

Automated Residual Plot Assessment with the R Package autovi and the Shiny App autovi.web

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Summary

Visually assessing residual plots is a common advice for linear model diagnostics, however this approach requires manual human evaluation and thereby is not scalable for assessing many models. Human evaluation also has the potential to produce inconsistent decisions from different analysts. Using a lineup protocol, where the residual plot is embedded among null plots, can help to alleviate inconsistency, but requires even more human effort. This is the type of task that in today's world we might employ a robot to do the tedious work for a human. Here we describe a new R package that includes a computer vision model for automated assessment of residual plots, and an accompanying Shiny app for ease of use. For a user-provided sample of residuals, it predicts a measure of visual signal strength (VSS) and provides a suite of supporting information to assist the analyst decide on the appropriateness of their model fit.

Key words: initial data analysis; statistical graphics; data visualization; visual inference; computer vision; machine learning; hypothesis testing; regression analysis; model diagnostics

1. Introduction

10 Regression analysis is a widely used statistical modeling technique for data in many
11 fields. There is a vast array of software for conducting regression modeling and
12 generating diagnostics. The package `lmtest` ([Zeileis & Hothorn 2002](#)) provides a
13 suite of conventional tests. The `stats` package ([R Core Team 2022](#)) offers standard

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diagnostic plots such as residuals vs. fitted values, quantile-quantile (Q-Q) plots, and residuals vs. leverage plots. Packages like `jtools` (Long 2022), `olsrr` (Hebbali 2024), `rockchalk` (Johnson 2022), and `ggResidpanel` (Goode & Rey 2019) provide similar graphical diagnostics, often with alternative aesthetics or interactive features. All of these tools deliver the types of diagnostic plots outlined in the classical text by Cook & Weisberg (1982). The `ecostats` package (Warton 2023) incorporates simulation envelopes into residual plots, while DHARMA (Hartig 2022) compares empirical quantiles (0.25, 0.5, and 0.75) of scaled residuals to their theoretical counterparts. DHARMA is particularly focused on detecting model violations such as heteroscedasticity, incorrect functional forms, and issues specific to generalized linear and mixed-effect models, like over/under-dispersion. It also includes conventional test annotations to help avoid misinterpretation.

However, relying solely on subjective assessments of these plots can lead to issues such as over-interpreting random patterns as model violations. Li et al. (2024a) demonstrated that visual methods using the lineup protocol (Buja et al. 2009) for assessing residuals are more useful, and also perform more practically than conventional tests due to their reduced sensitivity to minor departures. Packages such as `nullabor` (Wickham et al. 2020), `HLMdiag` (Loy & Hofmann 2014), and `regressinator` (Reinhart 2024), enable users to compare observed residual plots with plots of samples from null distributions, helping to quantify the significance of any detected patterns.

However, as discussed in Li et al. (2024b), the lineup protocol has significant limitations in large-scale applications due to dependence on human labor. Thus, a computer vision model was developed with an associated statistical testing procedure to automate the assessment of residual plots. This model takes a residual plot and a vector of auxiliary variables (such as the number of observations) as inputs and outputs the predicted visual signal strength (VSS). This strength estimates the distance between the residual distribution of the fitted regression model and the reference distribution assumed under correct model specification.

To make the statistical testing procedure and trained computer vision model widely accessible, we developed the R package `autovi`, and a web interface, `autovi.web` to make it easy for users to automatically read their residual plots with the trained computer vision model.

The remainder of this paper is structured as follows: Section 2 introduces the definition and computation of visual signal strength. Section 3 provides a detailed documentation of the `autovi` package, including its usage and infrastructure. Section 4 focuses on the

49 `autovi.web` interface, describing its design and usage, along with illustrative examples.
 50 Finally, Section 5 presents the main conclusions of this work.

