Package ‘odseq’

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Type Package
Title Outlier detection in multiple sequence alignments
Version 1.4.0
Date 2015-12-20
Author José Jiménez
Maintainer José Jiménez <jose@jimenezluna.com>
Description Performs outlier detection of sequences in a multiple sequence alignment using bootstrap of predefined distance metrics. Outlier sequences can make downstream analyses unreliable or make the alignments less accurate while they are being constructed. This package implements the OD-seq algorithm proposed by Jehl et al (doi 10.1186/s12859-015-0702-1) for aligned sequences and a variant using string kernels for unaligned sequences.
License MIT + file LICENSE
LazyData True
Encoding UTF-8
biocViews Alignment, MultipleSequenceAlignment
VignetteBuilder knitr
Suggests knitr(>= 1.11)
Depends R (>= 3.2.3)
Imports msa (>= 1.2.1), kebabs (>= 1.4.1), mclust (>= 5.1)
NeedsCompilation no

R topics documented:

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Description

Performs outlier detection of sequences in a multiple sequence alignment using bootstrap of pre-defined distance metrics. Outlier sequences can make downstream analyses unreliable or make the alignments less accurate while they are being constructed. This package implements the OD-seq algorithm proposed by Jehl et al (doi 10.1186/s12859-015-0702-1) for aligned sequences and a variant using string kernels for unaligned sequences.

Details

The DESCRIPTION file:

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License:       MIT + file LICENSE
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VignetteBuilder: knitr
Suggests:     knitr(>= 1.11)
Depends:      R (>= 3.2.3)
Imports:       msa (>= 1.2.1), kebabs (>= 1.4.1), mclust (>= 5.1)
NeedsCompilation: no

Index of help topics:

odmix Gaussian mixture modelling of distances in a multiple sequence alignment.
odseq Outlier detection in a multiple sequence alignment
odseq-package Outlier detection in multiple sequence alignments
odseq_unaligned Outlier detection provided a distance/similarity matrix of sequences.
seqs PFAM plus random data.

Author(s)

José Jiménez

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odmix

References

See Also
odseq odseq_unaligned

Examples
library(msa)
data(seqs)
al <- msa(seqs)
odseq(al, distance_metric = "affine", B = 1000, threshold = 0.025)

Description
This function performs clustering of biological sequences via fitting a Gaussian mixture model of the distances defined by the odseq algorithm

Usage
odmix(msa_object, distance_metric, groups)

Arguments
msa_object An object of formal class MsaAAMultipleAlignment, as provided by the msa package.
distance_metric A string indicating the type of distance metric to be computed. Either 'linear' and 'affine' is supported at the moment.
groups Number of groups to fit in the mixture model. If a numeric vector of size n, n models will be fitted and a list of BIC values will be given to choose a single model.

Value
A list containing the following items:
prob A numeric matrix of size n x groups where the probability of belonging to a group is provided for each sequence.
class The class assigned according to prob. Returns a numeric vector.
BIC BIC values for the models proposed in groups

Author(s)
José Jiménez <jose@jimenezluna.com>
See Also

odseq_unaligned odseq

Examples

library(msa)
data(seqs)
al <- msa(seqs)
odmix(al, distance_metric = "affine", groups = 2)

Description

This function will first compute a distance metric among every sequence in the multiple alignment. Then it will bootstrap an average score of these distance to provide information on the distribution of scores, which is used to distinguish outlier sequences with a certain threshold.

Usage

odseq(msa_object, distance_metric = "linear", B = 100, threshold = 0.025)

Arguments

msa_object An object of formal class MsaAMultipleAlignment, as provided by the msa package.
distance_metric A string indicating the type of distance metric to be computed. Either 'linear' and 'affine' is supported at the moment.
B Integer indicating the number of bootstrap replicates to be run. The higher the more robust the detection should be.
threshold Float indicating the probability to be left at the right of the bootstrap scores distribution when computing outliers. This parameter may need some tuning depending on each specific problem.

Value

Returns a logical vector, where TRUE indicates an outlier.

Author(s)

José Jiménez <jose@jimenezluna.com>

References


See Also

odseq_unaligned
**Examples**

```r
library(msa)
data(seqs)
al <- msa(seqs)
odseq(al, distance_metric = "affine", B = 1000, threshold = 0.025)
```

**Description**

Outlier detection provided a distance/similarity matrix of sequences. Provided a similarity matrix (like the ones provided using string kernels in kebabs). It will then compute a score for each sequence and perform bootstrap to provide information on the distribution of the scores, which is used to distinguish outlier sequences.

**Usage**

```r
odseq_unaligned(distance_matrix, B = 100, threshold = 0.025, type = "similarity")
```

**Arguments**

- `distance_matrix`: A numeric matrix representing either similarity or distance among unaligned sequences. Package kebabs may be useful for this task.
- `B`: Integer indicating the number of bootstrap replicates to be run. The higher the more robust the detection should be.
- `threshold`: Float indicating the probability to be left at the right of the bootstrap scores distribution when computing outliers. This parameter may need some tuning depending on each specific problem.
- `type`: A string indicating the type of distance metric used. Either 'similarity' or 'distance'.

**Value**

Returns a logical vector, where TRUE indicates an outlier.

**Author(s)**

José Jiménez <jose@jimenezluna.com>

**References**


**See Also**

odseq
library(kebabs)
data(seqs)
sp <- spectrumKernel(k = 3)
mat <- getKernelMatrix(sp, seqs)
odseq_unaligned(mat, B = 1000, threshold = 0.025, type = "similarity")

Description
Sequences from a certain PFAM family plus 100 random sequences.

Usage
data("seqs")

Value
An object of class AAStringSet.

Examples
data(seqs)
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