Package ‘jetset’

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Title One-to-One Gene-Probeset Mapping for Affymetrix Human Microarrays
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Depends R (>= 2.10)
Imports org.Hs.eg.db, AnnotationDbi
Description On Affymetrix gene expression microarrays, a single gene may be measured by multiple probe sets. This can present a mild conundrum when attempting to evaluate a gene “signature” that is defined by gene names rather than by specific probe sets. This package provides a one-to-one mapping from gene to “best” probe set for four Affymetrix human gene expression microarrays: hgu95av2, hgu133a, hgu133plus2, and u133x3p. This package also includes the pre-calculated probe set quality scores that were used to define the mapping.
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NeedsCompilation no
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Description

This function retrieves probe sets corresponding to the queried genes.

Usage

jmap(chip, eg, symbol, alias, ensembl)

Arguments

chip Chip name
eg A vector of Entrez GeneIDs (optional)
symbol A vector of gene symbols (optional)
alias A vector of gene aliases (optional)
ensembl A vector of Ensembl IDs (optional)

Details

Currently, chip can be "hgu95av2", "hgu133a", "hgu133plus2", or "u133x3p". Queried genes must be specified by either eg, symbol, alias, or ensembl. If the query is not recognized, or is ambiguous, or corresponds to a gene that is not detected by the array, NA will be returned. Details about the jetset algorithm are available in the vignette.

Value

A character vector of probe set IDs

References


See Also

The underlying Entrez ID to probeset data is available in (e.g.) scores.hgu95av2. Symbol, alias, and ensembl lookups are generated from e.g. org.Hs.egSYMBOL2EG.

Examples

genes <- c('MKI67', 'CHD5', 'ESR1', 'FGF19', 'ERBB2', 'NoSuchGene')

# This generates several informative warnings
jmap('hgu133a', symbol = genes)
jscores

Retrieve jetset scores for probe sets

Description

This function retrieves jetset scores, which indicate the predicted quality of individual probe sets on selected Affymetrix microarrays.

Usage

jscores(chip, probeset, eg, symbol, alias, ensembl)

Arguments

- chip: Chip name
- probeset: A vector of probe set IDs (optional)
- eg: A vector of Entrez GeneIDs (optional)
- symbol: A vector of gene symbols (optional)
- alias: A vector of gene aliases (optional)
- ensembl: A vector of Ensembl IDs (optional)

Details

Currently, chip can be "hgu95av2", "hgu133a", "hgu133plus2", or "u133x3p". If no further arguments are specified, the scores for all probe sets on the chip are returned.

If any of probeset, eg, symbol, alias, or ensembl are specified, these are used to filter the resulting data frame in a logical OR sense.

Details about the jetset algorithm are available in the vignette.

Value

A data frame in which each row corresponds to a probe set, with 8 columns:

- EntrezID: Entrez GeneID of the targeted gene (character).
- nProbes: Number of probes in the probe set (integer).
- process: Processivity requirement (integer).
- specificity: Specificity score (numeric).
- coverage: Coverage score (numeric).
- robust: Robustness score (numeric).
- overall: Overall score (numeric).
- symbol: HUGO gene symbol (character).

The rows are sorted by decreasing overall score.
References


See Also

The underlying data comes from (e.g.) scores.hgu95av2, with gene symbol lookups coming from org.Hs.eh5SYMBOL.

Examples

```r
genes <- c('MKB67', 'CHD5', 'ESR1', 'FGF19', 'ERBB2', 'NoSuchGene')

# This generates several informative warnings
jscores('hgu133a', symbol = genes)
```

---

**scores**

*Data: Probe set quality scores*

Description

This data set provides gene target and quality scores for each probe set on the corresponding Affymetrix gene expression microarrays.

Usage

scores.hgu95av2
scores.hgu133a
scores.hgu133plus2
scores.u133x3p

Format

A data frame with each row corresponding to a probe set, with 4 columns:

- **EntrezID** Entrez GeneID of the targeted gene (character).
- **process** Processivity requirement (integer).
- **specificity** Specificity score (numeric).
- **coverage** Coverage score (numeric).
Details

If there is a relative majority (plurality) of the probes in a probe set that are specific for a single gene, this is defined as the targeted gene. If no such majority exists, the targeted gene is defined as NA, as are the following scores.

The processivity requirement is the number of consecutive bases that must be synthesized to generate a target that can be detected by the probe set.

The specificity score is the fraction of the probes in a probe set that are likely to detect the targeted gene and unlikely to detect other genes.

The coverage score is the fraction of the splice isoforms belonging to the targeted gene that are detected by the probe set.

The following two scores are not contained in this data, but are calculated from the above scores; to see them use jscores.

The robustness score quantifies robustness against transcript degradation. The robustness score uses the processivity requirement to estimate the signal intensity of a probe set, relative to the ideal case of perfect processivity.

The overall score is the product of the specificity score, coverage score, and robustness score.

All scores can range from 0 to 1. A higher score indicates better (predicted) performance.

Details about the jetset algorithm are available in the vignette.

Note

This data is also available in CSV format from http://www.cbs.dtu.dk/biotoools/jetset/

Source

Scores are calculated from BLASTN alignments between probe sequences and Refseq transcript sequences, as described in the vignette and in the reference below.

The Refseq human RNA was downloaded from NCBI on 2017-04-04. The lookups were based on org.Hs.eg.db version 3.4.0.

References


See Also

jscores for a more convenient way to access this data

Examples

```r
## Here is the EntrezID for the ESR1 gene
id <- "2899"

## Extract the scores for all probe sets detecting ESR1
scores.hgu95av2[which(scores.hgu95av2$EntrezID == id), ]
```
## Compare to the recommended function 'jscores'

```r
jscores("hgu95av2", eg = "2099")
```
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