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FFTrees: A toolbox to create, visualize, and evaluate fast-and-frugal decision trees

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Abstract

Fast-and-frugal trees (FFTs) are simple algorithms that facilitate efficient and accurate decisions based on limited information. But despite their successful use in many applied domains, there is no widely available toolbox that allows anyone to easily create, visualize, and evaluate FFTs. We fill this gap by introducing the R package `FFTrees`. In this paper, we explain how FFTs work, introduce a new class of algorithms called fan for constructing FFTs, and provide a tutorial for using the `FFTrees` package. We then conduct a simulation across ten real-world datasets to test how well FFTs created by `FFTrees` can predict data. Simulation results show that FFTs created by `FFTrees` can predict data as well as popular classification algorithms such as regression and random forests, while remaining simple enough for anyone to understand and use.

Keywords: decision trees, heuristics, prediction.

1 Introduction

An emergency room physician facing a patient with chest pain needs to quickly decide whether to send him to the coronary care unit or to a regular hospital bed (L. Green & Mehr, 1997). A soldier guarding a military checkpoint needs to decide whether an approaching vehicle is hostile or not (Keller & Katsikopoulos, 2016). A stock portfolio adviser, upon seeing that, at 3:14 am, an influential figure tweeted about a company she is heavily invested in, needs to decide whether to move her shares or sit tight (Akane & Shane, 2017). Binary classification decisions like these have important consequences and must be made under time-pressure with limited information. How should people make such decisions? One effective way is to use a fast-and-frugal decision tree (FFT, Martignon, Katsikopoulos & Woike, 2008; Martignon, Vitouch, Takezawa & Forster, 2003). In contrast to compensatory decision algorithms such as regression, FFTs allow people to make fast, accurate decisions based on limited information without requiring statistical training or a calculation device. FFTs have been successfully used to both describe decision processes and to provide prescriptive guides for effective real-world decision making in a variety of domains, including medical (Fischer et al., 2002; Jenny, Pachur, Williams, Becker & Margraf, 2013; Super, 1984; Wegwarth, Gaissmaier & Gigerenzer, 2009), legal (Dhami, 2003; Dhami & Ayton, 2001; Dhami & Harries, 2001), financial (Aikman et al., 2014; Woike, Hoffrage & Petty, 2015) and managerial (Luan & Reb, 2017) decision making.

Despite their proven effectiveness, FFTs are still not used as often as other decision algorithms. We believe that there are two key reasons for this: First, while there are many tools in popular software packages to create regression models and non-frugal decision trees, no such tool currently exists to create FFTs. Although one could construct an FFT from data with a pencil, paper, and calculator using a heuristic tree construction algorithm (Martignon et al., 2008), the process can be tedious, especially for large datasets. Second, as complex, computationally demanding algorithms, such as random forests and support vector machines increase in popularity, simple algorithms like FFTs are increasingly perceived as being outdated and inferior prediction algorithms. This paper addresses both of these reasons by introducing `FFTrees` (Phillips, Neth, Woike & Gaissmaier, 2017b), a toolbox written in the free and open-source R language (R Core Team, 2016). As we will show, `FFTrees` makes it easy for anyone to create, visualize, and evaluate FFTs that can compete with the predictive power of more complex algorithms, while staying simple and transparent enough for anyone to apply in real-world decision environments.

The rest of this paper is structured as follows: Section 1 provides a theoretical background on binary classification tasks, explains how FFTs solve them and introduces a new class of "fan" algorithms for constructing FFTs. Section 2 provides a 4-step tutorial on using the `FFTrees` package to create and evaluate FFTs from data. Finally, Section 3 presents simulation results comparing the performance of the fan algorithms to existing FFT construction algorithms and more complex algorithms such as logistic regression and random forests.

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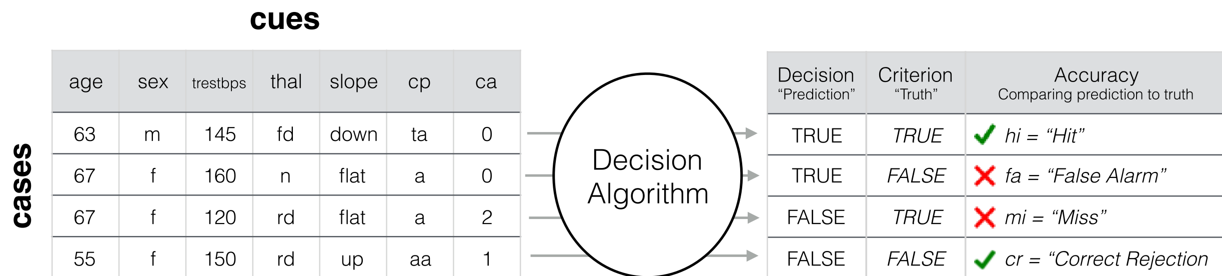


Figure 1: The structure of a binary classification task. The data underlying the task are arranged as a combination of cases (e.g., patients) and each case's values on several cues (e.g., age, sex, and various medical tests indicated by the labels trestbps, thal, slope, cp, and ca). Classification accuracy is evaluated by comparing the algorithm's decisions to the true criterion values. The goal of the algorithm is to maximize correct decisions (hits and correct rejections), while minimizing errors (misses and false-alarms).

2 Binary Classification Tasks

FFTs are supervised learning algorithms used to solve binary classification tasks. In a binary classification task, a decision maker seeks to predict a binary *criterion* value for each of a set of individual *cases* on the basis of each case's values on a range of *cues* (a.k.a., features, predictors). The structure of the task can be illustrated by a table in which each row represents a case, each column represents a cue, and individual cells represent cue values for specific cases. Figure 1 illustrates data from a set of patients (cases), where each case is characterized by their values on several measures (cues), ranging from demographic variables, such as sex and age, to biological measurements, such as cholesterol level and other medical tests. The binary criterion is the patients' heart disease status which can either be true (i.e., having heart disease) or false (i.e., not having heart disease). The true criterion values are assumed to be unknown at the time of the decision and must be inferred from the cue values. The goal of a decision maker presented with this information is to accurately classify each case into one of two categories (i.e., as high-risk or as low-risk), and make an actionable decision (i.e., send to the coronary care unit or a regular hospital bed) on the basis of this classification.

Theoretically, this structure of a binary classification task is captured by a variety of frameworks that range from the statistical analysis of clinical judgments (e.g., Hammond, 1955; Meehl, 1954) and comparisons between linear and non-linear regression models (Dawes, 1979; Einhorn & Hogarth, 1975) to the formalization of discrimination performance in signal detection theory (SDT, D. M. Green & Swets, 1966; Macmillan & Creelman, 2005). Practically, the key question that arises in this context is: How to make good classifications, and ultimately good decisions, based on cue information? One way to do this is to use an algorithm.

A *decision algorithm* (for brevity, we use only the term decision algorithm in this section, although the concepts apply equally to classification algorithms) is a formal mapping between cue values and a binary decision. We broadly distinguish between two families of decision algorithms: compensatory and non-compensatory. *Compensatory* algorithms, such as regression and random forests, tend to use most, if not all, of the available cue information because the value of one cue could potentially overturn the evidence given by one or more other cues.[1] By contrast, *non-compensatory* algorithms use only a partial subset of all cue information, because the value(s) of one or more cues can *not* be outweighed by any values of other cues. That is, non-compensatory algorithms deliberately ignore information because, once a decision is made based on some information, no additional information can change the decision.

Non-compensatory algorithms can have both practical and statistical advantages over compensatory algorithms. First, because they ignore information, non-compensatory algorithms typically use less information than compensatory algorithms. Second, because non-compensatory algorithms typically use information in a specific, sequential order, they can guide decision makers in gathering information. For these reasons, non-compensatory algorithms are especially well-suited to decision tasks for which information is costly (in terms of time, money, or processing resources) and when information must be gathered sequentially over time.

A prototypical non-compensatory algorithm is a *decision tree* (Breiman, Friedman, Olshen & Stone, 1984; Quinlan, 1986, 1987). A decision tree can be applied as a set of

[1] While many regression models are compensatory, specific cases of regression models can be non-compensatory. For example, a linear regression model with highly unequal coefficients applied to variables with restricted ranges, can be non-compensatory. Additionally, some compensatory algorithms, such as regression models built with the lasso do not use all available information (James, Witten, Hastie & Tibshirani, 2013).

ordered, conditional rules in the form "If A, then B" that are applied sequentially until a decision is reached. Formally, a decision tree is comprised of a sequence of *nodes*, representing cue-based questions, *branches*, representing answers to questions, and *leaves*, representing decisions. Decision trees are non-compensatory because, once a decision is made based on some subset of the available information (i.e., a higher node) no additional information (i.e., in lower nodes) is considered. However, just because decision trees ignore information does not guarantee that they are always simple. Without appropriate restrictions a decision tree can contain dozens of nodes forming a complex network of questions (Quinlan, 1986). When decision trees become overly complex, they become both more difficult for people to understand and use. Moreover, complex trees can be worse than simpler trees in predicting new data due to statistical problem known as overfitting (as we will explain below). This complexity problem is addressed by imposing strict restrictions on the size and shape of decision trees. One of the most restricted forms of a decision tree is a *fast-and-frugal tree* (Martignon et al., 2008, 2003).

2.1 Fast-and-Frugal Trees (FFTs)

Fast-and-frugal trees were defined by Martignon and colleagues as decision trees with exactly two branches extending from each node, where either one or both branches is an exit branch leading to a leaf (Martignon et al., 2008, 2003). In other words, in an FFT one answer (or in the case of the final node, both answers) to every question posed by a node will trigger an immediate decision. Because FFTs have an exit branch on every node, they typically make decisions faster than standard decision trees (to avoid confusion, we refer to decision trees that are not fast-and-frugal as *standard*) while simultaneously being easier to understand and use.

Figure 2 presents an FFT designed to classify patients as being at high or at low-risk for having heart disease. The three nodes in the FFT correspond to the results of three medical tests: thal indicates the result of a thallium scintigraphy, a nuclear imaging test that shows how well blood flows into the heart while exercising or at rest. The result of the test can either be normal (n), indicate a fixed defect (fd), or a reversible defect (rd). The second node uses the cue cp, indicating a patient's type of chest pain, which can be either typical angina (ta), atypical angina (aa), non-anginal pain (np), or asymptomatic (a). Finally, ca indicates the number of major vessels colored by fluoroscopy, a continuous x-ray imaging tool, whose values can range from 0 to 3.

To classify a patient with the FFT, begin with the first node (the parent node): If a patient's thal value is either rd or fd, then *immediately* classify the patient as high-risk, ignoring all other information about the patient. Otherwise, consider the next node: If a patient's cp value is aa, np, or ta, then *immediately* classify the patient as low-risk. Otherwise, consider the third and final node: If the ca value is positive, classify the patient as high-risk, otherwise classify the patient as low-risk.

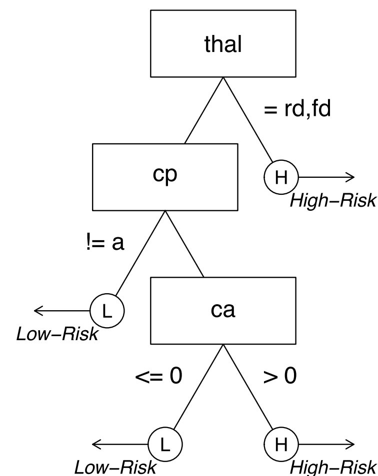


Figure 2: A fast-and-frugal tree (FFT) for classifying patients as either low or high-risk for heart disease based on up to three cues. Each cue is contained in a node, represented as rectangles. Decisions are made in leafs, represented as circles. Branches represent answers to questions to cue–based questions. Branches connecting nodes to leafs are called exit branches. One can use this tree to make a decision as follows: If a patient's thal (thallium scintigraphy result) value is rd (reversible defect) or fd (fixed defect), classify her as high-risk. If not, check her cp (chest pain type) value. If this is aa (atypical angina), np (non-anginal pain), or ta (typical angina), classify her low-risk. If not, check her ca (number of major vessels colored by flourosopy) value. If this is positive, classify her as high-risk, otherwise classify her as low-risk. Note: After creating the `heart.fft` object in the tutorial section "Using the `FFTrees` package", this plot can be generated by running `plot(heart.fft, stats = FALSE, decision.labels = c("Low-Risk", "High-Risk")`.

As an example, consider a 65 year old, female patient with a normal thal value, an atypical angina (cp = aa), and a *ca* value of 1. To classify this patient, we first check if her *thal* value is rd or fd. As it is not, we check if her cp value is aa, np, or ta. As this is the case, we classify her as low-risk and do not consider any additional information.

For this patient, the non-compensatory FFT in Figure 2 allows making a classifications based on two cues without requiring a calculator. To classify this patient using logistic regression—a common compensatory classification algorithm—will not be as easy. Logistic regression belongs to the larger family of general linear models that model criterion values as a weighted sum of cue values and cue weights.

