

Package ‘BASiNETEntropy’

July 21, 2025

Title Classification of RNA Sequences using Complex Network and Information Theory

Version 0.99.6

Description It makes the creation of networks from sequences of RNA, with this is done the abstraction of characteristics of these networks with a methodology of maximum entropy for the purpose of making a classification between the classes of the sequences. There are two data present in the 'BASiNET' package, ``mRNA", and ``ncRNA" with 10 sequences. These sequences were taken from the data set used in the article (LI, Aimin; ZHANG, Junying; ZHOU, Zhongyin, 2014) <[doi:10.1186/1471-2105-15-311](https://doi.org/10.1186/1471-2105-15-311)>, these sequences are used to run examples.

License GPL-3

Encoding UTF-8

Depends R (>= 4.1.0)

Imports igraph, Biostrings, randomForest

biocViews Software, BiologicalQuestion, GenePrediction, FunctionalPrediction, Network, Classification

RoxygenNote 7.2.0

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Murilo Montanini Breve [aut] (ORCID: <<https://orcid.org/0000-0002-5781-0480>>),
Matheus Henrique Pimenta-Zanon [aut] (ORCID: <<https://orcid.org/0000-0003-0698-6360>>),
Fabricio Martins Lopes [aut, cre] (ORCID: <<https://orcid.org/0000-0002-8786-3313>>)

Maintainer Fabricio Martins Lopes <fabricio@utfpr.edu.br>

Repository CRAN

Date/Publication 2023-08-16 18:24:35 UTC

Contents

classify	2
createedges	3
creatingDataframe	4
curveofentropy	4
entropy	5
filtering	5
matrixmultiplication	6
maxentropy	6
preprocessing	7
selectingEdges	7
training	8
Index	9

classify	<i>Performs the classification methodology using complex network and entropy theories</i>
----------	---

Description

Given three or two distinct data sets, one of mRNA, one of lncRNA and one of sncRNA. The classification of the data is done from the structure of the networks formed by the sequences, that is filtered by an entropy methodology. After this is done, the classification starts.

Usage

```
classify(  
  mRNA,  
  lncRNA,  
  sncRNA = NULL,  
  trainingResult,  
  save_dataframe = NULL,  
  save_model = NULL,  
  predict_with_model = NULL  
)
```

Arguments

mRNA	Directory where the file .FASTA lies with the mRNA sequences
lncRNA	Directory where the file .FASTA lies with the lncRNA sequences
sncRNA	Directory where the file .FASTA lies with the sncRNA sequences (optional)
trainingResult	The result of the training, (three or two matrices)
save_dataframe	save when set, this parameter saves a .csv file with the features in the current directory. No file is created by default.

save_model save when set, this parameter saves a .rds file with the model in the current directory. No file is created by default.

predict_with_model predict the input sequences with the previously generated model.

Value

Results

Author(s)

Murilo Montanini Breve

Examples

```
library(BASiNETEntropy)
arqSeqMRNA <- system.file("extdata", "mRNA.fasta", package = "BASiNETEntropy")
arqSeqLNCRNA <- system.file("extdata", "ncRNA.fasta", package = "BASiNETEntropy")
load(system.file("extdata", "trainingResult.RData", package = "BASiNETEntropy"))
r_classify <- classify(mRNA=arqSeqMRNA, lncRNA=arqSeqLNCRNA, trainingResult = trainingResult)
```

createedges

Creates an untargeted graph from a biological sequence

Description

A function that from a biological sequence generates a graph not addressed having as words vertices, this being able to have its size parameter set by the 'word' parameter. The connections between words depend of the 'step' parameter that indicates the next connection to be formed

Usage

```
createedges(sequence, word = 3, step = 1)
```

Arguments

sequence It is a vector that represents the sequence

word This integer parameter decides the size of the word that will be formed

step It is the integer parameter that decides the step that will be taken to make a new connection

Value

Returns the array used to creates the edge list

Author(s)

Murilo Montanini Breve

creatingDataframe	<i>Creates a feature matrix using complex network topological measures</i>
-------------------	--

Description

A function that from the complex network topological measures create the feature matrix.

