

# Supporting decision-makers in healthcare domain. A comparative study of two interpretative proposals for Random Forests

Massimo Aria, Corrado Cuccurullo, Agostino Gnasso

## 1. Introduction

Today, the availability of data is growing exponentially in all sectors, especially in the healthcare sector. Machine Learning (ML) techniques allow to analyze big data to extract knowledge and support healthcare activities (Miotto et al., 2018), such as models for the diagnosis of complex diseases (Dhillon and Singh, 2019), (Aria et al., 2020). Despite the use of ML is spreading in many applications, it is characterized by some limitations and disadvantages.

ML main drawback corresponds to its lack of interpretability which does not allow users to represent causal relationships and interactions between predictors and response. This leads to the inability to learn how particular decisions are made. From this problem derives the definition of the Black Box model, a highly accurate model with a large complexity that cannot be represented by a relational structure. In other words, it is not possible to visualize how it internally works.

Furthermore, the opaque nature of these models hinders application in various sectors, especially in critical ones such as healthcare. To undertake a decision-making process, having faith in a machine learning model is essential, to feel reassured when analyzing and using it.

Ribeiro et al. (2016) identify a different but at the same time-related definitions of trust: trust in a prediction and trust in a model. Trusting a prediction implies that the user will take a certain action based on it; it is important to determine this confidence given that the model will be used to make decisions think for example of the use of a decision-making process in the clinical field, the consequence of acting with absolute confidence on the predictions obtained without being able to understand how they are obtained. Having faith in a model is equivalent to evaluating the model as a whole and testing its ability to generalize with appropriate evaluation metrics. A problem that recurs in using data from real contexts is that they are often significantly different and the chosen metric may not be adequate, therefore an inspection procedure of individual predictions and their interpretations may be the optimal choice.

In this work, we pay attention to one of the most used, accurate, and performing models in Machine Learning, the Random Forest model (RF) (Breiman, 2001).

Random Forest is an evolution of Bagging which aims to reduce the variance of a statistical model, simulates the variability of data through the random extraction of bootstrap samples from a single training set, and aggregates predictions on a new record (see Breiman, 1996). Being an evolution of Bagging, Random Forest aims to obtain even more different and unrelated trees. It is known as an efficient ensemble learning model, as it ensures high predictive accuracy, flexibility, and immediacy; it is recognized as an intuitive and understandable approach to the construction process, but is also considered a Black Box model due to the large number of deep decision trees produced within it (Haddouchi and Berrado, 2019).

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FUP Best Practice in Scholarly Publishing (DOI 10.36253/fup\_best\_practice)

Massimo Aria, Corrado Cuccurullo, Agostino Gnasso, *Supporting decision-makers in healthcare domain. A comparative study of two interpretative proposals for Random Forests*, pp. 179-184, © 2021 Author(s), CC BY 4.0 International, DOI 10.36253/978-88-5518-461-8.34, in Bruno Bertaccini, Luigi Fabbris, Alessandra Petrucci (edited by), *ASA 2021 Statistics and Information Systems for Policy Evaluation. Book of short papers of the on-site conference*, © 2021 Author(s), content CC BY 4.0 International, metadata CC0 1.0 Universal, published by Firenze University Press (www.fupress.com), ISSN 2704-5846 (online), ISBN 978-88-5518-461-8 (PDF), DOI 10.36253/978-88-5518-461-8

The results deriving from the use of the Random Forest are valuable. Various studies have confirmed RF effectiveness in many sectors, such as biomedical for genetic selection (Díaz-Uriarte and De Andres, 2006). Breiman et al. (2001) states that Random Forest has A + performance but, having a prediction process that is difficult to understand, evaluates an F on interpretability. This leads to Occam’s dilemma (Domingos, 1998) (Domingos, 1999).

The poor interpretability has prevented the adoption of the model in some sectors where there is little or no tolerance for errors, such as healthcare and clinical context (Ahmad et al., 2018). Having set the common goal of interpretability, in recent years the scientific community has fueled considerable interest in Interpretable Machine Learning, which today is an extremely open and active research field with numerous approaches that continually emerge every year (Adadi and Berrada, 2018) (Du et al., 2019) (Guidotti et al., 2018).

