

Predictive Models: Explore, Explain, and Debug

Human-Centered Interpretable Machine Learning

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2019-07-17



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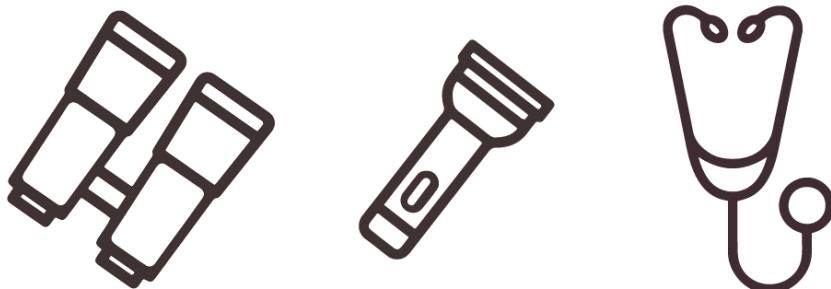
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Preface

Predictive Models

Explore, Explain and Debug

Human-Centered Interpretable Machine Learning



**Przemysław Biecek
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0.1 Introduction

0.1.1 Notes to readers

A note to readers: this text is a work in progress.

We've released this initial version to get more feedback. Feedback can be given at the GitHub repo https://github.com/pbiecek/PM_VEE/issues. Copyediting has not been done yet so read at your own risk.

We are primarily interested in the organization and consistency of the content, but any comments will be welcomed.

Thanks for taking the time to read this.

We'd like to thank everyone that contributed feedback, typos, or discussions while the book was being written. GitHub contributors included, [agosiewska](#), Rees Morrison.

0.1.2 The aim of the book

Predictive models are used to guess (statisticians would say: predict) values of a variable of interest based on other variables. As an example, consider prediction of sales based on historical data, prediction of risk of heart disease based on patient characteristics, or prediction of political attitudes based on Facebook comments.

Predictive models have been constructed through the entire human history. Ancient Egyptians, for instance, used observations of the rising of Sirius to predict flooding of the Nile. A more rigorous approach to model construction may be attributed to the method of least squares, published more than two centuries ago by Legendre in 1805 and by Gauss in 1809. With time, the number of applications in economy, medicine, biology, and agriculture has grown. The term *regression* was coined by Francis Galton in 1886. Initially, it was referring to biological applications, while today it is used for various models that allow prediction of continuous variables. Prediction of nominal variables is called *classification*, and its beginning may be attributed to works of Ronald Fisher in 1936.

During the last century, many statistical models that can be used for predictive purposes have been developed. These include linear models, generalized linear models, regression and classification trees, rule-based models, and many others. Developments in mathematical foundations of predictive models were boosted by increasing computational power of personal computers and availability of large datasets in the era of „big data” that we have entered.

With the increasing demand for predictive models, model features such as flexibility, ability to perform internally variable selection (feature engineering), and high precision of predictions are of interest. To obtain robust models, ensembles of models are used. Techniques like bagging, boosting, or model stacking combine hundreds or thousands of small models into a one super-model. Large deep neural models have over a billion parameters.

There is a cost of this progress. Complex models may seem to operate like „black boxes“. It may be difficult, or even impossible, to understand how thousands of coefficients affect the model prediction. At the same time, complex models may not work as well as we would like them to. An overview of real problems with large black-box models may be found in an excellent book of Cathy O’Neil ([O’Neil, 2016](#)) or in her TED Talk „*The era of blind faith in big data must end*“. There is a growing number of examples of predictive models with performance that deteriorated over time or became biased in some sense. For instance, IBM’s Watson for Oncology was criticized by oncologists for delivering unsafe and inaccurate recommendations ([Ross and Swetliz, 2018](#)). Amazon’s system for CV screening was found to be biased against women ([Dastin, 2018](#)). The COMPAS (Correctional Offender Management Profiling for Alternative Sanctions) algorithm for predicting recidivism, developed by Northpointe (now Equivant), is biased against blacks ([Larson et al., 2016](#)). These are examples of models and algorithms that led to serious violations of fairness and ethical principles. An example of situation when data drift led to deterioration in model performance is the Google Flu model, which gave worse predictions after two years than at baseline ([Salzberg, 2014](#)), [[Lazer et al Science 2014](#)].

A reaction to some of these examples and problems are new regulations, like the General Data Protection Regulation ([GDPR, 2018](#)). Also, new civic rights are being formulated ([Goodman and Flaxman, 2016](#)), ([Casey et al., 2018](#)), ([Ruiz, 2018](#)). A noteworthy example is the „*Right to Explanation*“, i.e., the right to be provided an explanation for an output of an automated algorithm ([Goodman and Flaxman, 2016](#)). To exercise the right, methods for verification, exploration, and explanation of predictive models are needed.

We can conclude that, today, the true bottleneck in predictive modelling is not the lack of data, nor the lack of computational power, nor inadequate algorithms, nor the lack of flexible models. It is the lack of tools for model validation, model exploration, and explanation of model decisions. Thus, in this book, we present a collection of methods that may be used for this purpose. As development of such methods is a very active area of research and new methods become available almost on a continuous basis, we do not aim at being exhaustive. Rather, we present the mind-set, key problems, and several examples of methods that can be used in model exploration.

0.1.3 A bit of philosophy: three laws of model explanation

Seventy-six years ago, Isaac Asimov formulated [Three Laws of Robotics](#): 1) a robot may not injure a human being, 2) a robot must obey the orders given it by human beings, and 3) a robot must protect its own existence.

Today’s robots, like cleaning robots, robotic pets, or autonomous cars are far from being conscious enough to fall under Asimov’s ethics. However, we are more and more surrounded by complex predictive models and algorithms used for decision making. Machine-learning models are used in health care, politics, education, justice, and many other areas. The models and algorithms have a far larger influence on our lives than physical robots. Yet, applications of such models are left unregulated despite examples of their potential harmfulness. See

Predictive Models: Visual Exploration, Explanation and Debugging

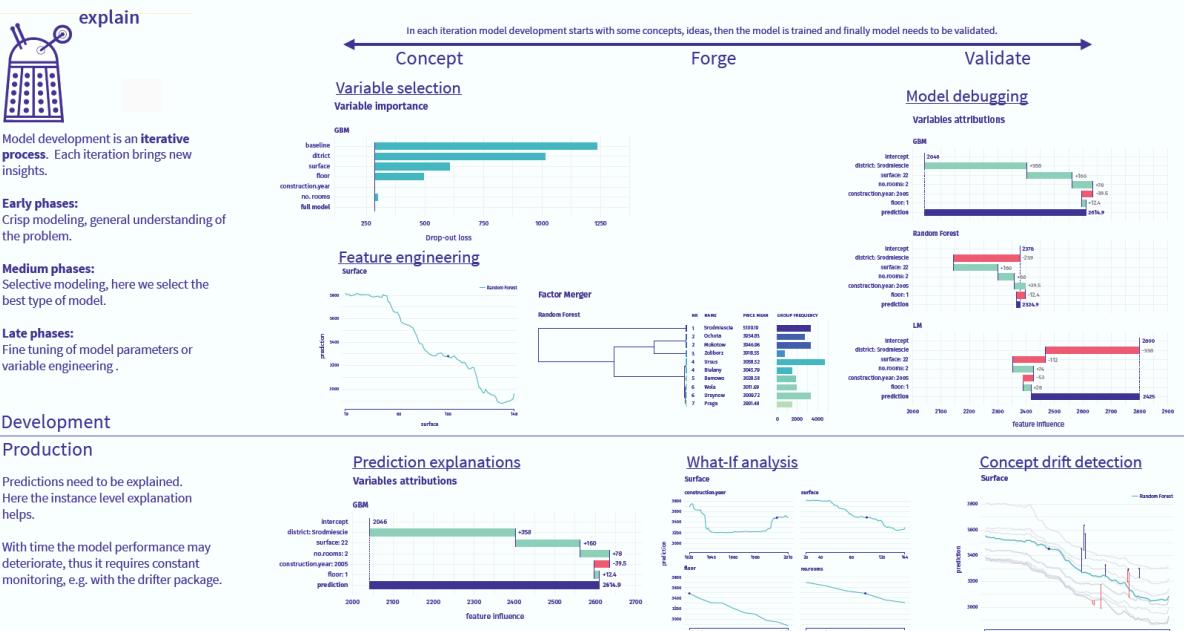


FIGURE 1 (fig:DrWhyAIPMVEE) Visual exploration of predictive models help in every phase of model life-cycle. Model level methods help in early crisp modeling. Instance level methods help in debugging. Feature effects help to cross-compare candidate models. Auditors help to identify weak sides of considered models.

Weapons of Math Destruction by Cathy O’Neil (O’Neil, 2016) for an excellent overview of selected problems.

It’s clear that we need to control the models and algorithms that may affect us. Thus, Asimov’s laws are referred to in the context of the discussion around [Ethics of Artificial Intelligence](#). Initiatives to formulate principles for AI development have been undertaken, for instance, in the UK [Olhede & Wolfe, Significance 2018, 15: 6-7]. Following Asimov’s approach, we propose three requirements that any predictive model should fulfill:

- **Prediction’s justification.** For every prediction of a model, one should be able to understand which variables affect the prediction and to what extent.
- **Prediction’s speculation.** For every prediction of a model, one should be able to understand how the model prediction would change if input variables changed.
- **Prediction’s validation.** For every prediction of a model, one should be able to verify how strong is the evidence that confirms the prediction.

We see two ways to comply with these requirements. One is to use only models that fulfill these conditions by design. However, the price for transparency may be a reduction in performance. Another way is to use tools that allow, perhaps by using approximations, to „explain” predictions for any model. In our book, we will focus on the latter approach.

0.1.4 Terminology

It is worth noting that, when it comes to predictive models, the same concepts have often been given different names in statistics and in machine learning. For instance, in the statistical-modelling literature, one refers to „explanatory variables,” with „independent variables,” „predictors,” or „covariates” as often-used equivalents. Explanatory variables are used in the model as means to explain (predict) the „dependent variable,” also called „predicted” variable or „response.” In machine-learning terminology, „input variables” or „features” are used to predict the „output” variable. In statistical modelling, models are fit to the data that contain „observations,” whereas in the machine-learning world a dataset may contain „instances.”

To the extent possible, in our book we try to consistently use the statistical-modelling terminology. However, the reader may find references to a „feature” here and there. Somewhat inconsistently, we also introduce the term „instance-level” explanation. Instance-level explanation methods are designed to extract information about the behavior of the model related to a specific observation (or instance). On the other hand, „global” explanation techniques allow obtaining information about the behavior of the model for an entire dataset.

We consider models for dependent variables that can be continuous or nominal. The values of a continuous variable can be represented by numbers with an ordering that makes some sense (zip codes or phone numbers are not considered as continuous variables). A continuous variable does not have to be continuous in the mathematical sense; counts (number of floors, steps, etc.) will be treated as continuous variables as well. A nominal variable can assume only a finite set of values that cannot be given numeric values.

In this book we focus on „black-box” models. We discuss them in a bit more detail in the next section.

0.1.5 Glass-box models vs. black-box models

Black-box models are models with a complex structure that is hard to understand by humans. Usually this refers to a large number of model coefficients. As people vary in their capacity to understand complex models, there is no strict threshold for the number of coefficients that makes a model a black-box. In practice, for most people this threshold is probably closer to 10 than to 100.

A „glass-box” (sometimes called white-box) model, which is opposite to a „black-box” one, is a model that is easy to understand (though maybe not by every person). It has a simple structure and a limited number of coefficients. The two most common classes of glass-box models are decision or regression trees, as an example in Figure 2, or models with an additive structure, like the following model for mortality risk in melanoma patients:

$$\text{RelativeRisk} = 1 + 3.6 * [\text{Breslow} > 2] - 2 * [\text{TILs} > 0]$$

In the model, two explanatory variables are used: an indicator whether the thickness of the lesion according to the Breslow scale is larger than 2 mm and an indicator whether the percentage of tumor-infiltrating lymphocytes (TILs) is larger than 0.

The structure of a glass box-model is, in general, easy to understand. It may be difficult to collect the necessary data, build the model, fit it to the data, or perform model validation, but once the model has been developed its interpretation and mode of working is straightforward.

Why is it important to understand the model structure? There are several important advantages. If the model structure is clear, we can easily see which variables are included in the model and which are not. Hence, for instance, we may be able to, question the model when a particular explanatory variable was excluded from it. Also, in the case of a model with a clear structure and a limited number of coefficients, we can easily link changes in model predictions with changes in particular explanatory variables. This, in turn, may allow us to challenge the model against domain knowledge if, for instance, the effect of a particular variable on predictions is inconsistent with previously established results. Note that linking changes in model predictions with changes in particular explanatory variables may be difficult when there are many variables and/or coefficients in the model. For instance, a classification tree with hundreds of nodes is difficult to understand, as is a linear regression model with hundreds of coefficients.

Comprehending the performance of a black-box models presents more challenges. The structure of a complex model, such as a neural-network model, may be far from transparent. Consequently, we may not understand which features influence the model decisions and by how much. Consequently, it may be difficult to decide whether the model is consistent with our domain knowledge. In our book we present tools that can help in extracting the information necessary for the evaluation of complex models.

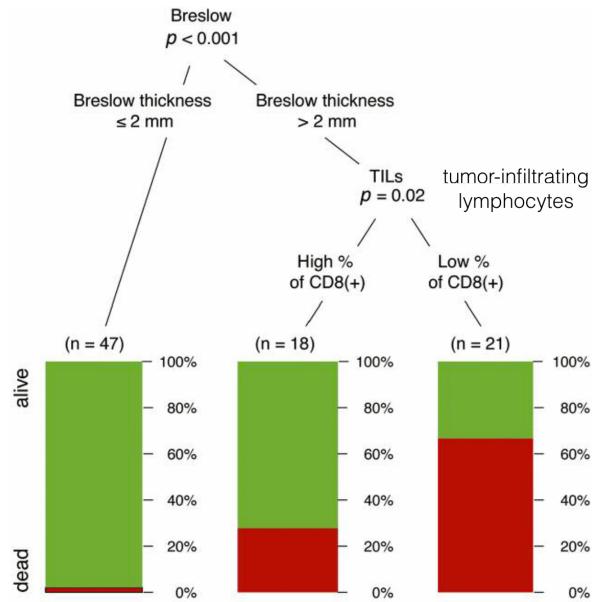


FIGURE 2 (fig:BILLCD8) Example tree model for melanoma risk

0.1.6 Model visualization, exploration, and explanation

In general, the lifecycle of a model can be divided, into three phases: development (or building), deployment, and maintenance.

Model development is the phase in which one is looking for the best available model. During this process, model exploration tools are useful. Exploration involves evaluation of the fit of the model, verification of the assumptions underlying the model (diagnostics), and assessment of the predictive performance of the model (validation). In our book we will focus on the visualization tools that can be useful in model exploration. We will not, however, discuss visualization methods for diagnostic purposes, as they are extensively discussed in many books devoted to statistical modelling.

Model deployment is the phase in which a predictive model is adopted for use. In this phase, it is crucial that the users gain confidence in using the model. It is worth noting that the users might not have been involved in the model development. Moreover, they may only have access to the binary implementation of the model, may not provide any insight into the details of the model structure. In this situation, model explanation tools can help to understand the factors that influence model predictions and boost confidence in the model. The tools are one of the main focus points of our book.

Finally, a deployed model requires maintenance. In this phase, one monitors a model performance by, for instance, checking the validity of predictions for different datasets. If issues are detected, model explanation tools may be used to find the source of the problem and to suggest a modification of the structure of the model.

0.1.7 Model-agnostic vs. model-specific approach

Some classes of models have been developed for a long period of time or have attracted intensive research. Consequently, those classes of models are equipped with excellent tools for model exploration or visualisation. For example:

- There are many tools for diagnostics and evaluation of linear models. Model assumptions are formally defined (normality, linear structure, homogenous variance) and can be checked by using normality tests or plots (normal qq-plot), diagnostic plots, tests for model structure, tools for identification of outliers, etc.
- For many more advanced models with an additive structure, like the proportional hazards model, many tools can be used for checking model assumptions.
- Random-forest models are equipped with the out-of-bag method of evaluating performance and several tools for measuring variable importance (Breiman et al., 2018). Methods have been developed to extract information from the model structure about possible interactions (Paluszynska and Biecek, 2017b). Similar tools have been developed for other ensembles of trees, like xgboost models (Foster, 2018).
- Neural networks enjoy a large collection of dedicated model-explanation tools that use, for instance, the layer-wise relevance propagation technique (Bach et al., 2015), or saliency maps technique (Simonyan et al., 2013), or a mixed approach.

Of course, the list of model classes with dedicated collections of model-explanation and/or diagnostics methods is much longer. This variety of model-specific approaches does lead to issues, though. For instance, one cannot easily compare explanations for two models with different structures. Also, every time a new architecture or a new ensemble of models is proposed, one needs to look for new methods of model exploration. Finally, for brand-new models no tools for model explanation or diagnostics may be immediately available.

For these reasons, in our book we focus on model-agnostic techniques. In particular, we prefer not to assume anything about the model structure, as we may be dealing with a black-box model with an unclear structure. In that case, the only operation that we may be able to perform is evaluation of a model for a selected observation.

However, while we do not assume anything about the structure of the model, we will assume that the model operates on p -dimensional vectors and, for a single vector, it returns a single value which is a real number. This assumption holds for a broad range of models for data such as tabular data, images, text data, videos, etc. It may not be suitable for, e.g., models with memory like seq2seq models (Sutskever et al., 2014) or Long Short Term Memory models (Hochreiter and Schmidhuber, 1997) in which the model output depends also on sequence of previous inputs.

0.1.8 Notation

Methods described in this book were developed by different authors, who used different mathematical notations. We try to keep the mathematical notation consistent throughout

the entire book. In some cases this may result in formulae with a fairly complex system of indices.

In this section, we provide a general overview of the notation we use. Whenever necessary, parts of the notation will be explained again in subsequent chapters.

We consider predictive models that operate on a p -dimensional input space \mathcal{X} . By $x \in \mathcal{X}$ we will refer to a single point in this input space.

In some cases models are described in context of a dataset with n observations. By x_i we refer to the i -th observation in this dataset. Of course, $x_i \in \mathcal{X}$.

Some explainers are constructed around an observation of interest which will be denoted by x_* . The observation may not necessarily belong to the analyzed dataset; hence, the use of the asterisk in the index. Of course, $x_* \in \mathcal{X}$.

Points in \mathcal{X} are p dimensional vectors. We will refer to the j -th coordinate by using j in superscript. Thus, x_i^j denotes the j -th coordinate of the i -th observation from the analyzed dataset. If \mathcal{J} denotes a subset of indices, then $x^{\mathcal{J}}$ denotes the elements of vector x corresponding to the indices included in \mathcal{J} .

We will use the notation x^{-j} to refer to a vector that results from removing the j -th coordinate from vector x . By $x^{j|=z}$, we denote a vector with the values at all coordinates equal to the values in x , except of the j -th coordinate, which is set equal to z . So, if $w = x^{j|=z}$, then $w^j = z$ and $\forall_{k \neq j} w^k = x^k$.

In this book, a model is a function $f : \mathcal{X} \rightarrow \mathbb{R}$ that transforms a point from \mathcal{X} into a real number. In most cases, the presented methods can be used directly for multi-variate dependent variables; however, we use examples with uni-variate responses to simplify the notation.

We will use $r_i = y_i - f(x_i)$ we refer to the model residual, i.e., the difference between the observed value of the dependent variable Y for the i -th observation from a particular dataset and the model prediction for the observation.

0.1.9 The structure of the book

Our book is split in two parts. In the part *Instance-level explainers*, we present techniques for exploration and explanation of model predictions for a single observation. On the other hand, in the part *Global explainers*, we present techniques for exploration and explanation of model's performance for an entire dataset.

Before embarking on the description of the methods, in Chapter 0.2, we provide a short description of R tools and packages that are necessary to replicate the results presented for various methods. In Chapter 0.4, we describe three datasets that are used throughout the book to illustrate the presented methods and tools.

The *Instance-level explainers* part of the book consists of Chapters 0.6-???. In Chapters 0.6-0.8, methods based on Ceteris-paribus (CP) profiles are presented. The profiles show the change

of model-based predictions induced by a change of a single variable; they are introduced in Chapter 0.6. Chapter 0.7 presents a CP-profile-based measure that summarizes the impact of a selected variable on model's predictions. The measure can be used to select the profiles that are worth plotting for a model with a large number of explanatory variables. Chapter 0.8 describes local-fidelity plots that are useful to investigate the sources of a poor prediction for a particular single observation.

Chapters 0.9-0.11 present methods to decompose variable contributions to model predictions. In particular, Chapter 0.9 introduces Break-down (BD) plots for models with additive effects. On the other hand, Chapter 0.10 presents a method for models including interactions. Finally, Chapter 0.11 describes an alternative method for decomposing model predictions that is closely linked with Shapley values (Shapley, 1953) developed originally for cooperative games.

Chapter 0.12 presents a different approach to explanation of single-instance predictions. It is based on a local approximation of a black-box model by a simpler, glass-box one. In particular, in the chapter, the Local Interpretable Model-Agnostic Explanations (LIME) method (Ribeiro et al., 2016) is discussed.

The final chapter of the first part, Chapter ??, presents a comparison of various instance-level explainers.

The *Global explainers* part of the book consists of Chapters ??-0.23.

In each part, every method is described in a separate chapter that has the same structure:
 * Subsection *Introduction* explains the goal of and the general idea behind the method.
 * Subsection *Method* shows mathematical or computational details related to the method. This subsection can be skipped if you are not interested in the details.
 * Subsection *Example* shows an exemplary application of the method with discussion of results.
 * Subsection *Pros and cons* summarizes the advantages and disadvantages of the method. It also provides some guidance regarding when to use the method.
 * Subsection *Code snippets* shows the implementation of the method in R and Python. This subsection can be skipped if you are not interested in the implementation.

Finally, we would like to signal that, **in this book, we do show**

- how to determine features that affect model prediction for a single observation. In particular, we present the theory and examples of methods that can be used to explain prediction like break down plots, ceteris paribus profiles, local-model approximations, or Shapley values.
- techniques to examine fully-trained machine-learning models as a whole. In particular, we review the theory and examples of methods that can be used to explain model performance globally, like partial-dependency plots, variable-importance plots, and others.
- charts that can be used to present key information in a quick way.
- tools and methods for model comparison.
- code snippets for R and Python that explain how to use the described methods.

On the other hand, **in this book, we do not focus on**

- any specific model. The techniques presented are model agnostic and do not make any assumptions related to model structure.
- data exploration. There are very good books on this topic, like R for Data Science <http://r4ds.had.co.nz/> or TODO
- the process of model building. There are also very good books on this topic, see An Introduction to Statistical Learning by Gareth James, Daniela Witten, Trevor Hastie and Robert Tibshirani <http://www-bcf.usc.edu/~gareth/ISL/> or TODO
- any particular tools for model building. These are discussed, for instance, in Applied Predictive Modeling by Max Kuhn and Kjell Johnson <http://appliedpredictivemodeling.com/>

0.1.10 Acknowledgements

Przemek's work on interpretability started during research trips within the RENOIR project (691152 - H2020/2016-2019). So he would like to thank Prof. Janusz Holyst for the chance to take part in this project.

Przemek would also like thank Prof. Chris Drake for her hospitality. This book would have never been created without perfect conditions that Przemek found at Chris's house in Woodland.

This book has been prepared using the **bookdown** package (Xie, 2018), created thanks to the amazing work of Yihui Xie.

0.2 Do-it-yourself With R

In our book we introduce different methods for instance-level and global explanation and exploration of predictive models. In each chapter, there is a section with code snippets for R that show how a particular method has been implemented. In this chapter we provide a short description of steps that will allow the reader to replicate the results presented for various methods.

0.2.1 What to install?

Obviously, R (R Core Team, 2018) is needed. It is always better to use the newest version, but at least R in version 3.5 should be used. R can be downloaded from <https://cran.r-project.org/>.

A good editor makes working with R much easier. There is a plenty of choices, but, especially for beginners, it is worth considering the RStudio editor, an open-source and enterprise-ready tool for R. It can be downloaded from <https://www.rstudio.com/>.

Once R and the editor are available, the required packages should be installed.

The most important one is the `DALEX` package. It is the entry point to solutions introduced in this book. The package can be installed by executing the following command from the R command line:

```
install.packages("DALEX")
```

Installation of `DALEX` will automatically take care about installation of other hard requirements (packages required by it), like the `ggplot2` package for data visualization.

To repeat all examples in this book, two additional packages are needed: `ingredients` and `iBreakDown`. The easiest way to get them, including other useful weak dependencies, is to execute the following command:

```
DALEX::install_dependencies()
```

0.2.2 How to work with `DALEX`?

To conduct model exploration with `DALEX`, first, a model has to be created. Then the model has got to be prepared for exploration.

There are many packages in R that can be used to construct a model. Some packages are structure-specific, like `randomForest` for Random-Forest Classification and Regression models (Liaw and Wiener, 2002a), `gbm` for Generalized Boosted Regression Models (Ridgeway, 2017), extensions for Generalized Linear Models (Harrell Jr, 2018), or many others. There is also a number of packages that can be used for constructing models with different structures. These include the `h2o` package (LeDell et al., 2019), `caret` (from Jed Wing et al., 2016) and its successor `parsnip` (Kuhn and Vaughan, 2019), a very powerful and extensible `mlr` (Bischl et al., 2016), or `keras` that is a wrapper to Python library with the same name (Allaire and Chollet, 2019).

While it is great to have such a large choice of tools for constructing models, the downside is that different packages have different interfaces and different arguments. Moreover, model-objects created with different packages may have different internal structures. The main goal of the `DALEX` package (Biecek, 2018) is to create a level of abstraction around a model that makes it easier to explore and explain the model.

Function `DALEX::explain` is THE function for model wrapping. The function requires five arguments:

- `model`, a model-object;
- `data`, a data frame with validation data;
- `y`, observed values of the dependent variable for the validation data; it is an optional argument, required for explainers focused on model validation and benchmarking.
- `predict_function`, a function that returns prediction scores; if not specified, then a default `predict()` function is used. Note that, for some models, the default `predict()` function

returns classes; in such cases you should provide a function that will return numerical scores.

- `label`, a name of a model; if not specified, then it is extracted from the `class(model)`. This name will be presented in figures, so it is recommended to make the name informative.

For an example, see Section 0.4.1.6.

0.2.3 How to work with `archivist`?

As we will focus on exploration of predictive models, we prefer not to waste space nor time on replication of the code necessary for model development. This is where the `archivist` packages helps.

The `archivist` package (Biecek and Kosinski, 2017) is designed to store, share, and manage R objects. We will use it to easily access R models and explainers. To install the package, the following command should be executed in the R command line:

```
install.packages("archivist")
```

Once the package has been installed, function `aread()` can be used to retrieve R objects from any remote repository. For this book, we use a GitHub repository `models` hosted at <https://github.com/pbiecek/models>. For instance, to download a model with the md5 hash `ceb40`, the following command has to be executed:

```
archivist::aread("pbiecek/models/ceb40")
```

Since the md5 hash `ceb40` uniquely defines the model, referring to the repository object results in using exactly the same model and the same explanations. Thus, in the subsequent chapters, pre-constructed model explainers will be accessed with `archivist` hooks.

0.2.4 DrWhy Packages

Here we present list of arguments in explainers from `drwhy` universe. All explainers use unified set of arguments. All of them are generic with two specific implementations `*.explainer` and `*.default`. The first one is working for objects created with `DALEX::explain()` function.

Common core arguments

- `x` a model to be explained, or an explainer created with function `DALEX::explain()`.
- `data` validation dataset. Used to determine univariate distributions, calculation of quantiles, correlations and so on. It will be extracted from `x` if it's an explainer.
- `predict_function` predict function that operates on the model `x`. Since the model is a black box, the `predict_function` is the only interface to access values from the model. It should be a function that takes at least a model `x` and `data` and returns vector of predictions. If model response has more than a single number (like multiclass models) then this function should return a matrix/data.frame of the size `m` x `d`, where `m` is the number of observations

while d is the dimensionality of model response. It will be extracted from x if it's an explainer.

- `new_observation` an observation/observations to be explained. Required for local/instance level explainers. Columns in `should` correspond to columns in the `data` argument.
- ... other parameters.
- `label` name of the model. By default it's extracted from the `class` attribute of the model

Function specific arguments

- `keep_distributions` if `TRUE`, then distributions of partial predictions is stored and can be plotted with the generic `plot()`.

0.3 Do-it-yourself With Python

0.4 Data Sets

We illustrate the methods presented in this book by using three datasets:

- *Sinking of the RMS Titanic*
- *Apartment prices*
- *Hire or fire*

The first dataset will be used to illustrate the application of the techniques in the case of a predictive model for a binary dependent variable. The second one will provide an example for models for a continuous variable. Finally, the third dataset will be used for illustration of models for a categorical dependent variable.

In this chapter, we provide a short description of each of the datasets, together with results of exploratory analyses. We also introduce models that will be used for illustration purposes in subsequent chapters.

0.4.1 Sinking of the RMS Titanic

Sinking of the RMS Titanic is one of the deadliest maritime disasters in history (during peacetime). Over 1500 people died as a consequence of collision with an iceberg. Projects like *Encyclopedia titanica* <https://www.encyclopedia-titanica.org/> are a source of rich and precise data about Titanic's passengers. The data are available in a dataset included in the `stablelearner` package. The dataset, after some data cleaning and variable transformations, is also available in the `DALEX` package. In particular, the 'titanic' data frame contains 2207 observations (for 1317 passengers and 890 crew members) and nine variables:



FIGURE 3 Titanic sinking by Willy Stöwer

- *gender*, person's (passenger's or crew member's) gender, a factor (categorical variable) with two levels (categories);
- *age*, person's age in years, a numerical variable; for adults, the age is given in (integer) years; for children younger than one year, the age is given as $x/12$, where x is the number of months of child's age;
- *class*, the class in which the passenger travelled, or the duty class of a crew member; a factor with seven levels
- *embarked*, the harbor in which the person embarked on the ship, a factor with four levels;
- *country*, person's home country, a factor with 48 levels;
- *fare*, the price of the ticket (only available for passengers; 0 for crew members), a numerical variable;
- *sibsp*, the number of siblings/spouses aboard the ship, a numerical variable;
- *parch*, the number of parents/children aboard the ship, a numerical variable;
- *survived*, a factor with two levels indicating whether the person survived or not.

The R code below provides more info about the contents of the dataset, values of the variables, etc.

```
library("DALEX")
head(titanic, 2)

##   gender age class      embarked      country    fare sibsp parch survived
## 1   male  42   3rd Southampton United States  7.11     0     0      no
## 2   male  13   3rd Southampton United States 20.05     0     2      no

str(titanic)

## 'data.frame':  2207 obs. of  9 variables:
## $ gender : Factor w/ 2 levels "female","male": 2 2 2 1 1 2 2 1 2 2 ...
## $ age    : num  42 13 16 39 16 25 30 28 27 20 ...
## $ class  : Factor w/ 7 levels "1st","2nd","3rd",...: 3 3 3 3 3 3 2 2 3 3 ...
## $ embarked: Factor w/ 4 levels "Belfast","Cherbourg",...: 4 4 4 4 4 4 2 2 2 4 ...
## $ country : Factor w/ 48 levels "Argentina","Australia",...: 44 44 44 15 30 44 17 17 26 16 ...
## $ fare   : num  7.11 20.05 20.05 20.05 7.13 ...
## $ sibsp  : num  0 0 1 1 0 0 1 1 0 0 ...
## $ parch  : num  0 2 1 1 0 0 0 0 0 0 ...
## $ survived: Factor w/ 2 levels "no","yes": 1 1 1 2 2 2 1 2 2 2 ...

levels(titanic$class)

## [1] "1st"          "2nd"          "3rd"
## [4] "deck crew"    "engineering crew" "restaurant staff"
## [7] "victualling crew"

levels(titanic$embarked)

## [1] "Belfast"      "Cherbourg"     "Queenstown"   "Southampton"
```

Models considered for this dataset will use *survived* as the (binary) dependent variable.

0.4.1.1 Data exploration

It is always advisable to explore data before modelling. However, as this book is focused on model exploration, we will limit the data exploration part.

Before exploring the data, we first do some pre-processing. In particular, the value of variables *age*, *country*, *sibsp*, *parch*, and *fare* is missing for a limited number of observations (2, 81, 10, 10, and 26, respectively). Analyzing data with missing values is a topic on its own (Little and Rubin 1987; Schafer 1997; Molenberghs and Kenward 2007). An often-used approach is to impute the missing values. Toward this end, multiple imputation should be considered (Schafer 1997; Molenberghs and Kenward 2007; van Buuren 2012). However, given the limited number of missing values and the intended illustrative use of the dataset, we will limit ourselves to, admittedly inferior, single imputation. In particular, we replace the missing *age* values by the mean of the observed ones, i.e., 30. Missing *country* will be coded by “X”. For *sibsp* and *parch*, we replace the missing values by the most frequently observed value, i.e., 0. Finally, for *fare*, we use the mean fare for a given *class*, i.e., 0 pounds for crew, 89 pounds for the 1st, 22 pounds for the 2nd, and 13 pounds for the 3rd class. The R code presented below implements the imputation steps.

```
# missing age is replaced by average (30)
titanic$age[is.na(titanic$age)] = 30
# missing country is replaced by "X"
titanic$country <- as.character(titanic$country)
titanic$country[is.na(titanic$country)] = "X"
titanic$country <- factor(titanic$country)
# missing fare is replaced by class average
titanic$fare[is.na(titanic$fare) & titanic$class == "1st"] = 89
titanic$fare[is.na(titanic$fare) & titanic$class == "2nd"] = 22
titanic$fare[is.na(titanic$fare) & titanic$class == "3rd"] = 13
# missing sibsp, parch are replaced by 0
titanic$sibsp[is.na(titanic$sibsp)] = 0
titanic$parch[is.na(titanic$parch)] = 0
```

After imputing the missing values, we investigate the association between survival status and other variables. Figures 4–9 present graphically the proportion non- and survivors for different levels of the other variables. The height of the bars (on the y-axis) reflects the marginal distribution (proportions) of the observed levels of the variable. On the other hand, the width of the bars (on the x-axis) provides the information about the proportion of non- and survivors. Note that, to construct the graphs for *age* and *fare*, we categorized the range of the observed values.

Figures 4 and 5 indicate that the proportion of survivors was larger for females and children below 5 years of age. This is most likely the result of the “women and children first” principle that is often evoked in situations that require evacuation of persons whose life is in danger. The principle can, perhaps, partially explain the trend seen in Figures 6 and 7, i.e., a higher proportion of survivors among those with 1–3 parents/children and 1–2 siblings/spouses aboard. Figure 8 indicates that passengers travelling in the first and second

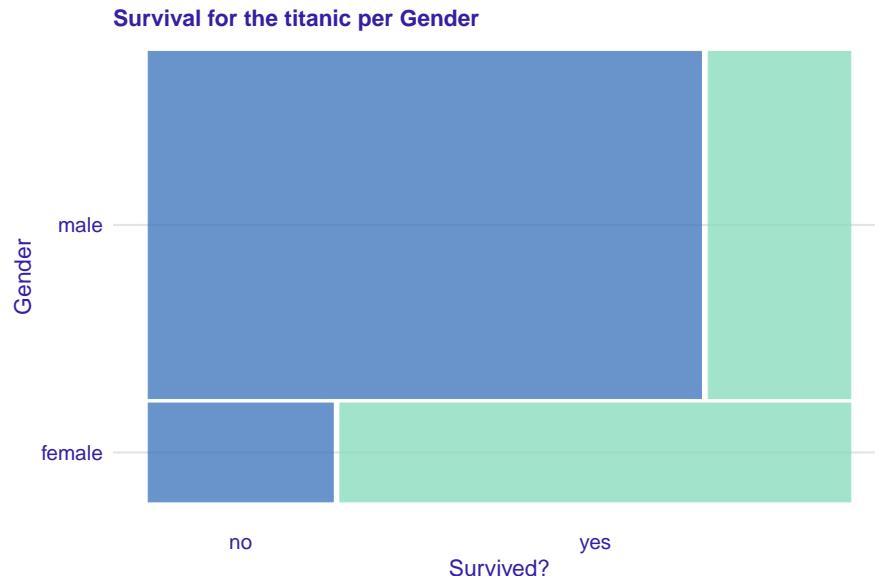


FIGURE 4 Survival according to gender in the Titanic data.

class had a higher chance of survival, perhaps due to the proximity of the location of their cabins to the deck. Interestingly, the proportion of survivors among crew deck was similar to the proportion of the first-class passengers. Figure 9 shows that the proportion of survivors increased with the fare, which is consistent with the fact that the proportion was higher for passengers travelling in the first and second class. Finally, Figures 10 and 11 do not suggest any noteworthy trends.

0.4.1.2 Logistic regression

The dependent variable of interest, *survival*, is binary. Thus, a natural choice to build a predictive model is logistic regression. We do not consider country as an explanatory variable. As there is no reason to expect a linear relationship between age and odds of survival, we use linear tail-restricted cubic splines, available in the `rcs()` function of the `rms` package (Harrell Jr, 2018), to model the effect of age. We also do not expect linear relation for the `fare` variable, but because of it's skewness, we do not use splines for this variable. The results of the model are stored in model-object `titanic_lmr_v6`, which will be used in subsequent chapters.

```
library("rms")
set.seed(1313)
titanic_lmr_v6 <- lrm(survived == "yes" ~ gender + rcs(age) + class + sibsp +
                        parch + fare + embarked, titanic)
titanic_lmr_v6

## Logistic Regression Model
##
## lrm(formula = survived == "yes" ~ gender + rcs(age) + class +
##       sibsp + parch + fare + embarked, data = titanic)
```

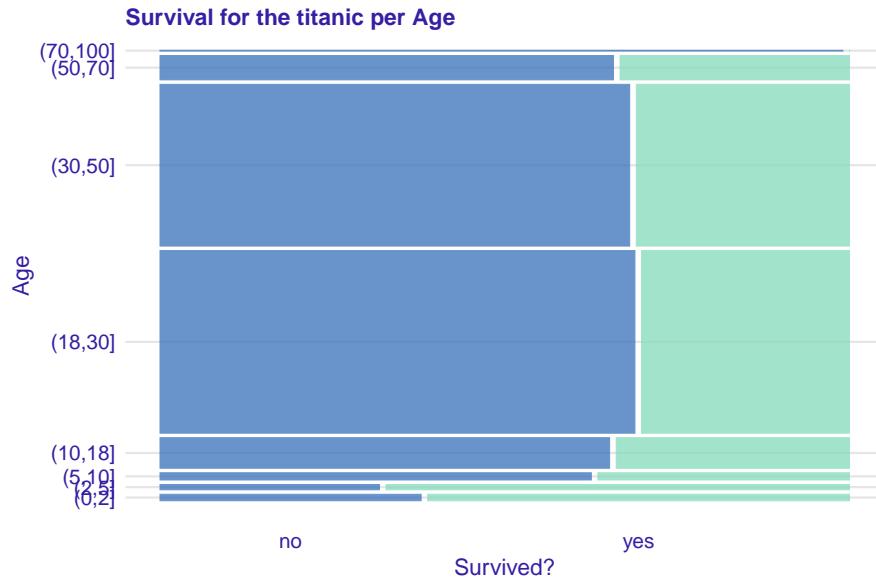


FIGURE 5 Survival according to age group in the Titanic data.

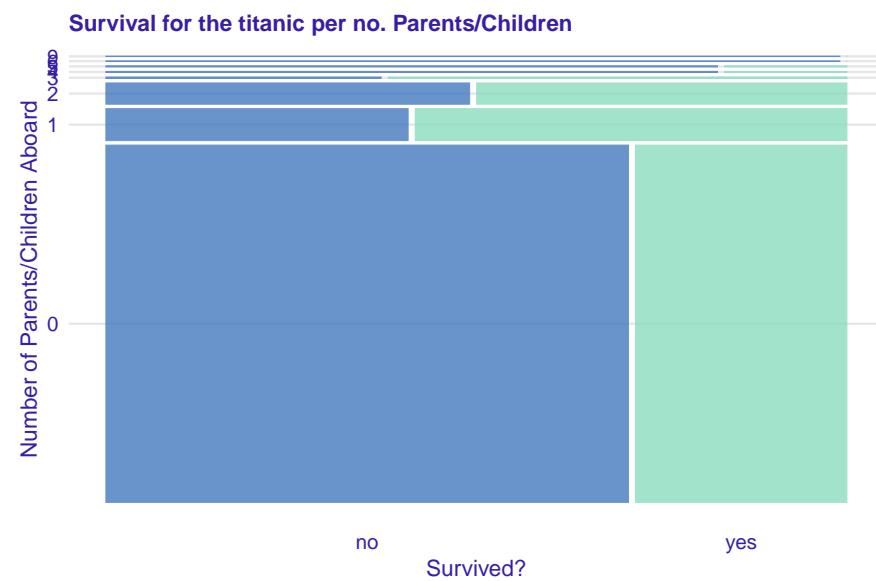


FIGURE 6 Survival according to the number of parents/children in the Titanic data.

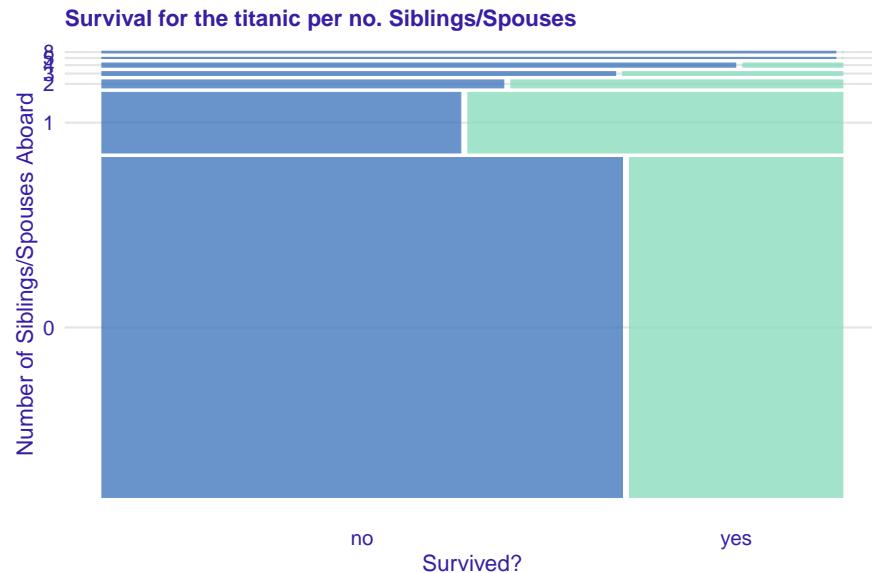


FIGURE 7 Survival according to the number of siblings/spouses in the Titanic data.

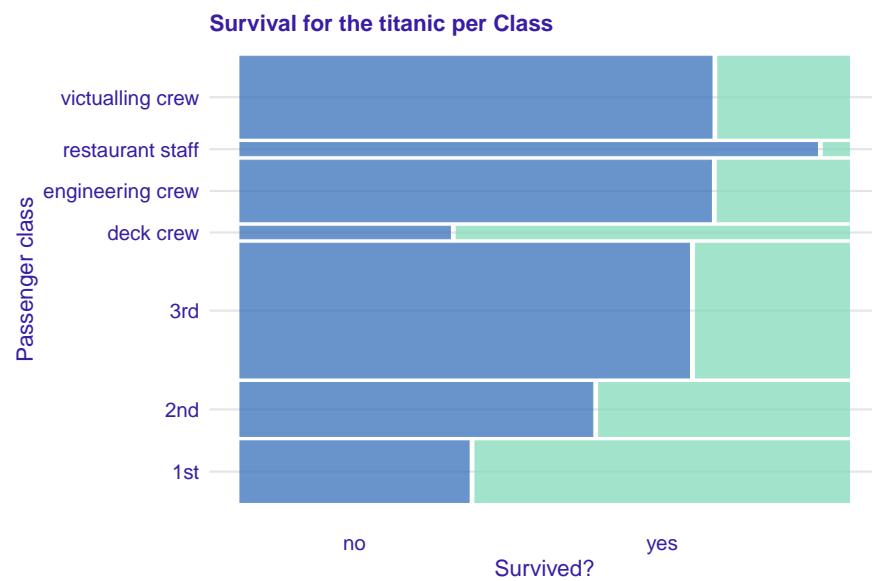


FIGURE 8 Survival according to the class in the Titanic data.

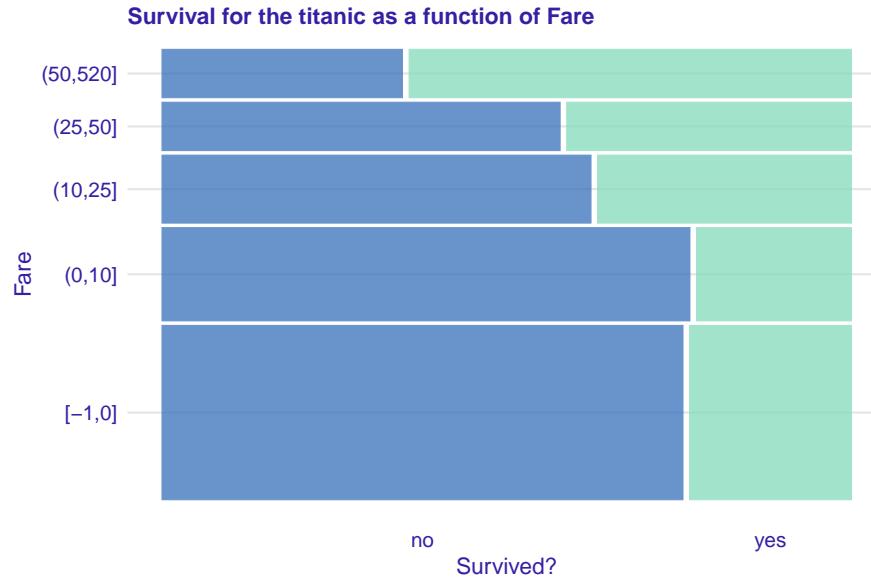


FIGURE 9 Survival according to fare in the Titanic data.

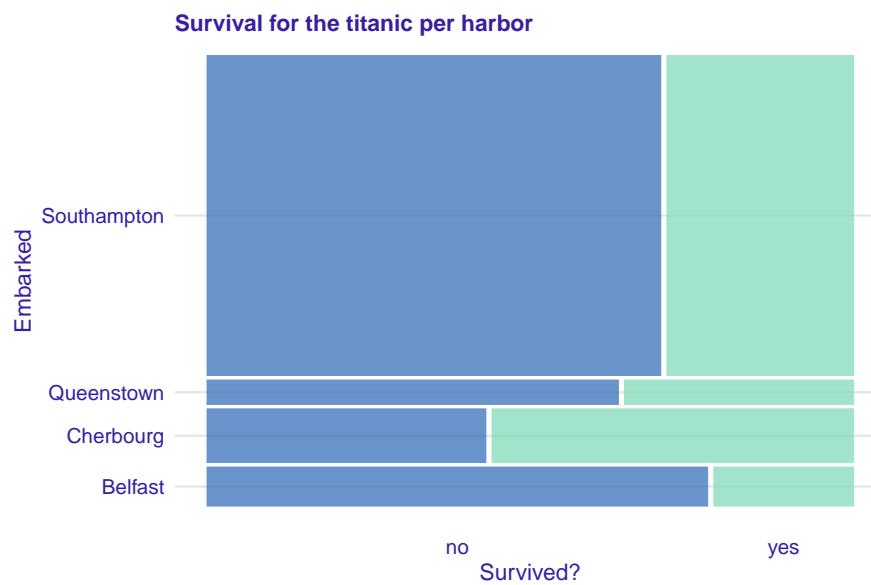


FIGURE 10 Survival according to the port of embarking in the Titanic data.

