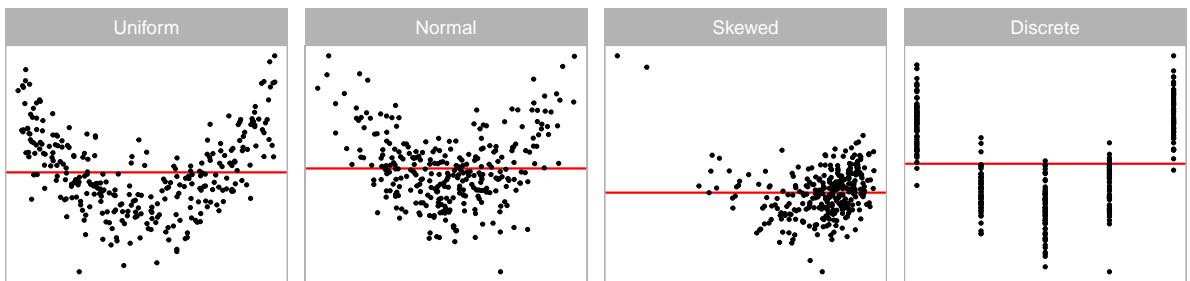


Figure 2.7: Variations in fitted values, that might affect perception of residual plots. Four different distributions are used.

2.4.2 Effect Size

The lineups are allocated to participants in a manner that uniformly covers the combination of experimental factors in Table 2.2. In addition, we use effect size to measure the signal strength, which helps in assigning a set of lineups with a range of difficulties to each participant.

Effect size in statistics measures the strength of the signal relative to the noise. It is surprisingly difficult to quantify, even for simulated data as used in this experiment.

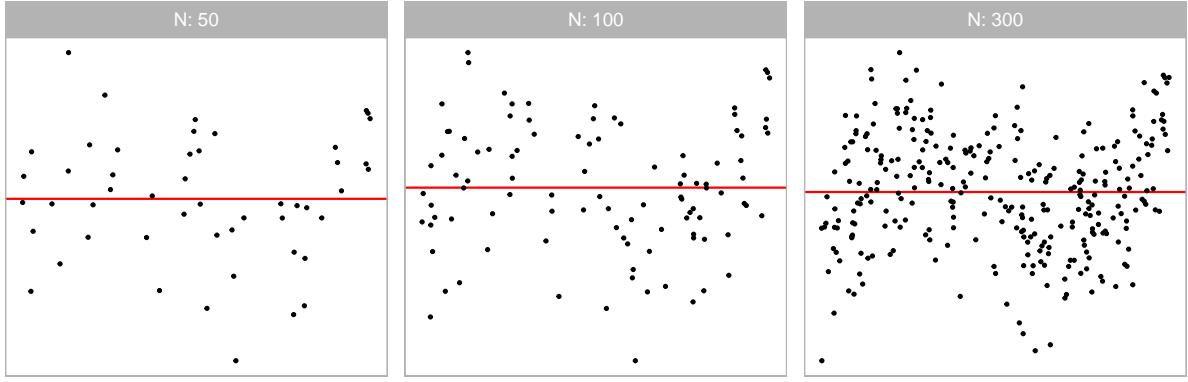


Figure 2.8: Examining the effect of signal strength for the three different values of n used in the experiment, for non-linear structure with fixed $\sigma = 1.5$, uniform fitted value distribution, and “S” shape. For these factor levels, only when $n = 300$ is the “S” shape clearly visible.

For the non-linearity model, the key items defining effect size are sample size (n) and the noise level (σ^2), and so effect size would be roughly calculated as \sqrt{n}/σ . Increasing sample size tends to boost the effect size, while heightened noise diminishes it. However, it is not clear how the additional parameter for the model polynomial order, j , should be incorporated. Intuitively, the large j means more complex pattern, which likely means effect size would decrease. Similarly, in the heteroskedasticity model, effect size relies on sample size (n) and the ratio of the largest to smallest variance, b . Larger values of both would produce higher effect size, but the role of the additional shape parameter, a , in this context is unclear.

For the purposes of our calculations we have chosen to use an approach based on Kullback-Leibler divergence (Kullback and Leibler 1951). This formulation defines effect size to be

$$E = \frac{1}{2} \left(\log \frac{|\text{diag}(\mathbf{R}\mathbf{V}\mathbf{R}')|}{|\text{diag}(\mathbf{R}\sigma^2)|} - n + \text{tr}(\text{diag}(\mathbf{R}\mathbf{V}\mathbf{R}')^{-1} \text{diag}(\mathbf{R}\sigma^2)) + \boldsymbol{\mu}'_z (\mathbf{R}\mathbf{V}\mathbf{R}')^{-1} \boldsymbol{\mu}_z \right),$$

where $\text{diag}(\cdot)$ is the diagonal matrix constructed from the diagonal elements of a matrix, \mathbf{X} is the design matrix, \mathbf{V} is the actual covariance matrix of the error term, $\mathbf{R} = \mathbf{I}_n - \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'$ is the residual operator, $\boldsymbol{\mu}_z = \mathbf{R}\mathbf{Z}\boldsymbol{\beta}_z$ is the expected values of residuals where \mathbf{Z} contains any higher order terms of \mathbf{X} left out of the regression equation, $\boldsymbol{\beta}_z$ contains the corresponding coefficients, and $\sigma^2\mathbf{I}_n$ is the assumed covariance matrix of the error term when H_0 is true. More details about the effect size derivation are provided in Appendix A.1.

2.5 Results

Data collection used a total of 1152 lineups, and resulted in a total of 7974 evaluations from 443 participants. Roughly half corresponded to the two models, non-linearity and heteroskedasticity, and the three collection periods had similar numbers of evaluations. Each participant received two of the 24 attention check lineups which were used to filter results of participants who were clearly not making an honest effort (only 11 of 454). To estimate α for calculating statistical significance (see Appendix A.1) there were 720 evaluations of 36 null lineups. Neither the attention checks nor null lineups were used in the subsequent analysis. The de-identified data, `vi_survey`, is made available in the R package, `visage`.

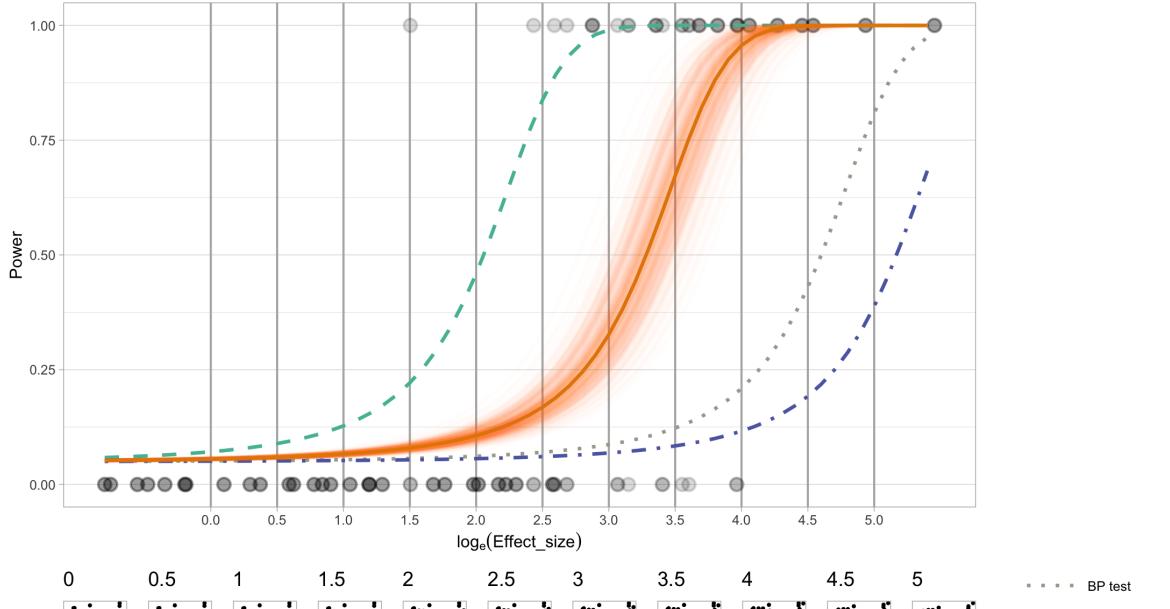
The data was collected on lineups constructed from four different fitted value distributions that stem from the corresponding predictor distribution: uniform, normal, skewed and discrete. Henceforth, we refer to these four different fitted value distributions with respect to their predictor distribution. More data was collected on the uniform distribution (each evaluated by 11 participants) than the others (each evaluated by 5 participants). The analysis in Section 2.5.1–Section 2.5.4 uses only results from lineups with uniform distribution, for a total 3069 lineup evaluations. This allows us to compare the conventional and visual test performance in an optimal scenario. Section 2.5.5 examines how the results may be affected if the fitted value distribution was different.

2.5.1 Power Comparison of the Tests

Figure 2.9 present the power curves of various tests plotted against the effect size in the residuals for non-linearity and heteroskedasticity. In each case the power of visual test is calculated for multiple bootstrap samples leading to the many (solid orange) curves. The effect size was computed at a 5% significance level and plotted on a natural logarithmic scale. To facilitate visual calibration of effect size values with the corresponding diagnostic plots, a sequence of example residual plots with increasing effect sizes is provided at the bottom of these figures. These plots serve as a visual aid to help readers understand how different effect size values translate to changes in the diagnostic plots. The horizontal lines of dots at 0 and 1 represent the non-rejection or rejection decisions made by visual tests for each lineup.

Figure 2.9A compares the power for the different tests for non-linear structure in the residuals. The test with the uniformly higher power is the RESET test, one that specifically tests for non-linearity. Note that the BP and SW tests have much lower power, which is expected because they are not designed to detect non-linearity. The bootstrapped power curves for the visual test

(A) Non-linearity



(B) Heteroskedasticity

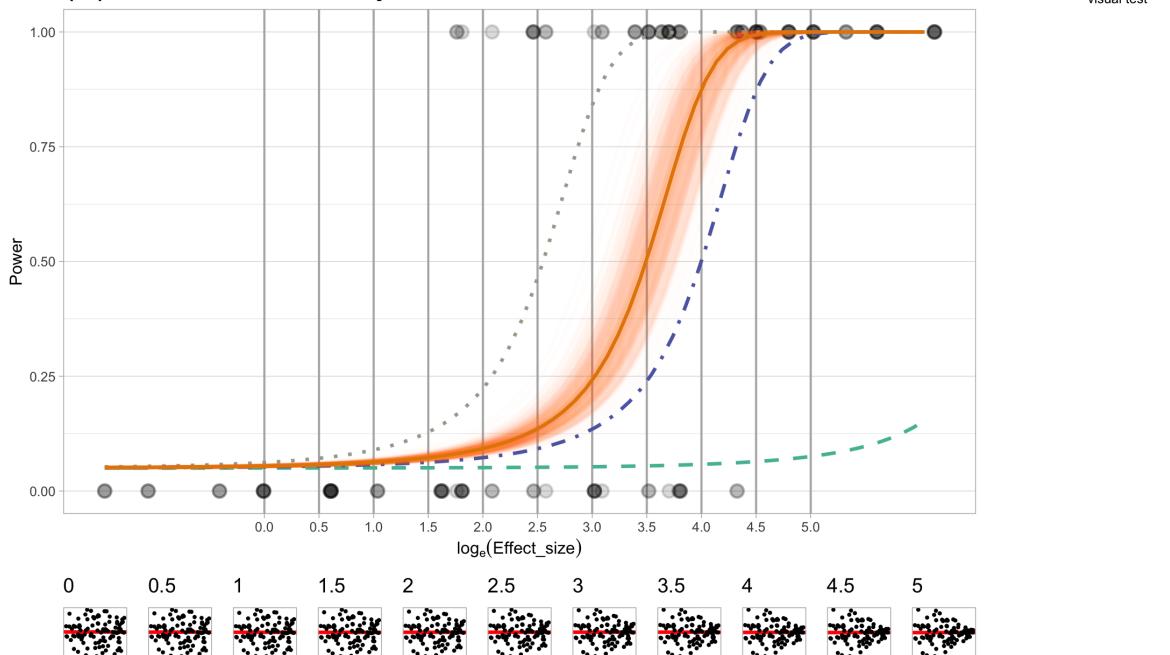


Figure 2.9: Comparison of power between different tests for (A) non-linear and (B) heteroskedasticity patterns (uniform fitted values only). Main plot shows the power curves, with dots indicating non-reject and reject in visual testing of lineups. The multiple lines for the visual test arise from estimating the power on many bootstrap samples. The row of scatterplots at the bottom are examples of residual plots corresponding to the specific effect sizes marked by vertical lines in the main plot.

are effectively a right shift from that of the RESET test. This means that the RESET test will reject at a lower effect size (less structure) than the visual test, but otherwise the performance will be similar. In other words, the RESET test is more sensitive than the visual test. This is not necessarily a good feature for the purposes of diagnosing model defects: if we scan the residual plot examples at the bottom, we might argue that the non-linearity is not sufficiently problematic until an effect size of around 3 or 3.5. The RESET test would reject closer to an effect size of 2, but the visual test would reject closer to 3.25, for a significance level of 0.05. The visual test matches the robustness of the model to (minor) violations of assumptions much better.

For the heteroskedasticity pattern, the power of BP test, designed for detecting heteroskedasticity, is uniformly higher than the other tests. The visual test power curve shifts to the right. This shows a similar story to the power curves for non-linearity pattern: the conventional test is more sensitive than the visual test. From the example residual plots at the bottom we might argue that the heteroskedasticity becomes noticeably visible around an effect size of 3 or 3.5. However the BP test would reject at around effect size 2.5. Interestingly, the power curve for the SW test (for non-normality) is only slightly different to that of the visual test, suggesting that it performs reasonably well for detecting heteroskedasticity, too. The power curve for the BP test suggests it is not useful for detecting heteroskedasticity, as expected.