51 **2. Definition and computation of visual signal strength**

52 To train a computer vision model, a measure of the visible pattern in a plot is needed.
 53 We call this the **visual signal strength** (VSS), which measures how prominently a
 54 specific set of visual patterns appears in an image. This can be computed for a training
 55 set of data, and plots, where the generating distributions are specified.
 56 In the context of regression model diagnostics, VSS describes the clarity of visual
 57 patterns on a diagnostic plot that may indicate model violations. Violations can be
 58 categorized as weak, moderate, or strong, but here we treat it as a continuous positive
 59 real variable. Importantly, its interpretation depends on how it is linked to a function
 60 of the data or the underlying data generating process. Consequently, the calculation of
 61 VSS can vary across different model classes or within the same model, depending
 62 on the generating function.
 63 VSS is an estimate of the distance between the residual distribution of a fitted classical
 64 normal linear regression model and a reference distribution; more details can be found
 65 in Li et al. (2024b). The distance measure is based on the Kullback-Leibler (KL)
 66 divergence:

$$D = \log(1 + D_{KL}),$$

67 where D_{KL} is given by:

$$D_{KL} = \int_{\mathbb{R}^n} \log \frac{p(\mathbf{e})}{q(\mathbf{e})} p(\mathbf{e}) d\mathbf{e},$$

68 here, $p(\cdot)$ and $q(\cdot)$ are the probability density functions of the reference residual
 69 distribution P and the true residual distribution Q , respectively.
 70 This distance measure depends on knowledge of the true residual distribution, which
 71 is often unknown. However, it can be estimated by identifying or approximating a
 72 mapping from a set of residuals to its corresponding distance measure. The computer
 73 vision model presented in Li et al. (2024b) approximates this mapping. It is trained
 74 on a large number of synthetic regression models, where the data-generating process

is known, allowing the distance measure to be explicitly calculated. The model takes a residual plot as input and outputs the corresponding distance measure. Additional details are provided in [Li et al. \(2024b\)](#).

78 3. R package: autovi

The main purpose of `autovi` is to provide rejection decisions and *p*-values for testing the null hypothesis (H_0) that the regression model is correctly specified. The package provides automated interpretation of residual plots using computer vision. The name `autovi` stands for **a**utomated **v**isual **i**nference. This functionality can be accessed through the R package `autovi`, or through a web interface, `autovi.web`, which allows use without the full installation of R, Python, and package dependencies on the user's system. locally.

86 3.1. Motivation

Figure 1 shows three sets of plots of residuals against fitted values. The simulated example in (a) might be interpreted as a heteroscedastic pattern, however the automated reading would predict this to have a visual signal strength (VSS) of 1.53, with a corresponding *p*-value of 0.25. This means it would be interpreted as a good residual plot, that there is nothing in the data to indicate a violation of model assumptions. Skewness in the predictor variables is generating the apparent heteroscedasticity, where the smaller variance in residuals at larger fitted values is due to smaller sample size only. The Breusch-Pagan test ([Breusch & Pagan 1979](#)) for heteroscedasticity would also not reject this as good residual plot.

The data in (b) is generated by fitting a linear model predicting `mpg` based on `hp` using the `datasets::mtcars`. It is a small data set, and there is a hint of nonlinear structure not captured by the model. The automated plot reading would predict a VSS of 3.57, which has a *p*-value less than 0.05. That is, the nonlinear structure is most likely real, and indicates a problem with the model. The conventional test, a Ramsey Regression Equation Specification Error Test (RESET) ([Ramsey 1969](#)) would also strongly detect the nonlinearity.

The third example is generated using the `surreal` package ([Balamuta 2024](#)) where structured residuals are hidden in data, to be revealed if the correct model is specified. Here a quote based on Tukey is used as the residual structure “visual summaries focus on unexpected values”. The automated plot reading predicts the VSS to be 5.87, with a *p*-value less than 0.05. This structure is blindingly obvious visually, but a RESET

108 test for nonlinear structure would not report a problem. (It would be detected by
 109 a Breusch-Pagan for heteroscedasticity and also Shapiro-Wilk test ([Shapiro & Wilk](#)
 110 [1965](#)) for non-normality.)

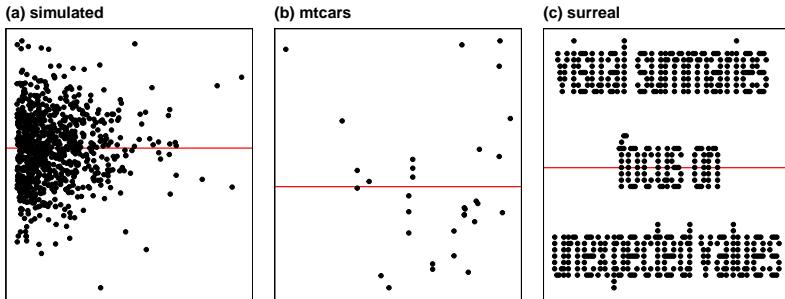


Figure 1. Reading residual plots can be a difficult task, particularly for students new to statistical modeling. The `autovi` package makes it easier. Here are three examples of residual plots, which may appear to have structure. According to `autovi`, the visual signal strengths (VSS) of these three examples are approximately (a) 1.53, (b) 3.57, (c) 5.87, resulting in (b), (c) being significant violations of good residuals, but (a) is consistent with a good residual plot.

