

Package ‘SigQBiC’

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Type Package

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

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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.

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RoxygenNote 7.1.0

Suggests testthat

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EnrichrPathwayAnalysis

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

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

Arguments

TF.list A list of affected TFs
 qvalue A numeric 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

```
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(input.twelvemers.list)
```

Arguments

twelvemers 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

```
GenerateQBiCScoresForTwelvemers
```

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

Description

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

Usage

```
GenerateQBiCScoresForTwelvemers(uPBM_QBiC_scores, twelvemers)
```

Arguments

uPBM_QBiC_scores	All QBiC scores for a universal PBM
twelvemers	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

GenerateSignatureWeightedDistributionPlots

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

Usage

```
GenerateSignatureWeightedDistributionPlots(
  uPBM_QBiC_scores,
  spectrum,
  output_name
)
```

Arguments

uPBM_QBiC_scores	All QBiC scores for a universal 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, p_values, spectrum)
```

Arguments

uPBM_QBiC_scores	All QBiC scores for a universal PBM
p_values	p_values for all twelvemers
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 GR and LR for each of 96 mutation types

PyrPenta	<i>Convert mutations to pyrimidine centred.</i>
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Description

This function converts trinucleotide context mutations to pyrimidine centred. For example, CGA > CAA will be converted to TCG > TTG

Usage

```
PyrPenta(mutstring)
```

Arguments

mutstring	A string with for characters: proceeding base - reference base - following base - mutated base (For example, CGA > CCA was input as CGAC)
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Value

A pyrimidine centred mutation

SignatureQBiC	<i>Generate GR and LR for a uPBM and a signature (Signature-QBiC)</i>
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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, p_values, spectrum)
```

Arguments

uPBM_QBiC_scores	All QBiC scores for a universal PBM
p_values	p_values for all twelvemers
spectrum	A list of possibilities for each mutation type(mutational spectrum) or a character of name of mutational signature(mutational signature)

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Value

A list of GR and LR

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