

# Package ‘rfPermute’

February 23, 2020

**Type** Package

**Title** Estimate Permutation p-Values for Random Forest Importance Metrics

**Description** Estimate significance of importance metrics for a Random Forest model by permuting the response variable. Produces null distribution of importance metrics for each predictor variable and p-value of observed. Provides summary and visualization functions for 'randomForest' results.

**Version** 2.1.81

**URL** <https://github.com/EricArcher/rfPermute>

**BugReports** <https://github.com/EricArcher/rfPermute/issues>

**Depends** R (>= 3.2.0), randomForest

**Imports** abind, dplyr, ggplot2, grDevices, gridExtra, magrittr, parallel, rlang, scales, stats, swfscMisc (>= 1.3), tibble, tidy, utils

**License** GPL (>= 2)

**RoxygenNote** 7.0.2

**NeedsCompilation** no

**Author** Eric Archer [aut, cre]

**Maintainer** Eric Archer <eric.archer@noaa.gov>

**Repository** CRAN

**Date/Publication** 2020-02-23 18:30:02 UTC

## R topics documented:

|                           |   |
|---------------------------|---|
| casePredictions . . . . . | 2 |
| classConfInt . . . . .    | 3 |
| cleanRFdata . . . . .     | 4 |
| confusionMatrix . . . . . | 4 |

|                              |           |
|------------------------------|-----------|
| exptdErrRate . . . . .       | 5         |
| impHeatmap . . . . .         | 6         |
| pctCorrect . . . . .         | 7         |
| plot.rp.importance . . . . . | 8         |
| plotConfMat . . . . .        | 9         |
| plotImpVarDist . . . . .     | 10        |
| plotInbag . . . . .          | 11        |
| plotNull . . . . .           | 11        |
| plotOOBtimes . . . . .       | 13        |
| plotPredictedProbs . . . . . | 13        |
| plotRFtrace . . . . .        | 14        |
| plotVotes . . . . .          | 15        |
| proximityPlot . . . . .      | 16        |
| rfPermute . . . . .          | 17        |
| rp.combine . . . . .         | 18        |
| rp.importance . . . . .      | 19        |
| symb.metab . . . . .         | 20        |
| <b>Index</b>                 | <b>22</b> |

---

|                 |                         |
|-----------------|-------------------------|
| casePredictions | <i>Case Predictions</i> |
|-----------------|-------------------------|

---

## Description

Get data frame of case predictions for training data along with vote distributions.

## Usage

```
casePredictions(rf)
```

## Arguments

`rf` an object inheriting from `randomForest`.

## Value

A data frame containing columns of original and predicted cases, whether they were correctly classified, and vote distributions.

## Author(s)

Eric Archer <eric.archer@noaa.gov>

## Examples

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars)
casePredictions(rf)
```

---

|              |  |
|--------------|--|
| classConfInt | <i>Classification Confidence Intervals</i> |
|--------------|--|

---

## Description

Calculate confidence intervals for Random Forest classifications

## Usage

```
classConfInt(rf, conf.level = 0.95, threshold = 0.8)
```

## Arguments

|            |   |
|------------|---|
| rf         | a <a href="#">randomForest</a> object                                   |
| conf.level | confidence level for the <a href="#">binom.test</a> confidence interval |
| threshold  | threshold to test observed classification probability against.          |

## Value

A matrix with the following columns for each class and overall:

**pct.correct** percent correctly classified

**LCI\_##, UCI\_##** the lower and upper central confidence intervals given `conf.level`

**Pr.gt\_##** the probability that the true classification probability is  $\geq$  threshold

## Author(s)

Eric Archer <[eric.archer@noaa.gov](mailto:eric.archer@noaa.gov)>

## Examples

```
data(symb.metab)

rf <- randomForest(type ~ ., symb.metab)
classConfInt(rf)
```

---

|             |                                       |
|-------------|---------------------------------------|
| cleanRFdata | <i>Clean Random Forest Input Data</i> |
|-------------|---------------------------------------|

---

**Description**

Removes cases for a Random Forest classification model with missing data and predictors that are constant.

**Usage**

