ARTICLE TEMPLATE

# Why aren't significance tests commonly used for linear regression diagnostics?

Weihao Li[a], Dianne Cook[a], Emi Tanaka[a], Susan VanderPlas[b]

[a]Department of Econometrics and Business Statistics, Monash University, Clayton, VIC, Australia; [b]Department of Statistics, University of Nebraska, Lincoln, Nebraska, USA

**ARTICLE HISTORY**
Compiled October 12, 2022

**ABSTRACT**
Abstract to fill.

**KEYWORDS**
data visualization; visual inference; hypothesis testing; residual plots;

## 1. Introduction

> *"Since all models are wrong the scientist must be alert to what is importantly wrong."* (Box 1976)

Diagnosing a model is the key to determining whether there is anything importantly wrong. For linear regression analysis, we typically interrogate the residuals for model diagnostics. 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. Residuals might be plotted, as a histogram or quantile-quantile plot to examine the distribution. Using the classical normal linear regression model as an example, if the distribution is symmetric and unimodal, it is well-behaved. But if the distribution is skewed, bimodal, multimodal, or contains outliers, there is cause for concern. The distribution could also be inspected by conducting a goodness of fit test, such as the Shapiro-Wilk Normality test (Shapiro and Wilk 1965).

Plotting the residuals against predicted values and each of the explanatory variables on a scatter plot is a recommend way to scrutinize their relationships. If there is any visually discoverable patterns, the model is potentially misspecified. However, correctly judging a residual plot where no pattern exists is a painstakingly difficult task for humans. It is especially common, particularly among new data analysts to report patterns when an experienced data analyst might quickly conclude that there are none. [ET: I don't know if the former statement is true?] Generally, one looks for noticeable departures from the model like non-linear dependency or heteroskedasticity. It is also possible to conduct hypothesis tests for non-linear dependence (Ramsey 1969),

CONTACT Weihao Li. Email: weihao.li@monash.edu, Dianne Cook. Email: dicook@monash.edu, Emi Tanaka. Email: emi.tanaka@monash.edu, Susan VanderPlas. Email: susan.vanderplas@unl.edu

and use a Breusch-Pagan test (Breusch and Pagan 1979) for heteroskedasticity.

Abundance of literature describe appropriate diagnostic methods for linear regression: Draper and Smith (1998), Montgomery and Peck (1982), Belsley, Kuh, and Welsch (1980), Cook and Weisberg (1999) and Cook and Weisberg (1982). The diligent reader of these sage writings will also notice sentences that express sentiments like *based on their experience, statistical tests are not widely used in regression diagnostics. The same or even larger amount of information can be provided by diagnostic plots than the corresponding tests in most empirical studies.* A common guidance by experts is that optimal method for diagnosing model fits is by plotting the data.

The persistence of this advice to check the plots is curious, and investigating why this might be common advice is the subject of this paper. The paper is structured as follows. The next background section describes the types of departures that one expects to detect, and describes a formal process for reading residual plots, called visual inference, that can avoid the concerns about subjectiveness of human readers [ET: CITATION HERE?]. Section 3 describes the experimental setup to compare the decision made by formal hypothesis testing, and how humans would read diagnostic plots. The results are reported in Section 4. We finish with a discussion on future work, in particular how the responsibility for residual plot reading might be passed on to computer vision.

## 2. Background

### 2.1. *Departures from good residual plots*

(This section discusses the visual patterns data analysts expect to see and their implications.)

Graphical summaries in which residuals are plotted against fitted values or other functions of the predictor variables that are approximately orthogonal to residuals are referred to as standard residual plots in Cook and Weisberg (1982). As shown in Figure 1, the top-left panel is a good residual plot with residuals evenly distributed at both sides of the horizontal zero line showing no noticeable patterns. There are various types of departures from a good residual plot.

Non-linearity, heterskedasticity and non-normality are perhaps the three mostly checked departures. Non-linearity is a type of model misspecification caused by failing to include higher order terms of the regressors in the regression equation. Any non-linear functional form of residuals on fitted values presented in the residual plot could be considered as an indicative of non-linearity. An example residual plot containing visual pattern of non-linearity is given at the top-right of Figure **??**. One can clearly observe the "S-shape" from the residual plot as the cubic term is not captured by the misspecified model.

Heteroskedasticity refers to the presence of nonconstant error variance in a regression model. It is mostly due to the strict but false assumptions on the variance-covariance matrix of the error term. The usual pattern of heteroskedasticity on a residual plot is the inconsistent spread of the residuals across the horizontal axis. Visually, it sometimes results in the so-called "butterfly" shape as shown in the bottom-left panel of Figure **??**, or the "left-triangle" and "right-triangle" shape where the smallest variance occurs at one side of the horizontal axis.

Compared to non-linearity and heteroskedasticity, non-normality is usually harder to detect from a residual plot since scatter plot do not readily reveal the marginal

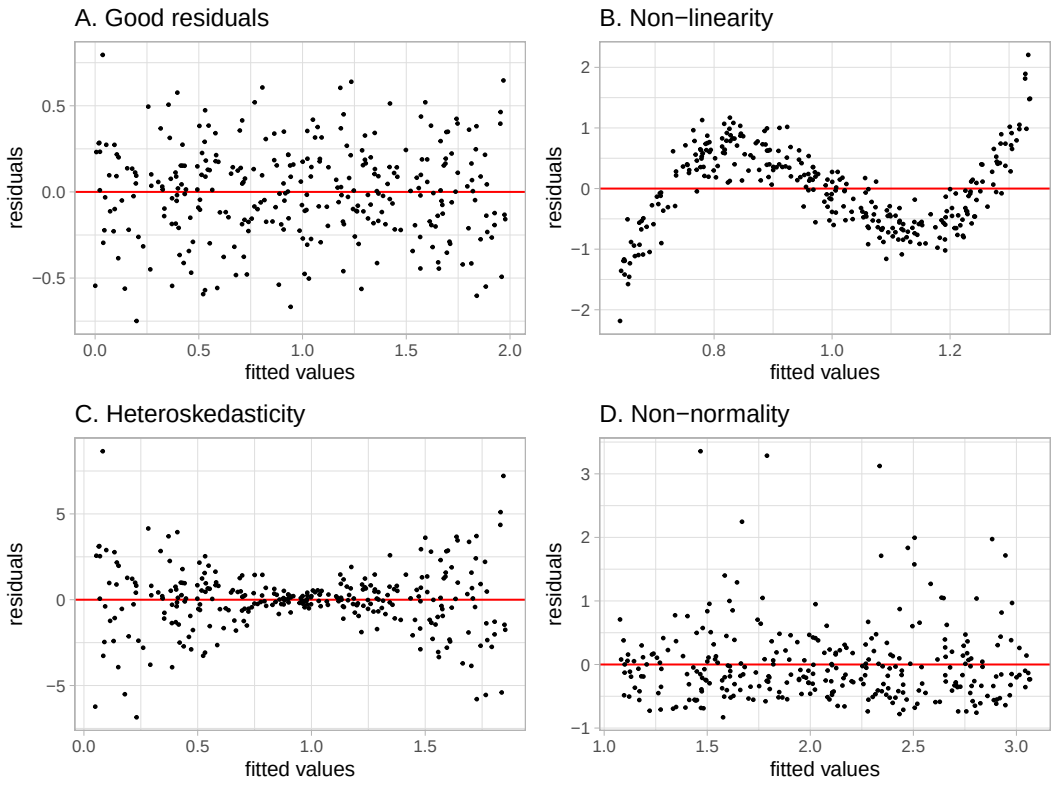



**Figure 1.** Example fitted vs residual plots: (A) classically good looking residuals, (B) non-linear pattern indicates that the model has not captured a non-linear association, (C) heteroskedasticity indicating that variance around the fitted model is not uniform, and (D) non-normality where the residual 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 plot.

distribution. A favourable graphical summary for this task is the quantile-quantile plot. However, for a consistent comparison, residual plot will be the focus of this paper. Besides, it is important to note that not all regression models assume normality for the error term, but a certain amount do including the classical normal linear regression model. In the case that the normality assumption is violated, it is expected to observe data points do not center around the horizontal axis and there is an uneven distribution of the number points at both below and above the horizontal axis. For example, given a skewed error distribution, fewer data points and more outliers are on one side of the horizontal axis as shown in plot D of Figure 1.

