```
"'
```

```
library(randomForest)
```

```
## randomForest 4.6-14
```

```
## Type rfNews() to see new features/changes/bug fixes.
```

```
library(FFTrees)
```

```
##
```

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##   / \
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##  F   O
```

```
##     / \
```

```
##    F   Trees 1.5.5
```

```
##
```

```
## Nathaniel.D.Phillips.is@gmail.com
```

```
## FFTrees.guide() opens the guide.
```

```
library(ggplot2)
```

```
##
## Attaching package: 'ggplot2'
```

```
## The following object is masked from 'package:randomForest':
##
##     margin
```

```
library(datasets)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following object is masked from 'package:randomForest':
##
##     combine
```

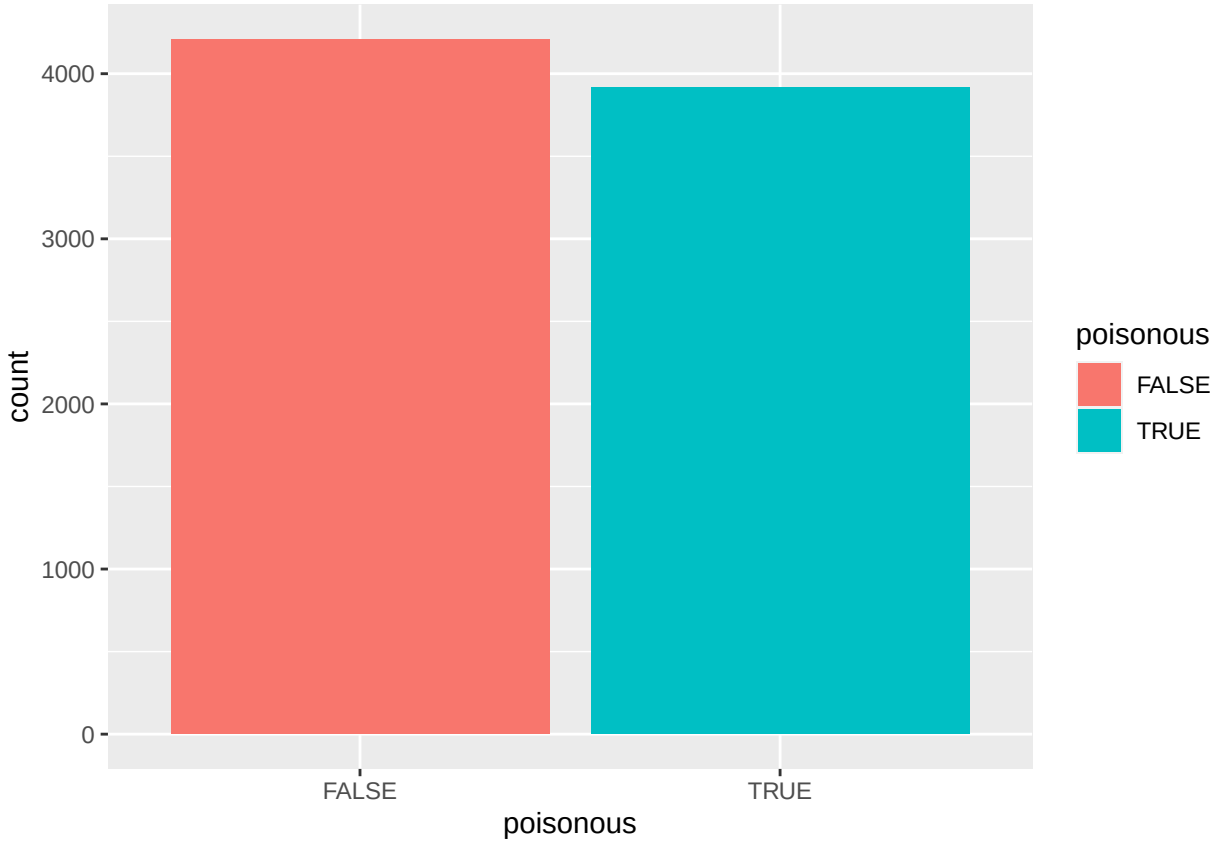
```
## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
head(mushrooms)
```

```
##   poisonous cshape csurface ccolor bruises odor gattach gspace gsize gcolor
## 1      TRUE      x        s      n       t    p       f      c     n      k
## 2     FALSE      x        s      y       t    a       f      c     b      k
## 3     FALSE      b        s      w       t    l       f      c     b      n
## 4      TRUE      x        y      w       t    p       f      c     n      n
## 5     FALSE      x        s      g       f    n       f      w     b      k
## 6     FALSE      x        y      y       t    a       f      c     b      n
##   sshape sroot ssaring ssbring scaring scbring vtype vcolor ringnum ringtype
## 1      e     e       s       s       w       w     p      w       o        p
## 2      e     c       s       s       w       w     p      w       o        p
## 3      e     c       s       s       w       w     p      w       o        p
## 4      e     e       s       s       w       w     p      w       o        p
## 5      t     e       s       s       w       w     p      w       o        e
## 6      e     c       s       s       w       w     p      w       o        p
##   sporepc population habitat
## 1       k          s       u
## 2       n          n       g
## 3       n          n       m
## 4       k          s       u
## 5       n          a       g
## 6       k          n       g
```