Overall, the results show that the conventional tests are more sensitive than the visual test. The conventional tests do have higher power for the patterns they are designed to detect, but they typically fail to detect other patterns unless those patterns are particularly strong. The visual test does not require specifying the pattern ahead of time, relying purely on whether the observed residual plot is detectably different from “good” residual plots. They will perform equally well regardless of the type of model defect. This aligns with the advice of experts on residual analysis, who consider residual plot analysis to be an indispensable tool for diagnosing model problems. What we gain from using a visual test for this purpose is the removal of any subjective arguments about whether a pattern is visible or not. The lineup protocol provides the calibration for detecting patterns: if the pattern in the data plot cannot be distinguished from the patterns in good residual plots, then no discernible problem with the model exists.

2.5.2 Comparison of Test Decisions Based on p -values

The power comparison demonstrates that the appropriate conventional tests will reject more aggressively than visual tests, but we do not know how the decisions for each lineup would agree or disagree. Here we compare the reject or fail to reject decisions of these tests, across all the

lineups. Figure 2.10 shows the agreement of the conventional and visual tests using a mosaic plot for both non-linearity patterns and heteroskedasticity patterns. For both patterns the lineups resulting in a rejection by the visual test are *all* also rejected by the conventional test, except for one from the heteroskedasticity model. This reflects exactly the story from the previous section, that the conventional tests reject more aggressively than the visual test.

For non-linearity lineups, conventional tests and visual tests reject 69% and 32% of the time, respectively. Of the lineups rejected by the conventional test, 46% are rejected by the visual test, that is, approximately half as many as the conventional test. There are no lineups that are rejected by the visual test but not by the conventional test.

In heteroskedasticity lineups, 76% are rejected by conventional tests, while 56% are rejected by visual tests. Of the lineups rejected by the conventional test, the visual test rejects more than two-thirds of them, too.

Surprisingly, the visual test rejects 1 of the 33 (3%) of lineups where the conventional test does not reject. Figure 2.11 shows this lineup. The data plot in position seventeen displays a relatively strong heteroskedasticity pattern, and has a strong effect size ($\log_e(E) = 4.02$), which is reflected by the visual test p -value = 0.026. But the BP test p -value = 0.056, is slightly above the significance cutoff of 0.05. This lineup was evaluated by 11 participants, it has experimental factors $a = 0$ (“butterfly” shape), $b = 64$ (large variance ratio), $n = 50$ (small sample size), and a uniform distribution for the predictor. It may have been the small sample size and the presence of a few outliers that may have resulted in the lack of detection by the conventional test.

Because the power curve of the visual tests are a shift to the right of the conventional test (Figure 2.9) we examined whether adjusting the significance level (to .001, .0001, .00001, ...) of the conventional test would generate similar decisions to that of the visual test. Interestingly, it does not: despite resulting in less rejections, neither the RESET or BP tests come to complete agreement with the visual test (see Appendix A.1).

2.5.3 Effect of Amount of Non-linearity

The order of the polynomial is a primary factor contributing to the pattern produced by the non-linearity model. Figure 2.12 explores the relationship between polynomial order and power of the tests. The conventional tests have higher power for lower orders of Hermite polynomials, and the power drops substantially for the “triple-U” shape. To understand why this is, we return to the application of the RESET test, which requires a parameter indicating degree of fitted values to test for, and the recommendation is to generically use four (Ramsey 1969). However,

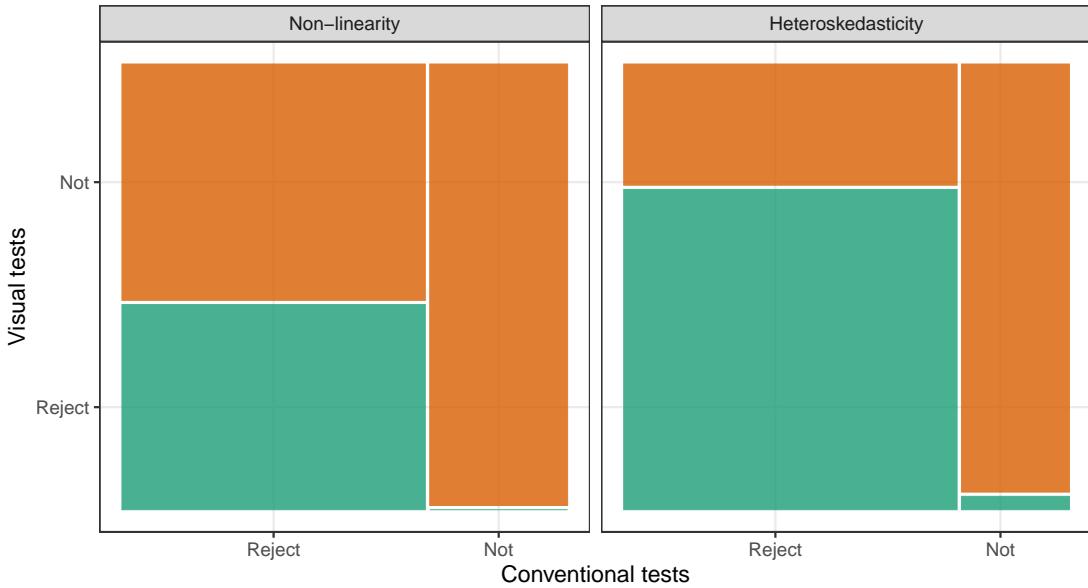


Figure 2.10: Rejection rate ($p\text{-value} \leq 0.05$) of visual test conditional on the conventional test decision on non-linearity (left) and heteroskedasticity (right) lineups (uniform fitted values only) displayed using a mosaic plot. The visual test rejects less frequently than the conventional test, and (almost) only rejects when the conventional test does. Surprisingly, one lineup in the heteroskedasticity group is rejected by the visual test but NOT the conventional test.

the “triple-U” shape is constructed from the Hermite polynomials using power up to 18. If the RESET test had been applied using a higher power of no less than six, the power curve of “triple-U” shape will be closer to other power curves. This illustrates the sensitivity of the conventional test to the parameter choice, and highlights a limitation: it helps to know the data generating process to set the parameters for the test, which is unrealistic in practice. However, we examined this in more detail (see Appendix A.1) and found that there is no harm in setting the parameter higher than four on the tests’ operation for lower order polynomial shapes. Using a parameter value of six, instead of four, yields higher power regardless of generating process, and is recommended.

For visual tests, we expect the “U” shape to be detected more readily, followed by the “S”, “M” and “triple-U” shape. From Figure 2.12, it can be observed that the power curves mostly align with these expectations, except for the “M” shape, which is as easily detected as the “S” shape. This suggests a benefit of the visual test: knowing the shape ahead of time is *not* needed for its application.

2.5.4 Effect of Shape of Heteroskedasticity

Figure 2.13 examines the impact of the shape of the heteroskedasticity on the power of both tests. The butterfly shape has higher power on both types of tests. The “left-triangle” and the

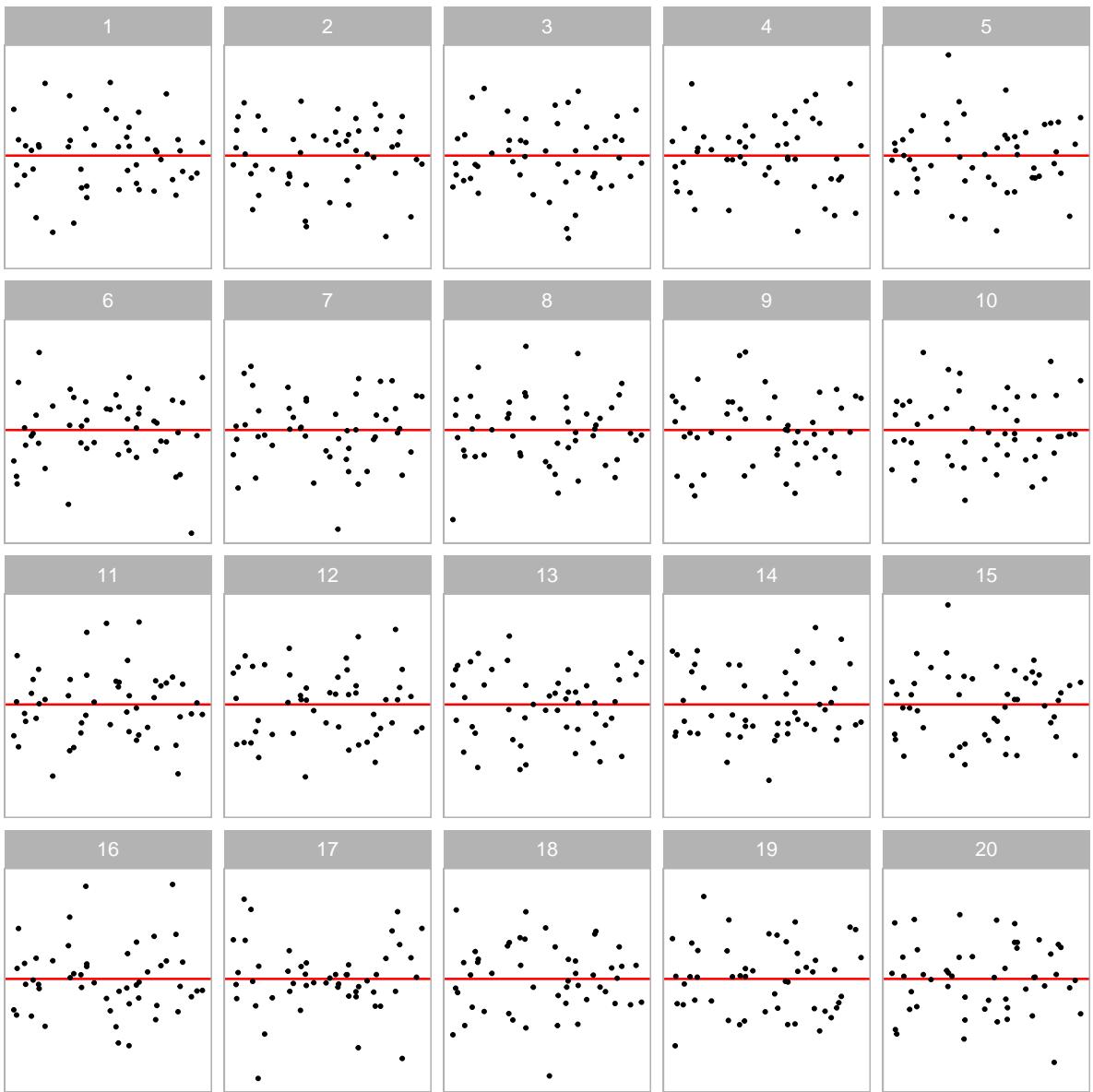


Figure 2.11: The single heteroskedasticity lineup that is rejected by the visual test but not by the BP test. The data plot (position 17) contains a “butterfly” shape. It visibly displays heteroskedasticity, making it somewhat surprising that it is not detected by the BP test.

“right-triangle” shapes are functionally identical, and this is observed for the conventional test, where the power curves are identical. Interestingly there is a difference for the visual test: the power curve of the “left-triangle” shape is slightly higher than that of the “right-triangle” shape. This indicates a bias in perceiving heteroskedasticity depending on the direction, and may be worth investigating further.

2.5.5 Effect of Fitted Value Distributions

In regression analysis, predictions are conditional on the observed values of the predictors, that is, the conditional mean of the dependent variable Y given the value of the independent variable

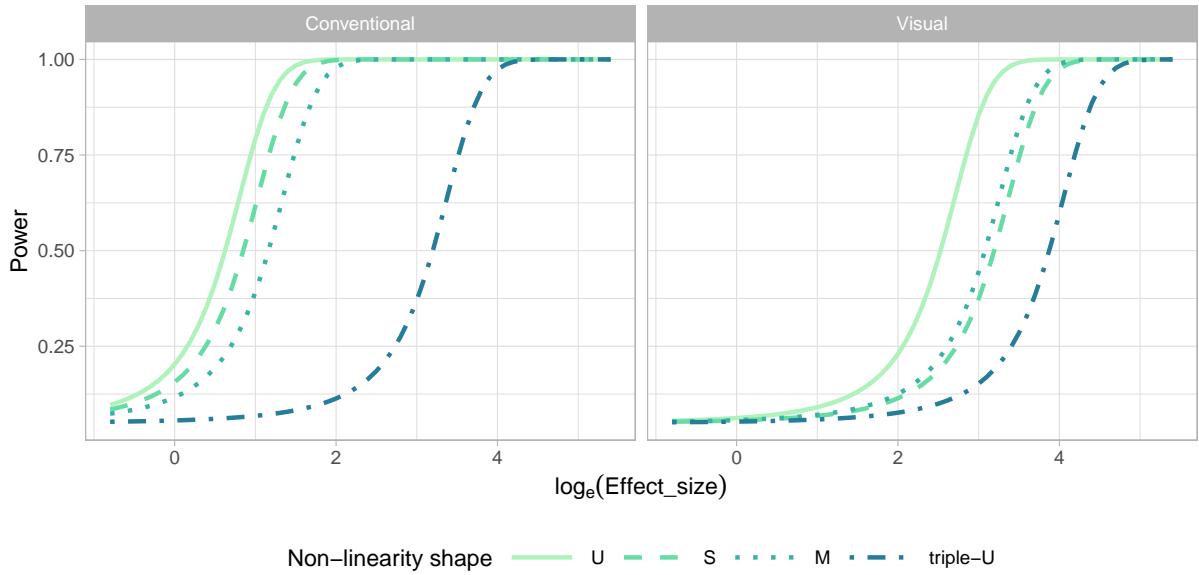


Figure 2.12: The effect of the order of the polynomial on the power of conventional and visual tests. Deeper colour indicates higher order. The default RESET tests under-performs significantly in detecting the “triple-U” shape. To achieve a similar power as other shapes, a higher order polynomial parameter needs to be used for the RESET test, but this higher than the recommended value.