This research focuses on the comparison between two approaches proposed in the literature that attempt to overcome the interpretative problem. These approaches, Node Harvest by Meinshausen (2010) and inTrees by Deng (2019), are based on a post-processing interpretation method. They are also defined as Rule Extraction (Haddouchi and Berrado, 2019) approaches as they are focused on the extraction of rule sets. Both proposals use an understandable model based on the rules extracted from a Random Forest. The general idea is to identify a representative weak model to provide the interpretation. This one is selected from the sequence of weak models generated by the ensemble procedure. In particular, Node Harvest selects the set of rules through weights that are assigned based on quadratic programming with linear inequality constraints. Performing this task manages to coincide with two objectives, such as interpretability and accuracy in prediction.

Similarly, inTrees obtain interpretable information through the extraction and processing of rules deriving from a tree ensemble sequence. The extracted rules are used for the realization of a learner, which serves to make predictions on new data.

inTrees works through a series of algorithms that, at first, extract the rules and classify them; subsequently, they carry out a pruning phase on each rule, eliminating the rules that produce background noise or that are irrelevant. Subsequently, these algorithms select a compact set of rules considered relevant and not redundant. Frequent interactions are extracted and finally, everything is summarized in a learner that will be used to make predictions on new data.

## 2. Comparison Study

We compare Node Harvest and inTrees on four health datasets. Comparison analysis is performed in an empirical context, where their performance is evaluated using performance metrics. These are obtained from the output and are compared to a reference standard (Aria et al., 2021).

The metrics that evaluate the performance of predictive models, when used for classification, are based on the confusion matrix, which contains the expected and observed class labels, as well as the predicted target category and the source category, as can be seen from Table 1 which represents the structure of a 2x2 confusion matrix.

Regarding comparison, the goal is to compare these approaches through the use of different health datasets. The analysis is conducted on four binary classification health datasets. These datasets are available in the UCI Machine Learning repository. They have different characteristics (see Table 2).

Table 1: Confusion Matrix

	Actual Positive Class	Actual Negative Class
Predicted Positive Class	<i>TP (True Positive)</i>	<i>FP (False Positive)</i>
Predicted Negative Class	<i>FN (False Negative)</i>	<i>TN (True Negative)</i>

Table 2: Main characteristics of the selected health datasets.

Datasets	Obs.	Qual. Feat.	Quant. Feat.	0/1 Response Rate	Unbalanced Response
<i>Diabetic Retinopathy Debrecen</i>	1151	3	16	118/120	False
<i>EEG Eye State</i>	14980	1	15	2375/1822	False
<i>Cardiovascular Disease</i>	10500	7	5	883/707	False
<i>Pima Indians Diabetes</i>	768	8	1	130/45	False

The analysis follows the following structure: we proceed with carrying out the random forest for each of the four datasets to obtain the performance of the standard model, in terms of the confusion matrix and prediction of the target variable; the extraction of the set of rules is carried out to investigate the paths taken by each observation, of which the most important and frequent rules of the set itself will also be shown.

Finally, the comparison of the various sets of rules obtained from the two investigated methodologies is performed. The final performance evaluation is conducted through nine parameters obtained from the confusion matrices: Accuracy, Precision, Sensitivity, Specificity, G-Mean, F1 Score, Youden’s Index, Balanced Accuracy, Kappa (see Sokolova et al., García et al., Akosa).

Examples are provided of the outputs obtained from the Node Harvest and inTrees approaches. These examples derive from the analysis conducted on Pima Indians Diabetes data: Node Harvest allows you to view the set of rules through an explanatory plot, provided in figure 1, while inTrees allows easy reading through summary tables that show the most frequent rule sets, such as in the table 3.