### 2.2. *Conventionally testing for departures*

(This section discusses the tests that will be used in the analysis and shows the results for the residual plots displayed in the previous section.)

Other than checking diagnostic plots, analysts may perform formal hypothesis testing for detecting model defects. Depending on the alternative hypothesis that is focused on, a variety of tests can be applied. For example, the presence of heteroskedasticity can usually be tested by applying the White test (White 1980) or the Breusch-Pagan 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. For testing non-linearity, one may apply the F-test as a model structural test to examine the significance of specific polynomial and non-linear forms of the regressors, or the significance of proxy variables as in the Ramsey Regression Equation Specification Error Test (RESET) (Ramsey 1969). And for testing normality, the Shapiro–Wilk test [ref here] is perhaps the most widely used test included by many of the statistical softwares. Another choice will be the Jarque–Bera test [ref here] which directly checks if the sample skewness and kurtosis match a normal distribution.

Example residual plots given in Figure 1 are examined by the corresponding model structural test, Breusch-Pagan test and Shapiro–Wilk test as shown in Table 1. In the example, both the Breusch-Pagan test and the Shapiro–Wilk test rejects the null hypothesis for departures that they do not intend to examine. As discussed in Cook and Weisberg (1982), most residual-based tests for a particular type of departure from model assumptions are sensitive to other types of departures. It is likely the null hypothesis is correctly rejected but for the wrong reason, which is known as the "Type III error". Additionally, outliers will often incorrectly trigger the rejection of the null hypothesis despite when majority of the residuals are well-behaved (Cook and Weisberg 1999). This can be largely avoided in diagnostic plots as experienced analysts can evaluate the acceptability of assumptions flexibly, even in the presence of outliers.

### 2.3. *Visual testing for departures*

(This section introduces the lineup protocol, and briefly discusses the method for sampling null data, calculating the p-value and estimating power.)

#### *2.3.1. Lineup protocol*

Unlike hypothesis testing built upon rigorous statistical procedures, reading diagnostic plots relies on graphical perception - human's ability to interpret and decode the

**Table 1.** Statistical significance testing for departures from good residuals for plots in Figure 1. Shown are the $p$-values calculated for the conventional Model structural, the Breusch-Pagan and the Shapiro–Wilk 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 | Model structural | Breusch-Pagan | Shapiro–Wilk |
|---|---|---|---|---|
| A | None | 0.434 | 0.133 | 0.728 |
| B | Non-linearity | *0.000* | *0.000* | *0.039* |
| C | Heteroskedasticity | 0.378 | *0.000* | *0.000* |
| D | Non-normality | 0.667 | 0.736 | *0.000* |

information embedded in the graph (Cleveland and McGill 1984), which is to some extent subjective and indecisive. Further, visual discovery suffers from its unsecured and unconfirmed nature where the degree of the presence of the visual features typically can not be measured quantitatively and objectively, which may lead to over or under-interpretations of the data. One such example is finding an over-interpretation of the separation between gene groups in a two-dimensional projection from a linear discriminant analysis when in fact there are no differences in the expression levels between the gene groups and separation is not an uncommon occurrence (Roy Chowdhury et al. 2015).

Visual inference was first introduced in a 1999 Joint Statistical Meetings (JSM) talk with the title "Inference for Data Visualization" by Buja, Cook, and Swayne (1999) as an idea to address the issue of valid inference for visual discoveries of data plots (Gelman 2004). Later, Buja et al. (2009) proposed the lineup protocol as a visual test inspired by the "police lineup" or "identity parade" which is the act of asking the eyewitness to identify criminal suspect from a group of irrelevant people. The protocol consists of $m$ randomly placed plots, where one plot is the actual data plot, and the remaining $m-1$ plots have the identical graphical production as the data plot except the data has been replaced with data consistent with the null hypothesis. Then, an observer who have not seen the actual data plot will be asked to point out the most different plot from the lineup. Under the null hypothesis, it is expected that the actual data plot would have no distinguishable difference with the null plots, and the probability of the observer correctly picks the actual data plot is $1/m$. If we reject the null hypothesis as the observer correctly picks the actual data plot, then the Type I error of this test is $1/m$.

Figure 2 is an example of a lineup protocol. If the actual data plot at position 11 is identifiable, then it is evidence for the rejection of the null hypothesis that the regression model is correctly specified. In fact, the actual residual plot is obtained from a misspecified regression model with non-linearity issue.

The effectiveness of lineup protocol has already been validated by Majumder, Hofmann, and Cook (2013) under relatively simple classical normal linear regression model settings with only one or two regressors. Their results suggest visual test is capable of testing the significance of a single regressor with a similar power as a t-test, though they expressed that in general it is unnecessary to use visual inference if there exists a conventional test and they didn't expect the visual test to perform equally well as the conventional test. In their third experiment, where there does not exist a proper conventional test, visual test outperforms the conventional test for a large margin. This is encouraging as it promotes the use of visual inference in border field of data science

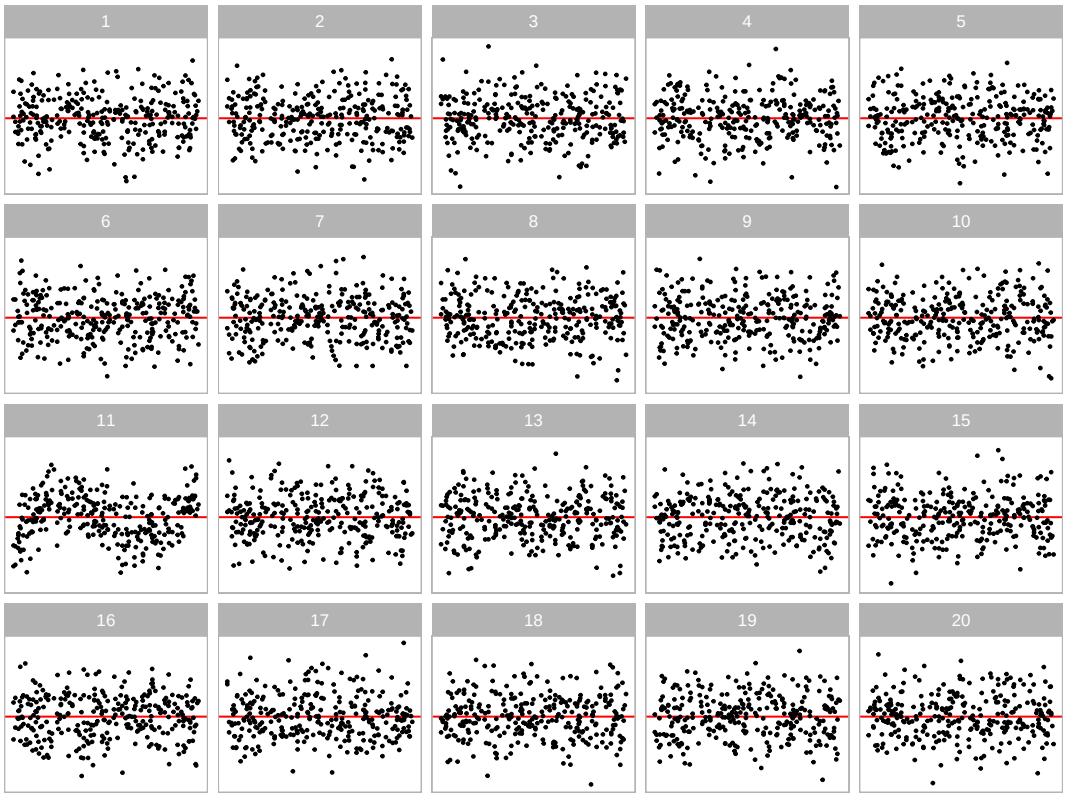



**Figure 2.** Visual testing is conducted using a lineup, as in the example here. The residual plot computed from the observed data (plot 11, exhibiting non-linearity) is embedded among 19 null plots, where the residuals were simulated from a standard error model. Computing the $p$-value requires that 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 plot 11.

where there are no existing statistical testing procedures. In fact, lineup protocol has been integrated successfully into diagnostic tools of hierarchical linear models (Loy and Hofmann 2013).