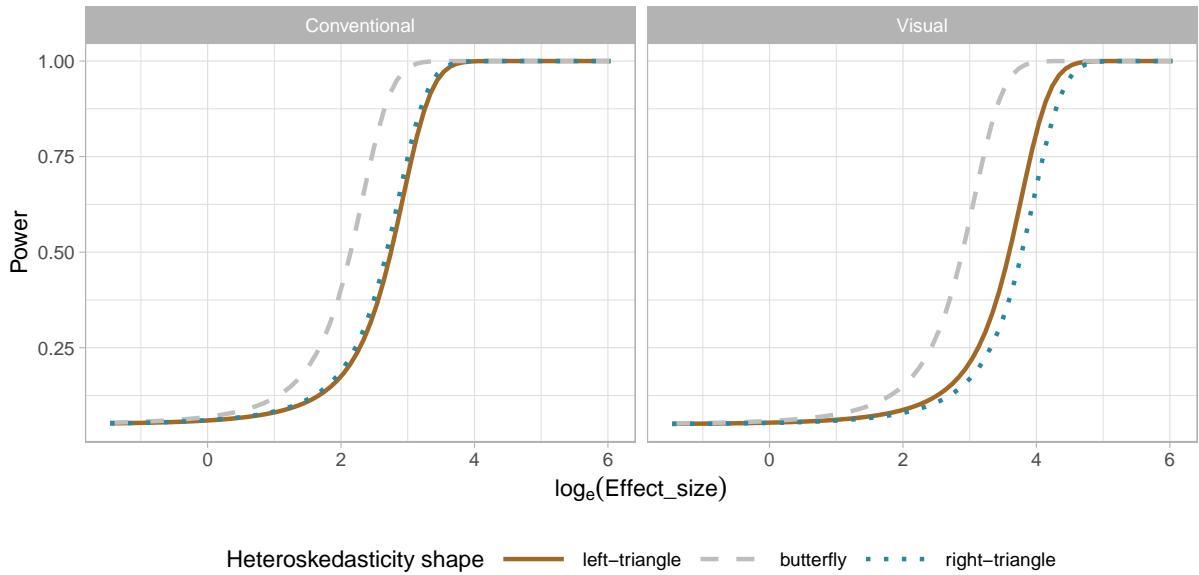


Figure 2.13: The effect of heteroskedasticity shape (parameter a) on the power of conventional and visual tests. The butterfly has higher power in both tests. Curiously, the visual test has a slightly higher power for the "left-triangle" than the "right-triangle" shape, when it would be expected that they should be similar, which is observed in conventional testing.

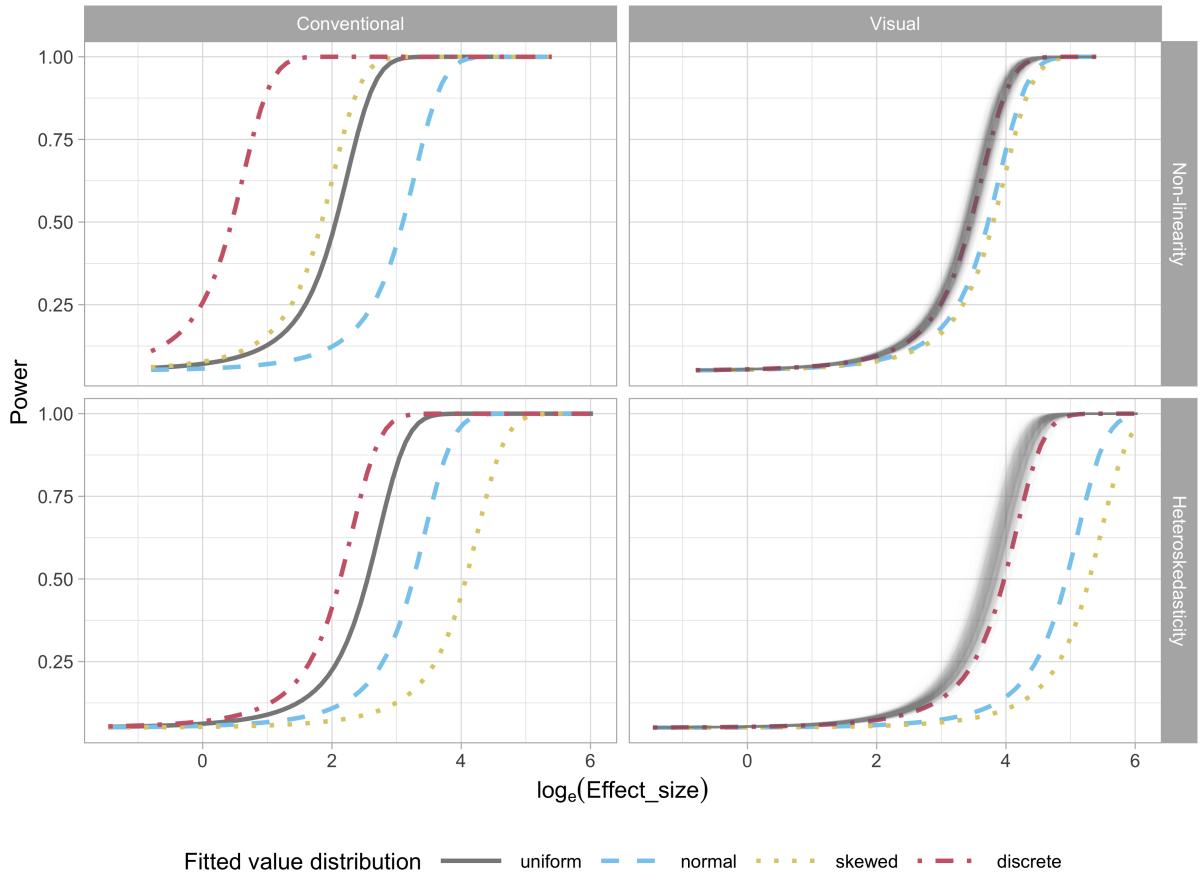


Figure 2.14: Comparison of power on lineups with different fitted value distributions for conventional and visual tests (columns) for non-linearity and heteroskedasticity patterns (rows). The power curves of conventional tests for non-linearity and heteroskedasticity patterns are produced by RESET tests and BP tests, respectively. Power curves of visual tests are estimated using five evaluations on each lineup. For lineups with a uniform fitted value distribution, the five evaluations are repeatedly sampled from the total eleven evaluations to give multiple power curves (solid grey). Surprisingly, the fitted value distribution has produces more variability in the power of conventional tests than visual tests. Uneven distributions, normal and skewed distributions, tend to yield lower power.

X , $E(Y|X)$. This is an often forgotten element of regression analysis but it is important. Where X is observed, the distribution of the X values in the sample, or consequently \hat{Y} , may affect the ability to read any patterns in the residual plots. The effect of fitted value distribution on test performance is assess using four different distributions of fitted values stemming from the predictor distributions: uniform, normal, discrete and lognormal (skewed). We expect that if all predictors have a uniform distribution, it is easier to read the relationship with the residuals.

Figure 2.14 examines the impact of the fitted value distribution on the power of conventional (left) and visual (right) tests for both the non-linearity (top) and heteroskedasticity (bottom) patterns. For conventional tests, only the power curves of appropriate tests are shown: RESET tests for non-linearity and BP tests for heteroskedasticity. For visual tests, more evaluations on

lineups with uniform fitted value distribution were collected, so to have a fair comparison, we randomly sample five from the 11 total evaluations to estimate the power curves, producing the multiple curves for the uniform condition, and providing an indication of the variability in the power estimates.

Perhaps surprisingly, the visual tests have more consistent power across the different fitted value distributions: for the non-linear pattern, there is almost no power difference, and for the heteroskedastic pattern, uniform and discrete have higher power than normal and skewed. The likely reason is that these latter two have fewer observations in the tails where the heteroskedastic pattern needs to be detected.

The variation in power in the conventional tests is at first sight, shocking. However, it is discussed, albeit rarely, in the testing literature. See, for example, Jamshidian et al. (2007), Olvera Astivia et al. (2019) and Zhang and Yuan (2018) which show derivations and use simulation to assess the effect of the observed distribution of the predictors on test power. The big differences in the power curves seen in Figure 2.14 is echoed in the results reported in these articles.

Chapter 3

Limitations and Practicality

One of the primary limitations of the lineup protocol lies in its reliance on human judgements. In this context, the effectiveness of a single lineup evaluation can be dependent on the perceptual ability and visual skills of the individual. However, when results from multiple individuals are combined the outcome is encouragingly high-quality and robust. For simple plots and strong patterns just a few individuals are needed to arrive at a clear answer, but more individuals will be needed when the plot design is complex, or the signal strength is weak.

Using a lineup protocol removes subjectiveness in interpreting patterns in plots. A plot is compared with draws from a null model, in much the same way as a test statistic is compared to its sampling distribution. It is important to remove plot elements that might introduce bias, such as axis labels, text and legends, or to make them generic.

The lineup protocol can be used cheaply and informally with the R package **nullabor**. There is evidence that it is being used fairly broadly, based on software download rates and citations of the original papers. For residual plot analysis we recommend that the lineup be the default first plot so that the data plot is only seen in the context of null plots. When a rigorous test is needed, we recommend using a crowd-sourcing service, as done in gene expression experiment described in Yin et al. (2013). While it takes extra effort it is not difficult today, and costs are tiny compared to the overall costs of conducting a scientific experiment. We do also expect that at some point a computer vision model can be developed to take over the task of employing people to evaluate residual plots.

For this study, simulated data was used to provide a precisely controlled environment within which to compare results from conventional testing to those from visual testing. We also explored only the most commonly used, the residual vs fitted value plots. However, we expect the behaviour of

the conventional test and the visual test to be similar when observed residuals are diagnosed with this type of plot or other residual plots. The conventional tests will be more sensitive to small departures from the null. They will also fail to detect departures when residuals have some contamination, like outliers or anomalies, as is often encountered when working with data. The lineup approach is well-suited for generally interpreting data plots, and also detecting unexpected patterns not related to the model. This is supported by earlier research (e.g. Loy et al. 2016; Loy and Hofmann 2015; Roy Chowdhury et al. 2015; VanderPlas and Hofmann 2016; Wickham et al. 2010).

Chapter 4

Conclusions

This paper has described experimental evidence providing support for the advice of regression analysis experts *that residual plots are indispensable methods for assessing model fit*, using the formal framework of the lineup protocol. We conducted a perceptual experiment on scatterplots of residuals vs fitted values, with two primary departures from good residuals: non-linearity and heteroskedasticity. We found that conventional residual-based statistical tests are more sensitive to weak departures from model assumptions than visual tests. That is, a conventional test concludes there are problems with the model fit almost twice as often as a human. Conventional tests often reject the null hypothesis when departures in the form of non-linearity and heteroskedasticity are not visibly different from null residual plots.

While it might be argued that the conventional tests are correctly detecting small but real effects, this can also be seen as the conventional tests are rejecting unnecessarily. Many of these rejections happen even when downstream analysis and results would not be significantly affected by the small departures from a good fit. The results from human evaluations provide a more practical solution, which reinforces the statements from regression experts that residual plots are an indispensable method for model diagnostics. Further work would be needed to *quantify* how much departure from good residuals is too much.

It is important to emphasize that this work also supports a change in common practice, which is to deliver residual plots as a lineup, embedded in a field of null plots, rather than be viewed out of context. A residual plot may contain many visual features, but some are caused by the characteristics of the predictors and the randomness of the error, not by the violation of the model assumptions. These irrelevant visual features have a chance to be filtered out by participants with a comparison to null plots, resulting in more accurate reading. The lineup

enables a careful calibration for reading structure in residual plots, and also provides the potential to discover interesting and important features in the data not directly connected to linear model assumptions.

Human evaluation of residuals is expensive, time-consuming and laborious. This is possibly why residual plot analysis is often not done in practice. However, with the emergence of effective computer vision, it is hoped this work helps to lay the foundation for automated residual plot assessment.

The experiment also revealed some interesting results. For the most part, the visual test performed similarly to the appropriate conventional test with a shift in the power curve. Unlike conventional tests, where one needs to specifically test for non-linearity or heteroskedasticity the visual test operated effectively across the range of departures from good residuals. If the fitted value distribution is not uniform, there is a small loss of power in the visual test. Surprisingly, there is a big difference in power of the conventional test across fitted value distributions. Another unexpected finding was that the direction of heteroskedasticity appears to affect the ability to visually detect it: both triangles being more difficult to detect than the butterfly, and a small difference in detection between left- and right-triangle.

Chapter 5

Automated assessment of residual plots with computer vision models

Plotting residuals is a standard practice in linear regression diagnostics, essential for identifying deviations from model assumptions such as linearity, homoscedasticity, and normality. Visual inference provides an inferential framework to assess whether residual plots contain patterns inconsistent with model assumptions, typically using a lineup protocol. However, the lineup protocol's reliance on human judgment limits its scalability. This study addresses this limitation by automating the interpretation of residual plots using computer vision models. We develop a distance measure based on Kullback-Leibler divergence to quantify the disparity between the residual distribution of a fitted classical normal linear regression model and the reference distribution. We propose a computer vision model to estimate this distance from residual plots, facilitating formal statistical testing and bootstrapping techniques to assess model specification. Our computer vision model shows strong performance, though it performs slightly less effectively on non-linearity visual patterns. The statistical tests based on the estimated distance exhibit lower sensitivity than conventional tests but higher sensitivity than human visual tests. Examples demonstrate the method's effectiveness across different scenarios, highlighting its value in automating the diagnostic process and supplementing traditional methods.

5.1 Introduction

Plotting residuals is commonly regarded as a standard practice in linear regression diagnostics [see Cook and Weisberg (1982); [belsley1980regression](#)]. This visual assessment plays a crucial role in identifying deviations from model assumptions, such as linearity, homoscedasticity, and

normality. It also helps in understanding the goodness of fit and various characteristics of the model.

Generating a residual plot in most statistical software is often as straightforward as executing a line of code or clicking a button. However, accurately interpreting a residual plot can be challenging. A residual plot can exhibit various visual features, but it is crucial to recognize that some may arise from the characteristics of predictors and the inherent randomness of the error, rather than indicating a violation of model assumptions (Li et al. 2023). Consider Figure 5.1 as an example, the residuals display a triangular shape pointing to the left. While this might suggest heteroskedasticity, it is important to avoid over-interpreting this visual pattern. In this case, the fitted regression model is correctly specified, and the triangular shape is actually a result of the skewed distribution of the predictors, rather than indicating a flaw in the model.