```
cleanRFdata(x, y, data, max.levels = 30)
```

**Arguments**

|            |   |
|------------|---|
| x          | columns used as predictor variables as character or numeric vector. |
| y          | column used as response variable as character or numeric.           |
| data       | data.frame containing x and y columns.                              |
| max.levels | maximum number of levels in response variable y.                    |

**Value**

a data.frame containing cleaned data.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

---

|                 |                         |
|-----------------|-------------------------|
| confusionMatrix | <i>Confusion Matrix</i> |
|-----------------|-------------------------|

---

**Description**

Generate a confusion matrix for Random Forest analyses with error rates translated into percent correctly classified, and columns for confidence intervals and expected classification rates (priors) added.

**Usage**

```
confusionMatrix(rf, conf.level = 0.95, threshold = 0.8)
```

**Arguments**

|            |   |
|------------|---|
| rf         | a <a href="#">randomForest</a> object.                                  |
| conf.level | confidence level for the <a href="#">binom.test</a> confidence interval |
| threshold  | threshold to test observed classification probability against.          |

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**See Also**

[classConfInt](#), [exptdErrRate](#)

**Examples**

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars, importance = TRUE)
confusionMatrix(rf)
```

---

|              |                            |
|--------------|----------------------------|
| exptdErrRate | <i>Expected Error Rate</i> |
|--------------|----------------------------|

---

**Description**

Calculate expected OOB error rates (priors) for randomForest classification model based on random assignment and class sizes.

**Usage**

```
exptdErrRate(rf)
```

**Arguments**

rf                    an object inheriting from link{randomForest}.

**Value**

a vector of expected error rates (priors) for each class.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars)
exptdErrRate(rf)
```

---

`impHeatmap`*Importance Heatmap*

---

**Description**

Plot heatmap of importance scores or ranks from a classification model

**Usage**

```
impHeatmap(  
  rf,  
  n = NULL,  
  ranks = TRUE,  
  plot = TRUE,  
  xlab = NULL,  
  ylab = NULL,  
  scale = TRUE,  
  alpha = 0.05  
)
```

**Arguments**

|                         |   |
|-------------------------|---|
| <code>rf</code>         | an object inheriting from <a href="#">randomForest</a> .  |
| <code>n</code>          | Plot <code>n</code> most important predictors.  |
| <code>ranks</code>      | plot ranks instead of actual importance scores?   |
| <code>plot</code>       | print the plot?   |
| <code>xlab, ylab</code> | labels for the x and y axes.  |
| <code>scale</code>      | For permutation based measures, should the measures be divided their "standard errors"?   |
| <code>alpha</code>      | a number specifying the critical alpha for identifying predictors with importance scores significantly different from random. This parameter is only relevant if <code>rf</code> is a <a href="#">rfPermute</a> object with p-values. Importance measures with p-values less than alpha will be denoted in the heatmap by a black border. If set to NULL, no border is drawn. |

**Details**

`rf` must be a classification model run with `importance = TRUE`.

**Value**

the ggplot object is invisibly returned.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
data(mtcars)

# A randomForest model
rf <- randomForest(factor(am) ~ ., mtcars, importance = TRUE)
importance(rf)
impHeatmap(rf, xlab = "Transmission", ylab = "Predictor")

# An rfPermute model with significant predictors identified
rp <- rfPermute(factor(am) ~ ., mtcars, nrep = 100, num.cores = 1)
impHeatmap(rp, xlab = "Transmission", ylab = "Predictor")
```

---

|            |                                     |
|------------|-------------------------------------|
| pctCorrect | <i>Percent Correctly Classified</i> |
|------------|-------------------------------------|

---

**Description**

Calculate the percent of individuals correctly classified in a specified percent of trees in the forest.

**Usage**

```
pctCorrect(rf, pct = c(seq(0.8, 0.95, 0.05), 0.99))
```

**Arguments**

**rf** a [randomForest](#) or `rfPermute` object.  
**pct** vector of minimum percent of trees voting for each class. Can be 0:1 or 0:100.