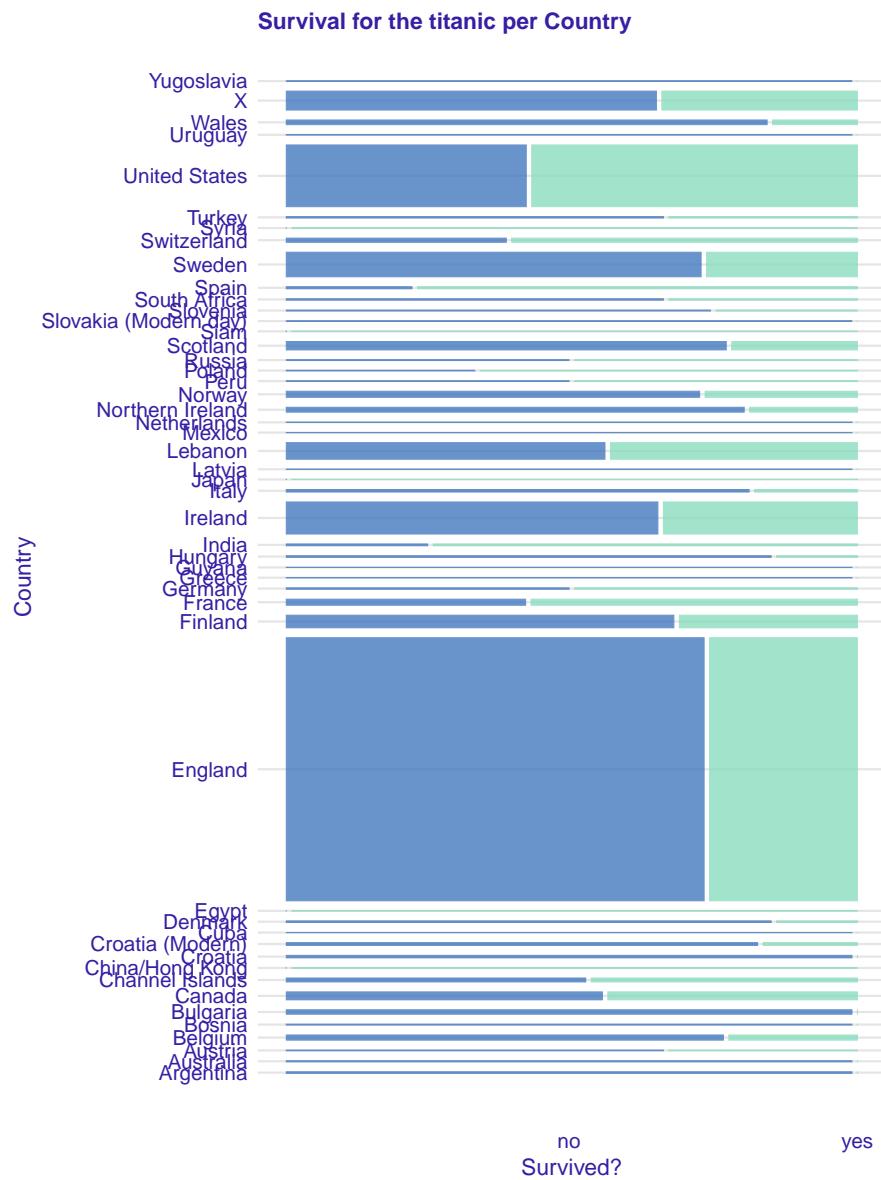


FIGURE 11 Survival according to country in the Titanic data.

```

##                                     Model Likelihood           Discrimination      Rank Discrim.
##                                     Ratio Test             Indexes          Indexes
##   Obs    2207    LR chi2    752.06      R2     0.404      C     0.817
##   FALSE   1496    d.f.        17      g     1.647    Dxy     0.635
##   TRUE     711  Pr(> chi2) <0.0001    gr     5.191  gamma     0.636
##   max |deriv| 0.0001                  gp     0.282  tau-a     0.277
##                                         Brier     0.146
##
##                                     Coef     S.E.    Wald Z Pr(>|Z|)
##   Intercept                 4.5746  0.5480     8.35 <0.0001
##   gender=male              -2.7687  0.1586   -17.45 <0.0001
##   age                      -0.1180  0.0221    -5.35 <0.0001
##   age'                     0.6313  0.1628     3.88 0.0001
##   age''                   -2.6583  0.7840    -3.39 0.0007
##   age'''                  2.8977  1.0130     2.86 0.0042
##   class=2nd                -1.1390  0.2501    -4.56 <0.0001
##   class=3rd                -2.0627  0.2490    -8.28 <0.0001
##   class=deck crew          1.0672  0.3498     3.05 0.0023
##   class=engineering crew   -0.9702  0.2648    -3.66 0.0002
##   class=restaurant staff  -3.1712  0.6583    -4.82 <0.0001
##   class=victualling crew  -1.0877  0.2596    -4.19 <0.0001
##   sibsp                   -0.4504  0.1006    -4.48 <0.0001
##   parch                   -0.0871  0.0987    -0.88 0.3776
##   fare                     0.0014  0.0020     0.70 0.4842
##   embarked=Cherbourg       0.7881  0.2836     2.78 0.0055
##   embarked=Queenstown     0.2745  0.3409     0.80 0.4208
##   embarked=Southampton    0.2343  0.2119     1.11 0.2689
##

```

0.4.1.3 Random forest

As an alternative to a logistic regression model, we consider a random forest model. Random forest is known for good predictive performance, is able to grasp low-level variable interactions, and is quite stable (Breiman, 2001). To fit the model, we apply the `randomForest()` function, with default settings, from the package with the same name (Liaw and Wiener, 2002b).

In the first instance, we fit a model with the same set of explanatory variables as the logistic regression model. The results of the model are stored in model-object `titanic_rf_v6`.


```
## Distribution not specified, assuming bernoulli ...
titanic_gbm_v6

## gbm(formula = survived == "yes" ~ class + gender + age + sibsp +
##       parch + fare + embarked, data = titanic, n.trees = 15000)
## A gradient boosted model with bernoulli loss function.
## 15000 iterations were performed.
## There were 7 predictors of which 7 had non-zero influence.
```

0.4.1.5 Model predictions

Let us now compare predictions that are obtained from the three different models. In particular, we will compute the predicted probability of survival for an 8-year-old boy who embarked in Belfast and travelled in the 1-st class with no parents nor siblings and with a ticket costing 72 pounds.

First, we create a data frame `johny_d` that contains the data describing the passenger.

```
johny_d <- data.frame(
  class = factor("1st", levels = c("1st", "2nd", "3rd", "deck crew", "engineering crew", "restaurant",
  gender = factor("male", levels = c("female", "male")),
  age = 8,
  sibsp = 0,
  parch = 0,
  fare = 72,
  embarked = factor("Belfast", levels = c("Belfast", "Cherbourg", "Queenstown", "Southampton"))
)
```

Subsequently, we use the generic function `predict()` to get the predicted probability of survival for the logistic regression model.

```
(pred_lmr <- predict(titanic_lmr_v6, johny_d, type = "fitted"))

##           1
## 0.7233413
```

The predicted probability is equal to 0.72.

We do the same for the random forest and gradient boosting models.

```
(pred_rf <- predict(titanic_rf_v6, johny_d, type = "prob"))

##      no    yes
## 1 0.626 0.374
## attr(,"class")
## [1] "matrix" "votes"

(pred_gbm <- predict(titanic_gbm_v6, johny_d, type = "response", n.trees = 15000))

## [1] 0.6700909
```

As a result, we obtain the predicted probabilities of 0.37 and 0.67, respectively.

The models lead to different probabilities. Thus, it might be of interest to understand the reason for the differences, as it could help us to decide which of the predictions we might want to trust.

Note that for some examples we will use another observation (instance) with lower chances of survival. Let's call this passenger Henry.

```
henry <- data.frame(
  class = factor("1st", levels = c("1st", "2nd", "3rd", "deck crew", "engineering crew", "restaurant crew"),
  gender = factor("male", levels = c("female", "male")),
  age = 47,
  sibsp = 0,
  parch = 0,
  fare = 25,
  embarked = factor("Cherbourg", levels = c("Belfast", "Cherbourg", "Queenstown", "Southampton"))
)
round(predict(titanic_lmr_v6, henry, type = "fitted"), 2)

##      1
## 0.43

round(predict(titanic_rf_v6, henry, type = "prob")[1, 2], 2)

## [1] 0.25

round(predict(titanic_gbm_v6, henry, type = "response", n.trees = 15000), 2)

## [1] 0.42
```

0.4.1.6 Explainers

Model-objects created with different libraries may have different internal structures. Thus, first, we have got to create a wrapper around the model. Toward this end, we use the `explain()` function from the `DALEX` package (Biecek, 2018). The function requires five arguments:

- `model`, a model-object;
- `data`, a validation data frame;
- `y`, observed values of the dependent variable for the validation data;
- `predict_function`, a function that returns prediction scores; if not specified, then a default `predict()` function is used;
- `label`, a function that returns prediction scores; if not specified, then it is extracted from the `class(model)`. In the example below we create explainers for the logistic regression, random forest, and gradient boosting models created for the Titanic data.

Each explainer wraps all elements needed to create a model explanation, i.e., a suitable `predict()` function, validation data set, and the model object. Thus, in subsequent chapters we will use the explainers instead of the model objects to keep code snippets more concise.

```

explain_titanic_lmr_v6 <- explain(model = titanic_lmr_v6,
                                     data = titanic[, -9],
                                     y = titanic$survived == "yes",
                                     predict_function = function(m, x) predict(m, x, type = "fitted"),
                                     label = "Logistic Regression v6")
explain_titanic_rf_v6 <- explain(model = titanic_rf_v6,
                                     data = titanic[, -9],
                                     y = titanic$survived == "yes",
                                     label = "Random Forest v6")
explain_titanic_rf_v3 <- explain(model = titanic_rf_v3,
                                     data = titanic[, -9],
                                     y = titanic$survived == "yes",
                                     label = "Random Forest v3")
explain_titanic_gbm_v6 <- explain(model = titanic_gbm_v6,
                                     data = titanic[, -9],
                                     y = titanic$survived == "yes",
                                     label = "Generalized Boosted Regression v6")

```

0.4.1.7 List of objects for the `titanic` example

In the previous sections we have built several predictive models for the `titanic` data set. The models will be used in the rest of the book to illustrate the model explanation methods and tools.

For the ease of reference, we summarize the models in Table 0.1. The binary model-objects can be downloaded by using the indicated `archivist` hooks (Biecek and Kosinski, 2017). By calling a function specified in the last column of the table, one can recreate a selected model in a local R environment.

TABLE 0.1: Predictive models created for the `titanic` dataset.

Model name	Model generator	Variables	Archivist hooks
<code>titanic_lmr_v6</code>	<code>rms:: lmr v.5.1.3</code>	gender, age, class, sibsp, parch, fare, embarked	Get the model: <code>archivist::: aread("pbiecek/models/ceb40")</code> . Get the explainer: <code>archivist::: aread("pbiecek/models/2b9b6")</code>
<code>titanic_rf_v6</code>	<code>randomForest::: randomForest v.4.6.14</code>	gender, age, class, sibsp, parch, fare, embarked	Get the model: <code>archivist::: aread("pbiecek/models/1f938")</code> . Get the explainer: <code>archivist::: aread("pbiecek/models/9b971")</code>

Model name	Model generator	Variables	Archivist hooks
<code>titanic_rf_v3</code>	<code>randomForest:: randomForest v.4.6.14</code>	gender, age, class	Get the model: <code>archivist:: aread("pbiecek/models/855c1")</code> Get the explainer: <code>archivist:: aread("pbiecek/models/92754")</code>
<code>titanic_gbm_v6</code>	<code>gbm:: gbm v.2.1.5</code>	gender, age, class, sibsp, parch, fare, embarked	Get the model: <code>archivist:: aread("pbiecek/models/24e72")</code> Get the explainer: <code>archivist:: aread("pbiecek/models/84d5f")</code>

Table 0.2 summarizes the data frames that will be used in examples in the subsequent chapters.

TABLE 0.2: Data frames created for the `titanic` example.

Description	No. rows	Variables	Link to this object
<code>titanic</code> dataset with imputed missing values	2207	gender, age, class, embarked, country, fare, sibsp, parch, survived	<code>archivist:: aread("pbiecek/models/27e5c")</code>
johny_d 8-year-old boy that travelled in the 1st class without parents	1	class, gender, age, sibsp, parch, fare, embarked	<code>archivist:: aread("pbiecek/models/e3596")</code>
henry 47-year-old male passenger from the 1st class, paid 25 pounds and embarked at Cherbourg	1	class, gender, age, sibsp, parch, fare, embarked	<code>archivist:: aread("pbiecek/models/a6538")</code>

0.4.2 Apartment prices

Predicting house prices is a common exercise used in machine-learning courses. Various datasets for house prices are available at websites like Kaggle (<https://www.kaggle.com>) or UCI Machine Learning Repository (<https://archive.ics.uci.edu>).



FIGURE 12 Warsaw skyscrapers by Artur Malinowski Flicker

In this book, we will work with an interesting variant of this problem. The `apartments` dataset is an artificial dataset created to match key characteristics of real apartments in Warszawa, the capital of Poland. However, the dataset is created in a way that two very different models, namely linear regression and random forest, have almost exactly the same accuracy. The natural question is then: which model should we choose? We will show that the model-explanation tools provide important insight into the key model characteristics and are helpful in model selection.

The dataset is available in the `DALEX` package (Biecek, 2018). It contains 1000 observations (apartments) and six variables:

- *m2.price*, apartment price per meter-squared (in EUR), a numerical variable;
- *construction.year*, the year of construction of the block of flats in which the apartment is located, a numerical variable;
- *surface*, apartment's total surface in squared meters, a numerical variable;
- *floor*, the floor at which the apartment is located (ground floor taken to be the first floor), a numerical integer variable with values from 1 to 10;
- *no.rooms*, the total number of rooms, a numerical variable with values from 1 to 6;
- *district*, a factor with 10 levels indicating the district of Warszawa where the apartment is located.

The R code below provides more info about the contents of the dataset, values of the variables, etc.

```
library("DALEX")
head(apartments, 2)

##   m2.price construction.year surface floor no.rooms      district
## 1      5897              1953     25     3        1 Srodmiescie
## 2      1818              1992    143     9        5      Bielany

str(apartments)

## 'data.frame': 1000 obs. of 6 variables:
## $ m2.price       : num  5897 1818 3643 3517 3013 ...
## $ construction.year: num  1953 1992 1937 1995 1992 ...
## $ surface         : num  25 143 56 93 144 61 127 105 145 112 ...
## $ floor           : int  3 9 1 7 6 6 8 8 6 9 ...
## $ no.rooms        : num  1 5 2 3 5 2 5 4 6 4 ...
## $ district        : Factor w/ 10 levels "Bemowo","Bielany",...: 6 2 5 4 3 6 3 7 6 6 ...

table(apartments$floor)

##
##   1   2   3   4   5   6   7   8   9   10
##  90 116  87  86  95 104 103 103 108 108

table(apartments$no.rooms)

##
```

```
##   1   2   3   4   5   6
## 99 202 231 223 198  47
levels(apartments$district)

## [1] "Bemowo"      "Bielany"       "Mokotow"       "Ochota"        "Praga"
## [6] "Srodmiescie" "Ursus"        "Ursynow"       "Wola"          "Zoliborz"
```

Models considered for this dataset will use *m2.price* as the (continuous) dependent variable.

Model predictions will be obtained for a set of six apartments included in data frame `apartments_test`, also included in the `DALEX` package.

```
head(apartments_test)
```

```
##      m2.price construction.year surface floor no.rooms district
## 1001    4644            1976     131     3         5 Srodmiescie
## 1002    3082            1978     112     9         4      Mokotow
## 1003    2498            1958     100     7         4      Bielany
## 1004    2735            1951     112     3         5       Wola
## 1005    2781            1978     102     4         4      Bemowo
## 1006    2936            2001     116     7         4      Bemowo
```

0.4.2.1 Data exploration

Note that `apartments` is an artificial dataset created to illustrate and explain differences between random forest and linear regression. Hence, the structure of the data, the form and strength of association between variables, plausibility of distributional assumptions, etc., is better than in a real-life dataset. In fact, all these characteristics of the data are known. Nevertheless, we conduct some data exploration to illustrate the important aspects of the data.

The variable of interest is *m2.price*, the price per meter-squared. The histogram presented

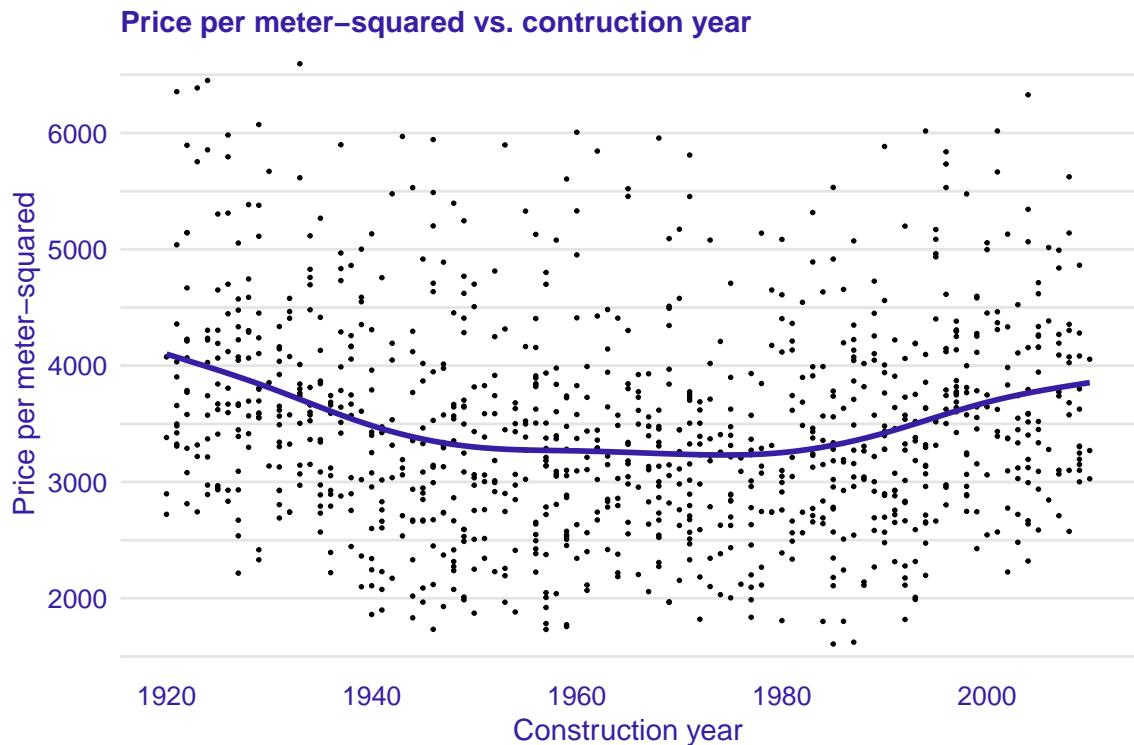


FIGURE 13 (fig:apartmentsMi2Construction) Price per meter-squared vs. construction year

in Figure ?? indicates that the distribution of the variable is slightly skewed to the right.

Distribution

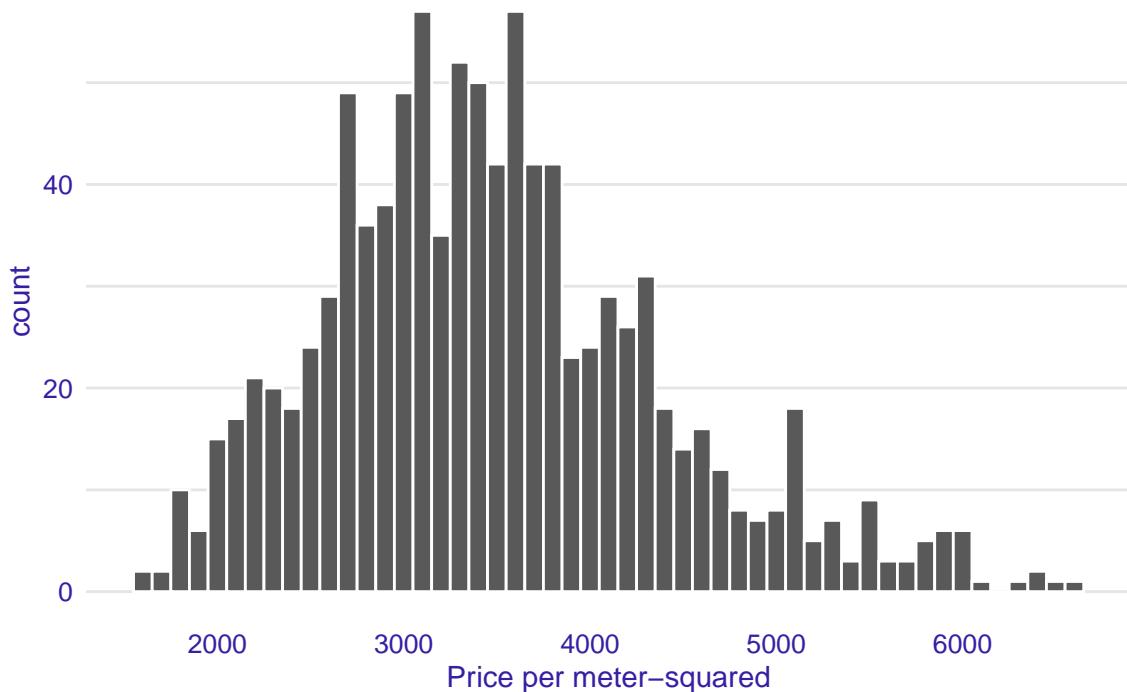


Figure 13 suggests (possibly) a nonlinear relation between *construction.year* and *m2.price*.

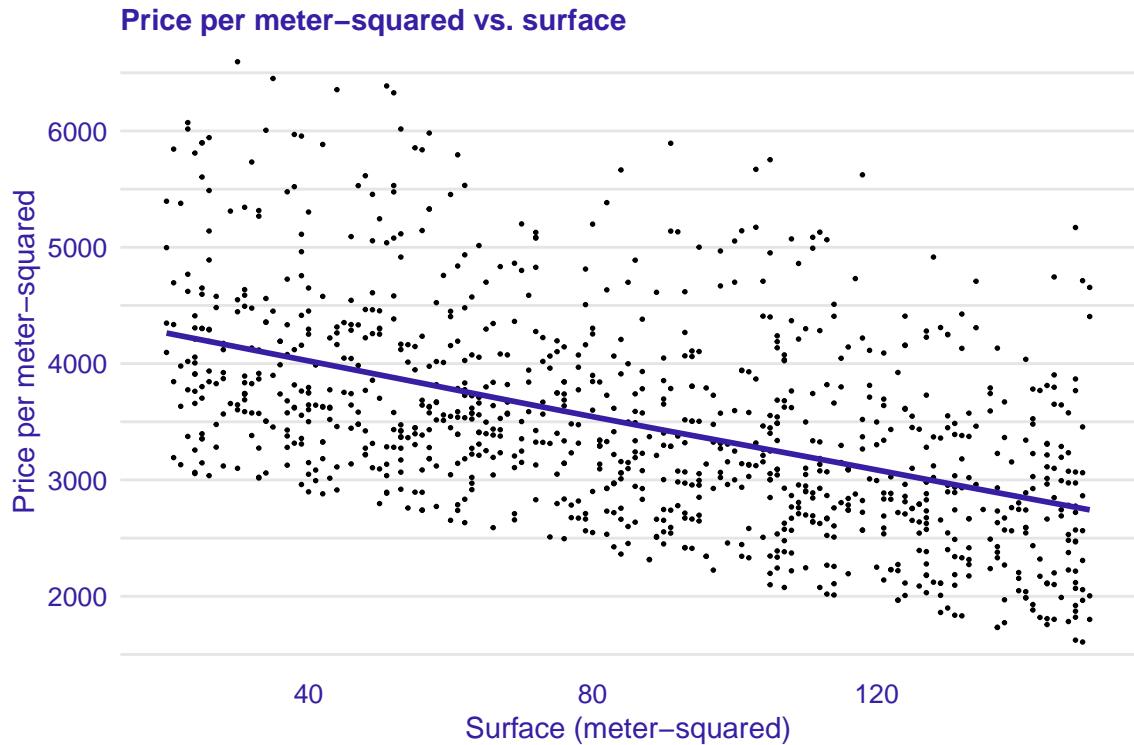


FIGURE 14 (fig:apartmentsMi2Surface) Price per meter-squared vs. surface

Figure 14 indicates a linear relation between *surface* and *m2.price*.

Relation between *floor* and *m2.price* is also close to linear, as seen in Figure 15.

There is a close to linear relation between *no.rooms* and *m2.price*, as suggested by Figure 16. It is worth noting that, quite naturally, surface and number of rooms are correlated (see Figure 17).

Prices depend on district. Violin plots in Figure 18 indicate that the highest prices per meter-squared are observed in Srodmiescie (Downtown).

0.4.2.2 Linear regression

The dependent variable of interest, *m2.price*, is continuous. Thus, a natural choice to build a predictive model is linear regression. We treat all the other variables in the `apartments` data frame as explanatory and include them in the model. The results of the model are stored in model-object `apartments_lm_v5`.

```
apartments_lm_v5 <- lm(m2.price ~ ., data = apartments)
apartments_lm_v5

## 
## Call:
## lm(formula = m2.price ~ ., data = apartments)
```

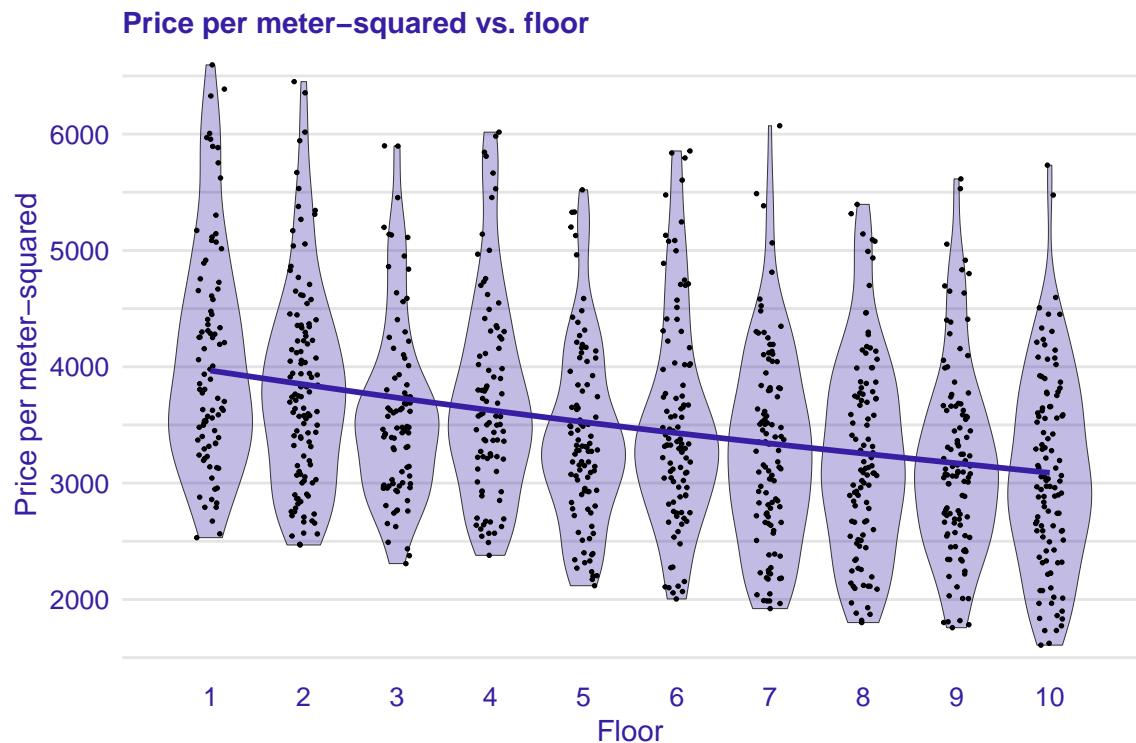


FIGURE 15 (fig:apartmentsMi2Floor) Price per meter-squared vs. floor

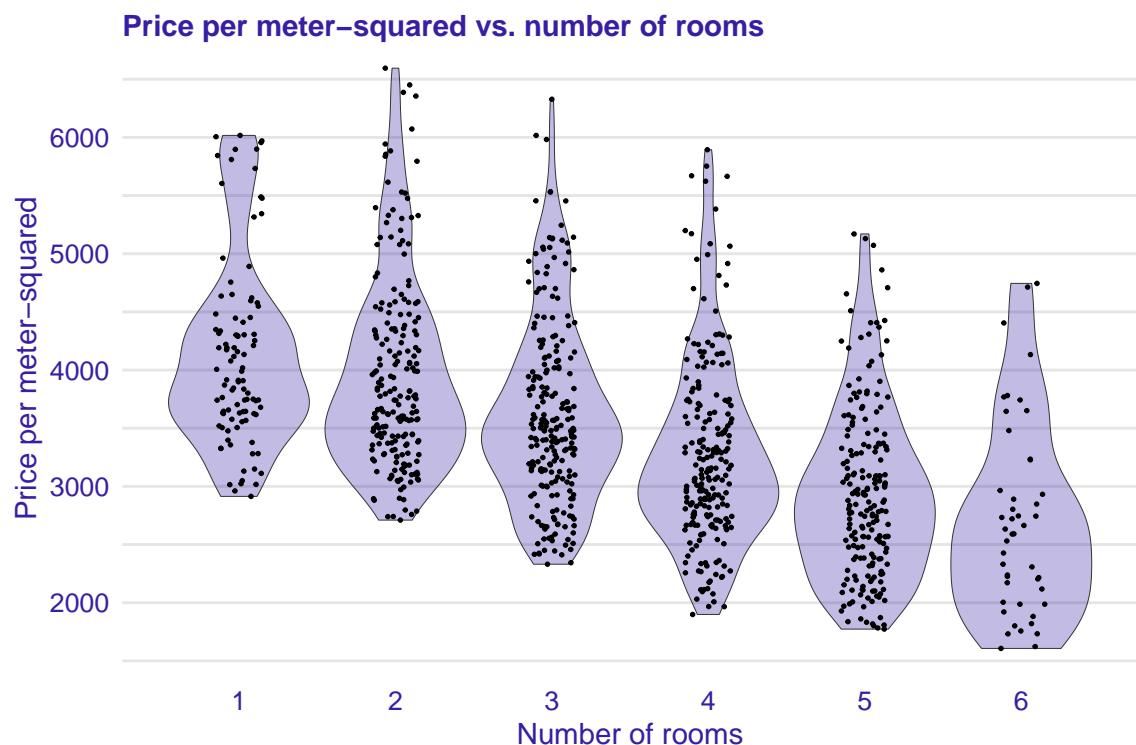


FIGURE 16 (fig:apartmentsMi2Norooms) Price per meter-squared vs. number of rooms

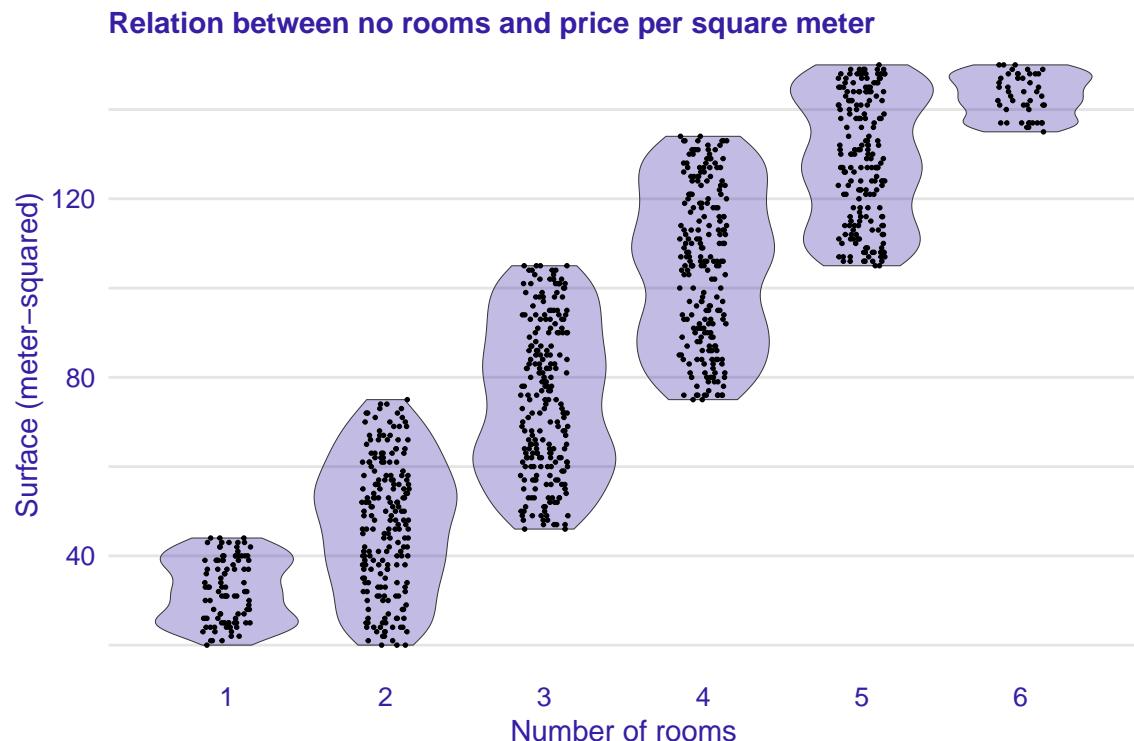


FIGURE 17 (fig:apartmentsSurfaceNorooms) Surface vs. number of rooms

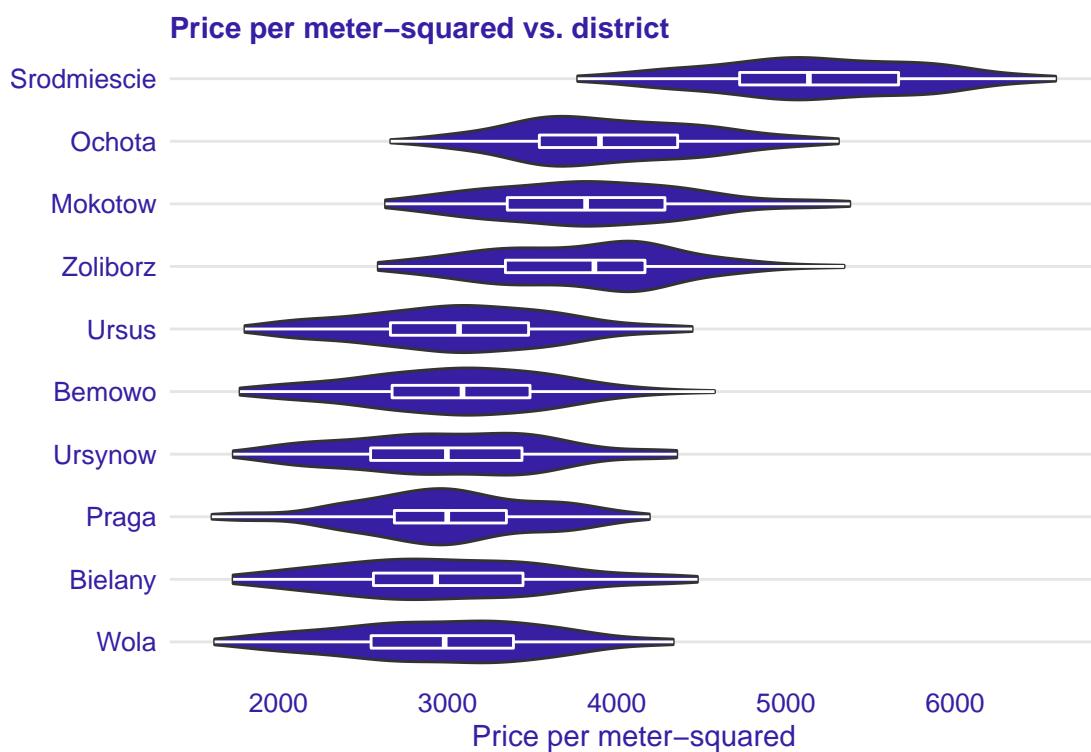


FIGURE 18 (fig:apartmentsMi2District) Price per meter-squared for different districts

```
## 
## Coefficients:
## (Intercept) construction.year surface
## 5003.248      -0.229     -10.238
## floor          no.rooms   districtBielany
## -99.482       -37.730      34.106
## districtPraga  districtUrsynow districtBemowo
## -20.214        -1.974      16.891
## districtUrsus  districtZoliborz districtMokotow
## 46.833         906.865     935.271
## districtOchota districtSrodmiescie
## 943.145        2097.502
```

0.4.2.3 Random forest

As an alternative to linear regression, we consider a random forest model. To fit the model, we apply the `randomForest()` function, with default settings, from the package with the same name (Liaw and Wiener, 2002b).

The results of the model are stored in model-object `apartments_rf_v5`.

```
library("randomForest")
set.seed(72)
apartments_rf_v5 <- randomForest(m2.price ~ ., data = apartments)
apartments_rf_v5
```

```
## 
## Call:
## randomForest(formula = m2.price ~ ., data = apartments)
##                 Type of random forest: regression
##                         Number of trees: 500
## No. of variables tried at each split: 1
##
##                 Mean of squared residuals: 79789.39
##                         % Var explained: 90.28
```

0.4.2.4 Model predictions

By applying the `predict()` function to model-object `apartments_lm_v5` with `apartments_test` as the data frame for which predictions are to be computed, we obtain the predicted prices for the testing set of six apartments for the linear regression model. Subsequently, we compute the mean squared difference between the predicted and actual prices for the test apartments. We repeat the same steps for the random forest model.

```
predicted_apartments_lm <- predict(apartments_lm_v5, apartments_test)
rmsd_lm <- sqrt(mean((predicted_apartments_lm - apartments_test$m2.price)^2))
rmsd_lm
```

```

## [1] 283.0865
predicted_apartments_rf <- predict(apartments_rf_v5, apartments_test)
rmsd_rf <- sqrt(mean((predicted_apartments_rf - apartments_test$m2.price)^2))
rmsd_rf

## [1] 282.9519

```

For the random forest model, the square-root of the mean squared difference is equal to 283. It is only minimally smaller than the value of 283.1, obtained for the linear regression model. Thus, the question we may face is: should we choose the more complex, but flexible random-forest model, or the simpler and easier to interpret linear model? In the subsequent chapters we will try to provide an answer to this question.

0.4.2.5 List of objects for the `apartments` example

In Sections 0.4.2.2 and 0.4.2.3 we have built two predictive models for the `apartments` data set. The models will be used in the rest of the book to illustrate the model explanation methods and tools.

For the ease of reference, we summarize the models in Table 0.3. The binary model-objects can be downloaded by using the indicated `archivist` hooks (Biecek and Kosinski, 2017). By calling a function specified in the last column of the table, one can recreate a selected model in a local R environment.

TABLE 0.3: Predictive models created for the `apartments` dataset.

Model name	Model generator	Variables	Archivist hooks
<code>apartments_lm_v5</code>	<code>stats:: lm</code> v.3.5.3	construction .year, surface, floor, no.rooms, district	Get the model: <code>archivist::: aread("pbiecek/models/55f19")</code> . Get the explainer: TODO: add if needed
<code>apartments_rf_v5</code>	<code>randomForest::: randomForest</code> v.4.6.14	construction .year, surface, floor, no.rooms, district	Get the model: <code>archivist::: aread("pbiecek/models/fe7a5")</code> . Get the explainer: TODO: add if needed

0.4.3 Hire or fire

Predictive models can be used to support decisions. For instance, they can be used in a human-resources department to decide whether, for instance, to promote an employee. An advantage of using a model for this purpose would be the objectivity of the decision, which

would not be subject to personal preferences of a manager. However, in such a situation, one would most likely want to understand what influences the model's prediction.

To illustrate such a situation, we will use the `HR` dataset that is available in the `DALEX` package (Biecek, 2018). It is an artificial set of data from a human-resources department of a call center. It contains 7847 observations (employees of the call center) and six variables:

- *gender*, person's gender, a factor with two levels;
- *age*, person's age in years, a numerical variable;
- *hours*, average number of working hours per week, a numerical variable;
- *evaluation*, the last evaluation score, a numerical variable with values 2 (fail), 3 (satisfactory), 4 (good), and 5 (very good);
- *salary*, the salary level, a numerical variable with values from 0 (lowest) to 5 (highest);
- *status*, a factor with three indicating whether the employee was fired, retained, or promoted.

The R code below provides more info about the contents of the dataset, values of the variables, etc.

```
library("DALEX")
head(HR, 4)

##   gender      age     hours evaluation salary status
## 1 male 32.58267 41.88626       3      1  fired
## 2 female 41.21104 36.34339      2      5  fired
## 3 male 37.70516 36.81718      3      0  fired
## 4 female 30.06051 38.96032      3      2  fired

str(HR)

## 'data.frame':    7847 obs. of  6 variables:
## $ gender    : Factor w/ 2 levels "female","male": 2 1 2 1 2 2 1 2 1 1 ...
## $ age       : num  32.6 41.2 37.7 30.1 21.1 ...
## $ hours     : num  41.9 36.3 36.8 39 62.2 ...
## $ evaluation: num  3 2 3 3 5 2 4 2 2 4 ...
## $ salary    : num  1 5 0 2 3 0 0 4 4 4 ...
## $ status    : Factor w/ 3 levels "fired","ok","promoted": 1 1 1 1 3 1 3 2 1 3 ...

table(HR$evaluation)

##
##      2      3      4      5
## 2371 2272 1661 1543

table(HR$salary)

##
##      0      1      2      3      4      5
## 1105 1417 1461 1508 1316 1040
```

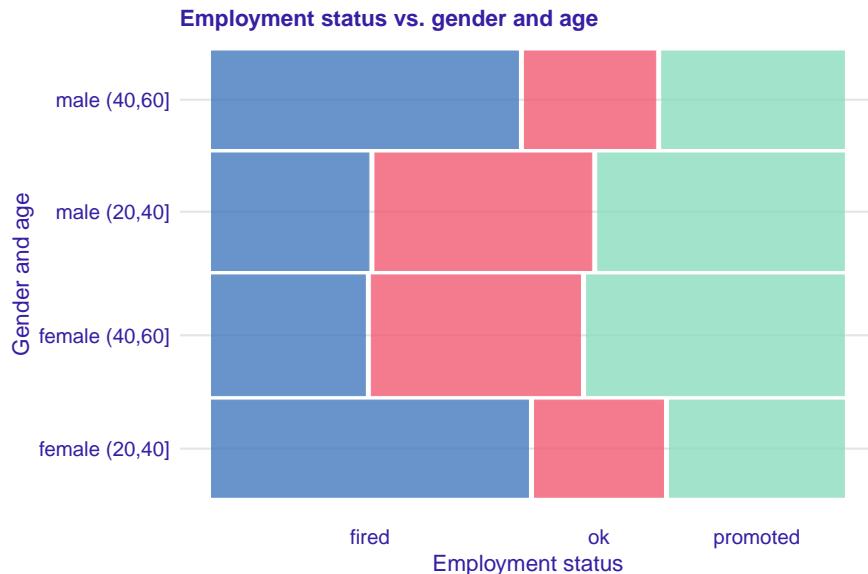


FIGURE 19 Employment status for age-groups and gender.

Models considered for this dataset will use *status* as the (categorical) dependent variable.

0.4.3.1 Data exploration

As it was the case for the `apartments` dataset (see Section 0.4.2), the `HR` data were simulated. Despite the fact that characteristics of the data are known, we conduct some data exploration to illustrate the important aspects of the data.

Figure 19 indicates that young females and older males were fired more frequently than older females and younger males.

Figure 20 indicates that the proportion of promoted employees was the lowest for the lowest and highest salary level. At the same time, the proportion of fired employees was the highest for the two salary levels.

Figure 21 indicates that the chance of being fired was larger for evaluation scores equal to 2 or 3. On the other hand, the chance of being promoted substantially increased for scores equal to 4 or 5.

0.4.3.2 Multinomial logistic regression

The dependent variable of interest, *status*, is categorical with three categories. Thus, a simple choice is to consider a multinomial logistic regression model (Venables and Ripley, 2010). We fit the model with the help of function `multinom` from package `nnet`. The function fits multinomial log-linear models by using the neural-networks approach. As a result, we obtain a complex model that is smoother as compared to a random forest model that relies on binary splits for continuous variables. We treat all variables other than *status* in the `HR` data



FIGURE 20 Employment status for different salary levels.

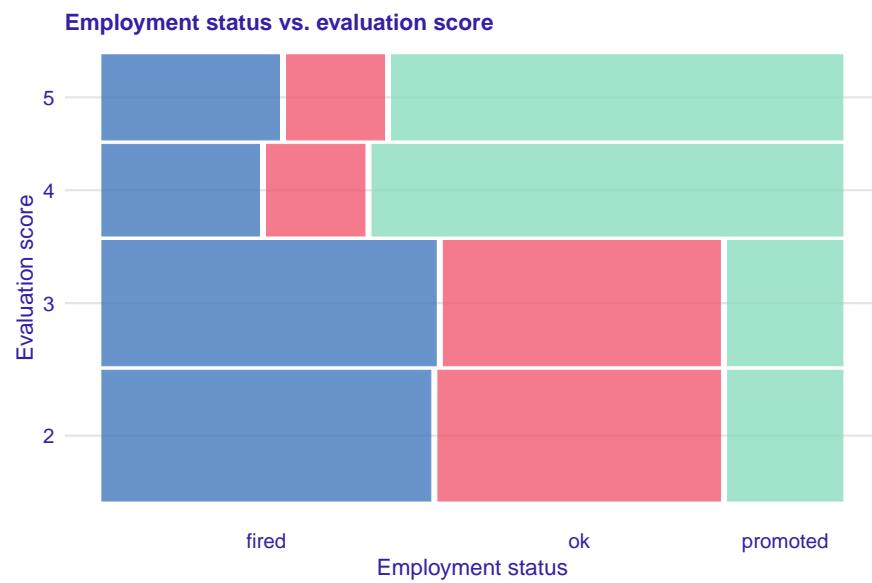


FIGURE 21 Employment status for different evaluation scores.

frame as explanatory and include them in the model. The results of the model are stored in model-object `HR_glm_v5`.

```
library("nnet")
set.seed(1313)
HR_glm_v5 <- multinom(status ~ gender + age + hours + evaluation + salary, data = HR)

## # weights: 21 (12 variable)
## initial value 8620.810629
## iter 10 value 7002.127738
## iter 20 value 6239.478146
## iter 20 value 6239.478126
## iter 20 value 6239.478124
## final value 6239.478124
## converged

HR_glm_v5

## Call:
## multinom(formula = status ~ gender + age + hours + evaluation +
##           salary, data = HR)
##
## Coefficients:
##             (Intercept) gendermale      age      hours   evaluation
## ok          -3.199741  0.05185293 0.001003521 0.06628055 -0.03734345
## promoted   -12.677639  0.11838037 0.003436872 0.16253343  1.26109093
##             salary
## ok          0.01680039
## promoted  0.01507927
##
## Residual Deviance: 12478.96
## AIC: 12502.96
```

0.4.3.3 Random forest

As an alternative to multinomial logistic regression, we consider a random forest model. To fit the model, we apply the `randomForest()` function, with default settings, from the package with the same name (Liaw and Wiener, 2002b). The results of the model are stored in model-object `HR_rf_v5`.

```
library("randomForest")
set.seed(1313)
HR_rf_v5 <- randomForest(status ~ gender + age + hours + evaluation + salary, data = HR)
HR_rf_v5

## 
## Call:
```

```
## randomForest(formula = status ~ gender + age + hours + evaluation + salary, data = HR)
##           Type of random forest: classification
##                  Number of trees: 500
## No. of variables tried at each split: 2
##
##          OOB estimate of error rate: 27.46%
## Confusion matrix:
##             fired   ok promoted class.error
## fired      2270  388      197  0.2049037
## ok         530 1243      448  0.4403422
## promoted    202  390     2179  0.2136413
```

0.4.3.4 Model predictions

Let us now compare predictions that are obtained from the multinomial regression and random forest models. In particular, we compute the predicted probabilities of being fired, retained in service, or promoted for Dilbert, a 58-year old male working around 42 hours per week for a salary at level 2, who got evaluation score equal to 2. Data frame `dilbert` contains the data describing the employee.

```
dilbert <- data.frame(gender = factor("male", levels = c("male", "female")),
                      age = 57.7,
                      hours = 42.3,
                      evaluation = 2,
                      salary = 2)
```

By applying the `predict()` function to model-objects `HR_rf_v5` and `HR_glm_v5`, with `dilbert` as the data frame for which predictions are to be computed, and argument `type="prob"`, we obtain the predicted probabilities of being fired, retained in service, or promoted for Dilbert.

```
pred_HR_rf <- predict(HR_rf_v5, dilbert, type = "prob")
pred_HR_rf
```

```
##    fired      ok promoted
## 1 0.778  0.218    0.004
## attr(),"class"
## [1] "matrix" "votes"
pred_HR_glm <- predict(HR_glm_v5, dilbert, type = "prob")
pred_HR_glm
```

```
##    fired      ok promoted
## 0.56369601 0.40630786 0.02999612
```

For both models, the predicted probability of promotion is low; it is more likely that Dilbert will be fired. It is of interest to understand why such prediction is made? Moreover, random forest yields a higher probability of firing (0.78) than the multinomial regression model (0.56).

We may want to learn where does this difference come from? We will try to answer these questions in subsequent chapters.

0.4.3.5 List of objects for the `HR` example

In Sections 0.4.3.2 and 0.4.3.3 we have built two predictive models for the `HR` data set. The models will be used in the remainder of the book to illustrate model-explanation methods and tools.