### *2.3.2. Sampling from the null distribution*

Data used in the $m-1$ null plots need to be simulated. In the context of regression diagnostics, sampling data from $H_0$ is equivalent to sampling data from the assumed model. As Buja et al. (2009) suggested, $H_0$ is usually composited by a collection of distributions 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 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. 2009). Essentially, null residuals can be simulated by regressing $N$ i.i.d standard normal random draws on the regressors, then rescaling it by the ratio of residual sum of square in two regressions.

### *2.3.3. Calculating p-values*

Further, a visual test can involve $K$ independent observers. Let $D_i = \{0, 1\}$ be a binomial random variable denoting whether subject $i$ correctly detecting the actual data plot, and $X = \sum_{i=1}^{K} X_i$ be the number of observers correctly picking the actual data plot. Then, by imposing a relatively strong assumption on the visual test that all $K$ evaluations are fully independent, under the null hypothesis, $X \sim \text{Binom}_{K,1/m}$. Therefore, the $p$-value of a lineup of size $m$ evaluated by $K$ observer is given as $P(X \geq x) = 1 - F(x) + f(x)$, where $F(.)$ is the cumulative distribution function, $f(.)$ is the probability mass function and $x$ is the realization of number of observers correctly picking the actual data plot (Majumder, Hofmann, and Cook 2013).

As pointed out by VanderPlas et al. (2021), the binomial model doesn't take into account the possible dependencies in the visual test due to repeated evaluations of the same lineup. And it is inapplicable to visual test where subjects are asked to select one or more "most different" plots from the lineup. They summarized three common scenarios in visual inference: (1) $K$ different lineups are shown to $K$ subjects, (2) $K$ lineups with different null plots but the same actual data plot are shown to $K$ subjects, and (3) the same lineup is shown to $K$ subjects. Out of these three scenarios, Scenario 3 is the most common in previous studies as it puts the least constraints on the experimental design. For Scenario 3, VanderPlas et al. (2021) modelled the probability of a plot $i$ being selected from a lineup as $\theta_i$, where $\theta_i \sim Dirichlet(\alpha)$ for $i = 1, ..., m$ and $\alpha > 0$. And defined $c_i$ to be the number of times plot $i$ being selected in $K$ evaluations. In case subject $j$ makes multiple selections, $1/s_j$ will be added to $c_i$ instead of one, where $s_j$ is the number of plots subject $j$ selected for $j = 1, ...K$. This ensured $\sum_i c_i = K$. Since we are only interested in the selections of the actual data plot $i$, the marginal model can be simplified to a beta-binomial model and thus the visual p-value is given as

$$P(C \geq c_i) = \sum_{x=c_i}^{K} \binom{K}{x} \frac{B(x+\alpha, K-x+(m-1)\alpha)}{B(\alpha,(m-1)\alpha)}, \tag{1}$$

where $B(.)$ is the beta function defined as

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

Note that Equation 1 only works with integer $c_i$. For non-integer $c_i$, linear approximation will be applied to calculate the p-value

$$P(C \geq c_i) = P(C \geq \lceil c_i \rceil) + (\lceil c_i \rceil - c_i)P(C = \lfloor c_i \rfloor), \quad \text{for} \quad c_i \notin \mathbb{Z}. \tag{3}$$

Besides, the parameter $\alpha$ used in Equation 1 is usually unknown and hence needs to be estimated from the survey data. For low values of $\alpha$, only a few plots are attractive to the observers and tend to be selected. For higher values of $\alpha$, the distribution of the probability of each plot being selected is more evenly. VanderPlas et al. (2021) defined that a plot is $c$-interesting if $c$ or more participants selected the plot as the most different. Given the definition, The expected number of plots selected at least $c$ times, $E[Z_c]$, is calculated as

$$E[Z_c(\alpha)] = \frac{m}{B(\alpha,(m-1)\alpha)} \sum_{\lceil c \rceil}^{K} \binom{K}{x} B(x+\alpha, K-x+(m-1)\alpha). \tag{4}$$

VanderPlas et al. (2021) suggested that $\alpha$ can be estimated using MLE and Equation 4. But for precise estimate of $\alpha$, additional responses to Rorschach lineups, which is a type of lineup consists of only null plots, are required.

#### *2.3.4. Power calculation*

As discussed in Majumder, Hofmann, and Cook (2013), individual's skill will affect the number of observers who identify the actual data plot from the lineup. Thus, the power of a visual test depends on the subject-specific abilities. Previously, it was addressed by modelling the probability of a subject $i$ correctly picking the actual data plot from a lineup $l$ using a mixed-effect logistic regression with the subject being treated as a random effect (Majumder, Hofmann, and Cook 2013). However, having this probability is insufficient to determine the power of a visual test allowed for multiple selections as it doesn't provide information about the number of selections made by the subject for p-value calculation.

Instead, we directly estimated the probability of a lineup being rejected using a logistic regression with the natural logarithm of the effect size as the only regressor formulated as

$$Pr(\text{reject } H_0|H_1, E) = \Lambda(\beta_0 + \beta_1 log_e(\boldsymbol{E})), \tag{5}$$

where $\Lambda(.)$ is the standard logistic function given as $\Lambda(z) = exp(z)/(1 + exp(z))$.

Effect $E$ is derived from the Kullback-Leibler divergence (see [appendix ref here]) formulated as

$$E = \frac{1}{2\sigma^2} \boldsymbol{X}'_b \boldsymbol{R}'_a (diag(\boldsymbol{R}_a))^{-1} \boldsymbol{R}_a \boldsymbol{X}_b, \tag{6}$$

where $diag(.)$ is the diagonal matrix constructed from the diagonal elements of $\boldsymbol{R}_a$.

To study various factors contributing to the power of the visual test, the same logistic regression model is fit on different subsets of the collated data grouped by levels of factors. This includes [expansion].

## 3. Experimental design

(This section discusses the experimental design including the motivation of the experiment, an overview of the experiment, the simulation setting of the depatures from good residual plots, parameter choices, allocation of the lineups and other technical details.)

Three experiments were conducted to investigate the difference between conventional hypothesis testing and visual inference in the application of linear regression diagnostics. The experiment I has ideal scenario for conventional testing, where the visual test is not expected to outperform the conventional test. Meanwhile, the experiment II is a scenario where the conventional test is an approximate test, in which the visual test may have a chance to match the performance of the conventional test. The experiment III is designed for collecting human responses to lineup with only good residual plots such that the parameter $\alpha$ in Equation 1 can be estimated. Overall, we planned to collect 7974 evaluations on 1152 uniqued lineups performed by 443 subjects throughout three experiment.

### 3.1. *Simulating departures*

Two types of departures, namely non-linearity and heteroskedasticity, were considered with the corresponding data generating process being designed for experiment I and II.