Table 3: inTrees (STEL) on Pima Indians Diabetes: set of decision rules that are easily applicable to new data. The impRRF value measures the relative percentage decrease in the Gini index for each rule derived from the random forest. The impRRF consider the length of each rule as a proxy of its complexity.

len	freq	err	condition	pred	impRRF
3	0.279	0.307	$X[2] > 129.5 \ \& \ X[3] \leq 102 \ \& \ X[6] > 27.2$	1	1
2	0.326	0.366	$X[2] > 114.5 \ \& \ X[8] > 28.5$	1	0.301
3	0.054	0.138	$X[1] > 6.5 \ \& \ X[7] > 0.6 \ \& \ X[7] \leq 1.41$	1	0.162
4	0.134	0.278	$X[2] > 96 \ \& \ X[5] \leq 34 \ \& \ X[6] > 29.8 \ \& \ X[8] > 30.5$	1	0.144
2	0.84	0.282	$X[2] \leq 165.5 \ \& \ X[3] > 39$	0	0.139
1	0.553	0.219	$X[8] \leq 30.5$	0	0.092
4	0.024	0.154	$X[1] \leq 4.5 \ \& \ X[2] \leq 168.5 \ \& \ X[5] > 250 \ \& \ X[6] > 29.85$	0	0.088
3	0.184	0.232	$X[2] > 127.5 \ \& \ X[6] > 31.4 \ \& \ X[8] > 24.5$	1	0.073
2	0.786	0.261	$X[2] \leq 162 \ \& \ X[6] \leq 40.75$	0	0.071
4	0.119	0.375	$X[3] \leq 77 \ \& \ X[5] \leq 118 \ \& \ X[6] > 27.55 \ \& \ X[8] > 30$	1	0.060

Table 4 shows the nine performance metrics calculated on the four health datasets. The highest score, for each metric, is marked in bold. First of all, the interpretative solutions



Table 4: Summary tables on the performance metrics performed on the four health datasets.

(a) <i>Diabetic Retinopathy Debrecen</i>				(b) <i>EEG Eye State</i>			
	<i>RF</i>	<i>NH</i>	<i>STEL</i>		<i>RF</i>	<i>NH</i>	<i>STEL</i>
Accuracy	0.64	0.64	<b>0.70</b>	Accuracy	0.92	0.68	<b>0.69</b>
Balanced Accuracy	0.64	0.65	<b>0.71</b>	Balanced Accuracy	0.92	0.67	<b>0.69</b>
Kappa	0.29	0.29	<b>0.41</b>	Kappa	0.84	0.34	<b>0.38</b>
Specifity	0.65	0.48	<b>0.68</b>	Specifity	0.89	0.48	<b>0.65</b>
Sensitivity	0.64	<b>0.82</b>	0.74	Sensitivity	0.94	<b>0.85</b>	0.73
Precision	0.63	0.59	<b>0.65</b>	Precision	0.91	0.66	<b>0.72</b>
G-mean	0.64	0.63	<b>0.71</b>	G-mean	0.92	0.64	<b>0.69</b>
F1	0.64	0.68	<b>0.69</b>	F1	0.93	<b>0.75</b>	0.73
Youden's Index	0.29	0.30	<b>0.42</b>	Youden's Index	0.83	0.33	<b>0.38</b>

  

(c) <i>Cardiovascular Disease</i>				(d) <i>Pima Indians Diabetes</i>			
	<i>RF</i>	<i>NH</i>	<i>STEL</i>		<i>RF</i>	<i>NH</i>	<i>STEL</i>
Accuracy	0.73	0.69	<b>0.71</b>	Accuracy	0.71	<b>0.74</b>	0.72
Balanced Accuracy	0.73	0.69	<b>0.71</b>	Balanced Accuracy	0.67	0.67	<b>0.69</b>
Kappa	0.47	0.38	<b>0.43</b>	Kappa	0.35	<b>0.39</b>	0.38
Specifity	0.69	0.55	<b>0.66</b>	Specifity	0.55	0.42	<b>0.57</b>
Sensitivity	0.78	<b>0.84</b>	0.77	Sensitivity	0.80	<b>0.93</b>	0.80
Precision	0.71	0.64	<b>0.70</b>	Precision	0.78	0.74	<b>0.78</b>
G-mean	0.73	0.68	<b>0.71</b>	G-mean	0.66	0.62	<b>0.68</b>
F1	0.74	0.72	<b>0.73</b>	F1	0.79	<b>0.82</b>	0.79
Youden's Index	0.47	0.38	<b>0.43</b>	Youden's Index	0.35	0.35	<b>0.38</b>

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