That is, each cue value is multiplied by a weight, added, and then transformed by an equation to produce a continuous (probability) prediction. A logistic regression solution for the heart disease classification problem can be represented as $ln(\frac{p}{1-p}) = -2.76 + 1.53 \cdot \text{sex} - 1.91 \cdot \text{cp_np} - 2.12 \cdot \text{cp_ta} + 0.02 \cdot \text{trestbps} + 1.24 \cdot \text{ca}$, where p is the estimated probability that a patient has heart disease. To use this equation, we need to know four cue values (the patient's sex, cp, trestbps and ca values) multiply them by a series of constants, sum them, and then transform the result with an inverse-logit function. We can then compute, using an external calculation device, the patient's probability of having heart disease as 70.7%. To finally classify the patient as having high or low-risk for heart disease, we need to compare this probability to a threshold. For example, using a threshold of 50%, we would classify the patient as high-risk

2.2 Why use FFTs?

Why use FFTs rather than regression? FFTs have three key advantages, based on their frugality, simplicity, and prediction accuracy (see also Gigerenzer, Czerlinski & Martignon, 1999; Martignon et al., 2008, 2003). First, FFTs tend to be both fast and frugal as they typically use very little information. The FFT for diagnosing heart disease in Figure 2 requires a maximum of three cue values, but as the previous example suggests, FFTs frequently make decisions after considering fewer cue values, as every node has an exit branch that can trigger an early decision. By contrast, regression typically requires more information and thus takes longer to implement. The logistic regression heart disease algorithm always requires four cue values, as the patient's value on any one of these cues could potentially change the final decision. Thus, FFTs are *heuristics* by virtue of ignoring information (Gigerenzer & Gaissmaier, 2011). The fact that heuristics like FFTs ignore information does not necessarily imply that they will perform worse than slower and less frugal algorithms. As heuristics are tools that tend to work well under conditions of uncertainty (Neth & Gigerenzer, 2015), it is an empirical question whether an FFT's gain in speed and frugality reduces its predictive accuracy relative to regression (Gigerenzer, Todd & the ABC Research Group, 1999).

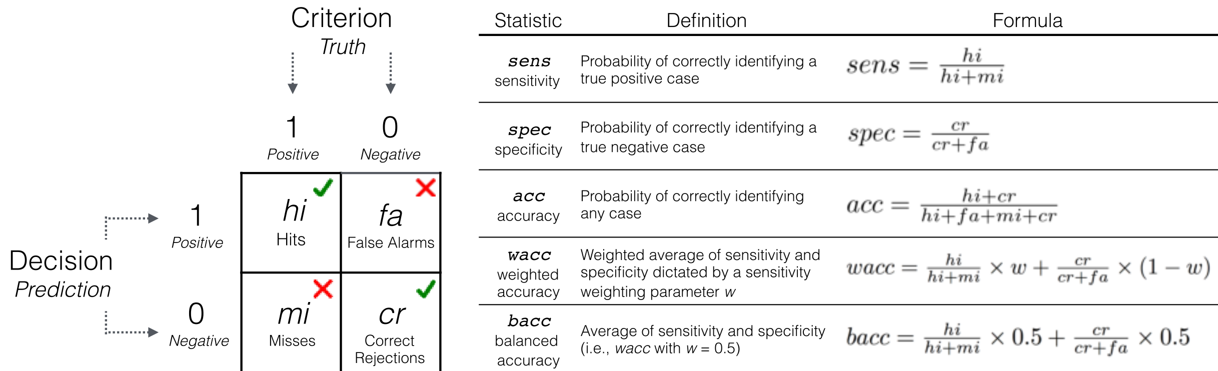
Second, FFTs are simple and transparent, allowing anyone to easily understand and use them. The heart disease FFT in Figure 2 can be quickly communicated, learned, and applied either by a computer or "in the head". By contrast, the regression variant requires training to understand, and usually a calculator to implement. The simplicity and transparency of FFTs make them particularly useful in domains where decision rules need to be quickly understood, implemented, communicated, or taught to decision makers.

Finally, FFTs can make good predictions even on the basis of a small amount of noisy data because they are relatively *robust* against a statistical problem known as *overfitting*. As we describe below, overfitting occurs when an algorithm has systematically lower accuracy in predicting new, unseen data compared to fitting old, known data. In contrast to regression (particularly in its classic, non-regularized form), FFTs tend to be robust against overfitting, and have been found to predict data at levels comparable with regression (Martignon et al., 2008; Woike, Hoffrage & Martignon, 2017).

2.3 Why are FFTs not more popular?

Given these advantages of FFTs, it is puzzling that FFTs are used far less than other classification algorithms such as regression. We believe that there are three main reasons for this: First, people use tools that are accessible and easy to use, and most standard software packages do not contain algorithms for creating FFTs. Second, people often evaluate decision algorithms based on their ability to fit known data, rather than their ability to predict new data. This is both theoretically and statistically problematic, as it favors overly complex models that are prone to fitting random noise (see Gigerenzer & Brighton, 2009; Pitt & Myung, 2002; Roberts & Pashler, 2000). Consequently, focusing on fitting punishes simple algorithms like FFTs that tend to be worse than complex algorithms at fitting past data, but as good, if not better, at predicting new data (see Gigerenzer & Brighton, 2009; Walsh, Einstein & Gluck, 2013, for a discussion of the bias-variance dilemma and the robustness of heuristics).

The third reason against a wider adoption of FFTs is skepticism that something as simple as an FFT can be as accurate as a more complex algorithm. This skepticism is partly due to a suspected trade-off between information frugality and prediction accuracy. According to this trade-off, the more information an algorithm uses, the more accurate it will be—in other words: "more is better." For someone subscribing to the more-is-better principle, the idea that a simple FFT that explicitly ignores information could be as accurate as a compensatory decision that uses all or most of the available information seems preposterous. But despite its intuitive plausibility, when it comes to building predictive models, the "more is better"-mantra is often mistaken (Dawes, 1979; Gigerenzer & Brighton, 2009; Gigerenzer & Goldstein, 1996). Several studies comparing the accuracy of simple FFTs to more complex decision algorithms have found that FFTs can closely match, and even outperform more complex algorithms in predicting new data in domains ranging from medical and legal to financial and military decision making (see Aikman et al., 2014; Dhami & Ayton, 2001; Fischer et al., 2002; 205 L. Green & Mehr, 1997; Jenny et al., 2013; Keller & Katsikopoulos, 2016; Martignon et al., 2008; Wegwarth et al., 2009, for examples). These results have shown that less can be more, and that FFTs need not necessarily sacrifice accuracy for the sake of simplicity, clarity, or speed. Rather, FFTs can be accurate *because* of their simplicity, not in spite of it (see Gigerenzer & Gaissmaier,



Statistic	Definition	Formula
sens sensitivity	Probability of correctly identifying a true positive case	$sens = \frac{hi}{hi+mi}$
spec specificity	Probability of correctly identifying a true negative case	$spec = \frac{cr}{cr+fa}$
acc accuracy	Probability of correctly identifying any case	$acc = \frac{hi+cr}{hi+fa+mi+cr}$
wacc weighted accuracy	Weighted average of sensitivity and specificity dictated by a sensitivity weighting parameter *w*	$wacc = \frac{hi}{hi+mi} \times w + \frac{cr}{cr+fa} \times (1-w)$
bacc balanced accuracy	Average of sensitivity and specificity (i.e., *wacc* with *w* = 0.5)	$bacc = \frac{hi}{hi+mi} \times 0.5 + \frac{cr}{cr+fa} \times 0.5$

Figure 3: A 2 x 2 confusion table and accuracy statistics used to evaluate a decision algorithm. Rows refer to the frequencies of algorithm decisions (predictions) and columns refer to the frequencies of criterion values (the truth). Cells *hi* and *cr* refer to correct decisions, whereas cells *fa* and *mi* refer to errors of different types. Five measures of decision accuracy are defined in terms of cell frequencies.

2011, for additional less-is-more effects).

In the following section we explain how to quantify the accuracy and efficiency of a decision algorithm, and show how `FFTrees` creates FFTs that are simultaneously fast, frugal, and accurate. We then present a 4-step tutorial on how to construct and visualize FFTs from data using `FFTrees`. Finally, we conduct a series of simulations on 10 real-world datasets to compare the prediction performance of `FFTrees` to several popular decision algorithms.

2.4 Evaluating and constructing FFTs

To reiterate, the decision problems we address are binary classification tasks for which data can be organized in a table (as in Figure 1), where several cases are characterized by their values on several cues. Cues can either be numeric, such as age, or nominal, such as sex. The criterion is a column of binary values—either positive (True or 1) or negative (False or 0)— that one wishes to predict.

In the present paper, we focus on building prescriptive FFTs that predict criterion values for any kind of data, whether it is behavioral data representing actual decisions, such as a doctor's diagnoses, or non-behavioral data representing true states of the world, such as a patient's health status. As we will return to in the Discussion, we do not claim that FFTs, specifically those created by `FFTrees`, are necessarily good (or bad) models of the decision process underlying behavioral data. The purpose of FFTs built by `FFTrees` is to efficiently and accurately predict binary criterion values on the basis of cues, without claiming that the tree does, or does not, capture the original data generating process.

2.4.1 Measuring accuracy

To define the accuracy of a decision algorithm, we contrast its decisions with true criterion values in a *confusion table* like the one shown in Figure 3. A confusion table cross-tabulates the decisions of the algorithm (rows) with true criterion values (columns) and contains counts of observations for all four resulting cells. Counts in cells *hi* and *cr* refer to correct decisions due to the match between predicted and criterion values, whereas counts in cells *fa* and *mi* refer to errors due to a mismatch between predicted and true criterion values. Both correct decisions and errors come in two types: Cell *hi* represents *hits*, positive criterion values correctly predicted to be positive, and cell *cr* represents *correct rejections*, negative criterion values correctly predicted to be negative. As for errors, cell *fa* represents *false alarms*, negative criterion values erroneously predicted to be positive, and cell *mi* represents *misses*, positive criterion values erroneously predicted to be negative. Given this structure, a decision algorithm aims to maximize frequencies in cells *hi* and *cr* while minimizing those in cells *fa* and *mi*.

There are many different ways to combine the cell frequencies in a confusion table into aggregate measures of accuracy. We focus on five measures: sensitivity (sens), specificity (spec), overall accuracy (acc), weighted accuracy (wacc), and balanced accuracy (bacc). The first two measures define accuracy separately for cases with positive and negative criterion values. An algorithm's *sensitivity* (a.k.a., hit-rate) is defined as $sens = hi/(hi + mi)$ and represents the percentage of cases with positive criterion values that are correctly predicted by the algorithm. Similarly, an algorithm's *specificity* (a.k.a., correct rejection rate, or the compliment of the false alarm rate) is defined as $spec = cr/(fa + cr)$ and represents the percentage of cases with negative criterion

values correctly predicted by the algorithm. The next three measures define accuracy across all cases. *Overall accuracy* is defined as the overall percentage of correct decisions $acc = (hi + cr)/(hi + fa + mi + cr)$, ignoring the difference between hits and correct rejections.

Although overall accuracy is an important and useful measure, it can be misleading and must be interpreted relative to the base rate of the criterion. For instance, in a dataset with a low base rate of 1% (e.g., 100 cases and only one case with a positive criterion value), a *baseline* algorithm that simply predicts *every* case to be negative would achieve an overall accuracy of 99%. Thus, baseline algorithms can have a high overall accuracy without being very useful because they do not distinguish between positive and negative cases. An extremely liberal baseline algorithm that always predicts "True" will never miss and thus have a seemingly desirable sensitivity of 100%. But this comes at the cost of many false alarms and a dismal specificity of 0%. By contrast, an extremely conservative algorithm that always predicts "False" will maximize correct rejections and exhibit an impressive specificity of 100%, but at the cost of many misses and a sensitivity of 0%. Indeed, there is an inevitable *sensitivity–specificity trade-off* in most classification tasks, such that an increase in one measure corresponds to a decrease in the other (Macmillan & Creelman, 2005). The shape of this trade-off can be expressed by a receiver operating characteristic (ROC) curve like the one in Figure 4, which shows the sensitivity-specificity trade-off of 7 different algorithms applied to the same data set. Here, algorithms with higher specificities tend to have lower specificities, and vice-versa.

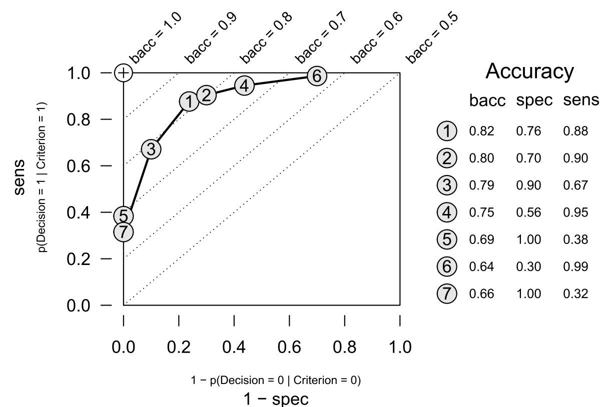


FIGURE 4: A receiver operating characteristic (ROC) curve illustrating the trade-off between sensitivity (sens) and specificity (spec) in classification algorithms. As sensitivity increases, specificity decreases (i.e., 1 − spec increases). Balanced accuracy (bacc) is the average of sensitivity and specificity. Ideal performance (bacc = 1.0), is represented by the cross in the upper-left corner. The numbered circles in the plot represent the accuracy of 7 different algorithms with different trade-offs between sensitivity and specificity. Their numbers represent the rank order of algorithm performance in terms of their bacc values. (Note: The circles correspond to the fan of 7 FFTs that will be created by the ifan algorithm for the heart disease dataset in the tutorial.)

