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

ANZJS Quarto Template

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Summary

Regression software is widely available, and there are many tools for generating diagnostics and computing conventional residual tests. However, the advice remains that the analyst should look at the residual plot to check the fit. Perhaps, one of the reasons is that conventional tests are too sensitive, strictly resulting in adequate models being abandoned. Visually assess the strength of patterns in residual plots requires human effort and suffers from the potential for 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 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 their model fit.

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

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1. Introduction

Regression analysis is a widely used statistical modeling technique widely for data in many fields. There are a vast array of software for conducting regression modeling and generating diagnostics. The package `lmtest` (Zeileis & Hothorn 2002) provides a suite of conventional tests. The `stats` package (R Core Team 2022) offers standard 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 samples from null distributions, helping to quantify the significance of any detected patterns. However, the

However, as discussed in Li et al. (2024b), the lineup protocol has significant limitations in large-scale applications due 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 provides a detailed documentation of the `autovi` package, including its usage and infrastructure. Section 3 focuses on the `autovi.web` interface, describing its design and usage, along with illustrative examples. Finally, Section 4 presents the main conclusions of this work.

2. 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 **auto**mated **v**isual **i**nference.

There are two ways to access the package, directly using R or through a web interface, `autovi.web`. The web interface has the advantage that it can be used without installing Python, R and the relevant packages locally.

2.1. Why use it

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

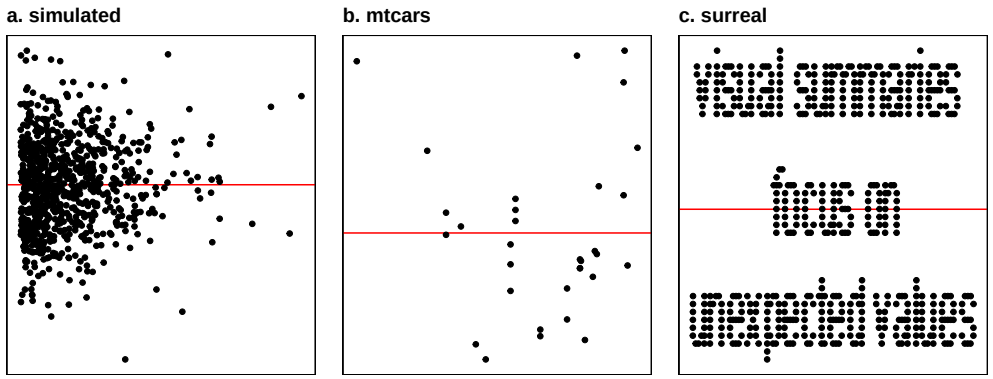

Figure 1. Reading residual plots can be a difficult task, particular for students new to statistical modeling. The autovi package makes it easier. Here are three examples of residual plots, which may appear to have structure. According to autovi, the visual signal strengths (VSS) of these three examples 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.

2.2. Implementation

The `autovi` package is built on the `bandicoot` object-oriented programming (OOP) system (Li 2024), marking a departure from R's traditional S3 generic system. This OOP architecture enhances flexibility and modularity, allowing users to redefine key functions through method overriding. While similar functionality could be achieved using R's S3 system with generic functions, the OOP framework offers a more structured and extensible foundation for the package.

The `autovi` infrastructure effectively integrates multiple programming languages and libraries into a comprehensive analytical tool. It relies on five core libraries from Python and R, each playing a critical role in the analysis pipeline. In Python, `pillow` (Clark et al. 2015) handles image processing tasks such as reading and resizing PNG files of residual plots, then converting them into input tensors for further analysis. The

`TensorFlow` (Abadi et al. 2016) library, a key component of modern machine learning, is used to predict the VSS of these plots through a pre-trained convolutional neural network.

In the R environment, `autovi` utilizes several libraries. `ggplot2` (Wickham 2016) generates the initial residual plots, saved as PNG files for visual input. The `cassowaryr` (Mason et al. 2022) library computes scagnostics (scatter plot diagnostics), providing numerical features that capture statistical properties of the plots. These scagnostics complement the visual analysis by offering quantitative metrics as secondary input to the computer vision model. The `reticulate` (Ushey, Allaire & Tang 2024) package bridges R and Python, enabling seamless communication between the two languages and supporting the integrated infrastructure.

2.3. Installation

The `autovi` package is available on CRAN. It is actively developed and maintained, with the latest updates accessible on GitHub. The code discussed in this paper is based on `autovi` version 0.4.1.

The package includes internal functions to check the current Python environment used by the `reticulate` package. If the necessary Python packages are not installed in the Python interpreter, an error will be raised. If you want to select a specific Python environment, you can do so by calling the `reticulate::use_python()` function before using the `autovi` package.

We recommend using the Shiny app `autovi.web` if encountering installation problems.

2.4. Numerical Summary

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

1. Load the `autovi` package using the `library()` function.
2. Create a checker object with a linear regression model.
3. Call the `check()` method of the checker, which, by default, predicts the VSS for the true residual plot, 100 null plots, and 100 bootstrapped plots, storing the predictions internally. A concise report of the check results is then printed.

The code to do this is:

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

It produces the following summary:

```
-- <AUTO_VI object>
Status:
 - Fitted model: lm
 - Keras model: UNKNOWN
    - Output node index: 1
 - Result:
    - Observed visual signal strength: 3.162 (p-value = 0.0396)
    - Null visual signal strength: [100 draws]
       - Mean: 1.274
       - Quantiles:

     25%    50%    75%    80%    90%    95%    99%
  0.8021 1.1109 1.5751 1.6656 1.9199 2.6564 3.3491

    - Bootstrapped visual signal strength: [100 draws]
       - Mean: 2.786 (p-value = 0.05941)
       - Quantiles:

    25%   50%   75%   80%   90%   95%   99%
  2.452 2.925 3.173 3.285 3.463 3.505 3.652

    - Likelihood ratio: 0.7275 (boot) / 0.06298 (null) = 11.55
```

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

than the observed VSS in both the bootstrapped data values and the simulated null values.

