Package 'AdvISERPYRO'

July 4, 2013

Type Package

Title Amplicon Identification using SparsE Representation of PYROsequencing signal

Version 1.0

Date 2013-01-10

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Depends penalized

Description Interpreting a pyrosequencing signal appears highly challenging when signal intensities are low (unitary peak heights smaller than 5) or when complex signals are produced by more than one target amplicon in the sample. AdvISER-PYRO is an efficient algorithm that can reliably be used to identify amplicons in pyrosequencing signals generated by Single Amplicon Samples (SAS) and Multiple Amplicon Samples (MAS). AdvISER-PYRO is based on a sparse regression model and deciphers each amplicon-specific signal that contributes to the resulting global signal.

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R topics documented:

AdvISERPYRO	*Amplicon Identification using SparsE Representation of PYROsequencing signal*

Usage

```
AdvISERPYRO(signaltest, dictionary, L1, L2, SCT)
```

Arguments

signaltest	Testing pyrosequencing signal of length n. Each element of this signal corresponds to a peak height. The length of the signal (n) is therefore equal to the number of dispensated nucleotides.
dictionary	Representative dictionnary that include at least one signal (of length n) for each potential amplicon.
L1	L1-norm penalty of the regression model used within AdvISERPYRO.
L2	L2-norm penalty of the regression model used within AdvISERPYRO.
SCT	Significant Contribution Threshold. Any amplicon having a contribution to the testing signal lower than the SCT is removed. A high value of SCT (>2) tends therefore to produce a sparse set of amplicons

Value

A dataframe with 3 columns and 1 line for each amplicon that was identified in the signal by AdvISERPYRO. The first column gives the name of the amplicon while the second column gives its corresponding contribution and the third column give a reliability index of the global identification (R). This index corresponds to the correlation between the n predicted values of the penalized regression model and the n values of the pyrosequenced signal. An R index close to 1 indicates therefore a reliable identification.

References

Ambroise J., Piette A.-S., Delcorps C., Rigouts L., de Jong B., Irenge L., Robert A., Gala J.-L.: AdvISER-PYRO: Amplicon Identification using SparsE Representation of PYROsequencing signal. Bioinformatics, 2013

dictionary	*A example of representative dictionary*

Description

The dictionary includes 34 atoms corresponding to 10 distinct amplicons. Each atom is a pyrosequencing signal with 26 values.

Usage

```
data(dictionary)
```

Format

A data frame with 26 (n = length of the signal) observations and 34 variables (p = number of atoms).

Examples

```
data(signal1)
data(dictionary)
AdvISERPYRO(signaltest=signal1,dictionary=dictionary,L1=0.05,L2=0,SCT=2)
```

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signal1   *Testing pyrosequencing signal of a Single Amplicon Sample*

Usage

```
data(signal1)
```

Examples

```
data(signal1)
data(dictionary)
AdvISERPYRO(signaltest=signal1,dictionary=dictionary,L1=0.05,L2=0,SCT=2)
```

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signal2   *Testing Pyrosequencing signal of a Multiple Amplicon Sample*

Usage

```
data(signal2)
```

Examples

```
data(signal2)
data(dictionary)
AdvISERPYRO(signaltest=signal2,dictionary=dictionary,L1=0.05,L2=0,SCT=2)
```

Index