For the ease of reference, we summarize the models in Table 0.4. The binary model-objects can be downloaded by using the indicated `archivist` hooks (Biecek and Kosinski, 2017). By calling a function specified in the last column of the table, one can recreate a selected model in a local R environment.

TABLE 0.4: Predictive models created for the `HR` dataset.

Model name	Model generator	Variables	Archivist hooks
<code>HR_rf_v5</code>	<code>randomForest::: randomForest</code> v.4.6.14	gender, age, hours, evaluation, salary	Get the model: <code>archivist::: aread("pbiecek/models/1ecfd")</code> . Get the explainer: TODO: add if needed
<code>HR_glm_v5</code>	<code>stats::: glm</code> v.3.5.3	gender, age, hours, evaluation, salary	Get the model: <code>archivist::: aread("pbiecek/models/f0244")</code> . Get the explainer: TODO: add if needed

0.5 Instance-level exploration

Instance-level explainers help to understand how a model yields a prediction for a single observation. We can think about the following situations as examples:

- We may want to evaluate the effects of explanatory variables on model predictions. For instance, we may be interested in predicting the risk of heart attack based on person's age, sex, and smoking habits. A model may be used to construct a score (for instance, a linear combination of the explanatory variables representing age, sex, and smoking habits) that could be used for the purposes of prediction. For a particular patient we may want to learn how much the different variables contribute to the patient's score?
- We may want to understand how models predictions would change if values of some of the explanatory variables changed. For instance, what would be the predicted risk of heart attack if the patient cut the number of cigarettes smoked per day by half?

Local Exploration, Explanation and Visualisation of Predictive Models



Introduction

When decisions from Machine Learning models are confronted with humans, following questions sparkle: Why? Why this decision was made? Which features support this decision? Can we trust this decision? How would it change if a single feature is slightly different?

Methods for local exploration/explanation are designed to improve our understanding of model predictions that refer to a particular observation.

Model preparation

Model exploration starts with a model to explore, and the observation of interest.

1. First we need to train a model

```
library("randomForest")
rf_model <- randomForest(
  status ~ gender + age + hours +
  evaluation + salary, data = HR)
```

2. Then we need to build an explainer - model enriched with additional metadata like validation data, predict function, true labels. Use the `explain()` function from the DALEX package.

```
library("DALEX")
explainer_rf <- explain(rf_model,
  data = HR,
  y = HR$status == "fired")
```

3. Local explainers work for a selected observation / point in a feature space.

```
John1960 <- data.frame(
  gender = factor("male",
    levels = c("male", "female")),
  age = 57.7,
  hours = 42.3,
  evaluation = 2,
  salary = 2)
```

Use-Case

As an use-case we are using `HR` dataset from the `DALEX` package. Five variables are used for a classification problem, would a given employee shall be fired, promoted or left as it is. It's an artificial dataset designed in a way that variable age and gender are in interaction.

```
library("DALEX")
head(HR, 2)
##   gender   age   hours evaluation salary   status
## 1  male 32.58267 41.88626      3     1   fired
## 2  female 41.21104 36.34339      2     5   fired
```

Presented tools are part of DALEXverse, set of tools for model agnostic exploration, explanation and visualisation of predictive models.

Find mode information about DALEX at the website https://pbiecek.github.io/DALEX_docs/ or online book https://pbiecek.github.io/PM_VEE/

Calculation of local explainers

What-if scenarios with Ceteris Paribus Profiles are supported with the `ceterisParibus` package, function. Use the function `ceteris_paribus()` with an explainer and the observation of interest as first arguments. You may also select variables of interest.

```
library("ceterisParibus")
cp_rf <- ceteris_paribus(explainer_rf, John1960,
  variables = c("age", "hours"))
cp_rf
## Top profiles :
##   gender   age   hours evaluation salary
## 1  male 20.00389 42.3      2     2
## 1.1 male 20.35994 42.3      2     2
##   yhat _vname_ _ids_   label_
## 1  0.4234617   age   1 randomForest
## 1.1 0.3761229   age   1 randomForest
```

Variable attributions are supported with the `breakDown` package.

```
library("breakDown")
bd_rf <- break_down(explainer_rf, John1960)
bd_rf
##             contribution
## (Intercept)        0.364
## * hours = 42       0.161
## * age:gender = 58:male 0.120
## * salary = 2       -0.045
## final_prognosis    0.648
```

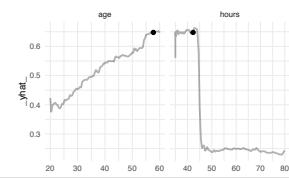
Local model approximation is supported with the `lime` package.

```
library("lime")
lm_rf <- local_approximation(explainer_rf,
  John1960, target_variable_name = "status")
lm_rf
## Explanation model:
## Name: regr.lm
## R-squared: 0.9889
```

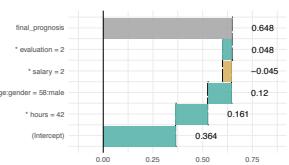
Visualisation of explainers

The generic function `plot()` works for every local explainer.

`plot(cp_rf)`



`plot(bd_rf)`



`plot(lm_rf)`

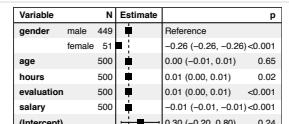


FIGURE 22 (fig:localDALEXsummary) Summary of three approaches to local model exploration and explanation.

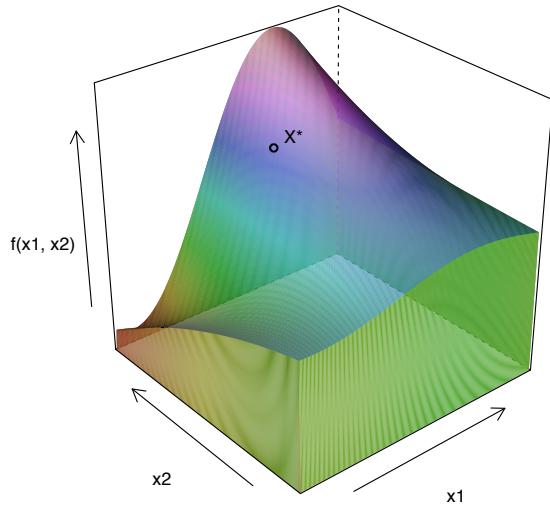


FIGURE 23 (fig:cutsSurfaceReady) Response surface for a model that is a function of two variables. We are interested in understanding the response of a model in a single point x^*

- We may discover that the model is providing incorrect predictions and we may want to find the reason. For instance, a patient with a very low risk-score experiences heart attack. What has driven that prediction?

A model is a function with a p -dimensional vector x as an argument. The plot of the value(s) of the function can be constructed in a $p + 1$ -dimensional space. An example with $p = 2$ is presented in Figure 23. We will use it as an illustration of key ideas. The plot provides an information about the values of the function in the vicinity of point x^* .

There are many different tools that may be used to explore the predictions of the model around a single point x^* . In the following sections we will describe the most popular approaches. They can be divided into three classes.

- One approach is to investigate how the model prediction changes if the value of a single explanatory variable changes. The approach is useful in the so-called „What-If” analyses. In particular, we can construct plots presenting the change in model-based predictions induced by a change of a single variable. Such plots are usually called Ceteris-paribus (CP) profiles. An example is provided in panel A of Figure 24. Chapters 0.6-0.8 introduce the CP profiles and methods based on them.
- Another approach is to analyze how the model prediction for point x^* is different from the average model prediction and how the difference can be distributed among explanatory

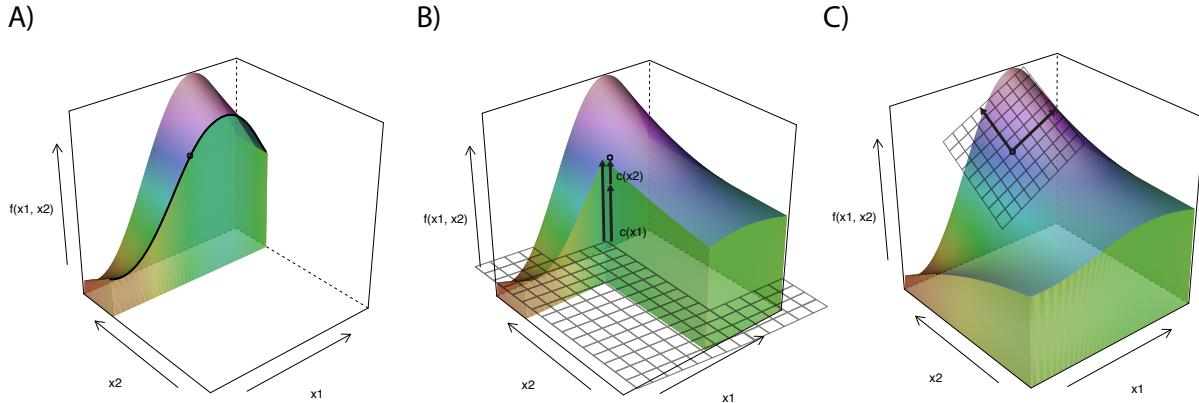


FIGURE 24 (fig:cutsTechnikiReady) Illustration of different approaches to instance-level explanation. Panel A presents a What-If analysis with Ceteris-paribus profiles. The profiles show the model response as a function of a value of a single variable, while keeping the values of all other explanatory variables fixed. Panel B illustrates the concept of variable attributions. Additive effects of each variable show how the model response differs from the average. Panel C illustrates the concept of local models. A simpler glass-box model is fitted around the point of interest. It describes the local behaviour of the black-box model.

variables. It is often called the „variable attributions” approach. An example is provided in panel B of Figure 24. Chapters 0.9-0.11 present various methods implementing this approach.

- Yet another approach is to analyze the curvature of the response surface (see Figure 23) around the point of interest x^* . Treating the model as a function, we are interested in the local behavior of this function around x^* . In case of a black-box model, we may approximate it with a simpler glass-box model around x^* . An example is provided in panel C of Figure 24. Chapter 0.12 presents the Local Interpretable Model-agnostic Explanations (LIME) method that exploits the concept of a „local model.”

Each method has its own merits and limitations. They are briefly discussed in the corresponding chapters. Chapter ?? offers a comparison of the methods.

0.6 Ceteris-paribus Profiles and What-If Analysis

0.6.1 Introduction

Ceteris paribus is a Latin phrase meaning “other things held constant” or “all else unchanged.” In this chapter, we introduce a technique for model exploration based on the *Ceteris paribus* principle. In particular, we examine the influence of each explanatory variable, assuming that effects of all other variables are unchanged. The main goal is to understand how changes in a single explanatory variable affects model predictions.

Explanation tools (explainers) presented in this chapter are linked to the second law introduced in Section 0.1.3, i.e. the law of “Prediction’s speculation.” This is why the tools are also known as *What-If model analysis* or *Individual Conditional Expectations* (Goldstein et al., 2015a). It appears that it is easier to understand how a black-box model is working if we can explore the model by investigating the influence of explanatory variables separately, changing one at a time.

0.6.2 Intuition

Panel A of Figure 25 presents response (prediction) surface for the `titanic_lmr_v6` model for two explanatory variables, `age` and `class`, from the `titanic` dataset (see Section 0.4.1). We are interested in the change of the model prediction induced by each of the variables. Toward this end, we may want to explore the curvature of the response surface around a single point with `age` equal to 47 and `class` equal to “1st,” indicated in the plot. Ceteris-paribus (CP) profiles are one-dimensional profiles that examine the curvature across each dimension, i.e., for each variable. Panel B of Figure 25 presents the profiles corresponding to `age` and `class`. Note that, in the CP profile for `age`, the point of interest is indicated by the black dot. In essence, a CP profile shows a conditional expectation of the dependent variable (response) for the particular explanatory variable.

CP technique is similar to the LIME method (see Chapter 0.12). LIME and CP profiles examine the curvature of response surface of a model. The difference between these two methods lies in the fact that LIME approximates the black-box model of interest locally with a simpler glass-box model. Usually, the LIME model is sparse, i.e., contains fewer explanatory variables. Thus, one needs to investigate a plot across a smaller number of dimensions. On the other hand, the CP profiles present conditional predictions for every variable and, in most cases, are easier to interpret.

0.6.3 Method

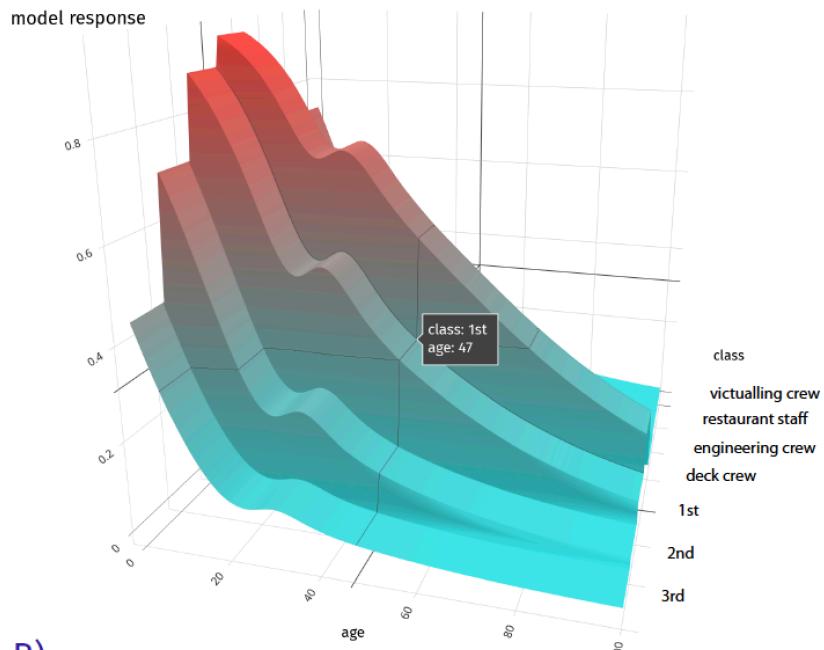
In this section, we introduce more formally one-dimensional CP profiles.

In predictive modeling, we are interested in a distribution of a dependent variable Y given vector x_* . The latter contains values of explanatory variables. In the ideal world, we would like to know the conditional distribution of Y given x_* . In practical applications, however, we usually do not predict the entire distribution, but just some of its characteristics like the expected (mean) value, a quantile, or variance. Without loss of generality we will assume that we model the conditional expected value $E_Y(Y|x_*)$.

Assume that we have got model $f()$, for which $f(x_*)$ is an approximation of $E_Y(Y|x_*)$, i.e., $E_Y(Y|x_*) \approx f(x_*)$. Note that we do not assume that it is a “good” model, nor that the approximation is precise. We simply assume that we have got a model that is used to estimate the conditional expected value and to form predictions of the values of the dependent variable. Our interest lies in the evaluation of the quality of the predictions. If the model

Ceteris Paribus Profiles for the model titanic_lmr_v6

A)



B)

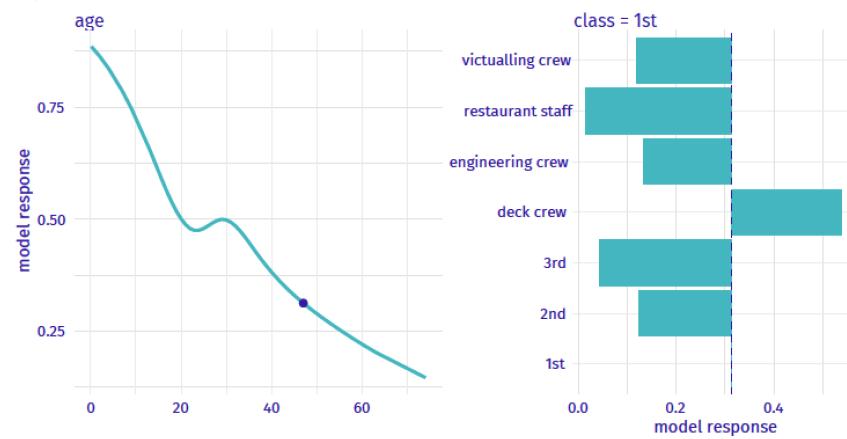


FIGURE 25 (fig:modelResponseCurveLine) A) Model response (prediction) surface. Ceteris-paribus (CP) profiles marked with black curves help to understand the curvature of the surface while changing only a single explanatory variable. B) CP profiles for individual variables, age (continuous) and class (categorical).

offers a “good” approximation of the conditional expected value, it should be reflected in its satisfactory predictive performance.

Recall (see Section 0.1.8) that we use x_i to refer to the vector corresponding to the i -th observation in a dataset. Let x_*^j denote the j -th element of x_* , i.e., the j -th explanatory variable. We use x_*^{j-} to refer to a vector resulting from removing the j -th element from x_* . By $x_*^{j|=z}$, we denote a vector resulting from changing the value of the j -th element of x_* to (a scalar) z .

We define a one-dimensional CP profile $h()$ for model $f()$, the j -th explanatory variable, and point x_* as follows:

$$h_{x_*}^{f,j}(z) \equiv f(x_*^{j|=z}).$$

CP profile is a function that provides the dependence of the approximated expected value (prediction) of Y on the value z of the j -th explanatory variable. Note that, in practice, z is taken to go through the entire range of values typical for the variable, while values of all other explanatory variables are kept fixed at the values specified by x_* .

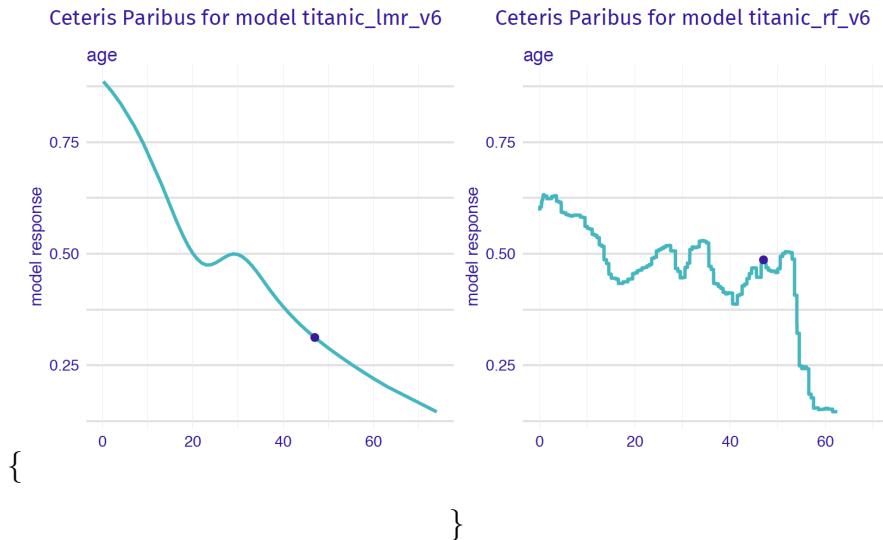
Note that in the situation when only a single model is considered, we will skip the model index and we will denote the CP profile for the j -th explanatory variable and the point of interest x_* by $h_{x_*}^j(z)$.

0.6.4 Example: Titanic

For continuous explanatory variables, a natural way to represent the CP function is to use a profile plot similar to the ones presented in Figure 0.6.4. In the figure, the dot on the curves marks an instance prediction, i.e., prediction $f(x_*)$ for a single observation x_* . The curve itself shows how the prediction would change if the value of a particular explanatory variable changed.

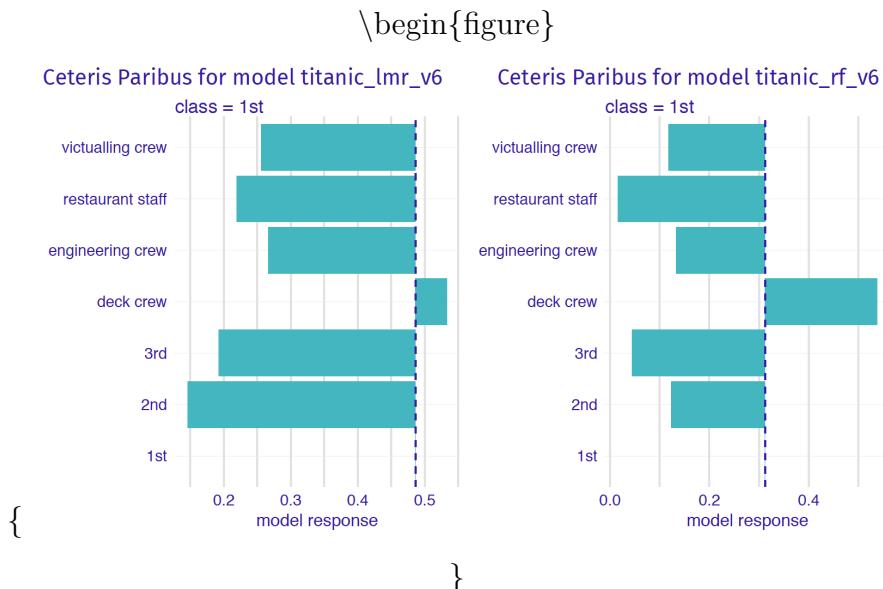
Figure 0.6.4 presents CP profiles for the *age* variable in the logistic regression and random forest models for the Titanic dataset (see Sections 0.4.1.2 and 0.4.1.3, respectively). It is worth observing that the profile for the logistic regression model is smooth, while the one for the random forest model shows more variability. For this instance (observation), the prediction for the logistic regression model would increase substantially if the value of *age* became lower than 20. For the random forest model, a substantial increase would be obtained if *age* became lower than 13 or so.

\begin{figure}



\caption{(fig:profileAgeRf) Ceteris-paribus profiles for variable `age` for the logistic regression (`titanic_lmr_v6`) and random forest (`titanic_rf_v6`) models that predict the probability of surviving based on the Titanic data} \end{figure}

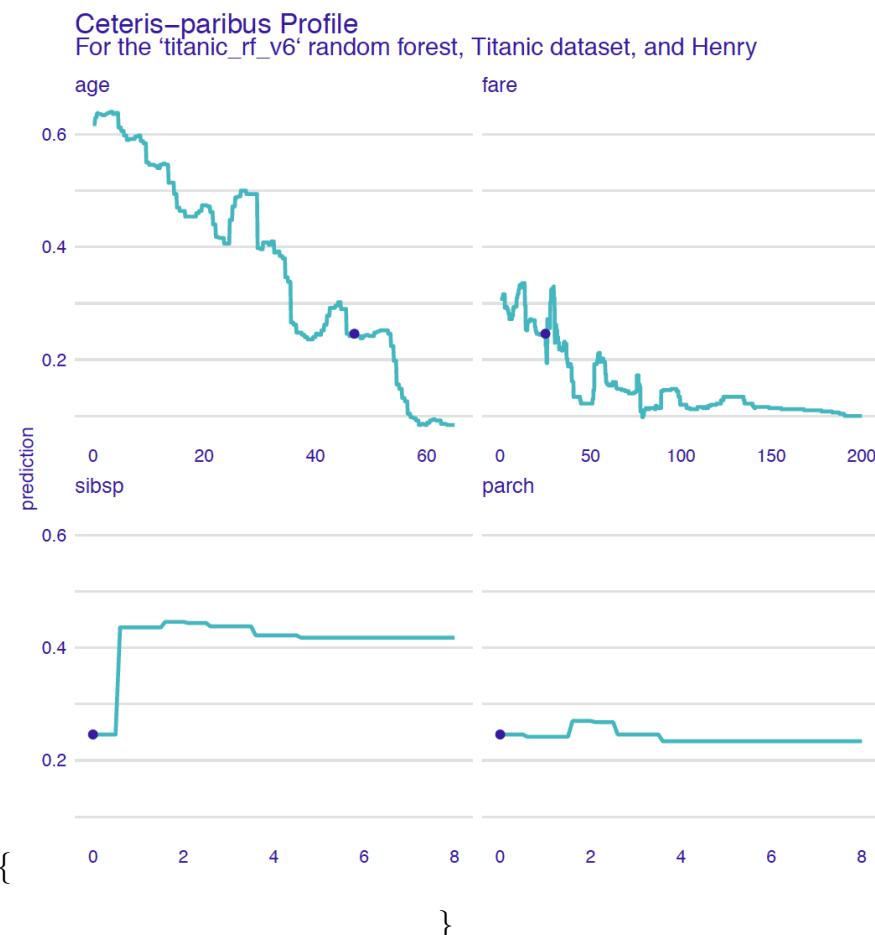
For a categorical explanatory variable, a natural way to represent the CP function is to use a barplot similar to the ones presented in Figure 0.6.4. The barplots in Figure 0.6.4 present CP profiles for the `class` variable in the logistic regression and random forest models for the Titanic dataset (see Sections 0.4.1.2 and 0.4.1.3, respectively). For this instance (observation), the predicted probability for the logistic regression model would decrease substantially if the value of `class` changed to “2nd”. On the other hand, for the random forest model, the largest change would be marked if `class` changed to “restaurant staff”.



\caption{(fig:profileAgeRf2) Ceteris-paribus profiles for variable `class` for the logistic regression (`titanic_lmr_v6`) and random forest (`titanic_rf_v6`) models that predict the probability of surviving based on the Titanic data} \end{figure}

Usually, black-box models contain a large number of explanatory variables. However, CP profiles are legible even for tiny subplots, created with techniques like sparklines or small multiples (Tufte, 1986). In this way we can display a large number of profiles at the same time keeping profiles for consecutive variables in separate panels, as shown in Figure 0.6.4 for the random forest model for the Titanic dataset. It helps if these panels are ordered so that the most important profiles are listed first. We discuss a method to assess the importance of CP profiles in the next chapter.

\begin{figure}



\caption{(fig:profileV4Rf) Ceteris-paribus profiles for all continuous explanatory variables for the random forest (`titanic_rf_v6`) model for the `titanic` dataset} \end{figure}

0.6.5 Pros and cons

One-dimensional CP profiles, as presented in this chapter, offer a uniform, easy to communicate and extendable approach to model exploration. Their graphical representation is easy to understand and explain. It is possible to show profiles for many variables or models in a single plot. CP profiles are easy to compare, thus we can juxtapose two or more models to better understand differences between models. We can also compare

two or more instances to better understand model stability. CP profiles are also a useful tool for sensitivity analysis.

There are several issues related to the use of the CP profiles. If explanatory variables are correlated, then changing one variable implies a change in the other. In such case, the application of the *Ceteris paribus* principle may lead to unrealistic settings, as it is not possible to keep one variable fixed while varying the other one. For example, apartment's price prediction features like surface and number of rooms are correlated thus it is unrealistic to consider very small apartments with extreme number of rooms. Special cases are interactions, which require the use of two-dimensional CP profiles that are more complex than one-dimensional ones. Also, in case of a model with hundreds or thousands of variables, the number of plots to inspect may be daunting. Finally, while barplots allow visualization of CP profiles for factors (categorical explanatory variables), their use becomes less trivial in case of factors with many nominal (unordered) categories (like, for example, a ZIP-code).

0.6.6 Code snippets for R

In this section, we present key features of the R package `ingredients` (Biecek, 2019a) which is a part of `DrWhy.AI` universe and covers all methods presented in this chapter. More details and examples can be found at <https://modeloriented.github.io/ingredients/>.

Note that there are also other R packages that offer similar functionality, like `condvis` (O'Connell et al., 2017), `pdp` (Greenwell, 2017a), `ICEbox` (Goldstein et al., 2015b), `ALEPlot` (Apley, 2018a), `iml` (Molnar et al., 2018a).

For illustration, we use two classification models developed in Chapter 0.4.1, namely the logistic regression model `titanic_lmr_v6` (Section 0.4.1.2) and the random forest model `titanic_rf_v6` (Section 0.4.1.3). They are developed to predict the probability of survival after sinking of Titanic. Instance-level explanations are calculated for a single observation `henry` - a 47 years old male passenger that travelled in the 1st class.

`DALEX` explainers for both models and the `henry` data frame are retrieved via the `archivist` hooks as listed in Section 0.4.1.7.

```
library("rms")
explain_lmr_v6 <- archivist::aread("pbiecek/models/2b9b6")

library("randomForest")
explain_rf_v6 <- archivist::aread("pbiecek/models/9b971")

library("DALEX")
henry <- archivist::aread("pbiecek/models/a6538")
henry

##   class gender age sibsp parch fare embarked
## 1   1st    male  47      0      0    25 Cherbourg
```

0.6.6.1 Basic use of the `ceteris_paribus` function

The easiest way to create and plot CP profiles is to call `ceteris_paribus()` function and then the generic `plot()` function. By default, profiles for all variables are being calculated and all numeric features are being plotted. One can limit the number of variables that should be considered with the `variables` argument.

To obtain CP profiles, the `ceteris_paribus()` function requires the explainer-object and the instance data frame as arguments. As a result, the function yields an object od the class `ceteris_paribus_explainer`. It is a data frame with model predictions.

```
library("ingredients")
cp_titanic_rf <- ceteris_paribus(explain_rf_v6, henry)
cp_titanic_rf

## Top profiles      :
##           class gender age sibsp parch fare embarked _yhat_ _vname_
## 1          3rd   male  47     0     0    25 Cherbourg  0.100  class
## 1.1        2nd   male  47     0     0    25 Cherbourg  0.054  class
## 1.2        1st   male  47     0     0    25 Cherbourg  0.246  class
## 1.3 engineering crew male  47     0     0    25 Cherbourg  0.096  class
## 1.4 victualling crew male  47     0     0    25 Cherbourg  0.098  class
## 1.5 restaurant staff male  47     0     0    25 Cherbourg  0.092  class
##       _ids_         _label_
## 1      1 Random Forest v6
## 1.1    1 Random Forest v6
## 1.2    1 Random Forest v6
## 1.3    1 Random Forest v6
## 1.4    1 Random Forest v6
## 1.5    1 Random Forest v6
##
##
## Top observations:
##           class gender age sibsp parch fare embarked _yhat_      _label_
## 1  1st   male  47     0     0    25 Cherbourg  0.246 Random Forest v6
##       _ids_
## 1      1
```

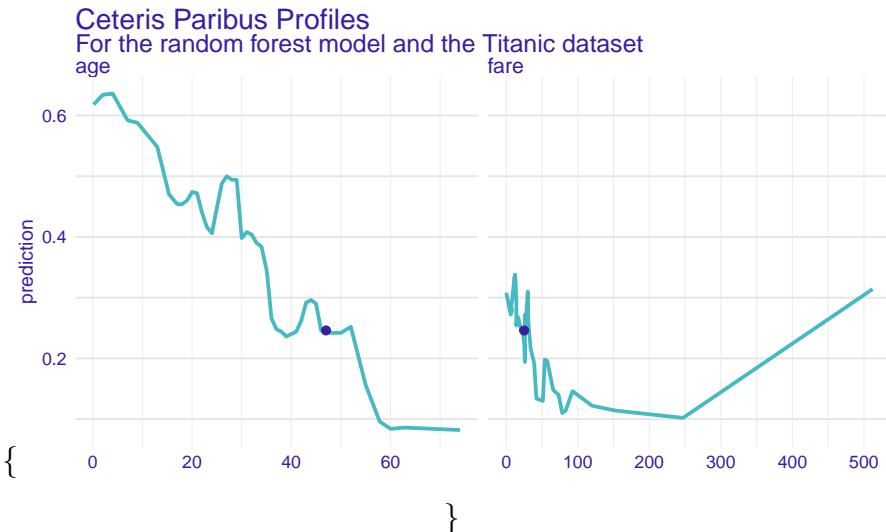
To obtain a graphical representation of CP profiles, the generic `plot()` function can be applied to the data frame returned by the `ceteris_paribus()` function. It returns a `ggplot2` object that can be processed further if needed. In the examples below, we use the `ggplot2` functions, like `ggtitle()` or `ylim()`, to modify plot's title or the range of the Y-axis.

The resulting plot can be enriched with additional data by applying functions `ingredients::show_rugs()` (adds rugs for the selected points), `ingredients::show_observations` (adds dots that shows observations), or `ingredients::show_aggregated_profiles`. All these functions can take additional arguments to modify size, color, or linetype.

Below we show an R snippet that can be used to replicate plots presented in the upper part of Figure 0.6.4.

```
library("ggplot2")
plot(cp_titanic_rf, variables = c("age", "fare")) +
  show_observations(cp_titanic_rf, variables = c("age", "fare")) +
  ggtitle("Ceteris Paribus Profiles", "For the random forest model and the Titanic dataset")
```

\begin{figure}



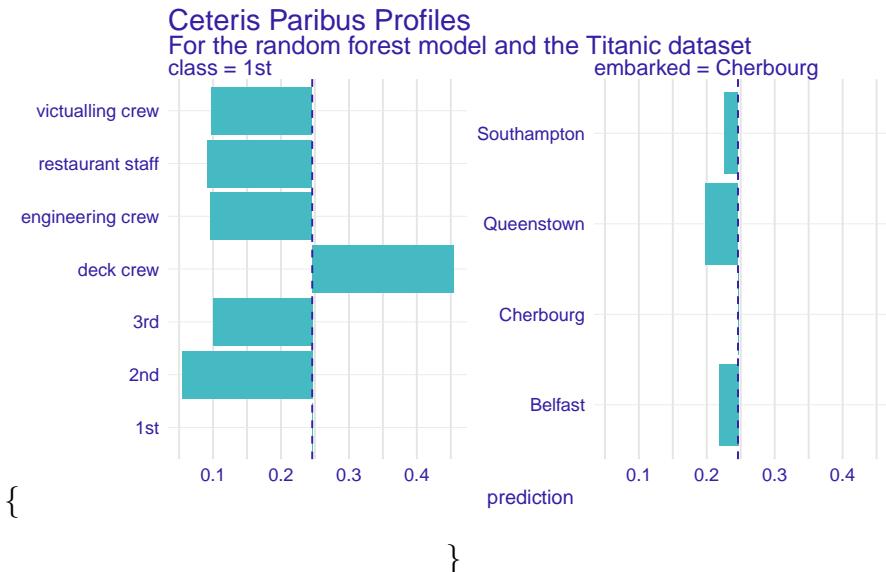
\caption{Ceteris-paribus profiles for `age` and `fare` variables and the `titanic_rf_v6` model.}

\end{figure}

By default, all numerical variables are plotted. To plot CP profiles for categorical variables, we have got to add the `only_numerical = FALSE` argument to the `plot()` function. The code below can be used to recreate the right-hand-side plot from Figure 0.6.4.

```
plot(cp_titanic_rf, variables = c("class", "embarked"), only_numerical = FALSE) +
  ggtitle("Ceteris Paribus Profiles", "For the random forest model and the Titanic dataset")
```

\begin{figure}



```
\caption{Ceteris-paribus profiles for class and embarked variables and the titanic_rf_v6 model.} \end{figure}
```

0.6.6.2 Advanced use of the `ceteris_paribus` function

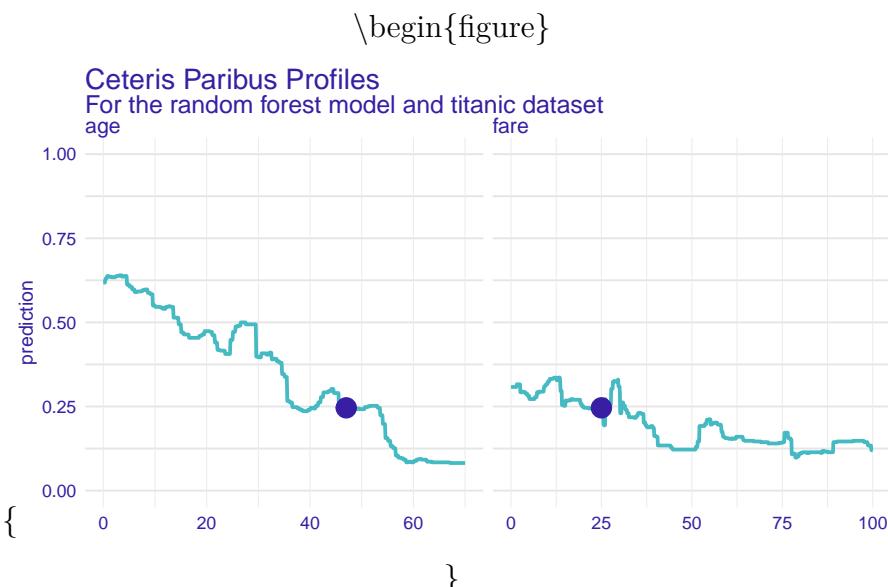
The `ceteris_paribus()` is a very flexible function. To better understand how it can be used, we briefly review its arguments.

- `x`, `predict_function`, `label` - information about a model. If `x` is created with the `DALEX::explain` function, then other arguments are extracted from `x`; this is how we use the function in this chapter. Otherwise, we have got to specify directly the model, the validation data, the predict function, and the model label.
 - `new_observation` - instance (one or more), for which we want to calculate CP profiles. It should be a data frame with same variables as in the validation data.
 - `y` - observed value of the dependent variable for `new_observation`. The use of this argument is illustrated in Section 0.8.1.
 - `variables` - names of explanatory variables, for which CP profiles are to be calculated. By default, the profiles will be constructed for all variables, which may be time consuming.
 - `variable_splits` - a list of values for which CP profiles are to be calculated. By default, these are all values for categorical variables. For continuous variables, uniformly-placed values are selected; one can specify the number of the values with the `grid_points` argument (the default is 101).

The code below allows to obtain the plots in the upper part of Figure 0.6.4. The argument `variable_splits` specifies the variables (`age` and `fare`) for which CP profiles are to be calculated, together with the list of values at which the profiles are to be evaluated.

```
cp_titanic_rf <- ceteris_paribus(explain_rf_v6, henry,  
variable_splits = list(age = seq(0, 70, 0.1),  
fare = seq(0, 100, 0.1)))
```

```
plot(cp_titanic_rf) +
  show_observations(cp_titanic_rf, variables = c("age", "fare"), size = 5) +
  ylim(0, 1) +
  ggtitle("Ceteris Paribus Profiles", "For the random forest model and titanic dataset")
```



\caption{Ceteris-paribus profiles for `class` and `embarked` variables and the `titanic_rf_v6` model. Blue dot stands for `henry`.} \end{figure}

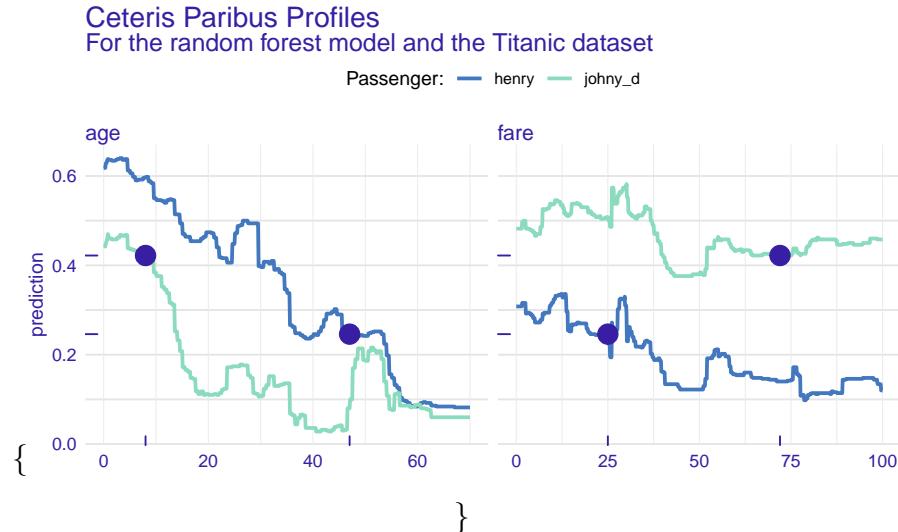
To enhance the plot, additional functions can be used. The generic `plot()` function creates a `ggplot2` object with a single `geom_line` layer. Function `show_observations` adds `geom_point` layer, `show_rugs` adds `geom_rugs`, while `show_profiles` adds another `geom_line`. All these functions take, as the first argument, an object created with the `ceteris_paribus` function. They can be combined freely to superpose profiles for different models or observations.

In the example below, we present the code to create XO profiles for two passengers, `henry` and `johny_d`. Their profiles are included in a plot presented in Figure 0.6.6.2. We use the `scale_color_manual` function to add names of passengers to the plot, and to control colors and positions.

```
johny_d <- archivist:::aread("pbiecek/models/e3596")
cn_titanic_rf2 <- ceteris.paribus(explain_rf_v6_rbind(henry, johny_d))
```

```
plot(cp_titanic_rf2, color = "_ids_") +
  show_observations(cp_titanic_rf2, size = 5, variables = c("age", "fare")) +
  show_rugs(cp_titanic_rf2, sides = "bl", variables = c("age", "fare")) +
  scale_color_manual(name = "Passenger:", breaks = 1:2, values = c("#4378bf", "#8bdcbc"), labels = c("henry" ,
  ggtitle("Ceteris Paribus Profiles", "For the random forest model and the Titanic dataset")
```

```
\begin{figure}
```



\caption{Ceteris-paribus profiles for the `titanic_rf_v6` model. Profiles for different passengers are color-coded.} \end{figure}

0.6.6.3 Champion-challenger analysis

One of the most interesting uses of the explainers is comparison of CP profiles for two or more of models.

To illustrate this possibility, first, we have go to construct profiles for the models. In our illustration, for the sake of clarity, we limit ourselves just to two models: the logistic regression and random forest models for the Titanic data. Moreover, we only consider the `age` and `fare` variables. We use `henry` as the instance, for which predictions are of interest.

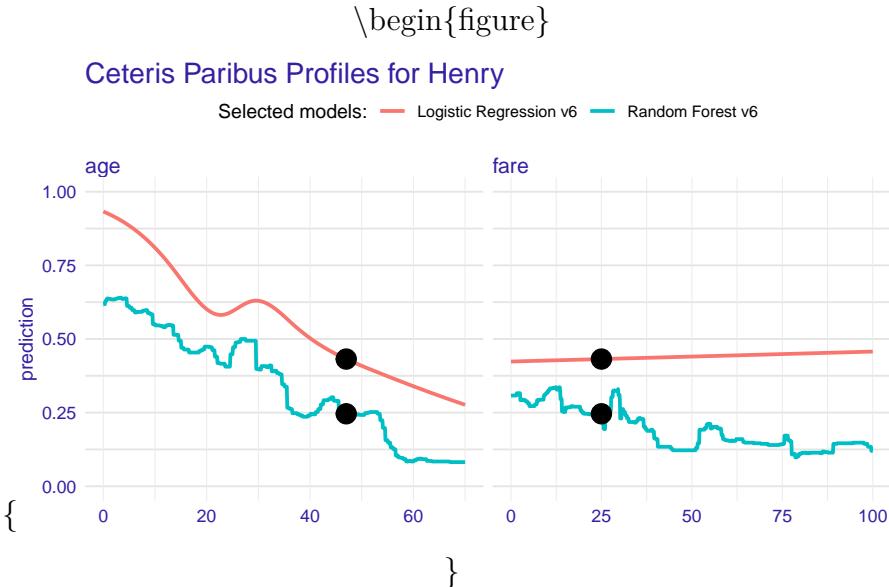
```
cp_titanic_rf <- ceteris_paribus(explain_rf_v6, henry)
cp_titanic_lmr <- ceteris_paribus(explain_lmr_v6, henry)
```

Subsequently, we construct the plot. The result is shown in Figure 0.6.6.3. Predictions for `henry` are slightly different, logistic regression returns in this case higher predictions than random forest. For `age` variable profiles of both models are similar, in both models we see decreasing dependency. While for `fare` the logistic regression model is slightly positive while random forest is negative. The larger the `fare` the larger is difference between these models.

Such analysis helps us to which degree different models agree on what if scenarios.

Note that every `plot` and `show_*` function can take a collection of explainers as arguments. Profiles for different models are included in a single plot. In the presented R snippet, models are color-coded with the help of the argument `color = "_label_"`, where `_label_` refers to the name of the column in the CP explainer that contains the model label.

```
plot(cp_titanic_rf, cp_titanic_lmr, color = "_label_") +
  show_observations(cp_titanic_rf, cp_titanic_lmr, color = "black", variables = c("age", "fare"), size = 5) +
  scale_color_discrete(name = "Selected models:") + ylim(0,1) +
  ggtitle("Ceteris Paribus Profiles for Henry")
```



\caption{Champion-challenger comparison of the `titanic_lmr_v6` and `titanic_rf_v6` models. Profiles for different models are color-coded.} \end{figure}

0.7 Ceteris-paribus Oscillations and Local Variable-importance

0.7.1 Introduction

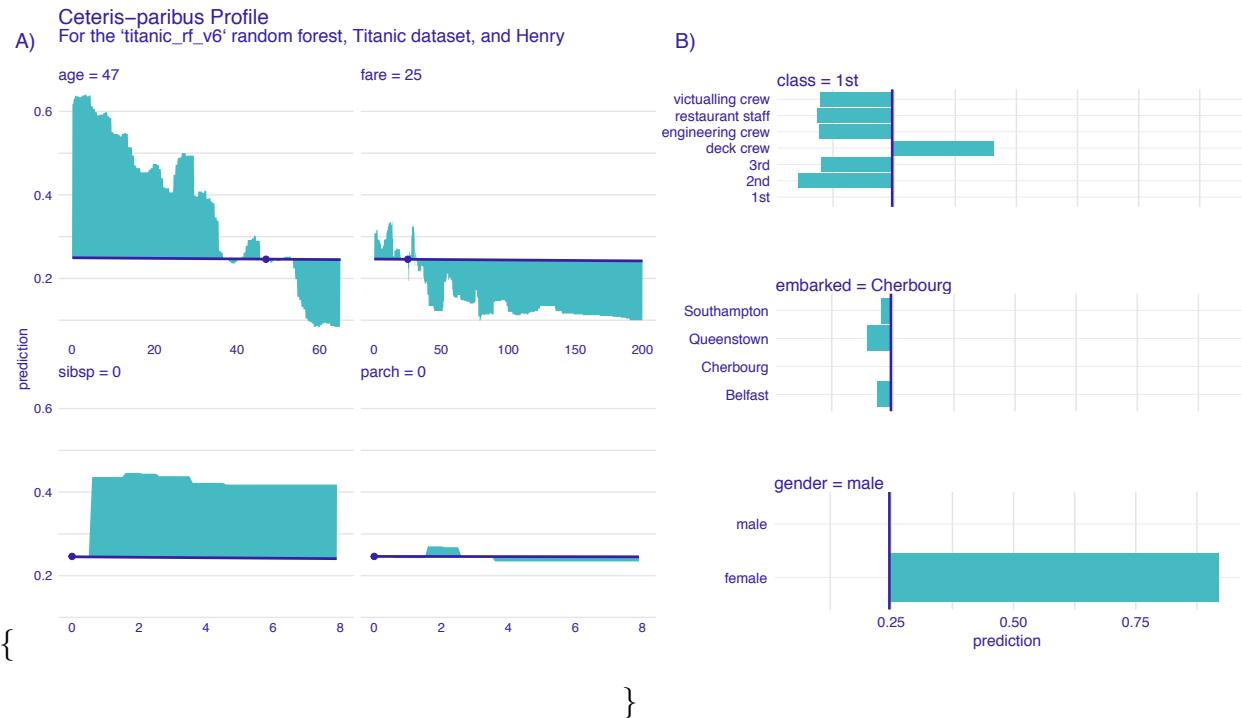
Visual examination of Ceteris-paribus (CP) profiles is insightful, but for a model with a large number of explanatory variables we may end up with a large number of plots which may be overwhelming. To prioritize between the profiles we need a measure that would summarize the impact of a selected variable on model's predictions. In this chapter we describe a solution closely linked with CP profiles. An alternative is discussed in the Chapters 0.9 and 0.11.

0.7.2 Intuition

To assign importance to CP profiles, we can use the concept of profile oscillations. In particular, the larger influence of an explanatory variable on prediction at a particular instance, the larger the fluctuations along the corresponding CP profile. For a variable that exercises little or no influence on model prediction, the profile will be flat or will barely change. In other words, the values of the CP profile should be close to the value of the model prediction for the particular instance. Consequently, the sum of differences between the profile and the value of the prediction, take across all possible values of the explanatory variable, should be close to zero. The sum can be graphically depicted by the area between the profile and the horizontal line representing the instance prediction. On the other hand,

for an explanatory variable with a large influence on the prediction, the area should be large. Figure 0.7.2 illustrates the concept. Panel A of the figure corresponds to the CP profiles presented in Figure 0.6.4. The larger the highlighted area in Figure 0.7.2, the more important is the variable for the particular prediction.

\begin{figure}



\caption{(fig:CPVIPprofiles) The value of the colored area summarizes the

Ceteris-paribus-profile oscillations and provides the mean of the absolute deviations between the CP profile and the instance prediction. Panel A shows plots for continuous explanatory variables, while panel B shows plots for categorical variables in the

`titanic_rf_v6` model.} \end{figure}

0.7.3 Method

Let us formalize this concept now. Denote by $g^j(z)$ the probability density function of the distribution of the j -th explanatory variable. The summary measure of the variable's importance for model prediction at point x_* , $vip_{CP}^j(x_*)$, computed based on the variable's CP profile, is defined as follows:

$$vip_{CP}^j(x_*) = \int_{\mathcal{R}} |h_{x_*}^j(z) - f(x_*)| g^j(z) dz = E_{X^j} [|h_{x_*}^j(X^j) - f(x_*)|]. \quad (0.1)$$

Thus, $vip_{CP}^j(x_*)$ is the expected absolute deviation of the CP profile from the model prediction for x_* over the distribution $g^j(z)$ for the j -th explanatory variable.

