

1 LazyModeler: An R package for automatic 2 simplification, check, and visualization of regression 3 models




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8 Summary

9 Setting up, simplifying, checking, and visualizing regression models continues to be a time-
10 consuming task involving multiple, sometimes concurrent, workflows and software packages.
11 This particularly applies to big data research where several models with different response
12 variables and many explanatory variables need to be set up and optimized. To tackle this
13 problem, we present LazyModeler - a statistical package for the programming language R that
14 allows to easily perform regression modeling. It includes removal of autocorrelated variables,
15 choice between several types of (non)linear regression models, standard stepwise model
16 simplification, various model quality checks, plotting of coefficient estimates and relationships,
17 and output generation. LazyModeler will significantly speed up regression modeling, enabling
18 people to analyze and illustrate their data in a statistically reliable and standardized manner.

Statement of need

19 Statistical modeling describes the process of finding a mathematical function with specific
20 statistical assumptions that best fits the observed data ([Crawley, 2007, 2015](#); [Henley et al., 2020](#)). This process attempts, in practice, to find a (causal) relationship between a dependent
21 response variable y and an independent predictor variable x for any postulated hypothesis. For
22 statistical inference and graphics in science, the programming environment R ([R Core Team, 2024](#))
23 has become highly popular.

24 Linear models, as one of the most basic and powerful tools, have been frequently applied in
25 this context ([Crawley, 2007, 2015](#); [Li, 2023](#); [Schielzeth et al., 2020](#)). Because of their flexibility,
26 they also allow for non-normally distributed response variables (e.g., in the case of binomial,
27 proportional, or count data), and any kind of transformation for numerical (e.g., polynomial or
28 logarithmic) and categorical (e.g., centered or one-hot/fractional encoded) predictor variables,
29 as well as interactions among them ([Cai et al., 2023](#); [Henley et al., 2020](#); [Karbstein et al., 2019, 2020, 2021](#);
30 [Liaw et al., 2021](#); [Römermann et al., 2016](#); [Schielzeth, 2010](#)). Regression
31 models also provide the ability to control for random effects that may influence the variables of
32 interest (e.g., [Bauer & Albrecht, 2020](#); [Schielzeth et al., 2020](#); [Wicke et al., 2016](#)). Although
33 other statistical technologies can outperform them in highly complex, non-linear scenarios,
34 regression models allow for detailed variable transformation and interaction, mathematical
35 formula specification, calculation of effect sizes, determination of variable significance, and
36 thus hypothesis testing and explanation ([Benjamin et al., 2018](#); [Bzdok & Ioannidis, 2019](#);
37 [Cai et al., 2023](#); [Karbstein et al., 2023](#); [Li, 2023](#); [Schulz et al., 2020](#)). Recent developments
38 make regression models also applicable to nonlinear scenarios (e.g., [Bates et al., 2024](#); [Hastie,](#)

2023). Consequently, they are of high practical value in finding and interpreting significant relationships.

In statistical modeling, and especially in real-world applications, multiple predictors are assumed for a given response variable. As a consequence, people strive to exclude the irrelevant from the relevant (statistically significant) information, which is called model simplification (Crawley, 2007, 2015; Forstmeier & Schielzeth, 2011). One of the most widely used optimization workflows is stepwise model simplification. For example, starting from a full/saturated model, the least significant variable ($p > 0.05$) is excluded until the final minimal adequate model is attained ['backward simplification'; Crawley (2007); Forstmeier & Schielzeth (2011); Crawley (2015)]. Each model simplification step will be justified with certain metrics (e.g., SSE, AIC, or BIC) (Henley et al., 2020). Given the number of models, variables of interest, and their data characteristics, this task can be extraordinarily time consuming. Currently, only AIC/BIC-based automated simplification is available (e.g., 'stepAIC,' Venables & Ripley, 2002). Nevertheless, model simplification continues to be a rather manual process [on Google Scholar, only ca. 5,000 "stepAIC" entries despite ca. 5,000,000 "linear regression model" studies (0.1%); e.g., Römermann et al. (2016); Karbstein et al. (2019); Henley et al. (2020); Karbstein et al. (2020); Cai et al. (2023); Li (2023)]. In addition, simplification and other aspects such as data cleaning, model comparison and quality control, and output visualization have not been automated. An easy-to-use, all-in-one function for the entire modeling process within a single software package is missing.