The concept of visual inference, as proposed by Buja et al. (2009b), provides an inferential framework to assess whether residual plots indeed contain visual patterns inconsistent with the model assumptions. The fundamental idea involves testing whether the true residual plot visually differs significantly from null plots, where null plots are plotted with residuals generated from the residual rotation distribution (Langsrud 2005), which is a distribution consistent with the null hypothesis H_0 that the linear regression model is correctly specified. Typically, the visual test is accomplished through the lineup protocol, where the real residual plot is embedded within a lineup alongside several null plots. If the real residual plot can be distinguished from the lineup, it provides evidence for rejecting H_0 .

The practice of delivering a residual plot as a lineup is generally regarded as a valuable approach. Beyond its application in residual diagnostics, the lineup protocol has integrated into the analysis of diverse subjects. For instance, (Loy and Hofmann 2013, 2014, 2015) illustrated its applicability in diagnosing hierarchical linear models. Additionally, Widen et al. (2016) demonstrated its utility in geographical research, while Krishnan and Hofmann (2021) explored its effectiveness in forensic examinations.

However, as pointed out by Li et al. (2023), a primary limitation of the lineup protocol lies in its reliance on human judgments. Unlike conventional statistical tests that can be performed computationally in statistical software, the lineup protocol requires human evaluation of images. This characteristic makes it less suitable for large-scale applications, given the associated high labour costs and time requirements.

There is a substantial need to develop an approach that alleviates analysts' workload by automating repetitive tasks and providing standardized results in a controlled environment. The

large-scale evaluation of lineups is impractical without the use of technology and machines.

The utilization of computers to interpret data plots has a rich history, with early efforts such as “Scagnostics” by Tukey and Tukey (1985), focusing on scatter plot diagnostics. Wilkinson et al. (2005) expanded on this work, introducing graph theoretic scagnostics, which encompassed computable measures applied to planar proximity graphs. These measures, including, but not limited to, “Outlying”, “Skinny”, “Stringy”, “Straight”, “Monotonic”, “Skewed”, “Clumpy”, and “Striated” aimed to characterize outliers, shape, density, trend, coherence and other characteristics of the data. While this approach has been inspiring, there is a recognition (Buja et al. 2009b) that it may not capture all the necessary visual features that differentiate true residual plots from null plots. A more promising alternative entails enabling machines to learn the function for extracting visual features from residual plots. Essentially, this means empowering computers to discern the crucial visual features for residual diagnostics and determining the method to extract them.

Modern computer vision models are well-suited for addressing this challenge. They rely on deep neural networks with convolutional layers (Fukushima and Miyake 1982). These layers leverage hierarchical patterns in data, downsizing and transforming images by summarizing information in a small space. Numerous studies have demonstrated the efficacy of convolutional layers in addressing various vision tasks, including image recognition (Rawat and Wang 2017). Despite the widespread use of computer vision models in fields like computer-aided diagnosis (Lee and Chen 2015), pedestrian detection (Brunetti et al. 2018), and facial recognition (Emami and Suciu 2012), their application in reading data plots remains limited. While some studies have explored the use of computer vision models for tasks such as reading recurrence plots for time series regression (Ojeda et al. 2020), time series classification (Chu et al. 2019; Hailesilassie 2019; Hatami et al. 2018; Zhang et al. 2020), anomaly detection (Chen et al. 2020), and pairwise causality analysis (Singh et al. 2017), the application of reading residual plots with computer vision models represents a relatively new field of study.

In this paper, we develop computer vision models and integrate them into the residual plots diagnostics workflow, addressing the need for automated visual inference. The paper is structured as follows. Section ?? discusses various specifications of the computer vision models. Section ?? defines the distance measure used to measure model violations. Section ?? explains how the computer vision models estimate this distance measure. Section ?? covers the statistical testing based on the estimated distance. Sections ??, ??, and ?? detail the data preparation, model architecture, and training process, respectively. The results are presented in Section ?. Finally,

we conclude with a discussion of our findings and propose ideas for future research directions.

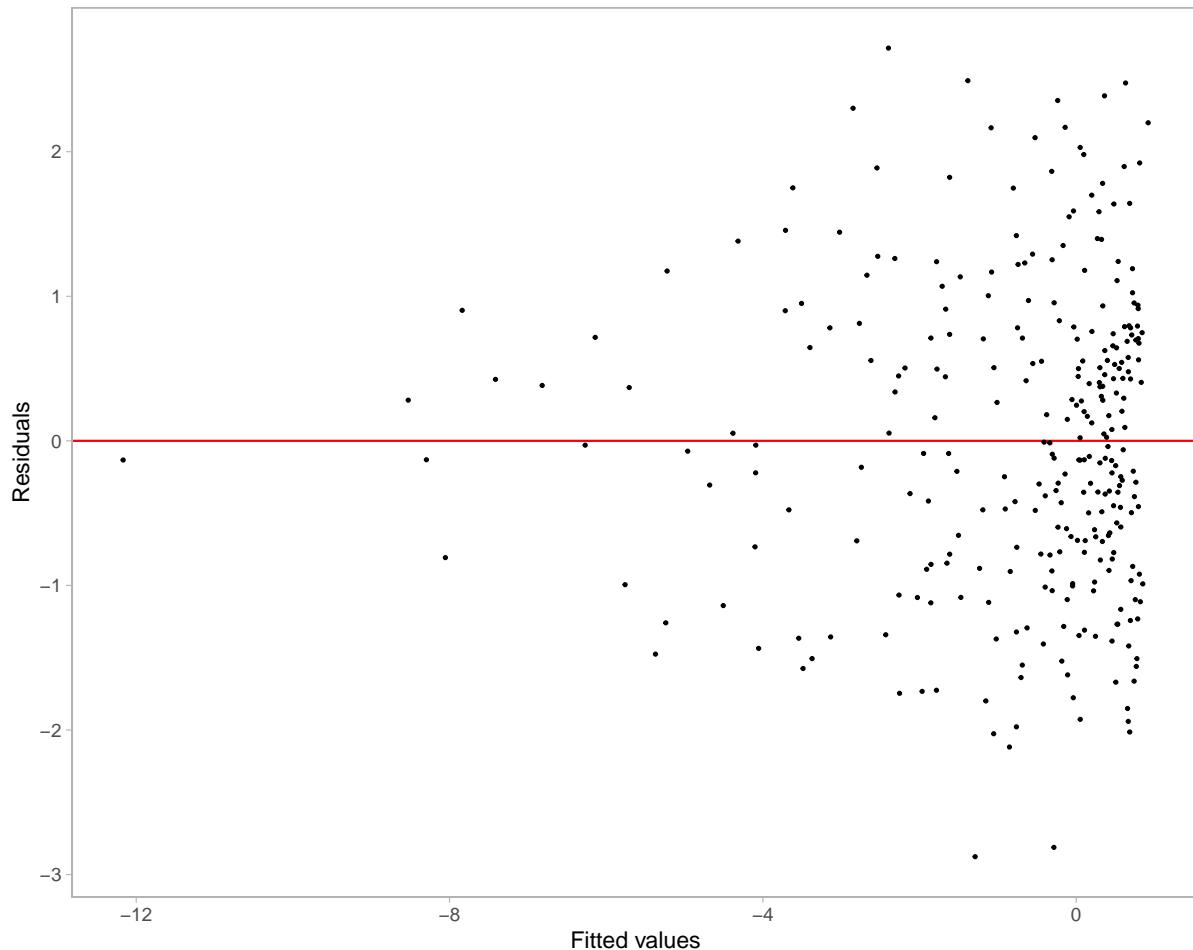


Figure 5.1: An example residual vs fitted values plot (red line indicates 0). The vertical spread of the data points varies with the fitted values. This often indicates the existence of heteroskedasticity. The Breusch-Pagan test rejects this residual plot at 95% significance level (p -value = 0.046).

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Appendix A

Appendix to “A Plot is Worth a Thousand Tests: Assessing Residual Diagnostics with the Lineup Protocol”

A.1 Additional Details of Testing Procedures

A.1.1 Statistical Significance

Within the context of visual inference, with K independent observers, the visual p -value can be seen as the probability of having as many or more participants detect the data plot than the observed result.

The approach used in Majumder et al. (2013b) is as follows. Define $X_j = \{0, 1\}$ to be a Bernoulli random variable measuring whether participant j detected the data plot, and $X = \sum_{j=1}^K X_j$ be the total number of observers who detected the data plot. Then, by imposing a relatively strong assumption that all K evaluations are fully independent, under H_0 $X \sim \text{Binom}_{K,1/m}$. Therefore, the p -value of a lineup of size m evaluated by K observer is estimated with $P(X \geq x) = 1 - F(x) + f(x)$, where $F(\cdot)$ is the binomial cumulative distribution function, $f(\cdot)$ is the binomial probability mass function and x is the realization of number of observers choosing the data plot.

As pointed out by VanderPlas et al. (2021), this basic binomial model is deficient. It does not

take into account the possible dependencies in the visual test due to repeated evaluations of the same lineup, or account for when participants are offered the option to select one or more “most different” plots, or none, from a lineup. They suggest three common lineup scenarios: (1) K different lineups are shown to K participants, (2) K lineups with different null plots but the same data plot are shown to K participants, and (3) the same lineup is shown to K participants. Scenario 3 is the most feasible to apply, but has the most dependencies to accommodate for the p -value calculation. For Scenario 3, VanderPlas et al propose modelling the probability of plot i being selected from a lineup as θ_i , where $\theta_i \sim \text{Dirichlet}(\alpha)$ for $i = 1, \dots, m$ and $\alpha > 0$. The number of times plot i being selected in K evaluations is denoted as c_i . In case participant j makes multiple selections, $1/s_j$ will be added to c_i instead of one, where s_j is the number of plots participant j selected for $j = 1, \dots, K$. This ensures $\sum_i c_i = K$. Since we are only interested in the selections of the data plot i , the marginal model can be simplified to a beta-binomial model and thus the visual p -value is given as

$$P(C \geq c_i) = \sum_{x=c_i}^K \binom{K}{x} \frac{B(x + \alpha, K - x + (m - 1)\alpha)}{B(\alpha, (m - 1)\alpha)}, \quad \text{for } c_i \in \mathbb{Z}_0^+ \quad (\text{A.1})$$

where $B(\cdot)$ is the beta function defined as

$$B(a, b) = \int_0^1 t^{a-1} (1-t)^{b-1} dt, \quad \text{where } a, b > 0. \quad (\text{A.2})$$

We extend the equation to non-negative real number c_i by applying a linear approximation

$$P(C \geq c_i) = P(C \geq \lceil c_i \rceil) + (\lceil c_i \rceil - c_i) P(C = \lfloor c_i \rfloor), \quad \text{for } c_i \in \mathbb{R}_0^+, \quad (\text{A.3})$$

where $P(C \geq \lceil c_i \rceil)$ is calculated using Equation A.1 and $P(C = \lfloor c_i \rfloor)$ is calculated by

$$P(C = c_i) = \binom{K}{c_i} \frac{B(c_i + \alpha, K - c_i + (m - 1)\alpha)}{B(\alpha, (m - 1)\alpha)}, \quad \text{for } c_i \in \mathbb{Z}_0^+. \quad (\text{A.4})$$

The parameter α used in Equation A.1 and Equation A.4 is usually unknown and will need to be estimated from the survey data. An interpretation of α is that when it is low only a few plots are attractive to the observers and tend to be selected, and when high, most plots are equally likely to be chosen. VanderPlas et al define c -interesting plot to be if c or more participants select the plot as the most different. The expected number of plots selected at least c times, $E[Z_c]$, is then calculated as

$$E[Z_c(\alpha)] = \frac{m}{B(\alpha, (m-1)\alpha)} \sum_{[c]}^K \binom{K}{x} B(x + \alpha, K - x + (m-1)\alpha). \quad (\text{A.5})$$

With Equation A.5, α can be estimated using maximum likelihood estimation. Precise estimation of α , is aided by evaluation of Rorschach lineups, where all plots are null plots. In a Rorschach, in theory all plots should be equally likely, but in practice some (irrelevant) visual elements may be more eye-catching than others. This is what α captures, the capacity for extraneous features to distract the observer for a particular type of plot display.

A.1.2 Effect Size Derivation

Effect size can be defined as the difference of a parameter for a particular model or distribution, or a statistic derived from a sample. Importantly, it needs to reflect the treatment we try to measure. Centred on a conventional statistical test, we usually can deduce the effect size from the test statistic by substituting the null parameter value. When considering the diagnostics of residual departures, there exist many possibilities of test statistics for a variety of model assumptions. Meanwhile, diagnostic plots such as the residual plot have no general agreement on measuring how strong a model violation pattern is. To build a bridge between various residual-based tests, and the visual test, we focus on the shared information embedded in the testing procedures, which is the distribution of residuals. When comes to comparison of distribution, Kullback-Leibler divergence (Kullback and Leibler 1951) is a classical way to represent the information loss or entropy increase caused by the approximation to the true distribution, which in our case, the inefficiency due to the use of false model assumptions.

Following the terminology introduced by Kullback and Leibler (1951), P represents the measured probability distribution, and Q represents the assumed probability distribution. The Kullback-Leibler divergence is defined as $\int_{-\infty}^{\infty} \log(p(x)/q(x))p(x)dx$, where $p(\cdot)$ and $q(\cdot)$ denote probability densities of P and Q .

Let \mathbf{X} denotes the $p+1$ predictors with n observations, $\mathbf{b} = (\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y}$ denotes the OLS solution, $\mathbf{R} = \mathbf{I}_n - \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'$ denotes the residual operator, and let $\varepsilon \sim N(\mathbf{0}, \sigma^2 \mathbf{I})$ denotes the error. The residual vector

$$\begin{aligned}
\mathbf{e} &= \mathbf{y} - \mathbf{X}\mathbf{b} \\
&= \mathbf{y} - \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}'\mathbf{y} \\
&= (\mathbf{I} - \mathbf{X}(\mathbf{X}'\mathbf{X})^{-1}\mathbf{X}')\mathbf{y} \\
&= \mathbf{R}\mathbf{y} \\
&= \mathbf{R}(\mathbf{X}\beta + \boldsymbol{\varepsilon}) \\
&= \mathbf{R}\boldsymbol{\varepsilon}.
\end{aligned}$$

Because $\text{rank}(\mathbf{R}) = n - p - 1 < n$, \mathbf{e} follows a degenerate multivariate normal distribution and does not have a density. Since the Kullback-Leibler divergence requires a proper density function, we need to simplify the covariance matrix of \mathbf{e} by setting all the off-diagonal elements to 0. Then, the residuals will be assumed to follow $N(\mathbf{0}, \text{diag}(\mathbf{R}\sigma^2))$ under the null hypothesis that the model is correctly specified. If the model is however misspecified due to omitted variables \mathbf{Z} , or a non-constant variance \mathbf{V} , the distribution of residuals can be derived as $N(\mathbf{R}\mathbf{Z}\beta_z, \text{diag}(\mathbf{R}\sigma^2))$ and $N(\mathbf{0}, \text{diag}(\mathbf{R}\mathbf{V}\mathbf{R}'))$ respectively.

