

# Package ‘banter’

June 11, 2025

**Type** Package

**Title** BioAcoustic eveNT classifier

**Description** Create a hierarchical acoustic event species classifier out of multiple call type detectors as described in Rankin et al (2017) <[doi:10.1111/mms.12381](https://doi.org/10.1111/mms.12381)>.

**Version** 0.9.8

**URL** <https://github.com/SWFSC/banter>

**BugReports** <https://github.com/SWFSC/banter/issues>

**Depends** R (>= 4.1.0)

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**Suggests** testthat

**License** GNU General Public License

**RoxygenNote** 7.3.2

**Encoding** UTF-8

**NeedsCompilation** no

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**Repository** CRAN

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banter-package	<i>BioAcoustic EveNT ClassifiER</i>
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### Description

banter

### References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

---

addBanterDetector	<i>Add a BANTER Detector Model</i>
-------------------	------------------------------------

---

### Description

Add a detector model to a BANTER classifier.

### Usage

```
addBanterDetector(
  x,
  data,
  name,
  ntree,
  sampsize = 1,
  importance = FALSE,
```

```

    num.cores = 1
  )

removeBanterDetector(x, name)

```

### Arguments

x	a <a href="#">banter_model</a> object.
data	detector data.frame or named list of detector data.frames. If a data.frame, then name must be provided.
name	detector name.
ntree	number of trees.
sampsize	number or fraction of samples to use in each tree. If < 1, then it will be used to select this fraction of the smallest sample size.
importance	retain importance scores in model? Defaults to FALSE and will be ignored if num.cores > 1.
num.cores	number of cores to use for Random Forest model. Set to NULL to use the maximum number detected on your system - 1.

### Value

a [banter\\_model](#) object with the detector model added or removed.

### Author(s)

Eric Archer <eric.archer@noaa.gov>

### References

Rankin, S., Archer, F., Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

### Examples

```

data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add the 'bp' (burst pulse) detector model
bant.mdl <- addBanterDetector(
  x = bant.mdl,
  data = train.data$detectors$bp,
  name = "bp",
  ntree = 50, sampsize = 1, num.cores = 1
)
bant.mdl

# remove the 'bp' detector model
bant.mdl <- removeBanterDetector(bant.mdl, "bp")

```

bant.mdl

---

banterGuide

*BANTER Guide*

---

### Description

Open a browser window displaying "BANTER: A User's Guide to Acoustic Classification".

### Usage

```
banterGuide()
```

### Author(s)

Eric Archer <eric.archer@noaa.gov>

### References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. Marine Mammal Science 33:520-540. doi:10.1111/mms.12381

---

getBanterModel

*Extract Random Forest Model*

---

### Description

Extract BANTER event or detector Random Forest model.

### Usage

```
getBanterModel(x, model = "event")
```

### Arguments

x                    a [banter\\_model](#) object.  
model                name of model to extract. Default is "event" to extract the event-level model.  
Can also be the name of a detector.

### Value

a [randomForest](#) model object.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**References**

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

**Examples**

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 1, num.cores = 1
)
# run BANTER event model
bant.mdl <- runBanterModel(bant.mdl, ntree = 1000, sampsize = 1)

# extract the event randomForest model
event.rf <- getBanterModel(bant.mdl)
event.rf

# extract the burst pulse (bp) detector model
bp.rf <- getBanterModel(bant.mdl, "bp")
bp.rf
```

---

getBanterModelData      *Extract Random Forest Model Data*

---

**Description**

Extract BANTER event data used for the Random Forest model.

**Usage**

```
getBanterModelData(x)
```

**Arguments**

x                    a `banter_model` object.

**Value**

the event data frame used to build the input model x.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**References**

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

**Examples**

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 1, num.cores = 1
)
# run BANTER event model
bant.mdl <- runBanterModel(bant.mdl, ntree = 1000, sampsize = 1)

event.df <- getBanterModelData(bant.mdl)
head(event.df)
```

---

getDetectorNames	<i>Detector Names</i>
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---

**Description**

Return names of detectors loaded in BANTER model.

**Usage**

```
getDetectorNames(x)
```

**Arguments**

x                    a `banter_model` object.

**Value**

a vector of names.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

## References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

## Examples

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 1, num.cores = 1
)
getDetectorNames(bant.mdl)
```

---

getSampSize

*Sample Size*

---

## Description

Return sample sizes used for a BANTER model.

## Usage

```
getSampSize(x, model = "event")
```

## Arguments

x                    a [banter\\_model](#) object.

model                name of model to extract. Default is "event" to return values for the event-level model. Can also be name of a detector.

## Value

a vector of sample sizes.

## Author(s)

Eric Archer <eric.archer@noaa.gov>

## References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

## Examples

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 2, num.cores = 1
)
# run BANTER event model
bant.mdl <- runBanterModel(bant.mdl, ntree = 1000, sampsize = 1)

# sample size for the event model
getSampSize(bant.mdl)

# sample size for the burst pulse (bp) detector model
getSampSize(bant.mdl, "bp")
```

---

initBanterModel	<i>Initialize BANTER model</i>
-----------------	--------------------------------

---

## Description

Initialize a BANTER model with event data.