The true distribution of j -th explanatory variable is, in most cases, unknown. Thus, there are several options how to calculate (0.1).

One is to calculate just the area under the CP curve, i.e., to assume that $g^j(z)$ is a uniform distribution for the range of variable x^j . It follows then that a straightforward estimator of $\widehat{vip}_{CP}^{j,uni}(x_*)$ is

$$\widehat{vip}_{CP}^{j,uni}(x_*) = \frac{1}{k} \sum_{l=1}^k |h_{x_*}^j(z_l) - f(x_*)|, \quad (0.2)$$

where z_l ($l = 1, \dots, k$) are the selected values of the j -th explanatory variable. For instance, one can select use all unique values of x^j in the considered dataset. Alternatively, for a continuous variable, one can use an equi-distant grid of values.

Another approach is to use the empirical distribution for x^j . This leads to the estimator of $\widehat{vip}_{CP}^{j,emp}(x_*)$ defined as

$$\widehat{vip}_{CP}^{j,emp}(x_*) = \frac{1}{n} \sum_{i=1}^n |h_{x_*}^j(x_i^j) - f(x_*)|, \quad (0.3)$$

where index i goes through all observations in a dataset.

The use of $\widehat{vip}_{CP}^{j,emp}(x_*)$ is preferred when there are enough data to accurately estimate the empirical distribution and when the distribution is not uniform. On the other hand, $\widehat{vip}_{CP}^{j,uni}(x_*)$ is in most cases quicker to compute and, therefore, it is preferred if we look for fast approximations.

It is worth noting that the importance of an explanatory variable for instance prediction may be very different for different points x_* . For example, consider model

$$f(x_1, x_2) = x_1 * x_2,$$

where x_1 and x_2 take values in $[0, 1]$. Consider prediction for an observation described by vector $x_* = (0, 1)$. In that case, the importance of X_1 is larger than X_2 . This is because the CP profile for the first variable, given by the values of function $f(z, 1) = z$, will have oscillations. On the other hand, the profile for the second variable will show no oscillations, because the profile is given by function $f(0, z) = 0$. Obviously, the situation is reversed for $x_* = (1, 0)$.

0.7.4 Example: Titanic

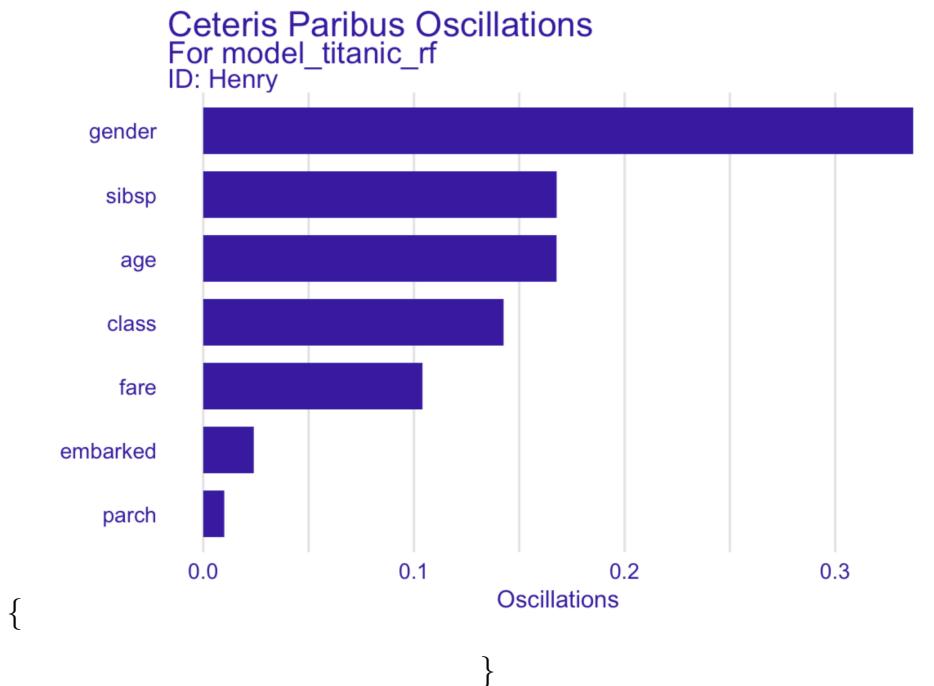
Figure 0.7.4 provides a barplot of variable importance measures for different continuous explanatory variables for the random forest model `titanic_rf_v6` for `henry`.

The longer the bar, the larger the CP-profile oscillations for a particular explanatory variable. Thus, Figure 0.7.4 indicates that the most important variable for prediction for the selected observation are `gender` and `sibsp`, followed by `age`.

From the Ceteris Paribus one can read that if Henry were older, this would significantly lower the chance of survival. One the other hand, were Henry not travelling alone, this would increase the chance.

From the oscillation's plot one can only read which features are important but one cannot read how they influence the prediction. This is why profile oscillations shall be accompanied by Ceteris Paribus profiles.

\begin{figure}



\caption{(fig:CPVIP1) Variable-importance measures calculated for Ceteris-paribus oscillations for `henry` based on the `titanic_rf_v6` model} \end{figure}

0.7.5 Pros and cons

Oscillations of CP profiles are easy to interpret and understand. By using the average of oscillations, it is possible to select the most important variables for an instance prediction.

The methodology can easily be extended to two or more variables.

There are several issues related to the use of the CP oscillations. For example, the oscillations may not be of help in situations when the use of CP profiles may itself be problematic (e.g., in the case of correlated explanatory variables or interactions - see Section 0.6.5). An important issue is that the local variable importance do not sum up to

the instance prediction for which they are calculated. In Chapters 0.9 and 0.11, we will introduce measures that address this problem.

0.7.6 Code snippets for R

In this section, we present key features of R package `ingredients` which is a part of the `DrWhy.AI` universe and covers all methods presented in this chapter. More details and examples can be found at <https://modeloriented.github.io/ingredients/>.

For illustration purposes we use the random forest model `titanic_rf_v6` (see Section ??). Recall that it is developed to predict the probability of survival from sinking of Titanic. Instance-level explanations are calculated for a single observation: `henry` - a 47-year-old passenger that travelled in the 1st class.

`DALEX` explainers for both models and the `Henry` data are retrieved via `archivist` hooks as listed in Section 0.4.1.7.

```
library("randomForest")
explain_rf_v6 <- archivist::aread("pbiecek/models/9b971")

library("DALEX")
henry <- archivist::aread("pbiecek/models/a6538")
henry
```

0.7.6.1 Basic use of the `calculate_oscillations` function

To calculate CP oscillations, we have got to calculate CP profiles for the selected observation. We use `henry` as the instance prediction of interest.

CP profiles are calculated by applying the `ceteris_paribus()` function to the wrapper object.

```
library("ingredients")
library("ggplot2")

cp_titanic_rf <- ceteris_paribus(explain_rf_v6, henry)
```

The resulting object can subsequently be processed with the `calculate_oscillations()` function to calculate the oscillations and the estimated value of the variable-importance measure (0.1).

```
oscillations_titanic_rf <- calculate_oscillations(cp_titanic_rf)
oscillations_titanic_rf

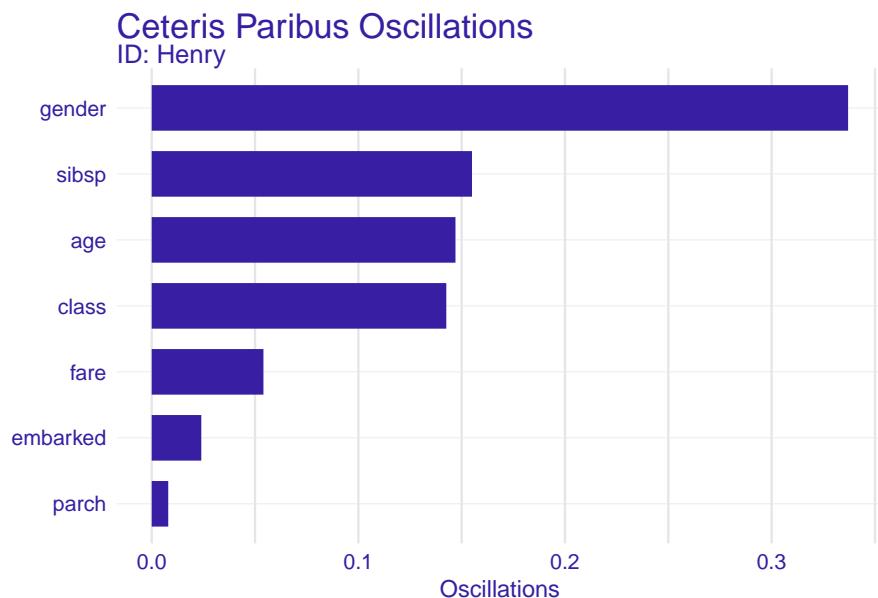
##      _vname_ _ids_ oscillations
## 2    gender     1   0.33700000
## 4    sibsp      1   0.15500000
## 3     age       1   0.14700000
## 1   class      1   0.14257143
```

```
## 6     fare      1  0.05407273
## 7 embarked    1  0.02400000
## 5     parch    1  0.00800000
```

Note that, by default, `calculate_oscillations()` estimates $\widehat{vip}_{CP}^j(x_*)$ by $\widehat{vip}_{CP}^{j,uni}(x_*)$, given in (0.2), using all unique values of the explanatory variable as the grid points.

The `calculate_oscillations()` function returns an object of class `ceteris_paribus_oscillations`, which has a form of a data frame, but has also an overloaded `plot()` function. We can use the latter function to plot the local variable-importance measures for the instance of interest.

```
oscillations_titanic_rf$`_ids_` <- "Henry"
plot(oscillations_titanic_rf) + ggtitle("Ceteris Paribus Oscillations")
```



0.7.6.2 Advanced use of the `calculate_oscillations` function

As mentioned in the previous section, `calculate_oscillations()` estimates $\widehat{vip}_{CP}^j(x_*)$ by $\widehat{vip}_{CP}^{j,uni}(x_*)$ using all unique values of the explanatory variable as the grid points. However, other approaches are also possible.

One is to use $\widehat{vip}_{CP}^j(x_*)$, but assuming an equi-distant grid of values for a continuous explanatory variable. Toward this aim, we have got to explicitly specify a dense uniform grid of values for such a variable. The `variable_splits` argument can be used for this purpose.

```
cp_titanic_rf_uniform <- ceteris_paribus(explain_rf_v6, henry,
                                             variable_splits = list(age = seq(0, 65, 0.1),
                                                       fare = seq(0, 200, 0.1),
                                                       sibsp = seq(0, 8, 0.1),
                                                       parch = seq(0, 8, 0.1),
                                                       gender = unique(titanic$gender),
```

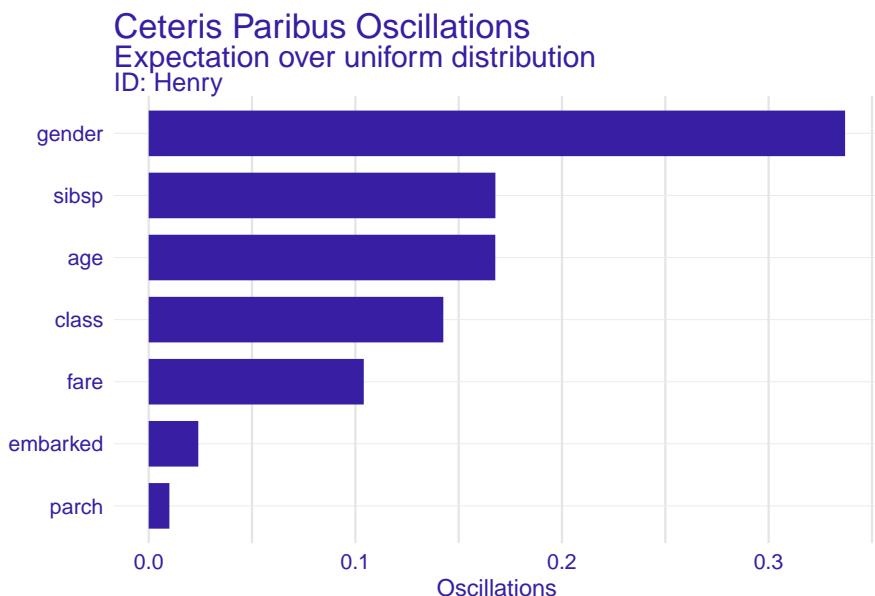
```
embarked = unique(titanic$embarked),  
class = unique(titanic$class)))
```

Subsequently, we apply the `calculate_oscillations()` function to compute the oscillations and the variable-importance measures.

```
oscillations_uniform <- calculate_oscillations(cp_titanic_rf_uniform)
oscillations_uniform$`_ids_` <- "Henry"
oscillations_uniform
```

```
##      _vname_ _ids_ oscillations
## 5    gender Henry    0.3370000
## 3   sibsp Henry    0.1677778
## 1     age Henry    0.1677235
## 7   class Henry    0.1425714
## 2    fare Henry    0.1040790
## 6 embarked Henry    0.0240000
## 4   parch Henry    0.0100000

plot(oscillations_uniform) + ggtitle("Ceteris Paribus Oscillations", "Expectation over uniform distribution")
```



Another approach is to calculate the expectation (0.1) over the empirical distribution of a variable, i.e., to use $\widehat{vip}_{CP}^{j,emp}(x_*)$, given in (0.3). Toward this aim, we use the `variable_splits` argument to explicitly specify the validation-data sample to define the grid of values.

```

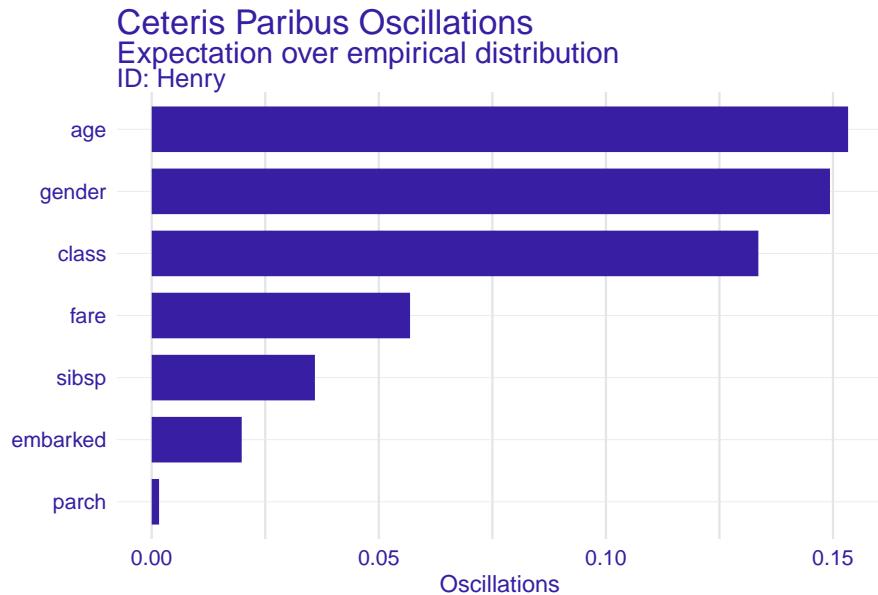
    parch = titanic$parch,
    gender = titanic$gender,
    embarked = titanic$embarked,
    class = titanic$class))

oscillations_empirical <- calculate_oscillations(cp_titanic_rf_empirical)
oscillations_empirical`_ids_` <- "Henry"
oscillations_empirical

##      _vname_ _ids_ oscillations
## 1      age Henry  0.153323969
## 5     gender Henry  0.149336656
## 7     class Henry  0.133567739
## 2      fare Henry  0.056883552
## 3     sibsp Henry  0.035932034
## 6  embarked Henry  0.019818758
## 4      parch Henry  0.001623924

plot(oscillations_empirical) + ggtitle("Ceteris Paribus Oscillations", "Expectation over empirical distribution")

```



0.8 Local Diagnostics With Ceteris-paribus Profiles

0.8.1 Introduction

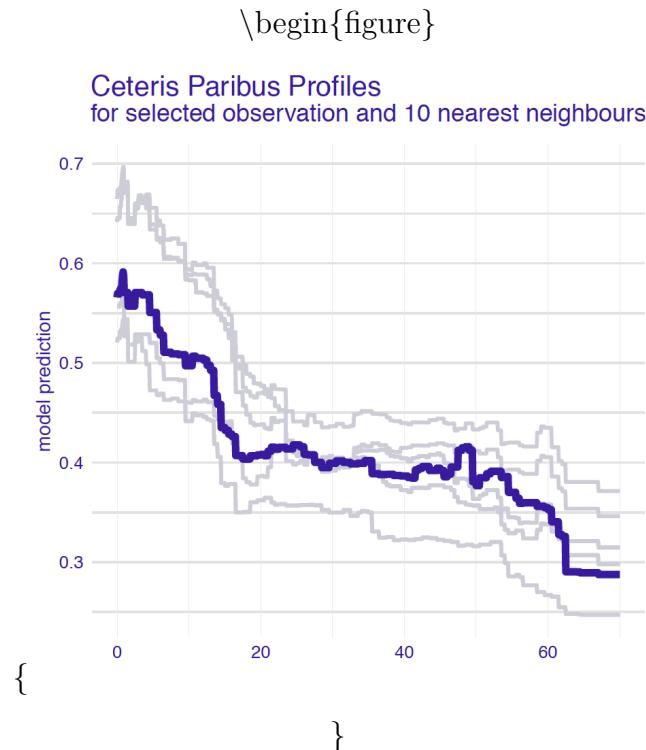
It may happen that, while the global predictive performance of the model is good, model predictions for some observations are very bad. In this chapter, we present two

local-diagnostics techniques that can address this issue. In particular, we focus on fidelity plots: the plot of CP profiles for nearest neighbors and the local-fidelity plot.

The idea behind fidelity plots is to select a number of observations (“neighbors”) from the validation dataset that are closest to the instance (observation) of interest. Then, for the selected observations, we plot CP profiles and check how stable they are. Additionally, if we know true values of the dependent variable for the selected neighbors, we may add residuals to the plot to evaluate the local fit of the model.

0.8.2 Intuition

One approach to local model diagnostics is to examine how the predictions vary for observations from the training dataset. Figure 0.8.2 presents CP profiles for the instance of interest and its 10 nearest neighbors for the random forest model for the Titanic dataset (Section 0.4.1.3). The profiles are almost parallel and very close to each other. This suggests that model predictions are stable around the instance of interest, because small changes in the explanatory variables (represented by the nearest neighbors) have not got much influence on the predictions.



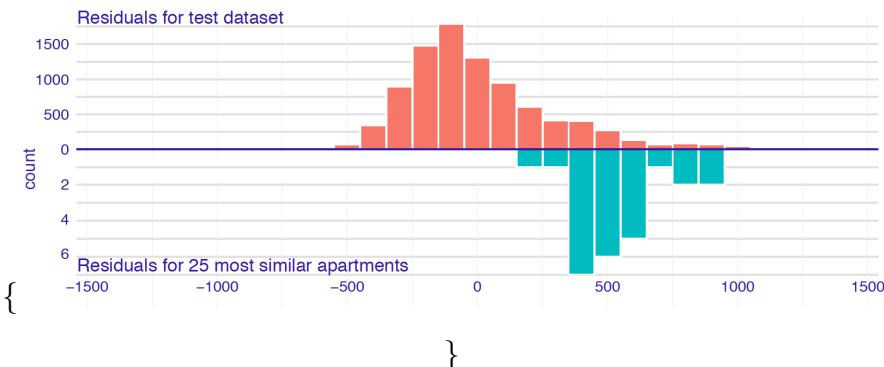
\caption{(fig:profileWith10NN) Ceteris-paribus profiles for a selected instance (dark violet line) and 10 nearest neighbors (light grey lines) for the `titanic_rf_b6` model. The profiles are almost parallel and close to each other what suggests the stability of the model.}
\end{figure}

Once we have selected the nearest neighbors, we can also look closer at the model fit around the point of interest. Figure 0.8.2 presents histograms of residuals for the entire

dataset and the selected neighbors for the random forest model for the Apartments dataset (Section 0.4.2.3). The distribution of residuals for the entire dataset is rather symmetric and centered around 0, suggesting a reasonable average performance of the model. On the other hand, the residuals for the selected neighbors are centered around the value of 500. This suggests that, on average, the model predictions are biased for the instance of interest.

\begin{figure}

Distribution of residuals for apartments_rf_v5



\caption{(fig:profileBack2BackHist) Histograms of residuals for the `apartments_rf_v5` model for the Apartments dataset. Upper panel: residuals calculated for all observations from the dataset. Bottom panel: residuals calculated for 25 nearest neighbors of the instance of interest.} \end{figure}

0.8.3 Method

The proposed method is based on three elements:

- identification of nearest neighbors,
- calculation and visualization of CP profiles for the selected neighbors, and
- analysis of residuals for the neighbors.

In what follows we discuss each of the elements in more detail.

0.8.3.1 Nearest neighbors

There are two important questions related to the selection of the neighbors “nearest” to the instance (observation) of interest:

- How many neighbors should we choose?
- What metric should be used to measure the “proximity” of observations?

The answer to both questions is, of course, *it depends*.

- The smaller the number of neighbors, the more local is the analysis. However, a very small number will lead to a larger variability of the results. In many cases we found that 20 neighbors works fine. However, one should always take into account computational time

(smaller number of neighbors results in quicker calculations) and the size of the dataset (for a small dataset, smaller sets of neighbors may be preferred).

- The metric if very important. The more explanatory variables, the more important is the choice. In particular, the metric should be capable of accommodating variables of different nature (categorical, continuous). Our default choice is the Gower similarity measure:

$$d_{gower}(x_i, x_j) = \frac{1}{p} \sum_{k=1}^p d^k(x_i^k, x_j^k),$$

where x_i is a p -dimensional vector of explanatory covariates for the i -th observation and $d^k(x_i^k, x_j^k)$ is the distance between values of the k -th variable for the i -th and j -th observations. Note that $d^k()$ depends on the nature of the variable. For instance, for a continuous variable it is equal to $|x_i^k - x_j^k| / \{max(x_1^k, \dots, x_n^k) - min(x_1^k, \dots, x_n^k)\}$, i.e., the absolute difference scaled by the observed range of the variable. On the other hand, for a categorical variable, it is simply $I(x_i^k = x_j^k)$, where $I()$ is the indicator function. Note that p may be equal to the number of all explanatory variables included in the model, or only a subset of them.

Once we have decided on the number of neighbors, we can use the chosen metric to select the required number observations “closest” to the one of interest.

0.8.3.2 Profiles for neighbors

Once nearest neighbors have been identified, we can graphically compare CP profiles for selected (or all) variables.

For a model with a large number of variables, we may end up with a large number of plots. In such a case a better strategy is to focus only on K most important variables, selected by using the variable-importance measure (see Chapter 0.7).

0.8.3.3 Local-fidelity plot

CP profiles are helpful to assess the model stability. In addition, we can enhance the plot by adding residuals to it to allow evaluation of the local model fit. For model $f()$ and observation i described by the vector of explanatory variables x_i , the residual is the difference between the observed and predicted value of the dependent variable Y_i , i.e.,

$$r_i = y_i - f(x_i).$$

Note that, for a binary variable, the residual is the difference between the value of 0 or 1, depending on how we code “success,” and the value of the predicted probability of “success.” This definition also applies to categorical responses, as it is common to define, in such case, a binary “success” indicator and compute the predicted probability of “success” for each category separately.

The plot that includes CP profiles for the nearest neighbors and the corresponding residuals is called a local-fidelity plot.

0.8.4 Example: Titanic

As an example, we will use the predictions for the random forest model for the Titanic data (see Section 0.4.1.3).

Figure 26 presents a detailed explanation of the elements of a local-fidelity plot for `age`, a continuous explanatory variable. The plot includes eight nearest neighbors of Henry (see Section 0.4.1.5). Profiles are quite apart from each other, which indicates potential instability of model predictions. However, the residuals included in the plots are positive and negative, indicating that, on average, the instance prediction should not be biased.

Figure 27 presents a local-fidelity plot for the categorical explanatory variable `class`. Henry and his neighbors traveled in the 1st class. In different panels we see how the predicted probability of survival changes if the 1st class is replaced, for instance, by the 2nd (in most cases, the probability will be reduced) or the `deck crew` (in most cases, the probability will increase). Such plots can help to detect interactions, as we see that the same change (let's say, from the 1st to the 3rd class) results in a different change of the model prediction.

0.8.5 Pros and cons

Local-fidelity plots may be very helpful to check if

- the model is locally additive, as for such models the CP profiles should be parallel;
- the model is locally stable, as in that case the CP profiles should be close to each other;
- the model fit for the instance of interest is good, as in that case the residuals should be small and their distribution should be balanced around 0.

The drawback is that such plots are quite complex and lack objective measures of the quality of the model fit. Thus, they are mainly suitable for an exploratory analysis.

0.8.6 Code snippets for R

In this section, we show how to use the R package `ingredients` (Biecek, 2019b) to construct local-fidelity plots. More details and examples can be found at

<https://modeloriented.github.io/ingredients/>.

We use the random forest model `titanic_rf_v6` developed for the Titanic dataset (see Section 0.4.1.3) as the example. Recall that we try to address a classification problem for a binary dependent variable - we want to predict the probability of survival for a selected passenger.

DALEX explainers for the model and the `henry` data frame are retrieved via `archivist` hooks, as listed in Section 0.4.1.7.

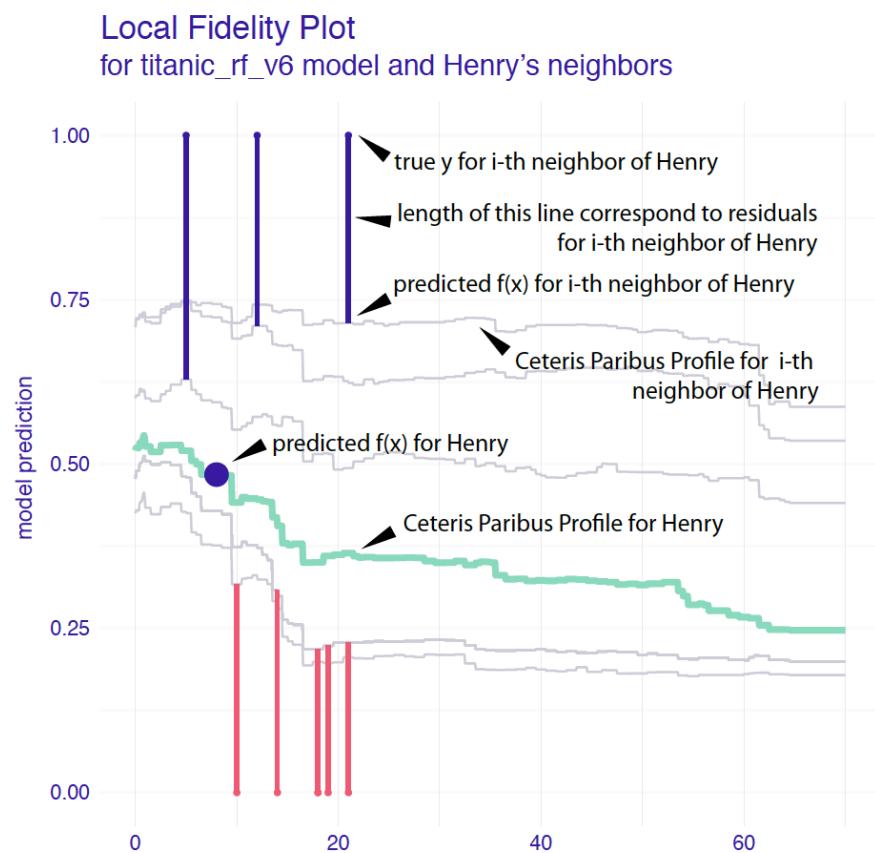


FIGURE 26 (fig:localFidelityPlots) Elements of a local-fidelity plot for a continuous explanatory variable. The green line shows the Ceteris-paribus profile for the instance of interest. Profiles of the nearest neighbors are marked with grey lines. The vertical intervals correspond to residuals; the shorter the interval, the smaller the residual and the more accurate prediction of the model. Blue intervals correspond to positive residuals, red intervals to negative intervals. Stable model will have profiles close to each other; additive model will have parallel lines.

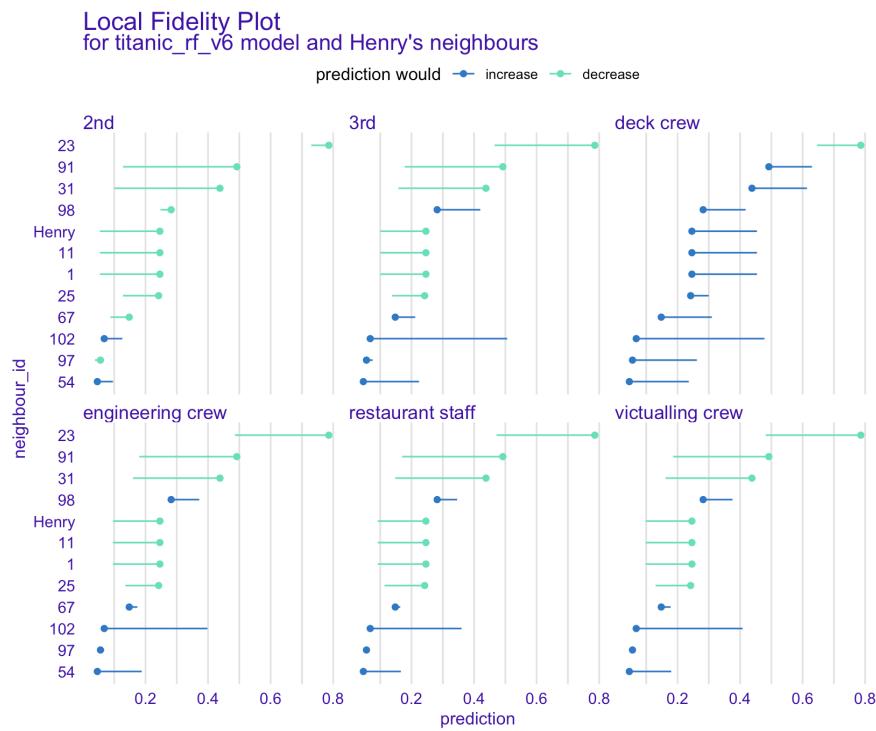


FIGURE 27 (fig:localFidelityPlots2) The local-fidelity plot for the categorical explanatory variable ‘class’ in the random effects model for the Titanic data, Henry, and his 10 neighbors. Each panel indicates how the model prediction would change if the class changed from ‘1st’ to another one. Dots indicate original model predictions for the neighbors; the end of the interval corresponds to model prediction after changing the class. The top-left panel indicates that, for the majority of the neighbors, the change from the ‘1st’ to the ‘2nd’ class reduces the predicted value of the probability of survival. On the other hand, the top-right panel indicates that changing the class to ‘deck crew’ members increases the predicted probability.

```

library("randomForest")
explain_rf_v6 <- archivist::aread("pbiecek/models/9b971")

library("DALEX")
henry <- archivist::aread("pbiecek/models/a6538")
henry

##   class gender age sibsp parch fare embarked
## 1  1st    male  47      0      0   25 Cherbourg

```

We will show how to construct Figure 0.8.2. Toward this aim we need some number of passengers most similar to `henry`. To select the “neighbors”, we use the `select_neighbours()` function from the `ingredients` package. It returns `n` observations (by default, 20) most similar to the observation of interest according to the `distance` measure (by default, the Gower distance is used).

In the example below, we select 10 nearest neighbors to `henry` find from the `titanic` dataset. Note that the similarity is based only on two explanatory variables, `gender`, and `class`, as indicated in the argument `variables`.

```

library("ingredients")
henry_neighbors <- select_neighbours(titanic,
                                      henry,
                                      n = 10,
                                      variables = c("class", "gender"))

```

Now we are ready to plot profiles for Henry and his neighbors. First, we have got to calculate the corresponding profiles with `ceteris_paribus()` function introduced in Section 0.6.6.

```

cp_henry <- ceteris_paribus(explain_rf_v6,
                             henry,
                             variable_splits = list(age = seq(0,80,0.1)))
cp_henry_neighbors <- ceteris_paribus(explain_rf_v6,
                                       henry_neighbors,
                                       variable_splits = list(age = seq(0,80,0.1)))

```

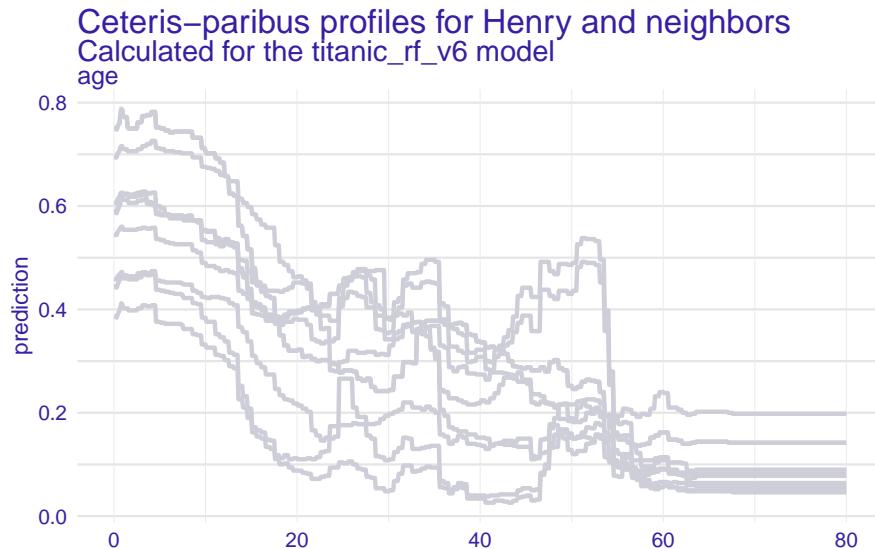
Subsequently, we can plot the profiles. Note that, in the example below, we do this only for a single variable `age`.

```

library("ggplot2")

plot(cp_henry_neighbors, color = '#ceced9') +
# show_profiles(cp_henry, size = 2) +
  ggtitle("Ceteris-paribus profiles for Henry and neighbors", "Calculated for the titanic_rf_v6 model")

```



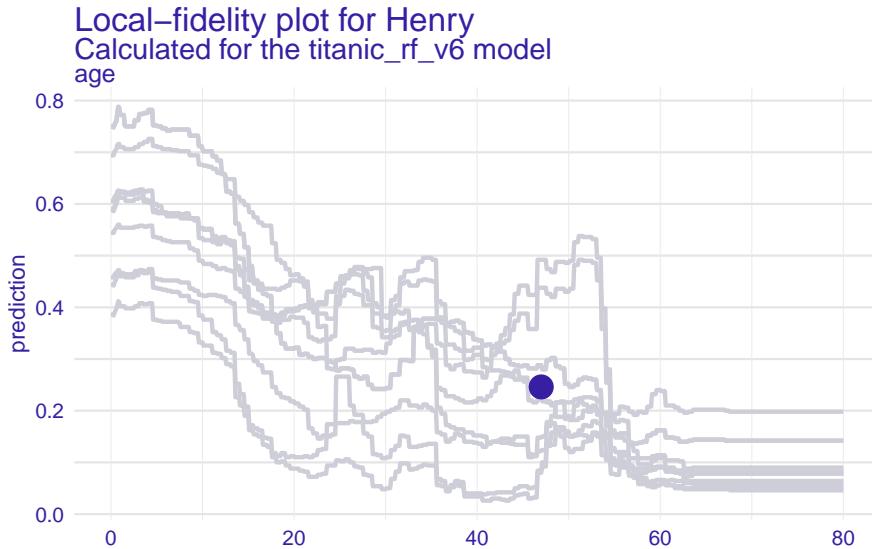
To construct the local-fidelity plot presented in Figure 26, we have got to add the information about the observed values of the dependent variable for the selected neighbors.

Toward this aim, we use the `y` argument in the `ceteris_paribus()` function. The argument takes numerical values. Our binary dependent variable `survived` assumes values `yes/no`; to convert them to numerical values, we use the `survived == "yes"` expression.

```
cp_henry_neighbors <- ceteris_paribus(explain_rf_v6,
                                         henry_neighbors,
                                         y = henry_neighbors$survived == "yes",
                                         variable_splits = list(age = seq(0,80,0.1)))
```

Finally, we add residuals to the plot by using the `show_residuals()` function. As a result, we obtain the local-fidelity plot for `henry`.

```
plot(cp_henry_neighbors, color = '#ceced9') +
# show_profiles(cp_henry, size = 2) +
show_observations(cp_henry, variables = "age", size = 5) +
# show_residuals(cp_henry_neighbors, variables = "age") +
ggtitle("Local-fidelity plot for Henry","Calculated for the titanic_rf_v6 model")
```



0.9 Break Down for Additive Variable Attributions

In the Section 0.7 we introduced a method for assessment of local variable importance based on Ceteris Paribus Profiles. But the main disadvantage of this method is that importance scores do not sum up to final model predictions.

In this chapter we introduce Break Down Plots which solve this problem. Note that the described method is also similar to the EXPLAIN algorithm introduced in (Robnik-Šikonja and Kononenko, 2008) and implemented in (Robnik-Sikonja, 2018) package.

0.9.1 Intuition

For any model we may repeat the intuition presented in the Section 0.25 to calculate variable contribution as shifts in expected model response after conditioning over consecutive variables. This intuition is presented in Figure 28.

Panel A shows distribution of model responses. The row `all data` shows the model response of the validation dataset. The red dot stands for average model response and it is an estimate of expected model response $E[f(x)]$.

Since we want to calculate effects of particular values of selected variables we then condition over these variables in a sequential manner. The next row in panel A corresponds to average model prediction for observations with variable `class` fixed to value `1st`. The next row corresponds to average model prediction with variables `class` set to `1st` and `age` set to `0`, and so on. The last row corresponds to model response for x_* .

Black lines in the panel A show how prediction for a single point changes after coordinate j is replaced by the x_*^j , so they span between $f(x)$ and $f(x^{j|x_*^j})$. But finally we are not

interested in particular changes, not even in distributions but only in averages - expected model responses.

The most minimal form that shows important information is presented in the panel C. Positive values are presented with green bars while negative differences are marked with red bar. They sum up to final model prediction, which is denoted by a violet bar in this example.

0.9.2 Method

Again, as in previous chapter, let $v(j, x_*)$ stands for the contribution of variable j to prediction of model f in point x_* .

We expect that such contribution will sum up to the model prediction in a given point (property called *local accuracy*), so

$$f(x_*) = v_0 + \sum_{j=1}^p v(j, x_*)$$

where v_0 stands for average model response (it may be different for different models).

Note that the equation above may be rewritten as

$$E[f(X)|X^1 = x_*^1, \dots, X^p = x_*^p] = E[f(X)] + \sum_{j=1}^p v(j, x_*)$$

what leads to quite natural proposition for $v(j, x_*)$, such as

$$v(j, x_*) = E[f(X)|X^1 = x_*^1, \dots, X^j = x_*^j] - E[f(X)|X^1 = x_*^1, \dots, X^{j-1} = x_*^{j-1}]$$

In other words the contribution of variable j is the difference between expected model response conditioned on first i variables minus the model response conditioned on first $j - 1$ variables.

To simplify notation, let's define a symbol $\Delta^{i|J}$ as

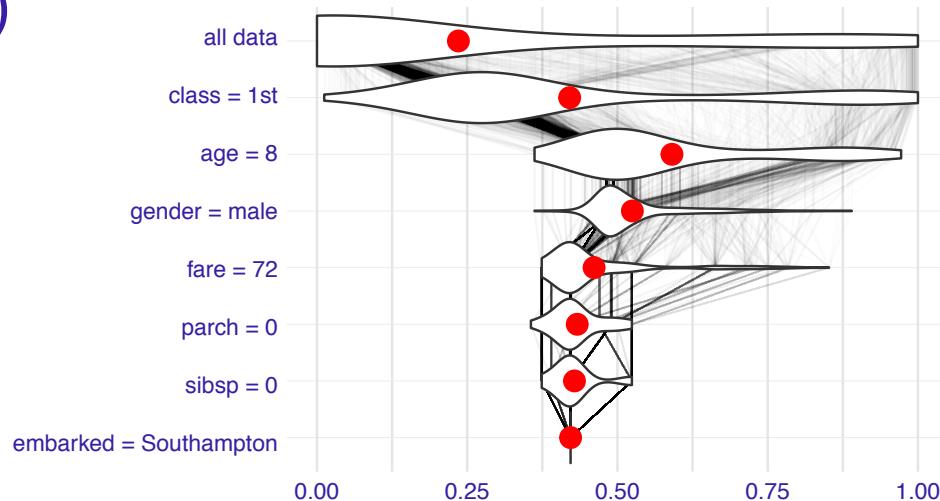
$$\Delta^{i|J} = E[f(X)|X^{J \cup \{i\}} = x_*^{J \cup \{i\}}] - E[f(X)|X^J = x_*^J],$$

So $\Delta^{i|J}$ is the change between expectation over variables from the set $J \cup \{i\}$ minus expectation over variables from the set J .

Then

$$v(j, x_*) = \Delta^{j|\{1, \dots, j-1\}}.$$

A)



B)



C)

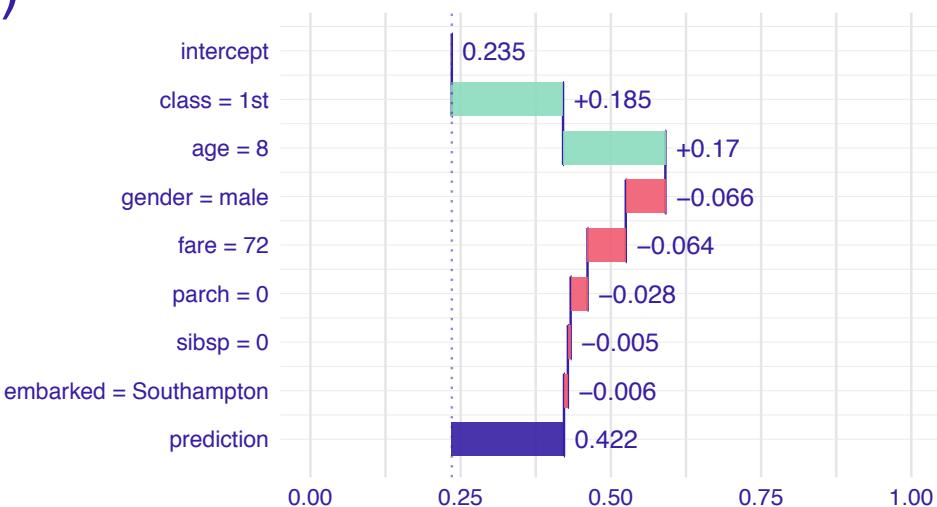


FIGURE 28 (fig:BDPrice4) Break Down Plots show how variables move the model prediction from population average to the model prognosis for a single observation. A) The first row

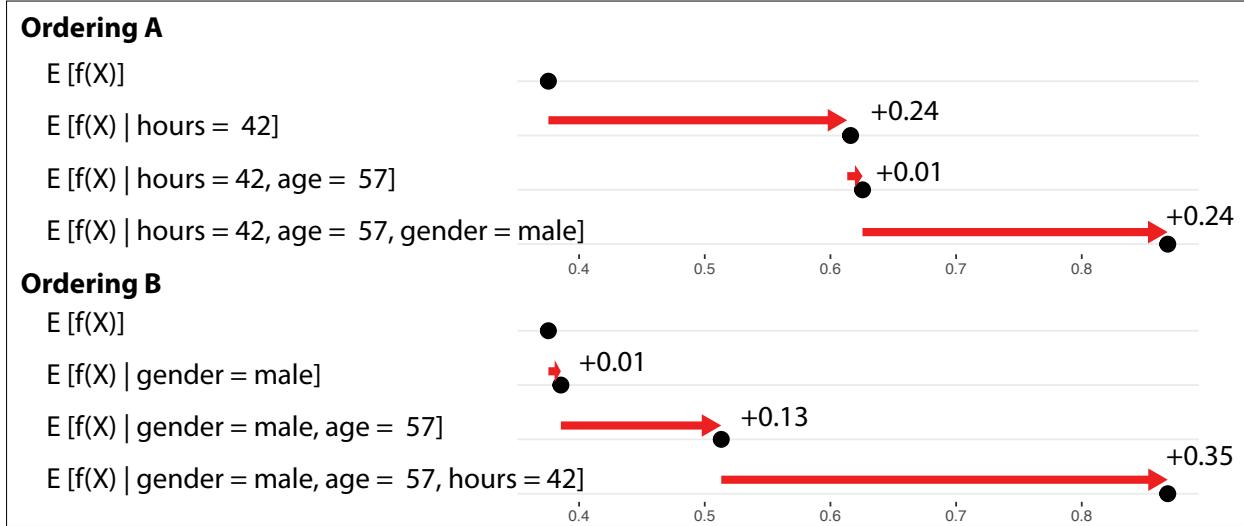


FIGURE 29 (fig:ordering) Two different paths between average model prediction and the model prediction for a selected observation. Black dots stand for conditional average, red arrows stands for changes between conditional averages.

Such proposition fulfills the *local accuracy* condition.

Unfortunately, for non-additive models, variable contributions depend on the ordering of variables. See for example Figure 29. In the first ordering the contribution of variable `age` is calculated as 0.01, while in the second the contribution is calculated as 0.13. Such differences are related to the lack of additivness of the model $f()$.

There are different attempts to solve the problem with the ordering.

A. choose an ordering in which variables with largest contributions are first. In this chapter we will describe a heuristic behind this approach. B. identify interactions that causes difference in attributions for different orderings and show these interactions. In the chapter 0.10 we will describe a heuristic behind this idea. C. calculate average across all possible orderings. There is $p!$ possible orderings, be the may quite accurately approximate the average. This approach will be presented in the chapter 0.11.

So, let's start with approach A. The easiest way to solve this problem is to use two-step procedure. In the first step variables are ordered and in the second step the consecutive conditioning is applied to ordered variables.

First step of this algorithm is to determine the order of variables for conditioning. It seems to be reasonable to include first variables that are likely to be most important, leaving the noise variables at the end. This leads to order based on following scores

$$\Delta^j = |E[f(X)] - E[f(X)|X^j = x_*^j]|$$

Note, that the absolute value is needed as variable contributions can be both positive and negative.

Once the ordering is determined in the second step variable contributions are calculated as

$$v(j, x_*) = E[f(X)|X^{J \cup \{i\}} = x_*^{J \cup \{i\}}] - E[f(X)|X^J = x_*^J] = \Delta^{i|J}$$

where J is the set of variables that have scores Δ^j smaller than score for variable i .

$$J = \{j : \Delta^j < \Delta^i\}$$

The time complexity of the first step is $O(p)$ where p is the number of variables and the time complexity of the second step is also $O(p)$.

0.9.3 Example: Titanic

Let us consider a random forest model `titanic_rf_v6` and the passenger `johny_d` as defined in section 0.4.1.7.

Average model response for all passengers for this model is $v_0 = 0.2356585$. For each coordinate of `johny_d` we can calculate scores Δ^j and they are presented in the table 0.5. These scores determine the order in which we do the conditioning.

TABLE 0.5: For each variable we calculated scores Δ^j . These scores are sorted in the decreasing order.

variable j	$E[f(X : x^j = x_*^j)]$	Δ^j
age	0.7407795	0.5051210
class	0.6561034	0.4204449
fare	0.6141968	0.3785383
sibsp	0.4786182	0.2429597
parch	0.4679240	0.2322655
embarked	0.4602620	0.2246035
gender	0.3459458	0.1102873

Once the order is determined we can calculate sequential contributions $\Delta^{i|J}$. For `johny_d` and the model unde consideration, these coefficients are listed in Table 0.6.