111 3.2. Implementation

112 The `autovi` package is built on the `bandicoot` object-oriented programming (OOP)
 113 system ([Li 2024](#)), marking a departure from R's traditional S3 generic system. This
 114 OOP architecture enhances flexibility and modularity, allowing users to redefine key
 115 functions through method overriding.

116 The `autovi` infrastructure effectively integrates multiple programming languages and
 117 libraries into a comprehensive analytical tool. It relies on five core libraries from
 118 Python and R, each playing a critical role in the analysis pipeline. In Python, `pillow`
 119 ([Clark et al. 2015](#)) handles image processing tasks such as reading and resizing PNG
 120 files of residual plots, then converting them into input tensors for further analysis.
 121 `TensorFlow` ([Abadi et al. 2016](#)), a key component of modern machine learning, is used
 122 to predict the VSS of these plots using a pre-trained convolutional neural network.

123 In the R environment, `autovi` utilizes several libraries. `ggplot2` ([Wickham 2016](#))
 124 generates the initial residual plots, saved as PNG files for visual input. `cassowaryr`
 125 ([Mason et al. 2022](#)) computes scagnostics (scatter plot diagnostics), providing numerical
 126 features that capture statistical properties of the plots. These scagnostics complement
 127 the visual analysis by offering quantitative metrics as secondary input to the

128 computer vision model. `reticulate` (Ushey, Allaire & Tang 2024) enables seamless
 129 communication between R and Python.

130 **3.3. Installation**

131 The `autovi` package is available on CRAN. It is actively developed and maintained,
 132 with the latest updates accessible on GitHub. This paper uses `autovi` version 0.4.1.
 133 The package includes internal functions to check the current Python environment used
 134 by the `reticulate` package. If the necessary Python packages are not installed in the
 135 Python interpreter, an error will be raised. If you want to select a specific Python
 136 environment, you can do so by calling the `reticulate::use_python()` function before
 137 using the `autovi` package.

138 We recommend using the Shiny app `autovi.web` if users encounter installation
 139 problems.

140 **3.4. Usage**

141 **3.4.1. Numerical summary**

142 Three steps are needed to get an automated assessment of a set of residuals and fitted
 143 values:

- 144 1. Load the `autovi` package using the `library()` function.
- 145 2. Create a checker object with a linear regression model.
- 146 3. Call the `check()` method of the checker, which, by default, predicts the VSS for
 147 the true residual plot, 100 null plots, and 100 bootstrapped plots. The method
 148 stores the predictions internally and prints a concise results report.

149 The code to do this is:

```
library(autovi)
checker <- residual_checker(lm(dist ~ speed, data = cars))
checker$check()
```

150 It produces the following summary:

```
151
152 -- <AUTO_VI object>
153 Status:
154 - Fitted model: lm
```

```

155 - Keras model: UNKNOWN
156   - Output node index: 1
157 - Result:
158   - Observed visual signal strength: 3.162 (p-value = 0.0396)
159   - Null visual signal strength: [100 draws]
160     - Mean: 1.274
161     - Quantiles:
162
163   25%      50%      75%      80%      90%      95%      99%
164   0.8021  1.1109  1.5751  1.6656  1.9199  2.6564  3.3491
165
166 - Bootstrapped visual signal strength: [100 draws]
167   - Mean: 2.786 (p-value = 0.05941)
168   - Quantiles:
169
170   25%      50%      75%      80%      90%      95%      99%
171   2.452  2.925  3.173  3.285  3.463  3.505  3.652
172
173 - Likelihood ratio: 0.7275 (boot) / 0.06298 (null) = 11.55

```

174 The summary includes observed VSS of the true residual plot and associated p -value
 175 of the automated visual test. The p -value is the proportion of null plots (out of the
 176 total 100) that have VSS greater than or equal to that of the true residual plot. The
 177 report also provides sample quantiles of VSS for null samples and bootstrapped data
 178 plots, providing more information about the sampling variability and a likelihood of
 179 model violations. The likelihood is computed from the proportion of values greater
 180 than the observed VSS in both the bootstrapped data values and the simulated null
 181 values.