2.5. Visual Summary

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

```
checker$plot_pair()
```

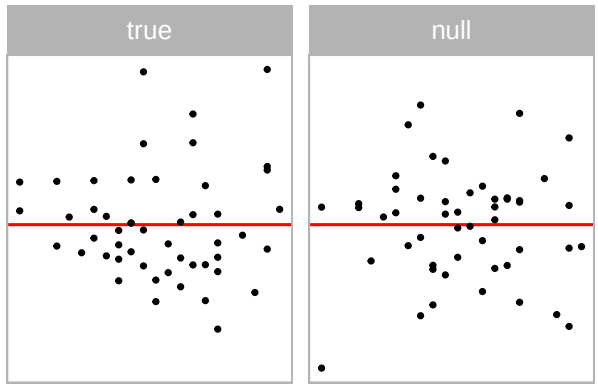

Figure 2. True plot alongside one null plot, for quick comparison.

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

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

```
checker$summary_plot()
```

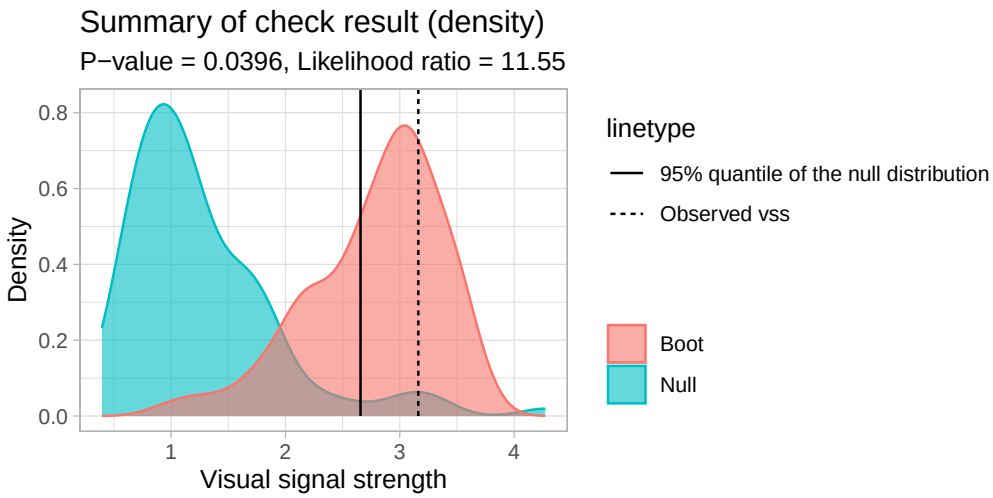

Figure 3. Summary plot comparing the densities of VSS for bootstrapped residual samples (red) relative to VSS for null plots (blue).

In the result, shown in Figure 3, the blue area represents the density of VSS for null residual plots, while the red area shows the density for bootstrapped residual plots. The dashed line indicates the VSS of the true residual plot, and the solid line marks the critical value at a 95% significance level. The p-value and the likelihood ratio are displayed in the subtitle. The likelihood ratio represents the ratio of the likelihood of observing the VSS of the true residual plot from the bootstrapped distribution compared to the null distribution.

Interpreting the plot involves several key aspects. If the dashed line falls to the right of the solid line, it suggests rejecting the null hypothesis. The degree of overlap between the red and blue areas indicates similarity between the true residual plot and null plots; greater overlap suggests more similarity. Lastly, the portion of the red area to the right of the solid line represents the percentage of bootstrapped models considered to have model violations.

This visual summary provides an intuitive way to assess the model's fit and potential violations, allowing users to quickly grasp the results of the automated analysis.

2.6. Modularized Infrastructure

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

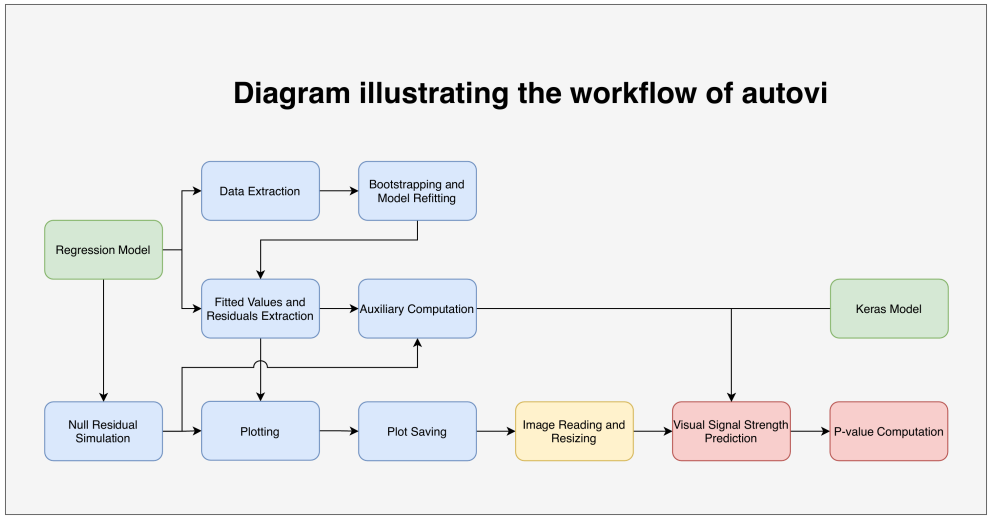

Figure 4. Diagram illustrating the infrastructure of the R package autovi. The modules in green are primary inputs provided by users. Modules in blue are overridable methods that can be modified to accommodate users' specific needs. The module in yellow is a pre-defined non-overridable method. The modules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

we sought to avoid limiting the potential for future extensions, whether by the original developers or other users. 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 on the software's website.

3. Web interface: autovi.web

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

The `autovi.web` interface is available at autoviweb.netlify.app. This section discusses the implementation based on `autovi.web` version 0.1.0.