By assuming both P and Q are multivariate normal density functions, the Kullback-Leibler divergence can be rewritten as

$$KL = \frac{1}{2} \left(\log \frac{|\Sigma_p|}{|\Sigma_q|} - n + \text{tr}(\Sigma_p^{-1}\Sigma_q) + (\mu_p - \mu_q)' \Sigma_p^{-1}(\mu_p - \mu_q) \right).$$

Then, we can combine the two residual departures into one formula

$$KL = \frac{1}{2} \left(\log \frac{|\text{diag}(\mathbf{R}\mathbf{V}\mathbf{R}')|}{|\text{diag}(\mathbf{R}\sigma^2)|} - n + \text{tr}(\text{diag}(\mathbf{R}\mathbf{V}\mathbf{R}')^{-1} \text{diag}(\mathbf{R}\sigma^2)) + \boldsymbol{\mu}_z' (\mathbf{R}\mathbf{V}\mathbf{R}')^{-1} \boldsymbol{\mu}_z \right).$$

When there are omitted variables but constant error variance, the formula can be reduced to

$$KL = \frac{1}{2} \left(\boldsymbol{\mu}_z' (\text{diag}(\mathbf{R}\sigma^2))^{-1} \boldsymbol{\mu}_z \right).$$

And when the model equation is correctly specified but the error variance is non-constant, the formula can be reduced to

$$KL = \frac{1}{2} \left(\log \frac{|\text{diag}(\mathbf{R}\mathbf{V}\mathbf{R}')|}{|\text{diag}(\mathbf{R}\sigma^2)|} - n + \text{tr}(\text{diag}(\mathbf{R}\mathbf{V}\mathbf{R}')^{-1} \text{diag}(\mathbf{R}\sigma^2)) \right).$$

Table A.1: Examining how decisions might change if $\hat{\alpha}$ was different. Percentage of lineups that where the p -value would switch to above or below 0.05, when $\hat{\alpha}$ is multiplied by a multiplier.

Multiplier	Reject to not reject	%	Not reject to reject	%
0.500	7	2.51	0	0.00
0.750	4	1.43	0	0.00
0.875	3	1.08	0	0.00
1.125	0	0.00	3	1.08
1.250	0	0.00	4	1.43
1.500	0	0.00	5	1.79

To compute the effect size for each lineup we simulate a sufficiently large number of samples from the same model with the number of observations n fixed for each sample. We then compute the effect size for each sample and take the average as the final value. This ensures lineups constructed with the same experimental factors will share the same effect size.

A.1.3 Sensitivity Analysis for α

The parameter α used for the p -value calculation needs to be estimated from responses to null lineups. With a greater value of $\hat{\alpha}$, the p -value will be smaller, resulting in more lineups being rejected. However, The way we generate Rorschach lineup is not strictly the same as what suggested in VanderPlas et al. (2021) and Buja et al. (2009b). Therefore, we conduct a sensitivity analysis in this section to examine the impact of the variation of the estimator α on our primary findings.

The analysis is conducted by setting up several scenarios, where the α is under or overestimated by 12.5%, 25% and 50%. Using the adjusted $\hat{\alpha}$, we recalculate the p -value for every lineup and show the results in Figure ???. It can be observed that there are some changes to p -values, especially when the $\hat{\alpha}$ is multiplied by 50%. However, Table ?? shows that adjusting $\hat{\alpha}$ will not result in a huge difference in rejection decisions. There are only a small percentage of cases where the rejection decision change. It is very unlikely the downstream findings will be affected because of the estimate of α .

A.1.4 Effect of Number of Evaluations on the Power of a Visual Test

When comparing power of visual tests across different fitted value distributions, we have discussed the number of evaluations on a lineup will affect the power of the visual test. Using the lineups with uniform fitted value distribution, we show in Figure A.2 the change of power of visual tests due to different number of evaluations. It can be learned that as the number of evaluations increases, the power will increase but the margin will decrease. Considering we have eleven

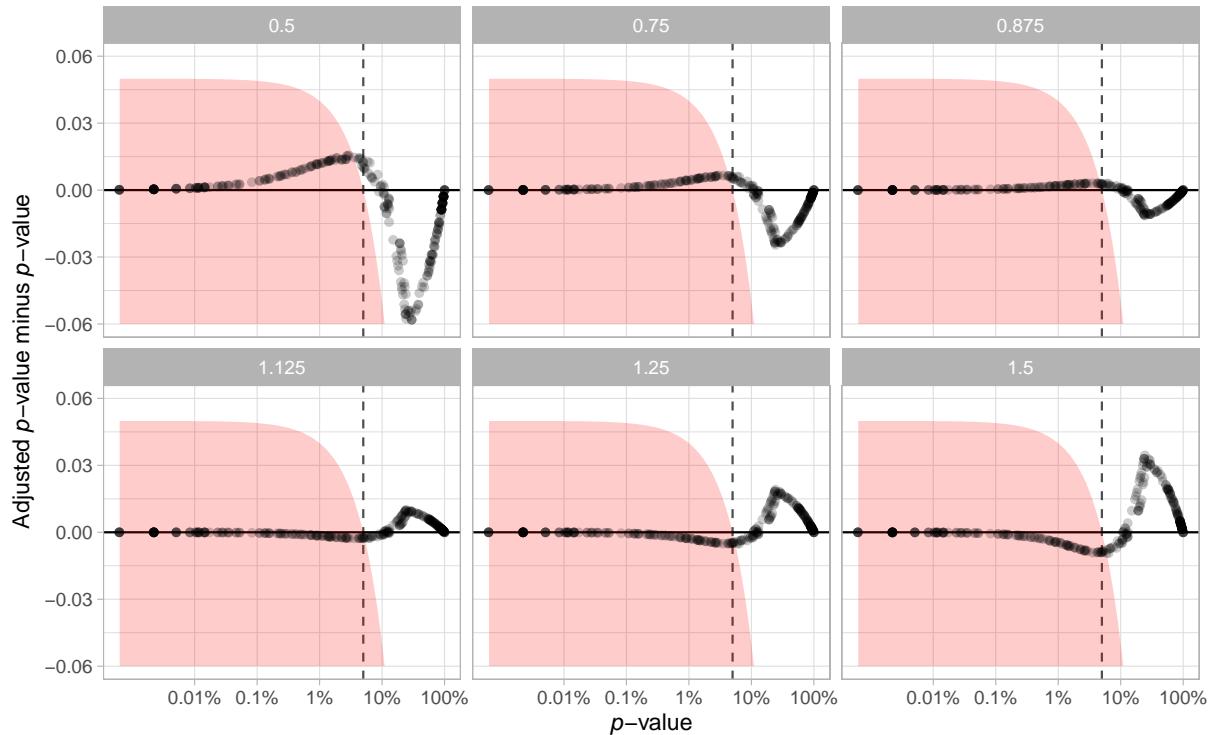


Figure A.1: Change of p -values with $\hat{\alpha}$ multiplied by 0.5, 0.75, 0.875, 1.125, 1.25 and 1.5. Only lineups with uniform fitted value distribution is used. The vertical dashed line indicates p -value = 0.05. The area coloured in red indicates adjusted p -value < 0.05 . The x-axis is drawn on logarithmic scale. For multipliers smaller than 1, the adjusted p -value will initially increase and decline when the p -value increases. The trend is opposite with multipliers greater than 1, but the difference eventually reaches 0.

evaluations on lineups with uniform fitted value distribution, and five evaluations on other lineups, it is necessary to use the same number of evaluations for each lineup in comparison.

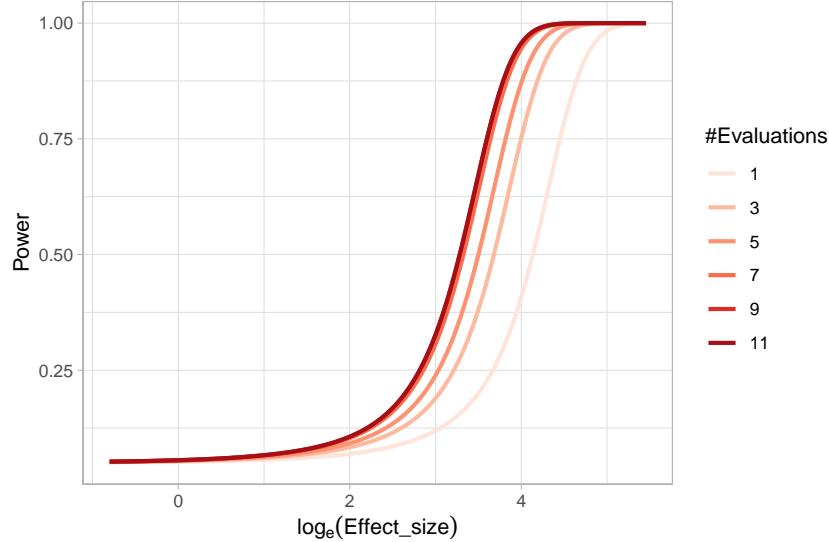


Figure A.2: Change of power of visual tests for different number of evaluations on lineups with uniform fitted value distribution. The power will increase as the number of evaluations increases, but the margin will decrease.

A.1.5 Power of a RESET Test under Different Auxiliary Regression Formulas

It is found in the result that the power of a RESET test will be affected by the highest order of fitted values included in the auxiliary formula. And we suspect that the current recommendation of the highest order - four, is insufficient to test complex non-linear structures such as the “triple-U” shape designed in this paper. Figure A.3 illustrates the change of power of RESET test while testing the “U” shape and the “triple-U” shape with different highest orders. Clearly, when testing a simple shape like the “U” shape, the highest order has very little impact on the power. But for testing the “triple-U” shape, there will be a loss of power if the recommended order is used. To avoid the loss of power, the highest order needs to be set to at least six.

A.1.6 Conventional Test Rejection Rate for Varying Significance Levels

In the main paper, Section 2.5.1 and Section 2.5.2 compared the power, and the decisions made by the conventional tests and the visual test. The power curves for the visual test is effectively a right-shift from the conventional test. The effect is that the visual test rejects less often than the conventional test, at the same significance level. We also saw that the visual test rejected a subset of those that the conventional tests rejected. This means that they agreed quite well - only residual plots rejected by the conventional tests were rejected by the visual test. There was little disagreement, where residual plots not rejected by the conventional test were rejected by

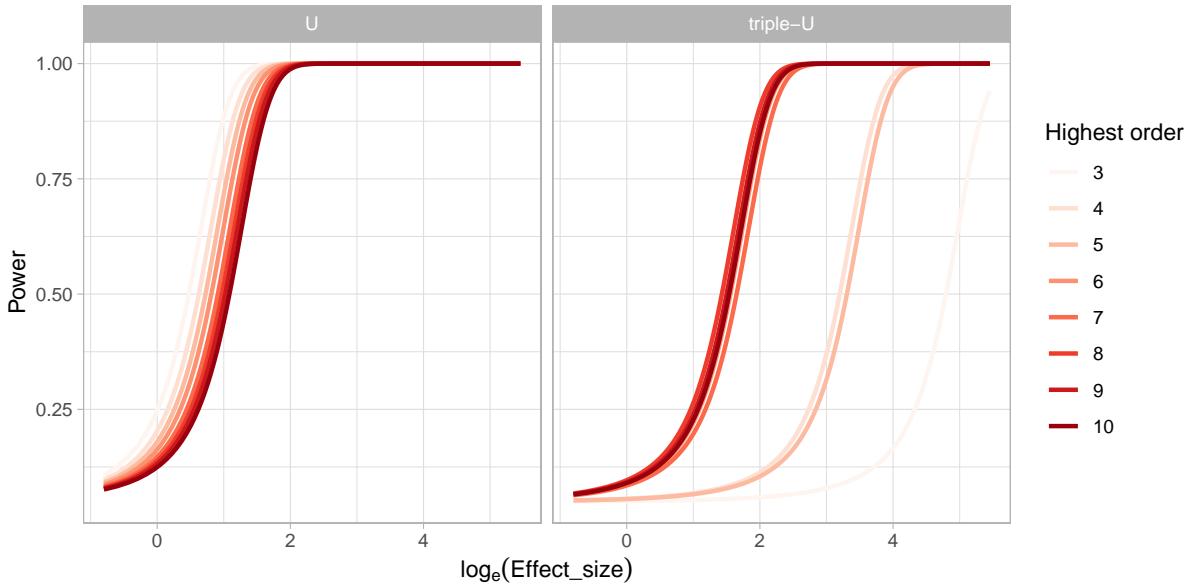


Figure A.3: Change of power of RESET tests for different orders of fitted values included in the auxiliary formula. The left panel is the power of testing the “U” shape and the right panel is the power of testing the “triple-U” shape. The power will not be greatly affected by the highest order in the case of testing the “U” shape. In the case of testing the “triple-U” shape, the highest order needs to be set to at least six to avoid the loss of power.

the visual test. The question arises whether the decisions made conventional test could be made similar to that of the visual test by reducing the significance level. Reducing the significance level from 0.05, to 0.01, 0.001, ... will have the effect of rejecting fewer of the residual plots.