## Usage

```
initBanterModel(x)
```

## Arguments

**x** a data.frame of events. Every row is a unique event. Must have columns named `event.id` and `species`. All other columns will be used as predictor variables for the BANTER event classifier model.

## Value

a `banter_model` object without any detector models.

## Note

Values in the column `species` are passed through the `make.names` function on creation to ensure they don't include invalid characters.

## Author(s)

Eric Archer <eric.archer@noaa.gov>

## References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

## Examples

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
bant.mdl
```

---

modelPctCorrect	<i>Model Percent Correct</i>
-----------------	------------------------------

---

## Description

Extract percent correctly classified by species for detector and event models.

## Usage

```
modelPctCorrect(x)
```

## Arguments

x                    a [banter\\_model](#) object.

## Value

a data.frame with the percent correctly classified for each model in x.

## Author(s)

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

## References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

## Examples

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 1, num.cores = 1
)
# run BANTER event model
bant.mdl <- runBanterModel(bant.mdl, ntree = 1000, sampsize = 1)
modelPctCorrect(bant.mdl)
```

---

numCalls	<i>Number and Proportion of Calls</i>
----------	---------------------------------------

---

## Description

Return the number and proportion of calls in BANTER detector models.

## Usage

```
numCalls(x, by = c("species", "event"))
```

```
propCalls(x, by = c("species", "event"))
```

## Arguments

x                    a [banter\\_model](#) object.

by                    return summary by "species" or "event".

## Author(s)

Eric Archer <eric.archer@noaa.gov>

## References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

## Examples

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 1, num.cores = 1
)
# run BANTER event model
bant.mdl <- runBanterModel(bant.mdl, ntree = 1000, sampsize = 1)

# number of calls by species and event
numCalls(bant.mdl, "species")
numCalls(bant.mdl, "event")

# proportion of calls by species and event
propCalls(bant.mdl, "species")
propCalls(bant.mdl, "event")
```

---

numEvents	<i>Number of Events</i>
-----------	-------------------------

---

## Description

Return the number of events in a BANTER model by species.

## Usage

```
numEvents(x, model = "event")
```

## Arguments

x	a <a href="#">banter_model</a> object.
model	name of model to extract. Default is "event" to summarize the event-level model. Can also be name of a detector.

## Value

a data.frame giving the number of events available for each species.

## Author(s)

Eric Archer <eric.archer@noaa.gov>

## References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

## Examples

```
data(train.data)
# initialize BANter model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 1, num.cores = 1
)
# run BANter event model
bant.mdl <- runBanterModel(bant.mdl, ntree = 1000, sampsize = 1)

# number of events in event model
numEvents(bant.mdl)

# number of events in burst pulse (bp) detector model
numEvents(bant.mdl, "bp")
```

---

plotDetectorTrace      *Plot BANter Detector Traces*

---

## Description

Plot traces of OOB error rates for detector Random Forest models.

## Usage

```
plotDetectorTrace(x, detector = NULL)
```

## Arguments

x                    a `banter_model` object.  
 detector            names of models to plot. If set to NULL, traces for all models will be shown.

## Author(s)

Eric Archer <eric.archer@noaa.gov>

## References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

**See Also**[plotTrace](#)**Examples**

```

data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 1, num.cores = 1
)

plotDetectorTrace(bant.mdl)

```

---

predict

*Predict BANTER events*


---

**Description**

Predict species of events for novel data from a BANTER model.

**Usage**

```

predict(object, ...)

## S3 method for class 'banter_model'
predict(object, new.data, ...)

## S4 method for signature 'banter_model'
predict(object, new.data, ...)

```

**Arguments**

object	a <a href="#">banter_model</a> object.
...	unused.
new.data	a list of event and detector data that has the same predictors as in the <code>banter_model</code> . It must contain elements called <code>events</code> and <code>detectors</code> . The <code>events</code> element must be a data.frame that has a column called <code>event.id</code> and the same predictor columns as the event data used to initialize the banter model (see <a href="#">initBanterModel</a> ). The <code>detectors</code> element must be a named list with the same detectors used to build the model (see <a href="#">addBanterDetector</a> ).

**Value**

A list with the following elements:

**events** the data frame used in the event model for predictions.

**predict.df** data.frame of predicted species and assignment probabilities for each event.

**detector.freq** data.frame giving the number of events available for each detector.

**validation.matrix** if species is a column in new.data, a table giving the classification rate for each event

**Note**

At least one detector in the model must be present in new.data. Any detectors in the training model that are absent will have all species proportions and the the detector propoprion set to 0. If a column called species is in new.data, columns for the original species designation and if that matches predicted (correct) will be added to the predict.df data.frame of the output.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**References**

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. Marine Mammal Science 33:520-540. doi:10.1111/mms.12381

**Examples**

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 2, num.cores = 1
)
# run BANTER event model
bant.mdl <- runBanterModel(bant.mdl, ntree = 1000, sampsize = 1)

# predict test data
data(test.data)
test.pred <- predict(bant.mdl, test.data)
test.pred
```