Our R package LazyModeler addresses these issues by automating variable selection, model optimization, and output illustration and generation. In detail, users will be enabled to automatically remove autocorrelated variables, choose between several types of (non)linear regression models (e.g., LM, GLM, LMER, GLMER, GAM, or NLMER), perform stepwise model simplification, check model quality, plot coefficient estimates and relationships, and generate the output of the final model.

Overview and major functions

LazyModeler automatizes all necessary steps needed for use of (non)linear regression models. It comprises three major functions that are included within the main function `optimize_model`.

The first major function `remove_autocorrelations` checks for any autocorrelations ($|r| > 0.7$) (Dormann et al., 2013) given a list of variables sorted by relevance. Automatic removal of these autocorrelations is possible through the use of a function parameter. Removal will follow the order of the list of variables, ensuring that the user's expertise on the importance of features is respected. A named list is returned with a) a vector containing all removed predictors, and b) a dataframe listing autocorrelations and information on deleted variables.

The main function provides the model formula to the second major function `simplify_model`. If autocorrelations were detected, the formula is updated accordingly. The regression model is then calculated. Options for the models are: `lm`, `glm`, `lmer`, `glmer`, `gam`, or `nlmer`, with all possible distributions of the response variable being allowed. Stepwise backward simplification or forward model selection takes place using an iterative process where each time the metric(s) specified by the user are applied on the model to check whether further simplification/selection is needed. Main variables are kept when they are involved in interactions. Options for the metrics are: `aov`, `aic`, `aicc`, or `bic`. The final model is returned to the main function alongside its metadata as well as simplification history if requested by the user.

Using the third major function `plot_model_features`, the final model then undergoes multiple visualization steps. Plots to assess model quality are created using the standard plot function available through base R, or model check included in the performance R package (Lüdtke et al., 2021). Furthermore, the script produces regression, box, or violin plots for each numerical or categorical coefficient as well as plots depicting effects sizes and estimates. All generated

90 plots are returned to the user within a named list. The main function additionally returns the
91 output of both the model simplification/selection and autocorrelation functions as well as the
92 summary of the final model.

93 LazyModeler makes use of the R package `corrplot` (Wei & Simko, 2021) to calculate
94 correlations between variables, `lme4` (Bates et al., 2024) and `lmerTest` (Kuznetsova et al.,
95 2017) for regression modeling, `tidyverse` (Wickham et al., 2019) for data handling, and `MuMIn`
96 (Bartoń, 2024) for calculation of AICc scores. For generation of plots visualizing regression,
97 effect size, and estimates, the script further leverages `tidyverse` and color palettes included in
98 the `colorspace` (Zeileis et al., 2020) and `viridis` (Garnier et al., 2024) R packages.

99 Example

```
# import example data
data(plants)

# check data structure
str(plants)
summary(plants)

# testing dataset (subset) based on Karbstein et al. 2021
#(https://onlinelibrary.wiley.com/doi/10.1111/mec.15919)

results_example <- optimize_model(plants, quote(sexual_seed_prop ~
altitude + latitude_gps_n + longitude_gps_e + (solar_radiation +
annual_mean_temperature + isothermality)^2 + I(isothermality^2) +
habitat + ploidy), autocorrelation_cols = c("solar_radiation",
"annual_mean_temperature", "isothermality", "altitude",
"latitude_gps_n", "longitude_gps_e"), automatic_removal=TRUE,
autocorrelation_threshold = 0.8, correlation_method="spearman",
model_type = "glm", model_family = "quasibinomial",
assessment_methods=c("anova"), simplification_direction="backward",
omit.na="overall", scale_predictor=TRUE,
plot_quality_assessment="performance", round_p=3,
cor_use="complete.obs", plot_relationships=TRUE, jitter_plots=TRUE,
plot_type="violinplot", stat_test="wilcox",
backward_simplify_model=TRUE, trace=TRUE)
```