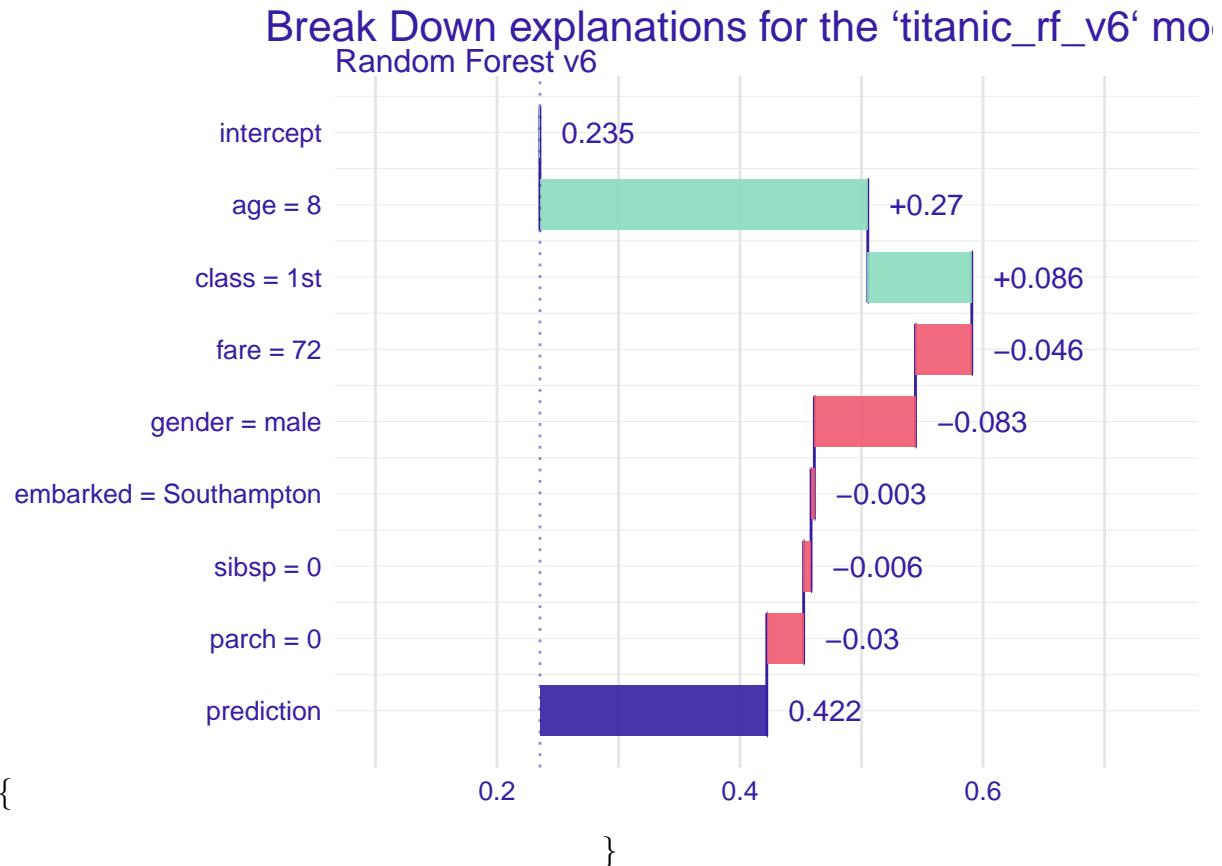
TABLE 0.6: Following order defined by Δ^i we calculate sequential conditioning $E[f(X|x^I = x_*^I)]$ where I is an increasing set of already considered coefficients.

variable i	$E[f(X : x^I = x_*^I)]$	$\Delta^{i J}$
intercept	0.2353095	0.2353095

variable i	$E[f(X : x^I = x_*^I)]$	$\Delta^{i J}$
age = 8	0.5051210	0.2698115
class = 1st	0.5906969	0.0855759
fare = 72	0.5443561	-0.0463407
gender = male	0.4611518	-0.0832043
embarked = Southampton	0.4584422	-0.0027096
sibsp = 0	0.4523398	-0.0061024
parch = 0	0.4220000	-0.0303398
prediction	0.4220000	0.4220000

These results can be visually presented with waterfall plot as in the Figure 0.9.3.

\begin{figure}



\caption{(fig:BDjohnyExample) Break Down explanations for the `titanic_rf_v6` model and `johnny_d` passenger.} \end{figure}

0.9.4 Pros and cons

Break Down approach is model agnostic, can be applied to any predictive model that returns a single number. It leads to additive variable attribution. Below we summarize key strengths and weaknesses of this approach.

Pros

- Break Down Plots are easy to understand and decipher.
- Break Down Plots are compact; many variables may be presented in a small space.
- Break Down Plots are model agnostic yet they reduce to intuitive interpretation for linear Gaussian and generalized models.
- Complexity of Break Down Algorithm is linear in respect to the number of variables.

Cons

- If the model is non-additive then showing only additive contributions may be misleading.
- Selection of the ordering based on scores is subjective. Different orderings may lead to different contributions.
- For large number of variables the Break Down Plot may be messy with many variables having small contributions.

0.9.5 Code snippets for R

In this section we present key features of the `iBreakDown` package for R (Gosiewska and Biecek, 2019a) which is a part of `DrWhy.AI` universe. This package covers all features presented in this chapter. It is available on CRAN and GitHub. Find more examples at the website of this package <https://modeloriented.github.io/iBreakDown/>.

In this section, we use a random forest classification model developed in the chapter 0.4.1, namely the `titanic_rf_v6` model. It is trained to predict probability of survival from sinking of Titanic. Instance level explanations are calculated for a single observation `johny_d` - 8 years old passenger that travels 1st class.

`DALEX` explainers for both models and the Henry data are retrieved via `archivist` hooks as listed in Chapter 0.4.1.7.

```
library("randomForest")
explain_rf_v6 <- archivist::aread("pbiecek/models/9b971")

library("DALEX")
johny_d <- archivist::aread("pbiecek/models/e3596")
johny_d
```

0.9.5.1 Basic usage for the `break_down` function

The `iBreakDown::break_down()` function calculates Break Down contributions for a selected model around a selected observation.

The result from `break_down()` function is a data frame with additive attributions for selected observation.

The simplest use case is to set only the arguments - model explainers and observation of interest.

Note that the table below recreates values presented in Table 0.6.

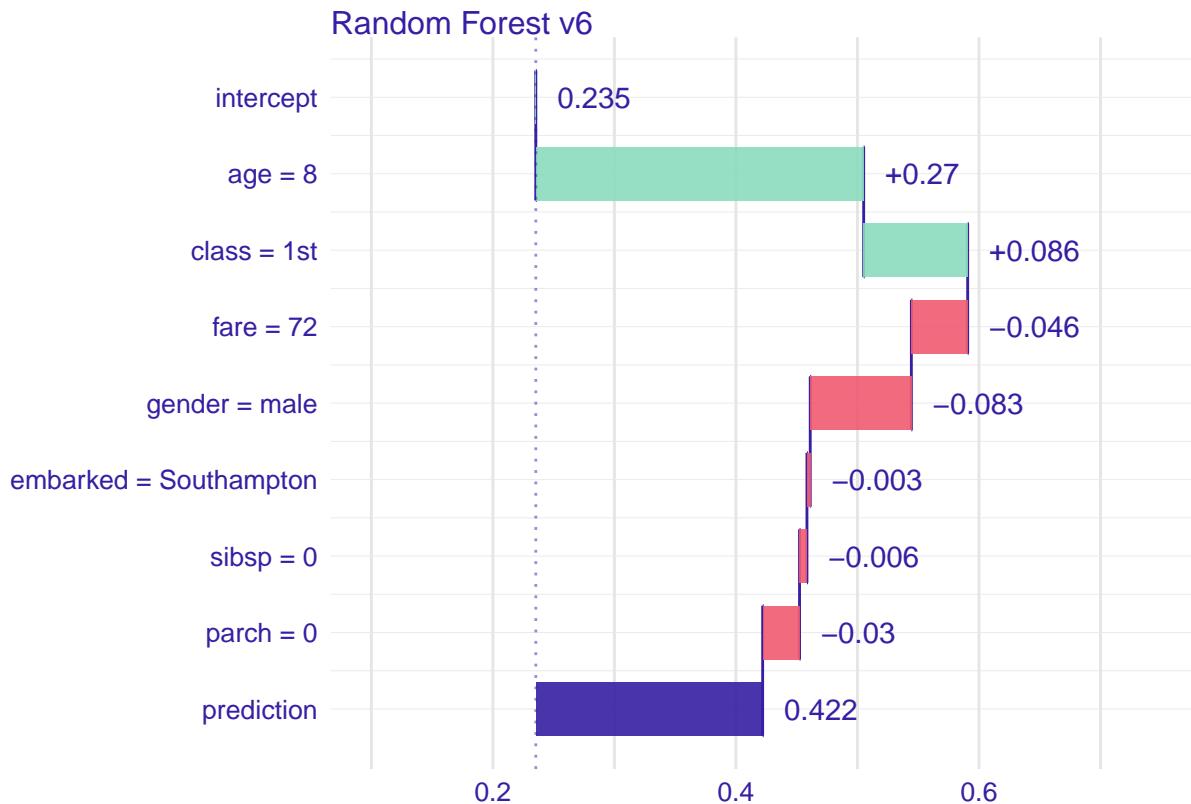
```
library("iBreakDown")
bd_rf <- break_down(explain_rf_v6,
                      johny_d)
bd_rf
```

	contribution
## Random Forest v6: intercept	0.235
## Random Forest v6: age = 8	0.270
## Random Forest v6: class = 1st	0.086
## Random Forest v6: fare = 72	-0.046
## Random Forest v6: gender = male	-0.083
## Random Forest v6: embarked = Southampton	-0.003
## Random Forest v6: sibsp = 0	-0.006
## Random Forest v6: parch = 0	-0.030
## Random Forest v6: prediction	0.422

The generic `plot()` function creates Break Down plots.

Note that the plot below recreates Figure 0.9.3.

```
plot(bd_rf)
```



0.9.5.2 Advanced usage for the `break_down` function

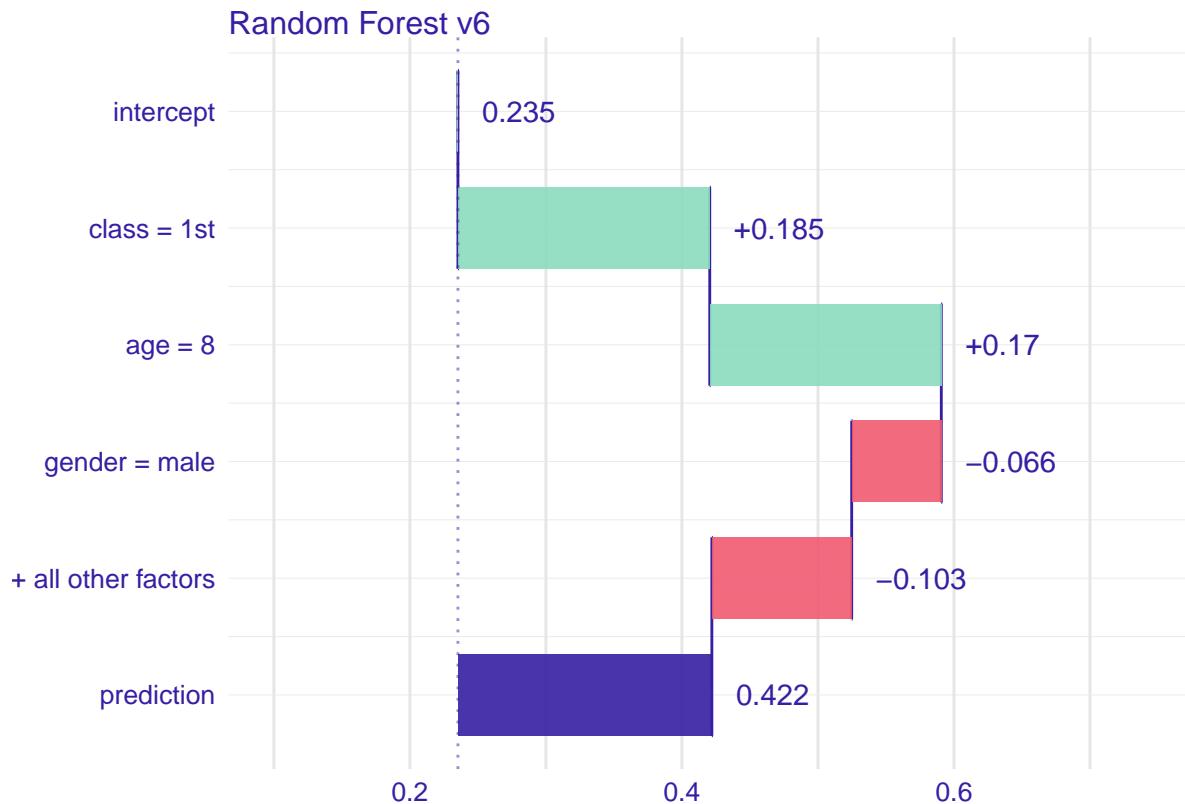
The function `break_down()` can take more arguments. The most commonly used are:

- `x` a wrapper over a model created with function `DALEX::explain()`,
- `new_observation` an observation to be explained is should be a data frame with structure that matches the training data,
- `order` if specified then it can be a vector of characters (column names) or integers (column indexes) that specify order of variable conditioning. If not specified (default) then a one-step heuristic is used to determine the order,
- `keep_distributions` logical value.
if `TRUE`, then additional diagnostic information is about conditional distributions is stored and can be plotted with the generic `plot()` function.

Let's see these additional arguments in action.

First we will specify `order`. You can use integer indexes or variable names. Note that the second option is in most cases better because of higher readability. Additionally, to reduce clutter in the plot we set `max_features = 3` argument in the `plot()` function.

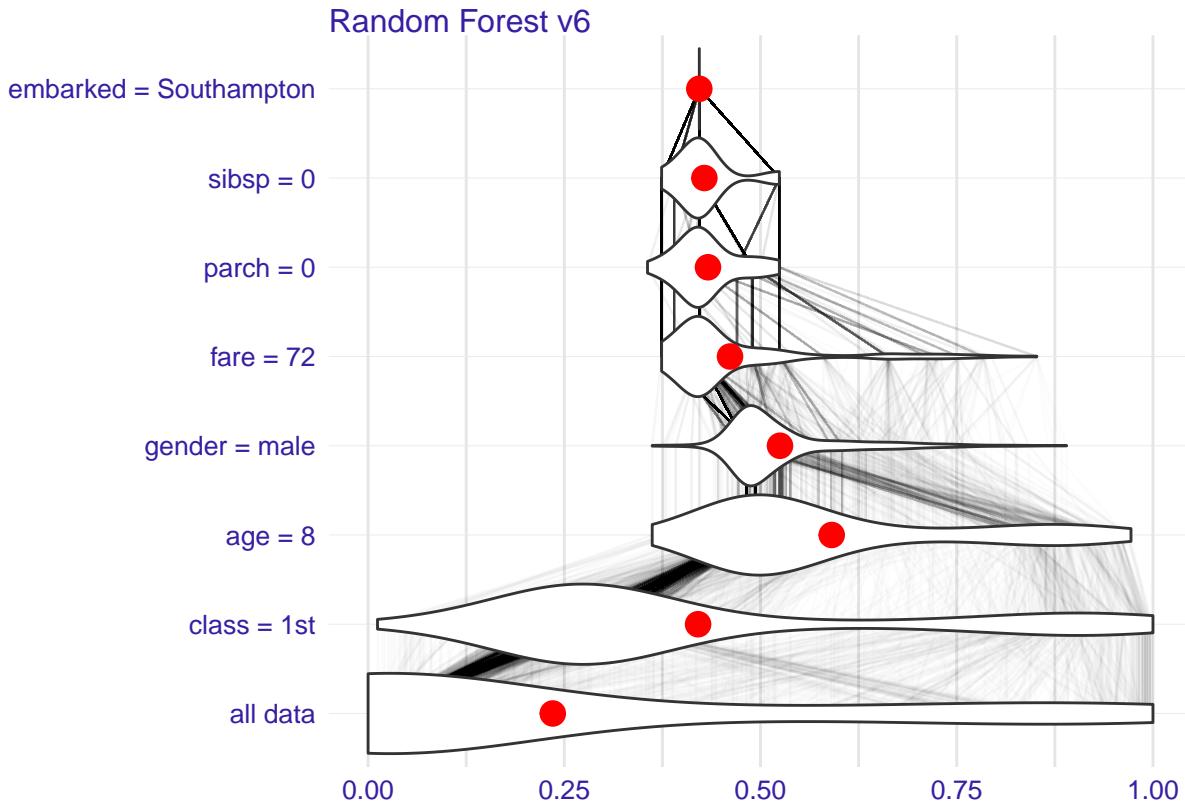
```
library("iBreakDown")
bd_rf_order <- break_down(explain_rf_v6,
                           johny_d,
                           order = c("class", "age", "gender", "fare", "parch", "sibsp", "embarked"))
plot(bd_rf_order, max_features = 3)
```



The `plot_distributions = TRUE` argument of `break_down()` function enriches model response with additional information about conditional distribution.

It can be presented after setting `plot_distributions = TRUE` in the `plot()` function. Conditional distributions are presented as vioplots. Red dots stand for conditional average model response. Thin black lines between vioplots correspond to predictions for individual observations. With them we can trace how model predictions change after consecutive conditioning.

```
bd_rf_distr <- break_down(explain_rf_v6,
  johny_d,
  order = c("class", "age", "gender", "fare", "parch", "sibsp", "embarked"),
  keep_distributions = TRUE)
plot(bd_rf_distr, plot_distributions = TRUE)
```



0.10 iBreakDown for Variable Attributions with Interactions

In the Section 0.9 we presented a model agnostic approach to additive decomposition of model predictions. We also showed that for non-additive models the proposed attribution depends on the ordering of variables.

Lack of additivity means, that effect of one variable is modulated by another variable(s). In such pair (or larger tuple) a single variable does not contribute independently, therefore in model explanations they should be presented together.

In this section we present an algorithm that identifies interactions between pairs of variables and include such interactions in variable decomposition plots. Here we present an algorithm for pairs of variables, but it can be easily generalized to larger number of variables.

0.10.1 Intuition

First, let's see an example of an interaction between two variables. We will use real data from the Titanic dataset. Table 0.7 shows survival statistics for men on Titanic. For the sake of simplicity, in this example we consider only two variables - `age` and `class`. In the

data `age` is a continuous variable, but again, for simplicity we have dychotomized it into two levels: boys (0-16 years old) and adults (17+ years old).

Suppose that we would like to explain factors that contribute to the survival of kids from the second class. As we can read, the survival for young passengers from 2nd class is 91.7% (survived 11 out of 12 male passengers in this group). It is higher than survival for men on titanic which is 20.5% (survived 352 out of 1716 men). So the question is, how age and class contribute to this higher survival?

Let us consider two explanations, that correspond to two different orderings:

- Overall men survival is 20.5%, but when we condition on male passengers from 2nd class the survival is even lower, i.e. 13.5%. Thus effect of the 2nd class is negative, it decreases the probability of survival by 7 percent points. Being a kid in the 2nd class is very lucky though. It changes of survival increase from 13.5% (male 2nd class) to 91.7% (boys from 2nd class). It's an increase by 78.2 percent points. So the contributions are -7% for class and +78.2% for age.
- Overall men survival is 20.5%, but when we condition on young man then the survival is higher, i.e. 40.7%. Thus the effect of age is positive, being a boy increases the probability of survival by 20.2 percent points. Being a kid in 2nd class is even better, it changes the survival increase from 40.7% (boys) to 91.7% (boys from 2nd class). It's an increase by 51 percent points. So the contributions are +51% for class and +20.2% for age.

As we see these two paths leads to two very different explanations. They differ not only in the size but also in the sign of attributed importance. It has happened because one variable modulates effect on the second variable as the model is not additive. Below we will show how to deal with such cases.

TABLE 0.7: Survival rates for men on Titanic. Ratios show how many survived in each Class/Age category.

Class / Age	Kids (0-16)	Adults (>16)	Total
1st	5/5 = 100%	57/175 = 32.6%	62/180 = 34.4%
2nd	11/12 = 91.7%	13/166 = 7.8%	24/178 = 13.5%
3rd	17/61 = 27.9%	58/430 = 13.5%	75/491 = 15.3%
deck crew		43/66 = 65.2%	43/66 = 65.2%
engineering crew		71/324 = 21.9%	71/324 = 21.9%
restaurant staff		1/67 = 1.5%	1/67 = 1.5%
victualling crew	0/3 = 0%	76/407 = 18.7%	76/410 = 18.5%
Total	33/81 = 40.7%	319/1635 = 19.5%	352/1716 = 20.5%

The key intuition behind an iBreakDown algorithm is to include variable interactions to the visual explanations. To do this we need to identify some candidates for interactions.

Here we propose a very simple algorithm that will do this in two steps.

1. First it will calculate variable contributions for each variable independently.

2. Second it will calculate joint effect for each pair of variables. If this effect is different than the sum of separate variables then such pair is identified as candidate for an interaction.

0.10.2 Method

Identification of interactions in the model is performed in three steps ([Gosiewska and Biecek, 2019a](#))

- Calculate a *single-step* contribution for each variable.
- Calculate a *single-step* contribution for every pair of variables. Subtract individual contributions to assess the size of non additivity.
- Order interaction effects and additive effects in a list to determine the final order for conditioning/explanations.

This simple intuition may be generalized into higher order interactions.

0.10.2.1 Single step contributions

For a feature x_i we may define a single-step contribution as

$$\Delta^j = \mathbb{E}[f(x)|x^j = x_*^j] - \mathbb{E}[f(x)].$$

The expected model prediction $\mathbb{E}[f(x)]$ is sometimes called baseline or intercept and may be denoted as Δ_\emptyset .

Expected value $\mathbb{E}[f(x)|x^j = x_*^j]$ corresponds to an average prediction of a model f if feature x_j is fixed on x_*^j coordinate from the observation to explain x_* .

I.e. the Δ^j is the difference between expected model response after conditioning on j variable minus the expected model response. Δ^j measures a naive single-step local variable importance, it indicates how much the average prediction of model f changes if feature x^j is set on x_*^j .

0.10.2.2 Two steps contributions

For a pair of variables x_i, x_j we introduce a single-step contribution as

$$\Delta^{ij} = \mathbb{E}[f(x)|x^i = x_*^i, x^j = x_*^j] - \mathbb{E}[f(x)].$$

And non additive component of this contribution as

$$\Delta_I^{ij} = \mathbb{E}[f(x)|x^i = x_*^i, x^j = x_*^j] - \mathbb{E}[f(x)|x^i = x_*^i] - \mathbb{E}[f(x)|x^j = x_*^j] + \mathbb{E}[f(x)].$$

Or equivalently

$$\Delta_I^{ij} = \Delta^{ij} - \Delta^i - \Delta^j.$$

0.10.2.3 Sequential contributions

The Δ_I^{ij} is the difference between collective effect of variables x^i and x^j denoted as Δ^{ij} and their additive effects Δ^i and Δ^j . Therefore, Δ_I^{ij} measures the importance of local lack-of-additivnes (aka. interaction) between features i and j . For additive models Δ_I^{ij} should be small~for any i, j .

Note that contributions Δ^i do not sum to final model prediction. We only use them to determine the order of features in which the instance shall be explained. To calculate contributions that have the property of *local accuracy* we need to introduce one more symbol, that corresponds to the added contribution of feature i to the set of features $\sim J$.

$$\Delta^{i|J} = \mathbf{E}[f(X)|x^{J \cup \{i\}} = x_*^{J \cup \{i\}}] - \mathbf{E}[f(X)|x^J = x_*^J] = \Delta^{J \cup \{i\}} - \Delta^J.$$

And for pairs of features

$$\Delta^{ij|J} = \mathbf{E}[f(X)|x^{J \cup \{i,j\}} = x_*^{J \cup \{i,j\}}] - \mathbf{E}[f(X)|x^J = x_*^J] = \Delta^{J \cup \{i,j\}} - \Delta^J.$$

Once the order of single-step importance is determined based on Δ^i and Δ_I^{ij} scores, the final explanation is the attribution to the sequence of $\Delta^{i|J}$ scores. These contributions sum up to the model predictions, because

$$\Delta^{1,2,\dots,p} = f(x_*) - E[f(X)].$$

This approach can be generalized to interactions between any number of variables.

The complexity of the calculation of single step attributions is $O(p)$ where p stands for the number of variables, while complexity for all pairs is $O(p^2)$. The complexity of the consecutive conditioning is $O(p)$, thus the complexity of whole algorithm is $O(p^2)$.

0.10.3 Example: Titanic

In this example we will use a random forest model for Titanic data and Johny D example - an 8 years old boy from 1st class.

In Table 0.8 we showed expected model responses $\mathbb{E}[f(x)|x^i = x_*^i, x^j = x_*^j]$, single-step effects Δ^{ij} and non-additive effects Δ_I^{ij} for each variable and each pair of variables. All

these values are calculated locally for Johny D. These values are sorted along local importance, most important to the top.

Based on this ordering a following sequence of variables are indentified as informative: `age`, `fare:class`, `gender`, `embarked`, `sibsp` and `parch`.

Once the ordering is specified, in the table 0.9 we showed how the sequential attribution is calculated. These values are then presented in the iBreakDown plot 30.

TABLE 0.8: For each variable and each pair of variables we calculated the expected conditional model response, the difference between conditional model response and the baseline and for pairs of variables the non-additive contribution. Rows are sorted according to the absolute value of the last column (if provided).

Variable	$E[f(x) : x^{ij} = x_*^{ij}]$	Δ^{ij}	Δ_I^{ij}
age	0.505	0.270	
fare:class	0.333	0.098	-0.231
class	0.420	0.185	
fare:age	0.484	0.249	-0.164
fare	0.379	0.143	
gender	0.110	-0.125	
age:class	0.591	0.355	-0.100
age:gender	0.451	0.215	0.070
fare:gender	0.280	0.045	0.027
embarked	0.225	-0.011	
embarked:age	0.504	0.269	0.010
parch:gender	0.100	-0.136	-0.008
sibsp	0.243	0.008	
sibsp:age	0.520	0.284	0.007
sibsp:class	0.422	0.187	-0.006
embarked:fare	0.374	0.138	0.006
sibsp:gender	0.113	-0.123	-0.005
fare:parch	0.380	0.145	0.005
parch:sibsp	0.236	0.001	-0.004
parch	0.232	-0.003	
parch:age	0.500	0.264	-0.002
embarked:gender	0.101	-0.134	0.002
embarked:parch	0.223	-0.012	0.001
fare:sibsp	0.387	0.152	0.001
embarked:class	0.409	0.173	-0.001
gender:class	0.296	0.061	0.001
embarked:sibsp	0.233	-0.002	0.001
parch:class	0.418	0.183	0.000



FIGURE 30 (fig.iBreakDownTitanicExamplePlot) Break Down Plots with interactions for Johny D.

TABLE 0.9: Based on identified order we calculated the expected conditional model response and the difference between conditional model response with and without a specified variable. These values are plotted in the iBreak-Down plot.

Variable	$\Delta^{i:J}$	$\Delta^{J \cup \{i\}}$
intercept		0.235
age = 8	0.269	0.505
fare:class = 72:1st	0.039	0.544
gender = male	-0.083	0.461
embarked = Southampton	-0.002	0.458
sibsp = 0	-0.006	0.452
parch = 0	-0.030	0.422

0.10.4 Pros and cons

Break Down for interactions shares many features of Break Down for single variables. Below we summarize unique strengths and weaknesses of this approach.

Pros

- If interactions are present in the model, then additive contributions may be misleading. In such case the identification of interactions leads to better explanations.
- Complexity of Break Down Algorithm is quadratic, what is not that bad if number of features is small or moderate.

Cons

- For large number of variables, the consideration of all interactions is both time consuming and sensitive to noise as the number of pairs grow faster than number of variables.
- Identification of interaction is not based on significance testing, it's purely based on absolute empirical effects, thus for small samples this procedure is prone to errors.

0.10.5 Code snippets for R

In this section we present key features of the `iBreakDown` package for R (Gosiewska and Biecek, 2019a). This package covers all features presented in this chapter. It is available on CRAN and GitHub. Find more examples at the website of this package

<https://modeloriented.github.io/iBreakDown/>.

All steps are very similar to these presented in the previous chapter for variable attributions. The only difference is that the `break_down()` function will now take `interactions = TRUE` argument.

Model preparation

As in previous chapters we will use the random forest (Breiman et al., 2018) model `titanic_rf_v6` developed for the Titanic dataset (see Section 0.4.1). Using the same model will help us (1) to understand how the Break Down method works, (2) to compare these explanations against methods presented in previous chapters.

So let restore the `explain_rf_v6` explainer

```
library("randomForest")
explain_rf_v6 <- archivist::aread("pbiecek/models/9b971")

library("DALEX")
johny_d <- archivist::aread("pbiecek/models/e3596")
johny_d

##   class gender age sibsp parch fare      embarked
## 1   1st    male   8      0      0    72 Southampton
```

The `iBreakDown::break_down()` function calculates Break Down contributions for a selected model around a selected observation.

The result from `break_down()` function is a data frame with additive attributions for selected observation.

The simplest use case is to set only the arguments - model explainers and observation of interest.

By default only additive attributions are calculated. Use `interactions = TRUE` argument to look for interactions.

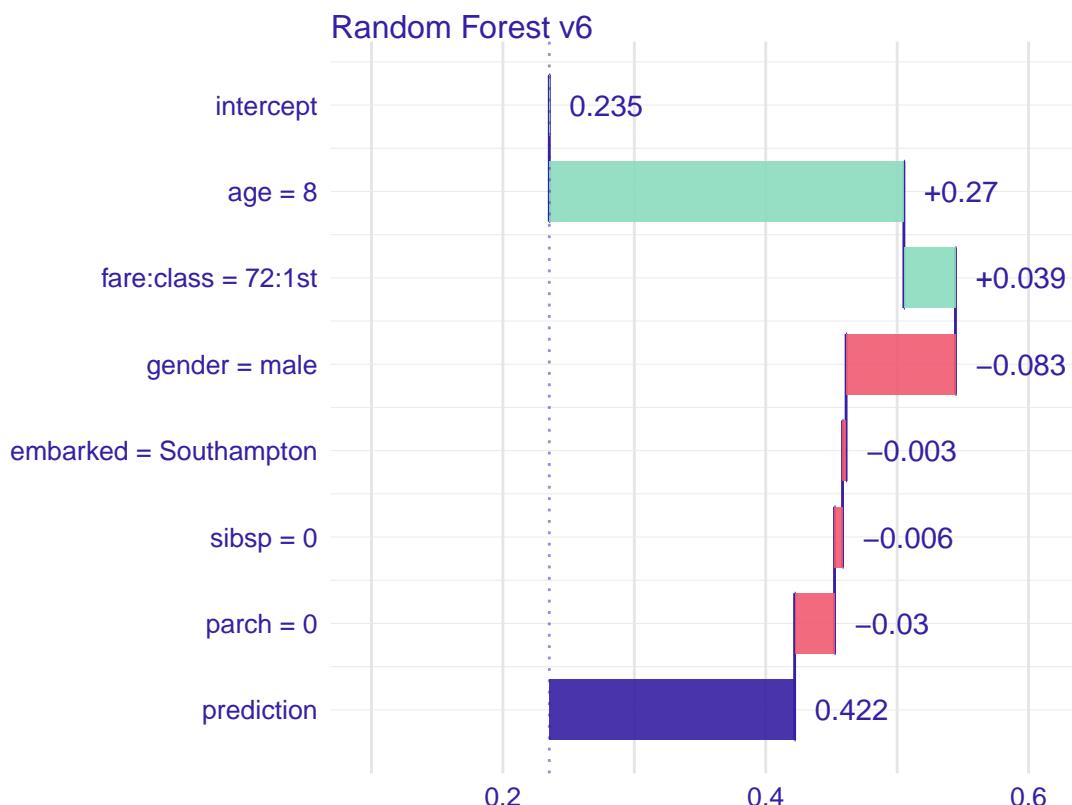
```
library("iBreakDown")
bd_rf <- break_down(explain_rf_v6,
                      johny_d,
                      interactions = TRUE)
```

```
bd_rf
```

	contribution
## Random Forest v6: intercept	0.235
## Random Forest v6: age = 8	0.270
## Random Forest v6: fare:class = 72:1st	0.039
## Random Forest v6: gender = male	-0.083
## Random Forest v6: embarked = Southampton	-0.003
## Random Forest v6: sibsp = 0	-0.006
## Random Forest v6: parch = 0	-0.030
## Random Forest v6: prediction	0.422

The generic `plot()` function creates a Break Down plots.

```
plot(bd_rf)
```



0.11 SHapley Additive exPlanations (SHAP) and Average Variable Attributions

In the Section 0.9 we show a procedure that attributes parts of model prediction to input features. We also show that in the presence of interactions attributions depend on the feature ordering. One solution to this problem is to find an ordering that put most important features to the front. Other solution is introduced in the Section 0.10 - identify interactions and show interactions in model explanations.

In this section we introduce another, very popular approach that deal with feature ordering. Basically, the problem of ordering is solved by averaging over all possible orderings. Or at least some large number of sampled orderings. Additionally, such average is closely linked with Shapley values developed originally for cooperative games.

This approach was first introduced in ([Strumbelj and Kononenko, 2010](#)) and ([Štrumbelj and Kononenko, 2014](#)). Wide adoption of this method comes with a NIPS 2017 paper ([Lundberg and Lee, 2017](#)) and python library SHAP ([Lundberg, 2019](#)). Authors of the SHAP (SHapley Additive exPlanations) method introduced an efficient algorithm for tree-based models ([Lundberg et al., 2018](#)) and show that Shapley values is an unification of a collection of different commonly used techniques for model explanations.

0.11.1 Intuition

Figure 31 shows Break Down attributions for 10 random orderings for Titanic dataset. As we see there are differences in feature attribution. The most striking ones are linked with features `fare` or `class`. Their attribution may be positive or negative depending on the ordering

SHAP attributions are averages across all (or at least large number) of different orderings. See for example Figure 32. In a single plot we summarize all orderings from Figure 31. Violet boxplots show distributions for attributions for a selected variable, while length of the bar stands for an average attribution.

0.11.2 Method

SHapley Additive exPlanations are based on *Shapley Values*, a solution concept in cooperative game theory developed by Lloyd Shapley.

Consider a following problem. A coalition of players cooperates, and obtains a certain overall gain from that cooperation. Players are not identical, different players may have different importance. Cooperation is beneficial, from cooperation they got more than from individual actions. The problem to solve is how to distribute the generated surplus among

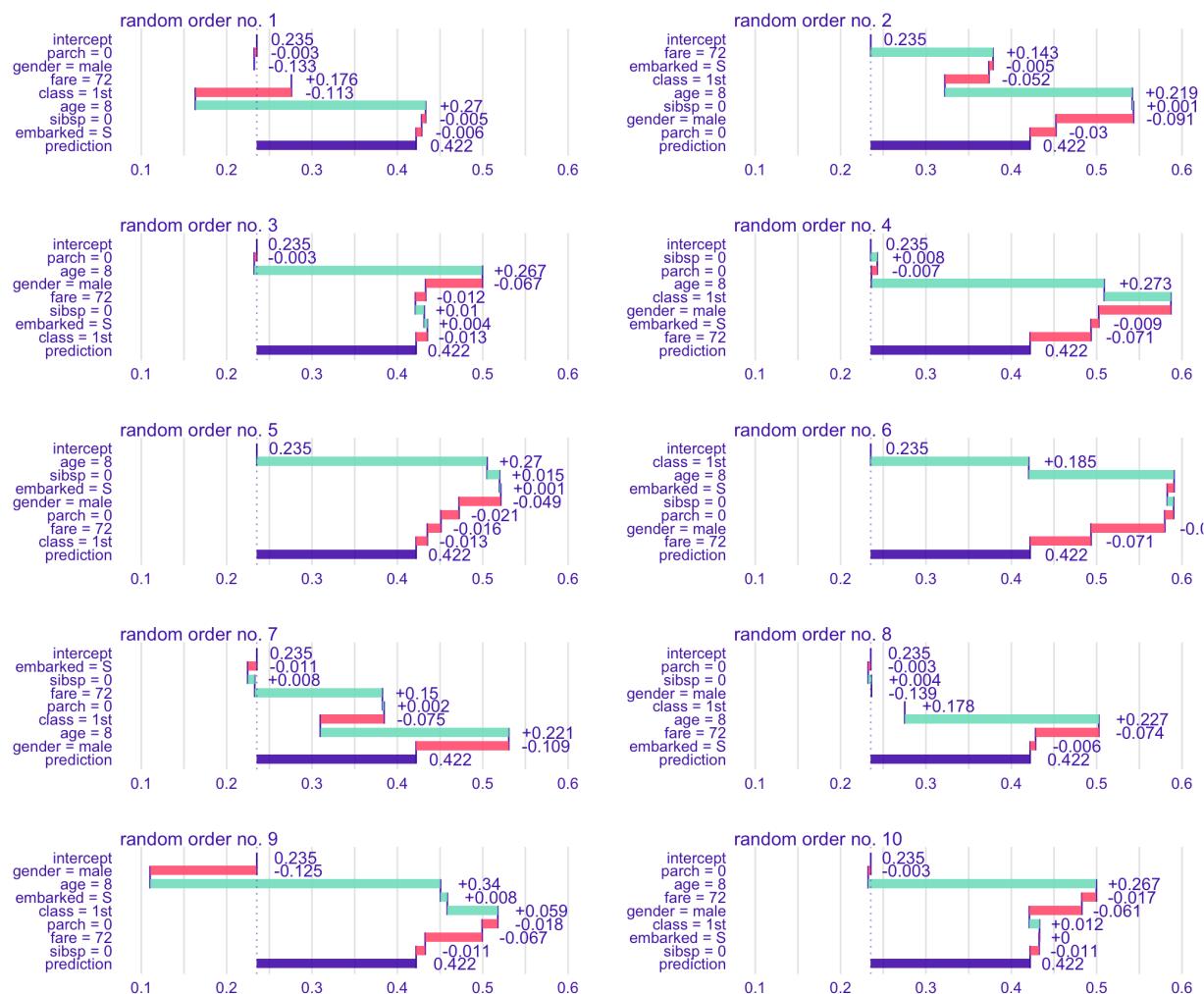


FIGURE 31 (fig:shap10orderings) Break Down plots for 10 random orderings. Each panel shows a single ordering

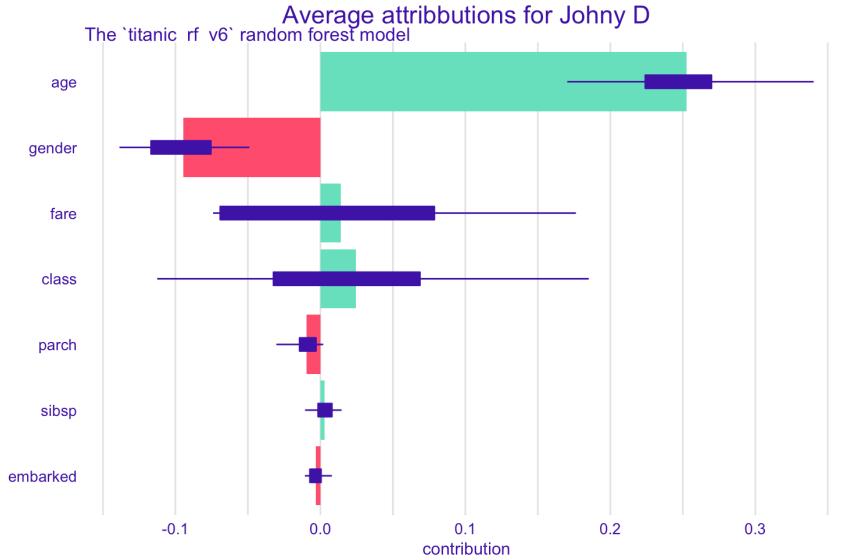


FIGURE 32 (fig:shapOrdering) Summary for 10 random orderings. Boxplots show distribution of feature attributions. Bars stand for average attributions.

the players? The Shapley value provides one possible fair answer to this question ([Shapley, 1953](#)).

Now let's translate this problem to machine learning settings. Instead of players we have features and instead of coalitions we have specific settings of values for features in the coalition. The payoff from a coalition is the model response for a selected setting. Problem to solve: how to distribute model response to particular features. Shapley values are defined for a single instance x^* . The idea of using Shapley values for feature attribution was introduced in ([Strumbelj and Kononenko, 2010](#)). Here we present a different notation more suited with approach presented in previous sections.

Let $v(S)$ stand for value of coalition of S features, defined as

$$v(x^*, S) = E[f(X)|X_S = x_S^*].$$

The value is defined as expected model response given features in the set S are set to values in the selected instance x^* . Expected value averages across all features that are not in the set S .

A special case is for empty coalition. Its value is an expected model response

$$v(x^*, \emptyset) = E[f(X)].$$

Shapley values may be defined as

$$\varphi(i) = \frac{1}{p!} \sum_{\pi} [v(x^*, \pi(i) \cup \{i\}) - v(x^*, \pi(i))]$$

where p is a number of all features, $p!$ is number of all possible orderings, π is an ordering

and $\pi(i)$ are all features in the ordering π that appear before feature i . Thus the $v(\pi(i) \cup \{i\}) - v(\pi(i))$ corresponds to a difference in value of a coalition $v(\pi(i))$ when feature i is added to it.

Of course for large p it is not feasible to consider all $p!$ permutations. A Monte Carlo estimator of this value was introduced in ([Štrumbelj and Kononenko, 2014](#)) and efficient implementation of Shapley values was introduced in ([Lundberg and Lee, 2017](#)). Later in this chapter we will use a crude estimator on $\varphi(i)$ in which instead of all $p!$ permutations we average across B randomly selected permutations.

Alternative formulation of Shapley values averages across coalitions not orderings.

$$\varphi(i) = \frac{1}{p} \sum_{S \subseteq \{1:p\} \setminus \{i\}} \binom{p-1}{|S|}^{-1} [v(x^*, S \cup \{i\}) - v(x^*, S)]$$

Note that the number of all subsets is 2^{p-1} is much smaller than number of all orderings $p!$. Binomial coefficients weight according to number of ordering with selected prefix coalition.

Properties

Shapley values are proven to be fair. And here fairness means that they are a single unique solution with following properties. Proved for cooperative games and then translated to machine learning.

- Symmetry. If two features are interchangeable, i.e. contribute equally to all coalitions

$$\forall_S v(x^*, S \cup \{i\}) = v(x^*, S \cup \{j\})$$

then they should have equal Shapley values

$$\varphi(i) = \varphi(j).$$

- Dummy feature. If a features does not contribute to any coalitions

$$\forall_S v(x^*, S \cup \{i\}) = v(x^*, S)$$

then it should have Shapley value equal to 0

$$\varphi(i) = 0.$$

- Additivity. If a model f is sum of two other models g and h then Shapley value calculated for model f is a sum of Shapley values for g and h .

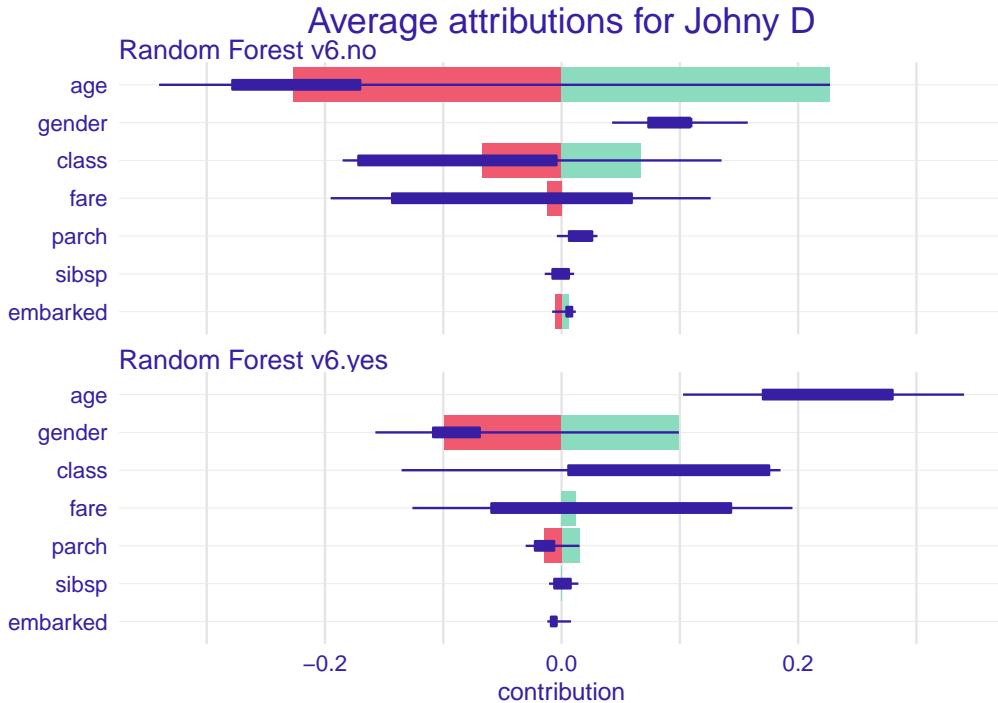


FIGURE 33 (fig:shappJohny02) Average attributions for Johny D. Violet boxplots show distributions of attributions.

- Local accuracy. Sum of Shapley values is equal to the model response

$$f(x^*) - v(x^*, \emptyset) = \sum_{i=1}^p \varphi(i).$$

0.11.3 Example: Titanic

Let us again consider explanation for prediction of the `titanic_rf_v6` model for *Johny D*, an 8-years old boy from 1st class.

In Figure 33 we have presented distribution of attributions for random 25 orderings. As we see, young age of Johny D has positive effect in all orderings. An average age-effect is equal 0.2525. Similarly, effect of being male is in all cases negative for this model, on average the negative effect is -0.0908 .

Things get complicated for `fare` and `class` features. Depending on the order one or another is largely positive or negative. In the section 0.10 we showed them as a pair, which should not be separated. Here we show average attributions for each feature.

Note, that in most applications the detailed information about distribution of orderings will be unnecessary complicated. So it is more common to keep only information about Shapley values as it is presented in Figure 34.

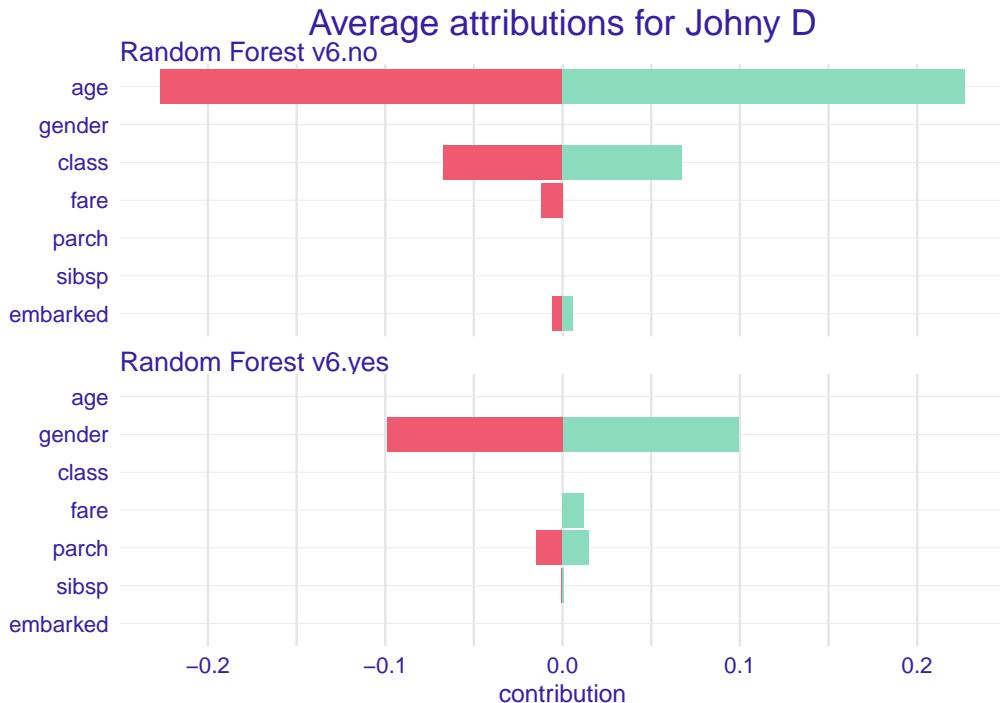


FIGURE 34 (fig:shappJohny01) Average attributions for Johny D.

Table 0.10 shows average attributions for Johny D.

TABLE 0.10: Average attributions for Johny D.

feature	avg. attribution
age = 8	0.2525
class = 1st	0.0246
embarked = Southampton	-0.0032
fare = 72	0.0140
gender = male	-0.0943
parch = 0	-0.0097
sibsp = 0	0.0027

0.11.4 Pros and cons

Shapley Values give a uniform approach to decompose model prediction into parts that can be attributed additively to variables. Below we summarize key strengths and weaknesses of this approach.