#### *3.1.1. Non-linearity*

Experiment I is designed to study the ability of human subjects to detect the effect of a non-linear term $\boldsymbol{z}$ constructed using Hermite polynomials [Hermite ref here] on random vector $\boldsymbol{x}$ formulated as

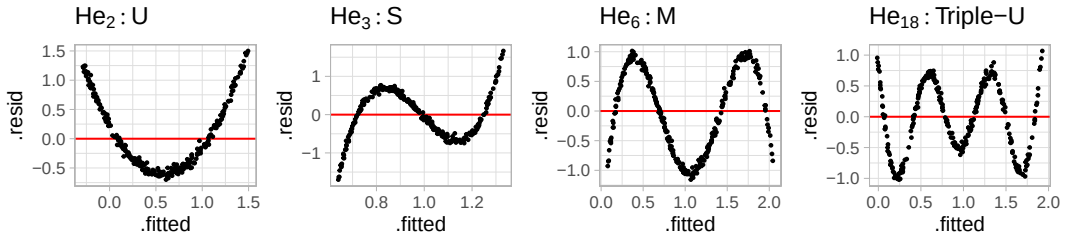



**Figure 3.** Polynomial forms generated for the residual plots used in experiment I. The four shapes are generated by varying the order of polynomial given by $j$ in $He_j(.)$.

**Table 2.** Summary of factors involved in the study.

| Order of Hermite polynomial ($j$) | Distribution of $X_{raw}$ | Standard deviation of polynomial model ($\sigma$) | Shape of heteroskedasticity ($a$) | Variance factor of heteroskedasticity model ($b$) | Sample size ($n$) |
|---|---|---|---|---|---|
| 2 | $U(-1,1)$ | 0.25 | -1 | 0.25 | 50 |
| 3 | $N(0,0.3^2)$ | 1 | 0 | 1 | 100 |
| 6 | $lognormal(0,0.6^2)/3$ | 2 | 1 | 4 | 300 |
| 18 | $U\{1,5\}$ | 4 | | 16 | |
| | NA | | | 64 | |

$$\boldsymbol{y} = 1 + \boldsymbol{x} + \boldsymbol{z} + \boldsymbol{\varepsilon}, \tag{7}$$

$$\boldsymbol{x} = g(\boldsymbol{x}_{raw}, 1), \tag{8}$$

$$\boldsymbol{z} = g(\boldsymbol{z}_{raw}, 1), \tag{9}$$

$$\boldsymbol{z}_{raw} = He_j(g(\boldsymbol{z}, 2)), \tag{10}$$

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

$$g(\boldsymbol{x}, k) = (\boldsymbol{x} - min(\boldsymbol{x}))/max(\boldsymbol{x} - min(\boldsymbol{x}))2k - k, \quad \text{for} \quad k > 0. \tag{11}$$

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

$$\boldsymbol{y} = \beta_0 + \beta_1 \boldsymbol{x} + \boldsymbol{u}, \tag{12}$$

where $\boldsymbol{u} \sim N(\boldsymbol{0}, \sigma^2 \boldsymbol{I}_n)$.

Since $z = O(x^j)$, for $j > 1$, $z$ is a higher order term leaves out by the null regression, which will result in model misspecification. Visual patterns of non-linearity were simulated using four different order of probabilist's Hermite polynomials ($j = 2, 3, 6, 18$) and four different distribution of $X_{raw}$: (1) $U(-1, 1)$, (2) $N(0, 0.3^2)$, (3) $lognormal(0, 0.6^2)/3$ and (4) $u\{1, 5\}$. A summary of the factors is given in Table 2.

The values of $j$ was chosen so that distinct shapes of non-linearity were included in the residual plot. A greater value of $j$ will result in a curve with more turning points. As shown in Figure 3, it includes "U" shape, "S" shape, "M" shape and "Triple-U" shape. It is expected that the "U" shape will be the easiest one to detect because complex shape tends to be concealed by cluster of data points.

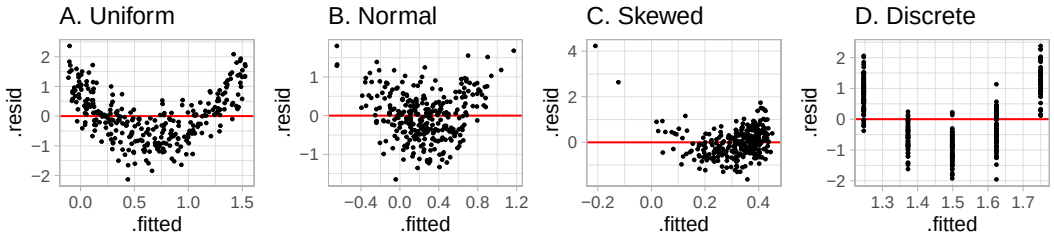



**Figure 4.** Variations in fitted values, that might affect perception of residual plots. Four different distribution of $x_{raw}$ are used in the experiment to provide various visual patterns.

Four different distribution were used to generate $X_{raw}$ as shown in Figure 4. The uniform and the normal distribution are symmetric and commonly assumed in statistical models. The adjusted log-normal distribution provides skewed density, while the discrete uniform distribution provides discreteness in residual plot, which could enrich the pool of visual patterns.

Figure 5 shows one of the lineups used in experiment I. This lineup was produced under $j = 6$ and $X_{raw} \sim N(0.0.3^2)$. The actual data plot location was four. All five subjects correctly identified the actual data plot for this lineup.

### *3.1.2. Heteroskedasticity*

Experiment II is designed to study the ability of human subjects to detect the appearance of a heteroskedasticity pattern under a simple linear regression model setting:

$$\boldsymbol{y} = 1 + \boldsymbol{x} + \boldsymbol{\varepsilon}, \tag{13}$$

$$\boldsymbol{x} = g(\boldsymbol{x}_{raw}, 1) \tag{14}$$

$$\boldsymbol{\varepsilon} \sim N(\boldsymbol{0}, 1 + 2 - |a|b(\boldsymbol{x} - a)^2\boldsymbol{I}), \tag{15}$$

$$\tag{16}$$

where $\boldsymbol{y}$, $\boldsymbol{x}$, $\boldsymbol{\varepsilon}$ are vectors of size $n$ and $g(.)$ is the scaling function defined in 11.

The null regression model used to fit the realizations generated by the above model is formulated exactly the same as Equation 12.

For $b \neq 0$, the variance-covariance matrix of the error term $\boldsymbol{\varepsilon}$ is correlated with the regressor $x$, which will lead to the presence of heteroskedasticity. Visual patterns were simulated using three different shapes ($a$ = -1, 0, 1) and the same four different distribution of $X_{raw}$ used in experiment I. A summary of the factors is given in Table 2.

The values of $a$ was chosen so that different shapes of heteroskedasticity were included in the residual plot. These include left-triangle shape, butterfly shape and right-triangle shape as displayed in Figure 6.

An example lineup of this model is shown in Figure 7 with $a = -1$ and $X_{raw} \sim U(-1, 1)$. The actual data plot location was 15. 8 out of 11 subjects correctly identified the actual data plot for this lineup.