3.1. Implementation

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

Determining the best way to implement the interface was difficult. In our initial planning for `autovi.web`, we considered implementing the entire web application using the `webr` framework (Moon 2020), which would have allowed the entire application to run directly in the user's browser. However, this approach was not feasible at the time of writing this paper. The reason is that one of the R packages `autovi` depends on the R package `splancs` (Rowlingson & Diggle 2023), which uses compiled Fortran code. A working Emscripten (Zakai 2011) version of this package, which would be required for `webr`, was not available.

We also explored the possibility of implementing the web interface using frameworks built on other languages, such as Python. However, server hosting domains that natively support Python servers typically do not have the latest version of R installed. Additionally, calling R from Python is typically done using the `rpy2` Python library (Gautier 2024), but this approach can be awkward when dealing with language syntax related to non-standard evaluation. Another option we considered was renting a server where we could have full control, such as those provided by cloud platforms like Google Cloud Platform (GCP) or Amazon Web Services (AWS). However, correctly setting up

the server and ensuring a secure deployment requires significant expertise. Ultimately, the most practical solution was to use the `shiny` and `shinydashboard` frameworks, which are well-established in the R community and offer a solid foundation for web application development.

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

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

In contrast to `autovi`, `autovi.web` does not use the native Python version of `TensorFlow`. Instead, it leverages `TensorFlow.js`, a JavaScript library that allows the execution of machine learning models directly in the browser. This choice enables native browser execution, enhancing compatibility across different user environments, and shifts the computational load from the server to the client-side. `TensorFlow.js` also offers better scalability and performance, especially when dealing with resource-intensive computer vision models on shinyapps.io.

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

To allow communication between `TensorFlow.js` and other components of the Shiny application, the `shinyjs` R package is used. This package allows calling custom JavaScript code within the Shiny framework. The specialized JavaScript code for initializing `TensorFlow.js` and calling `TensorFlow.js` for VSS prediction is deployed alongside the Shiny application as additional resources.

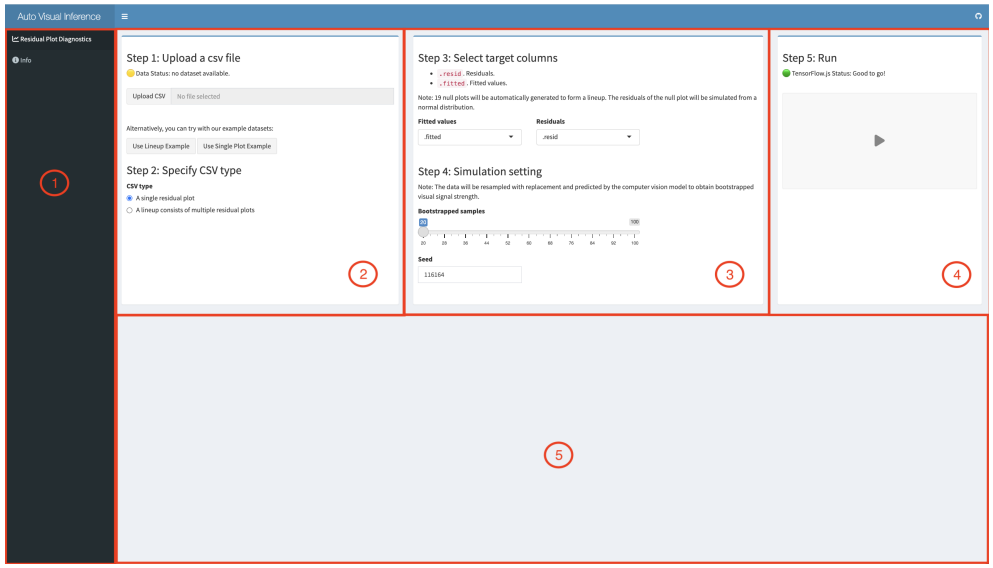

Figure 5. Overview of the `autovi.web` graphical user interface (GUI). This default view may change based on user interactions. Region 1 is the sidebar menu, containing the residual assessment tab and the information tab. Region 2 is the data upload panel, where users can provide a CSV file and specify the type of data it contains. Region 3 includes dropdown menus for selecting the columns to be analyzed, a slider to control the number of bootstrapping samples, and a numeric input box for setting the simulation seed. Region 4 displays the initialization status and offers a button to start the analysis. Region 5 is empty in the default view but will be populated with results once the analysis is started.

3.2. Design

While the R package `autovi` aims to provide tools that can be extended to broader visual inference applications, `autovi.web` is only focus on providing a straightforward and clean user interface. An overview of the graphical user interface of `autovi.web` is provided in Figure 5. This is the default view of the web application, and there are five regions that user can mainly interact with. Region 1 of Figure 5 is a sidebar menu which can switch between the analysis page and the information page. The analysis page is the focus of this section.

Region 2 of Figure 5 is a panel for data uploading and CSV type selection. Clicking the "upload CSV" button opens a window where the user can select a file from their local system. The data status displayed above the button provides information about the number of rows and columns in the current dataset. Additionally, there are two example datasets available beneath the "upload CSV" button: one is a lineup example using a CSV file with three columns, and the other is a single plot example using a

CSV file with two columns. More details about these example datasets are be discussed in Section 3.3.

While the `autovi` package typically expects a fitted regression model object provided by the user, this approach is impractical for a web interface. Saving the R model object to the filesystem involves extra steps and requires users to have specific knowledge, which does not align with the goal of the web application. Moreover, the regression model object may contain sensitive, non-shareable data, making it unsuitable for uploading. Additionally, model objects are often unnecessarily large, containing extra information not needed for residual diagnostics. In contrast, a CSV file is easier to generate using various software programs, not just R. CSV files are widely accepted and can be easily viewed and modified using common desktop applications like Excel. They are generally less sensitive than raw data, as they exclude most information about the predictors.