182 **3.4.2. Visual summary**

183 Users can visually inspect the original residual plot alongside a sample null plot using
 184 `plot_pair()` or a lineup of null plot `plot_lineup()`. This visual comparison can
 185 clarify why H_0 is either rejected or not, and help identify potential remedies.

```
checker$plot_pair()
```

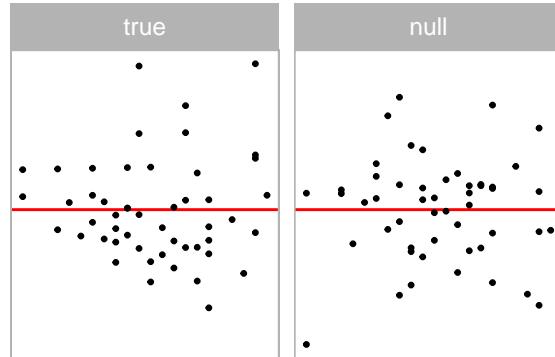


Figure 2. True plot alongside one null plot, for quick comparison.

186 The `plot_pair()` method (Figure 2) displays the true residual plot on the left and a
 187 single null plot on the right. If a full lineup was shown, the true residual plot would
 188 be embedded in a page of null plots. Users should look for any distinct visual patterns
 189 in the true residual plot that are absent in the null plot. Running these functions
 190 multiple times can help any visual suspicions, as each execution generates new random
 191 null plots for comparison.

192 The package offers a straightforward visualization of the assessment result through
 193 the `summary_plot()` function.

```
checker$summary_plot()
```

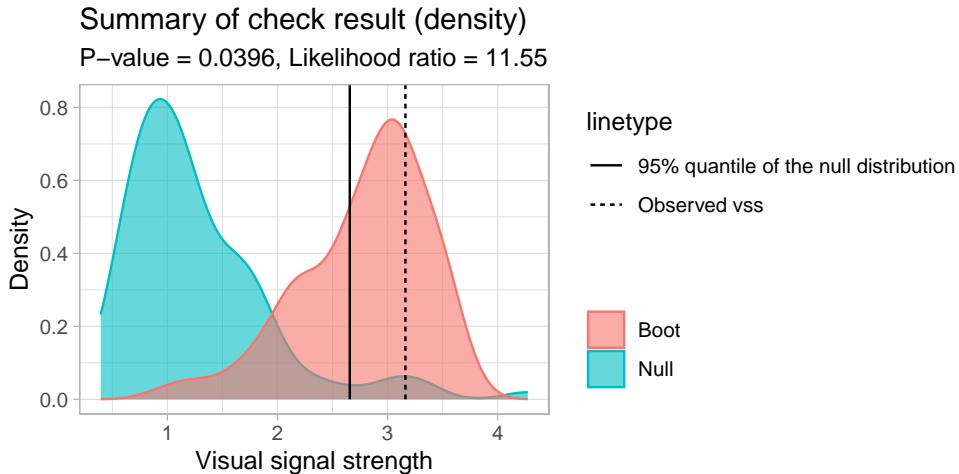


Figure 3. Summary plot comparing the densities of VSS for bootstrapped residual samples (red) relative to VSS for null plots (blue).

- 194 In the result, shown in Figure 3, the blue area represents the density of VSS for null
 195 residual plots, while the red area shows the density for bootstrapped residual plots.
 196 The dashed line indicates the VSS of the true residual plot, and the solid line marks
 197 the critical value at a 95% significance level. The p -value and the likelihood ratio are
 198 displayed in the subtitle. The likelihood ratio represents the ratio of the likelihood
 199 of observing the VSS of the true residual plot from the bootstrapped distribution
 200 compared to the null distribution.
- 201 Interpreting the plot involves several key aspects. If the dashed line falls to the right of
 202 the solid line, it suggests rejecting the null hypothesis. The degree of overlap between
 203 the red and blue areas indicates similarity between the true residual plot and null
 204 plots; greater overlap suggests more similarity. Lastly, the portion of the red area to
 205 the right of the solid line represents the percentage of bootstrapped models considered
 206 to have model violations.
- 207 This visual summary provides an intuitive way to assess the model's fit and potential
 208 violations, allowing users to quickly grasp the results of the automated analysis.