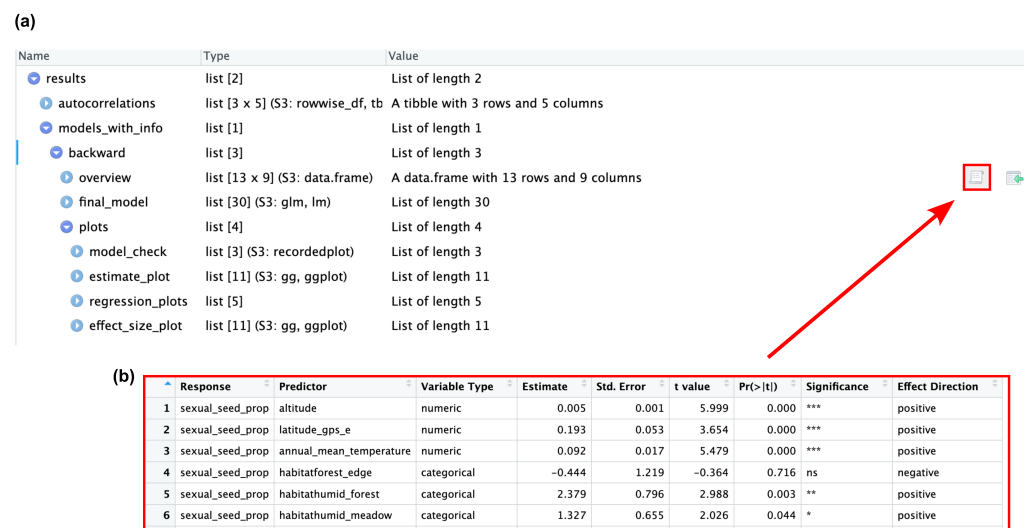


Figure 1: Navigating through the output. For example, (a) simply click on dataframe button highlighted with a red arrow to (b) illustrate the final model output.

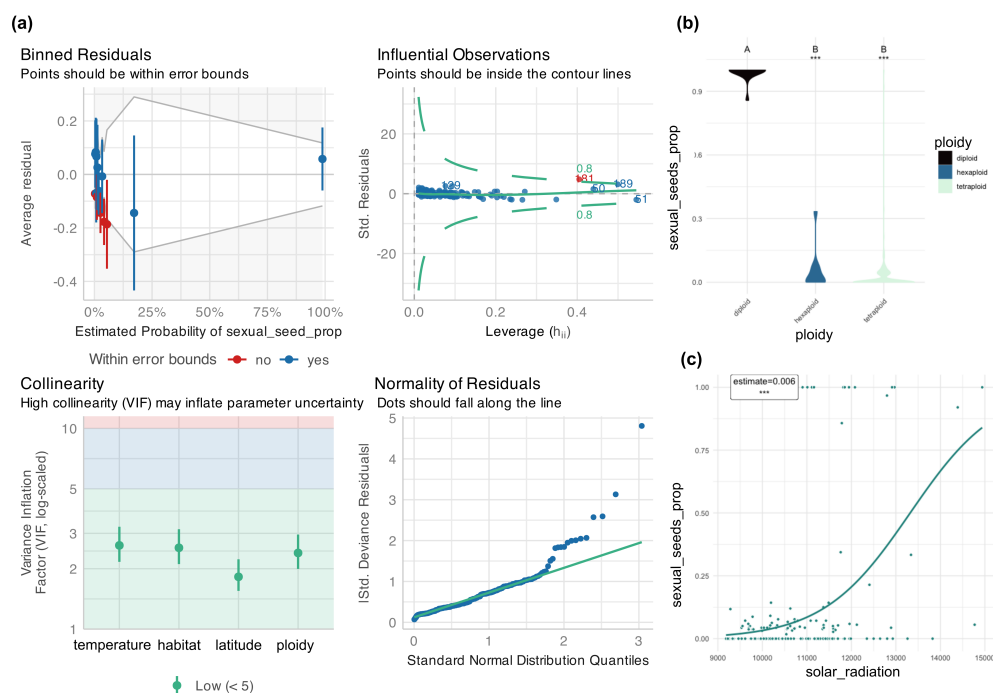


Figure 2: (a) Model quality check and (b,c) exemplary output plots of significant relationships.