---

runBanterModel	<i>Run BANTER Model</i>
----------------	-------------------------

---

**Description**

Build full event classifier model

**Usage**

```
runBanterModel(x, ntree, sampsize = 1)
```

**Arguments**

x	a <a href="#">banter_model</a> object.
ntree	number of trees.
sampsize	number or fraction of samples to use in each tree.

**Value**

a [banter\\_model](#) object with the complete BANTER model.

**Author(s)**

Eric Archer <eric.archer@noaa.gov>

**References**

Rankin, S., Archer, F., Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

**Examples**

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 1, num.cores = 1
)
# run BANTER event model
bant.mdl <- runBanterModel(bant.mdl, ntree = 1000, sampsize = 1)
summary(bant.mdl)
```

---

subsampleDetections    *Subsample Detections*

---

### Description

Extract a random subsample of detections for each event and detector.

### Usage

```
subsampleDetections(data, n)
```

### Arguments

data	a detector data.frame or list of detector data.frames.
n	a value giving the number ( $n \geq 1$ ) or fraction ( $n$ between 0 and 1) of detections per event per detector to select. Detections are randomly selected without replacement. If $n$ is greater than the number of detections in an event, all detections for that event will be retained.

### Value

a detector data.frame or list of detector data.frames with no more than  $n$  detections per event per detector.

### Author(s)

Eric Archer <eric.archer@noaa.gov>

### References

Rankin, S., Archer, F., Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. *Marine Mammal Science* 33:520-540. doi:10.1111/mms.12381

### Examples

```
data(train.data)

# initial number of detections per event per detector
sapply(train.data$detectors, function(x) table(x$event.id))

# select half of all detectors
detect.half <- subsampleDetections(train.data$detectors, 0.5)
sapply(detect.half, function(x) table(x$event.id))

# select 20 detections
detect.20 <- subsampleDetections(train.data$detectors, 20)
sapply(detect.20, function(x) table(x$event.id))
```

```
# select 10 detections fro 'ec' detector
ec.10 <- subsampleDetections(train.data$detectors$ec, 10)
table(ec.10$event.id)
```

---

summary

*BANTER Classifier Model Summary*


---

## Description

Display summaries for event and detector models

## Usage

```
summary(object, ...)

## S3 method for class 'banter_model'
summary(object, model = "event", n = 0.5, bins = 20, ...)

## S4 method for signature 'banter_model'
summary(object, model = "event", n = 0.5, bins = 20, ...)
```

## Arguments

object	a <a href="#">banter_model</a> object.
...	ignored.
model	name of model to summarize. Default is "event" to summarize the event-level model. Can also be name of a detector.
n	number of final iterations to summarize OOB error rate for. If between 0 and 1 is taken as a proportion of chain.
bins	number of bins in inbag histogram.

## Value

In the plot that is created, the upper panel shows the trace of the Random Forest model OOB rate across sequential trees in the forest. The lower plot shows a frequency histogram of the number of times each sample was inbag (used as training data in a tree in the forest). The vertical red lines indicate the expected inbag rate for samples of each species.

## Author(s)

Eric Archer <eric.archer@noaa.gov>

## References

Rankin, S. , Archer, F. , Keating, J. L., Oswald, J. N., Oswald, M. , Curtis, A. and Barlow, J. (2017), Acoustic classification of dolphins in the California Current using whistles, echolocation clicks, and burst pulses. Marine Mammal Science 33:520-540. doi:10.1111/mms.12381

## Examples

```
data(train.data)
# initialize BANTER model with event data
bant.mdl <- initBanterModel(train.data$events)
# add all detector models
bant.mdl <- addBanterDetector(
  bant.mdl, train.data$detectors,
  ntree = 50, sampsize = 1, num.cores = 1
)
# run BANTER event model
bant.mdl <- runBanterModel(bant.mdl, ntree = 1000, sampsize = 1)
summary(bant.mdl)
```

---

test.data	<i>Testing events and detectors</i>
-----------	-------------------------------------

---

## Description

A list of events and call data from detectors for testing BANTER model

## Usage

```
data(test.data)
```

## Format

list

---

train.data	<i>Training events and detectors</i>
------------	--------------------------------------

---

## Description

A list of events and call data from detectors for training BANTER model

## Usage

```
data(train.data)
```

## Format

list

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