209 3.5. Modularized infrastructure

- 210 The initial motivation for developing `autovi` was to create a convenient interface for
 211 sharing the models described and trained in Li et al. (2024b). However, recognizing
 212 that the classical normal linear regression model represents a restricted class of

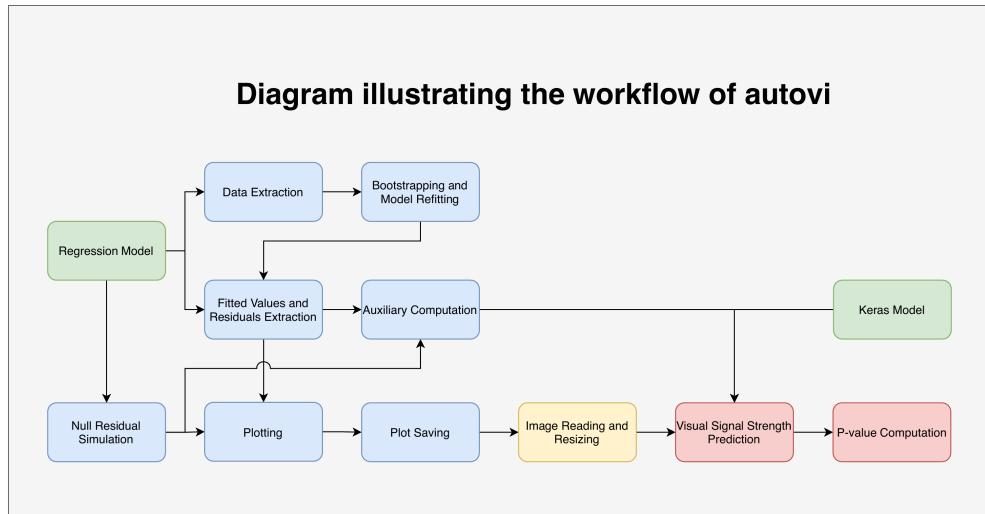


Figure 4. Diagram illustrating the infrastructure of the R package **autovi**. The modules in green are primary inputs provided by users. Modules in blue are overridable methods that can be modified to accommodate users' specific needs. The module in yellow is a pre-defined non-overridable method. The modules in red are primary outputs of the package.

models, we sought to avoid limiting the potential for future extensions, whether by the original developers or other developers. As a result, the package was designed to function seamlessly with linear regression models with minimal modification and few required arguments, while also accommodating other classes of models through partial infrastructure substitution. This modular and customizable design allows **autovi** to handle a wide range of residual diagnostics tasks.

The infrastructure of **autovi** consists of ten core modules: data extraction, bootstrapping and model refitting, fitted values and residuals extraction, auxiliary computation, null residual simulation, plotting, plot saving, image reading and resizing, VSS prediction, and *p*-value computation. Each module is designed with minimal dependency on the preceding modules, allowing users to customize parts of the infrastructure without affecting its overall integrity. An overview of this infrastructure is illustrated in Figure 4.

The modules for VSS prediction and *p*-value computation are predefined and cannot be overridden, although users can interact with them directly through function arguments. Similarly, the image reading and resizing module is fixed but will adapt to different Keras models by checking their input shapes. The remaining seven modules are designed to be overridable, enabling users to tailor the infrastructure to their specific needs. These modules are discussed in detail in the package documentation.

232

4. Web interface: `autovi.web`

233 The `autovi.web` shiny application extends the functionality of `autovi` by offering a
234 user-friendly web interface for automated residual plot assessment. This eliminates the
235 common challenges associated with software installation, so users can avoid managing
236 Python environments or handling version requirements for R libraries. The platform
237 is cross-platform and accessible on various devices and operating systems, making it
238 suitable even for users without R programming experience. Additionally, updates are
239 managed centrally, ensuring that users always have access to the latest features. This
240 section discusses the implementation based on `autovi.web` version 0.1.0.

241 **4.1. Implementation**

242 The interface `autovi.web` is built using the `shiny` (Chang et al. 2022) and
243 `shinydashboard` (Chang & Borges Ribeiro 2021) R packages. Hosted on the
244 `shinyapps.io` domain, the application is accessible through any modern web browser.
245 The R packages `htmltools` (Cheng et al. 2024) and `shinycssloaders` (Sali & Attali
246 2020) are used to render markdown documentation in shiny application, and for loading
247 animations for shiny widgets, respectively.

