Package 'SigQBiC'

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Type Package

Title Signature-QBiC:Predict the effect of mutational signatures on TF binding

Version 0.1.2

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Description Signature-QBiC integrates mutational signature profiles with the QBiC method to investigate the effect of mutational signatures on the binding of TFs.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Suggests testthat

R topics documented:

Generate96ChannelSpectrumFromTwelvemers

Generate mutation spectrum from twelvemers

Description

This function generates a mutation spectrum of 96 mutation classes (mutations on pyrimidine centered trinucleotide) from a list of twelvemers

Usage

```
Generate96ChannelSpectrumFromTwelvemers(twelvemers.list)
```

Arguments

twelvemers.list

          A list of twelvemers, with a 11mer centered at the mutation base and 1 mutated base appended

Value

A mutation spectrum with 96 mutation types

GenerateQBiCScoresFromTwelvemers

          Generate QBiC scores for all uPBMs for a given list of twelvemers

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Description

This function generates QBiC scores for all uPBM experiments for given twelvemers

Usage

GenerateQBiCScoresFromTwelvemers(uPBM_QBiC_scores, twelvemers.list)

Arguments

uPBM_QBiC_scores

          All QBiC scores for a universal PBM

twelvemers.list

          A list of twelvemers, with a 11mer centered at the mutation base and 1 mutated base appended

Value

A list of scores for the given twelvemers list

GenerateSignatureWeightedQBiCScoresDistribution

          Plot histogram for each mutation class for a given signature and uPBM experiment name

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Usage

GenerateSignatureWeightedQBiCScoresDistribution(uPBM_QBiC_scores, spectrum, output_name)

Arguments

uPBM_QBiC_scores

          All QBiC scores for a PBM

spectrum   A list of GR/LR generated by Signature-QBiC from observed mutation spectrum

Value

A plot of histograms

MutationTypeContribution

Compute the contribution

Description

Compute the contribution

Usage

```
MutationTypeContribution(uPBM_QBiC_scores, spectrum)
```

Arguments

uPBM_QBiC_scores

      QBiC scores of a uPBM experiment

spectrum   A list of possibilities for each mutation type(mutational spectrum) or a character of name of mutational signature(mutational signature)

Value

A matrix with contribution to the gain-binding and loss-binding for each of 96 mutation types

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Pathway_Selection   *Identify pathways that enriched with affected TFs by a given mutational signature*

Description

A function gives the pathways enriched with affected TFs by a given mutational signature

Usage

```
Pathway_Selection(TF.list, qvalue, dbs.selected)
```

Arguments

TF.list   A list of affected TFs

qvalue   A number of qvalue as filter

dbs.selected   A character of database name in 'enrichR'. In our paper, we used 'Reactome_2016'

Value

A matrix of pathways enriched with given TFs

SignatureQBiC	*Generate GR and LR for a uPBM and a signature (Signature-QBiC)*

Description

SignatureQBiC model. This function generates Gain Ratio and Loss Ratio for a TF (represented by universal PBM) with a mutational signature (or a mutation spectrum)

Usage

```
SignatureQBiC(uPBM_QBiC_scores, spectrum)
```

Arguments

uPBM_QBiC_scores

           All QBiC scores for a universal PBM

spectrum   A list of possibilities for each mutation type(mutational spectrum) or a character of name of mutational signature(mutational signature)

Value

A list of GR and LR

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