Different tasks and decision maker preferences can influence the extent to which sensitivity should be weighted relative to specificity. For example, consider the head of airport security who needs to construct a decision algorithm for bag screening, where any bag can be either truly safe (i.e., does not contain a safety threat) or unsafe (i.e., does contain a threat). To construct a good decision algorithm, she needs to take into account the relative cost of a false-alarm (falsely identifying a safe bag as unsafe), to the cost of a miss (falsely identifying an unsafe bag as safe). But what are these costs? There is no definitive answer to this question because the relative costs of both errors depend on the specific decision made for each case after it is classified. For example, consider the following two decision rules: "If a bag is classified as unsafe, hold it for an additional 30 minutes of manual screening to be certain of its contents. If a bag is classified as safe, let it pass without additional screening." Here, the cost of a miss is the potential loss of life due to a missed threat, while the cost of a false-alarm is an additional 30 minutes of screening time. Clearly, the cost of a miss in this scenario exceeds the cost of a false-alarm and thus calls for a decision algorithm that prioritizes sensitivity over specificity.[2] As this example shows, a good decision algorithm should be able to balance sensitivity and specificity as a function of the specific error costs of a domain.

To quantify how an algorithm balances sensitivity and specificity, we use *weighted accuracy*. Formally, weighted accuracy is defined as $wacc = w \cdot sens + (1 - w) \cdot spec$, where w (labeled sens.w in `FFTrees`) is a parameter between 0 and 1 that specifies how sensitivity is weighed relative to specificity. In decision tasks where sensitivity is more important than specificity (like threat detection in airport screening), wacc could be calculated with a value of w larger than 0.5. In cases where both measures are equally important, the sensitivity weight w can be set to 0.5. In this special case, weighted accuracy is called *balanced accuracy* (bacc).

There are many alternative measures to quantify the accuracy of an algorithm across all cases, most notably d-prime (d') and area under the curve (AUC). For simplicity, we focus on wacc (with bacc as a special case) for the remainder of this paper, as it provides a simple way to account for

[2] The specific costs of false-alarm and misses depend on the specific decision policy. For example, if the bag screening policy was "If a bag is classified as unsafe, destroy it immediately, otherwise, let it pass" then the cost of a miss would substantially increase because the cost of destroying a safe bag is higher than the cost of holding it for an additional 30 minutes of screening.

both false-alarms and misses, while using an interpretable scale of values ranging from 0 to 1 (where 0 indicates no accuracy, and 1 equals perfect accuracy, see Figure 4).

2.4.2 Measuring speed and frugality

Although prediction accuracy is an important characteristic of an algorithm, algorithms should also be evaluated based on their efficiency. If two algorithms have similar accuracy, but one is more efficient than the other, then the more efficient algorithm should be preferred because it will be cheaper (in terms of time and/or money) to implement, while being easier to understand, and communicate. For this reason, in addition to measuring an algorithm's accuracy, we also measure its efficiency in terms of speed and frugality. Previous FFT literature has operationalized an algorithm's speed and frugality with a single measure, usually as the number of cues used when implementing the algorithm, averaged across cases (e.g., Dhami & Ayton, 2001; Gigerenzer & Goldstein, 1996; Jenny et al., 2013). By contrast, we measure speed and frugality with two distinct measures that separate how rapidly an algorithm reaches a conclusion (its speed) from how much information it ignores (its frugality).

We quantify an algorithm's *speed* with the measure *mean cues used* (mcu), the average number of cue values used in making a decision, averaged across all cases. For example, an algorithm that uses 1 cue to make a decision for half of the cases, and 2 cues for the remaining half, would have an mcu value of 1.5. This is the same measure used in previous FFT research as an overall measure of both speed and frugality.

We separately define an algorithm's *frugality* with the measure *percent cues ignored* (pci), defined as 1 minus an algorithm's mcu divided by the total number of cues in the dataset (i.e., the maximum possible mcu value). This measure quantifies the percentage of information an algorithm *ignores* when it is implemented on a specific dataset. For example, in a dataset with 10 cues, an algorithm that uses 1 cue value to make a decision for every case (resulting in an mcu value of 1) would ignore 9 cue values for every case, resulting in a pci value of $1 - 1/10 = 90\%$. By contrast, an algorithm that uses 9 cue values to classify every case would ignore very little information, and thus have a pci value of $1 - 9/10 = 10\%$. Thus, the more data an algorithm ignores (i.e., the higher its pci value), the more frugal it is.

It is important to distinguish between an algorithm's speed (measured by mcu) and its frugality (measured by pci) for the following reason: A fast algorithm is not necessarily frugal, nor is a frugal algorithm necessarily fast. For example, when presented with a large dataset containing 100 cues, an algorithm that uses 10 cues on average (mcu = 10) to classify each case would, by most standards, not considered to be very fast. However, the algorithm would nonetheless be quite frugal (pci = 90%) relative to a complex algorithm that uses all available information. By contrast, the same algorithm applied to a smaller dataset that includes only the 10 cues actually used by the algorithm would no longer be frugal (pci = 0%) because it does not ignore any information. This example illustrates a second important point beyond the distinction between frugality and speed: While some algorithms will be faster and/or more frugal than others on average, the speed and frugality of an algorithm also depend on the data to which it is applied. In other words, an algorithm that is fast and frugal for one dataset could be slow and wasteful for another. For this reason, we consider and provide both measures when evaluating and comparing algorithms across datasets.

2.4.3 Training (fitting) vs. testing (prediction)

Regardless of the specific accuracy and efficiency measures used, a decision algorithm must always be evaluated in reference to one of two phases in the modeling process. In the *training* phase (a.k.a., *fitting* phase) true criterion values are provided to the algorithm so that it can adjust its free parameters to the specific decision task. In regression, these parameters take the form of regression weights. In an FFT, they are its cues, decision thresholds, cue order, and exits. In the *testing* phase (a.k.a., *prediction* phase) the algorithm must predict the criterion values of new data (i.e., data not used during training) by using the specific parameter values derived during the training phase. Thus, the purpose of the testing phase is to evaluate an algorithm's ability to make true predictions for data that it has not encountered before.

There is an important reason why one should always distinguish between an algorithm's accuracy in training and testing: Algorithms can have systematically higher accuracy in training data compared to their accuracy in testing data. The reason for this discrepancy is a statistical phenomenon known as *overfitting* (James et al., 2013). To understand overfitting, it is helpful to view a dataset as a combination of signal and noise, where the signal is a stable and systematic pattern in the data and noise is unpredictable variability due to measurement error or other random influences. As noise, by definition, cannot be predicted, while signal can, a good decision algorithm should detect and model signal and ignore noise (Gigerenzer & Brighton, 2009; Kuhn & Johnson, 2013; Silver, 2012). Generally speaking, overfitting occurs when an algorithm mistakes noise in a dataset for a signal, and as a result, changes its parameters to accommodate noise rather than (correctly) ignoring it. This leads to an inflated level of accuracy that can not possibly be maintained when predicting future data that will inevitably be contaminated with unpredictable noise. When decision makers want to maximize their ability to predict new data, decision algorithms should be evaluated based on their prediction accuracy in the testing phase rather than on their fitting accuracy in the training phase. The *robustness* of a decision algorithm

can then be expressed in terms of its resistance to overfitting: An algorithm that avoids confusing noise for a signal is robust in the sense that it achieves similar levels of accuracy for training and testing data. Equipped with these measures and conceptual distinctions, we can now describe the algorithms available in the `FFTrees` package that can be used to construct FFTs.

2.5 FFT construction algorithms

Constructing an FFT refers to the training phase in which the parameters of an FFT are tailored to a specific dataset. An FFT construction algorithm must solve the following four tasks (but not necessarily in this order): 1. Select cues; 2. Determine a decision threshold for each cue; 3. Determine the order of cues; and 4. Determine the exit (positive or negative) for each cue. Each of these tasks is critical in constraining how, and how well, an FFT will perform.

Two FFT construction algorithms, *max* and *zig-zag*, have been proposed and tested by Martignon and colleagues (Martignon et al., 2008, 2003; Woike et al., 2017). Both algorithms use several heuristics that simplify the process of tree construction. The basic steps in each algorithm are as follows: First, to determine the decision thresholds of numeric cues, both algorithms use the observed median value of numeric cues rather than using a value that optimizes any performance criteria. Second, the individual, marginal *positive predictive* and *negative predictive* validities[3] of each cue are calculated, ignoring any potential dependencies between cues. For the max algorithm, cues are ranked in order of the maximum value of their positive and negative validities. Cues with higher positive than predictive validities are then assigned positive exits, while those with higher negative than positive predictive validities are given negative exits.

In contrast to max, zig-zag determines the exit direction for each node before determining cue order. Specifically, after the first node is given a positive or negative exit, all sequential nodes then are given alternating exits.[4] Once exits are determined, zig-zag recursively assigns the cue with the highest positive predictive value to the next node with a positive exit, and the cue with the highest negative predictive value to the next node with a negative exit.

The max and zig-zag algorithms have been shown to produce FFTs that can compete with logistic regression and standard decision trees in predictive accuracy (Martignon et al., 2008). Moreover, because they use several simplifying heuristics throughout the construction process, they require very few calculations and can in principle be implemented with a pencil and paper.

Although max and zig-zag are simple and effective, they lack two features that can make them unsuited for certain decision problems. First, they do not have sensitivity and specificity weighting parameters. This means that they cannot create FFTs tailored to decision tasks where false-alarms are more (or less) costly than misses. Second, the algorithms do not have explicit size restrictions or a process of removing nodes from a tree (a.k.a., "pruning"). This means that max and zig-zag create FFTs that use *all* cues in a dataset, regardless of whether or not the cues are actually used in classification. In datasets with only a few cues, this does not pose a problem; however, in datasets with dozens or even hundreds of cues, this can lead to extremely long trees containing nodes that may never be used in practice.

To address the sensitivity weighting and tree size issues present existing FFT construction algorithms, we introduce a new class of algorithms called *fan* with two variants: *ifan* and *dfan*. These algorithms account for different sensitivity and specificity weights by taking advantage of the effect of an FFT's *exit structure*, its particular sequence of negative and positive exits, on its balance between sensitivity and specificity. By definition, every node in an FFT must have either a negative or a positive exit (or both in the case of the final node). Martignon et al. (2008) and Luan, Schooler, and Gigerenzer (2011) have shown that the exit structure of an FFT can dramatically affect its balance between sensitivity and specificity. For example, an FFT with either all positive or all negative exits (except for the last node which must contain both a positive and a negative exit), known as a *rake* (Martignon et al., 2003), tends to maximize one metric to the detriment of the other. An FFT with only positive exits until the last node, a "positive-rake", exhibits high sensitivity at the expense of low specificity because every node in the tree can trigger a positive decision. By contrast, an FFT with only negative exits until the last node, a "negative-rake", exhibits high specificity at the expense of low sensitivity because every node in the tree can trigger a negative decision. In contrast, an FFT with alternating positive and negative exit directions, known as a "zig-zag" tree, will tend to balance sensitivity and specificity. Thus, just as a judge can adjust her decision criterion in the signal detection theory framework to shift her balance in decision errors, so can an FFT change its exit structure (Luan et al., 2011).

Inspired by the role an FFT's exit structure has on its error balance, the ifan and dfan algorithms explore a virtual "fan" of several FFTs with different exit structures and error trade-offs, ranging from negative-rakes, to zig-zag trees, to positive-rakes. After the fan is created, the algorithms select the tree with the exit structure that maximizes the statistic the unique error trade-off (i.e., weighted accuracy) desired by the

[3]Using the notation of Figure 3, *positive predictive validity* (ppv) is calculated as $hi/(hi + fa)$, while *negative predictive validity* (npv) is calculated as $cr/(mi + cr)$. Thus, while sensitivity and specificity are calculated conditionally on true criterion values, ppv and npv are also calculated conditionally on decision values.

[4]There are slightly different variants of the zig-zag algorithm that change how the exit of the first node is determined. In our simulations, we use the Z_0 algorithm that determines the first exit direction as a function of the positive and negative predictive value of the highest ranked cue (Woike et al., 2017).

decision maker. They also have parameters that both limit the size of FFTs, and remove nodes deemed to be unnecessary because they either do not classify enough cases (the default), or because they do not substantially increase accuracy.