The web application is designed to assess either a single residual plot or a lineup of residual plots. Therefore, it accepts only two types of CSV files: one with at least two columns representing the fitted values and residuals of a single residual plot, and another with at least three columns, where the additional column serves as the label or identifier for a lineup of multiple residual plots. For a single residual plot, 19 null plots are generated by simulating normal random draws from a distribution with the same variance as the original residual plot, and comparisons are made with the original residual plot. For a lineup, comparisons are made among the plots within the lineup. After uploading the CSV file, the user must select the correct format to ensure the web interface interprets the data correctly.

Region 3 of Figure 5 is a panel for column selection and simulation settings. As shown in Figure 5, if the CSV type is set to a single residual plot, there will be two dropdown menus for specifying the columns for fitted values and residuals, respectively. The default variable names for these columns are `.fitted` and `.resid`. After uploading the CSV file, the content of these dropdown menus will be updated to reflect the existing columns in the dataset. As displayed in Figure 6, for the CSV type that is a lineup of multiple residual plots, an additional dropdown menu will appear for specifying the column of residual plot labels. The default variable name for this column is `.sample`. If this variable name does not exist in the dataset, the dropdown menu will remain empty, allowing the user to specify the correct column. The number of levels for each option in this dropdown menu will be displayed to help avoid the selection of a variable with too many levels, which could significantly slow down the application due to extensive computation.

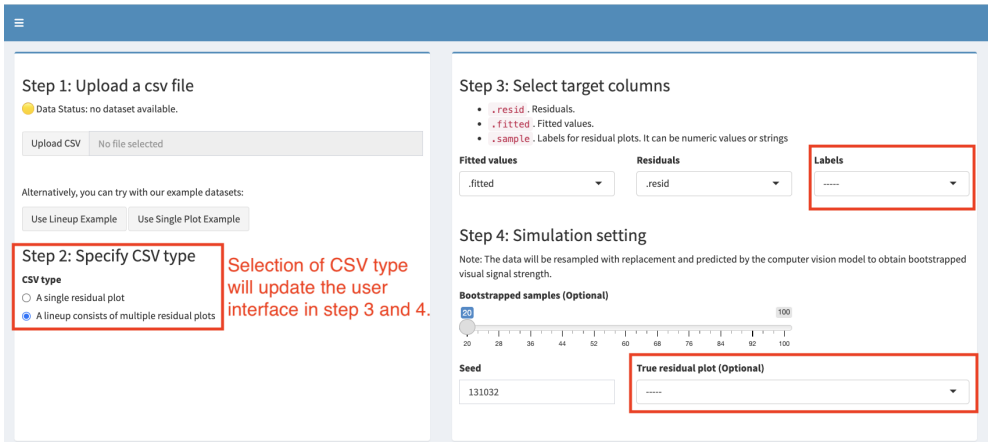

Figure 6. The panels for selecting target columns and simulation settings are updated when a different CSV type is selected in the left panel. Compared to Figure 5, where the CSV type is a single residual plot, choosing a CSV type that includes a lineup of multiple residual plots adds a dropdown menu for specifying a column for the residual plot identifier. Additionally, an optional dropdown menu for specifying the true residual plot identifier will appear under the simulation settings.

Under the simulation settings, there is a slider for specifying the number of bootstrapped samples needed for the assessment. A higher value on this slider will result in a more accurate bootstrap distribution estimation, though it will require more computation time. The simulation seed can be set in a numeric input box below the slider to control the reproducibility of the assessment. By default, a random seed is set each time the web page is refreshed. When the CSV type is a lineup of multiple residual plots, an optional dropdown menu will appear next to the simulation seed input box, allowing the user to specify an identifier for the true residual plot. If no label is provided for the true residual plot, the assessment will only estimate the VSS for each residual plot in the lineup, without providing a p-value, as it cannot be computed. Consequently, some result panels may be missing due to insufficient information. This option is useful when the lineup consists solely of null plots or if the user simply wants to obtain the VSS for multiple residual plots.

Region 4 of Figure 5 is the panel for triggering the assessment. It contains a large play button to start the assessment. Above the play button, a text message displays the status of `TensorFlow.js`, allowing users to monitor whether the JavaScript library and Keras model have been loaded correctly. The play button will remain disabled until both the data status in Region 1 and the `TensorFlow.js` status in Region 4 indicate that everything is ready, with both showing a green status.

Once the play button is clicked, region 5 of Figure 5 will be populated with panels displaying the assessment results. Generally, there will be four result panels, as shown in Figure 7 and Figure 8.

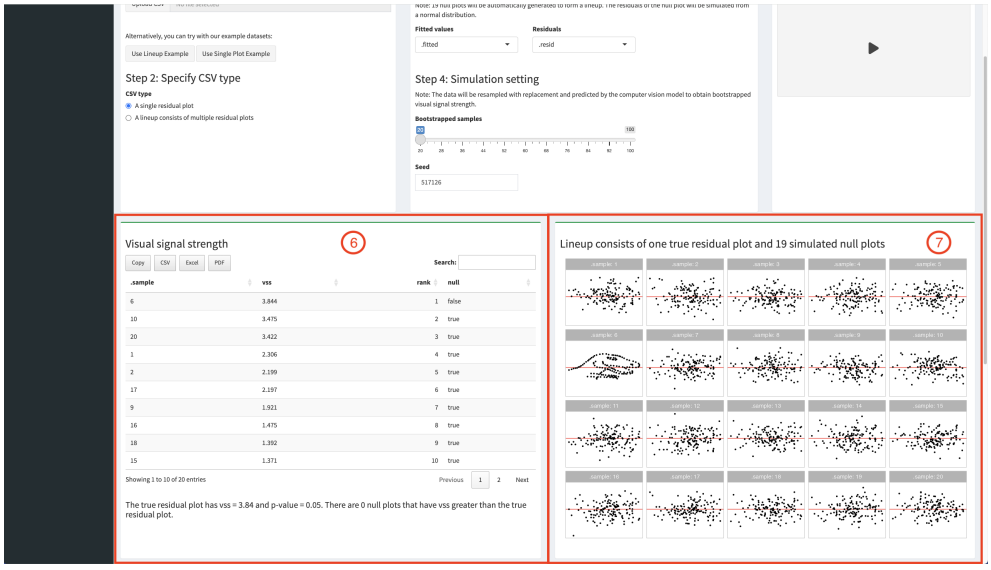

Figure 7. The first two panels of results from the automated residual assessment are shown. The application provides four results panels in total, and these screenshots display the first two. In region 1, there is an interactive table detailing the VSS, with a summary of the analysis provided in the paragraph below. Region 2 displays a lineup of residual plots.