It would be interesting if a different conventional test significance level results in both the visual tests and conventional tests reject only the same residual plots, and fails to reject the same residual plots. This would be a state where both systems agree perfectly. Figure ?? examines this. Plot A shows the percentage of residual plots rejected by the visual test, given the conventional test rejected (solid lines) or failed to reject (dashed lines). The vertical grey line marks significance level 0.05. When the significance level gets smaller, it is possible to see that the visual tests reject (nearly) 100% of the time that the conventional test rejects. However, there is no agreement, because the visual tests also increasingly reject residual plots where the conventional test failed to reject. Plot B is comparable to an ROC curve, where the percentage visual test rejection conditional on conventional test decision is plotted: Reject conditional on reject is plotted against reject conditional on fail to reject, for different significance levels. The non-linearity pattern results are close to being ideal, that the percentage of reject relative to fail to reject increases very slowly as the reject relative to reject converges to 100. The heteroskedasticity pattern is more problematic, and shows that the cost of rejecting less with the conventional test is disagreement with the visual test.

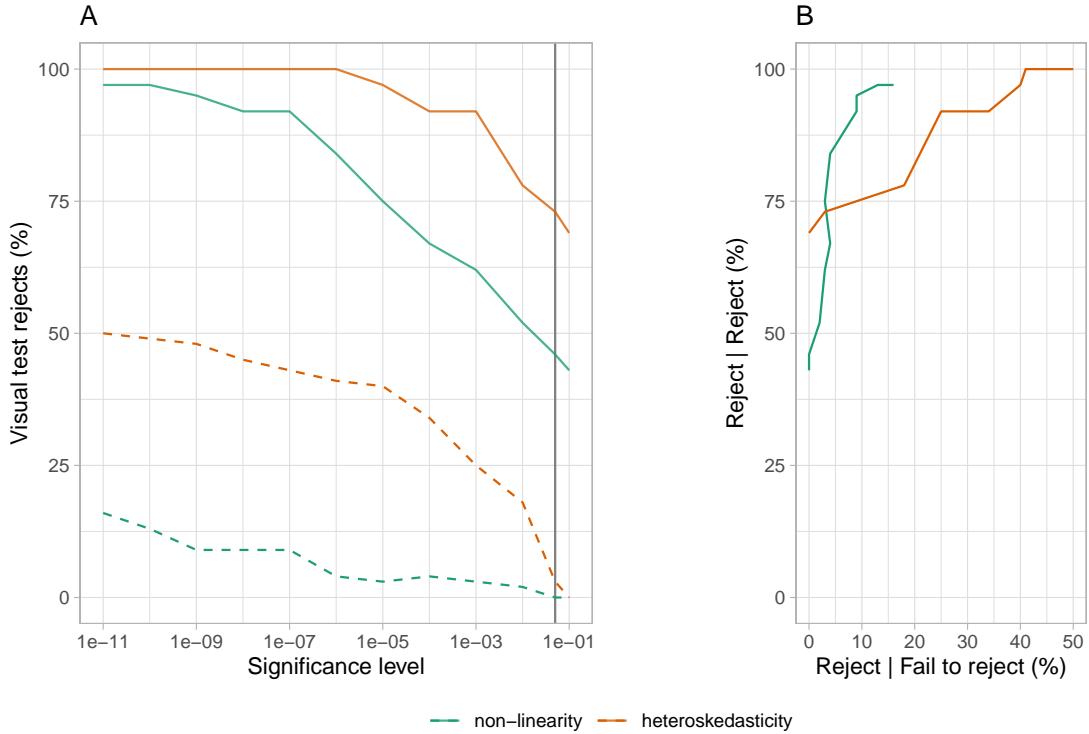


Figure A.4: Changing the significance level of the conventional test will change the rejection rate. A: Percentage of conventional tests also rejected by the visual test: rejected (solid), not rejected (dashed). As the significance level is reduced, the percentage rejected by the visual test that has been rejected by the conventional test approaches 100. The percentage of tests not rejected by the conventional test also increases, as expected, but the percentage of these that are rejected by the visual test increases too. B: ROC curve shows that forcing the conventional test to not reject creates a discrepancy with the visual test. Many of the residual plots not rejected by the conventional test are rejected by the visual test. It is not possible to vary the significance level of the conventional test to match the decisions made by the visual test.

A.2 Additional Details of Experimental Setup

A.2.1 Non-linearity Model

The non-linearity model used in the experiment includes a non-linear term \mathbf{z} constructed using Hermite polynomials on random vector \mathbf{x} formulated as

$$\begin{aligned}
 \mathbf{y} &= \mathbf{1}_n + \mathbf{x} + \mathbf{z} + \varepsilon, \\
 \mathbf{x} &= g(\mathbf{x}_{raw}, 1), \\
 \mathbf{z} &= g(\mathbf{z}_{raw}, 1), \\
 \mathbf{z}_{raw} &= He_j(g(\mathbf{x}, 2)),
 \end{aligned}$$

where \mathbf{y} , \mathbf{x} , $\boldsymbol{\varepsilon}$, \mathbf{x}_{raw} , \mathbf{z}_{raw} are vectors of size n , $\mathbf{1}_n$ is a vector of ones of size n , $He_j(\cdot)$ is the j th-order probabilist's Hermite polynomials (Hermite 1864; originally by Laplace 1820), $\boldsymbol{\varepsilon} \sim N(\mathbf{0}_n, \sigma^2 \mathbf{I}_n)$, and $g(\mathbf{x}, k)$ is a scaling function to enforce the support of the random vector to be $[-k, k]^n$ defined as

$$g(\mathbf{x}, k) = 2k \cdot \frac{\mathbf{x} - x_{min} \mathbf{1}_n}{x_{max} - x_{min}} - k, \quad \text{for } k > 0. \quad (\text{A.6})$$

where $x_{min} = \min_{i \in \{1, \dots, n\}} x_i$, $x_{max} = \max_{i \in \{1, \dots, n\}} x_i$ and x_i is the i -th entry of \mathbf{x} . The function `hermite` from the R package `mpoly` (Kahle 2013) is used to simulate \mathbf{z}_{raw} to generate Hermite polynomials.

The null regression model used to fit the realizations generated by the above model is formulated as

$$\mathbf{y} = \beta_0 \mathbf{1}_n + \beta_1 \mathbf{x} + \mathbf{u}, \quad (\text{A.7})$$

where $\mathbf{u} \sim N(\mathbf{0}, \sigma^2 \mathbf{I}_n)$. Here \mathbf{z} is a higher order term of \mathbf{x} and leaving it out in the null regression results in model misspecification.

A.2.2 Heteroskedasticity Model

The heteroskedasticity model used in the experiment is formulated as

$$\begin{aligned} \mathbf{y} &= \mathbf{1}_n + \mathbf{x} + \boldsymbol{\varepsilon}, \\ \mathbf{x} &= g(\mathbf{x}_{raw}, 1), \\ \boldsymbol{\varepsilon} &\sim N(\mathbf{0}_n, \mathbf{1}_n + (2 - |a|)(\mathbf{x} - a\mathbf{1}_n)'(\mathbf{x} - a\mathbf{1}_n)b\mathbf{I}_n), \end{aligned}$$

where \mathbf{y} , \mathbf{x} , $\boldsymbol{\varepsilon}$ are vectors of size n and $g(\cdot)$ is the scaling function defined in Equation A.6. The null regression model used to fit the realizations generated by the above model is formulated exactly the same as Equation A.7.

For $b \neq 0$, the variance-covariance matrix of the error term $\boldsymbol{\varepsilon}$ is correlated with the predictor \mathbf{x} , which will lead to the presence of heteroskedasticity.

Since $\text{supp}(X) = [-1, 1]$, choosing a to be -1 , 0 and 1 can generate “left-triangle”, “butterfly” and “right-triangle” shapes. The term $(2 - |a|)$ maintains the magnitude of residuals across

different values of a .

A.2.3 Controlling the Signal Strength

The three parameters n , σ and b are important for controlling the strength of the signal to generate lineups with a variety difficulty levels. This will ensure that estimated power curves will be smooth and continuous, and that participants are allocated a set of lineups with a range of difficulty.

Parameter $\sigma \in \{0.5, 1, 2, 4\}$ and $b \in \{0.25, 1, 4, 16, 64\}$ are used in data collection periods I and II respectively. A large value of σ will increase the variation of the error of the non-linearity model and decrease the visibility of the visual pattern. The parameter b controls the variation in the standard deviation of the error across the support of the predictor. A larger value of b generates a larger ratio between its smallest and highest values, making the visual pattern more obvious. The sample size n sharpens (or blurs) a pattern when it is larger (or smaller).

A.2.4 Lineup Allocation to Participants

There are a total of $4 \times 4 \times 3 \times 4 = 192$ and $3 \times 5 \times 3 \times 4 = 180$ combinations of parameter values for the non-linearity model and heteroskedasticity models respectively. Three replications for each combination results in $192 \times 3 = 576$ and $180 \times 3 = 540$ lineups, respectively.

Each lineup needs to be evaluated by at least five participants. From previous work, and additional pilot studies for this experiment, we decided to record evaluations from 20 lineups for each participant. Two of the 20 lineups with clear visual patterns were used as attention checks, to ensure quality data. Thus, $576 \times 5/(20 - 2) = 160$ and $540 \times 5/(20 - 2) = 150$ participants were needed to cover the experimental design for the data collection periods I and II, respectively. The factor levels and range of difficulty was assigned relatively equally among participants.

Data collection period III was primarily to obtain Rorschach lineup evaluations to estimate α , and also to obtain additional evaluations of lineups made with uniform fitted value distribution to ensure consistency in the results. To construct a Rorschach lineup, the data is generated from a model with zero effect size, while the null data are generated using the residual rotation technique. This procedure differs from that of the canonical Rorschach lineup, where all 20 plots are generated directly from the null model, so the method suggested in VanderPlas et al. (2021) for typical lineups containing a data plot is used to estimate α . The $3 \times 4 = 12$ treatment levels of the common factors, replicated three times results in 36 lineups. And 6 more evaluations on the 279 lineups with uniform fitted value distribution, results in at least

$(36 \times 20 + 279 \times 3 \times 6)/(20 - 2) = 133$ participants needed.

A.2.5 Mapping of Participants to Experimental Factors

Mapping of participants to experimental factors is an important part of experimental design. Essentially, we want to maximum the difference in factors exposed to a participant. For this purpose, we design an algorithm to conduct participant allocation. Let L be a set of available lineups and S be a set of available participants. According to the experimental design, the availability of a lineup is associated with the number of participants it can assign to. For lineups with uniform fitted value distribution, this value is 11. And other lineups can be allocated to at most five different participants. The availability of a participant is associated with the number of lineups that being allocated to this participant. A participant can view at most 18 different lineups.

The algorithm starts from picking a random participant $s \in S$ with the minimum number of allocated lineups. It then tries to find a lineup $l \in L$ that can maximise the distance metric D and allocate it to participant s . Set L and S will be updated and the picking process will be repeated until there is no available lineups or participants.

Let F_1, \dots, F_q be q experimental factors, and f_1, \dots, f_q be the corresponding factor values. We say f_i exists in L_s if any lineup in L_s has this factor value. Similarly, $f_i f_j$ exists in L_s if any lineup in L_s has this pair of factor values. And $f_i f_j f_k$ exists in L_s if any lineup in L_s has this trio of factor values. The distance metric D is defined between a lineup l and a set of lineups L_s allocated to a participant s if L_s is non-empty:

$$D = C - \sum_{1 \leq i \leq q} I(f_i \text{ exists in } L_s) - \sum_{\substack{1 \leq i \leq q-1 \\ i < j \leq q}} I(f_i f_j \text{ exists in } L_s) - \sum_{\substack{1 \leq i \leq q-2 \\ i < j \leq q-1 \\ j < k \leq q}} I(f_i f_j f_k \text{ exists in } L_s)$$

where C is a sufficiently large constant such that $D > 0$. If L_s is empty, we define $D = 0$.

The distance measures how different a lineup is from the set of lineups allocated to the participant in terms of factor values. Thus, the algorithm will try to allocate the most different lineup to a participant at each step.

In Figure A.5 and Figure A.6, we present examples of lineup allocations generated by our algorithm for data collection periods I and II, respectively. These figures illustrate the factor values presented to the first 20 participants recruited during each period. It can be observed that the algorithm effectively distributed almost all possible one-way and two-way factor combinations among the participants, thereby ensuring a diverse set of lineups for each participant.

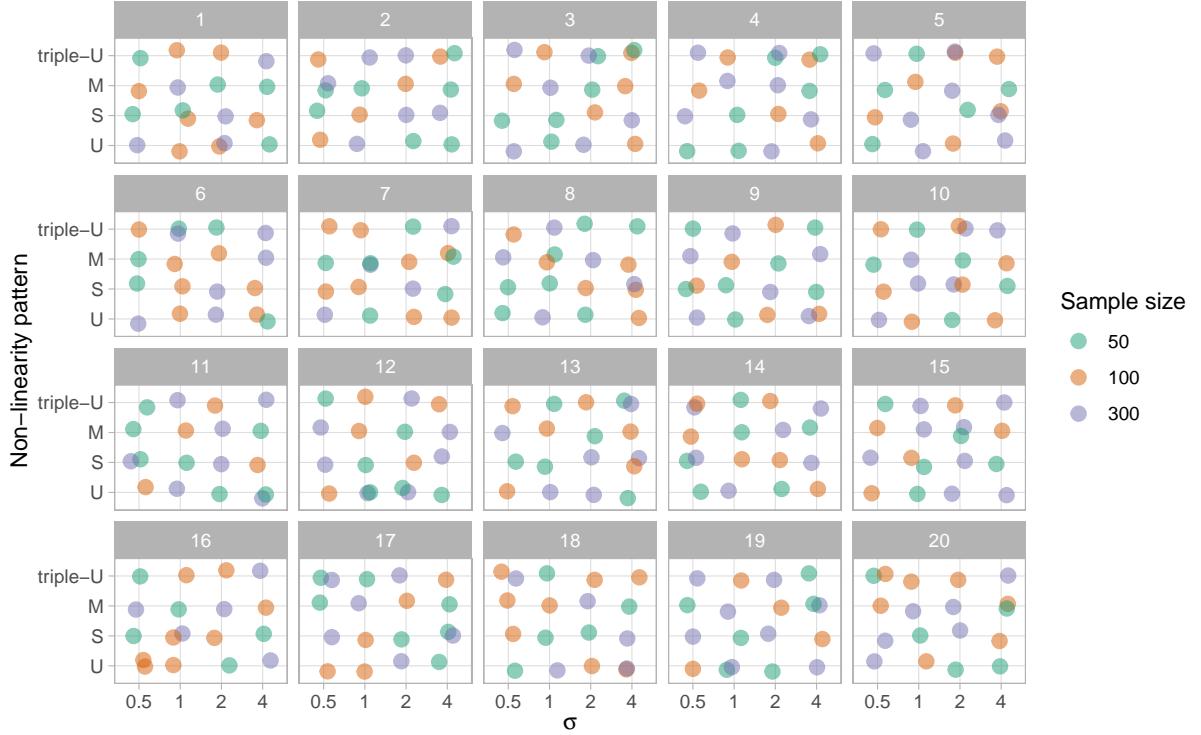


Figure A.5: Factor values assigned to the first 20 participants recruited during data collection period I, with data points slightly jittered to prevent overlap. Each participant have been exposed to all one-way and two-way factor combinations.