```r
ggplot(mushrooms,aes(poisonous, fill = poisonous)) + geom_bar()
```




```
rows <- sample(nrow(mushrooms), nrow(mushrooms)*.7, replace=FALSE)

train <- mushrooms[rows,]
test <- mushrooms[-rows,]
```

```
model <- FFTrees(poisonous ~ . , train)
```

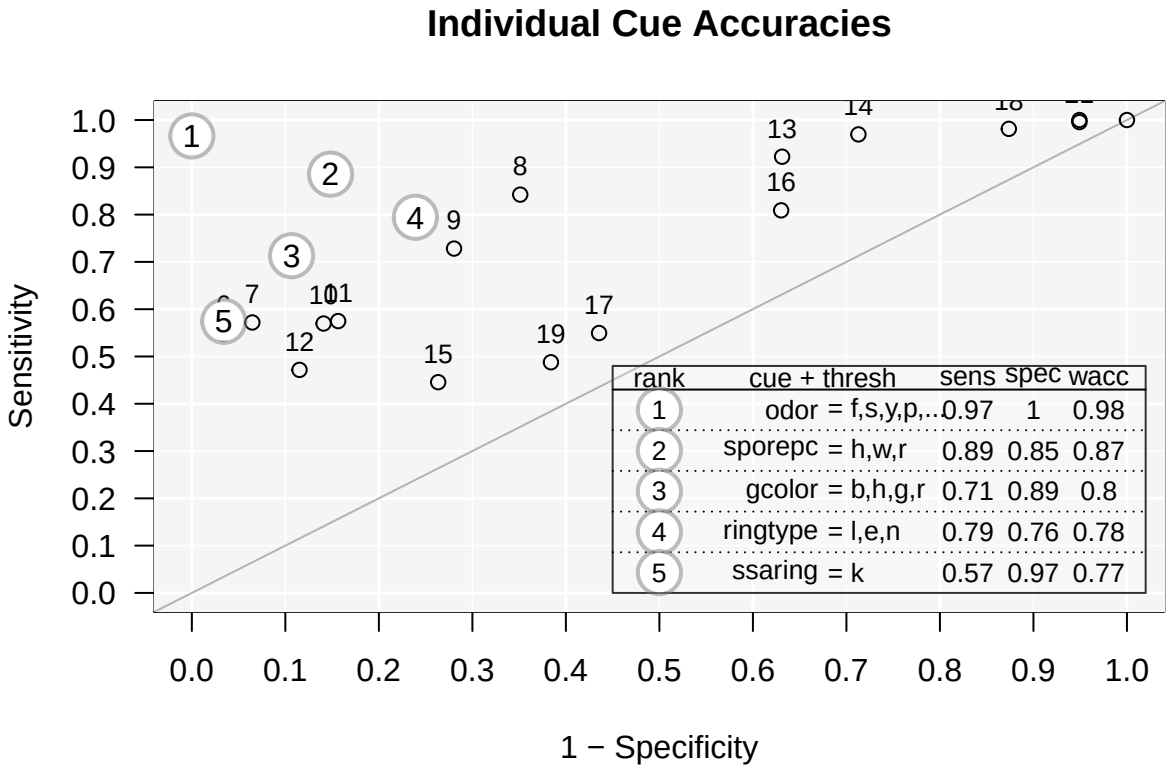
```
## Setting goal = 'wacc'

## Setting goal.chase = 'waccc'

## Setting cost.outcomes = list(hi = 0, mi = 1, fa = 1, cr = 0)

## Growing FFTs with ifan

## Fitting other algorithms for comparison (disable with do.comp = FALSE) ...
```

```
model
```

```
## FFTrees
## - Trees: 6 fast-and-frugal trees predicting poisonous
## - Outcome costs: [hi = 0, mi = 1, fa = 1, cr = 0]
##
```

```
## FFT #1: Definition
## [1] If odor != {f,s,y,p,c,m}, decide False.
## [2] If sporepc != {h,w,r}, decide False, otherwise, decide True.
##
## FFT #1: Training Accuracy
## Training Data: N = 5,686, Pos (+) = 2,733 (48%)
##
## |         | True +   | True -   |
## |---------|----------|----------|
## |Decide + | hi 2,328 | fa 0     | 2,328
## |Decide - | mi 405   | cr 2,953 | 3,358
## |---------|----------|----------|
##             2,733      2,953      N = 5,686
##
## acc  = 92.9%  ppv  = 100.0%  npv  = 87.9%
## bacc = 92.6%  sens = 85.2%  spec = 100.0%
## E(cost) = 0.071
##
## FFT #1: Training Speed and Frugality
## mcu = 1.46, pci = 0.93
```

```
plot(model, what = 'cues')
```




```
pred <- predict(model, test)
table(pred, test$poisonous)
```

```
##
## pred    FALSE TRUE
##   FALSE  1255  163
##   TRUE      0 1020
```