248 Determining the best way to implement the backend was difficult. In our initial
249 planning for `autovi.web`, we considered implementing the entire web application using
250 the `webr` framework (Moon 2020), which would have allowed the entire application to
251 run directly in the user’s browser. However, `webr` does not support packages which use
252 compiled fortran code, which is required by `splancs` (Rowlingson & Diggle 2023), a
253 dependency of `autovi`. In the future, it is possible that a working Emscripten (Zakai
254 2011) version of this package may allow full `webr` support.

255 We also explored the possibility of implementing the web interface using frameworks
256 built on other languages, such as Python. However, server hosting domains that
257 natively support Python servers typically do not have the latest version of R installed.
258 Additionally, calling R from Python is typically done using the `rpy2` Python library
259 (Gautier 2024), but this approach can be awkward when dealing with language syntax
260 related to non-standard evaluation. Another option we considered was renting a server
261 where we could have full control, such as those provided by cloud platforms like
262 Google Cloud Platform (GCP) or Amazon Web Services (AWS). However, deploying
263 and maintaining the server securely requires some expertise. Ultimately, the most
264 practical solution was to use the `shiny` and `shinydashboard` frameworks, which are

265 well-established in the R community and offer a solid foundation for web application
266 development.

267 The server-side configuration of `autovi.web` is carefully designed to support its
268 functionality. Most required Python libraries, including `pillow` and `numpy`, are pre-
269 installed on the server. These libraries are integrated into the Shiny application using
270 the `reticulate` package, which provides an interface between R and Python.

271 Due to the resource allocation policy of shinyapps.io, the server enters a sleep mode
272 during periods of inactivity, resulting in the clearing of the local Python virtual
273 environment. Consequently, when the application “wakes up” for a new user session,
274 these libraries need to be reinstalled. While this ensures a clean environment for each
275 session, it may lead to slightly longer loading times for the first user after a period of
276 inactivity.

277 In contrast to `autovi`, `autovi.web` leverages `TensorFlow.js`, a JavaScript library
278 that allows the execution of machine learning models directly in the browser. This
279 choice enables native browser execution, enhancing compatibility across different user
280 environments, and shifts the computational load from the server to the client-side.
281 `TensorFlow.js` also offers better scalability and performance, especially when dealing
282 with resource-intensive computer vision models on the web.

283 While `autovi` requires downloading the pre-trained computer vision models from
284 GitHub, these models in “.keras” file format are incompatible with `TensorFlow.js`.
285 Therefore, we extract and store the model weights in JSON files and include
286 them as extra resources in the Shiny application. When the application initializes,
287 `TensorFlow.js` rebuilds the computer vision model using these pre-stored weights.

288 To allow communication between `TensorFlow.js` and other components of the Shiny
289 application, the `shinyjs` R package ([Attali 2021](#)) is used. This package allows calling
290 custom JavaScript code within the Shiny framework. The specialized JavaScript
291 code for initializing `TensorFlow.js` and calling `TensorFlow.js` for VSS prediction is
292 deployed alongside the Shiny application as additional resources.

293 4.2. Usage

294 The workflow of `autovi.web` is designed to be straightforward, with numbered
295 steps displayed in each panel. There are two example datasets provided by the
296 web application. The single residual plot example uses the `dino` dataset from the
297 R package `datasauRus` ([Davies, Locke & D'Agostino McGowan 2022](#)). The lineup

example uses residuals from a simulated regression model that has a non-linearity issue. We walk through the lineup example to further demonstrate the workflow of the web application.

4.2.1. Reading data and setting parameters

The user can select to upload data as either a single set of residuals and fitted values in a two (or more) column CSV file or a pre-computed lineup of residuals and null datasets in a three (or more) column CSV file (i.e. multiple sets of residuals and fitted values with a column indicating the set label). Here we illustrate use with lineup example data sets (Figure 5). To use the lineup example data, click the “Use Lineup Example” button. The data status will then update to show the number of rows and columns in the dataset, and the CSV type will automatically be selected to the correct option. Since the example dataset follows the variable naming conventions assumed by the web application, the columns for fitted values, residuals, and labels of residual plots are automatically mapped such that the column named as `.fitted` is mapped to fitted values, `.resid` is mapped to residuals and if applicable, `.sample` to labels of the residual set (middle image). If the user is working with a custom dataset, these options must be set accordingly. Whenever a data containing a lineup, the user must manually select the label for the true residual plot, otherwise the web application does not provide all the results. The last step is to click the play button (right image) to start the assessment.