**Value**

a matrix giving the percent of individuals correctly classified in each class and overall for each threshold value specified in `pct`.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars, importance = TRUE)
pctCorrect(rf)
```

---

plot.rp.importance      *Plot Random Forest Importance Distributions*

---

### Description

Plot the Random Forest importance distributions, with significant p-values as estimated in rfPermute.

### Usage

```
## S3 method for class 'rp.importance'
plot(
  x,
  alpha = 0.05,
  sig.only = FALSE,
  type = NULL,
  n = NULL,
  main = NULL,
  ...
)
```

### Arguments

|          |  |
|----------|--|
| x        | An object produced by a call to <a href="#">rp.importance</a> .  |
| alpha    | Critical alpha to identify "significant" predictors.   |
| sig.only | Plot only the significant ( $\leq$ alpha) predictors?  |
| type     | character vector listing which importance measures to plot. Can be class names or names of overall importance measures (e.g., "MeanDecreaseAccuracy") in the <a href="#">rp.importance</a> object. |
| n        | Plot n most important predictors.  |
| main     | Main title for plot.   |
| ...      | Optional arguments which will be ignored.  |

### Details

The function will generate a panel of plots, one for each importance type.

### Author(s)

Eric Archer <eric.archer@noaa.gov>

### See Also

[rfPermute](#), [rp.importance](#)



## Examples

```
# A regression model using the ozone example
data(airquality)
ozone.rfP <- rfPermute(
  Ozone ~ ., data = airquality, ntree = 100,
  na.action = na.omit, nrep = 50, num.cores = 1
)

# Plot the unscaled importance distributions and highlight significant predictors
plot(rp.importance(ozone.rfP, scale = FALSE))

# ... and the scaled measures
plot(rp.importance(ozone.rfP, scale = TRUE))
```

---

plotConfMat

*Plot Confusion Matrix*

---

## Description

Plot confusion matrix heatmap.

## Usage

```
plotConfMat(rf, title = NULL, plot = TRUE)
```

## Arguments

|       |  |
|-------|--|
| rf    | an object inheriting from <a href="#">randomForest</a> . |
| title | a title for the plot.                                    |
| plot  | display the plot?  |

## Value

the ggplot2 object is invisibly returned.

## Author(s)

Eric Archer <eric.archer@noaa.gov>

## Examples

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars)
plotConfMat(rf)
```

---

plotImpVarDist                    *Plot Important Variable Distribution*

---

### Description

Plot distribution of predictor variables on classes sorted by order of importance in model.

### Usage

```
plotImpVarDist(rf, df, class.col, max.vars = 16, plot = TRUE)
```

### Arguments

|           |   |
|-----------|---|
| rf        | an object inheriting from <a href="#">randomForest</a> .    |
| df        | data.frame with predictors in rf model.                     |
| class.col | response column name in df.                                 |
| max.vars  | number of variables to plot (from most important to least). |
| plot      | display the plot?   |

### Value

the ggplot2 object is invisibly returned.

### Note

If the model in rf was run with importance = TRUE, then 'MeanDecreaseAccuracy' is used as the importance measure. Otherwise, 'MeanDecreaseGini' is used.

### Author(s)

Eric Archer <eric.archer@noaa.gov>

### Examples

```
data(mtcars)
df <- mtcars
df$am <- factor(df$am)

rf <- randomForest(am ~ ., df, importance = TRUE)
plotImpVarDist(rf, df, "am")
```

---

|           |                                |
|-----------|--------------------------------|
| plotInbag | <i>Plot inbag distribution</i> |
|-----------|--------------------------------|

---

**Description**

Plot distribution of sample inbag rates

**Usage**

```
plotInbag(rf, sampsize = NULL, bins = 20, plot = TRUE)
```

**Arguments**

|          |  |
|----------|--|
| rf       | an object inheriting from <a href="#">randomForest</a> . |
| sampsize | optional vector of sample sizes used in rf model.        |
| bins     | number of bins in histogram.                             |
| plot     | display the plot?  |

**Value**

the ggplot2 object is invisibly returned. The red vertical lines mark the expected values for the classes in the model based on their frequency and sample sizes.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars)
plotInbag(rf)
```

---

|          |   |
|----------|---|
| plotNull | <i>Plot Random Forest Importance Null Distributions</i> |
|----------|---|

---

**Description**

Plot the Random Forest null distributions importance metrics, observed values, and p-values for each predictor variable from the object produced by a call to [rfPermute](#).

**Usage**