Region 6 of Figure 7 contains an interactive table created with the R package `DT` (Xie, Cheng & Tan 2024), which provides the VSS. This table includes four columns: `.sample`, `vss`, `rank`, and `null`. The `.sample` column shows the residual plot labels. For a CSV type that is a lineup, these labels are taken from an identifier column in the dataset specified by the user. In the case of the CSV type is a single residual plot, labels are automatically generated from 1 to 20, with the true residual plot receiving a randomly assigned label. The `vss` column displays the VSS for each residual plot, rounded to three decimal places. The `rank` column indicates the ranking of each residual plot based on VSS. The `null` column reveals whether the plot is a null plot. For the CSV type that is a single residual plot, only the true residual plot will have "false" in this column, while all other plots will be marked "true." For the CSV type that is a lineup, if the true residual plot identifier has not been provided, this column will show "NA" to represent missing values. If the identifier is provided by user, the column behaves as if the CSV type is a single residual plot.

Figure 8. The last two panels of results from the automated residual assessment are shown. The application provides four results panels in total, and these screenshots display the final two. Region 1 presents a density plot comparing the bootstrapped VSS with the null VSS. Region 2 includes an attention map of the true residual plot.

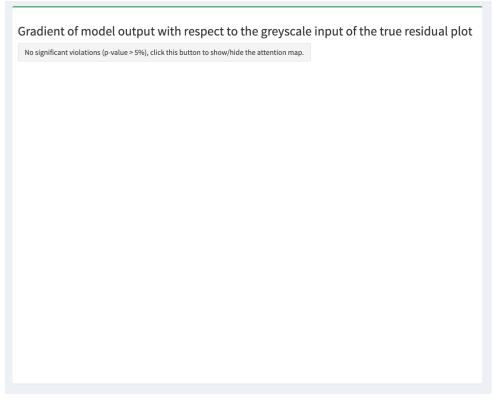

Figure 9. The attention map is hidden if the assessment indicates a p-value greater than 0.05. A button is available to toggle the display of the attention map.

The `DT` table provides several interactive features. Users can download the table in four formats, including text, CSV, Excel, and PDF, using the buttons located above the table. Additionally, the table is searchable via the text input field also positioned above it. Below the table, a text message displays the p-value of the assessment for the true residual plot and summarizes the number of null plots with VSS greater than

that of the true residual plot. This helps the user determine whether the true residual plot shows visual patterns that suggest model violations.

Region 7 of Figure 7 provides a lineup of plots corresponding to each `.sample` value from the table in Region 6. Due to space limitations, a maximum of 20 residual plots will be displayed, ensuring that the true residual plot, if known, will be included in the lineup. The plots are generated using `ggplot2`, the same as in `autovi`. Users can perform a visual test with this lineup to check if the true residual plot is distinguishable from the other plots, helping to determine the significance of model violations.

Region 8 of Figure 8 displays the density plot for bootstrapped VSS and null VSS. The densities are shown in distinct colors that are friendly for colorblind users. A solid vertical line marks the VSS of the true residual plot, while rug lines at the bottom of the plot provide a clearer view of individual cases. Below the plot, a text message indicates the number and percentage of bootstrapped residual plots that would be rejected by the visual test when compared to the null plots. Note that the bootstrapped residual plots in this application are generated differently from `autovi`. Since we do not have the R model object, we can not refit the regression model with bootstrapped data. Instead, we bootstrap the residuals of the true residual plot directly to obtain bootstrapped residual plots. As as result, this panel will disappear when the true residual plot is unknown.

Region 9 of Figure 8 displays an attention map for the true residual plot, generated by computing the gradient of the Keras model's output with respect to the greyscale input of the plot. The attention map helps to understand how the Keras model predicts VSS and which areas it is focusing on. We use a greyscale input because it is easier to generate a clear attention map in this format, and it usually conveys all the essential information, as most of the important details of the plot are drawn in black. If the p-value of the true residual plot is greater than 0.05, checking the attention map is not necessary. However, to provide users with the option to review it if they wish, a button will be available, as shown in Figure 9. This button allows users to toggle the display of the attention map.

3.3. Workflow

The workflow of `autovi.web` is designed to be straightforward, with numbered steps displayed in each panel shown in Figure 5. There are two example datasets provided by the web application, as mentioned in Section 3.2. The single residual plot example uses the `dino` dataset from the 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 will walk through the lineup example to further demonstrate the workflow of the web application.

As shown in Figure 10, 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 set automatically (Figure 11). If the user is working with a custom dataset, these options must be set accordingly. Regardless of the dataset, the user must manually select the label for the true residual plot, as the web application allows assessments without this label. The next step is to click the play button to start the assessment.

Results are provided in multiple panels as displayed in Figure 12, Figure 13, Figure 14 and Figure 15. In Figure 12, the first row of the table is the most crucial to check, as it provides the VSS and the rank of the true residual plot among the other plots. The summary text beneath the table provides the p-value, which can be used for quick decision-making. In Figure 13, the lineup is for manual inspection, and the user should see if the true residual plot is visually distinguishable from the other plots, to confirm if the model violation is serious. The density plot in Figure 14 offers a more robust result, allowing the user to compare the distribution of bootstrapped VSS with the distribution of null VSS. Finally, the grayscale attention map shown in Figure 15 can be used to check if the target visual features, like the non-linearity present in the lineup example, are captured by the computer vision model, ensuring the quality of the assessment.