Conclusions

In summary, LazyModeler streamlines the process of building, simplifying, and visualizing regression models in R. By automating key steps such as autocorrelation removal, model selection, quality assessment, and output generation, it significantly reduces manual effort. The package is especially valuable for researchers dealing with large and complex datasets who seek a reproducible and statistically sound regression modeling workflow. We anticipate that LazyModeler will serve as a practical and accessible tool for both novice and experienced users in the scientific community.

Important note

The model selection procedures implemented in LazyModeler are provided for convenience and exploratory analysis, and reflect practices recommended in widely used applied statistics literature (Crawley, 2007, 2015). Users should be aware, however, that statistical inference reported from a model chosen in a data-driven way may be anti-conservative (e.g., p-values may appear smaller than they truly are, confidence intervals narrower). This issue is known as post-selection inference (PSI). Specialized methods have been developed to address it, for instance (Lee et al., 2016), but they are not yet broadly applicable across the full range of model classes supported by LazyModeler. We have implemented PSI for (generalized) linear regression models based on the 'selcorr' R package (Cattaneo, 2021), but users are free to use the retained model from LazyModeler for more sophisticated PSI analyses.

Code availability

The code including basic documentation and an exemplary testing dataset will be made available upon publication on [Github](#) and on [Comprehensive R Archive Network \(CRAN\)](#).

Acknowledgements

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References

- Bartoń, K. (2024). *MuMIn: Multi-model inference*. <https://doi.org/10.32614/cran.package.mumin>
- Bates, D., Maechler, M., Bolker, B., & Walker, S. (2024). *lme4 - Linear mixed-effects models using 'Eigen' and S4*. <https://github.com/lme4/lme4/>
- Bauer, M., & Albrecht, H. (2020). Vegetation monitoring in a 100-year-old calcareous grassland reserve in Germany. *Basic and Applied Ecology*, 42, 15–26. <https://doi.org/10.1016/j.baae.2019.11.003>
- Benjamin, A. S., Fernandes, H. L., Tomlinson, T., Ramkumar, P., VerSteeg, C., Chowdhury, R. H., Miller, L. E., & Kording, K. P. (2018). Modern machine learning as a benchmark for fitting neural responses. *Frontiers in Computational Neuroscience*, 12(July), 1–13. <https://doi.org/10.3389/fncom.2018.00056>
- Bzdok, D., & Ioannidis, J. P. A. (2019). Exploration, Inference, and Prediction in Neuroscience and Biomedicine. *Trends in Neurosciences*, 42(4), 251–262. <https://doi.org/10.1016/j.tins.2019.02.001>