```
plotNull(
  x,
  preds = NULL,
  imp.type = NULL,
  scale = TRUE,
  plot.type = c("density", "hist"),
  plot = TRUE
)
```

**Arguments**

|           |  |
|-----------|--|
| x         | An object produced by a call to <code>rfPermute</code> .                               |
| preds     | a character vector of predictors to plot. If NULL, then all predictors are plotted.    |
| imp.type  | Either a numeric or character vector giving the importance metric(s) to plot.          |
| scale     | Plot importance measures scaled (divided by) standard errors?                          |
| plot.type | type of plot to produce: "density" for smoothed density plot, or "hist" for histogram. |
| plot      | display the plot?  |

**Details**

The function will generate an plot for each predictor, with faceted importance metrics. The vertical red line shows the observed importance score and the p-value is given in the facet label.

**Value**

A named list of the ggplot figures produced is invisibly returned.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
# A regression model using the ozone example
data(airquality)
ozone.rfP <- rfPermute(
  Ozone ~ ., data = airquality, ntree = 100,
  na.action = na.omit, nrep = 50, num.cores = 1
)

# Plot the null distributions and observed values.
plotNull(ozone.rfP)
```

---

|              |                       |
|--------------|-----------------------|
| plotOOBtimes | <i>Plot Times OOB</i> |
|--------------|-----------------------|

---

**Description**

Plot histogram of times samples were OOB.

**Usage**

```
plotOOBtimes(rf, bins = NULL, plot = TRUE)
```

**Arguments**

|      |   |
|------|---|
| rf   | an object inheriting from <a href="#">randomForest</a> .        |
| bins | number of bins in histogram. Defaults to number of samples / 5. |
| plot | display the plot?   |

**Value**

the ggplot2 object is invisibly returned.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars)
plotOOBtimes(rf)
```

---

|                    |                                     |
|--------------------|-------------------------------------|
| plotPredictedProbs | <i>Plot Predicted Probabilities</i> |
|--------------------|-------------------------------------|

---

**Description**

Plot histogram of assignment probabilities to predicted class. This is used for determining if the model differentiates between correctly and incorrectly classified samples in terms of how well they are classified.

**Usage**

```
plotPredictedProbs(rf, bins = 30, plot = TRUE)
```

**Arguments**

`rf` an object inheriting from `randomForest`.  
`bins` number of bins in histogram. Defaults to number of samples / 5.  
`plot` display the plot?

**Value**

the `ggplot2` object is invisibly returned.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars)
plotPredictedProbs(rf, bins = 20)
```

---

plotRFtrace

*OOB Trace*

---

**Description**

Plot trace of cumulative OOB error rate by number of trees

**Usage**

```
plotRFtrace(rf, plot = TRUE)
```

**Arguments**

`rf` an object inheriting from `randomForest`.  
`plot` display the plot?

**Value**

the `ggplot2` object is invisibly returned.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars)
plotRFtrace(rf)
```

---

|           |                               |
|-----------|-------------------------------|
| plotVotes | <i>Plot Vote Distribution</i> |
|-----------|-------------------------------|

---

**Description**

Plot distribution of votes for each sample in each class.

**Usage**

```
plotVotes(rf, type = NULL, freq.sep.line = TRUE, plot = TRUE)
```

**Arguments**

|               |   |
|---------------|---|
| rf            | an object inheriting from <a href="#">randomForest</a> .  |
| type          | either area for stacked continuous area plot or bar for discrete stacked bar chart. The latter is preferred for small numbers of cases. If not specified, a bar chart will be used if all classes have $\leq 30$ cases. |
| freq.sep.line | put frequency of original group on second line in facet label? If FALSE, labels are single line. If NULL frequencies will not be included in labels.  |
| plot          | display the plot?   |

**Value**

the ggplot2 object is invisibly returned.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
data(mtcars)

rf <- randomForest(factor(am) ~ ., mtcars)
plotVotes(rf)
```

---

`proximityPlot`*Plot Random Forest Proximity Scores*

---

### Description

Create a plot of Random Forest proximity scores using multi-dimensional scaling.