A.2.6 Data Collection Process

The survey data is collected via a self-hosted website designed by us. The complete architecture is provided in Figure A.7. The website is built with the `Flask` (Grinberg 2018) web framework and hosted on `PythonAnywhere` (PythonAnywhere LLP 2023). It is configured to handle HTTP requests such that participants can correctly receive webpages and submit responses. Embedded in the resources sent to participants, the `jsPsych` front-end framework (De Leeuw 2015) instructs participants' browsers to render an environment for running behavioural experiments. During the experiment, this framework will automatically collect common behavioural data such as response time and clicks on buttons. Participants' responses are first validated by a scheduled `Python` script run on the server, then push to a Github repository. Lineup images shown to users are saved in multiple Github repositories and hosted in corresponding Github pages. The URLs to these images are resolved by `Flask` and bundled in HTML files.

Once the participant is recruited from Prolific (Palan and Schitter 2018), it will be redirected to the entry page of our study website. An image of the entry page is provided in Figure A.8. Then, the participant needs to submit the online consent form and fill in the demographic information as shown in Figure A.9 and Figure A.10 respectively. Before evaluating lineups, participant also

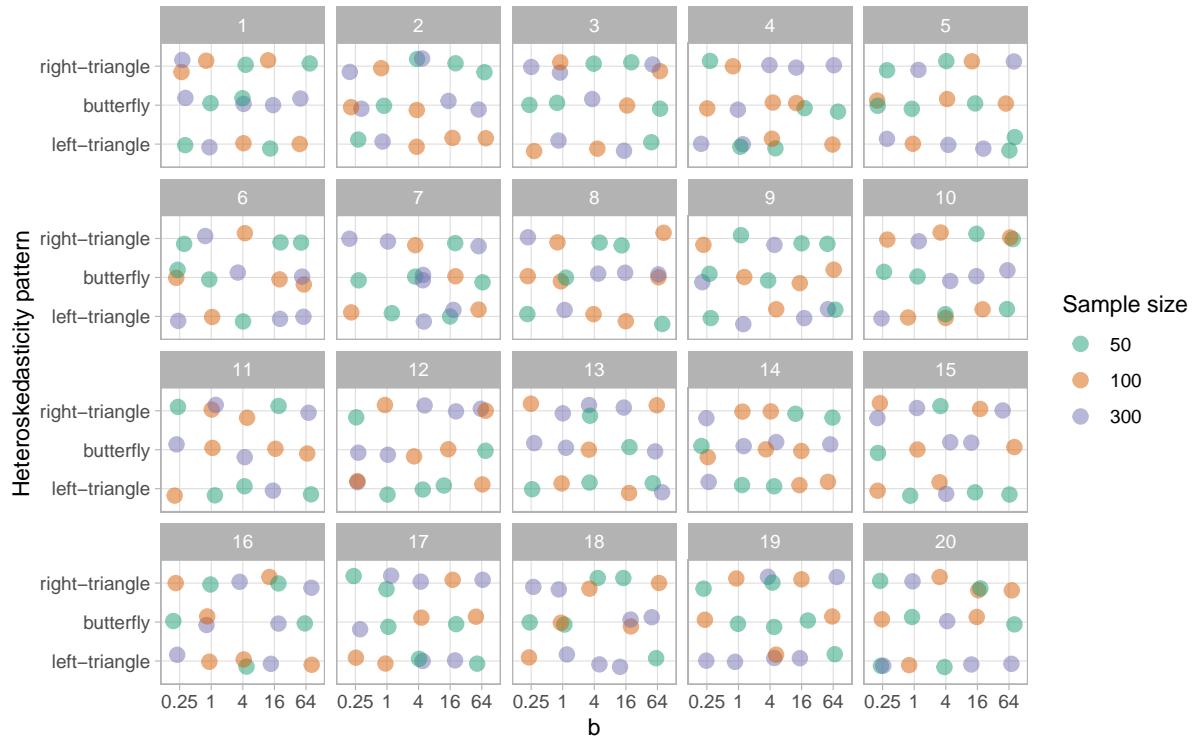


Figure A.6: Factor values assigned to the first 20 participants recruited during data collection period II, with data points slightly jittered to prevent overlap. Each participant appears to have been exposed to almost all one-way and two-way factor combinations. However, two participants, namely participant 16 and participant 18, were not presented with lineups containing a butterfly shape with $b = 4$. Additionally, participant 7 did not encounter a lineup featuring a butterfly shape with $b = 1$.

need to read the training page as provide in Figure A.11 to understand the process. An example of the lineup page is given in Figure A.12. A half of the page is taken by the lineup image to attract participant's attention. The button to skip the selections for the current lineup is intentionally put in the corner of the bounding box with smaller font size, such that participants will not misuse this functionality.

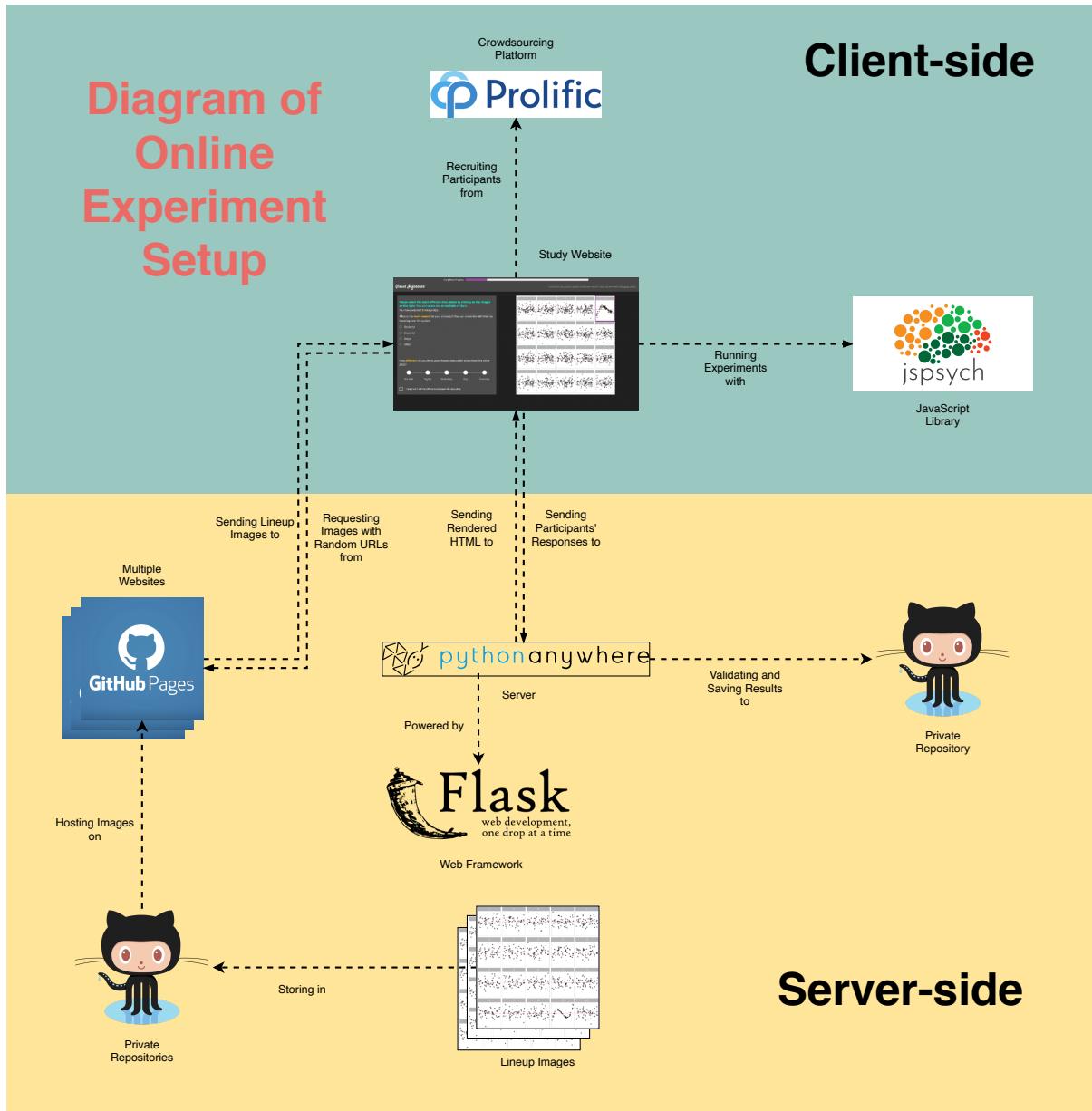


Figure A.7: Diagram of online experimental setup. The server-side of the study website uses Flask as backend hosted on PythonAnywhere. And the client-side uses jsPsych to run experiment.

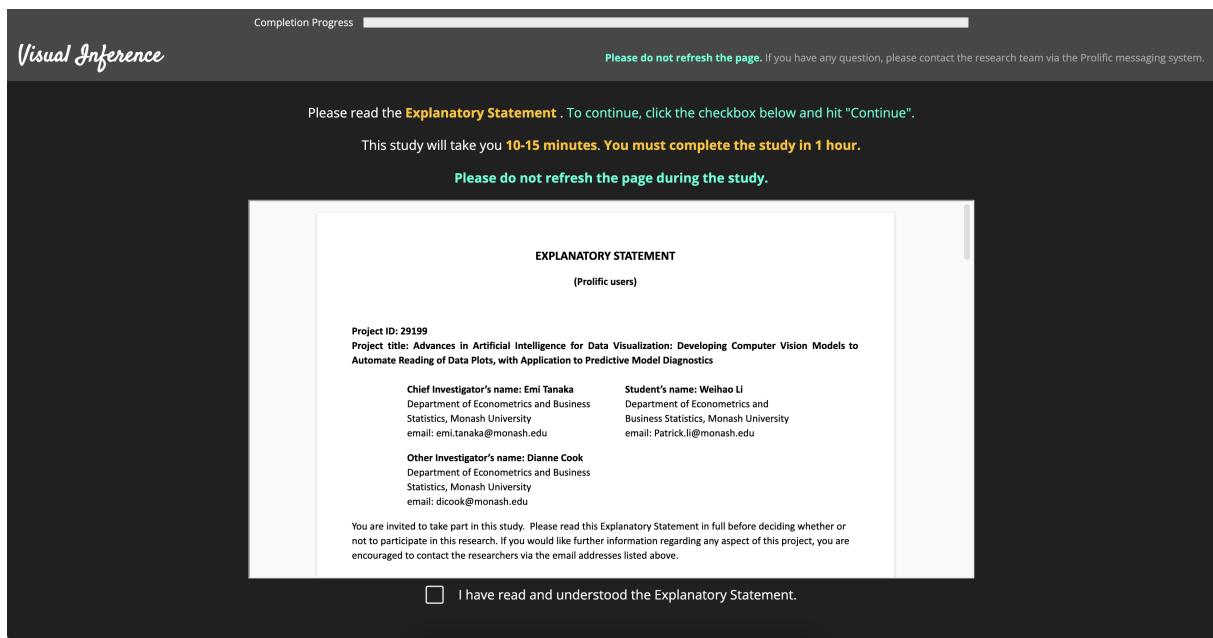


Figure A.8: The entry page of the study website.

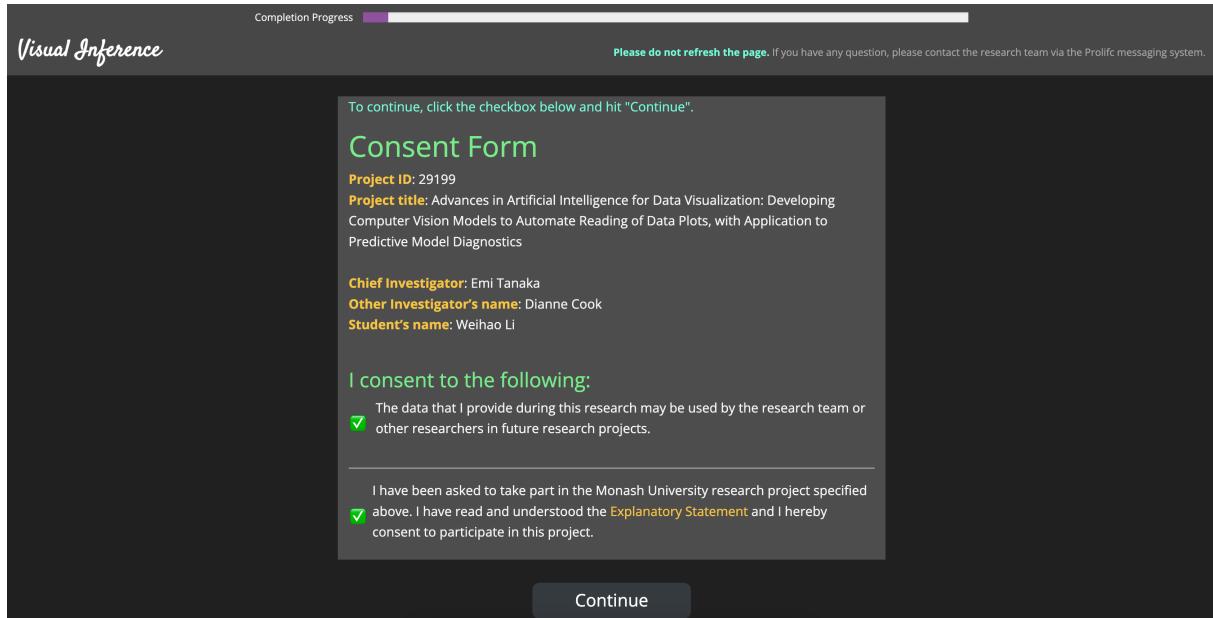


Figure A.9: The consent form provided in the study website.