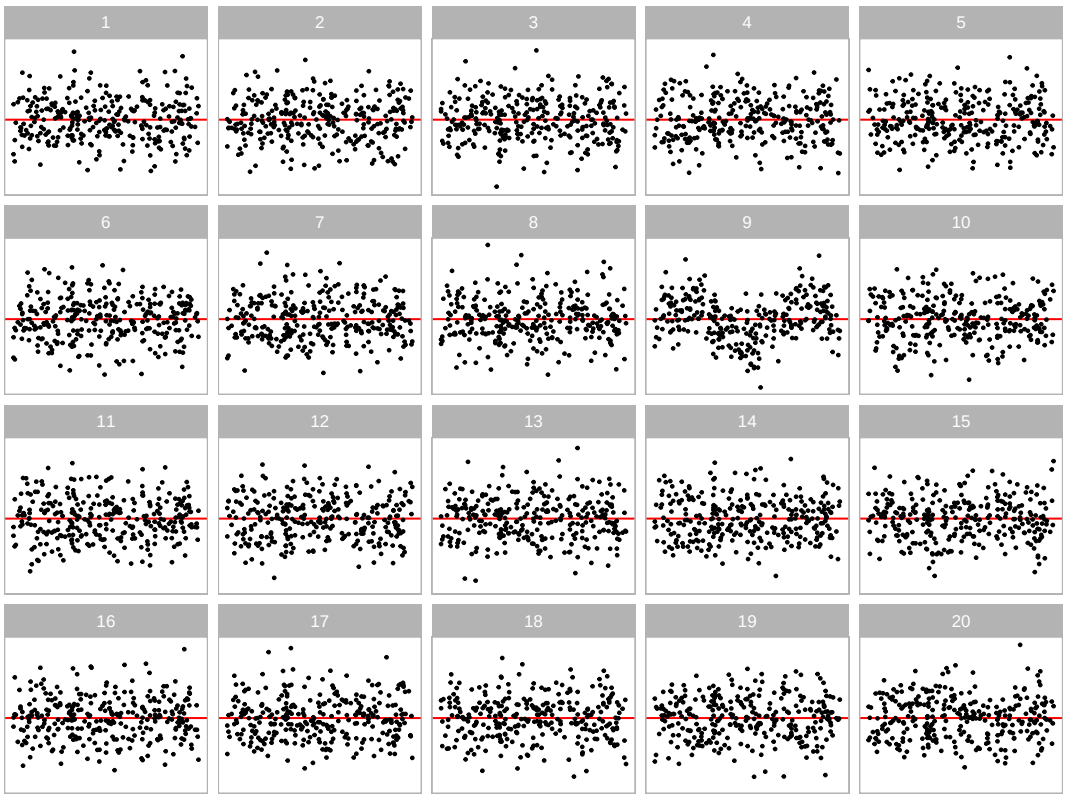



**Figure 5.** Lineup poly-24 in experiment I. Can you spot the most different plot?

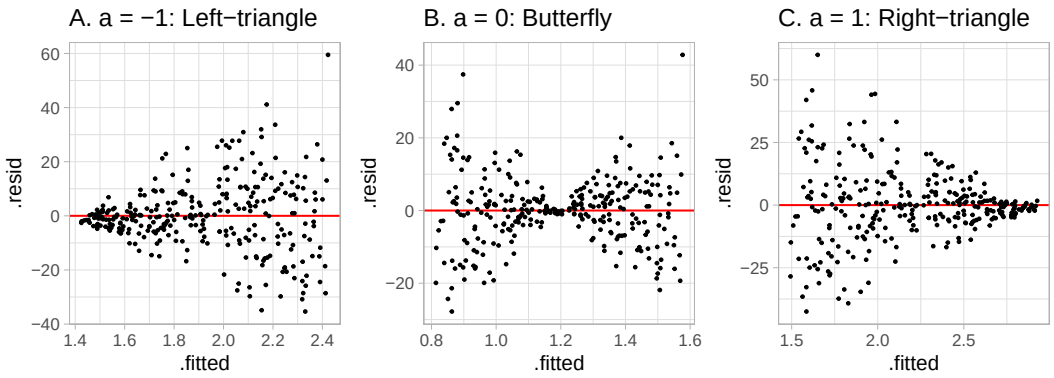



**Figure 6.** Heteroskedasticity forms used in experiment II. Three different shapes (a = -1, 0, 1) are used in the experiment to create left-triangle, butterfly and right-triangle shapes.

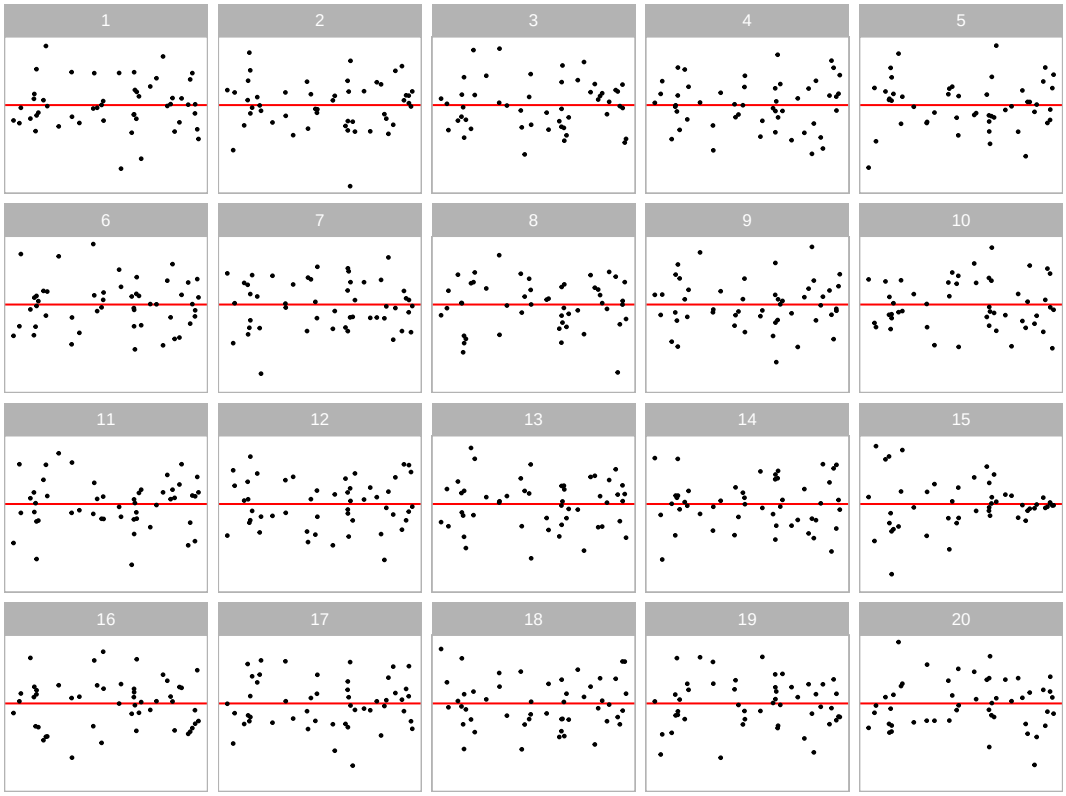



**Figure 7.** Lineup heter-169 in experiment II. Can you spot the most different plot?

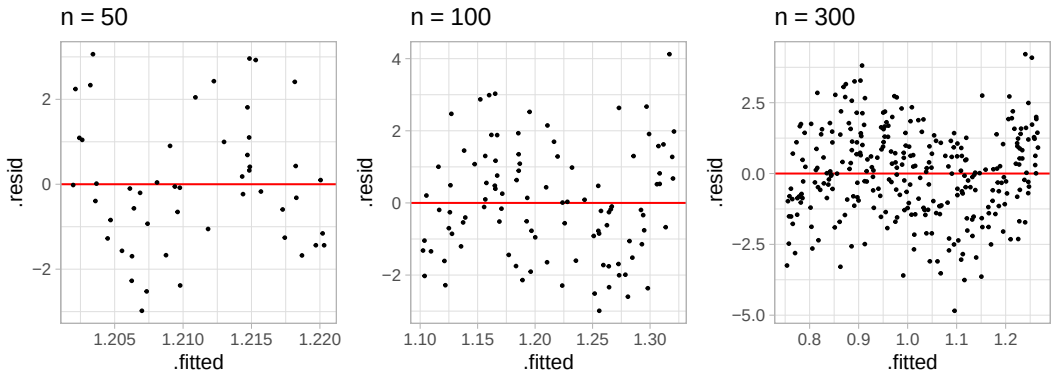



**Figure 8.** Three different values of $n$ are used in experiment I, II and III to control the strength of the signal.

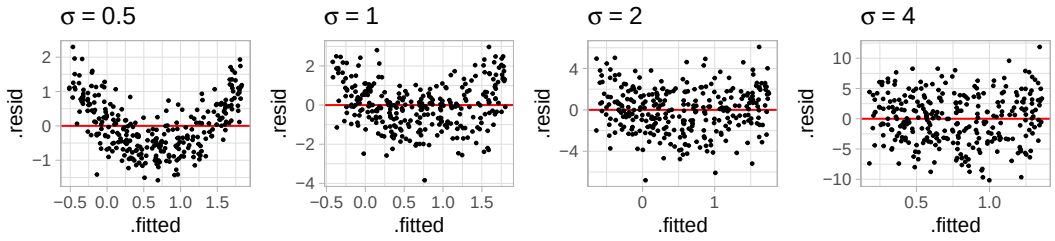



**Figure 9.** Four different values of $\sigma$ are used in the experiment I to control the strength of the signal.

## 3.2. *Experimental setup*

### *3.2.1. Controlling the strength of the signal*

As summarised in Table 2, three additional parameters $n$, $\sigma$ and $b$ were used to control the strength of the signal so that different difficulty levels of lineups were generated, and therefore, the estimated power curve would be smooth and continuous. Parameter $\sigma \in \{0.5, 1, 2, 4\}$ and $b \in \{0.25, 1, 4, 16, 64\}$ were used in experiment I and II respectively. Figure 9 and 10 demonstrate the impact of these two parameters. A large value of $\sigma$ will increase the variation of the error of the non-linear model and decrease the visibility of the visual pattern. The parameter $b$ controls the ratio of the standard deviation of the heteroskedasticity across the domain of the regressor. Given $x \neq a$, a larger value of $b$ will lead to a larger ratio of the variance at $x$ to the variance at $x - a = 0$, making the visual pattern more obvious.