- 140 Cai, L., Kreft, H., Taylor, A., Denelle, P., Schrader, J., Essl, F., Kleunen, M. van, Pergl, J.,
141 Pyšek, P., Stein, A., Winter, M., Barcelona, J. F., Fuentes, N., Inderjit, Karger, D. N.,
142 Kartesz, J., Kuprijanov, A., Nishino, M., Nickrent, D., ... Weigelt, P. (2023). Global models
143 and predictions of plant diversity based on advanced machine learning techniques. *New*
144 *Phytologist*, 237(4), 1432–1445. <https://doi.org/10.1111/nph.18533>
- 145 Cattaneo, M. (2021). *Selcorr: Post-selection inference for generalized linear models*. <https://CRAN.R-project.org/package=selcorr>
- 147 Crawley, M. J. (2007). *The R Book* (p. 942). John Wiley & Sons, Ltd. <https://doi.org/10.1002/9780470515075>
- 149 Crawley, M. J. (2015). *Statistics: an introduction using R* (sec. ed., p. 339). John Wiley &
150 Sons. ISBN: 1118448960
- 151 Dormann, C. F., Elith, J., Bacher, S., Buchmann, C., Carl, G., Carré, G., Marquéz, J. R.
152 G., Gruber, B., Lafourcade, B., Leitão, P. J., Münkemüller, T., McClean, C., Osborne, P.
153 E., Reineking, B., Schröder, B., Skidmore, A. K., Zurell, D., & Lautenbach, S. (2013).
154 Collinearity: a review of methods to deal with it and a simulation study evaluating their
155 performance. *Ecography*, 36(1), 27–46. <https://doi.org/10.1111/j.1600-0587.2012.07348.x>
- 157 Forstmeier, W., & Schielzeth, H. (2011). Cryptic multiple hypotheses testing in linear models:
158 overestimated effect sizes and the winner's curse. *Behavioral Ecology and Sociobiology*,
159 65(1), 47–55. <https://doi.org/10.1007/s00265-010-1038-5>
- 160 Garnier, Simon, Ross, Noam, Rudis, Robert, Camargo, Pedro, A., Sciaini, Marco, Scherer,
161 & Cédric. (2024). *viridis(Lite) - colorblind-friendly color maps for r*. <https://doi.org/10.5281/zenodo.4679423>
- 163 Hastie, T. (2023). *gam: Generalized Additive Models*. <https://cran.r-project.org/web/packages/gam/index.html>
- 165 Henley, S. S., Golden, R. M., & Kashner, T. M. (2020). Statistical modeling methods:
166 challenges and strategies. *Biostatistics & Epidemiology*, 4(1), 105–139. <https://doi.org/10.1080/24709360.2019.1618653>
- 168 Karbstein, K., Prinz, K., Hellwig, F., & Römermann, C. (2020). Plant intraspecific functional
169 trait variation is related to within-habitat heterogeneity and genetic diversity in *Trifolium*
170 *montanum* L. *Ecology and Evolution*, 10(11), 5015–5033. <https://doi.org/10.1002/ece3.6255>
- 172 Karbstein, K., Römermann, C., Hellwig, F., & Prinz, K. (2023). Population size affected
173 by environmental variability impacts genetics, traits, and plant performance in *Trifolium*
174 *montanum* L. *Ecology and Evolution*, 13(8), 1–19. <https://doi.org/10.1002/ece3.10376>
- 175 Karbstein, K., Tomasello, S., Hodač, L., Lorberg, E., Daubert, M., & Hörandl, E. (2021).
176 Moving beyond assumptions: Polyploidy and environmental effects explain a geographical
177 parthenogenesis scenario in European plants. *Molecular Ecology*, 30(11), 2659–2675.
178 <https://doi.org/10.1111/mec.15919>
- 179 Karbstein, K., Tomasello, S., & Prinz, K. (2019). Desert-like badlands and surrounding
180 (semi-)dry grasslands of Central Germany promote small-scale phenotypic and genetic
181 differentiation in *Thymus praecox*. *Ecology and Evolution*, 9(24), 14066–14084. <https://doi.org/10.1002/ece3.5844>
- 183 Kuznetsova, A., Brockhoff, P. B., & Christensen, R. H. B. (2017). lmerTest package: Tests
184 in linear mixed effects models. *Journal of Statistical Software*, 82(13), 1–26. <https://doi.org/10.18637/jss.v082.i13>
- 186 Lee, J. D., Sun, D. L., Sun, Y., & Taylor, J. E. (2016). Exact post-selection inference, with
187 application to the lasso. *Annals of Statistics*, 44(3), 907–927. <https://doi.org/10.1214/>