Pros

- There is a nice theory based on cooperative games.
- (Lundberg and Lee, 2017) shows that this method unifies different approaches to additive features attribution, like DeepLIFT, Layer-Wise Relevance Propagation, LIME.
- There is an efficient implementation available for Python and ports or reimplementations for R

0.11.5 Code snippets for R

In this section we present key features of the R package `iBreakDown` (Gosiewska and Biecek, 2019a) which is a part of `DrWhy.AI` universe and covers methods presented in this chapter. More details and examples can be found at <https://modeloriented.github.io/iBreakDown/>.

Note that there are also other R packages that offer similar functionality, like `shapper` (Gosiewska and Biecek, 2019b) which is a wrapper over SHAP python library (Lundberg, 2019) and `iml` (Molnar et al., 2018a).

In this section, we use the random forest (Breiman et al., 2018) model `titanic_rf_v6` developed for the Titanic dataset (see Chapter 0.4.1).

So let restore the `titanic_rf_v6` model and explainer created with the `explain()` function from `DALEX` package (Biecek, 2018).

```
library("randomForest")
explain_rf_v6 <- archivist::aread("pbiecek/models/9b971")

library("DALEX")
johny_d <- archivist::aread("pbiecek/models/e3596")
johny_d
```

Here again we will use a data frame `johny_d` with a single row, that describes an 8-years old boy that travels in the first class without parents and siblings. Then, we obtain the model prediction for this instance with the help of the ‘`predict()`’ function.

```
predict(explain_rf_v6, johny_d)

## [1] 0.422
```

First, we will recreate Figure 34. To do this we use function `iBreakDown::shap()` that calculates B random orderings and average Shapley contributions. This function takes an explainer created with `DALEX::explain()` function and an observation for which attributions shall be calculated. Additionally one can specify B number of orderings to sample.

The generic function `plot()` shows Shapley values with corresponding boxplots.

```
library("iBreakDown")

shap_johny <- shap(explain_rf_v6, johny_d, B = 25)
plot(shap_johny)
```

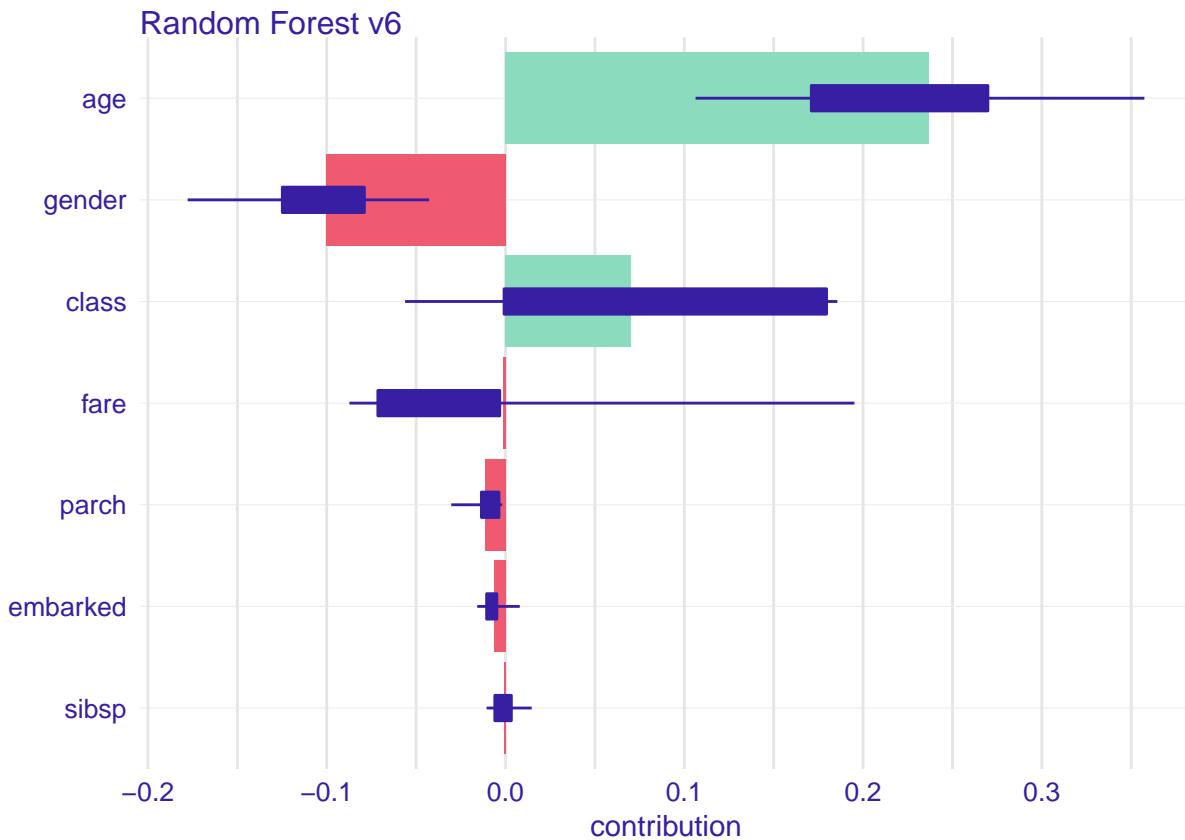
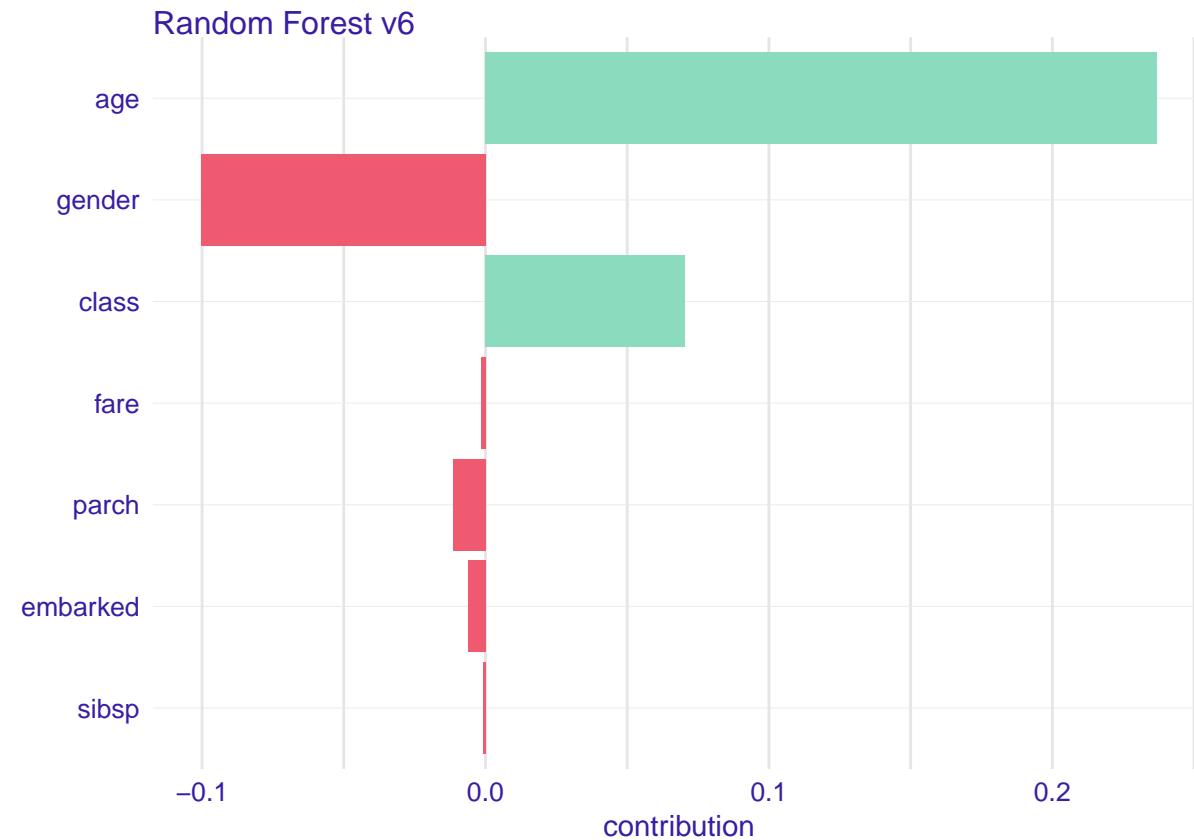


Figure 33 is generated in the same way. The only difference is that boxplots are not plotted.

Use the `show_boxplots` argument to decide whatever they shall be added or not.

```
plot(shap_johny, show_boxplots = FALSE)
```



Function `shap()` results a data frame with attributions for every ordering. Having all these values we can calculate not only Shapley values (averages) but also some other statistics, like quintiles or range for feature attributions.

```
shap_johny
```

```
##                                     min          q1      median
## Random Forest v6-age    0.10631717  0.1710566380  0.252221985
## Random Forest v6-class -0.05615224 -0.0008022202  0.060401903
## Random Forest v6-embarked -0.01580879 -0.0105541459 -0.007472134
## Random Forest v6-fare   -0.08729950 -0.0713928410 -0.045135931
## Random Forest v6-gender -0.17778251 -0.1248278206 -0.105988219
## Random Forest v6-parch  -0.03033983 -0.0134748527 -0.009966017
## Random Forest v6-sibsp -0.01059538 -0.0059755324 -0.001904848
##                                     mean          q3      max
## Random Forest v6-age    0.2370556593  0.269811509  0.357347531
## Random Forest v6-class  0.0703436701  0.179579067  0.185606706
## Random Forest v6-embarked -0.0063245310 -0.004847558  0.007968283
## Random Forest v6-fare   -0.0014576167 -0.003210340  0.195174445
## Random Forest v6-gender -0.1004931944 -0.078935433 -0.042726778
## Random Forest v6-parch  -0.0116046398 -0.003649751 -0.001842320
## Random Forest v6-sibsp -0.0008288174  0.003267784  0.014658813
```

```

library("dplyr")
shap_johny %>%
  group_by(variable) %>%
  summarise(avg = mean(contribution),
            q10 = quantile(contribution, 0.1),
            q90 = quantile(contribution, 0.9)) %>%
  arrange(-abs(avg))

## # A tibble: 7 x 4
##   variable      avg      q10      q90
##   <fct>        <dbl>     <dbl>     <dbl>
## 1 age         0.237    0.158    0.313
## 2 gender      -0.100   -0.133   -0.0555
## 3 class        0.0703   -0.0293   0.185
## 4 parch       -0.0116   -0.0303  -0.00304
## 5 embarked    -0.00632  -0.0124   0.00348
## 6 fare        -0.00146  -0.0714   0.146
## 7 sibsp       -0.000829 -0.00835  0.00824

```

0.12 Local Interpretable Model-Agnostic Explanations (LIME)

0.12.1 Introduction

Ceteris Paribus profiles introduced in the Chapter 0.6 work best for models with small number of interpretable features. In this case it makes sense to explore feature by feature and analyze how a single feature affects model predictions

Break Down and Shapley attributions introduced in the Chapter 0.9 work best for small and moderate number of features. These attributions are not as detailed as Ceteris Paribus profiles, but can handle more variables that are presented by narrow bars.

Both these approaches are not well suited for high-dimensional data. For instance in bioinformatics when working with gene expression, mutations or methylation it is not uncommon to have thousands or even million of features. If most of them are binary low/high, present/absent, wild/mutated then Ceteris Paribus and Break Down plots become unreadable. In such cases an useful alternatives are sparse explainers. The most popular example of such explainers is LIME and its modifications.

The LIME method was originally proposed in the paper *Why Should I Trust You?: Explaining the Predictions of Any Classifier* (Ribeiro et al., 2016). The acronym stands for Local Interpretable Model-Agnostic Explanations. The key idea behind this method is to locally approximate a black-box model by a sparse local glass-box surrogate model, which is easier to interpret.

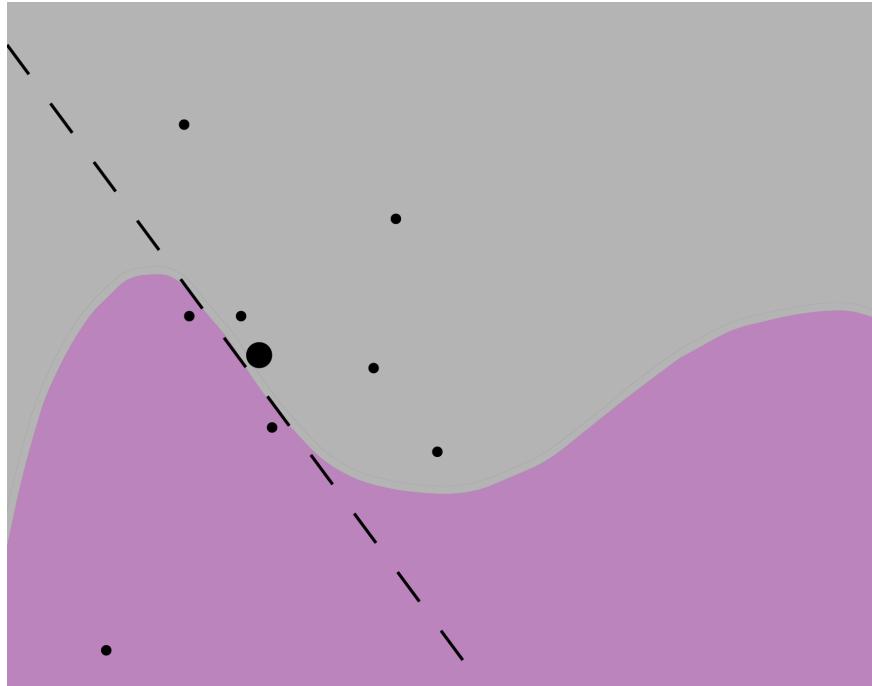


FIGURE 35 (fig:limeEx) A schematic idea behind local model approximations. Colors stand for decision regions for black-box model. We want to explain model decision for the largest black point. To do this we create artificial points around point of interest and train a glass-box model. Here it's a logistic regression presented as a dashed line.

0.12.2 Intuition

The intuition behind LIME is presented in Figure 35. We want to understand a complex black-box model around a single instance. Here the black box model is a binary classifier and colored areas in the plot correspond to its decision regions. We are interested in instance explanation, and the instance of interest is marked with large black dot. Having some artificial dataset around this black dot we can train a glass-box model that will locally approximate the black-box model. The glass-box model may then serve as local explainer for the complex model.

We may select different classes of glass-box models, e.g. linear models. The important part is to keep it sparse and low-dimensions, this way the surrogate model is easier to explain. The most typical choices for glass-box models are regularized linear models like LASSO regression or decision trees.

0.12.3 Method

The objective is to find a local model M_* that approximates a black box model f around the point of interest x_* . This intuition can be formalized in a following formula

$$M(x_*) = \arg \min_{g \in G} L(f, g, \Pi_{x_*}) + \Omega(g).$$

For a selected instance x_* we are looking for a local model g from the class G of interpretable models. The model shall be simple so we add penalty for the model complexity measured as $\Omega(g)$. And the white-box model g shall approximate well the black-box model f locally, where locality is defined by neighborhood Π_{x_*} of x^* . The L stands for some goodness of fit measure like for example likelihood.

Note that functions f and g may work on different data representations. The black-box $f(x) : \mathcal{X} \rightarrow \mathcal{R}$ works on original feature space \mathcal{X} while the glass-box function $g : \mathcal{X}' \rightarrow \mathcal{R}$ usually works on an interpretable feature space \mathcal{X}' , which is in many applications smaller.

We will present some examples for \mathcal{X}' in the next section, but for now let's just assume that function h transforms \mathcal{X} on \mathcal{X}' .

Let's limit the class G of interpretable models to sparse linear models. Following algorithm may be used to find an interpretable surrogate model that selects K most important interpretable features.

```

Input: N - length of sample for surrogate model
Input: K - length of explanation
1. Let  $x' = h(x)$  be an interpretable version of  $x$ 
2. for i in 1...N {
3.    $z'[i] \leftarrow \text{sample\_around}(x')$ 
4.    $y'[i] \leftarrow f(z[i])$  # prediction for a new observation
5.    $w'[i] \leftarrow \text{similarity}(x, z[i])$ 
6. }
7. return K-LASSO( $y'$ ,  $x'$ ,  $w'$ )

```

Where $K - LASSO(y', x', w')$ stands for weighted LASSO linear regression that selects K most important features based on new dataset (y', x') weighted with w' . This algorithm selects K most important interpretable features.

As it is presented in the paper (Ribeiro et al., 2016), the LIME method has following properties:

- *model-agnostic*, they do not imply any assumptions on model structure, f can be any function,
- *interpretable representation*, model input is transformed into a feature space that is easier to understand. One of applications comes from image data, single pixels are not easy to interpret, thus the LIME method decompose image into a series of super pixels, that are easier to interpret to humans,
- *local fidelity* means that the explanations shall be locally well fitted to the black-box model.

Where it comes to the implementation of this idea there are at least three important steps, which will be presented in consecutive subsections.



FIGURE 36 (fig:duckHorse06) The left panel shows an ambiguous picture, half horse and half duck. The right panel shows 100 superpixels identified for this figure.

0.12.3.1 Interpretable data representation

It is important to remember that functions f and g may work on different data representations.

For example, let's consider a VGG16 neural network trained for ImageNet data. Such network takes an image of the size 244x244 pixels as an input and predicts an image category out of 1000 classes. The original input space is $3 \times 244 \times 244 = 178608$ dimensional as single dimensional is a single color channel for a single pixel. Explanations in such input space would be hard to interpret. Instead, the input space is transformed into superpixels - binary features that can be turned on or off. Figure 36 shows an example 100 superpixels created for some ambiguous picture.

In this case the black box model f works on \mathcal{X} which is \mathcal{R}^{178608} while g works on interpretable binary space of 100 superpixels $\mathcal{X}' = [0, 1]^{100}$.

Superpixels are frequent choices for image data. For text data words are frequently used as interpretable features. For tabular data sometimes continuous features are discretized.

0.12.3.2 Sampling around point of interest

In order to fit surrogate local model g we need new data points around point of interest. It is not enough to sample points from original dataset, because in very highdimensional space the input dataset is very sparse and points are „far” from each other.

This is why the training data for surrogate model is created through some perturbations of the point of interest.

For binary interpretable input space the common choice is to sample subset of features (i.e. new datapoints are the point of interest with some random number of features switched to 0).

For nonbinary features various propositions are introduced in different papers.

In our example with the duck-horse samples around the image are subsets of superpixels.

0.12.3.3 Fitting a glass-box model

Once the new data are sampled around the point of interest we are ready to create an interpretable model g from class G .

The most common choices for G are linear models (for regression) or generalized linear models (for classification). In order to get sparse models the LASSO or similar regularisation/feature selection is used. An alternative choice is classification and regression trees.

In our example we are using $K - LASSO$ method which selects K super pixels that are the most influential when it comes to model prediction. In the Figure 37 we present explanations for the top 2 classes selected by the model VGG16. For each class the top K superpixels / interpretable features are highlighted

Interesting to see that the superpixel that shows the nib is influential when it comes to prediction ‘*goose*’ and superpixels linked with white fur are linked with prediction ‘*standard poodle*’.

0.12.4 Example: Titanic

Let us again consider explanation for prediction of the `titanic_rf_v6` model for *Johny D*, an 8-years old boy from 1st class.

In Figure 38 we have presented explanations generated with the LIME method. Three variables were identified as the most influential, age, gender and class.

It is important here to mention how interpretable features are created. For tabular data the most common approach is to discretized continuous variables and combine levels in categorical variables.

Figure 39 shows how interpretable feature can be extracted from Ceteris Paribus Profile for the variable `age`.

Different implementations of the LIME method have different algorithms for extraction of interpretable features, different methods for sampling and different methods for weighting.

In the section *Code snippets for R* we present different available implementations.



FIGURE 37 (fig:duckHorse04) LIME explanations for two classes identified by the VGG16 network with ImageNet weights.

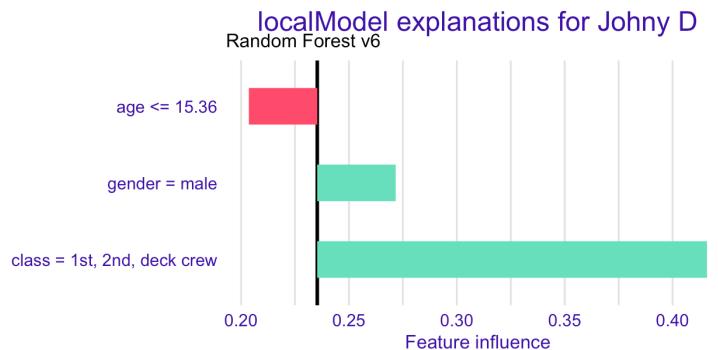


FIGURE 38 (fig:LIMEexample01) LIME explanations for single instance Johny D and generated for Random Forest v6 model.

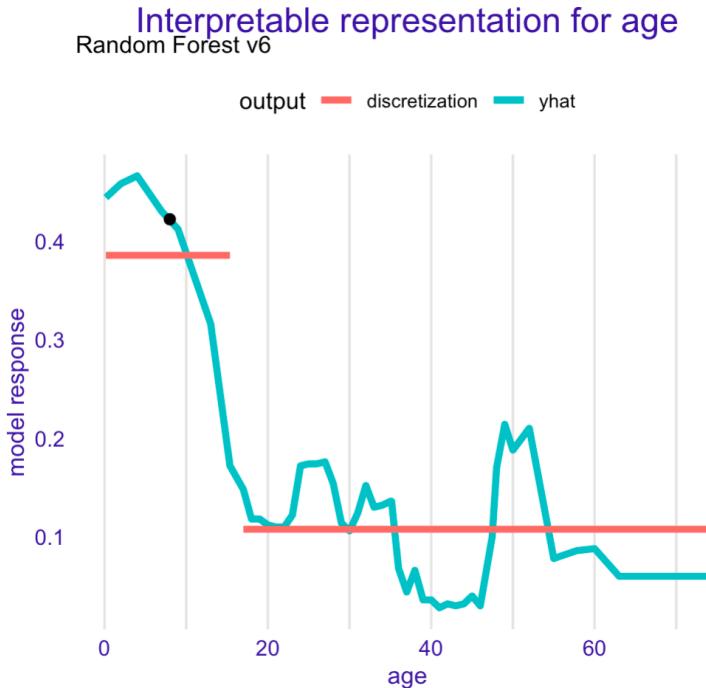


FIGURE 39 (fig:LIMEexample02) Interpretable local feature generated for age variable. LIME explanations for single instance Johny D and generated for Random Forest v6 model

0.12.5 Pros and cons

Local approximations are model agnostic, can be applied to any predictive model. Below we summarize key strengths and weaknesses of this approach.

Pros

- This method is highly adopted in text analysis and image analysis, in part thanks to the interpretable data representations.
- The intuition behind the method is straightforward, fit simple model to approximate a complex model.
- Model explanations are sparse, thus only small number of features are in the surrogate models used what makes it easier to explain.
- The LIME method can be applied to high dimensional models.

Cons

- For continuous variables and tabular data it is not that easy to find interpretable representations. IMHO this problem is not solved yet.
- The black-box model approximated the data and the glass-box model approximates the black box model. We do not have control over the quality of local fit of the glass-box model, thus the surrogate model may be misleading.
- Due to the *curse of dimensionality*, for high dimensional space points are sparse. Measuring of being local is tricky.

0.12.6 Code snippets for R

The LIME methods and it's clones are now implemented in various R and python packages, see for example `lime` (Pedersen and Benesty, 2018) which is a port of LIME python library (Lundberg, 2019), `lime` (Staniak and Biecek, 2018) and `localModel` (Staniak and Biecek, 2019) and `iml` (Molnar et al., 2018a).

These packages are different in a way how they turn continuous variables into interpretable features. For example, package `lime` performs global discretization using quartiles, `localModel` performs local discretization using Ceteris Paribus profiles, while `lime` and `iml` works directly on continuous variables. Also they differ in terms of which surrogate models they use and how new instances are being sampled. For these reasons these packages results different explanations.

Below we present explanations returned for these four methods for the Johny D and `titanic_rf_v6` model.

```
library("DALEX")
library("randomForest")

titanic <- archivist::aread("pbiecek/models/27e5c")
titanic_rf_v6 <- archivist::aread("pbiecek/models/31570")
johny_d <- archivist::aread("pbiecek/models/e3596")
```

0.12.6.1 The lime package

An example code snippet for the `lime` package is presented below. Key parts are function `lime::lime` which creates an explainer and `lime::explain` which evaluates explanations.

Resulting explanations are presented in Figure 40.

For continuous variables `lime` package discretizes features by using quartiles. This is why in the explanation we have `age < 22`.

```
library("lime")
model_type.randomForest <- function(x, ...) "classification"
lime_rf <- lime(titanic[, colnames(johny_d)], titanic_rf_v6)
lime_expl <- lime::explain(johny_d, lime_rf, labels = "yes", n_features = 4, n_permutations = 1000)
lime_expl

#   model_type case label label_prob  model_r2 model_intercept model_prediction
#1 classification    1    no     0.602 0.5806297      0.5365448      0.5805939
#2 classification    1    no     0.602 0.5806297      0.5365448      0.5805939
#3 classification    1    no     0.602 0.5806297      0.5365448      0.5805939
#4 classification    1    no     0.602 0.5806297      0.5365448      0.5805939
#   feature feature_value feature_weight  feature_desc          data prediction
#1   fare            72     0.00640936 21.00 < fare 1, 2, 8, 0, 0, 72, 4 0.602, 0.398
#2   gender           2     0.30481181 gender = male 1, 2, 8, 0, 0, 72, 4 0.602, 0.398
```

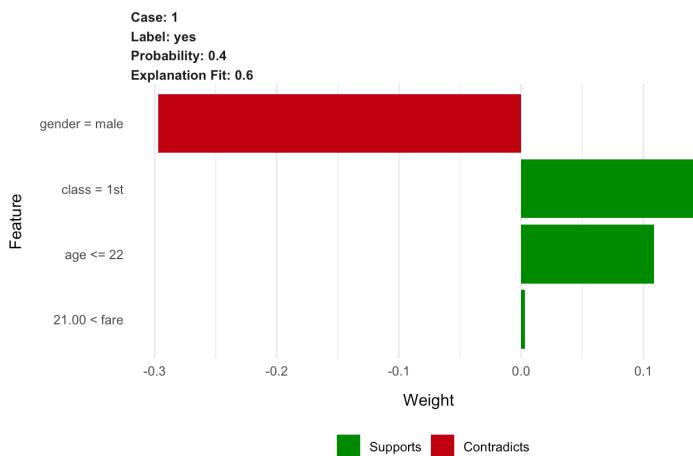


FIGURE 40 (fig:limeExplLIMETitanic) Explanations for Johny D generated by the lime package.

```
#3   class          1    -0.16690730  class = 1st 1, 2, 8, 0, 0, 72, 4 0.602, 0.398
#4   age            8    -0.10026475  age <= 22 1, 2, 8, 0, 0, 72, 4 0.602, 0.398

plot_features(lime_expl)
```

0.12.6.2 The localModel package

An example code snippet for the `localModel` package is presented below. Key parts are function `DALEX:::explain` which creates an explainer and `individual_surrogate_model` which fits a local model.

Resulting explanations are presented in Figure 41.

For continuous variables `localModel` package discretizes features by using local Ceteris Paribus Profiles. This is why in the explanation we have `age < 15`. As we show in the Ceteris Paribus Chapter 0.6 the largest drop in survival is observed around 15 years old boys.

```
library("localModel")

localModel_rf <- DALEX:::explain(model = titanic_rf_v6,
                                    data = titanic[, colnames(johny_d)])
localModel_lok <- individual_surrogate_model(localModel_rf, johny_d,
                                               size = 1000, seed = 1313)
localModel_lok
#   estimated           variable dev_ratio response
#1 0.23479837        (Model mean) 0.6521442
#2 0.14483341        (Intercept) 0.6521442
#3 0.08081853 class = 1st, 2nd, deck crew 0.6521442
```

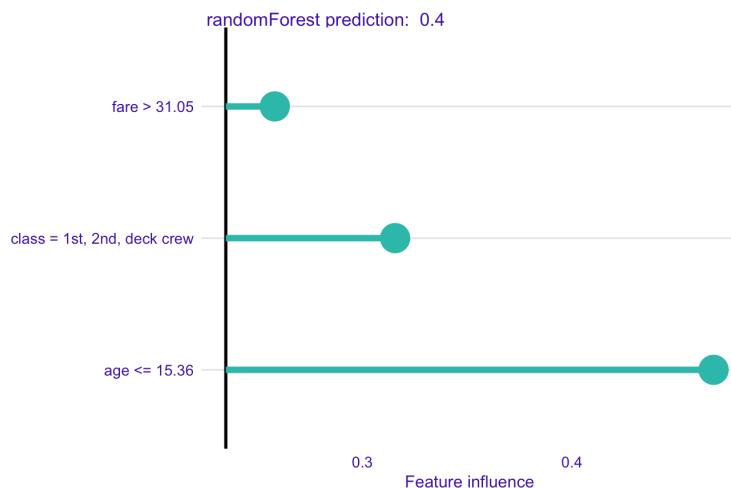


FIGURE 41 (fig:limeExplLocalModelTitanic) Explanations for Johny D generated by the localModel package.

```
#4 0.00000000      gender = female, NA, NA 0.6521442
#5 0.23282293      age <= 15.36 0.6521442
#6 0.02338929      fare > 31.05 0.6521442
plot(localModel_lok)
```

0.12.6.3 The iml package

An example code snippet for the `iml` package is presented below. Key parts are function `Predictor$new` which creates an explainer and `LocalModel$new` which fits local model.

Resulting explanations are presented in Figure 42.

For continuous variables like `age` the `iml` package approximates this feature without any discretization. As we showed in the Ceteris Paribus Chapter 0.6, the profile for `age` is constant in the interval 0-15, this is why here `age` is not an important feature.

```
library("iml")
iml_rf = Predictor$new(titanic_rf_v6, data = titanic[, colnames(johny_d)])
iml_glass_box = LocalModel$new(iml_rf, x.interest = johny_d, k = 6)
iml_glass_box
#Interpretation method: LocalModel
#
#Analysed predictor:
#Prediction task: unknown
#
#Analysed data:
#Sampling from data.frame with 2207 rows and 7 columns.
#
```

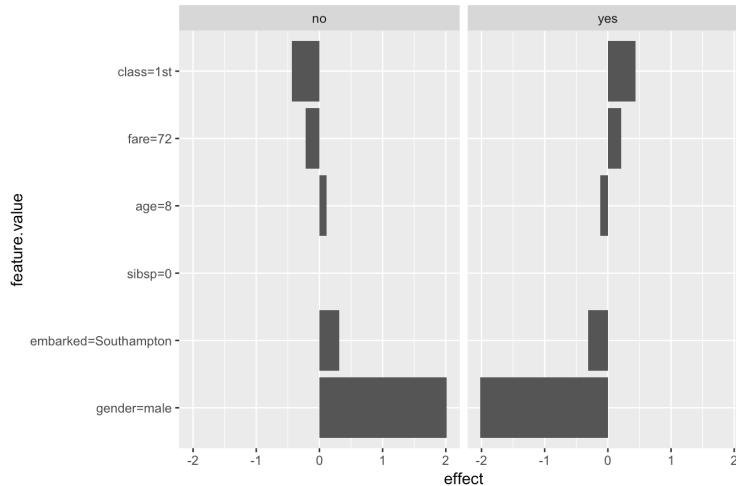


FIGURE 42 (fig:limeExplIMLTitanic) Explanations for Johny D generated by the iml package.

```
#Head of results:
#       beta x.recoded      effect x.original      feature
#1 -0.158368701      1 -0.1583687      1st    class=1st
#2  1.739826204      1  1.7398262     male   gender=male
#3  0.018515945      0  0.0000000      0      sibsp
#4 -0.001484918    72 -0.1069141      72      fare
#5  0.131819869      1  0.1318199 Southampton embarked=Southampton
#6  0.158368701      1  0.1583687      1st    class=1st

plot(iml_glass_box)
```

0.13 Summary of Instance-level Explainers

This part of the book was devoted to tools for exploration, explanation and debugging of predictive models around single prediction/single instance.

In Chapters 0.6-0.8 we discussed methods related to the concept of feature oriented exploration, aka. Ceteris Paribus Profils. Chapters 0.9-0.11 show methods that calculate contributions of individual feature to model predictions. Chapter 0.12 presens an alternative approach focused on sparse explanations. All these chapters were method-oriented. In this chapter we will compare these methods, discuss options how they can be used together and when they serves a different needs.

Local Exploration :

- *What If ?*
- *Why ?*
- *What about similar ?*

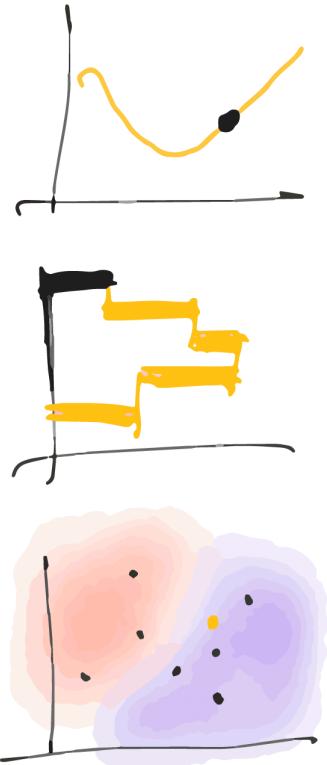


FIGURE 43 figure/localExplainers.png

0.13.1 Number of features, size of the data

0.13.2 Questions in mind

TODO compare pros and cons of different techniques

TODO: Sparse model approximation / variable selection / feature ranking

TODO comparison of different approach for Johny D

TODO Champion-Challenger explainers

0.13.3 When to use?

There are several use-cases for such explainers. Think about following.

- Model improvement. If model works particularly bad for a selected observation (the residual is very high) then investigation of model responses for miss fitted points may give some hints how to improve the model. For individual predictions it is easier to notice that selected variable should have a different effect.
- Additional domain specific validation. Understanding which factors are important for

model predictions helps to be critical about model response. If model contributions are against domain knowledge then we may be more skeptical and willing to try another model. On the other hand, if the model response is aligned with domain knowledge we may trust more in these responses. Such trust is important in decisions that may lead to serious consequences like predictive models in medicine.

- Model selection. Having multiple candidate models one may select the final response based on model explanations. Even if one model is better in terms of global model performance it may happen that locally other model is better fitted. This moves us towards model consultations that identify different options and allow human to select one of them.

Enslaving the Algorithm: From a ‘Right to an Explanation’ to a ‘Right to Better Decisions’? ([Edwards and Veale, 2018](#))

0.14 Model-level exploration

Model level explainers help to understand how the model works in general, for some population of interest. This is the main difference from the instance level explainers that were focused on a model behaviour around a single observation. Model level explainers work in the context of a population or subpopulation.

Think about following use-cases

- One wants to know which variables are important in the model. Think about model for heart accident in which features come from additional medical examinations. Knowing which examinations are not important one can reduce a model by removing unnecessary variables.
- One wants to understand how a selected variable affects the model response. Think about a model for prediction of apartment prices. You know that apartment location is an important factor, but which locations are better and how much a given location is worth? Model explainers help to understand how values of a selected variable affect the model response.
- One wants to know if there are any unusual observations that do not fit to the model. Observations with unusually large residuals. Think about a model for survival after some very risky treatment. You would like to know if for some patients the model predictions are extremely incorrect.

All cases mentioned above are linked with either model diagnostic (checking if model behaves along our expectations) or knowledge extraction (model was trained to extract some knowledge about the discipline).

0.14.1 Approaches to model explanations

Model level explanations are focused on four main aspects of a model.

- Model performance. Here the question is how good is the model, is it good enough (better than some predefined threshold), is a model A better than model B?
- Variable importance. How important are variables, which are the most important and which are not important at all?
- Variable effects. What is the relation between a variable and model response, can the variable be transformed to create a better model?
- Model residuals. Is there any unusual pattern related to residuals, are they biased, are they correlated with some additional variable?

0.14.2 A bit of philosophy: Three Laws for Model Level Explanations

In the spirit of three laws introduced in the chapter [0.1.3](#) here we propose three laws for model level explanations.

- **Variable importance.** For every model we shall be able to understand which variables are important and which are not.
 - **Model audit.** For every model we shall be able to verify basic checks like if residuals are correlated with variables and if there are unusual observations.
 - **Second opinion.** For every model we shall be able to compare it against other models to verify if they capture different stories about the data.
-

0.15 Feature Importance

Methods presented in this chapter are useful for assessment of feature importance. There are many possible applications of such methods, for example:

- Feature importance scores may be used for feature filtering. Features that are not important may be removed from the model training procedure. Removal of the noise shall lead to better models.
- Identification of the most important features may be used as a validation of a model against domain knowledge. Just to make sure that it's not like a single random feature dominates model predictions.
- Identification of the most important features may lead to new domain knowledge. Well, we have identified important features.
- Comparison of feature importance between different models helps to understand how different models handle particular features.
- Ranking of feature importance helps to decide in what order we shall perform further model exploration, in what order we shall examine particular feature effects.

There are many methods for assessment of feature importance. In general we may divide them into two groups, methods that are model specific and methods that are model agnostic.

Some models like random forest, gradient boosting, linear models and many others have their own ways to assess feature importance. Such method are linked with the particular structure of the model. In terms of linear models such specific measures are linked with normalized regression coefficients or p-values. For tree based ensembles such measures may be based on utilization of particular features in particular trees, see ([Foster, 2017](#)) for gradient boosting or ([Paluszynska and Biecek, 2017a](#)) for random forest.

But in this book we are focused on methods that are model agnostic. The may reason for that is

- First, be able to apply this method to any predictive model or ensemble of models.
- Second, (which is maybe even more important) to be able to compare feature importance between models despite differences in their structure.

Model agnostic methods cannot assume anything about the model structure and we do not want to refit a model. The method that is presented below is described in details in the ([Fisher et al., 2018](#)). The main idea is to measure how much the model fit will decrease if a selected feature or group of features will be cancelled out. Here cancellation means perturbations like resampling from empirical distribution of just permutation.

The method can be used to measure importance of single features, pairs of features or larger tuples. For the simplicity below we describe algorithm for single features, but it is straight forward to use it for larger subsets of features.

0.15.1 Permutation Based Feature Importance

The idea behind is easy and in some sense borrowed from Random Forest ([Breiman et al., 2018](#)). If a feature is important then after permutation model performance shall drop. The larger drop the more important is the feature.

Let's describe this idea in a bit more formal way. Let $\mathcal{L}(f(x), y)$ be a loss function that assess goodness of fit for a model $f(x)$ while let \mathcal{X} be a set of features.

1. For each feature $x_i \in \mathcal{X}$ do steps 2-5
2. Create a new data $x^{*, -i}$ with feature x_i resampled (or permuted).
3. Calculate model predictions for the new data $x^{*, -i}$, they will be denoted as $f(x^{*, -i})$.
4. Calculate loss function for models predictions on perturbed data

$$L^{*, -i} = \mathcal{L}(f(x^{*, -i}), y)$$

5. Feature importance may be calculated as difference or ratio of the original loss and loss on perturbed data, i.e. $vip(x_i) = L^{*, -i} - L$ or $vip(x_i) = L^{*, -i}/L$.

Note that ranking of feature importance will be the same for the difference and the ratio since the loss L is the same.

Note also, that the main advantage of the step 5 is that feature importance is kind of

normalized. But in many cases such normalization is not needed and in fact it makes more sense to present raw $L^{*, -i}$ values.

0.15.2 Example: Titanic

Let's use this approach to a random forest model created for the Titanic dataset. The goal is to predict passenger survival probability based on their sex, age, class, fare and some other features available in the `titanic` dataset.

```
head(titanic)
```

```
##   gender age class      embarked      country  fare sibsp parch survived
## 1   male  42   3rd Southampton United States 7.11    0    0     no
## 2   male  13   3rd Southampton United States 20.05   0    2     no
## 3   male  16   3rd Southampton United States 20.05   1    1     no
## 4 female 39   3rd Southampton       England 20.05   1    1    yes
## 5 female 16   3rd Southampton        Norway  7.13    0    0    yes
## 6   male  25   3rd Southampton United States 7.13    0    0    yes
##   age_cat fare_cat
## 1 (30,50]  (0,10]
## 2 (10,18]  (10,25]
## 3 (10,18]  (10,25]
## 4 (30,50]  (10,25]
## 5 (10,18]  (0,10]
## 6 (18,30]  (0,10]
```

Permutation based feature importance can be calculated with the `feature_importance{ingredients}`. By default it permutes values feature by feature.

Instead of showing normalized feature importance we plot both original L and loss after permutation $L^{*, -i}$. This way we can read also how good was the model, and as we will see in next subsection it will be useful for model comparison.

```
library("ingredients")
fi_rf <- feature_importance(explain_titanic_rf)
plot(fi_rf) + ggtitle("Permutation based feature importance", "For Random Forest model and Titanic data")
```

It's interesting that the most important variable for Titanic data is the Sex. So it have been „women first” after all. Then the three features of similar importance are passenger class (first class has higher survival), age (kids have higher survival) and fare (owners of more pricy tickets have higher survival).

Note that drawing permutations evolves some randomness. Thus to have higher repeatability of results you may either set a seed for random number generator or replicate the procedure few times. The second approach has additional advantage, that you will learn the uncertainty behind feature importance assessment.

Here we present scores for 10 repetition of the process.

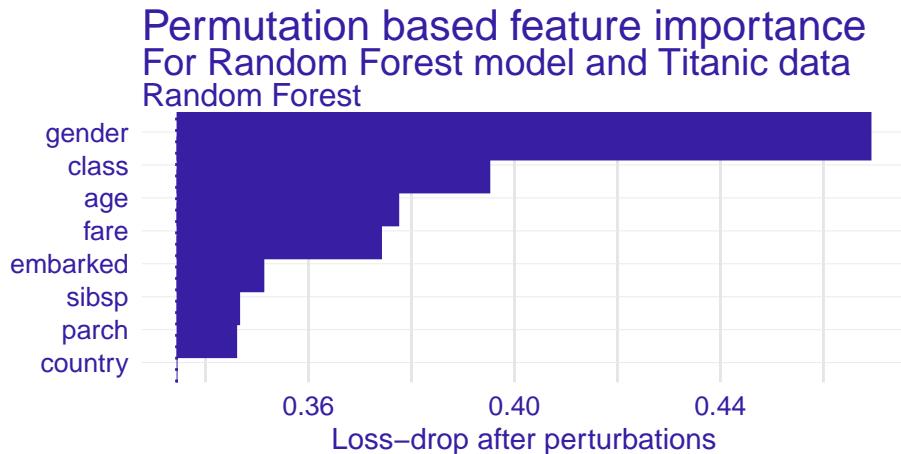


FIGURE 44 Feature importance. Each interval presents the difference between original model performance (left end) and the performance on a dataset with a single feature perturbed

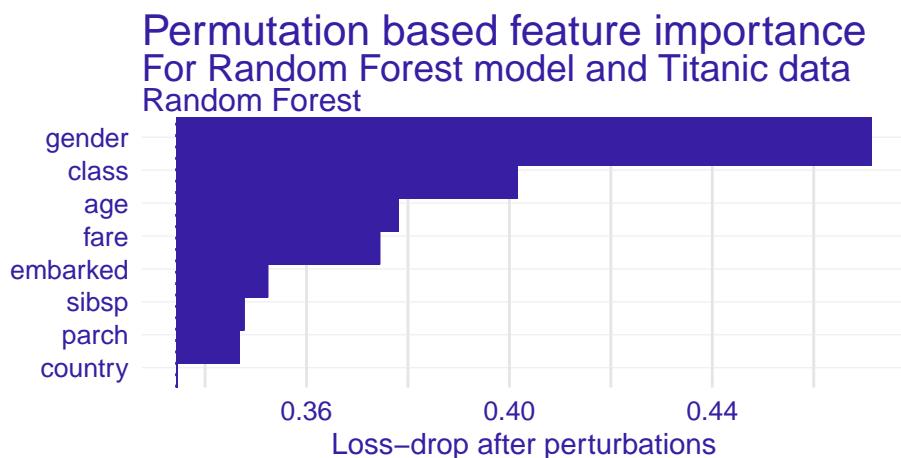


FIGURE 45 Feature importance for 10 replication of feature importance assessment

```
fi_rf10 <- replicate(10, feature_importance(explain_titanic_rf), simplify = FALSE)
do.call(plot, fi_rf10) + ggtitle("Permutation based feature importance", "For Random Forest model and Titanic data")
```

It is much easier to assess feature importance if they come with some assessment of the uncertainty. We can read from the plot that Age and passenger class are close to each other.

Note that intervals are useful for model comparisons. In the Figure @ref{titanic5} we can read feature importance for random forest, gradient boosting and logistic regression models. Best results are achieved by the random forest model and also this method consume more features than others. A good example is the *Fare* variable, not used in gradient boosting nor logistic regression (as a feature highly correlated with passenger class) but consumed in the random forest model.

```
fi_rf <- feature_importance(explain_titanic_rf)
fi_gbm <- feature_importance(explain_titanic_gbm)
```

```
fi_glm <- feature_importance(explain_titanic_lmr)

plot(fi_rf, fi_gbm, fi_glm)
```

0.15.3 Example: Price prediction

Let's create a regression model for prediction of apartment prices.

```
library("DALEX")
library("randomForest")
set.seed(59)
model_rf <- randomForest(m2.price ~ construction.year + surface + floor +
                           no.rooms + district, data = apartments)
```

A popular loss function for regression model is the root mean square loss

$$L(x, y) = \sqrt{\frac{1}{n} \sum_{i=1}^n (x_i - y_i)^2}$$

```
loss_root_mean_square(
  predict(model_rf, apartments),
  apartments$m2.price
)
```

```
## [1] 193.8477
```

Let's calculate feature importance

```
explainer_rf <- explain(model_rf,
  data = apartmentsTest[,2:6], y = apartmentsTest$m2.price)
```

```
vip <- variable_importance(explainer_rf,
  loss_function = loss_root_mean_square)
vip
```

	variable	dropout_loss	label
## 1	_full_model_	794.5552	randomForest
## 2	no.rooms	822.6120	randomForest
## 3	construction.year	853.5165	randomForest
## 4	floor	855.3036	randomForest
## 5	district	860.7501	randomForest
## 6	surface	871.8285	randomForest
## 7	_baseline_	1130.2765	randomForest

On a diagnostic plot is useful to present feature importance as an interval that start in a loss and ends in a loss of perturbed data.