Three different sample sizes were used (n = 50, 100, 300) in all three experiments. It can be observed from Figure 8 that with fewer data points drawn in a residual plot, the visual pattern is more difficult to be detected.

### *3.2.2. Subject allocation*

Three replications are made for each of the parameter values shown in Table **??** resulting in $(4 \times 4 \times 4 \times 3 + 4 \times 3 \times 5 \times 3) \times 3 = 1116$ different lineups. In addition, each lineup is designed to be evaluated by five different subjects. After attempting some pilot studies internally in our research group, we decide to present a block of 20 lineups to every subject. And to ensure the quality of the survey data, two lineups with obvi-

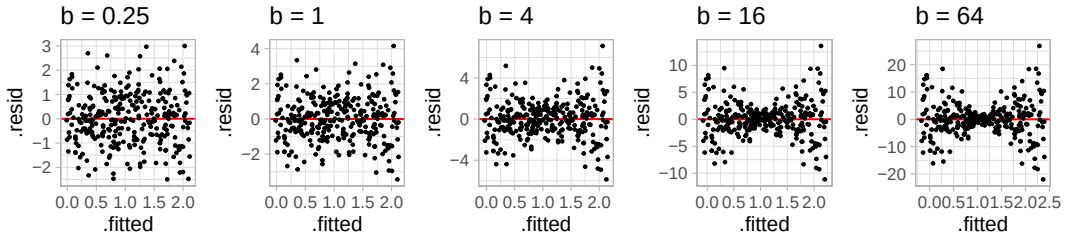



**Figure 10.** Five different values of $b$ are used in experiment II to control the strength of the signal.

ous visual patterns are included as attention checks. Thus, $576 \times 5/(20-2) = 160$ and $540 \times 5/(20-2) = 150$ subjects were recruited to satisfy the design of the experiment I and experiment II respectively.

As mentioned in Section [the alpha section], $\alpha$ used in Equation **??** needs to be estimated using Rorschach lineups. Hence, 36 Rorschach lineups with all combinations of $n$ and $X_{raw}$ and three replications are designed to be included in experiment III. All Rorschach lineups are planned to be evaluated by 20 subjects. However, presenting only Rorschach lineups to subjects are considered to be bad practices as subjects will lose interest quickly. We planned to also collect 6 more evaluations on the 279 lineups with uniform distribution, resulted in $(36 \times 20 + (4 \times 4 \times 3 + 3 \times 5 \times 3) \times 3)/(20-2) = 133$ subjects recruited for experiment III.

#### *3.2.3. Collecting results*

Subjects for all three experiments were recruited from an crowdsourcing platform called Prolific [ref here]. Prescreening procedure was applied during the recruitment, subjects were required to be fluent in English, with 98% minimum approval rate in other studies and 10 minimum submissions. During the experiment, every subject was presented with a block of 20 lineups. For each lineup, the actual data plot was drawn as a standard residual plot of the null model 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 helping line. The 19 null datasets were generated by the residual rotation technique, and plotted in the same way. The lineup consisted of 20 residual plots with one randomly placed actual data plot. And for every lineup, the subject 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 were from others. If there was no noticeable difference between plots in a lineup, subjects were permitted to select zero plots without providing the reason. No subject was shown the same lineup twice. Information about preferred pronoun, age group, education, and previous experience in visual experiment were also collected. A subject's submission was only accepted if the actual data plot was identified for at least one attention check. Data of rejected submissions were discarded automatically to maintain the overall data quality.

## 4. Results

### 4.1. *Data overview*

Subjects recruited from Prolific received a fixed payment for participating in the experiment. However, some subjects will try to maximize their earnings for minimum

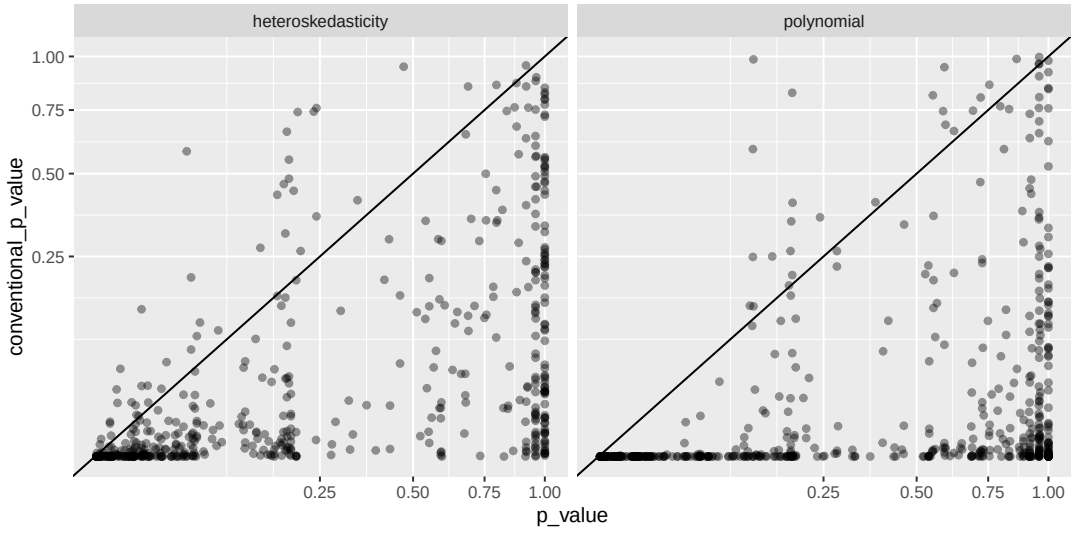



**Figure 11.** ...

effort. During the review of submissions, if we found a subject objectively demonstrated clear low-effort throughout the experiment, e.g., failed all attention checks, we rejected the submission. The rejected submissions will be removed immediately, and Prolific will automatically recruit another subject as substitution. Therefore, we only paid for approved submissions and no further data screening procedure needed to be applied on the collected data.

In overall, there were a total of 8860 lineup evaluations made by 443 subjects in experiment I, experiment II and experiment III, where 886 lineup evaluations were attention checks and were not used in the following analysis.

The collated dataset is provided in `vi_survey` of the `visage R` package.

### 4.2. *P-value comparison*

Visual inference and conventional hypothesis testing are two distinct statistical procedures. As displayed in Figure 11, the visual test almost always gives higher p-values than the conventional test in both polynomial and heteroskedasticity models, suggesting that humans have lower confidence and much higher tolerance of the residual departures than the numerical procedure. In fact, only around 58% of the cases, both tests will agree on the rejection decision given 95% confidence level. And in 41% of the cases, visual test does not reject the null hypothesis but conventional test does. Although we know that the all the designed lineups contain various degrees of residual departures and the conventional test is telling truth, analysts and general public as the consumers of the output will possibly not believe in or at least not response to the "false alarm" if they can not see the departures directly from the data plot and view it as impactful. The sensitivity of the conventional test may distract and discourage us from finding a good linear approximation to the data we try to model. This also partly explains why abundance of literature suggesting the use of data plot in regression diagnostics.