188 15-AOS1371

- 189 Li, J. (2023). Overview of high dimensional linear regression models. *Theoretical and Natural*
190 *Science*, 5(1), 656–661. <https://doi.org/10.54254/2753-8818/5/20230427>
- 191 Liaw, K., Khomik, M., & Arain, M. A. (2021). Explaining the shortcomings of log-transforming
192 the dependent variable in regression models and recommending a better alternative:
193 Evidence from soil CO₂ emission studies. *Journal of Geophysical Research: Biogeosciences*,
194 126(5), 1–18. <https://doi.org/10.1029/2021JG006238>
- 195 Lüdecke, D., Ben-Shachar, M. S., Patil, I., Waggoner, P., & Makowski, D. (2021). Performance:
196 An r package for assessment, comparison and testing of statistical models. *Journal of Open*
197 *Source Software*, 6(60), 3139. <https://doi.org/10.21105/joss.03139>
- 198 R Core Team. (2024). *R: a language and environment for statistical computing*. R Foundation
199 for Statistical Computing. <http://www.r-project.org/>
- 200 Römermann, C., Bucher, S. F., Hahn, M., & Bernhardt-Römermann, M. (2016). Plant
201 functional traits – fixed facts or variable depending on the season? *Folia Geobotanica*,
202 51(2), 143–159. <https://doi.org/10.1007/s12224-016-9250-3>
- 203 Schielzeth, H. (2010). Simple means to improve the interpretability of regression coefficients.
204 *Methods in Ecology and Evolution*, 1(2), 103–113. <https://doi.org/10.1111/j.2041-210X.2010.00012.x>
- 205
- 206 Schielzeth, H., Dingemanse, N. J., Nakagawa, S., Westneat, D. F., Alaguer, H., Teplitsky, C.,
207 Réale, D., Dochtermann, N. A., Garamszegi, L. Z., & Araya-Ajoy, Y. G. (2020). Robustness
208 of linear mixed-effects models to violations of distributional assumptions. *Methods in*
209 *Ecology and Evolution*, 11(9), 1141–1152. <https://doi.org/10.1111/2041-210X.13434>
- 210 Schulz, M.-A., Yeo, B. T. T., Vogelstein, J. T., Mourao-Miranada, J., Kather, J. N., Kording,
211 K., Richards, B., & Bzdok, D. (2020). Different scaling of linear models and deep learning
212 in UKBiobank brain images versus machine-learning datasets. *Nature Communications*,
213 11(1), 4238. <https://doi.org/10.1038/s41467-020-18037-z>
- 214 Venables, W. N., & Ripley, B. D. (2002). *Modern Applied Statistics with S* (Fourth). Springer.
215 ISBN: 0-387-95457-0
- 216 Wei, T., & Simko, V. (2021). *R package 'corrplot': Visualization of a correlation matrix*.
217 <https://github.com/taiyun/corrplot>
- 218 Wicke, S., Müller, K. F., DePamphilis, C. W., Quandt, D., Bellot, S., & Schneeweiss, G. M.
219 (2016). Mechanistic model of evolutionary rate variation en route to a nonphotosynthetic
220 lifestyle in plants. *Proceedings of the National Academy of Sciences of the United States*
221 *of America*, 113(32), 9045–9050. <https://doi.org/10.1073/pnas.1607576113>
- 222 Wickham, H., Averick, M., Bryan, J., Chang, W., McGowan, L. D., François, R., Golemund,
223 G., Hayes, A., Henry, L., Hester, J., Kuhn, M., Pedersen, T. L., Miller, E., Bache, S. M.,
224 Müller, K., Ooms, J., Robinson, D., Seidel, D. P., Spinu, V., ... Yutani, H. (2019). Welcome
225 to the tidyverse. *Journal of Open Source Software*, 4(43), 1686. <https://doi.org/10.21105/joss.01686>
- 226
- 227 Zeileis, A., Fisher, J. C., Hornik, K., Ihaka, R., McWhite, C. D., Murrell, P., Stauffer, R.,
228 & Wilke, C. O. (2020). colorspace: A toolbox for manipulating and assessing colors and
229 palettes. *Journal of Statistical Software*, 96(1), 1–49. <https://doi.org/10.18637/jss.v096.i01>
- 230