Usage

```
creatingDataframe(measures, tamM, tamLNC, tamSNC)
```

Arguments

measures	The complex network topological measures
tamM	mRNA sequence size
tamLNC	lncRNA sequence size
tamSNC	snRNA sequence size

Value

Returns the feature matrix in scale 0-1

Author(s)

Murilo Montanini Breve

curveofentropy	<i>Creates an entropy curve</i>
----------------	---------------------------------

Description

A function that from the entropy measures and threshold creates an entropy curve.

Usage

```
curveofentropy(H, threshold)
```

Arguments

H	The 'training' return for the entropy measures
threshold	The 'training' return for the threshold

Value

Returns a entropy curve

Author(s)

Murilo Montanini Breve

entropy*Calculates the entropy*

Description

A function that calculates the entropy

Usage

entropy(x)

Arguments

x The probabilities P0 and P1

Value

Returns the entropy

Author(s)

Murilo Montanini Breve

filtering*Filters the edges*

Description

A function that filters the edges after the maximum entropy is obtained

Usage

filtering(edgestoselect, edgestofilter)

Argumentsedgestoselect The selected edges
edgestofilter The edges used to filter**Value**

Returns the filtered edges

Author(s)

Murilo Montanini Breve

matrixmultiplication *Compares the matrices*

Description

A function that compares the matrices 'trainingResult' and the adjacency matrix to produce a filtered adjacency matrix.

Usage

```
matrixmultiplication(data, histodata)
```

Arguments

data	Adjacency matrix
histodata	'trainingResult' data

Value

Returns the filtered adjacency matrix

Author(s)

Murilo Montanini Breve

maxentropy *Calculates the maximum entropy*

Description

A function that calculates the maximum entropy

Usage

```
maxentropy(histogram)
```

Arguments

histogram	The histogram (used in 'training' function)
-----------	---

Value

Returns the maximum entropy

Author(s)

Murilo Montanini Breve

preprocessing	<i>Rescales the results between values from 0 to 1</i>
---------------	--

Description

Given the results the data is rescaled for values between 0 and 1, so that the length of the sequences does not influence the results. The rescaling of the sequences are made separately

Usage

```
preprocessing(datah, tamM, tamLNC, tamSNC)
```

Arguments

datah	Array with results numerics
tamM	Integer number of mRNA sequences
tamLNC	Integer number of lncRNA sequences
tamSNC	Integer number of sncRNA sequences

Value

Returns the array with the rescaled values

Author(s)

Murilo Montanini Breve

selectingEdges	<i>Selects the edges of the adjacency matrix</i>
----------------	--

Description

A function that selects the edges of the adjacency matrix

Usage

```
selectingEdges(MAX, data)
```

Arguments

MAX	The maximum entropy
data	The adjacency matrix

Value

Returns the selected edges of the adjacency matrix

Author(s)

Murilo Montanini Breve

training

Trains the algorithm to select the edges that maximize the entropy

Description

A function that trains the algorithm to select the edges that maximize the entropy

Usage

```
training(mRNA, lncRNA, sncRNA = NULL)
```

Arguments

mRNA	Directory where the file .FASTA lies with the mRNA sequences
lncRNA	Directory where the file .FASTA lies with the lncRNA sequences
sncRNA	Directory where the file .FASTA lies with the sncRNA sequences (optional)

Value

Returns the edge lists and the 'curveofentropy' function inputs

Author(s)

Murilo Montanini Breve

Index

classify, [2](#)
createedges, [3](#)
creatingDataframe, [4](#)
curveofentropy, [4](#)

entropy, [5](#)

filtering, [5](#)

matrixmultiplication, [6](#)
maxentropy, [6](#)

preprocessing, [7](#)

selectingEdges, [7](#)

training, [8](#)