### 4.3. *Power comparison*

Figure 12 shows the estimated power of visual test on lineups with uniform distribution $X_{raw}$ against natural logarithm of the effect with comparison to the power of an exact test - F-test, and the power of two other residual-based conventional tests commonly used in regression diagnostics but for testing other departures from the model assumptions. In overall, the power of all four tests increases as the effect becomes larger. The power curve of F-test climbs aggressively from 25% to around 90% as $log_e(E)$ increases from 0 to 2, while others respond inactively to the change of effect and remain lower than 25% throughout the period, showing that as an exact test, the F-test is relatively more sensitive to the type of model defects that being considered. The power of visual test arises steadily and nearly linearly to around 90% as $log_e(E)$ increases from 2 to 5, suggesting that the effect starts to make noticeable impact on the degree of the presence of the designed visual features. Other two inappropriate conventional tests shows improvement at the same time but at a lower rate. This coincides the point made by Cook and Weisberg (1982) mentioned in **??** that residual-based tests for a specific type of model defect are sensitive to other types of model defects. At $log_e(E) \approx 6$, the power curve of F-test reaches almost 100% followed by the visual test by a small margin. The power of Breusch–Pagan test and Shapiro–Wilk test reach around 75% and 30% respectively.

What truly impress us is the huge difference between the estimated power of visual test and the estimated power of F-test. The margin is largest at around $log_e(E) = 2$. An example lineup is included in Figure 12 where none of subjects detect the actual data plot positioned at panel 10. It demonstrates that at this level of difficulty, the designed visual feature is rarely visible, making the actual data plot indistinguishable from residual plots simulated from the assumed model. From a communication perspective, given the fact that the visual difference is unperceivable, the argument that non-linearity present in the fitted model is less convincing to the public even though it is true. At around $log_e(E) = 3$, the margin gets smaller as the chance of identifying the actual data plot becomes larger. At this level of difficulty, the designed visual features are usually detectable but it may not stand out from the lineup as other null plots may happen to include outliers or visual patterns that are are considered to be more attractive by human, and thus recognized as the most different plot. Without knowing the designed visual features beforehand, it is actually hard to identify the actual data plot by pure image comparison. The corresponding example lineup for $log_e(E) = 3$ shown in Figure **??** has the actual data plot positioned at panel 7, where four of 11 subjects detect it. It can be observed that a "U-shape" is presented in plot 7, but the signal is not strong enough to attract all five subjects, resulting in a visual p-value sightly above the desired significance level $\alpha = 0.05$. At $log_e(E) = 4$, the designed visual features become much clear and attractive, leading to a high percentage of rejection of the null hypothesis. Figure **??** gives example lineups of such cases. It is also interesting to observe that the power curve of visual test behaves similarly to those inappropriate conventional tests until the designed visual features really becomes visible.

### 4.4. *Distribution of regressor*

The impact of the distribution of $X_raw$ on the power is displayed in Figure 13. The power curve of F-test is stable across different distributions, while the visual test has a steeper power curve for normal and uniform distribution. BP-test performs worse for

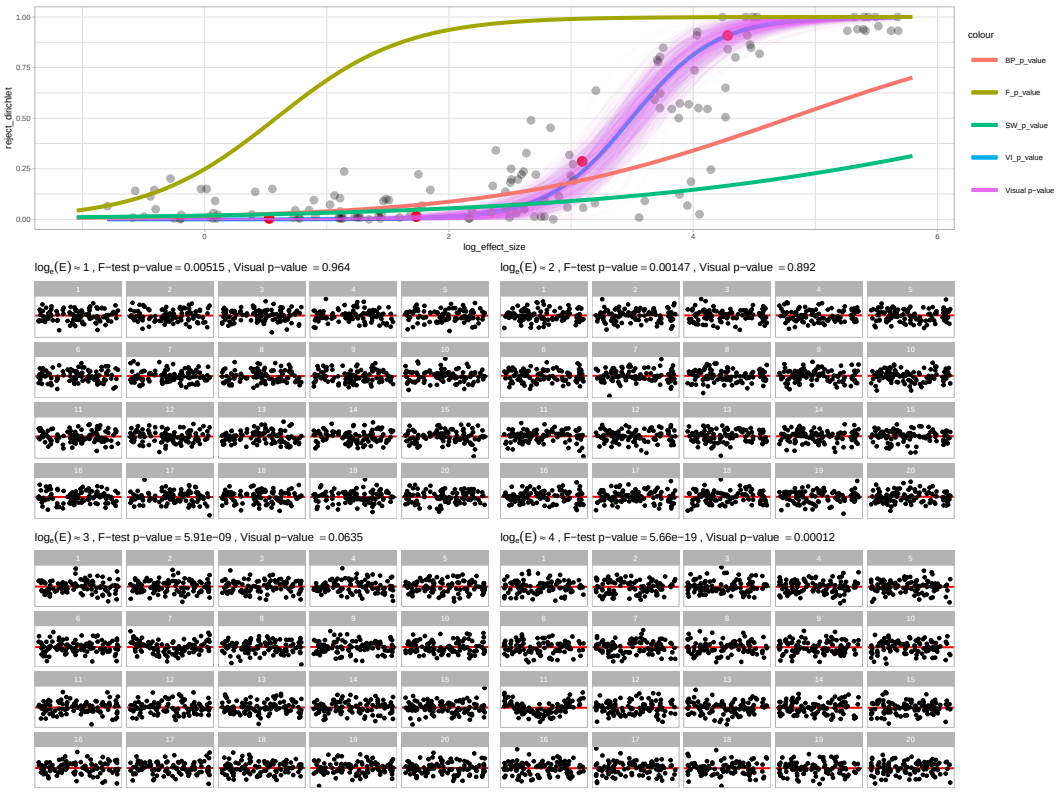

reject_dirichlet
log_effect_size
colour
BP_p_value
F_p_value
SW_p_value
VI_p_value
Visual p−value
log$_n$(E) ≈ 1 , F−test p−value = 0.00515 , Visual p−value = 0.964
log$_n$(E) ≈ 2 , F−test p−value = 0.00147 , Visual p−value = 0.892
log$_n$(E) ≈ 3 , F−test p−value = 5.91e−09 , Visual p−value = 0.0635
log$_n$(E) ≈ 4 , F−test p−value = 5.66e−19 , Visual p−value = 0.00012