### Usage

```
proximityPlot(  
  rf,  
  dim.x = 1,  
  dim.y = 2,  
  legend.loc = c("top", "bottom", "left", "right"),  
  point.size = 2,  
  circle.size = 8,  
  circle.border = 1,  
  hull.alpha = 0.3,  
  plot = TRUE  
)
```

### Arguments

|   |  |
|---|--|
| <code>rf</code>                         | A <code>randomForest</code> object.  |
| <code>dim.x</code> , <code>dim.y</code> | Numeric values giving x and y dimensions to plot from multidimensional scaling of proximity scores.                                |
| <code>legend.loc</code>                 | Character keyword specifying location of legend. Can be "bottom", "top", "left", "right".  |
| <code>point.size</code>                 | Size of central points.  |
| <code>circle.size</code>                | Size of circles around correctly classified points as argument to 'cex'. Set to NULL for no circles.                               |
| <code>circle.border</code>              | Width of circle border.  |
| <code>hull.alpha</code>                 | value giving alpha transparency level for convex hull shading. Setting to NULL produces no shading. Ignored for regression models. |
| <code>plot</code>                       | logical determining whether or not to show plot.   |

### Details

Produces a scatter plot of proximity scores for `dim.x` and `dim.y` dimensions from a multidimensional scale (MDS) conversion of proximity scores from a `randomForest` object. For classification models, a convex hull is drawn around the a-priori classes with points colored according to original (inner) and predicted (outer) class.

### Value

a list with `prox.cmd`: the MDS scores of the selected dimensions, and `g` the `ggplot` object.



**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**Examples**

```
data(symb.metab)

rf <- randomForest(type ~ ., symb.metab, proximity = TRUE)
proximityPlot(rf)
```

---

rfPermute

*Estimate Permutation p-values for Random Forest Importance Metrics*

---

**Description**

Estimate significance of importance metrics for a Random Forest model by permuting the response variable. Produces null distribution of importance metrics for each predictor variable and p-value of observed.

**Usage**

```
rfPermute(x, ...)

## Default S3 method:
rfPermute(x, y, ..., nrep = 100, num.cores = 1)

## S3 method for class 'formula'
rfPermute(formula, data = NULL, ..., subset, na.action = na.fail, nrep = 100)
```

**Arguments**

`x`, `y`, `formula`, `data`, `subset`, `na.action`, ...  
See [randomForest](#) for definitions.

`nrep`            Number of permutation replicates to run to construct null distribution and calculate p-values (default = 100).

`num.cores`       Number of CPUs to distribute permutation results over. Defaults to NULL which uses one fewer than the number of cores reported by [detectCores](#).

**Details**

All other parameters are as defined in `randomForest.formula`. A Random Forest model is first created as normal to calculate the observed values of variable importance. The response variable is then permuted `nrep` times, with a new Random Forest model built for each permutation step.

**Value**

An rfPermute object which contains all of the components of a randomForest object plus:

|           |   |
|-----------|---|
| null.dist | A list containing two three-dimensional arrays of null distributions for unscaled and scaled importance measures. |
| pval      | A three dimensional array containing permutation p-values for unscaled and scaled importance measures.            |

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**See Also**

[plotNull](#) for plotting null distributions from the rfPermute objects.  
[rp.importance](#) for extracting importance measures.  
[rp.combine](#) for combining multiple rfPermute objects.  
[proximityPlot](#) for plotting case proximities.  
[impHeatmap](#) for plotting a heatmap of importance scores.  
[randomForest](#)

**Examples**

```
# A regression model using the ozone example
data(airquality)
ozone.rfP <- rfPermute(
  Ozone ~ ., data = airquality, ntree = 100,
  na.action = na.omit, nrep = 50, num.cores = 1
)

# Plot the null distributions and observed values.
plotNull(ozone.rfP)

# Plot the unscaled importance distributions and highlight significant predictors
plot(rp.importance(ozone.rfP, scale = FALSE))

# ... and the scaled measures
plot(rp.importance(ozone.rfP, scale = TRUE))
```

---

rp.combine

---

*Combine rfPermute Objects*


---

**Description**

Combines two or more ensembles of rfPermute objects into one, combining randomForest results, null distributions, and re-calculating p-values.