4. Conclusions

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

The `autovi` R package, introduced in this paper, automates the assessment of residual plots by incorporating a computer vision model, eliminating the need for time-consuming and potentially inconsistent human interpretation. This automation

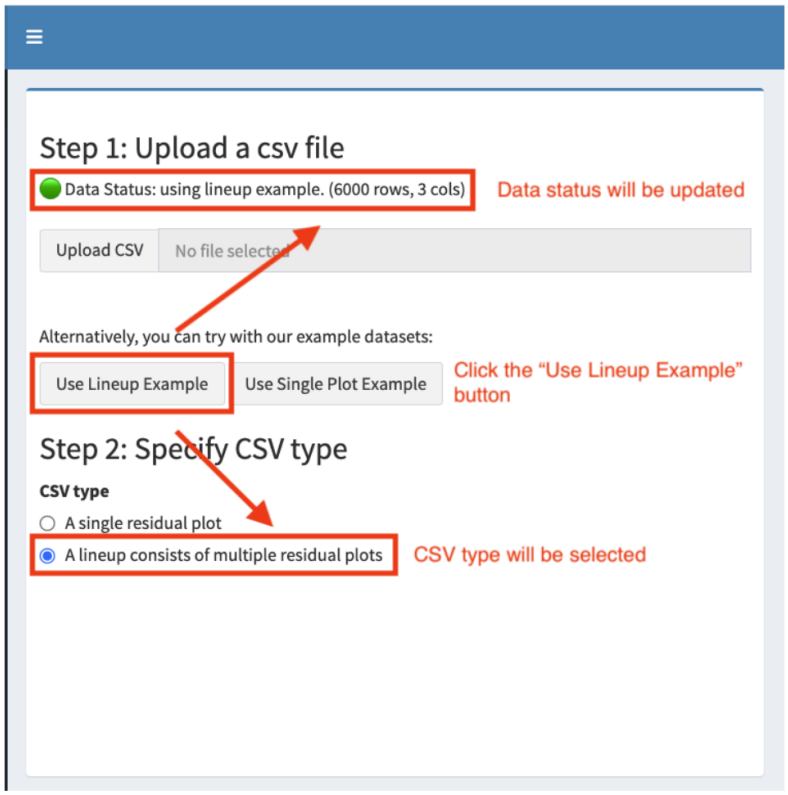

Figure 10. To begin the workflow for `autovi` using the lineup example dataset, the user clicks the "Use Lineup Example" button to load the example dataset, during which the data status and CSV type will be automatically updated.

improves the efficiency of the diagnostic process and promotes consistency in model evaluation across different users and studies.

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

The combination of `autovi` and `autovi.web` offers a comprehensive solution to the challenges of residual plot interpretation in regression analysis. These tools have the potential to significantly improve the quality and consistency of model diagnostics across various fields, from academic research to industry applications. By automating a critical aspect of model evaluation, they allow researchers and analysts to focus more

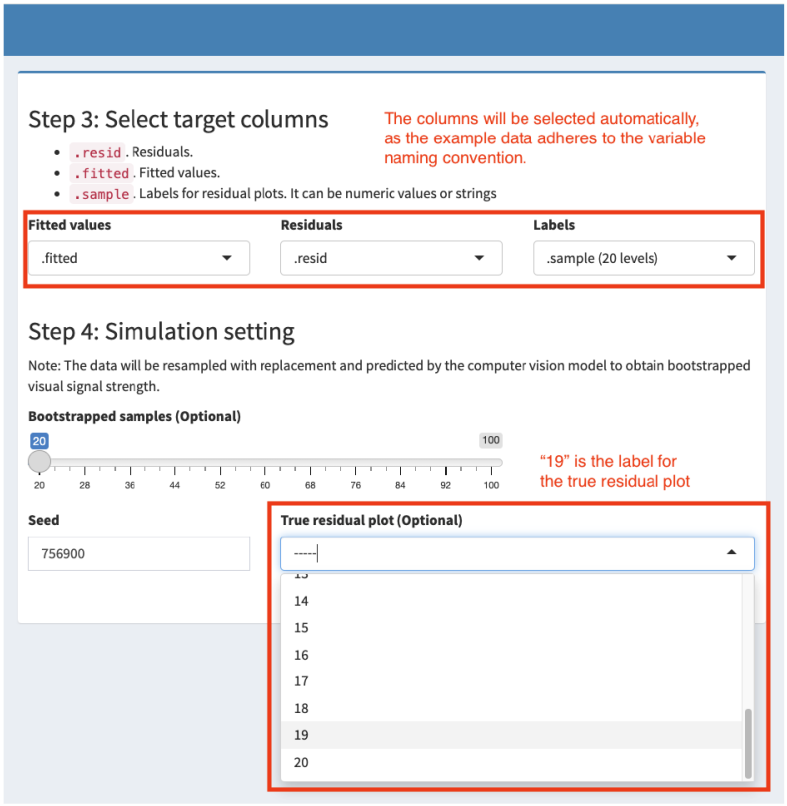

Figure 11. After clicking the button in Figure 10, the target columns are selected automatically, though the user must manually select the label for the true residual plot, as the web application permits assessment without this label.

443 on interpreting results and refining models, rather than grappling with the intricacies
444 of plot assessment.

445 The framework established by `autovi` and `autovi.web` opens up exciting possibilities
446 for further research and development. Future work could explore the extension of these
447 automated assessment techniques to other types of diagnostic plots and statistical
448 models, potentially revolutionizing how we approach statistical inference using visual
449 displays more broadly.