Full descriptions of the ifan and dfan algorithms are presented in the Appendix. Here, we describe the algorithms' rationale more generally. The ifan algorithm works as follows: Like max and zig-zag, ifan first calculates a decision threshold t for each cue. For numeric cues, thresholds are single values, whereas for factors (i.e., nominal or character cues), thresholds are sets of one or more factor values. Thresholds are also combined with decision *directions* to indicate how the threshold would be used to make a positive classification decision. For example, in using the cue age to predict the presence of heart disease risk, a threshold and direction could be > 65, indicating that people over the age of 65 are predicted to be at high risk for having heart disease. Unlike max and zig-zag, ifan is not restricted to using cue medians as thresholds for numeric cues. Instead, it tests several different thresholds (for numeric cues, the default value is 20) to find one that that maximizes the cue's accuracy goal.chase (by default, goal.chase = bacc) when applied to entire training dataset and ignoring all other cues.

Next, ifan ranks the cues in order of their maximum values of goal (by default, goal = bacc).[5] It then selects the top max.levels cues (by default, `max.levels = 4`), and discards all remaining cues. The algorithm then creates a set of $2^{\text{max.levels}-1}$ FFTs with these cues, keeping their order constant, using all possible exit structures. This set of trees represents the "fan". For example, the seven points in Figure 4 represent seven different FFTs within one fan. Next, the algorithm removes any lower nodes in the FFTs that classify fewer than stopping.par (by default, stopping.par = 10%) percent of the data.[6] If lower nodes are removed, the final remaining node is forced to have both a positive and a negative exit branch. Due to the option of removing low-data nodes, the final number of cues in an FFT may be lower than, but cannot exceed max.levels.

Once the set of FFTs has been created, ifan selects the tree with the highest goal value. By default, its goal is weighted accuracy (wacc), calculated with a sensitivity weight parameter (sens.w) specified by the user. To be clear, by default, the value of sens.w does not change how the set of FFTs are constructed (as long as `goal.chase = bacc`): rather, it changes which specific tree in the set of FFTs with different exit structures is selected to make classification decisions.[7]

A key restriction that ifan shares with max and zig-zag is that it ignores potential interactions between cues—both in their decision thresholds and their ranked accuracy. That is, these algorithms calculate decision thresholds and then rank cues based on their marginal accuracy. Does assuming cue independence hurt the performance of an algorithm? Intuition suggests that it would, as one can easily imagine scenarios where cues are not independent. For example, in diagnosing heart disease, we could hypothesize an interaction between weight and sex such that relationship between weight and heart disease is, substantially and reliably, not the same for men and for women. If so, a decision algorithm would make better predictions by calculating a different decision threshold for the weight of men versus women. Indeed, most algorithms for constructing standard decision trees (such as ID3 and C4.5, Quinlan, 1986, 1993) implicitly take cue interactions into account by sequentially calculating new thresholds during tree construction. However, one must be careful in assuming cue dependence for following reason stated by Martignon et al.: "the fact that cue interactions can exist [...], does not imply that they must exist; it says nothing about the frequency of their occurrence" (2003, p. 210). The reason why one should be careful in assuming cue interactions is that this assumption can come at a cost: If an algorithm that takes cue interactions into account is applied to a dataset where cue interactions either do not exist, or cannot be reliably estimated from training data, then the algorithm is likely to overfit the training data and can lead to poorer predictions than an algorithm that explicitly ignores cue interactions (see Gigerenzer & Brighton, 2009; Martignon & Hoffrage, 2002, for a more detailed discussion). In other words, algorithms that routinely incorporate cue interactions may commit false-alarms in detecting (and subsequently predicting) cue interactions that may be spurious or unreliable. For this reason, many successful heuristics (such as as take-the-best, Gigerenzer & Goldstein, 1996) and FFT construction algorithms (such as max and zig-zag, Martignon et al., 2008, 2003) explicitly ignore cue interactions to reduce both processing time and the risk of overfitting.

In decision domains where substantial interactions between cues are likely to exist and can reliably be measured in training data, FFT construction algorithms that assume dependencies between cues may provide better predictions than algorithms that do not. To provide users with a fitting FFT construction tool for such tasks, we provide a variant called *dfan* that does not assume cue independence. The dfan algorithm starts like ifan by ranking cues based on goal (by default, goal = bacc). But instead of calculating cue thresholds based on all cases and ranking cues based on their

[5] In their FFT construction algorithm, Luan et al. (2011) rank cues by *d'*, which is the difference in standardized values of sensitivity and 1 – specificity. We do not claim that bacc is necessarily a better metric for ranking cues than *d'*.

[6] This 10% value is arbitrary and can be adjusted by the user using the stopping.par argument in `FFTrees()`.

[7] In our experience, having ifan use wacc (with values of sens.w other than 0.5) in actually *constructing* FFTs (i.e., selecting cue thresholds and ranking cues) leads to FFTs of lower overall weighted accuracy (wacc) than constructing FFTs by chasing balanced accuracy (bacc) (and using wacc only to select FFTs after a fan of trees have been constructed). However, if users of `FFTrees` should wish to maximize wacc with sens.w values other than 0.5 for selecting cues and calculating cue thresholds, they can do so by using the optional argument goal.chase = 'wacc'.

accuracy only once, it iteratively re-calculates cue thresholds and accuracies based on the subsets of cases that occur dynamically as the FFT is being constructed. This allows dfan to detect and exploit cues that may exhibit poor overall accuracy, but are highly predictive for specific subsets of cases partitioned by other cues.

In the next section, we provide a tutorial for creating, evaluating, and visualizing FFTs with the `FFTrees` package. We illustrate each step with example code from a dataset on heart disease (Detrano et al., 1989), which is included in the `FFTrees` package, and ultimately arrive at the exact FFT for predicting heart disease presented in Figure 2, and the ROC curve in Figure 4. While we use the heart disease data throughout, we remind the reader that `FFTrees` is in no way restricted to medical data and can be used to model any dataset with a binary criterion.

3 FFTrees Tutorial

`FFTrees` should be used with versions 2.1.0 of R or greater. R can be downloaded for free from https://cloud.r-project.org. We recommend also using the RStudio programming environment from https://www.rstudio.com/products/rstudio/. Reproducible code corresponding to the tutorial is provided in Figure 5 and is also available at https://osf.io/m726x/ (Phillips, Neth, Woike & Gaissmaier, 2017a). The code and documentation presented here is valid for `FFTrees` version 1.3.2, but should also be valid for future package versions. The latest developer version of `FFTrees` is available at http://www.github.com/ndphillips/FFTrees. We welcome bug reports, feature requests, and code contributions at http://www.github.com/ndphillips/FFTrees/issues.

3.1 Step 1: Install the FFTrees package

`FFTrees` can be installed from CRAN by evaluating `install.packages("FFTrees")`. Once the package has been installed on a computer, it does not need to be installed again (except to check for a more recent version). Once the package is installed and loaded, a package guide containing instructions and examples can be opened by running `FFTrees.guide()`.

3.2 Step 2: Create FFTs with FFTrees()

The main function for creating FFTs is `FFTrees()`. The function has two mandatory arguments `formula` and `data`. The `formula` argument should be of the form `formula = criterion ~ a + b + ...` specifying the criterion (`criterion`) and one or more cues (`a, b, ...`) to be considered, but not necessarily used in the FFT. For example, including `formula = diagnosis ~ sex + age` will create FFTs predicting diagnosis that only consider the cues `sex` and `age`. One can also use the generic `formula = criterion ~ .` notation, which allows to consider all cues in the training data. Unless there are specific cues in the training data that should, or should not, be considered, we recommend using the generic formula notation.

The second mandatory argument to the `FFTrees()` function is `data`, a training dataset containing all cues specified in `formula`. The training data should be stored as a data frame consisting of m rows (cases) and n columns. One of the columns must be the binary criterion specified in the formula argument. Although there are no explicit restrictions on the number and classes of cues, we recommend not including factor cues with many (i.e., more than 20) unique cue values, as this can lead to long processing times and potential overfitting. Missing values are (currently) not permitted.

The optional `data.test` argument allows specifying a testing dataset used to test the prediction performance of the tree. In the absence of separate training and test datasets, one can use the `train.p = p` argument to automatically split the original training data (specified with the `data` argument) into separate training and test subsets. Setting `train.p = p` will split all cases contained in `data` into a proportion `p` used for training and 1−`p` for testing. For example, setting `train.p = .10` will randomly split the original data into a 10% training set, and a 90% testing set.[8]

Additional optional arguments include `main` and `decision.labels`, with which users can specify verbal labels for the dataset and/or decision outcomes. These arguments are passed to other functions such as `plot()`. There are several additional optional arguments one can use to customize how the trees are constructed. The `algorithm` argument specifies the FFT construction algorithm. The default algorithm is ifan (i.e., `algorithm = "ifan"`), however, the user can also specify `"max"`, `"zig-zag"`, or `"dfan"` to create FFTs using one of these algorithms. For the fan algorithms, the arguments max.levels and sens.w, additionally control tree size and sensitivity weights (for the ifan and dfan algorithms only), while goal and goal.chase specify which accuracy statistic is maximized when growing the tree(s), and selecting the final tree, respectively. Additional details about these and other arguments are provided in the package documentation.

3.3 Step 3: Inspect FFTs

The `FFTrees()` function returns an object of the `FFTrees` class. An overview of the trees contained in the object is available in three ways: by printing the object to the console, by summarizing it with `summary()`, or by obtaining a verbal description of it with `inwords()`. Most of the following

[8] Due to the random split, this can yield different results every time the `FFTrees(train.p = p)` function is evaluated. For reproducible results, we advise either fixing the sampling seed (via `set.seed()`) or creating an explicit `data.test` set.

```r
# ------------------------------------------------------------
# 4 Steps to create and visualize a fast-and-frugal tree (FFT)
#  predicting heart disease using FFTrees
# ------------------------------------------------------------

# Step 0: Install the FFTrees package (only necessary once)
install.packages("FFTrees")

# Step 1: Load the FFTrees package and open the package guide
library("FFTrees")                # Load the package
FFTrees.guide()                   # Open the package guide

# Step 2: Create FFTs from training data and test on testing data
heart.fft <- FFTrees(formula = diagnosis ~ ., # Criterion
                     data = heart.train,      # Training data
                     data.test = heart.test,  # Testing data
                     main = "Heart Disease",  # Optional labels
                     decision.labels = c("Low-Risk", "High-Risk"))

# Step 3: Inspect and summarize FFTs
heart.fft          # Print statistics of the final FFT
inwords(heart.fft) # Print a verbal description of the final FFT
summary(heart.fft) # Print statistics of all FFTs

# Step 4: Visualize the final FFT and performance results
# a) plot final FFT applied to test data:
plot(heart.fft, data = "test")

# b) plot individual cue accuracies in ROC space:
plot(heart.fft, what = "cues")
```

Figure 5: Complete, reproducible code showing four basic steps to create, visualize, and evaluate FFTs predicting heart disease with `FFTrees`. The datasets used for training (`heart.train`) and testing (`heart.test`) are included in `FFTrees` and an expanded tutorial for this code is available in the package by evaluating `vignette("FFTrees_heart")`. A link to a video tutorial corresponding to this code is also available at https://osf.io/m726x/ (Phillips et al., 2017a).

TABLE 1: Printing an FFTrees object provides summary statistics on the created FFTs, selects the FFT with the highest weighted accuracy (wacc) in training and shows its performance measures for training and testing data.

Heart Disease
7 FFTs predicting diagnosis (Low-Risk vs. High-Risk)
FFT #1 contains 3 cues: {thal, cp, ca}

Measure	Label	Training	Testing
cases	n	150	153
speed	mcu	1.74	1.73
frugality	pci	0.88	0.88
accuracy	acc	0.80	0.82
weighted accuracy	wacc	0.80	0.82
sensitivity	sens	0.82	0.88
specificity	spec	0.79	0.76

functions will automatically return details of the FFT with the highest weighted accuracy (wacc) in the training data. However, users can also return results from other trees in the fan by specifying an integer value in the `tree` argument.

Printing an `FFTrees` object (i.e., evaluating the object by its name) displays basic statistics—including the number of cases and metrics for accuracy, speed, and frugality in training vs. testing data—to the console (see Table 1).

Applying the `summary()` function to an `FFTrees` object returns detailed information on each of the FFTs, including their cues, decision thresholds, exits and exit directions, as well as accuracy and efficiency statistics.

Finally, applying the `inwords()` function to an `FFTrees` object returns a verbal description of the tree. For example, evaluating `inwords(heart.fft)` on the heart disease `FFTrees` object returns the sentence: "If thal = {rd, fd}, predict High-Risk. If cp != {a}, predict Low-Risk. If ca <= 0, predict Low-Risk, otherwise, if ca > 0, predict High-Risk."