**Usage**

```
rp.combine(...)
```

**Arguments**

... two or more objects of class rfPermute, to be combined into one.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**See Also**

[combine](#)

**Examples**

```
data(iris)
rp1 <- rfPermute(
  Species ~ ., iris, ntree = 50, norm.votes = FALSE, nrep = 100, num.cores = 1
)
rp2 <- rfPermute(
  Species ~ ., iris, ntree = 50, norm.votes = FALSE, nrep = 100, num.cores = 1
)
rp3 <- rfPermute(
  Species ~ ., iris, ntree = 50, norm.votes = FALSE, nrep = 100, num.cores = 1
)
rp.all <- rp.combine(rp1, rp2, rp3)

layout(matrix(1:6, nrow = 2))
plotNull(rp.all)
layout(matrix(1))
```

---

rp.importance

*Extract rfPermute Importance Scores and p-values.*

---

**Description**

Extract a matrix of the observed importance scores and p-values from the object produced by a call to rfPermute

**Usage**

```
rp.importance(x, scale = TRUE, sort.by = NULL, decreasing = TRUE)
```

**Arguments**

|            |   |
|------------|---|
| x          | An object produced by a call to rfPermute.  |
| scale      | For permutation based measures, should the measures be divided their "standard errors"?   |
| sort.by    | character vector giving the importance metric(s) or p-values to sort by. If NULL, defaults to "MeanDecreaseAccuracy" for classification models and "%IncMSE" for regression models. |
| decreasing | logical. Should the sort order be increasing or decreasing?   |

**Details**

p-values can be given to the sort.by argument by adding '.pval' to the column name of the desired column from the importance element of the rfPermute object.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**See Also**

[rfPermute](#), [plot.rp.importance](#)

**Examples**

```
# A regression model using the ozone example
ozone.rfP <- rfPermute(
  Ozone ~ ., data = airquality, ntree = 100,
  na.action = na.omit, nrep = 50, num.cores = 1
)
imp.unscaled <- rp.importance(ozone.rfP, scale = TRUE)
imp.unscaled

imp.scaled <- rp.importance(ozone.rfP, scale = TRUE)
imp.scaled
```

---

symb.metab

*Symbiodinium type metabolite profiles*

---

**Description**

A data.frame of 155 metabolite relative concentrations for 64 samples of four Symbiodinium clade types.

**Usage**

```
data(symb.metab)
```

**Format**

data.frame

**References**

Klueter, A.; Crandall, J.B.; Archer, F.I.; Teece, M.A.; Coffroth, M.A. Taxonomic and Environmental Variation of Metabolite Profiles in Marine Dinoflagellates of the Genus *Symbiodinium*. *Metabolites* 2015, 5, 74-99.

# Index

- \*Topic **classif**
  - rfPermute, 17
- \*Topic **datasets**
  - symb.metab, 20
- \*Topic **regression**
  - rfPermute, 17
- \*Topic **tree**
  - rfPermute, 17
  
- binom.test, 3, 4
  
- casePredictions, 2
- classConfInt, 3, 5
- cleanRFdata, 4
- combine, 19
- confusionMatrix, 4
  
- detectCores, 17
  
- exptdErrRate, 5, 5
  
- ggplot, 16
  
- impHeatmap, 6, 18
  
- pctCorrect, 7
- plot.rp.importance, 8, 20
- plotConfMat, 9
- plotImpVarDist, 10
- plotInbag, 11
- plotNull, 11, 18
- plotOOBtimes, 13
- plotPredictedProbs, 13
- plotRFtrace, 14
- plotVotes, 15
- proximityPlot, 16, 18
  
- randomForest, 2–4, 6, 7, 9–11, 13–15, 17, 18
- rfPermute, 6, 8, 11, 12, 17, 20
- rp.combine, 18, 18
- rp.importance, 8, 18, 19
  
- symb.metab, 20