

Package ‘AdvISERMHPYRO’

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Type Package

Title Analysis of human SNP Multiplex PYROsequencing signal

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Depends penalized

Description AdvISER-MH-PYRO is an extension of AdvISER-M-PYRO. It allows to analyse multiplex pyro-signal from human (bi-allelic) SNP.

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AdvISERMHPYRO *Amplicon Identification using SparsE Representation of Multitplex Human PYROsequencing signal*

Usage

```
AdvISERMHPYRO(signaltest, dictionary, L1 = 0.05, SCT = 1, dispensation)
```

Arguments

signaltest	Testing Multiplex 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 dispensed nucleotides.
dictionary	Representative dictionary that include at least one signal (of length n) for each potential Genotype in each genomic region.
L1	L1-norm penalty of the regression model used within AdvISERMPYRO. Default value = 0.05.
SCT	Significant Contribution Threshold. Any genotype having a contribution to the testing signal lower than the SCT is removed. Default value = 1.
dispensation	Nucleotide Dispensation order. This information is used to generate the graphical result.

Value

A vector with that includes for each genomic region, the amplicon that was identified by AdvISERMPYRO and its contribution to the signal. This vector also includes 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.

Author(s)

Ambroise J.

References

Ambroise J., Deccache Y., Ireng L., Encho S., Robert A., Gala J.-L.: Amplicon Identification using Sparse Representation of Multiplex PYROsequencing signal (AdvISER-M-PYRO): Application to bacterial resistance genotyping. Bioinformatics, 2014

Examples

```
data(dictionaryQuadruplex)
data(PyrosignalQuadruplex)
data(dispensationQuadruplex)
AdvISERMHPYRO(signaltest=PyrosignalQuadruplex,dictionary=dictionaryQuadruplex,L1=0.05,SCT=1,dispensation=d

data(dictionaryQuintuplex)
data(PyrosignalQuintuplex)
data(dispensationQuintuplex)
AdvISERMHPYRO(signaltest=PyrosignalQuintuplex,dictionary=dictionaryQuintuplex,L1=0.05,SCT=1,dispensation=d
```

dictionaryQuadruplex *Dictionary for the quadruplex assay that includes theoretical and experimental uniplex pyrosequencing signals for each genotype that can be found in each genomic region.*

Usage

```
data(dictionaryQuadruplex)
```

Format

the data frame includes 1 column for each signal in the dictionary. Several signals can correspond to the same genotype. The number of rows corresponds to the length of the dispensation order.

Details

The first 9 letters must correspond to the genomic region label while the next letters must correspond to the UNS label.

Examples

```
data(dictionaryQuadruplex)
```

dictionaryQuintuplex	<i>Dictionary for the quintuple assay that includes theoretical and experimental uniplex pyrosequencing signals for each genotype that can be found in each genomic region.</i>
----------------------	---

Usage

```
data(dictionaryQuintuplex)
```

Format

the data frame includes 1 column for each signal in the dictionary. Several signals can correspond to the same genotype. The number of rows corresponds to the length of the dispensation order.

Details

The first 9 letters must correspond to the genomic region label while the next letters must correspond to the UNS label.

Examples

```
data(dictionaryQuintuplex)
```

dispensationQuadruplex

Nucleotide dispensation order that has been used for the quadruplex assay.

Usage

data(dispensationQuadruplex)

Format

The format is: chr [1:14] "C" "T" "G" "C" "A" "T" "G" "A" "C" "T" "C" "G" "A" "T"

Examples

data(dispensationQuadruplex)

dispensationQuintuplex

Nucleotide dispensation order that has been used for the quadruplex assay.

Usage

data(dispensationQuintuplex)

Format

The format is: chr [1:15] "A" "G" "A" "T" "C" "G" "C" "T" "A" "C" "G" "A" "C" "T" "G"

Examples

data(dispensationQuintuplex)

PyroSignalQuadruplex *Quadruplex pyro-signal generated for 1 patient with pyrosequencer PyroMark PSQ 96 MA*

Usage

data(PyroSignalQuadruplex)

Format

This numerical vector contains the peak heights of the multiplex pyro-signal.

Examples

data(PyroSignalQuadruplex)

PyroSignalQuintuplex *Quintuplex pyro-signal generated for 1 patient with pyrosequencer PyroMark PSQ 96 MA*

Usage

```
data(PyroSignalQuintuplex)
```

Format

This numerical vector contains the peak heights of the multiplex pyro-signal.

Examples

```
data(PyroSignalQuintuplex)
```

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