3.4 Step 4: Visualize and evaluate FFTs

To visualize a specific FFT contained in an `FFTrees` object, as well as its associated accuracy statistics when applied to either the training or testing data, apply the generic `plot()` function to the object. By default, the FFT with the highest weighted accuracy (wacc) in the training data is shown. Figure 6 shows heart disease FFT applied to the testing data. Colored icon arrays (Galesic, Garcia-Retamero & Gigerenzer, 2009) illustrate how the tree made decisions for all 153 cases in the testing data. The bottom panel provides cumulative accuracy statistics. Additionally, the accuracies of each tree in the fan of seven FFTs generated by ifan are visible in the ROC curve in the bottom-right of the plot (these are identical to the points in Figure 4). Using the additional arguments `tree` and `data` allows users to select which FFT in the fan is plotted, and which dataset (training or testing) is displayed.

To visualize the marginal accuracy of every cue in the dataset, include the `what = "cues"` argument when plotting an `FFTrees` object. This option illustrates the individual, marginal accuracies for each cue in ROC space. Figure 7 shows the resulting plot for the heart disease data. Inspecting the graph reveals that the three cues (thal, cp, ca) used in FFT #1 (shown in Figure 6) have the highest individual balanced accuracies. Note that this is to be expected as the ifan algorithm explicitly selects and ranks cues by this statistic by default. Figure 7 also shows that the two next best cues are oldpeak and slope. This information can be useful in guiding a top-down process of future FFT construction. For example, if those cues were of particular interest, one could build a new FFT with these cues by evaluating `heart2.fft <- FFTrees(formula = diagnosis ~ thal + oldpeak + slope, data = heart)`, and then compare the performance of the two trees.

3.5 Additional options

The commands described so far cover the four basic steps in constructing and evaluating FFTs with the `FFTrees` package. Although these steps will be sufficient for many datasets and applications, the package offers additional functions and options that users might find helpful. We will now briefly describe five of the additional functionalities and direct users to the documentation and package guide (by evaluating `FFTrees.guide()`) for additional options and examples.

3.5.1 Accessing additional outputs

An `FFTrees` object created with the `FFTrees()` function contains several detailed outputs that can be accessed by evaluating `x$output`, where `x` is an `FFTrees` object created by the `FFTrees()` function, and `output` is a named output of that object. To see all named outputs from an `FFTrees` object, run `names(x)`. Key outputs include: `x$cue.accuracies`, which contains the decision thresholds and marginal accuracies for each cue; `x$decision`, which contains the classification decisions for all cases; `x$levelout`, which indicates at which level in the FFT each case was classified; and `x$levelstats`, which shows the cumulative classification statistics for each level of the FFTs.

3.5.2 Predicting classes of new data

To make classification predictions for a new dataset using an `FFTrees` object, use the `predict(x, newdata)` function, where `x` is an `FFTrees` object, and `newdata` is a data frame of new data. For example, one could use the heart

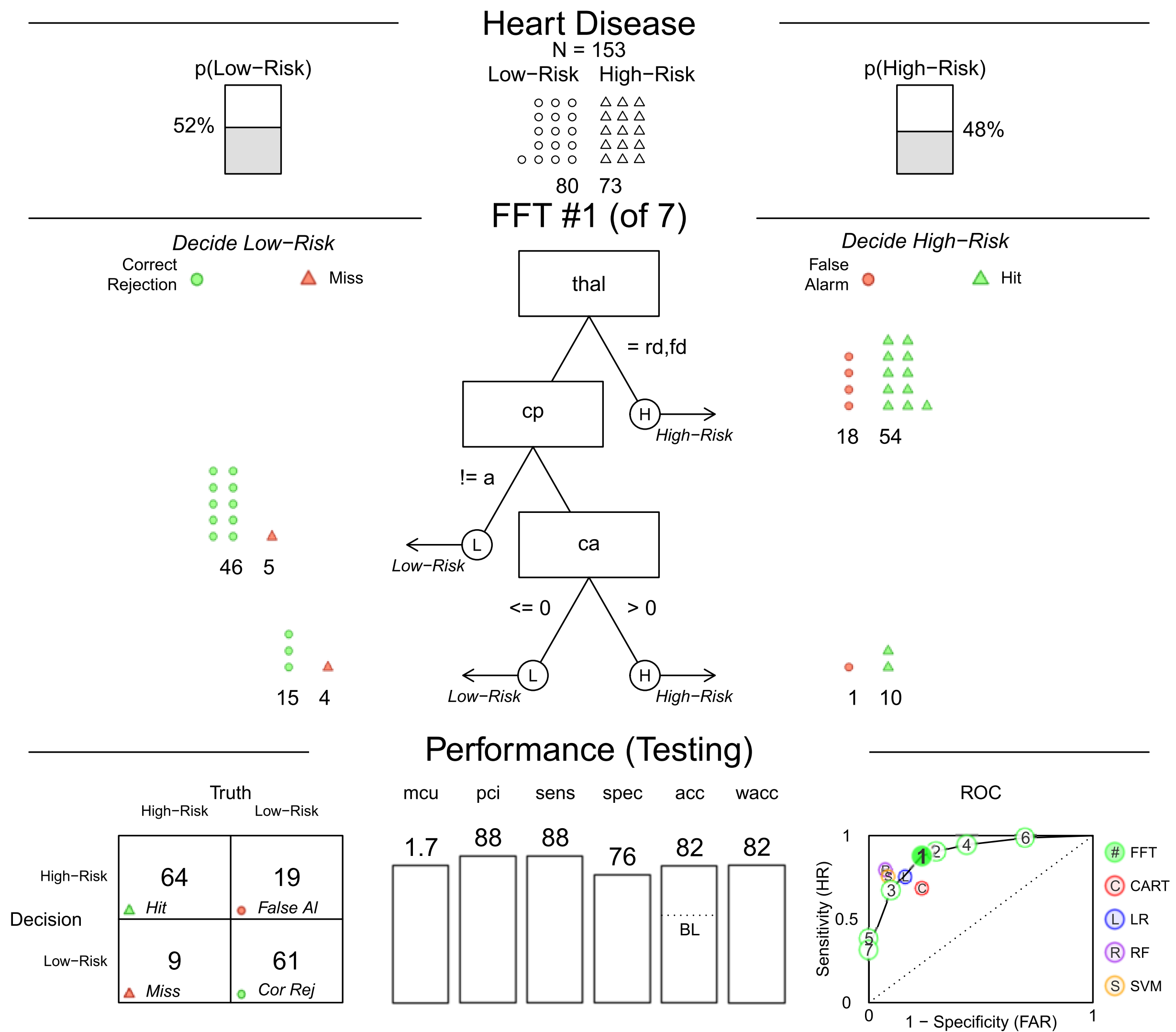


Figure 6: Visualization of an FFTrees object created by `plot(heart.fft, data = "test")`. The top panel shows information about the dataset, including the frequencies and base rates of negative and positive criterion classes. The middle panel contains the FFT and icon arrays showing the the number and accuracy of cases classified at each node. This particular FFT's interpretation has been described above (on p. 346 and in Figure 2). The bottom panel shows the FFT's cumulative classification performance, including a confusion table and levels for a range of statistics. The bottom right plot shows the performance of all seven FFTs created by the `FFTrees()` function in ROC space (green circles with numbers correspond to FFTs). The FFT currently being plotted is highlighted (here, FFT #1, with the highest weighted accuracy in training). Additional points in this plot correspond to the performance of competing classification algorithms (see Simulation section): standard decision trees (CART), logistic regression (LR), random forests (RF), and support vector machines (SVM). In this case, FFT #1 has a higher sensitivity than competing algorithms, but at the cost of a lower specificity. Additionally, FFT #1 dominates CART in this example by having a higher sensitivity and comparable specificity.

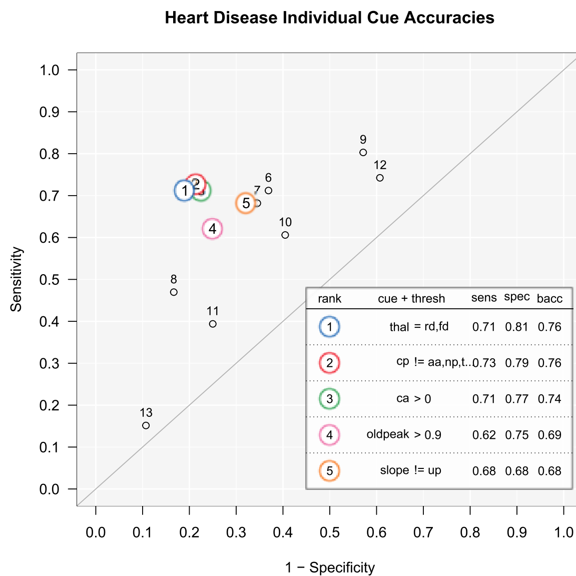


Figure 7: Visualizing marginal (training) cue accuracies from the `heart.fft` object by running `plot(heart.fft, what = "cues", data = "train")`. Accuracy statistics are calculated for each cue using the threshold that maximizes bacc. Numbers indicate a cue's ranked accuracy across all cues in terms of bacc. The top five cues are colored and described in the legend. All other cues in the data are shown as black points.

disease FFT (`heart.fft`) to predict the diagnoses of a new set of patients whose cue information is stored in a data frame called `heart.new` by running `predict(heart.fft, heart.new)`. This will return a vector of classification predictions for each case in `heart.new`.

3.5.3 Defining an FFT in words

Some users might wish to implement a specific FFT to data, rather than using an FFT construction algorithm to construct an optimized FFT. To do this, users can verbally define a tree as a sentence by using the `my.tree` argument when calling the `FFTrees()` function. `FFTrees` will attempt to extract the cues, decision thresholds, directions and exits from the sentence, and then apply the FFT described to the specified data. For example, in the heart disease data, one can directly define and implement a new heart disease FFT by running the code: `FFTrees(diagnosis ~ ., data = heart.train, my.tree = "If chol > 350, predict True. If cp != {a} predict False. If age <= 35, predict False. Otherwise, predict True")`. Additional grammatical rules for verbally defining FFTs are available in the package documentation.

3.5.4 Including cue costs

If the cues in a dataset have specific and known implementation costs—like the financial cost of a measurement, or the amount of time it takes to implement—they can be included as a data frame in the `cost.cues` argument when creating an `FFTrees` object. The `cost.cues` data frame should have two columns: one specifying the name of a cue, and one specifying the cost of that cue. The specific units used in specifying costs (e.g., hours or $) are arbitrary, as long as they are comparable across different cues. When `cost.cues` is included, `FFTrees` will calculate the classification cost of each case when applying an FFT to data. For example, in the heart disease data, each cue has a cost ranging from a minimum of $1 (age) to $102.9 for the thallium scintigraphy (thal) test.[9] The costs are stored in the `FFTrees` package as a data frame called `heart.cost`, with a column `cue` indicating the names of the cues, and a column `cost` indicating their costs. By including the argument `cost.cues = heart.cost` when creating the heart disease FFT in Figure 6, one can see in the summary output that using this FFT would cost approximately $123 per patient on average. In contrast, using all cues in classification would have cost approximately $300 per patient, more than twice as much. Note that including cue costs does *not* affect how trees are constructed. We will return to the topic of incorporating cue costs in FFT construction in the Discussion.

3.5.5 Creating a forest of FFTs

Additional insights into the role of cues in a dataset can be gained by using the `FFForest()` function. This function conducts a bootstrap simulation that applies the `FFTrees()` function to random subsets of the data, thus creating a forest of many FFTs, each constructed from different sets of cases.[10] This forest of FFTs can be used to explore the importance of each cue in a dataset, where cue importance is defined as the proportion of FFTs in the forest for which a particular cue is selected. The more often a cue is selected, the more important it is deemed to be. Moreover, information about the co-occurrence of cues within FFTs across the forest allows judging whether two cues tend to jointly contribute to classification decisions within an FFT, or if they tend to replace one another between FFTs.

[9] We retrieved the costs of the heart disease data from https://archive.ics.uci.edu/ml/machine-learning-databases/heart-disease/costs/. The three cues of the FFT (thal, cp, and ca) have costs of $102.90, $1.00, and $100.90, respectively. When applied to the data displayed in Figure 6, the total cost of the FFT would be $102.90 for each of the 72 patients classified at the first node, $103.90 ($102.90 + $1.00) for each of the 51 patients classified at the second node and $204.80 ($102.90 + $1.00 + $100.90) for each of the 30 patients classified at the third node.

[10] By default, `FFForest()` creates 10 FFTs created from 10 random 50% subsets of the original data. The number of simulations and size of the subsetting can be specified using arguments `ntree` and `train.p`. Additional arguments such as `sens.w` and `algorithm` can also be specified.

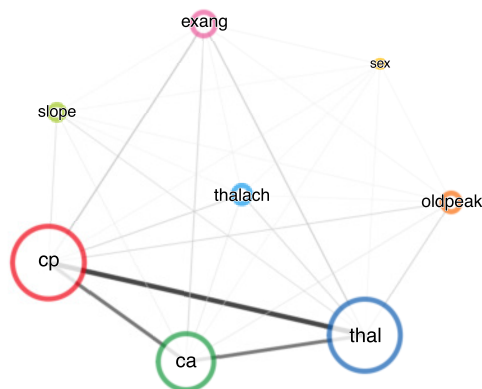


FIGURE 8: Network plot of relationships between cues in the heart disease data created by plotting an `FFForest` object. The object represents a bootstrap simulation of 100 FFTs trained on different random subsets of the heart disease data. The size of a node reflects how often it occurs across different FFTs in the forest (i.e., its importance), while the weight of the connection between two nodes reflects how often they co-occur within individual FFTs.