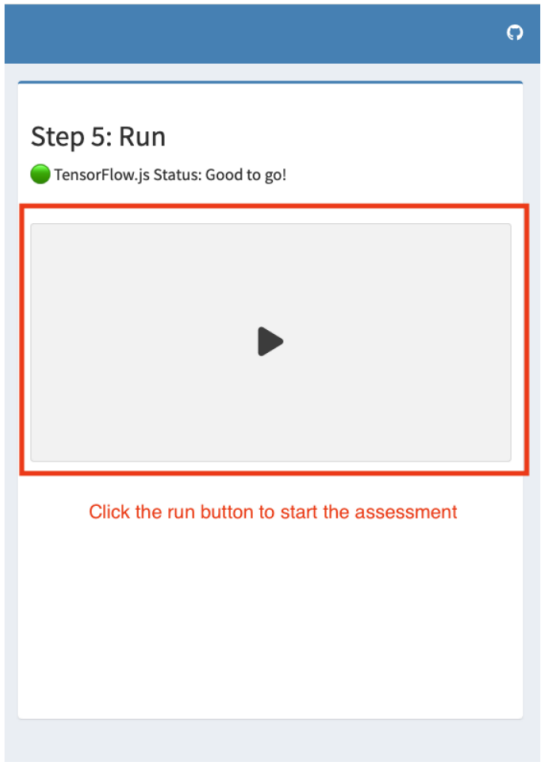

Figure 12. After finishing the required steps in Figure 10 and Figure 11, the user initiates the assessment of the lineup example data by clicking the run button.

5. Resources and Supplementary Material

The the current version of `autovi` can be installed from CRAN, and source code for both packages are available at https://github.com/TengMCing/autovi. The web interface is available from autoviweb.netlify.app.

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

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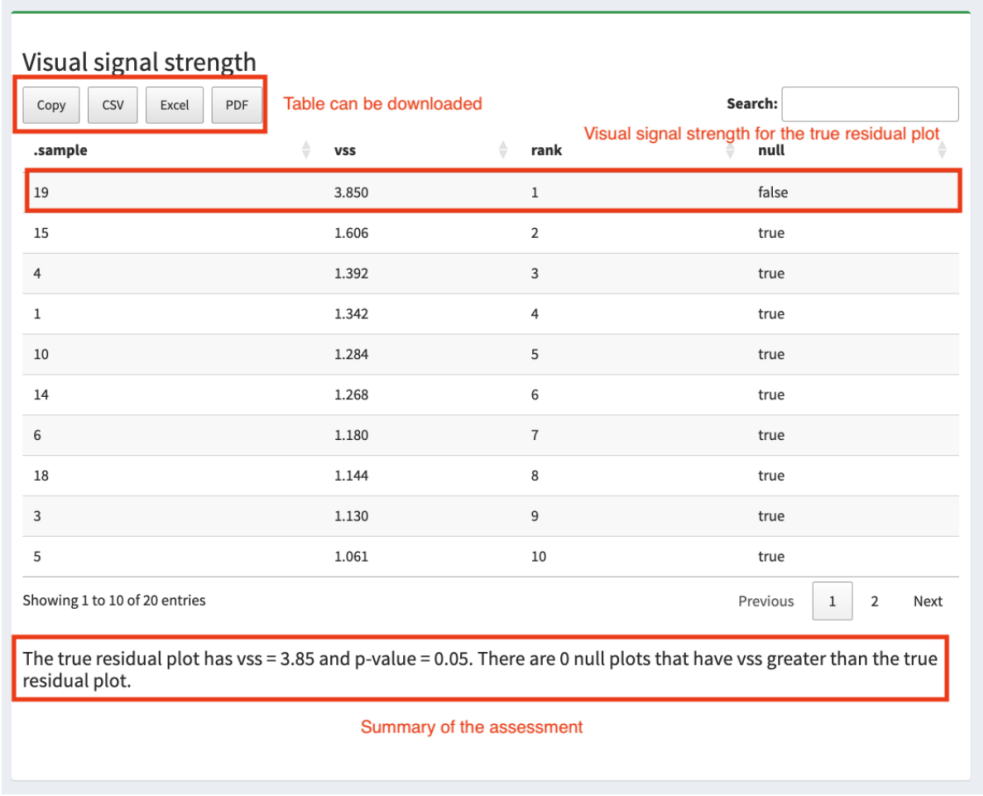

Figure 13. The VSS of the true residual plot is displayed in the first row of the table, with a summary text beneath the table providing the p-value to aid in decision-making.

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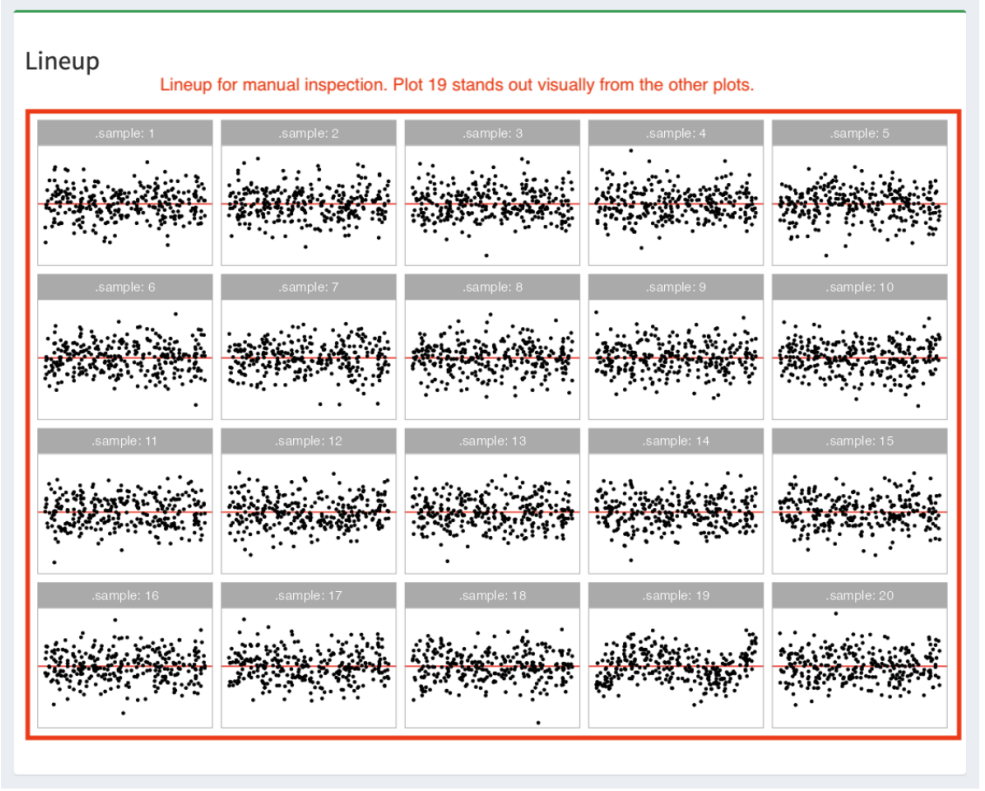

Figure 14. A lineup of residual plots allows for manual inspection.