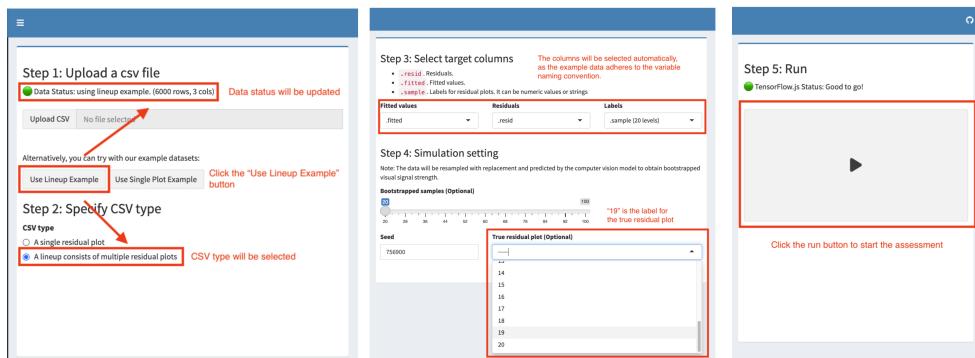


Figure 5. To begin the workflow for `autovi` using the lineup example dataset, the user clicks the “Use Lineup Example” button (left) to load the example dataset, during which the data status and CSV type will be automatically updated. The user must manually select the label for the true residual plot (middle) to compute further results. The user initiates the assessment of the lineup example data by clicking the run button (right).

318 **4.2.2. Results provided**

319 Results are provided in multiple panels. The first row of the table Figure 6 is the most
 320 crucial to check, as it provides the VSS and the rank of the true residual plot among
 321 the other plots. The summary text beneath the table provides the *p*-value, which can
 322 be used for quick decision-making. The lineup is for manual inspection, and the user
 323 should see if the true residual plot is visually distinguishable from the other plots, to
 324 confirm if the model violation is serious.

325 The density plot in Figure 7 offers a more robust result, allowing the user to compare
 326 the distribution of bootstrapped VSS with the distribution of null VSS. Finally, the
 327 grayscale attention map (right image) can be used to check if the target visual features,
 328 like the non-linearity present in the lineup example, are captured by the computer
 329 vision model, ensuring the quality of the assessment.

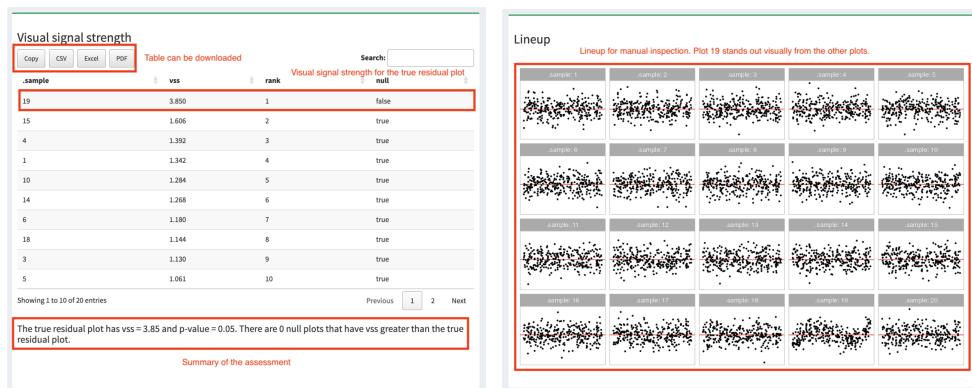


Figure 6. Results for the lineup. The VSS of the true residual plot is displayed in the first row of the table of VSS values for all the null plots (left image), with a summary text beneath the table providing the *p*-value to aid in decision-making. A lineup of residual plots allows for manual inspection (right image).

330

5. Conclusions

331 This paper presents new regression diagnostics software, the R package **autovi** and
 332 its accompanying web interface, **autovi.web**. It addresses a critical gap in the current
 333 landscape of statistical software. While regression tools are widely available, effective
 334 and efficient diagnostic methods have lagged behind, particularly in the field of residual
 335 plot interpretation.