Figure 8 shows the result of plotting the result of `FFForest()` applied to the heart disease data.[11] This shows that the three cues (thal, cp, ca) of the FFT shown in Figure 6 were deemed the most important (i.e., most commonly occurring) cues over the entire range of FFTs (as indicated by their size) and were most likely to co-occur (as indicated by the width of their connecting lines). This increases our confidence that the three chosen cues are robust across a wide range of subsets of the original data.

4 Prediction Simulation

FFTs are decision algorithms designed to provide simple rules of thumb that can be easily understood and applied under cognitive and time constraints, rather than solely maximizing decision accuracy. That said, accuracy is certainly an important criterion in selecting a decision algorithm. Moreover, while people might not be able to implement complex algorithms "in the head", they now often have easy access to a computer or mobile phone that can quickly implement a computationally intensive decision algorithm in negligible time. So how well do FFTs predict data relative to more complex algorithms when there are no computational restrictions? Prior research has suggested that FFTs can predict data as well as algorithms such as logistic regression and standard decision trees (Martignon et al., 2008; Woike, Hoffrage & Hertwig, 2012; Woike et al., 2017). However, logistic regression (in a non-regularised form) and standard decision trees have strong competition from other algorithms. Support vector machines (SVM) and random forests (RF, Kuhn & Johnson, 2013) are known to be highly robust against overfitting and thus should provide a stronger challenge to FFTs. Thus, we are left with an important question: If computational resources are no issue and we only care about prediction performance, how good are FFTs created by the `FFTrees` package relative to the benchmarks provided by complex compensatory algorithms? To answer this question, we conducted a series of prediction simulations.

4.1 Simulation method

We obtained 10 real-world datasets from the UCI machine learning repository (Lichman, 2013). A summary of the datasets is presented in Table 2. The datasets differed in a variety of ways, from their content domain, to the amount of cases (ranging from 68 to 17,895), to the number (from 6 to 280) and classes (numeric and factor) of cues, to the base-rate of the criterion.

We implemented the prediction simulations using the `benchmark` function in the `mlr` package (Bischl et al., 2016). Each simulation proceeded as follows: The original dataset was split into a 50% training set for model fitting and a 50% testing set for prediction. FFTs were constructed using four different algorithms: ifan, dfan, max, and zig-zag. For both ifan and dfan, the maximum number of levels was set to 4. As the max and zig-zag algorithms do not specify size restrictions or pruning procedures (Martignon et al., 2008), we did not restrict the size of FFTs created by either algorithm. Model prediction performance was measured with balanced accuracy (bacc) in the testing set. For simplicity, we do not consider other accuracy measures such as weighted accuracy with sensitivity weights other than 0.5, or overall accuracy, and do not claim that our results will generalize to these or other accuracy measures. The speed and frugality of the FFTs was measured by mcu and pci.

In addition to the four FFT construction algorithms, we performed similar simulations for five competing decision algorithms: standard decision trees (CART), using the `rpart` package (Therneau, Atkinson & Ripley, 2015); logistic regression (LR), using the `stats` package (R Core Team, 2016);[12] regularised regression (RLR), using the `glmnet` package (Friedman, Hastie & Tibshirani, 2010); naïve Bayes (NB), using the `e1071` package (Meyer, Dimitriadou, Hornik, Weingessel & Leisch, 2015); random forests (RF), using the `randomForest` package (Liaw & Wiener, 2002); and support vector machines (SVM), also using the `e1071` package (Meyer et al., 2015). We used default param-

[11] For this example, 100 FFTs were constructed from 100 simulations using 50% of the full heart disease data.

[12] Because GLM models in R cannot make predictions for data with new factor values unseen during training, we forced the logistic regression model to predict `FALSE` (the most common class) for all simulations in which new factor values were present. In addition, in predicting data with logistic regression, we included all predictors, not just significant ones.

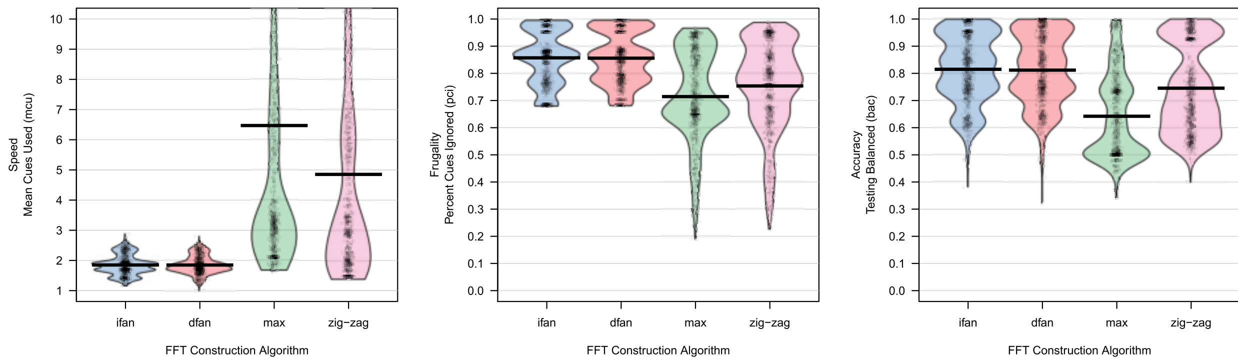


Figure 9: Comparisons of the four different fast-and-frugal tree construction algorithms collapsed across all simulations and datasets. For the left panel (speed, measured by mean cues used, mcu), lower values are better. For the middle and right panels (measuring frugality by percent cues ignored, pci, and balanced accuracy, bacc) higher values are better. Horizontal lines in distributions represent means. Plots were created using the `yarrr` package (Phillips, 2016).

eter values for all of these algorithms. We conducted 100 simulations for each dataset, resulting in a total of 100 simulations for each model-data combination. Complete simulation code and results are available on the Open Science Framework at https://osf.io/m726x/ (Phillips et al., 2017a).

4.2 Simulation results

We begin by comparing the four FFT construction algorithms, before comparing the performance of FFTs to alternative prediction algorithms.

4.2.1 Comparing FFT construction algorithms

The results for speed (mcu), frugality (pci), and balanced accuracy (bacc) collapsed across all simulations and testing datasets are presented in Figure 9. The two fan algorithms had virtually identical performance in all measures; therefore, we report their results simultaneously. With respect to efficiency, the fan algorithms were faster[13] and more frugal than both max and zig-zag. Both fan algorithms had mean mcu values of 1.85 (IQR = [1.65, 2.0]), whereas zig-zag had a mean mcu value of 4.85 (IQR = [2.0, 6.2]), and max had a mean mcu value of 6.5 (IQR = [2.6, 7.1]).[14] Both fan algorithms were also more accurate than max and zig-zag. The fan algorithms both had mean bacc values of 0.81 (IQR = [0.73, 0.93]) compared to means of 0.64 (IQR = [0.50, 0.74]) and 0.75 (IQR = [0.61, 0.93]) for max and zig-zag, respectively.

4.2.2 Comparing FFTs to other algorithms

We now compare the predictive accuracy of FFTs built with ifan to alternative prediction algorithms. The mean prediction balanced accuracy for each algorithm and dataset across all simulations are presented in Table 2 and Figure 10. Results show that FFTs were competitive with other algorithms in prediction performance. Collapsed across all datasets, the best performing algorithm was support vector machines (SVM), with a mean balanced accuracy of 0.86, followed closely by fast-and-frugal trees (FFT), regularized logistic regression (RLR), and random forests (RF), each with mean balanced accuracy scores of 0.83.[15]

Figure 11 shows the complete distribution of prediction performance within each individual dataset as well as an FFT constructed from the entire dataset.[16] These results show that there was variability in the rank order of algorithms across datasets, but FFTs were consistently competitive in their prediction performance. Relative to other algorithms, FFTs performed worst in the occupancy dataset, achieving a mean balanced accuracy of .96, while most other algorithms

[13]The fan algorithms were not faster in terms of actual tree construction processing times. Using a 2015 Apple Macbook Pro with 16GB of RAM and a 3.1Ghz Intel Core i7 processor, the max and zig-zag algorithms had median processing times of 0.59 and 0.57 seconds respectively, while the ifan and dfan algorithms had median times of 2.61 and 15.93 seconds, up to 30 times slower than max and zig-zag.

[14]These results parallel those of Newell, Rakow, Weston and Shanks (2004) who found that take-the-best, a strategy which—like max and zig-zag—ranks cues by positive and predictive validity, can be less frugal than a strategy that ranks cues by other measures, such as their likelihood of discriminating cases.

[15]As the SVM algorithm repeatedly crashed for both the arrhythmia and audiology data for unknown reasons, the mean balanced accuracy of SVM does not reflect its performance in these datasets.

[16]To clarify, our simulations produced different FFTs for different random training datasets. Thus, the variability in performance for the `FFTrees` algorithm is due to *both* different datasets and different FFTs.

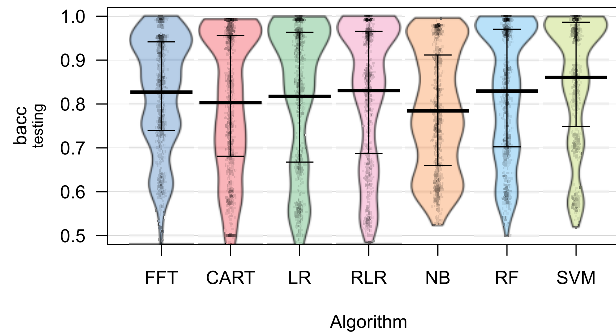


FIGURE 10: Distributions of prediction performance, measured as balanced accuracy (bacc) in testing across datasets. FFT results are for FFTs built with the ifan construction algorithm. The SVM results do not include data for the arrhythmia or audiology datasets due to repeated crashing. Wide horizontal lines represent means and vertical lines represent the 25th and 75th percentiles. Credible intervals for means are not shown because they are virtually identical to the sample means. Distributions for individual datasets are presented in Figure 11.

TABLE 2: Dataset descriptions, FFT efficiency, and prediction accuracy measured in balanced accuracy (bacc) in the prediction simulations. All FFTs were constructed using the ifan algorithm. The efficiency measures apply only to FFTs.

Dataset				Efficiency[1]		Prediction accuracy (bacc)[2]						
Title	Cases	Cues	Base rate	mcu	pci	FFT	CART	LR	RLR	NB	RF	SVM
arrhythmia	68	280	0.29	1.81	0.99	0.66	0.64	0.52	0.70	0.71	0.69	—[3]
audiology	226	70	0.10	1.65	0.98	0.84	0.65	0.93	0.85	0.83	0.72	—[3]
breast	683	10	0.35	1.42	0.86	0.94	0.94	0.96	0.96	0.97	0.97	0.97
cmc	1,473	10	0.35	2.20	0.78	0.61	0.58	0.56	0.53	0.59	0.59	0.57
credit	666	16	0.45	1.88	0.88	0.85	0.85	0.83	0.87	0.76	0.87	0.87
dermatology	358	35	0.31	1.69	0.95	0.99	0.98	0.99	0.99	0.69	1.00	1.00
heart	303	14	0.46	1.74	0.88	0.78	0.76	0.81	0.82	0.82	0.81	0.82
occupancy	17,895	6	0.21	1.89	0.68	0.96	0.99	0.99	0.99	0.98	0.99	0.99
voting	435	17	0.61	1.51	0.91	0.92	0.96	0.92	0.96	0.90	0.96	0.95
yeast	1,484	9	0.16	1.84	0.80	0.74	0.69	0.67	0.64	0.60	0.70	0.71
Overall	—	—	—	1.76	0.87	0.83	0.80	0.82	0.83	0.78	0.83	0.86

[1] Efficiency measures only apply to FFTs: mcu is mean cues used per case (speed), and pci is percent of cues ignored (frugality).

[2] Prediction accuracy measures show mean balanced accuracy (bacc) for six algorithms: FFT = fast-and-frugal trees using the ifan construction algorithm, CART = standard decision trees, LR = logistic regression, RLR = regularized logistic regression, NB = naïve Bayes, RF = random forests, and SVM = support vector machines.

[3] The SVM algorithm was unable to make predictions for both the arrhythmia or the audiology datasets due to repeated crashing. The overall accuracy prediction accuracy value for SVM thus only includes results from the other eight datasets.

reached .99. In the cmc and yeast datasets, FFTs slightly outperformed all other algorithms on average.

The 100% training FFTs in Figure 11 also illustrate the diversity of FFTs created for different datasets. For example, while some datasets such as breast and dermatology required only small FFTs with a maximum of two cues, other datasets, such as audiology, credit and bridges, produced larger FFTs that contained four cues (the maximum allowed).