**Figure 12.** ...

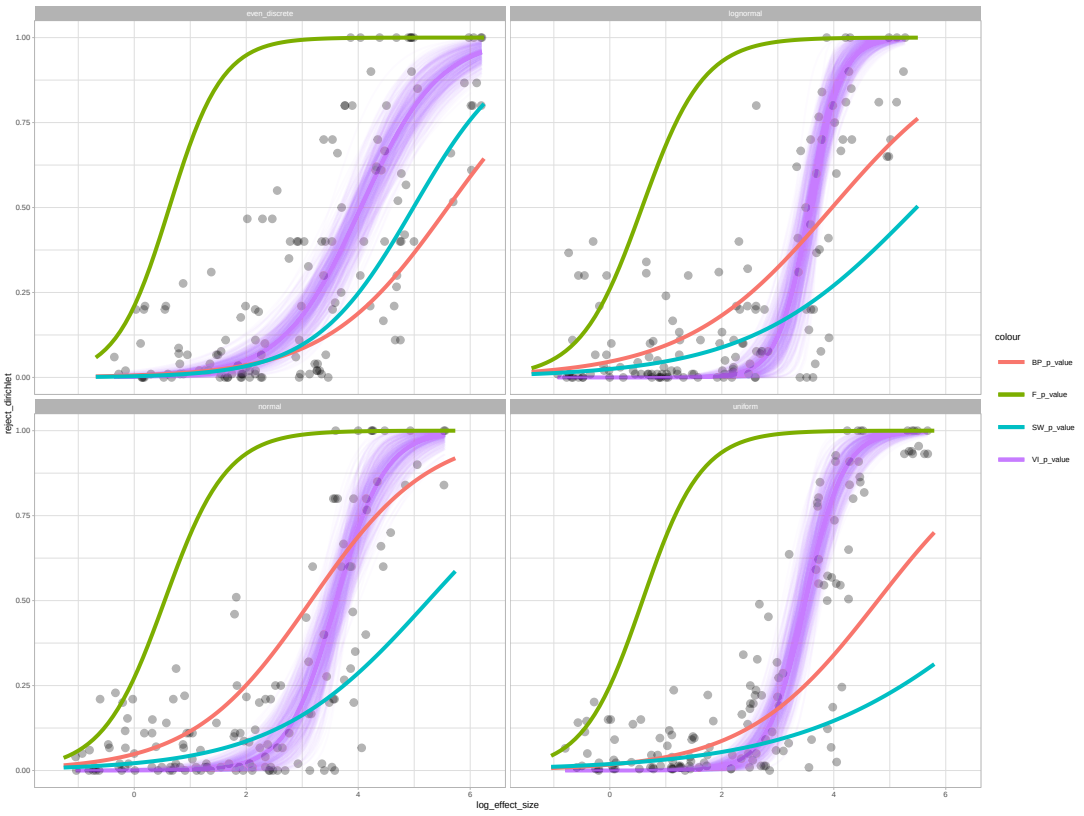
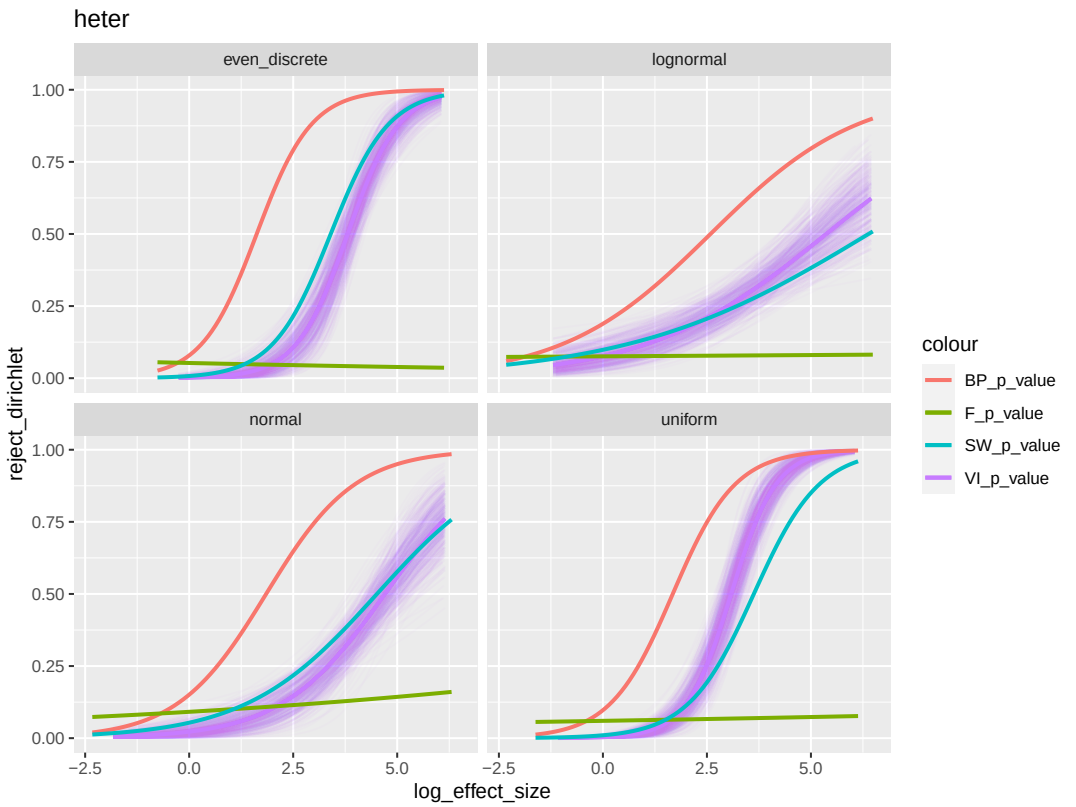



**Figure 13.** ...

discrete uniform distribution and uniform distribution but has relatively high power for normal distribution. SW-test outperforms BP-test for discrete uniform distribution but remains as the worst test for other distributions. The results indicate those inappropriate residual-based tests are sensitive to the distribution of the regressor.




−>
−>

## References


Belsley, David A, Edwin Kuh, and Roy E Welsch. 1980. *Regression diagnostics: Identifying influential data and sources of collinearity*. John Wiley & Sons.

Box, George EP. 1976. "Science and statistics." *Journal of the American Statistical Association* 71 (356): 791–799.

Breusch, T. S., and A. R. Pagan. 1979. "A Simple Test for Heteroscedasticity and Random Coefficient Variation." *Econometrica* 47 (5): 1287–1294.

Buja, Andreas, Dianne Cook, Heike Hofmann, Michael Lawrence, Eun-Kyung Lee, Deborah F. Swayne, and Hadley Wickham. 2009. "Statistical inference for exploratory data analysis and model diagnostics." *Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences* 367 (1906): 4361–4383.

Buja, Andreas, Dianne Cook, and D Swayne. 1999. "Inference for data visualization." In *Joint Statistics Meetings, August*, .

Cleveland, William S., and Robert McGill. 1984. "Graphical Perception: Theory, Experimentation, and Application to the Development of Graphical Methods." *Journal of the American Statistical Association* 79 (387): 531–554.

Cook, R Dennis, and Sanford Weisberg. 1982. *Residuals and influence in regression*. New York: Chapman and Hall.

Cook, R Dennis, and Sanford Weisberg. 1999. *Applied regression including computing and graphics*. John Wiley & Sons.

Draper, Norman R, and Harry Smith. 1998. *Applied regression analysis*. Vol. 326. John Wiley & Sons.

Gelman, Andrew. 2004. "Exploratory Data Analysis for Complex Models." *Journal of Computational and Graphical Statistics* 13 (4): 755–779.

Loy, Adam, and Heike Hofmann. 2013. "Diagnostic tools for hierarchical linear models." *Wiley Interdisciplinary Reviews: Computational Statistics* 5 (1): 48–61.

Majumder, Mahbubul, Heike Hofmann, and Dianne Cook. 2013. "Validation of Visual Statistical Inference, Applied to Linear Models." *Journal of the American Statistical Association* 108 (503): 942–956.

Montgomery, DC, and EA Peck. 1982. *Introduction to linear regression analysis*.

Ramsey, J. B. 1969. "Tests for Specification Errors in Classical Linear Least-Squares Regression Analysis." *Journal of the Royal Statistical Society. Series B (Methodological)* 31 (2): 350–371.

Roy Chowdhury, Niladri, Dianne Cook, Heike Hofmann, Mahbubul Majumder, Eun-Kyung Lee, and Amy L. Toth. 2015. "Using visual statistical inference to better understand random class separations in high dimension, low sample size data." *Computational Statistics* 30 (2): 293–316.

Shapiro, Samuel Sanford, and Martin B Wilk. 1965. "An analysis of variance test for normality (complete samples)." *Biometrika* 52 (3/4): 591–611.

Silvey, Samuel D. 1959. "The Lagrangian multiplier test." *The Annals of Mathematical Statistics* 30 (2): 389–407.

VanderPlas, Susan, Christian Röttger, Dianne Cook, and Heike Hofmann. 2021. "Statistical significance calculations for scenarios in visual inference." *Stat* 10 (1): e337.

White, Halbert. 1980. "A Heteroskedasticity-Consistent Covariance Matrix Estimator and a Direct Test for Heteroskedasticity." *Econometrica* 48 (4): 817–838.