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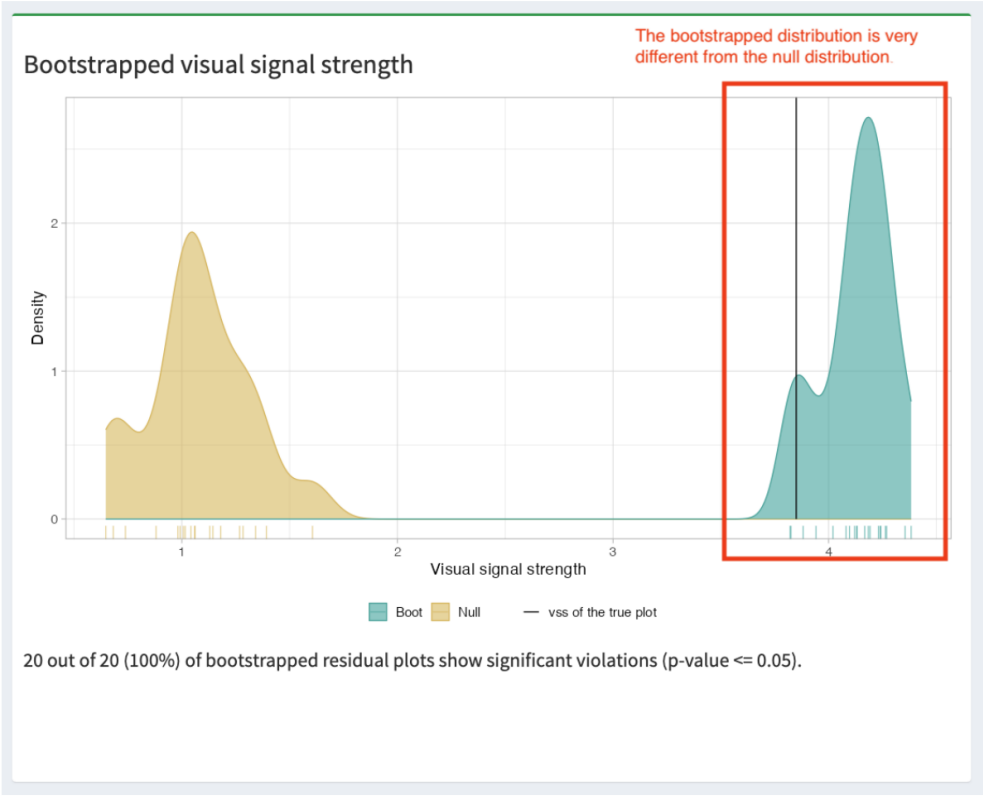

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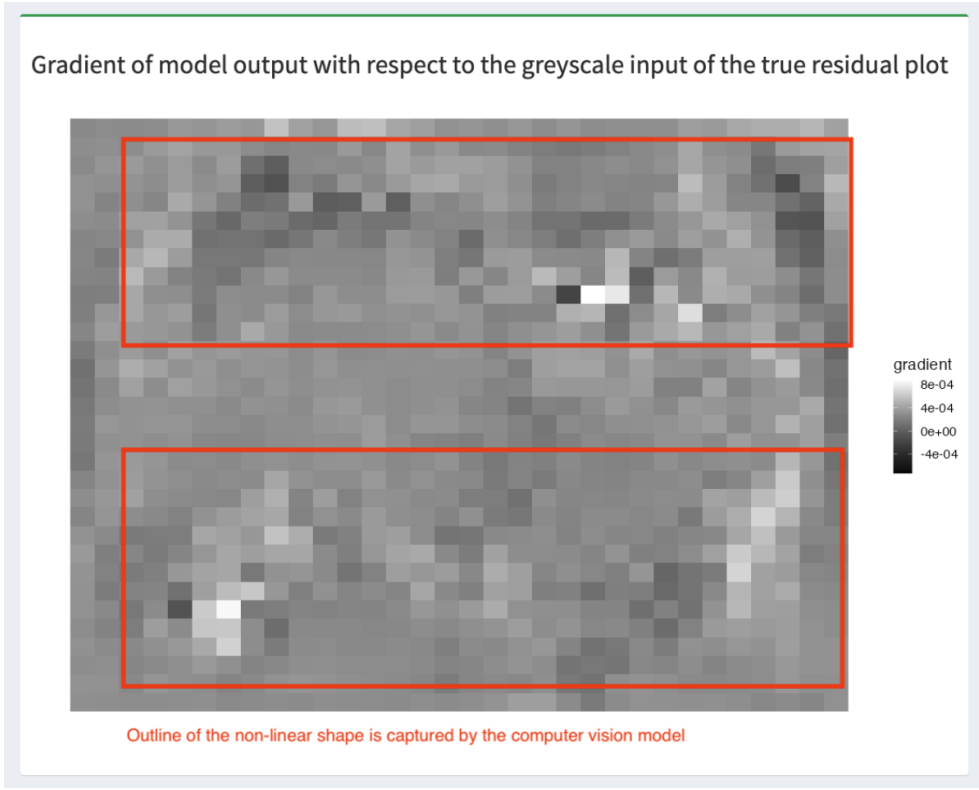

Figure 16. The attention map offers insights into whether the computer vision model has captured the intended visual features of the true residual plot.

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