336 The **autovi** R package, introduced in this paper, automates the assessment of residual
 337 plots by incorporating a computer vision model, reducing reliance on time-consuming

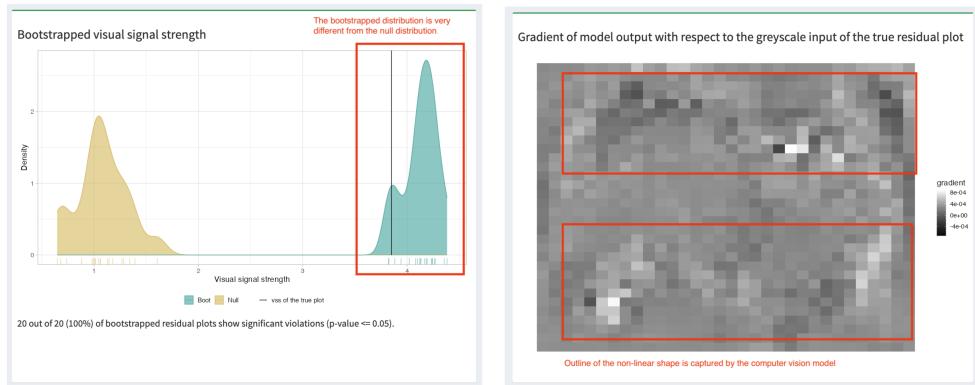


Figure 7. Summaries assessing the strength of the pattern and which elements of the plot contribute. The density plot helps verify if the bootstrapped distribution differs from the null distribution (left image). The attention map (right image) offers insights into whether the computer vision model has captured the intended visual features of the true residual plot.

338 and potentially inconsistent human interpretation. This automation improves the
 339 efficiency of the diagnostic process and promotes consistency in model evaluation
 340 across different users and studies.

341 The development of the accompanying Shiny app, **autovi.web**, expands access to these
 342 advanced diagnostic tools, by providing a user-friendly interface. It makes automated
 343 residual plot assessment accessible to a broader audience, including those who may not
 344 have extensive programming experience. This web-based solution effectively addresses
 345 the potential barriers to adoption, such as complex dependencies and installation
 346 requirements, that are often associated with advanced statistical software.

347 The combination of **autovi** and **autovi.web** offers a comprehensive solution to the
 348 challenges of residual plot interpretation in regression analysis. These tools have the
 349 potential to significantly improve the quality and consistency of model diagnostics
 350 across various fields, from academic research to industry applications. By automating
 351 a critical aspect of model evaluation, they allow researchers and analysts to focus more
 352 on interpreting results and refining models, rather than grappling with the intricacies
 353 of plot assessment.

354 The framework established by **autovi** and **autovi.web** opens up exciting possibilities
 355 for further research and development. Future work could explore the extension of these
 356 automated assessment techniques to other types of diagnostic plots and statistical
 357 models, potentially revolutionizing how we approach statistical inference using visual
 358 displays more broadly.

359 **6. Resources and supplementary material**

360 The current version of `autovi` can be installed from CRAN, and source
 361 code for both packages are available at github.com/TengMCing/autovi and
 362 github.com/TengMCing/autovi_web respectively. The web interface is available from
 363 autoviweb.netlify.app.

364 This paper is reproducibly written using Quarto ([Allaire et al. 2024](#)) powered by
 365 Pandoc ([MacFarlane, Krewinkel & Rosenthal 2024](#)) and pdfTeX. The full source code
 366 to reproduce this paper is available at github.com/TengMCing/autovi_paper.

367 These R packages were used for the work: `tidyverse` ([Wickham et al. 2019](#)), `lmtest`
 368 ([Zeileis & Hothorn 2002](#)), `kableExtra` ([Zhu 2021](#)), `patchwork` ([Pedersen 2022](#)),
 369 `rcartocolor` ([Nowosad 2018](#)), `glue` ([Hester & Bryan 2022](#)), `here` ([Müller 2020](#)),
 370 `magick` ([Ooms 2023](#)), `yardstick` ([Kuhn, Vaughan & Hvitfeldt 2024](#)) and `reticulate`
 371 ([Ushey, Allaire & Tang 2024](#)).

372 **References**

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 375 heterogeneous distributed systems. *arXiv preprint arXiv:1603.04467* .
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