In addition to making accurate predictions, the FFTs created by `FFTrees` were very efficient. Average mcu values,

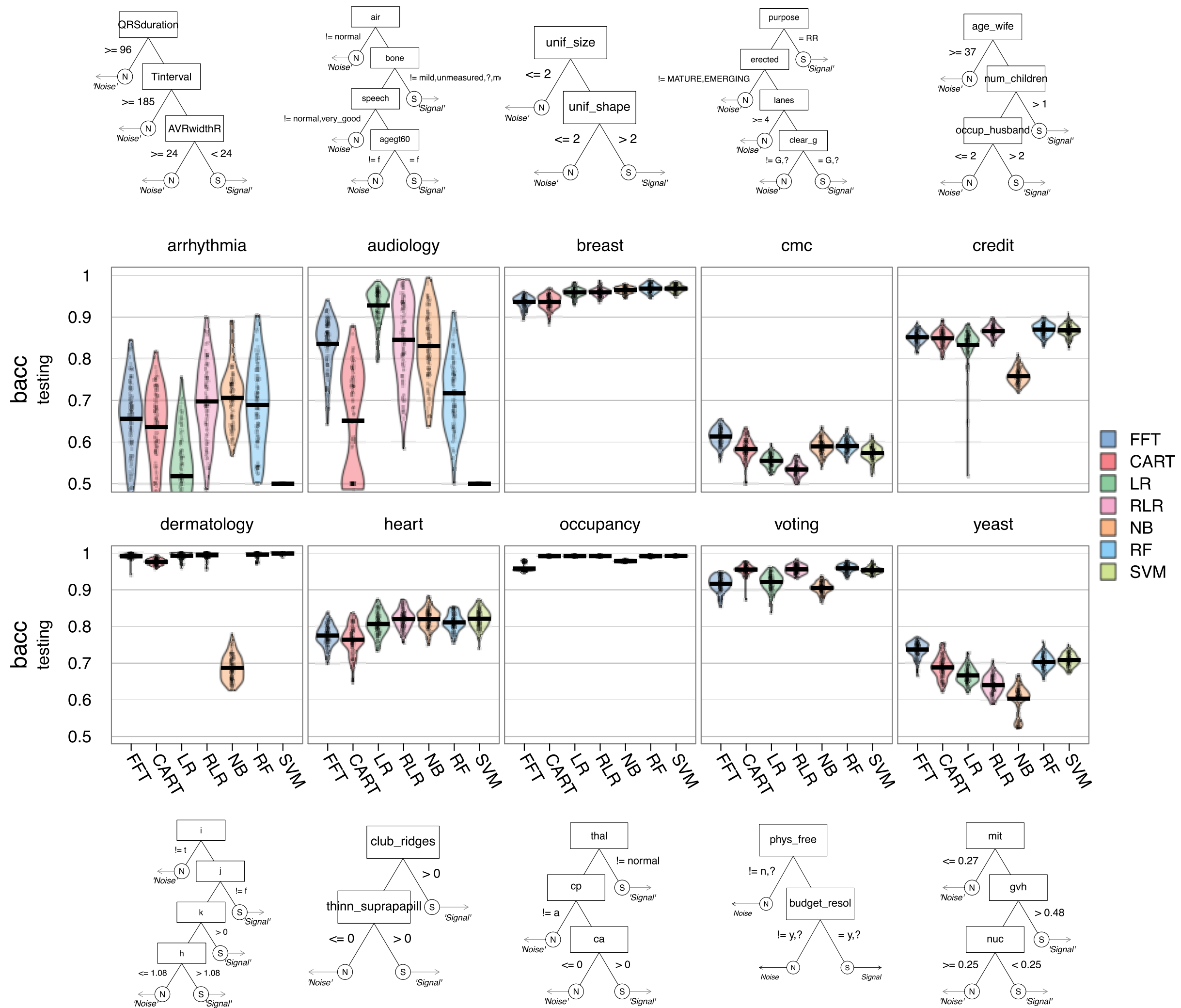


Figure 11: Distributions of prediction balanced accuracy (bacc) for each model and dataset in the prediction simulation. Horizontal lines within plots represent means. FFT results are for FFTs built with the ifan construction algorithm. The support vector machines (SVM) algorithm could not make predictions in the arrhythmia and audiology datasets due to repeated crashes. Next to each simulation is a 100% training FFT produced by the ifan algorithm applied to the full dataset.

representing how much information was necessary to make decisions, were low, ranging from a minimum of 1.42 in the breast dataset, to a maximum of 2.20 in the cmc dataset. Across all datasets, the mean mcu value was 1.76, indicating that the FFTs required fewer than two cues on average to make a fast classification decision. FFTs were not just fast, they were also frugal. Mean pci values, representing how much information the FFTs ignored, ranged from a minimum of 68% in the occupancy dataset, to a maximum of 99% in the arrhythmia dataset. Across all datasets, the mean pci value was 87%, indicating that FFTs ignored 87% of all available data. Together, these simulation results replicate and extend the findings of others (Martignon et al., 2008; Woike et al., 2017): Despite their simplicity and deliberate ignorance, FFTs can compete with state-of-the-art decision algorithms in pure prediction accuracy.

5 Discussion

FFTs are elegant, transparent and effective algorithms for making binary classification decisions. Because they are predictive, efficient and easy to implement, they have successfully been used in many applied domains ranging from

terrorism threat detection (Keller & Katsikopoulos, 2016) to depression diagnosis (Jenny et al., 2013). However, until now there has been no straightforward toolbox for anyone to easily create FFTs from data. The `FFTrees` package fills this gap. Importantly, our simulation results show that FFTs, especially those constructed with the ifan algorithm, can be as accurate as state-of-the-art classification algorithms. This reinforces previous research showing that there is no inherent trade-off between frugality and accuracy (Gigerenzer, Todd & the ABC Research Group, 1999). Thus, users of the `FFTrees` package not only can construct FFTs, but can use them with confidence for making important predictions.

5.1 When and how should we use an FFT?

Although we have argued that FFTs are under-utilized, we also believe that there are domains where an FFT is *not* the most appropriate algorithm to use. To help decision makers decide whether to consider FFTs or a alternative algorithm for making binary classification decisions we recommend using the FFT presented in Figure 12. It answers the question "Should I consider an FFT?" by considering four cues that matter when choosing a classification algorithm: implementation, cost, transparency, and prediction accuracy.

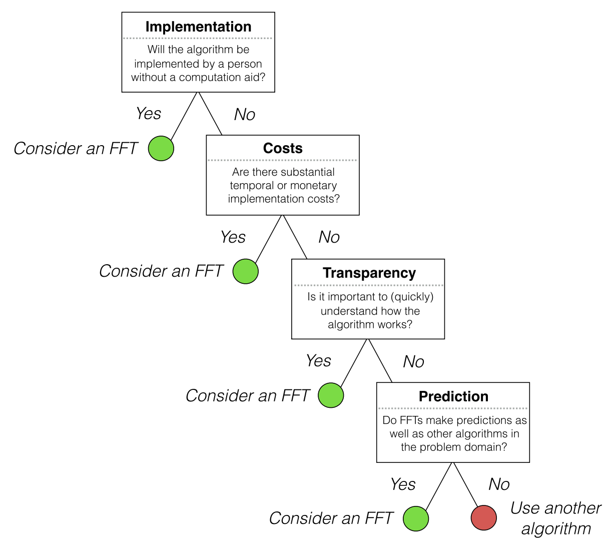


Figure 12: An FFT to decide whether to consider an FFT or use an alternative algorithm for classifying cases for a decision task. The list of cues in this FFT are meant to be illustrative and not exhaustive.

Implementation Will the algorithm be implemented by a person without a computational aid? If a decision needs to be implemented in real time by a human mind without a computational aid then FFTs provide a functional and accurate tool that can be quickly learned and easily used.

Costs Are there substantial monetary or temporal costs involved with implementing the decision? If it is costly to gather decision-relevant information, then FFTs are particularly effective because they use so little information, reducing costs in terms of money, time, and unnecessary tests (Gigerenzer, 2015; Luan et al., 2011; Martignon et al., 2003). Consider the domain of medical decision making: Here, the speed and frugality of effective FFTs are attractive because medical tests can be expensive. As we have shown in the heart disease dataset, the FFT in Figure 6 would have been almost 60% cheaper to implement than an algorithm that uses all possible cues, with perhaps no decrease in accuracy.

Transparency Is it important to understand how the algorithm works? Because an FFT can be explained either visually or verbally as a set of simple rules, it is easy for decision makers to understand how an FFT works and communicate it to others. By contrast, it is difficult for anyone without extensive statistical training to understand and implement more complex models like regression.

The transparency of FFTs not only makes them easier to understand, use, and communicate, it also facilitates troubleshooting when they *fail*. As with a simple machine with only a few moving parts, it should be relatively straightforward to see where and why an FFT might be going wrong. For example, imagine a doctor making heart disease diagnoses using the FFT presented in Figure 6. In her first year using the FFT, the tree has a balanced accuracy of 90%, but in the following year, its accuracy suddenly drops to 50%. What went wrong? Is one of the cues in the tree no longer accurate? If so, which one? To find out, the doctor could perform a few relatively simple checks. She could start by first considering the first node: "If the thallium scintigraphy test (thal) shows either a reversible defect (rd) or a fixed defect (fd), predict high-risk." To see if the accuracy of classifications made by this cue has changed, she could compare the classification of this node (i.e., those with reversible or fixed defects) between years. If she finds that the accuracy rate for patients classified at this node decreased from 85% to 40%, this might suggest that the test is not being administered correctly, or that her patient population has changed and that the test is less accurate for this new population. On the other hand, if there was no substantial change in accuracy for patients diagnosed at this node in the FFT, she could be confident that the problem lies with a node further down the tree.

In short, the simplicity and transparency of FFTs is not only beneficial when the algorithm works well, but also allows decision makers faced with a poorly performing tree to quickly diagnose why and where it is failing. In contrast, detecting the cause(s) behind a failing compensatory decision algorithm, which could hide behind a variety of parameters, is considerably more difficult.

Prediction accuracy Do FFTs reach similar (or better) prediction performance as other algorithms in the problem domain? Like all decision algorithms, FFTs are neither inherently good nor bad at prediction (Gigerenzer, Todd & the ABC Research Group, 1999). Rather, their performance depends on their match to the task environment, and the demands of the decision maker. Indeed, there is "no free lunch" in classification tasks, meaning that no single learning algorithm is better *a priori* than any other when facing an unknown dataset (Wolpert, 1996). Our simulations across 10 diverse datasets have shown that FFTs *can* compete with complex machine learning algorithms in data prediction alone, they do not prove that FFTs always will.

This raises an important question: When can we expect that FFTs will perform well and when can we expect that they will not? While a complete answer to this question is beyond the scope of this paper, we can point to one general class of datasets for which FFTs will not predict data as well as compensatory algorithms: namely, those with many cues that each are weakly predictive of the criterion, but where a function of the cues (i.e., a weighted linear combination) is highly predictive. For example, one could generate a dataset containing 10 cues $X_1, X_2, \ldots, X_{10}$, with a binary, Bernoulli-distributed criterion y and a probability of success defined by $logit(1 \cdot X_1 + 1 \cdot X_2 + 1 \cdot X_3 + \ldots + 1 \cdot X_{10})$. An FFT would tend to make poor predictions for this data as each individual cue is not very predictive of the criterion. By contrast, a logistic regression model with a sufficiently large training dataset could make accurate predictions for these data because the sum of all cues, which a regression equation can easily capture, is highly predictive of the criterion. However, if we allow for some cues to be more predictive than others, then FFTs can make good predictions even when the true generative model is a linear weighed combination of the cues. For example, if the probability of success was defined as a weighted sum of the cues with highly *skewed* weights, such as $logit(100 \cdot X_1 + 50 \cdot X_2 + 25 \cdot X_3 + \ldots + 1 \cdot X_{10})$, an FFT could perform quite well by focusing on a few highly predictive cues (i.e., X_1, X_2, and X_3), and ignoring the rest.

Ultimately, the question which algorithm yields the best predictive performance for a dataset is an empirical, rather than an ideological question. While it is helpful to understand which properties of data generally affect the relative performance of different decision algorithms, one should be cautious in discarding an algorithm *a priori*, without actually evaluating its prediction (rather than fitting) performance for a dataset. When viewing prediction algorithms as tools, whose function partly depends on their fit to the features of specific datasets, even algorithms that, by all logic "should" fail can be surprisingly successful.

5.2 Future directions

The `FFTrees` package is a growing toolbox for creating, customizing, and applying fast-and-frugal trees. As such, the FFT construction algorithms, metrics, and visualizations currently included in `FFTrees` provide just a starting point rather than a final product. Although we have ideas and plans for extensions, the goals and directions of future versions will also depend on the feedback from users, inputs from developers, and needs of practitioners. We now identify three key areas for further developing `FFTrees`.