Completion Progress 

Visual Inference

Please do not refresh the page. If you have any question, please contact the research team via the Prolific messaging system.

Survey Questions

Please enter your Prolific ID:

Prolific ID _____

Please select your age category:



18-24 25-39 40-54 55-64 65 or above

Please select your highest level of education:



High school or below Diploma and Bachelor Degree Honours Degree Masters Degree Doctoral Degree

Please select your preferred pronoun:

- He
- She
- They
- Other

Have you participated in any research that requires reading data graphs?

- Yes
- No

Figure A.10: The form to provide demographic information.

Completion Progress 

Visual Inference

Please do not refresh the page. If you have any question, please contact the research team via the Prolific messaging system.

Please read the [Training Page](#). To continue, click the checkbox below and hit "Continue".

Training Page (3 min read)

This document will provide you with the essential knowledge to finish the study.

1 Webpage layout

When you start the study, you will see a webpage like this:

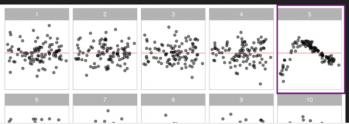
Completion Progress 

Visual Inference

Please select the most different data plot(s) by clicking on the images on the right. You can select one or multiple of them.
You have selected 0 data plot(s).

What is the **main reason** for your choice(s)? (You can check the definition by hovering over the option)

- Outlier(s)



I have read and understood the Training Page.

Figure A.11: The training page of the study website.

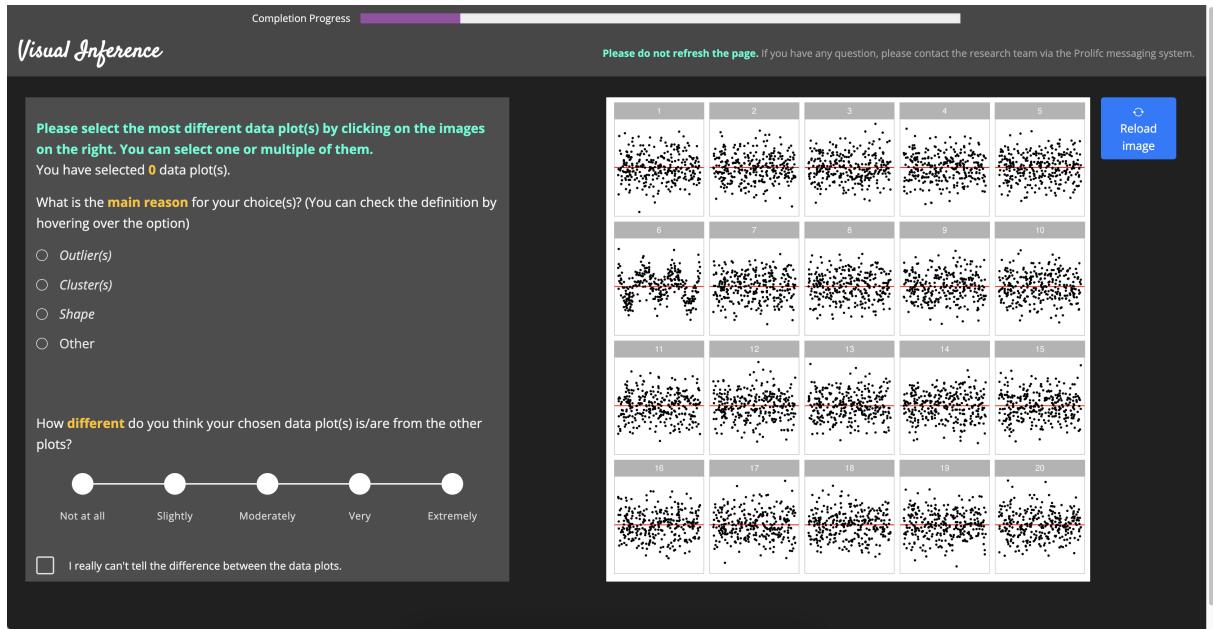


Figure A.12: The lineup page of the study website.

Table A.2: Count of lineups, evaluations and participants over departure types and data collection periods.

Number	Non-linearity			Heteroskedasticity			Total
	I	II	III	I	II	II	
Lineups	576	0	144	0	540	135	1116
Evaluations	2880	0	864	0	2700	810	7254
Participants	160	0	123	0	160	123	443

A.3 Analysis of Results Relative to Data Collection Process

A.3.1 Demographics

Throughout the study, we have collected 7254 evaluations on 1116 non-null lineups. Table A.2 gives further details about the number of evaluations, lineups and participants over pattern types and data collection periods.

Along with the responses to lineups, we have collected a series of demographic information including age, pronoun, education background and previous experience in studies involved data visualization. Table A.3, Table A.4, Table A.5 and Table A.6 provide summary of the demographic data.

It can be observed from the tables that most participants have Diploma or Bachelor degrees, followed by High school or below and the survey data is gender balanced. Majority of participants are between 18 to 39 years old and there are slightly more participants who do not have previous experience than those who have.

Table A.3: Summary of pronoun distribution of participants recruited in this study.

Pronoun	Period I	%	Period II	%	Period III	%	Total	%
He	77	17.4	79	17.8	61	13.8	217	49.0
She	78	17.6	77	17.4	61	13.8	216	48.8
Other	5	1.1	4	0.9	1	0.2	10	2.3
	160	36.1	160	36.1	123	27.8	443	100.0

Table A.4: Summary of age distribution of participants recruited in this study.

Age group	Period I	%	Period II	%	Period III	%	Total	%
18-24	83	18.7	86	19.4	51	11.5	220	49.7
25-39	69	15.6	63	14.2	63	14.2	195	44.0
40-54	6	1.4	8	1.8	6	1.4	20	4.5
55-64	2	0.5	3	0.7	3	0.7	8	1.8
	160	36.1	160	36.1	123	27.8	443	100.0

Table A.5: Summary of education distribution of participants recruited in this study.

Education	Period I	%	Period II	%	Period III	%	Total	%
High School or below	41	9.3	53	12.0	33	7.4	127	28.7
Diploma and Bachelor Degree	92	20.8	79	17.8	66	14.9	237	53.5
Honours Degree	6	1.4	15	3.4	6	1.4	27	6.1
Masters Degree	21	4.7	13	2.9	16	3.6	50	11.3
Doctoral Degree	0	0.0	0	0.0	2	0.5	2	0.5
	160	36.1	160	36.1	123	27.8	443	100.0

Table A.6: Summary of previous experience distribution of participants recruited in this study.

Previous experience	Period I	%	Period II	%	Period III	%	Total	%
No	96	21.7	88	19.9	67	15.1	251	56.7
Yes	64	14.4	72	16.3	56	12.6	192	43.3
	160	36.1	160	36.1	123	27.8	443	100.0

A.3.2 Data Collection Periods

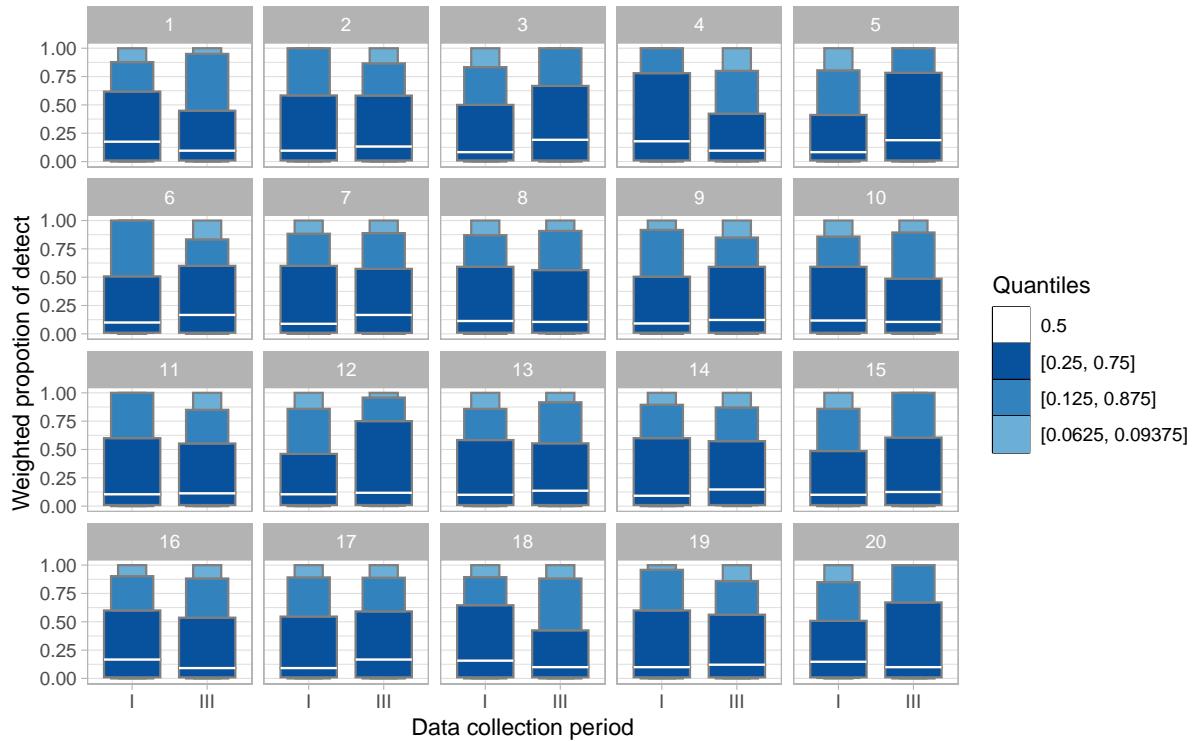


Figure A.13: A lineup of “letter-value” boxplots of weighted proportion of detect for lineups over different data collection periods for non-linearity model. Can you find the most different boxplot? The data plot is positioned in panel $2^3 - 1$.

We have the same type of model collected over different data collection periods, that may lead to unexpected batch effect. Figure A.13 and Figure A.14 provide two lineups to examine whether there is an actual difference across data collection periods for non-linearity model and heteroskedasticity model respectively. To emphasize the tail behaviour and display fewer outliers, we use the “letter-value” boxplot (Hofmann et al. 2017) which is an extension of the number of “letter value” statistics to check the weighed proportion of detect over different data collection period. The weighted proportion of detect is calculated by taking the average of c_i of a lineup over a data collection period. Within our research team, we can not identify the data plot from the null plots for these two lineups, result in p -values much greater than 5%. Thus, there is no clear evidence of batch effect.

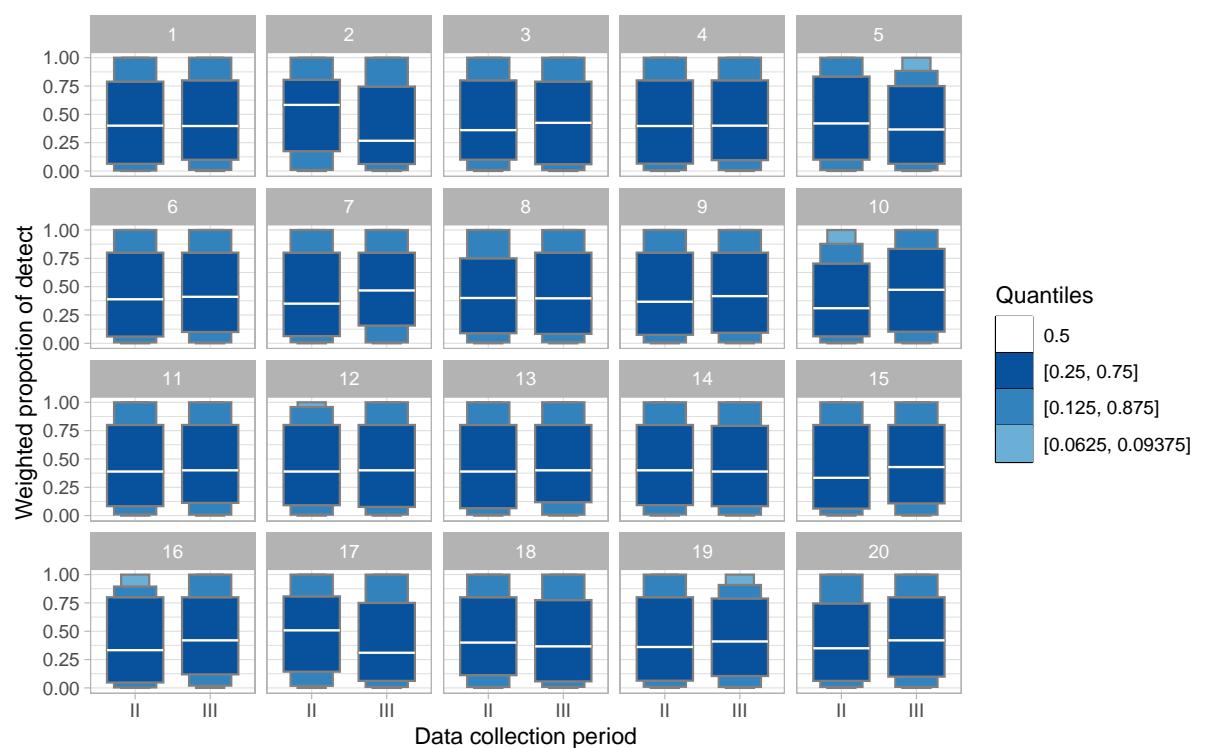


Figure A.14: A lineup of “letter-value” boxplots of weighted proportion of detect for lineups over different data collection periods for heteroskedasticity model. Can you find the most different boxplot? The data plot is positioned in panel $2^4 - 2$.