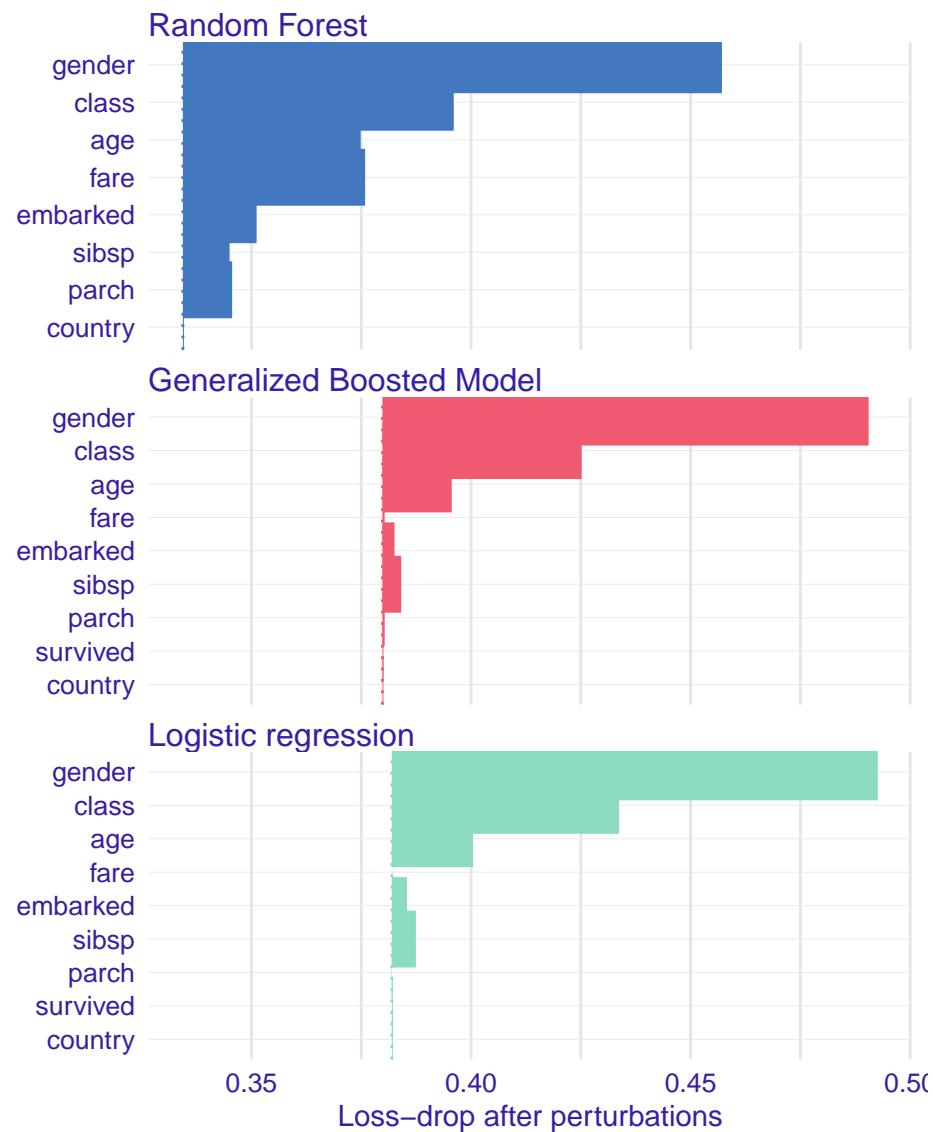
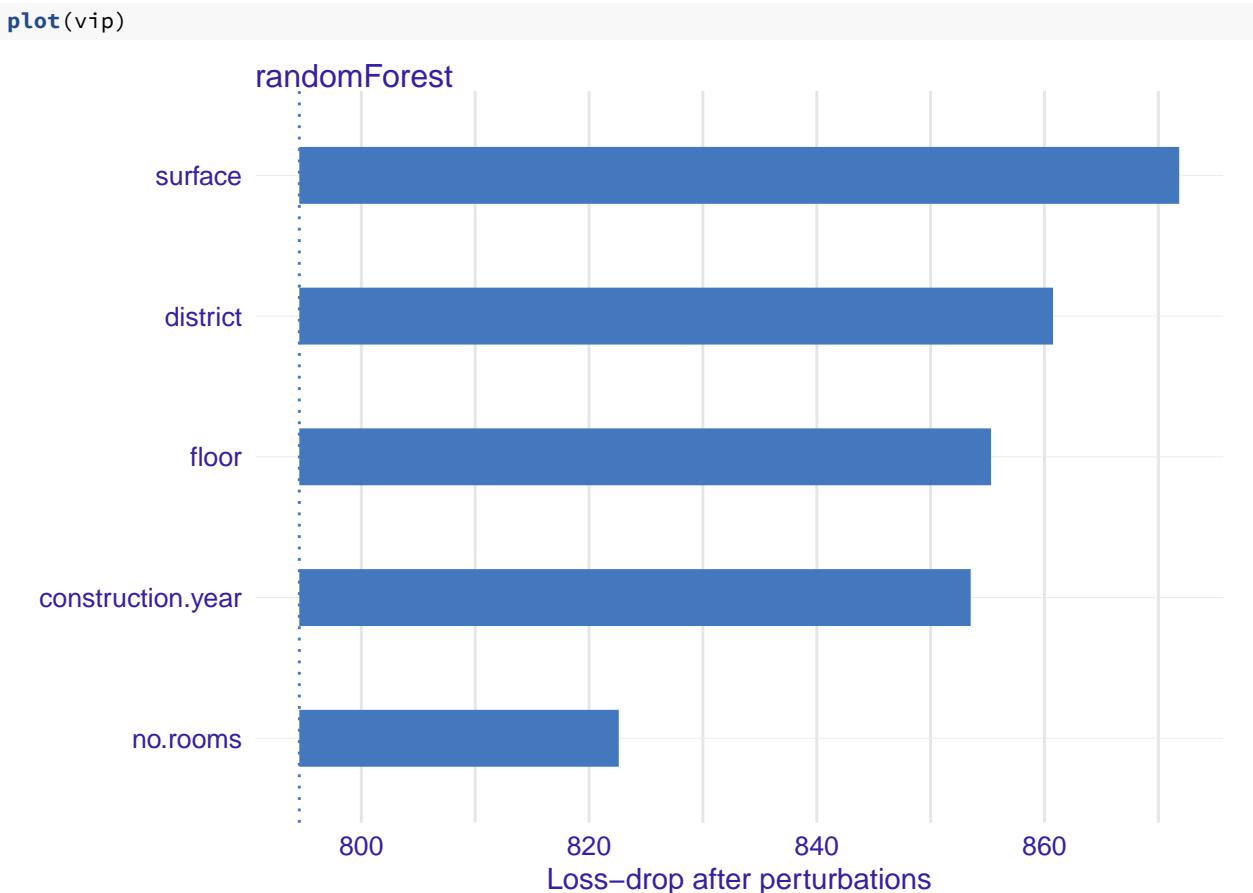


FIGURE 46 Feature importance for random forest, gradient boosting and logistic regression models



0.15.4 More models

Much more can be read from feature importance plots if we compare models of a different structure. Let's train three predictive models trained on `apartments` dataset from the `DALEX` package. Random Forest model (Breiman et al., 2018) (elastic but biased), Support Vector Machines model (Meyer et al., 2017) (large variance on boundaries) and Linear Model (stable but not very elastic). Presented examples are for regression (prediction of square meter price), but the CP profiles may be used in the same way for classification.

Let's fit these three models.

```
library("DALEX")
model_lm <- lm(m2.price ~ construction.year + surface + floor +
                 no.rooms + district, data = apartments)

library("randomForest")
set.seed(59)
model_rf <- randomForest(m2.price ~ construction.year + surface + floor +
                           no.rooms + district, data = apartments)
```

```
library("e1071")
model_svm <- svm(m2.price ~ construction.year + surface + floor +
                  no.rooms + district, data = apartments)
```

For these models we use DALEX explainers created with `explain()` function. These explainers wrap models, predict functions and validation data.

```
explainer_lm <- explain(model_lm,
                         data = apartmentsTest[,2:6], y = apartmentsTest$m2.price)
vip_lm <- variable_importance(explainer_lm,
                               loss_function = loss_root_mean_square)
vip_lm
```

```
##           variable dropout_loss label
## 1      _full_model_    282.0062   lm
## 2 construction.year    281.9007   lm
## 3       no.rooms     292.8398   lm
## 4          floor      492.0857   lm
## 5        surface     614.9198   lm
## 6      district    1002.3487   lm
## 7     _baseline_    1193.6209   lm
```

```
explainer_rf <- explain(model_rf,
                         data = apartmentsTest[,2:6], y = apartmentsTest$m2.price)
vip_rf <- variable_importance(explainer_rf,
                               loss_function = loss_root_mean_square)
vip_rf
```

```
##           variable dropout_loss      label
## 1      _full_model_    799.9382 randomForest
## 2       no.rooms     827.8470 randomForest
## 3 construction.year   852.1447 randomForest
## 4      district     857.3774 randomForest
## 5          floor     874.5364 randomForest
## 6        surface     898.5794 randomForest
## 7     _baseline_    1104.9754 randomForest
```

```
explainer_svm <- explain(model_svm,
                         data = apartmentsTest[,2:6], y = apartmentsTest$m2.price)
vip_svm <- variable_importance(explainer_svm,
                               loss_function = loss_root_mean_square)
vip_svm
```

```
##           variable dropout_loss label
## 1      _full_model_    960.1219   svm
## 2      district     902.5403   svm
## 3       no.rooms     956.8193   svm
```

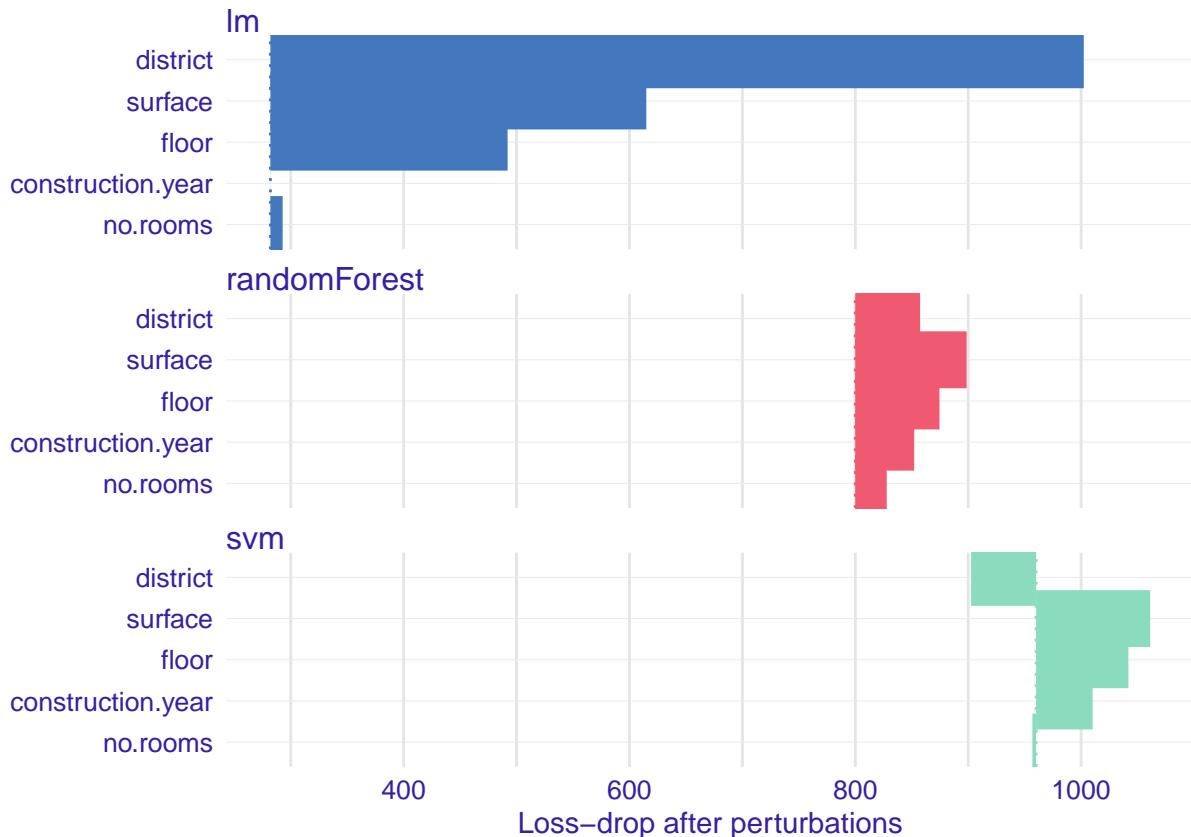
```
## 4 construction.year    1010.1792  svm
## 5          floor        1041.8232  svm
## 6         surface       1061.1809  svm
## 7 _baseline_      1248.4173  svm
```

Let's plot feature importance for all three models on a single plot.

Intervals start in a different values, thus we can read that loss for SVM model is the lowest.

When we compare other features it looks like in all models the `district` is the most important feature followed by `surface` and `floor`.

```
plot(vip_rf, vip_svm, vip_lm)
```



There is interesting difference between linear model and others in the way how important is the `construction.year`. For linear model this variable is not importance, while for remaining two models there is some importance.

In the next chapter we will see how this is possible.

0.15.5 Level frequency

What does the feature importance mean? How it is linked with a data distribution.

0.16 Feature effects

In following chapters we introduce tools for extraction of the information between model response and individual model inputs. These tools are useful to summarize how „in general” model responds to the input of interest. All presented approaches are based on Ceteris Paribus Profiles introduced in Chapter @ref{ceterisParibus} but they differ in a way how individual profiles are merged into a global model response.

We use the term „feature effect” to refer to global model response as a function of single or small number of model features. Methods presented in this chapter are useful for extraction information of feature effect, i.e. how a feature is linked with model response. There are many possible applications of such methods, for example:

- Feature effect may be used for feature engineering. The crude approach to modeling is to fit some elastic model on raw data and then use feature effects to understand the relation between a raw feature and model output and then to transform model input to better fit the model output. Such procedure is called surrogate training. In this procedure an elastic model is trained to learn about link between a feature and the target. Then a new feature is created in a way to better utilized the feature in a simpler model (Gosiewska et al., 2019). In the next chapters we will show how feature effects can be used to transform a continuous variable in to a categorical one in order to improve the model behavior.
- Feature effect may be used for model validation. Understanding how a model utilizes a feature may be used as a validation of a model against domain knowledge. For example if we expect monotonic relation or linear relation then such expectations can be verified. Also if we expect smooth relation between model and its inputs then the smoothness can be visually examined. In the next chapters we will show how feature effects can be used to warn a model developer that model is unstable and should be regularized.
- In new domains an understanding of a link between model output and the feature of interest may increase our domain knowledge. It may give quick insights related to the strength or character of the relation between a feature of interest and the model output.
- The comparison of feature effects between different models may help to understand how different models handle particular features. In the next chapters we will show how feature effects can be used learn limitations of particular classes of models.

0.16.1 Global level vs instance level explanations

The plot below shows Ceteris Paribus Profiles for the random forest `rf_5` for 10 selected passengers. Different profiles behave differently. In following chapter we discuss different approaches to aggregation of such profiles into model level feature effects.

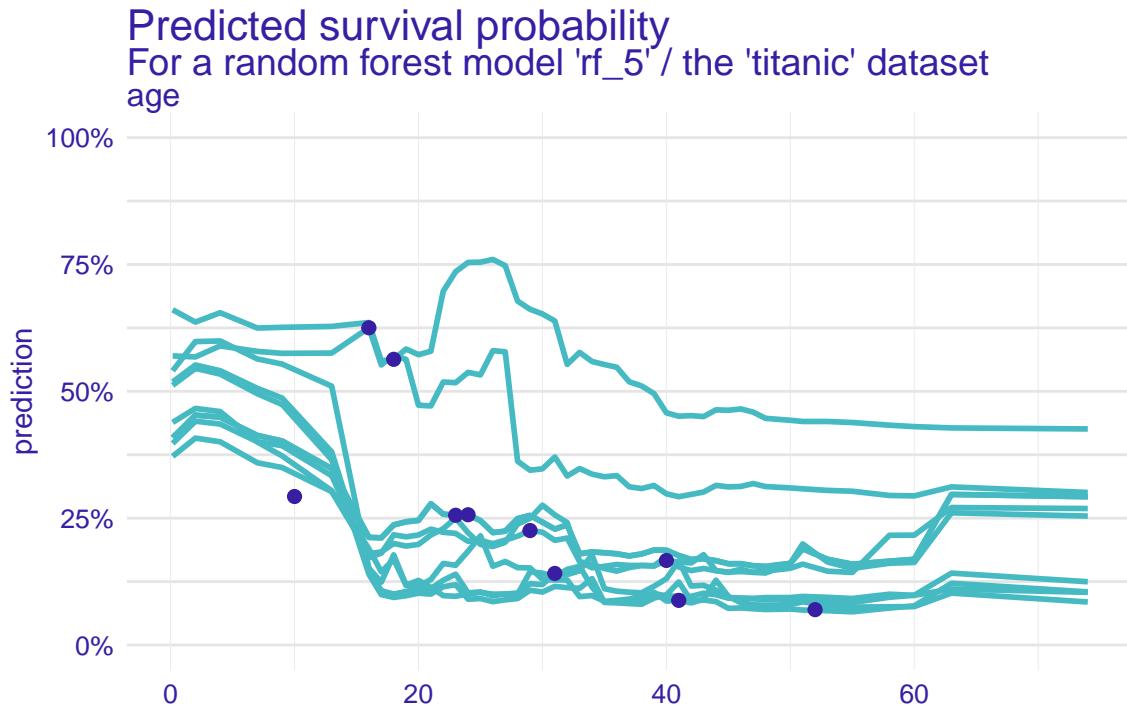


FIGURE 47 (#fig:pdp_part_1A) Ceteris Paribus profiles for 10 passengers and the random forest model

0.17 Partial Dependency Profiles

One of the first and the most popular tools for inspection of black-box models on the global level are Partial Dependence Plots (sometimes called Partial Dependence Profiles).

PDP were introduced by Friedman in 2000 in his paper devoted to Gradient Boosting Machines (GBM) - new type of complex yet effective models (Friedman, 2000). For many years PDP as sleeping beauties stay in the shadow of the boosting method. But this has

changed in recent years. PDP are very popular and available in most of data science languages. In this chapter we will introduce key intuitions, explain the math beyond PDP and discuss strengths and weaknesses.

General idea is to show how the expected model response behaves as a function of a selected feature. Here the term „expected” will be estimated simply as the average over the population of individual Ceteris Paribus Profiles introduced in 0.6.

0.17.1 Definition

Partial Dependency Profile for a model f and a variable x^j is defined as

$$g_{PD}^{f,j}(z) = E[f(x^j = z, X^{-j})] = E[f(x|j = z)].$$

So it's an expected value for $x^j = z$ over **marginal** distribution X^{-j} or equivalently expected value of f after variable x^j is set to z .

Exercise

Let $f = x_1 + x_2$ and distribution of (x_1, x_2) is given by $x_1 \sim U[0, 1]$ and $x_2 = x_1$.

Calculate $g_{PD}^{f,1}(z)$.

Answer $g_{PD}^{f,1}(z) = z + 0.5$.

0.17.2 Estimation

Let's see how they are constructed step by step. Here we will use a random forest `rf_5` model for the *titanic* dataset. Examples are related to a single variable *age*.

The expectation cannot be calculated directly as we do not know fully neither the distribution of X^{-j} nor the $f()$. Yet this value may be estimated by as average from CP profiles.

$$\hat{g}_{PD}^{f,j}(z) = \frac{1}{n} \sum_{i=1}^N f(x_i^j = z, x_i^{-j}) = \frac{1}{n} \sum_{i=1}^N f(x_i|j = z).$$

1. Calculate Ceteris Paribus Profiles for observations from the dataset

As it was introduced in @ref{ceterisParibus} Ceteris Paribus profiles are calculated for observations. They show how model response change is a selected variable in this observation is modified.

$$CP^{f,j,x}(z) := f(x|j = z).$$

Such profiles can be calculated for example with the `ceteris_paribus{ingredients}` function.

So for a single model and a single variable we get a bunch of *what-if* profiles. In the figure @ref{pdp_part_1} we show an example for 100 observations. Despite some variation (random forest are not as stable as we would hope) we see that most profiles are decreasing.

So the older the passengers is the lower is the survival probability.

2. Aggregate Ceteris Paribus into a single Partial Dependency Profile

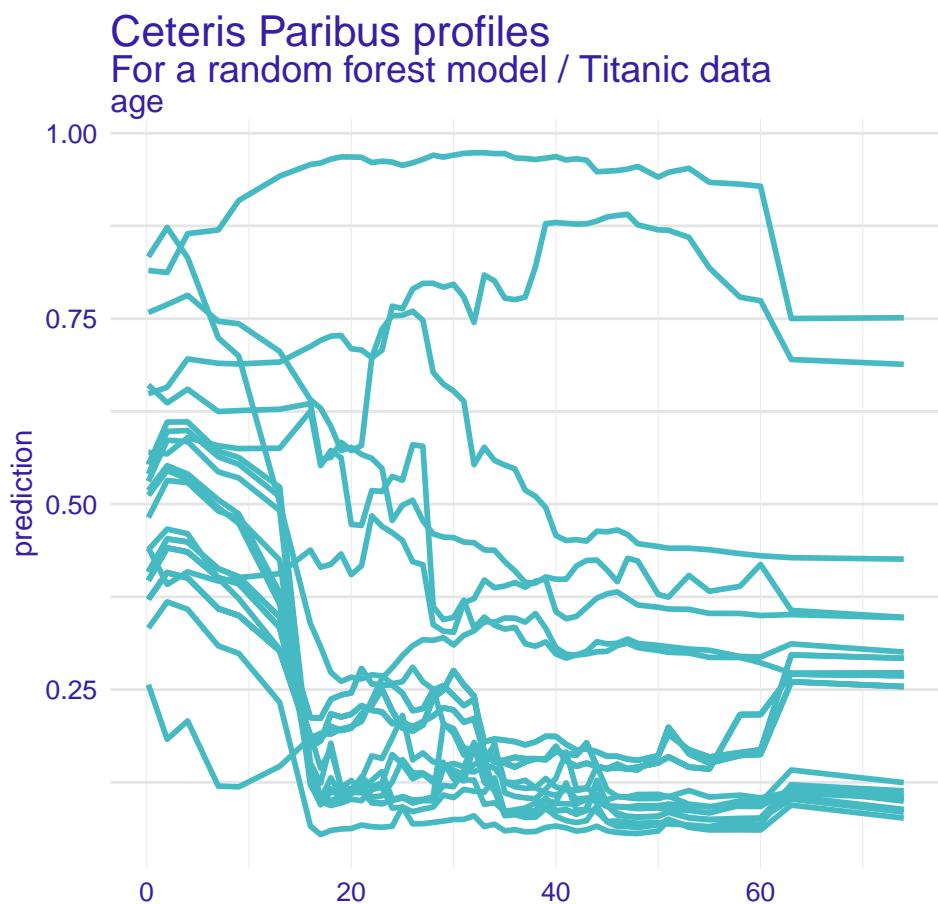


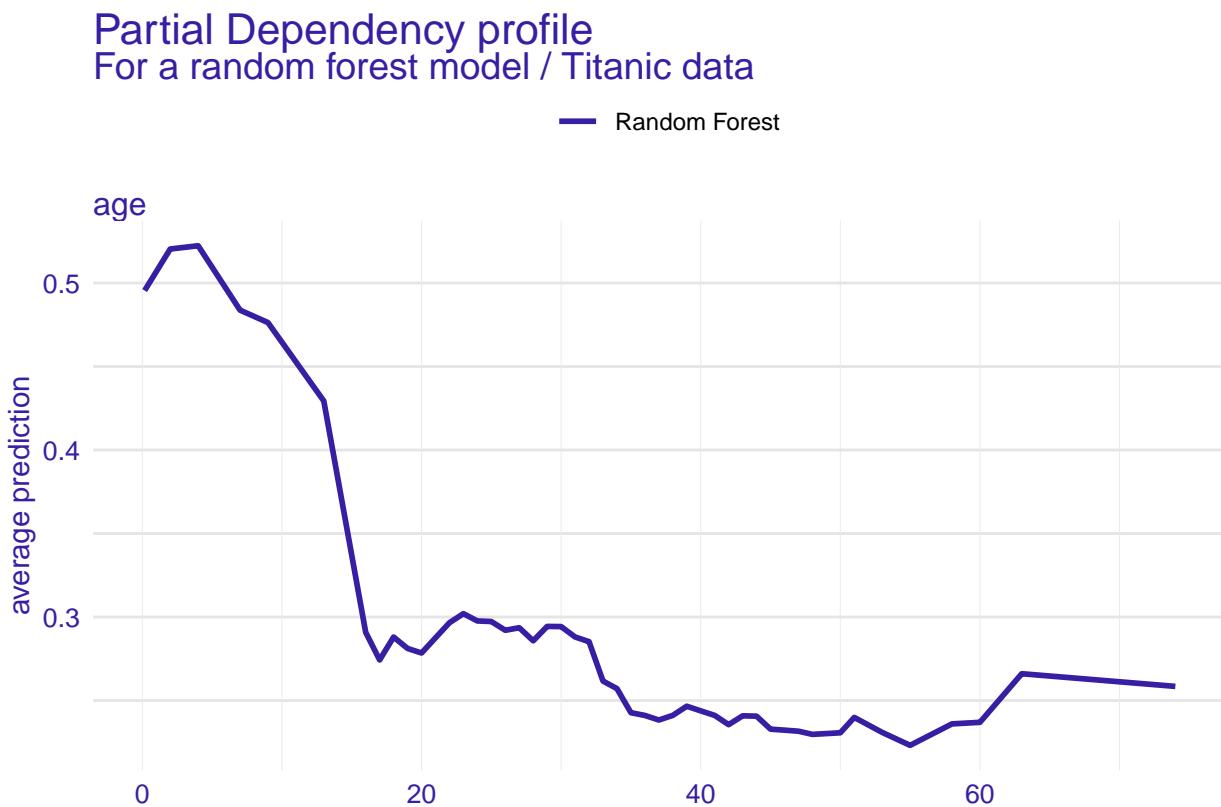
FIGURE 48 (#fig:pdp_part_1)Ceteris Paribus profiles for 100 observations, the age variable and the random forest model

Simple pointwise average across CP profiles. If number of CP profiles is large, it is enough to sample some number of them to get reasonably accurate PD profiles.

Here we show profiles calculated with `ingredients` package, but find similar implementation in the `pdp` package (Greenwell, 2017b), `ALEPlots` package (Apley, 2018b) or `iml` (Molnar et al., 2018b) package.

Such average can be calculated with the `aggregate_profiles{ingredients}` function.

```
pdp_rf <- aggregate_profiles(cp_rf)
plot(pdp_rf) +
  ggtitle("Partial Dependency profile", "For a random forest model / Titanic data")
```



So for a single model and a single variable we get a profile. See an example in figure @ref{pdp_part_2}. It is much easier than following 100 separate curves, and in cases in which Ceteris Paribus are more or less parallel, the Partial Dependency is a good summary of them.

The average response is of course more stable (as it's an average) and in this case is more or less a decreasing curve. It's much easier to notice that the older the passenger is the lower the survival probability. Moreover it is easier to notice that the largest drop in survival changes happen for teenagers. On average the survival for adults is 30 percent points smaller than for kids.

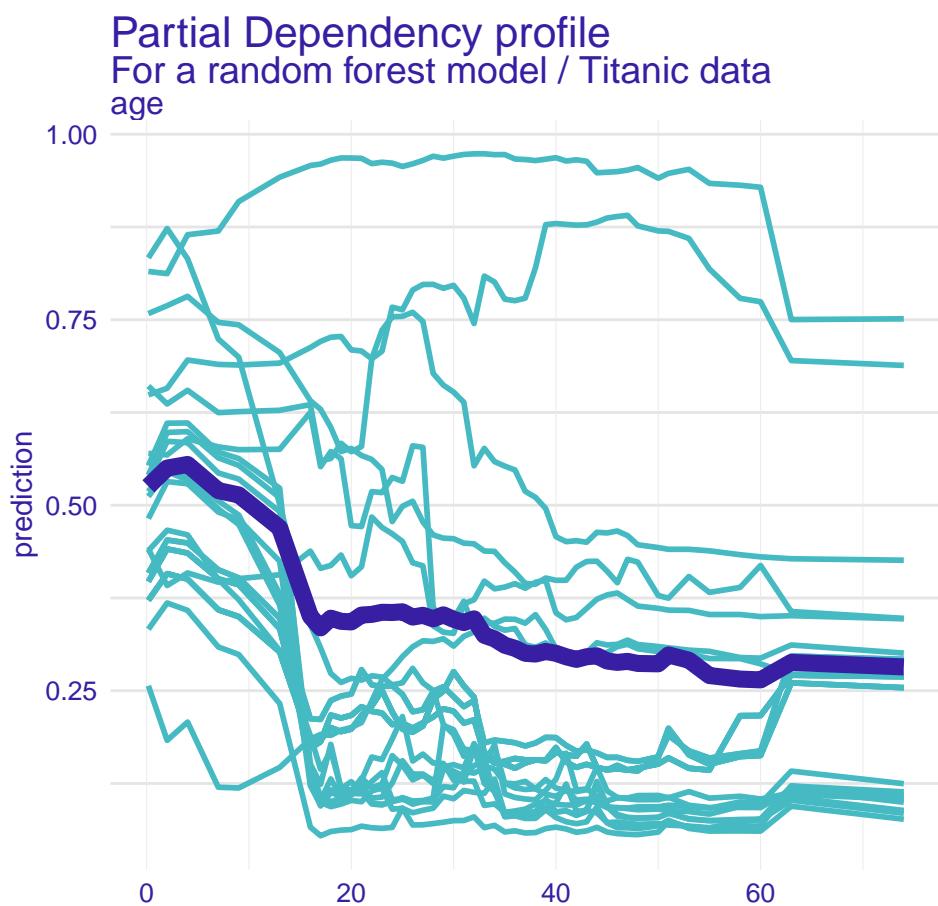


FIGURE 49 (#fig:pdp_part_2) Partial Dependency profile as an average for 100 observations

0.17.3 Clustered Partial Dependency Profiles

As we said in the previous section, Partial Dependency is a good summary if Ceteris Paribus profiles are similar, i.e. parallel. But it may happen that the variable of interest is in interaction with some other variable. Then profiles are not parallel because the effect of variable of interest depends on some other variables.

So on one hand it would be good to summaries all this Ceteris Paribus profiles with smaller number of profiles. But on another hand a single aggregate may not be enough. To deal with this problem we propose to cluster Ceteris Paribus profiles and check how homogenous are these profiles.

The most straightforward approach would be to use a method for clustering, like k-means algorithm or hierarchical clustering, and see how these cluster of profiles behave. Once clusters are established we can aggregate within clusters in the same way as in case of Partial Dependency Plots.

Such clusters can be calculated with the `cluster_profiles{ingredients}` function. We choose the hierarchical clustering with Ward linkage as it gives most stable results.

So for a single model and a single variable we get k profiles. The common problem in clustering is the selection of k . However in our case, as it's an exploration, the problem is simpler, as we are interesting if $k = 1$ (Partial Dependency is a good summary) or not (there are some interactions).

See an example in Figure @ref{pdp_part_4}. It is easier to notice that Ceteris Paribus profiles can be groups in three clusters. Group of passengers with a very large drop in the survival (cluster 1), moderate drop (cluster 2) and almost no drop in survival (cluster 3). Here we do not know what other factors are linked with these clusters, but some additional exploratory analysis can be done to identify these factors.

0.17.4 Grouped Partial Dependency Profiles

Once we see that variable of interest may be in interaction with some other variable, it is tempting to look for the factor that distinguish clusters.

The most straightforward approach is to use some other variable as a grouping variable. This can be done by setting the `groups` argument in the `aggregate_profiles{ingredients}` function.

```
library("ingredients")
selected_passangers <- select_sample(titanic, n = 100)
cp_rf <- ceteris_paribus(explain_titanic_rf, selected_passangers)
pdp_Sex_rf <- aggregate_profiles(cp_rf, variables = "age",
                                    groups = "gender")
```

See an example in Figure @ref{pdp_part_5}. Clearly there is an interaction between Age and Sex. The survival for woman is more stable, while for man there is more sudden drop

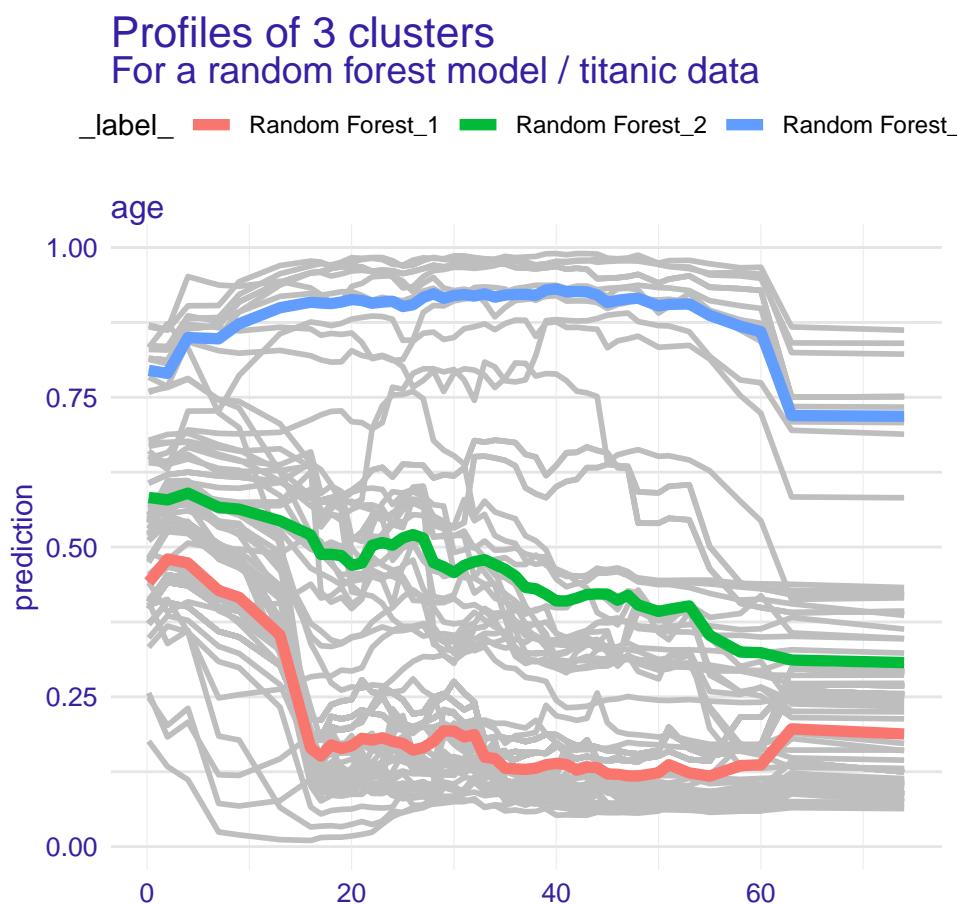


FIGURE 50 (#fig:pdp_part_4) Cluster profiles for 3 clusters over 100 Ceteris Paribus profiles

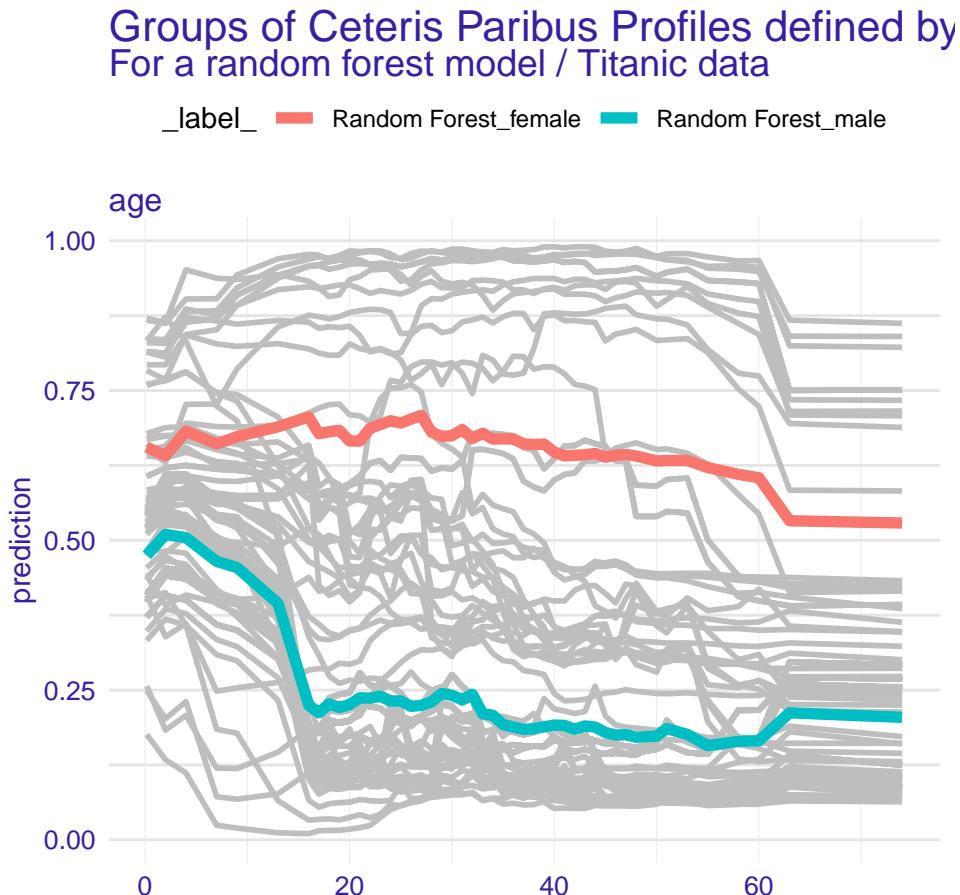


FIGURE 51 (#fig:pdp_part_5) Grouped profiles with respect to the gender variable

in Survival for older passengers. Check how the interaction for `Pclass` (passenger class) looks like.

0.17.5 Contrastive Model Comparisons

Contrastive comparisons of Partial Dependency Plots are useful not only for subgroups of observations but also for model comparisons.

Why one would like to compare models? There are at least three reasons for it.

- *Agreement of models will calm us.* Some models are known to be more stable other to be more elastic. If profiles for models from these two classes are not far from each other we can be more convinced that elastic model is not over-fitted.
- *Disagreement of models helps to improve.* If simpler interpretable model disagree with an elastic model, this may suggest a feature transformation that can be used to improve the interpretable model. For example if random forest learned non linear relation then it can be captured by a linear model after suitable transformation.
- *Validation of boundary conditions.* Some models are known to have different behavior on the boundary, for largest or lowest values. Random forest is known to shrink predictions

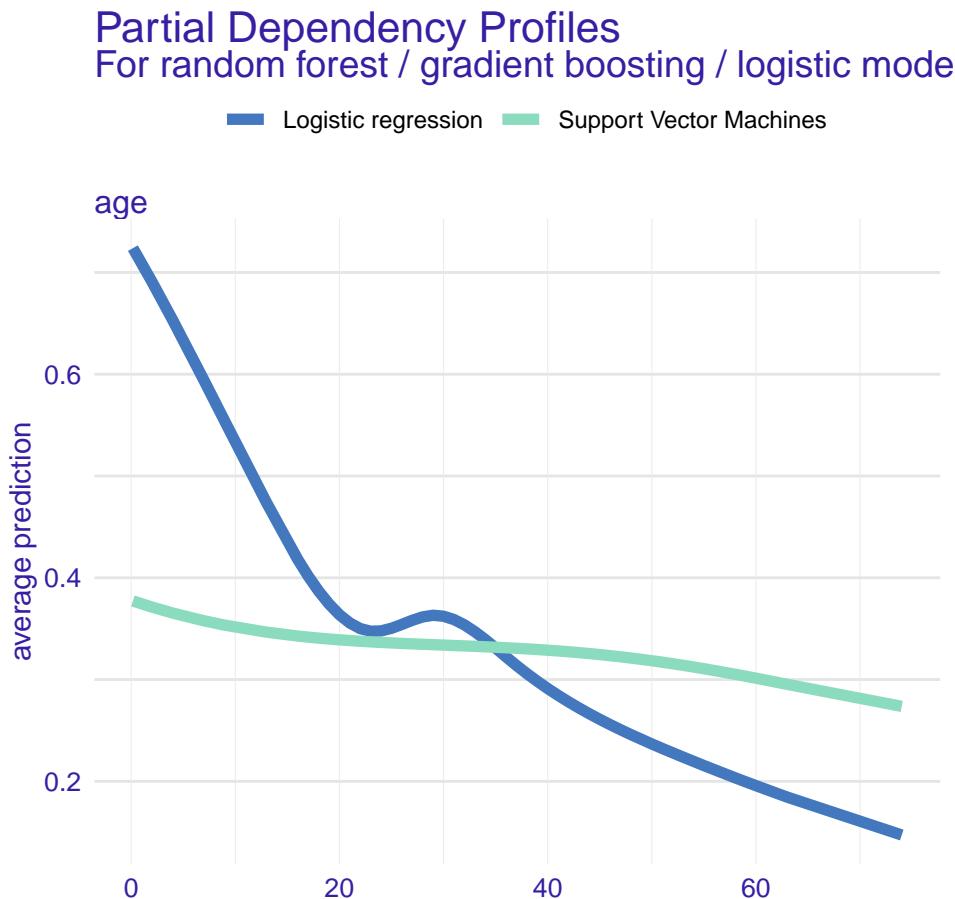


FIGURE 52 (#fig:pdp_part_7) Comparison on three predictive models with different structures.

towards the average, while support vector machines are known to have larger variance at edges. Contrastive comparisons may help to understand differences in boundary behavior.

Generic `plot{ingredients}` function handles multiple models as consecutive arguments.

See an example in Figure @ref{pdp_part_7}. Random forest is compared with gradient boosting model and generalized linear model (logistic regression). All three models agree when it comes to a general relation between Age and Survival. Logistic regression is of course the most smooth. Gradient boosting has on average higher predictions than random forest.

0.18 Conditional Dependency Profiles

One of the largest advantages of the Partial Dependency Profiles is that they are easy to explain, as they are just an average across Ceteris Paribus profiles. But one of the largest

disadvantages lies in expectation over marginal distribution which implies that x^j is independent from x^{-j} . In many applications this assumption is violated. For example, for the *apartments* dataset one can expect that features like *surface* and *number.or.rooms* are strongly correlated as apartments with larger number of rooms usually have larger surface. It may makes no sense to consider an apartment with 10 rooms and 20 square meters, so it may be misleading to change $x^{surface}$ independently from $x^{number.of.rooms}$. In the *titanic* dataset we shall expect correlation between *fare* and *passenger class* as tickets in the 1st class are the most expensive.

There are several attempts to fix this problem. Here we introduce Local Dependency Profiles presented in the (Apley, 2018b) under the name M-profiles.

The general idea is to use conditional distribution instead of marginal distribution to accomodate for the dependency between x^j and x^{-j} .

0.18.1 Definition

Conditional Dependency Profile for a model f and a variable x^j is defined as

$$g_{CD}^{f,j}(z) = E[f(X^j, X^{-j})|X^j = z].$$

So it's an expected value over **conditional** distribution $(X^j, X^{-j})|X^j = z$.

Exercise

Let $f = x_1 + x_2$ and distribuition of (x_1, x_2) is given by $x_1 \sim U[0, 1]$ and $x_2 = x_1$.

Calculate $g_{CD}^{f,1}(z)$.

Answer $g_{CD}^{f,1}(z) = 2 * z$.

0.18.2 Estimation

Partial Dependency Profiles are defined as an expected value from Ceteris Paribus Profiles.

$$g_i^{PD}(z) = E_{X_{-i}}[f(x|^{i=z}, x^{-i})].$$

And can be estimated as average from CP profiles.

$$\hat{g}_i^{PD}(z) = \frac{1}{n} \sum_{j=1}^n f(x|^{i=z}, x_j^{-i}).$$

As it was said, if X_i and X_{-i} are related it may have no sense to average CP profiles over

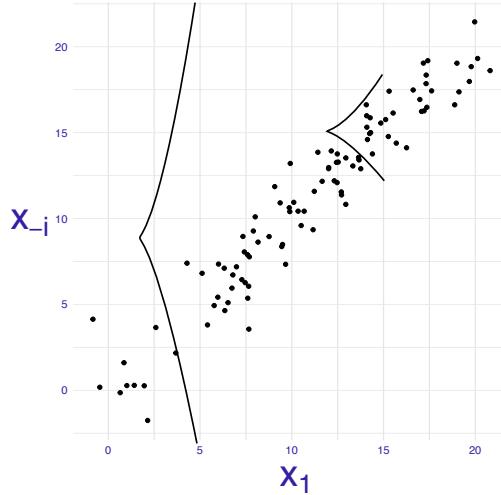


FIGURE 53 (fig:accumulatedCor)

marginal X_{-i} . Instead, an intuitive approach would be to use a conditional distribution $X_{-i}|X_i = x_i$.

$$g_i^M(z) = E_{X_{-i}|X_i=x_i}[f(x|^i = z, x^{-i})].$$

0.18.3 Example

See Figure ?? for illustration of difference between marginal and conditional distribution.

Such profiles are called Conditional Dependency Profiles and are estimated as

$$\hat{g}_i^M(z) = \frac{1}{|N_i|} \sum_{j \in N_i} f(x|^i = z, x_j^{-i}).$$

where N_i is the set of observations with x_i close to z .

As it is justified in (Apley, 2018b), there is a serious problem with this approach, illustrated by a following observation. If y depends on x_2 but not x_1 then the correlation between x_1 and x_2 will produce a *false* relation in the Marginal profiles for feature x_1 . This problem is also illustrated in the Figure ??.

0.19 Accumulated Local Profiles

As we showed in the previous chapter, Conditional Dependency Profiles takes into account dependency between features, but it is both advantage and disadvantage. The advantage is

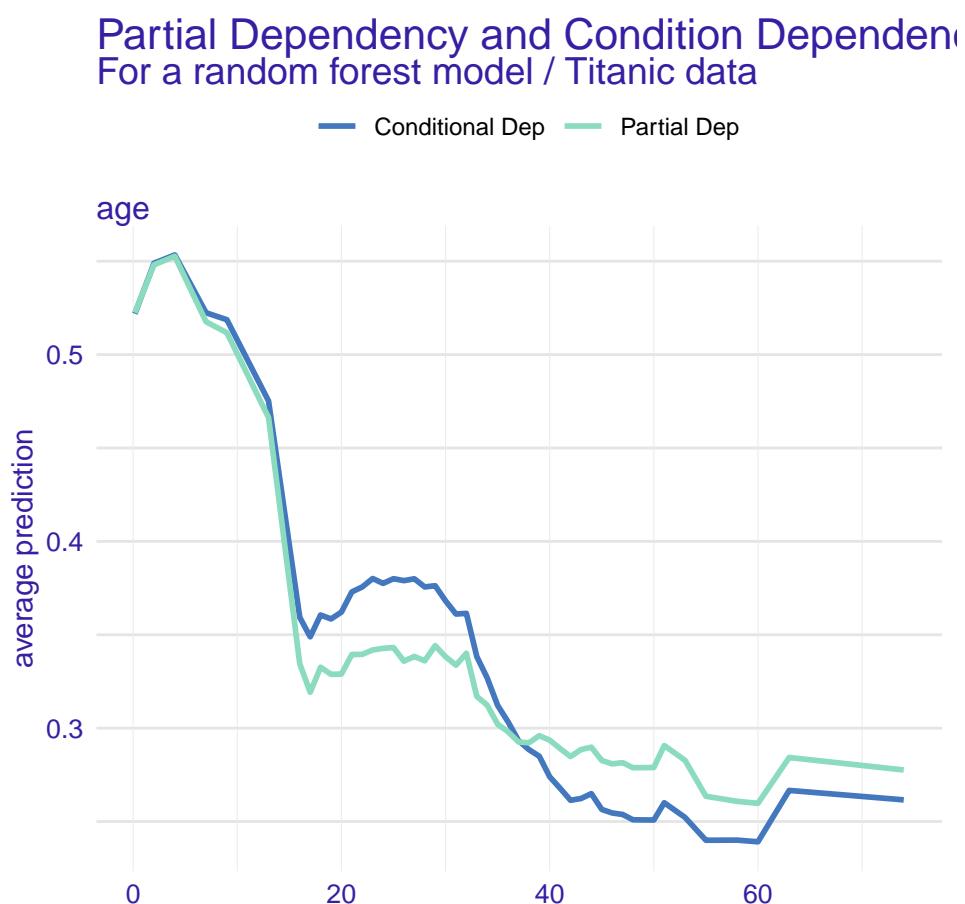


FIGURE 54 (#fig:mp_part_1) Conditional Dependency Profile for 100 observations

that in some cases the dependency is real and should be taken into account when computing expected value of f . The disadvantage is that in the Conditional Dependency Profiles we see both effects of the feature of interest x^j and other features that are dependent on it. Accumulated Local Profiles disentangle effects of a feature of interest and features correlated with it.

For example, for the *apartments* dataset one can expect that features like *surface* and *number.or.rooms* are correlated but we can also imagine that each of these variables affect the apartment price somehow. Partial Dependency Profiles show how the average price changes as a function of surface, keeping all other variables unchanged. Conditional Dependency Profiles show how the average price changes as a function of surface adjusting all other variables to the current value of the surface. Accumulated Local Profiles show how the average price changes as a function of surface adjusting all other variables to the current value of the surface but extracting changes caused by these other features.

Accumulated Local Dependency Profiles presented in the (Apley, 2018b) paper.

The general idea is to accumulate local changes in model response affected by single feature x^j .

0.19.1 Definition

Accumulated Local Profile for a model f and a variable x^j is defined as

$$g_{AL}^{f,j}(z) = \int_{z_0}^z E \left[\frac{\partial f(X^j, X^{-j})}{\partial x_j} | X^j = v \right] dv + c,$$

where z_0 if the lower boundry of x^j . The profile $g_{AL}^{f,j}(z)$ is calculated up to some constant c .

Usually the constant c is selected to keep average $g_{AL}^{f,j}$ equal to 0 or average f .

The equation may be a bit complex, but the intuition is not that complicated. Instead of aggregation of Ceteris Paribus we just look locally how quickly CP profiles are changing.

And AL profile is reconstructed from such local partial changes.

So it's an cummulated expected change of the model response along where the expected values are calculated over **conditional** distribution $(X^j, X^{-j}) | X^j = v$.

Exercise

Let $f = x_1 + x_2$ and distribuion of (x_1, x_2) is given by $x_1 \sim U[0, 1]$ and $x_2 = x_1$.

Calculate $g_{AD}^{f,1}(z)$.

Answer $g_{AD}^{f,1}(z) = z$.