5.2.1 Incorporating cue costs in FFT construction

In decision tasks such as medial diagnoses, information can come at significant costs in terms of time, money, or other factors, such as physical and psychological stress. As we have described, FFTs are almost inherently cheap to use as they typically require very little information to make a decision. However, this does not mean that all FFTs are equally cost efficient—one FFT might be much cheaper to use than another, either because it uses less expensive cues, or because it uses them in a more cost efficient order. While `FFTrees` can calculate classification costs when applying FFTs to data (when the user specifies cue costs using the `cost.cues` argument) these costs are not currently used during FFT construction. When cue costs are ignored, an FFT construction algorithm might construct trees containing cues that are relatively expensive to use, but miss slightly less accurate trees that would be much cheaper to implement. For instance, in the heart disease dataset, `FFTrees` puts a relatively expensive cue (`thal`: $102.90) at the first node of the FFT, and a very cheap cue (`cp`: $1) at the second node. However, inspecting the cue accuracies in Figure 7 shows that the cues have comparable accuracies. Thus, we would expect that simply changing the order of these cues could substantially reduce the cost of applying the FFT with very little reduction in decision accuracy. As the ifan construction algorithm ignored cue costs, it returned a relatively expensive FFT and missed a much cheaper variant that may yield a similar accuracy. The issue of considering explicit costs for test construction has been discussed in the medical decision making literature (e.g., Hershey, Cebul & Williams, 1986), and costs have been incorporated into standard decision tree construction algorithms (Lomax & Vadera, 2013). One major feature of a future `FFTrees` toolbox would be to allow users to specify the cost of obtaining values from each cue, and then incorporate both cue costs and decision accuracy in constructing FFTs.

5.2.2 Detecting and adapting to performance changes

Many decision tasks occur in dynamic environments, where conditions are not static, but can change over time. Terrorists can change how they approach military checkpoints (Keller

& Katsikopoulos, 2016), financial institutions can vary their investment strategies (Aikman et al., 2014), and new patient populations can enter emergency rooms (Trzeciak & Rivers, 2003). In decision tasks where FFTs are applied to potentially dynamic data, a change detection algorithm such as those used in image processing (e.g., Radke, Andra, Al-Kofahi & Roysam, 2005) and time series (e.g., Kim, 2000; Ray & Tsay, 2002) could be useful in tracking changes in the performance of an FFT over time as it is applied to new batches of data (see Todd & Dieckmann, 2004, for a similar discussion). Consider how a change detection algorithm could improve doctors' use of the heart disease FFT. Given historical training data, a change detection algorithm could maintain a series of expected probabilities that future patients will be classified at each exit branch in the tree, as well as the probability of classification success at each branch. For example, the algorithm might predict that 50% of future patients should be classified at the first node of the tree, and of those patients, 75% should be correctly classified. As new patients are classified using the tree over time, the algorithm could compare the classification rates of new patients to its expectations from historical data. If the algorithm determines that the new classification rates are substantially different from what was expected, `FFTrees` could notify the user that a meaningful change may have occurred. This could spur the user to re-evaluate how well specific cue values are being measured (i.e., a malfunctioning medical test) or to consider constructing a new FFT trained on more recent data.

5.2.3 Modeling behavioral data

In this paper, we have focused on using FFTs to predict matters of fact or objective states (like patients with high vs. low risks for heart disease). However, `FFTrees` could also be used to model behavioral data with binary outcomes (like doctors' decisions based on classifying patients). Both fast-and-frugal and standard decision trees have successfully been used to model decision making processes in memory (Batchelder & Riefer, 1990) and quantitative judgments (Gigerenzer & Goldstein, 1999; Gigerenzer, Todd & the ABC Research Group, 1999; Rieskamp & Hoffrage, 1999). Software packages such as `multiTree` (Moshagen, 2010) exist that automate the modeling process. `FFTrees` could also in principle be used to model individual-level decision processes. While we support such efforts, we also caution against a naive interpretation of FFTs as process models without a modicum of skepticism and additional supporting evidence. When applied to behavioral data, the FFT construction algorithms in `FFTrees` will prefer cues that predict the criterion value without any consideration of their their psychological plausibility. An FFT could rank cues in an order that makes no psychological sense, or might select cues that were not even encoded by the decision maker. While a good fit—or better, successful prediction—of some statistical model may be necessary to be considered as a process model, it is not sufficient. A convincing case for FFTs as process models should include process predictions (Johnson, Schulte-Mecklenbeck & Willemsen, 2008), such as increasing response latencies corresponding to lower levels of a tree (see Fific, Little & Nosofsky, 2010, for a a related example), and a conceptual scope of the decision making process (Jarecki, Tan & Jenny, 2016).

6 Conclusion

The purpose of this article is to highlight the effectiveness of fast-and-frugal trees, and to make them accessible to interested users via `FFTrees`. By focusing on the creation and evaluation of FFTs, we have been silent about how they are or should be used. For instance, FFTs can model someone's judgment or some objective state or fact, and can be interpreted in both a descriptive or a normative fashion. Irrespective of one's stance in this debate, an FFT is designed to provide accurate and robust predictions at low costs. If it achieves this goal, its transparency provides a suggestion for revising our beliefs about the causal texture of a particular task or domain. Thus, while it would seem inflated to view any successful FFT as a process model or theory, it could certainly serve as a tool to inform our theorizing.

Realizing that simple FFTs can be as accurate as far more complex models raises new issues regarding their acceptance and justification. Even if skeptics were persuaded that frugality does not always decrease accuracy it will remain a challenge how ignoring information can be *justified* when errors occur. Imagine a doctor making a frugal classification decision that proves to be wrong. Can she really claim with authority and confidence that it was legitimate and in the patient's best interest to ignore most of the available information? Given our results, there is no *a priori* reason to believe that a more comprehensive or complex algorithm would have been less error-prone than an FFT. Nevertheless, it is clear that a society or institution that primarily aims to assign blame, rather than learn from errors, may be reluctant to adopt fast-and-frugal algorithms.

At the same time, practical concerns and persistent pressures to reduce costs push decision makers towards more frugal models. Just as ignoring information may be hard to justify, it is difficult to insist on using irrelevant information that provides no benefit in predictive accuracy. Thus, answering the question if and how FFTs should be used touches upon many issues of public policy and of legal or moral responsibility. Whenever making predictions for important tasks, we ultimately strive for an acceptable balance between accuracy and frugality. The `FFTrees` package helps us to find, measure, and better understand this balance.

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Appendix

6.1 FFT fan construction algorithms

The following are descriptions of the fan FFT construction algorithms, ifan and dfan as implemented in `FFTrees` version 1.3.2. Our terminology is as follows:

Criterion: Y is a binary vector of length M indicating the true criterion value (True or False) for all cases.

Cue Matrix: Z is an $M \cdot N$ matrix (or in R terms, a data frame) of cues (predictors), containing M rows (cases) and N columns (cues).

Cues: X_i, $i \in 1, 2, \ldots N$ are N cue vectors of length M, where some vectors are nominal factors, and others are on a numeric (either continuous or discrete) scale.

Decision threshold and decision direction: T_i is a decision threshold, and D_i is a decision direction for the i-th cue that jointly map cue values to *positive* (i.e., criterion = True or 1) decisions. For numeric cues, T_i is a number and D_i a direction $D_i \in \{>, <\}$. For example, for a numeric cue age, the threshold and direction combination age > `30`, where $T = 30$ and $D =>$, means that age values greater than 30 are predicted to have positive criterion values, while age values less than or equal to 30 are predicted to have negative (i.e., criterion = False or 0) criterion values. For factor cues, T_i is a set of factor values and $D_i \in \{\in, \notin\}$ For example, $color \in \{blue, green\}$ has a decision threshold $T = \{blue, green\}$ and decision direction $D = \in$, meaning that colors equal to blue or green are predicted to have positive criterion values, and colors *not* equal to blue or green ($\notin$) are predicted to have negative criterion values.

6.2 Fan algorithm parameters

Both fan algorithms have the following five parameters:

goal.chase: A statistic that is maximized when calculating cue thresholds and ranking cues. Default: `goal.chase = bacc`.

goal: A statistic that is maximized when selecting a final FFT from an existing set of FFTs. Default: `goal = wacc`.

max.levels: The maximum number of levels allowed in an FFT. Default: `max.levels = 4`.

max.numcat: The number of (equally spaced) numeric thresholds compared when calculating thresholds for numeric cues. Default: `max.numcat = 20`.

stopping.par: The minimum percentage of training data required by each node. Default: `stopping.par = .10`.

6.3 The ifan algorithm

The ifan algorithm assumes independence between cues and is defined as follows:

1. *Calculate decision thresholds and directions for each cue*: For each cue X_i, calculate a decision threshold T_i and decision direction D_i that maximizes goal.chase when the decisions made by this cue (and ignoring all other cues) are compared to the true criterion values for all M cases. In version 1.3.0 of `FFTrees`, this is done in a brute-force fashion and comprises several sub-steps that distinguish between numeric and factor cues:

   (a) For numeric cues, test max.numcat $\cdot$ 2 different thresholds and direction pairs by combining all possible combinations of max.numcat (with a default value of 20) decision thresholds (equally spaced numeric values ranging from the minimum to the maximum cue value) with 2 decision directions (> and <). Select the threshold-direction pair with the highest goal.chase value.

   (b) For factor cues, the exit direction for each factor level is determined in a two-step procedure:

      i. Calculate the goal.chase of all possible combinations of individual factor levels and decision directions ($\in$ and $\notin$). For example,

given a cue *color* with three possible values *red*, *green* and *blue*, test six combinations of decision thresholds and directions: $color \in red$, $color \notin red$, $color \in green$, $color \notin green$, $color \in blue$, $color \notin blue$.

ii. For each factor level, remove the decision direction with the lower goal.chase value from the set. For example, if $color \in red$ has a balanced accuracy of 0.75, and $color \notin red$ has a balanced accuracy of 0.45, then remove the combination $color \notin red$.

iii. For each decision direction, rank cue thresholds in order of goal.chase. For example, considering the $\in$ direction, the color thresholds could be ranked as $color \in red = 0.75$, $color \in green = 0.6$ (here, we assume that the $color \in blue$ threshold was removed because the threshold $color \notin blue$ had a higher value of `goal.chase`).

iv. Determine a candidate set of cue thresholds by sequentially combining individual thresholds in order of rank, starting with the highest ranked threshold. As each additional threshold is added to the set, re-calculate the goal.chase of the set. Continue adding factor values to the set as long as goal.chase increases. As soon as goal.chase decreases with an additional factor value, stop the process and use the previously defined threshold set. Complete this process for both the $\in$ and the $\notin$ decision directions, resulting in two candidate sets of factor values (one for the $\in$ direction and one for the $\notin$ direction).

v. Compare the goal.chase values of the final two sets of factor values and select the set with the higher goal.chase value as the final decision threshold, with a corresponding decision direction.

2. *Rank order cues by* goal.chase: Rank order cues (combined with their corresponding decision thresholds and directions calculated in Step 1) by their goal.chase values. Select the top max.levels cues and discard the rest.
3. *Create a fan of several FFTs*: Create $2^{\text{max.levels}-1}$ FFTs $\{F_1, F_2, \ldots, F_{2^{\text{max.levels}-1}}\}$ by placing the cues selected and ordered in Step 2 in sequential nodes, using all possible FFT exit structures, where nodes 1 through max.levels − 1 can have either a positive or a negative exit, and the final max.levels node has both a positive and negative exit.
4. *Prune FFTs*: For each tree F_i, classify all cases. If any lower nodes in the tree contain fewer than stopping.par percent of all cases, remove those nodes and force the final remaining (lowest) node in the tree to have both a positive and negative exit.
5. *Select FFT with highest* goal: Calculate the goal value of each tree. Select the tree with the highest goal value as the final tree.

6.4 The dfan algorithm

The dfan algorithm assumes dependencies (or interactions) between cues and is defined as follows:

1. *Create FFTs with different exit structures*: Given max.levels, create $2^{\text{max.levels}-1}$ FFTs $\{F_1, F_2, \ldots\ F_{2^{\text{max.levels}-1}}\}$ by using all possible FFT exit structures, where nodes 1 through max.levels − 1 can have either a positive or a negative exit, and the final (max.levels.) node has both a positive and a negative exit. For example, if max.levels = 3, then four FFT skeletons are created: FFT #1 = {0, 0, .5}, FFT #2 = {0, 1, .5}, FFT #3 = {1, 0, .5}, FFT #4 = {1, 1, .5}, where 0, 1, and .5 represent negative exits, positive exits, and both negative and positive exits, respectively.
2. *Create new decision thresholds, rank cues, and select top ranked cue for next empty level*: Calculate decision thresholds, and directions for all cues using the procedure outlined in Step 1 of the ifan algorithm. Rank order cues by their goal.chase values. Select the top ranked cue and assign to the current node.
3. *Classify cases in current node*: Make classification decisions for cases that satisfy the decision criteria for the current node.
4. *Repeat Steps 2 and 3*: Recursively repeat Steps 2 and 3, calculating new decision thresholds and directions for each cue based on cases not yet classified by earlier nodes, and assigning the cue with the highest goal.chase to the next empty node. Repeat until all cases are classified.
5. *Prune FFTs*: See ifan Step 4 (above).
6. *Select FFT with highest* goal: See ifan Step 5 (above).