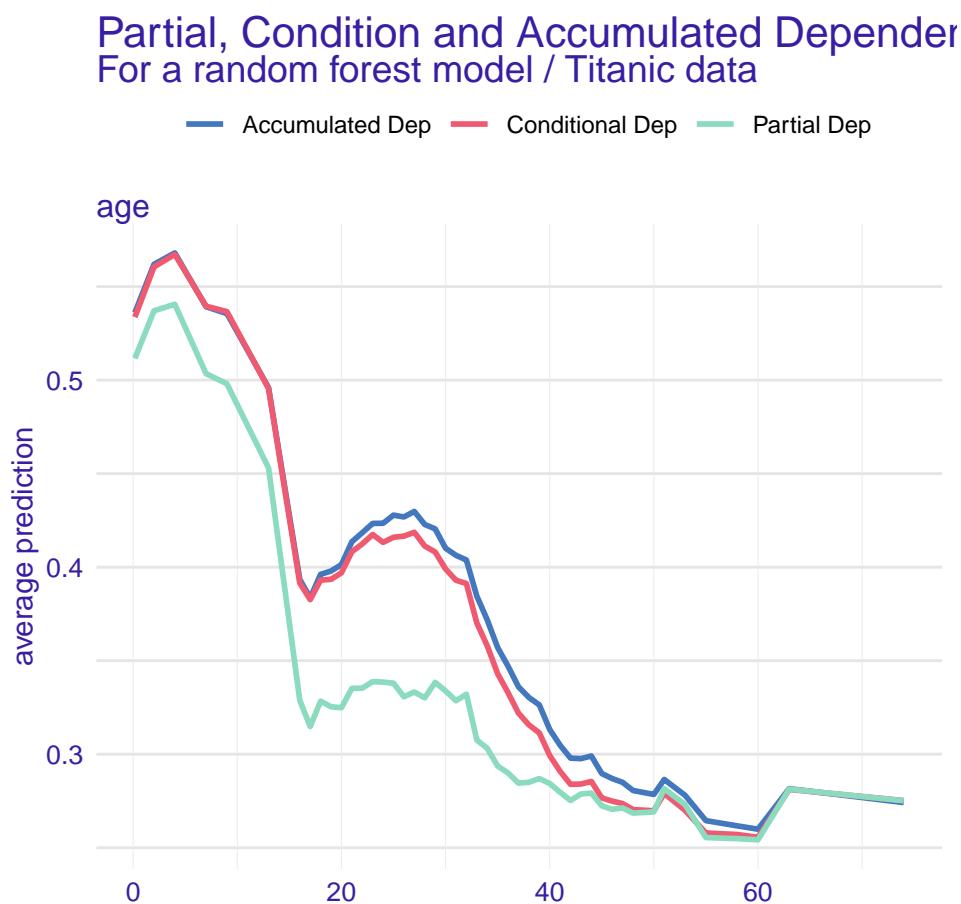


FIGURE 55 (#fig:ale_part_1) Accumulated Local Effects for 100 observations

0.20 Summary of Explainers for Feature Effects

In previous chapters we introduced different ways to calculate model level explainers for feature effects. A natural question is how these approaches are different and which one should we choose.

An example that illustrates differences between these approaches is presented in Figure @ref{accumulatedLocalEffects}. Here we have a model $f(x_1, x_2) = x_1 * x_2 + x_2$ and what is important features are correlated $x_1 \sim U[-1, 1]$ and $x_2 = x_1$.

We have 8 points for which we calculated instance level profiles.

x_1	x_2
-1	-1
-0.71	-0.71
-0.43	-0.43
-0.14	-0.14
0.14	0.14
0.43	0.43
0.71	0.71
1	1

Panel A) shows Ceteris Paribus for 8 data points, the feature x_1 is on the OX axis while f is on the OY. Panel B) shows Partial Dependency Profiles calculated as an average from CP profiles.

$$g_{PD}^{f,1}(z) = E[z * x^2 + x^2] = 0$$

Panel C) shows Conditional Dependency Profiles calculated as an average from conditional CP profiles. In the figure the conditioning is calculated in four bins, but knowing the formula for f we can calculate it directly as.

$$g_{CD}^{f,1}(z) = E[X^1 * X^2 + X^2 | X^1 = z] = z^2 + z$$

Panel D) shows Accumulated Local Effects calculated as accumulated changes in conditional CP profiles. In the figure the conditioning is calculated in four bins, but knowing the formula for f we can calculate it directly as.

$$g_{AL}^{f,1}(z) = \int_{z_0}^z E \left[\frac{\partial(X^1 * X^2 + X^2)}{\partial x_1} | X^1 = v \right] dv = \int_{z_0}^z E [X^2 | X^1 = v] dv = \frac{z^2 - 1}{2},$$

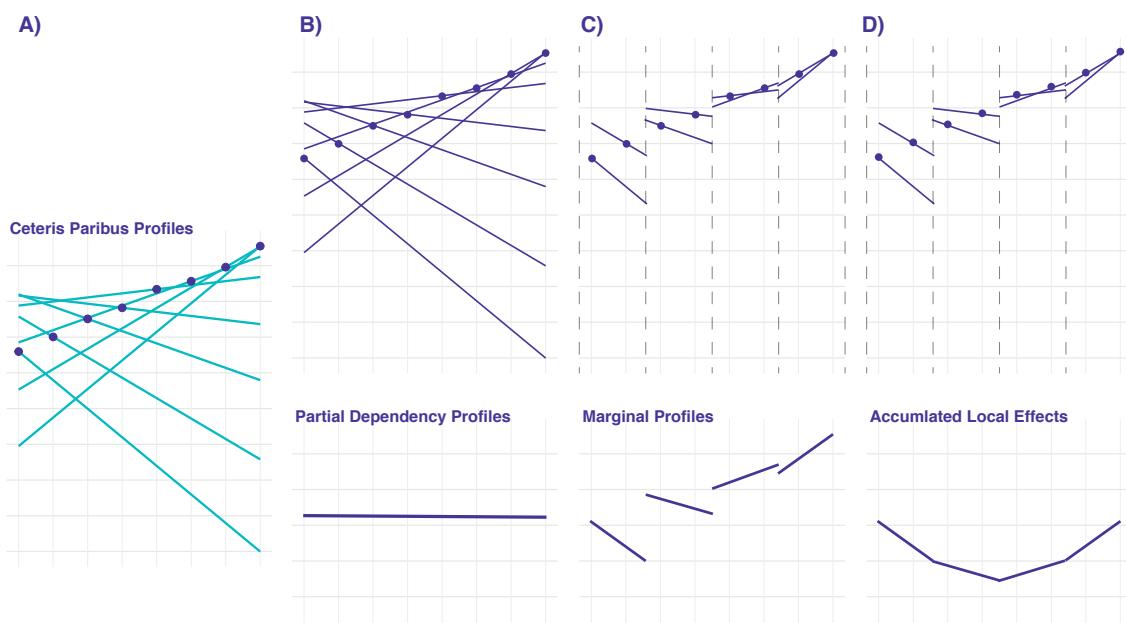


FIGURE 56 (fig:accumulatedLocalEffects) Differences between Partial Dependency, Marginal and Accumulated Local Effects profiles. Panel A) shows Ceteris Paribus Profiles for 8 points. Panel B) shows Partial Dependency profiles, i.e. an average out of these profiles. Panel C shows Marginal profiles, i.e. an average from profiles similar to the point that is being explained. Panel D shows Accumulated Local Effects, i.e. effect curve that takes into account only changes in the Ceteris Paribus Profiles.

```
## Distribution not specified, assuming bernoulli ...
```

0.20.1 Merging Path Plots and Others

(Demšar and Bosnić, 2018)

(Greenwell, 2017c) (Puri et al., 2017)

(Sitko et al., 2018)

(Strobl et al., 2007) (Strobl et al., 2008) - variable importance

(Fisher et al., 2018)

Beware Default Random Forest Importances

Terence Parr, Kerem Turgutlu, Christopher Csiszar, and Jeremy Howard March 26, 2018.

<http://explained.ai/rf-importance/index.html>

```
library(factorMerger)
```

0.20.2 Other topics

(Paluszynska and Biecek, 2017b) (Goldstein et al., 2017) (Apley, 2018b)

(Tatarynowicz et al., 2018)

0.21 Performance Diagnostic

Goal: how good is the model, which is better

(Piltaver et al., 2016) how good is the tree explainer

Model selection

- ROC / RROC / LIFT

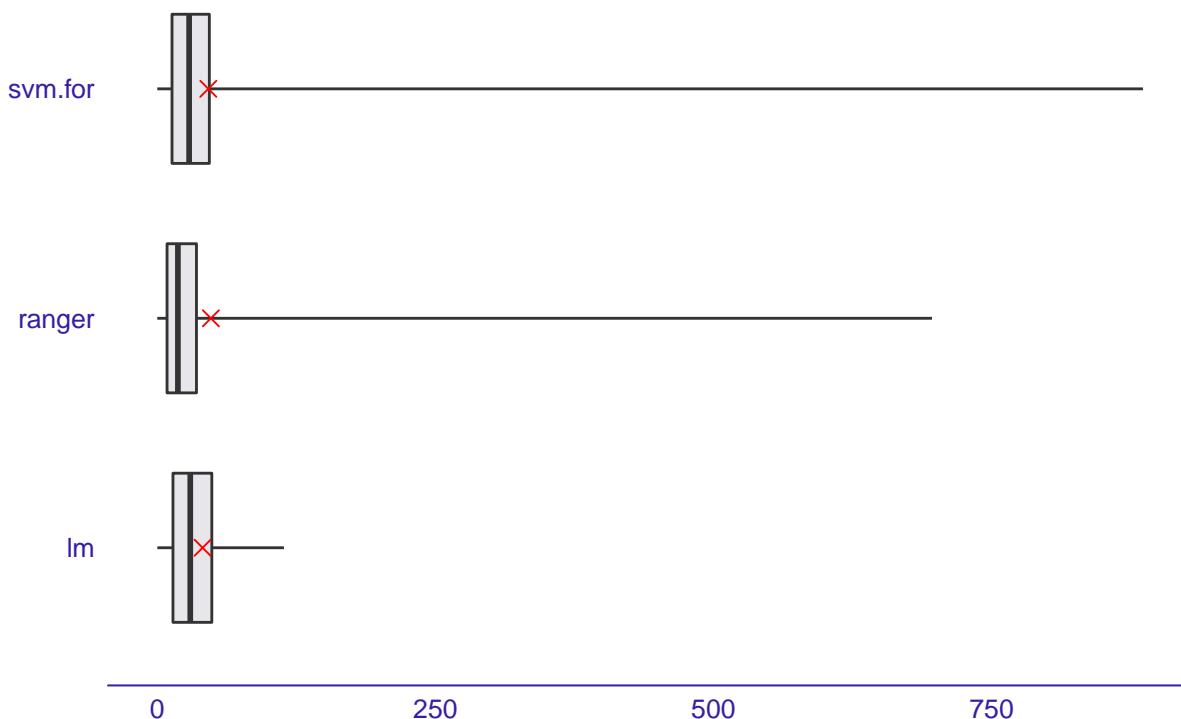
```
library("auditor")
library("DALEX2")
library("ranger")
library("e1071")

rf_model <- ranger(life_length ~ ., data = dragons)
lm_model <- lm(life_length ~ ., data = dragons)
svm_model <- svm(life_length ~ ., data = dragons)
```

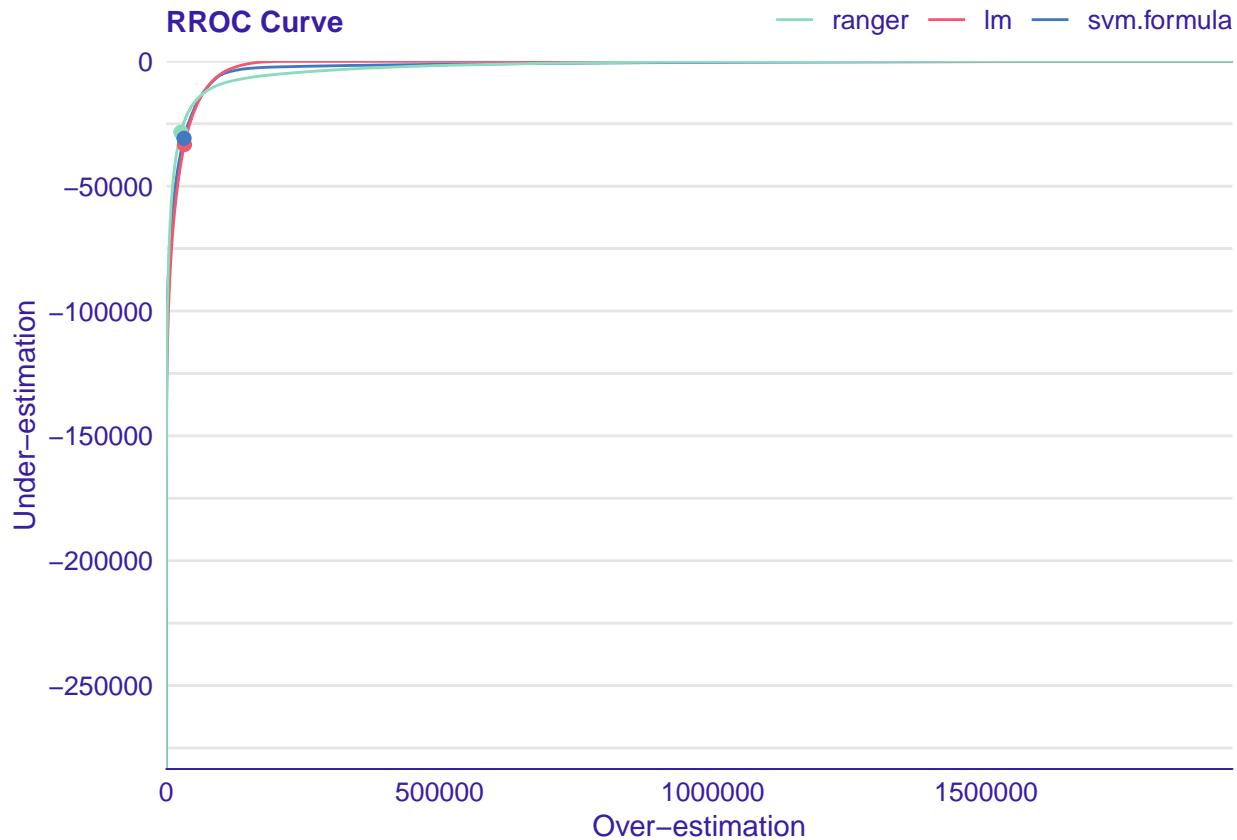
```
predict_function <- function(m,x,...) predict(m, x, ...)$predictions
rf_au <- audit(rf_model, data = dragons, y = dragons$life_length,
                 predict.function = predict_function)
lm_au <- audit(lm_model, data = dragons, y = dragons$life_length)
svm_au <- audit(svm_model, data = dragons, y = dragons$life_length)

plotResidualBoxplot(rf_au, lm_au, svm_au)
```

Absolute residuals



```
plotRROC(rf_au, lm_au, svm_au)
```



0.22 Residual Diagnostic

Goal: verify if model is ok

(Gosiewska and Biecek, 2018)

```
library("auditor")
library("DALEX2")
library("ranger")

rf_model <- ranger(life_length ~ ., data = dragons)
predict_function <- function(m,x,...) predict(m, x, ...)$predictions
rf_au <- audit(rf_model, data = dragons, y = dragons$life_length,
               predict.function = predict_function)
#check_residuals(rf_au)

#plotResidualBoxplot(rf_au)
#plotResidual(rf_au, variable = "Observed response")
plotScaleLocation(rf_au)
```

```
plotRROC(rf_au)
plotAutocorrelation(rf_au)
```

0.23 Concept Drift

Machine learning models are often fitted and validated on historical data under silent assumption that data are stationary. The most popular techniques for validation (k-fold cross-validation, repeated cross-validation, and so on) test models on data with the same distribution as training data.

Yet, in many practical applications, deployed models are working in a changing environment. After some time, due to changes in the environment, model performance may degenerate, as model may be less reliable.

Concept drift refers to the change in the data distribution or in the relationships between variables over time. Think about model for energy consumption for a school, over time the school may be equipped with larger number of devices or with more power-efficient devices that may affect the model performance.

In this chapter we define basic ideas behind concept drift and propose some solutions.

0.23.1 Introduction

In general, concept drift means that some statistical properties of variables used in the model change over time. This may result in degenerated performance. Thus the early detection of concept drift is very important, as it is needed to adapt quickly to these changes.

The term `concept` usually refers to target variable, but generally, it can also refer to model input of relations between variables.

The most general formulation of a concept drift refers to changes in joint distribution of $p(X, y)$. It is useful to define also following measures.

- Conditional Covariate Drift as change in $p(X|y)$
- Conditional Class Drift as change in $p(y|X)$
- Covariate Drift or Concept Shift as changes in $p(X)$

Once the drift is detected one may re-fit the model on newer data or update the model.

0.23.2 Covariate Drift

Covariate Drift is a change in distribution of input, change in the distribution of $p(X)$. The input is a p -dimensional vector with variables of possible mixed types and distributions.

Here we propose a simple one-dimensional method, that can be applied to each variable separately despite of its type. We do not rely on any formal statistical test, as the power of the test depends on sample size and for large samples the test will detect even small differences.

We also consider an use-case for two samples. One sample gathers historical „old” data, this may be data available during the model development (part of it may be used as training and part as test data). Second sample is the current „new” data, and we want to know is the distribution of X_{old} differs from the distribution of X_{new} .

There is a lot of distances between probability measures that can be used here (as for example Wasserstein, Total Variation and so on). We are using the Non-Intersection Distance due to its easy interpretation.

For categorical variables P and Q non-intersection distance is defined as

$$d(P, Q) = 1 - \sum_{i \in \mathcal{X}} \min(p_i, q_i)$$

where \mathcal{X} is a set of all possible values while p_i and q_i are probabilities for these values in distribution P and Q respectively. An intuition behind this distance is that it's amount of the distribution P that is not shared with Q (it's symmetric). The smaller the value the closer are these distributions.

For continuous variables we discretize their distribution in the spirit of χ^2 test.

0.23.3 Code snippets

Here we are going to use the `drifter` package that implements some tools for concept drift detection.

As an illustration we use two datasets from the `DALEX2` package, namely `apartments` (here we do not have drift) and `dragons` (here we do have drift).

```
library("DALEX2")
library("drifter")

# here we do not have any drift
head(apartments, 2)

## #> #> m2.price construction.year surface floor no.rooms district
## #> 1 5897 1953 25 3 1 Srodmiescie
## #> 2 1818 1992 143 9 5 Bielany
```

```

d <- calculate_covariate_drift(Apartments, Apartments_test)
d

##           Variable Shift
## -----
##      m2.price      4.9
## construction.year    6.0
##      surface      6.8
##      floor       4.9
## no.rooms      2.8
## district      2.6

# here we do have drift
head(Dragons, 2)

##   year_of_birth   height   weight scars colour year_of_discovery
## 1      -1291 59.40365 15.32391     7   red            1700
## 2      1589 46.21374 11.80819     5   red            1700
##   number_of_lost_teeth life_length
## 1                      25     1368.433
## 2                      28     1377.047

d <- calculate_covariate_drift(Dragons, Dragons_test)
d

##           Variable Shift
## -----
##      year_of_birth     8.9
##      height      15.3  .
##      weight      14.7  .
##      scars       4.6
##      colour      17.9  .
##      year_of_discovery 97.5 ***
##   number_of_lost_teeth    6.3
##      life_length     8.6

```

0.23.4 Residual Drift

Perhaps the most obvious negative effect of the concept drift is that the model performance degrades over time.

But this is also something that is straightforward to verify. One can calculate distribution of residuals on new data and compare this distribution with residuals obtained on old data.

Again, we have two samples, residuals calculated on the old dataset

$$r_{old} = y_{old} - \hat{y}_{old} = y_{old} - f_{old}(X_{old})$$

versus residuals calculated on the new dataset

$$r_{new} = y_{new} - \hat{y}_{new} = y_{new} - f_{old}(X_{new})$$

We can use any distance between distributions to compare r_{new} and r_{old} , for example the non-intersection distance.

0.23.5 Code snippets

Here we are going to use the `drifter` package.

```
library("DALEX2")
library("drifter")
library("ranger")

data_old <- apartments_test[1:4000,]
data_new <- apartments_test[4001:8000,]

predict_function <- function(m,x,...) predict(m, x, ...)$predictions
model_old <- ranger(m2.price ~ ., data = apartments)
calculate_residuals_drift(model_old,
                           data_old, data_new,
                           data_old$m2.price,
                           data_new$m2.price,
                           predict_function = predict_function)

##             Variable   Shift
## ----- 
##      Residuals    3.9
```

0.23.6 Model Drift

Model Drift is a change in the relation between target variable and input variables, change in $p(y|X)$. The input is a p -dimensional vector with variables of possible mixed types and distributions.

Here we propose a simple one-dimensional method based on Partial Dependency Plots introduced in the Chapter ???. PDP profiles summaries marginal relation between \hat{y} and variable x_i . The idea behind concept drift is to compare two models, the old model f_{old} and model refitted on the new data f_{new} and compare these models through PDP profiles.

For each variable we can obtain scores for drift calculated as L_2 distance between PDP profiles for both models.

$$drift_i = \frac{1}{|Z_i|} \int_{z \in Z_i} (PDP_i(f_{old}) - PDP_i(f_{new}))^2 dz$$

where Z_i is the set of values for variable x_i (for simplicity we assume that it's an interval) while $PDP_i(f_{new})$ is the PDP profile for variable i calculated for the model f_{new} .

0.23.7 Code snippets

Here we are going to use the `drifter` package. Instead of using `old` and `new` data here we compare model trained on data with males versus new dataset that contain data for females. But, because of the interaction of gender and age, models created on these two datasets are different.

```
library("DALEX2")
library("drifter")
library("ranger")

predict_function <- function(m,x,...) predict(m, x, ..., probability=TRUE)$predictions[,1]
data_old = HR[HR$gender == "male", -1]
data_new = HR[HR$gender == "female", -1]
model_old <- ranger(status ~ ., data = data_old, probability = TRUE)
model_new <- ranger(status ~ ., data = data_new, probability = TRUE)
calculate_model_drift(model_old, model_new,
                       HR_test,
                       HR_test$status == "fired",
                       max_obs = 1000,
                       predict_function = predict_function)

library("ceterisParibus2")
prof_old <- individual_variable_profile(model_old,
                                           data = data_new,
                                           new_observation = data_new[1:1000,],
                                           label = "model_old",
                                           predict_function = predict_function)
prof_new <- individual_variable_profile(model_new,
                                           data = data_new,
                                           new_observation = data_new[1:1000,],
                                           label = "model_new",
                                           predict_function = predict_function)
plot(prof_old, prof_new,
      variables = "age", aggregate_profiles = mean,
      show_observations = FALSE, color = "_label_", alpha = 1)
```

Appendices

0.24 Ceteris-paribus Two-dimensional Profiles - a Tool for Pairwise Interactions

0.24.1 Introduction

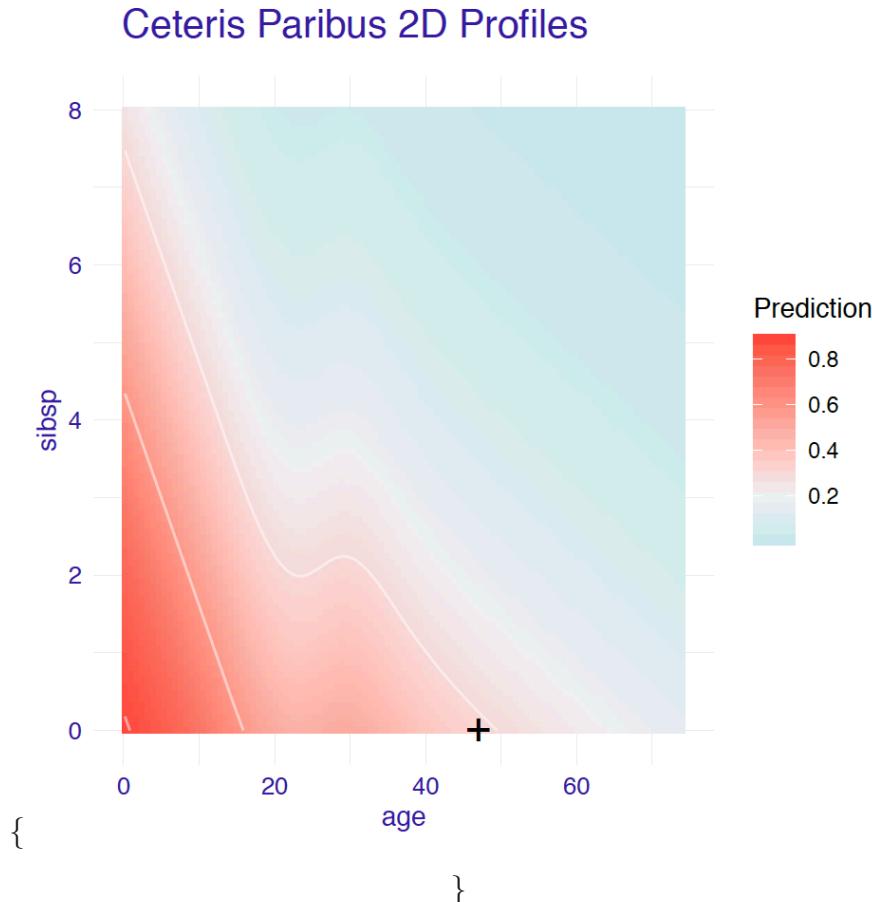
The definition of Ceteris-paribus (CP) profiles, given in Section 0.6, may be easily extended to two or more explanatory variables. Also, the definition of the variable importance measure $vip_j^{CP}(x^*)$ have a straightforward extension for a larger number of variables. The extensions are useful to identify or visualize pairwise interactions between explanatory variables.

0.24.2 Intuition

Figure 0.24.2 presents response (prediction) surface for the `titanic_lmr_v6` model for two explanatory variables, `age` and `sibsp`, from the `titanic` dataset (see Section 0.4.1). We are interested in the change of the model prediction induced jointly by the variables.

[TOMASZ: THIS IS A BIT WEAK. WHAT INTUITIVE IS ABOUT THE PLOT? WHAT CAN BE SEEN DIFFERENTLY THAN IN AN 1D CP PROFILE? WHICH STRUCTURE WOULD WE LOOK FOR?]

\begin{figure}



\caption{(fig:profile2d) Ceteris-paribus profile for `age` and `sibsp` explanatory variables for the `titanic_lmr_v6` model.} \end{figure}

0.24.3 Method

The definition of one-dimensional CP profiles (see Section 0.6.3) may be easily extended to two or more explanatory variables. A two-dimensional CP profile for model $f()$, explanatory variables j and k , and point x^* is defined as follows:

$$CP^{f,(j,k),x^*}(z_1, z_2) \equiv f(x^* |^{(j,k)} = (z_1, z_2)).$$

Thus, a two-dimensional (2D) CP profile is a function that provides the dependence of the instance prediction of the model on the values of j -th and k -th explanatory variables Z_1 and Z_2 , respectively. The values of Z_1 and Z_2 are taken to go through the range of values typical for the variables. All other explanatory variables are kept fixed at the values given by x^* .

The corresponding variable importance measure is defined as follows:

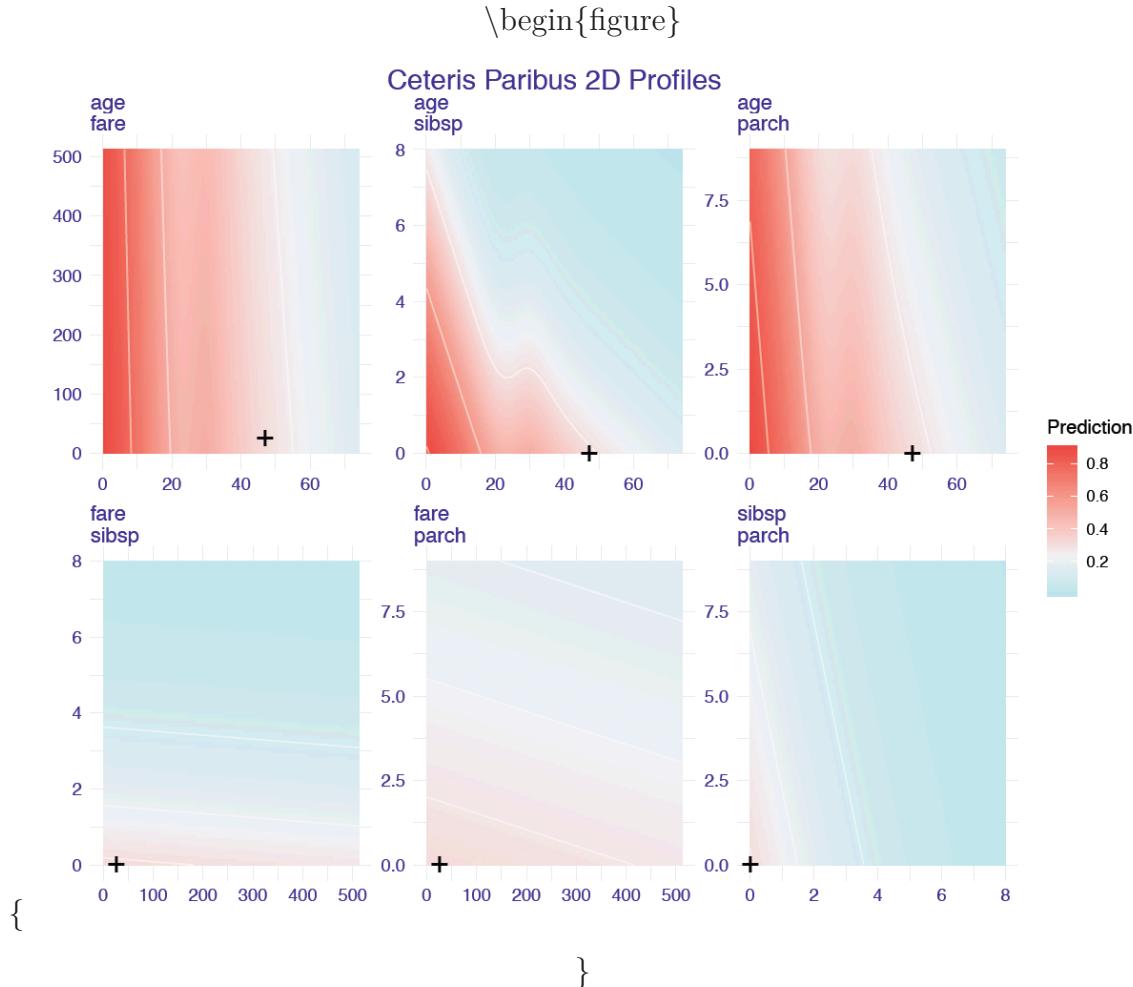
$$vip_{j,k}^{CP}(x^*) = \int_{\mathcal{R}} \int_{\mathcal{R}} |CP^{f,(j,k),x^*}(z_1, z_2) - f(x^*)| g^{j,k}(z_1, z_2) dz_1 dz_2 = E_{X_j, X_k} [|CP^{f,j,x^*}(X_j, X_k) - f(x^*)|],$$

where the expected value is taken over the joint distribution of the j -th and k -th explanatory variable.

Such multi-dimensional extensions are useful to check if, for instance, the model involves interactions. In particular, presence of pairwise interactions may be detected with 2D CP profiles.

0.24.4 Example: Titanic data

A natural way to visualize 2D CP profiles is to use a heat map for all pairs of explanatory variables as, in Figure 0.24.4.



\caption{(fig:profile2dAll) Two-dimensional ceteris-paribus profiles for all pairs of explanatory variables for the `titanic_lmer_v6` model. Black-cross marks the point of interest.} \end{figure}

If the number of pairs of explanatory variables is small or moderate, then it is possible to present 2D CP profiles for all pairs of variables.

If the number of pairs is large, we can use the variable importance measure to order the pairs based on their importance and select the most important pairs for purposes of illustration.

[TOMASZ: WE SHOULD INCLUDE HERE A MORE SUBSTANTIVE DISCUSSION REFERRING TO “HENRY”.]

0.24.5 Pros and cons

Two-dimensional CP profiles can be used to identify the presence and the influence of pairwise interactions in a model. However, for models with a large number of explanatory variables, the number of pairs will be large. Consequently, inspection of all possible 2D CP profiles may be challenging. Moreover, the profiles are more difficult to read and interpret than the 1D CP profiles.

[TOMASZ: 2D CP PROFILES FOR FACTORS?]

0.24.6 Code snippets for R

In this section, we present key features of the R package `ingredients` (Biecek, 2019a) which is a part of `DALEXverse` and covers all methods presented in this chapter. More details and examples can be found at <https://modeloriented.github.io/ingredients/>.

There are also other R packages that offer similar functionality, like `condvis` (O’Connell et al., 2017) or `ICEbox` (Goldstein et al., 2015b).

We use the random forest model `titanic_rf_v6` developed for the Titanic dataset (see Section @ref(model_titanic_rf)) as the example. Recall that we deal with a binary classification problem - we want to predict the probability of survival for a selected passenger.

```
titanic <- archivist::aread("pbiecek/models/27e5c")
titanic_rf_v6 <- archivist::aread("pbiecek/models/31570")
```

First, we have got to create a wrapper around the model (see Section 0.6.6).

```
library("DALEX")
library("randomForest")

explain_titanic_rf <- explain(model = titanic_rf_v6,
                                data = titanic[,-9],
                                y = titanic$survived == "yes",
                                label = "Random Forest v6")
```

To calculate oscillations we need to first calculate CP profiles for the selected observation. Let us use `henry` as the instance prediction of interest.

[TOMASZ: WHY NOT USING THE PRE-DEFINED DATA FRAME?]

```
henry <- data.frame(
  class = factor("1st", levels = c("1st", "2nd", "3rd", "deck crew", "engineering crew",
                                    "restaurant staff", "victualling crew")),
  gender = factor("male", levels = c("female", "male")),
  age = 8,
  sibsp = 0,
  parch = 0,
  fare = 72,
  embarked = factor("Southampton", levels = c("Belfast", "Cherbourg", "Queenstown", "Southampton"))
)
```

2D profiles are calculated by applying the `ceteris_paribus_2d()` function to the wrapper object. By default, all pairs of continuous explanatory variables are used, but one can limit number of variables for consideration through the `variables` argument. [TOMASZ: FACTORS?]

```
library("ingredients")
library("ggplot2")

wi_rf_2d <- ceteris_paribus_2d(explain_titanic_rf, observation = henry, variables = c("age", "sibsp", "parch"))
head(wi_rf_2d)
```

As a result, we obtain an object of class `ceteris_paribus_2d_explainer` with overloaded `print()` and `plot()` functions. We can use the latter function to obtain plots of the constructed 2D CP profilest.

[TOMASZ: LABELLING OF THE AXES COULD BE IMPROVED. IT IS UNCLEAR WHICH VARIABLES DEFINE THE Y- AND X AXES.]

```
plot(wi_rf_2d) +
  theme(legend.position = "right", legend.direction = "vertical") + ggtitle("Ceteris Paribus 2D Profiles")
```

The plot suggests that `age` and `sibsp` importantly influence the model response. [TOMASZ: WHY? WHICH FEATURE OF THE PLOTS DISTINGUISHES THIS PAIR FROM THE THREE OTHERS?]

[TOMASZ: WE SHOULD DISCUSS “HENRY” IN THE EXAMPLE SECTION. IN THE SNIPPETS, WE SHOULD SIMPLY SHOW THE UNDERLYING CODE.]

0.25 Variable attribution for linear models

0.25.1 Introduction

In this chapter we introduce the concept and the intuitions underlying “variable attribution,” i.e., the decomposition of the difference between the single-instance and the average model predictions among the different explanatory variables. We can think about the following examples:

- Assume that we are interested in predicting the risk of heart attack based on person’s age, sex, and smoking habits. A patient may want to know which factors have the highest impact on the his/her risk score.
- Consider a model for prediction of apartment prices. An investor may want to know how much of the predicted price may be attributed to, for instance, the location of an apartment.
- Consider a model for credit scoring. A customer may want to know if factors like gender, age, or number of children influence model predictions.

In each of those cases we want to attribute a part of the model prediction to a single explanatory variable. This can be done directly for linear models. Hence, in this chapter we focus on those models. The method can be easily extended to generalized linear models.

Model-agnostic approaches will be presented in Chapters 0.9 and 0.11.

0.25.2 Intuition

Assume a classical linear model for response Y with p explanatory variables collected in the vector $X = (X_1, X_2, \dots, X_p)$ and coefficients $\beta = (\beta_0, \beta_1, \dots, \beta_p)$, where β_0 is the intercept. The prediction for Y at point $X = x = (x_1, x_2, \dots, x_p)$ is given by the expected value of Y conditional on $X = x$. For a linear model, the expected value is given by the following linear combination:

$$E_Y(Y|x) = f(x) = \beta_0 + x_1\beta_1 + \dots + x_p\beta_p.$$

We are interested in the contribution of the i -th explanatory variable to model prediction $f(x^*)$ for a single observation described by x^* . In this case, the contribution is equal to $x_i^*\beta_i$, because the i -th variable occurs only in this term. As it will become clear in the sequel, it is easier to interpret the variable’s contribution if x_i is centered by subtracting a constant \hat{x}_i (usually, the mean of x_i). This leads the following, intuitive formula for the variable attribution:

$$v(f, x^*, i) = \beta_i(x_i^* - \hat{x}_i).$$

0.25.3 Method

We want to calculate $v(f, x^*, i)$, which is the contribution of the i -th explanatory variable to the prediction of model $f()$ at point x^* . Assume that $E_Y(Y|x^*) \approx f(x^*)$, where $f(x^*)$ is the value of the model at x^* . A possible approach to define $v(f, x^*, i)$ is to measure how much the expected model response changes after conditioning on x_i^* :

$$v(f, x^*, i) = E_Y(Y|x^*) - E_{X_i}\{E_Y[Y|(x_1^*, \dots, x_{i-1}^*, X_i, x_{i+1}^*, x_p^*)]\} \approx f(x^*) - E_{X_i}[f(x_{-i}^*)],$$

where x_{-i}^* indicates that variable X_i in vector x_{-i}^* is treated as random. For the classical linear model, if the explanatory variables are independent, $v(f, x^*, i)$ can be expressed as follows:

$$v(f, x^*, i) = f(x^*) - E_{X_i}[f(x_{-i}^*)] = \beta_0 + x_1^*\beta_1 + \dots + x_p^*\beta_p - E_{X_i}[\beta_0 + x_1^*\beta_1 + \dots + \beta_i X_i + \dots + x_p^*\beta_p] = \beta_i[x_i^* - E_{X_i}(X_i)].$$

In practice, given a dataset, the expected value of X_i can be estimated by the sample mean \bar{x}_i . This leads to

$$v(f, x^*, i) = \beta_i(x_i^* - \bar{x}_i).$$

Note that the linear-model-based prediction may be re-expressed in the following way:

$$\begin{aligned} f(x^*) &= [\beta_0 + \bar{x}_1\beta_1 + \dots + \bar{x}_p\beta_p] + [(x_1^* - \bar{x}_1)\beta_1 + \dots + (x_p^* - \bar{x}_p)\beta_p] \\ &\equiv [\text{average prediction}] + \sum_{j=1}^p v(f, x^*, j). \end{aligned}$$

Thus, the contributions of the explanatory variables are the differences between the model prediction for x^* and the average prediction.

** NOTE for careful readers **

Obviously, sample mean \bar{x}_i is an estimator of the expected value $E_{X_i}(X_i)$, calculated using a dataset. For the sake of simplicity we do not emphasize these differences in the notation.

Also, we ignore the fact that, in practice, we never know the model coefficients and we work with an estimated model.

Also, we assumed that the explanatory variables are independent, which may not be the case. We will return to this problem in Section 0.10, when we will discuss interactions.

0.25.4 Example: Wine quality

Figure 57 shows the relation between alcohol and wine quality, based on the wine dataset (Cortez et al., 2009). The linear model is

$$\text{quality(alcohol)} = 2.5820 + 0.3135 * \text{alcohol}.$$

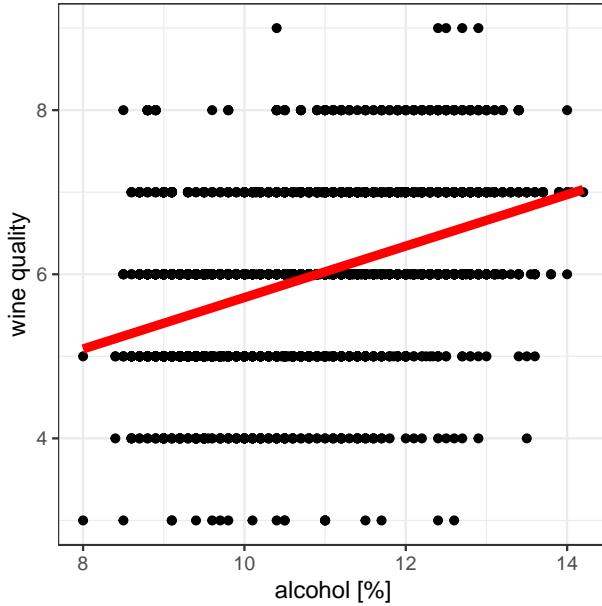


FIGURE 57 (fig:attribution1a) Relation between wine quality and concentration of alcohol assessed with linear model

The weakest wine in the dataset has 8% of alcohol, while the average alcohol concentration is 10.51%. Thus, the contribution of alcohol to the model prediction for the weakest wine is $0.3135 \cdot (8 - 10.51) = -0.786885$. This means that low concentration of alcohol for this wine (8%) decreases the predicted quality by -0.786885 .

Note, that it would be misleading to use $x_i^* \beta_i = 0.3135 * 8 = 2.508$ as the alcohol contribution to the quality. The positive value of the product would not correspond to the intuition that, in the presence of a positive relation, a smaller alcohol concentration should imply a lower quality of the wine.

0.25.5 Pros and Cons

The introduced values $v(f, x^*, i)$ do not depend on neither scale nor location of X_i ; hence, it is easier to understand than, for instance, the standardized value of β_i . For the classical linear model, $v(f, x^*, i)$ is not an approximation and it is directly linked with the structure of a model. An obvious disadvantage is that the definition of $v(f, x^*, i)$ is very much linear-model based. Also, it does not, in any way, reduce the model complexity; if model has 10 parameters then the prediction is decomposed into 10 numbers. Maybe these numbers are easier to understand, but dimensionality of model description has not changed.

0.25.6 Code snippets

In this section, we present an example of computing variable attributions using the `HR` dataset (see Section ?? for more details).

To calculate variable attributions for a particular point, first we have got to define this point:

```
dilbert <- data.frame(gender = factor("male", levels = c("male", "female")),
                      age = 57.7,
                      hours = 42.3,
                      evaluation = 2,
                      salary = 2)
```

Variable attributions for linear and generalized linear models may be directly extracted by applying the `predict()` function, with the argument `type = "terms"`, to an object containing results of fitting of a model. To illustrate the approach for logistic regression, we build a logistic regression model for the binary variable `status == "fired"` and extract the estimated model coefficients:

```
library("DALEX")
model_fired <- glm(status == "fired" ~ ., data = DALEX::HR, family = "binomial")
coef(model_fired)

## (Intercept) gendermale      age      hours   evaluation
## 5.737945729 -0.066803609 -0.001503314 -0.102021120 -0.425793369
##          salary
## -0.015740080
```

For the new observation, the predicted value of the logit of the probability of being fired is obtained by applying the `predict()` function:

```
as.vector(pred.inst <- predict(model_fired, dilbert)) # new prediction

## [1] 0.3858406
```

On the other hand, variable attributions can be obtained by applying the `predict()` function with the `type="terms"` argument:

```
(var.attr <- predict(model_fired, dilbert, type = "terms")) # attributions

##       gender      age      hours   evaluation      salary
## 1 -0.03361889 -0.02660691  0.7555555  0.5547197  0.007287334
## attr(,"constant")
## [1] -0.8714962
```

The largest contributions to the prediction come from variables “hours” and “evaluation.” Variables “gender” and “age” slightly decrease the predicted value. The sum of the attributions is equal to

```
sum(var.attr)

## [1] 1.257337
```

The attribute `constant` of object `var.attr` provides the “average” prediction, i.e., the

predicted logit for an observation defined by the means of the explanatory variables, as can be seen from the calculation below:

```
coef(model_fired) %*% c(1, mean((HR$gender=="male")), mean(HR$age), mean(HR$hours),
mean(HR$evaluation), mean(HR$salary))
```

```
## [1] -0.8714962
```

Adding the “average” prediction to the sum of the variable attributions results in the new-observation prediction:

```
attributes(var.attr)$constant + sum(var.attr)
```

```
## [1] 0.3858406
```

Below we illustrate how to implement this approach with the DALEX package. Toward this end, functions `explain()` and `single_prediction()` can be used. Object `model_fired` stores the definition of the logistic-regression model used earlier in this section. The contents of object `attribution` correspond to the results obtained by using function `predict()`.

```
library("DALEX")
```

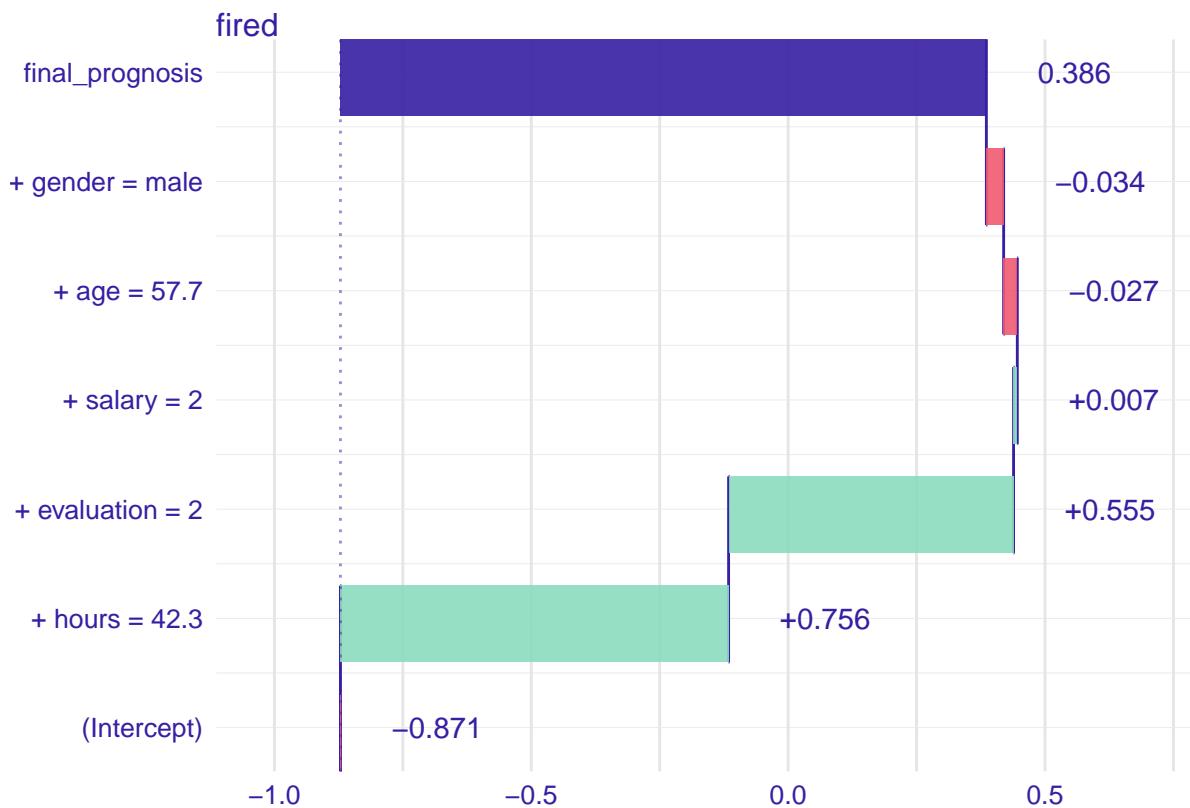
```
explainer_fired <- explain(model_fired,
  data = HR,
  y = HR$status == "fired",
  label = "fired")

(attribution <- single_prediction(explainer_fired, dilbert))
```

	variable	contribution	variable_name	variable_value
## 1	(Intercept)	-0.871496150	Intercept	1
## hours	+ hours	= 42.3 0.755555494	hours	42.3
## evaluation	+ evaluation	= 2 0.554719716	evaluation	2
## salary	+ salary	= 2 0.007287334	salary	2
## age	+ age	= 57.7 -0.026606908	age	57.7
## gender	+ gender	= male -0.033618893	gender	male
## 11	final_prognosis	0.385840593		
##	cummulative	sign	position	label
## 1	-0.8714962	-1	1	fired
## hours	-0.1159407	1	2	fired
## evaluation	0.4387791	1	3	fired
## salary	0.4460664	1	4	fired
## age	0.4194595	-1	5	fired
## gender	0.3858406	-1	6	fired
## 11	0.3858406	X	7	fired

After object `attribution` has been created, a plot presenting the variable attributions can be easily constructed:

```
plot(attribution)
```



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