Package ‘JohnsonKinaseData’

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Kinase PWMs based on data published by Johnson et al. 2023  
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**Description** The packages provides position specific weight matrices (PWMs) for 303 human serine/threonine kinases originally published in Johnson et al. 2023. It includes gene annotation for each kinase PWM and PWM matching scores for a set of 85603 curated human phosphosites which can be used to map a PWM score to its percentile rank. The package also includes basic functionality to score user provided phosphosites.

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**URL** https://github.com/fgeier/JohnsonKinaseData/

**BugReports** https://support.bioconductor.org/t/JohnsonKinaseData

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Description

The JohnsonKinaseData package provides position specific weight matrices (PWMs) for 303 human serine/threonine kinases originally published in Johnson et al. 2023.

It also includes pre-computed PWM scores ("background scores") for a large collection of curated human phosphosites.

The package additionally offers functionality to match kinase PWMs against user-provided phosphopeptides and to rank PWM scores relative to the background scores ("percentile rank").

Author(s)

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References


See Also

Useful links:

- https://github.com/fgeier/JohnsonKinaseData/
- Report bugs at https://support.bioconductor.org/t/JohnsonKinaseData
**getBackgroundScores**

Get precomputed PWM scores for a large set of curated human phosphosites

**Description**

The background scores are derived from matching each PWM to the 85,603 unique phosphosites published in Johnson et al. 2023. The data frame contains the log2-odds score per phosphosite and PWM.

**Usage**

```r
getBackgroundScores()
```

**Value**

A data frame with log2-odds scores per phosphosite (rows) and PWMs (columns)

**Examples**

```r
bg <- getBackgroundScores()
```

**getKinaseAnnotation**

Get annotation data for all 303 human serine/threonine kinase PWMs

**Description**

The annotation data records for each of the 303 human serine/threonine kinase PWMs originally published in Johnson et al. the PWM matrix name, gene symbol and description, Uniprot ID and Entrez ID as well as the kinase family.

**Usage**

```r
getKinaseAnnotation()
```

**Value**

A data frame with columns MatrixName, GeneName, UniprotID, EntrezID, Description and KinaseFamily

**Examples**

```r
anno <- getKinaseAnnotation()
```
getKinasePWM

Get a list of position specific weight matrices (PWMs)

Description

The function returns a list of PWMs for the 303 human serine/threonine kinases originally published in Johnson et al. 2023. Each PWM stores the log2-odds score per amino acid (23 rows) and position (10 columns) in matrix format. Beside the 20 standard amino acids also phosphorylated serine, threonine and tyrosine residues are included.

Usage

getKinasePWM(includeSTfavorability = TRUE)

Arguments

includeSTfavorability

Include serine vs. threonine favorability for the central phospho-acceptor?

Details

The central phospho-acceptor position of each PWM is either serine or threonine. By default, this position quantifies the favorability of serine over threonine. This favorability can be omitted when setting `includeSTfavorability=FALSE` in which case the central position doesn’t contribute to the PWM score.

Value

A named list of numeric matrices (PWMs).

References


Examples

pwms <- getKinasePWM()
**getScoreMaps**

*Map log2-odds score to percentile rank*

**Description**

For each kinase PWM, get a function that maps its log2-odds score to the percentile rank in the background score distribution. The percentile rank of a given score is the percentage of scores in corresponding background score distribution that are less than or equal to that score. The background score distribution per PWM is derived from matching each PWM to the 85'603 unique phosphosites published in Johnson et al. 2023.

**Usage**

```r
getScoreMaps()
```

**Details**

The background sites used by Johnson et al. don’t contain non-central phosphorylated residues (phospho-priming). Therefore any input sites which include phospho-priming will be capped to 100 percentile rank, if their PWM score exceeds the largest observed background score for that PWM.

Internally, `stats::approxfun` is used to linearly interpolate between the PWM score and its 0.1% quantile in the distribution over background scores. This approximation allows for a lower memory footprint compared with the full set of background scores.

**Value**

A named list of functions, one for each kinase PWM. Each function is taking a vector of PWM log2-odds scores and maps them to a percentile rank in the range 0 to 100.

**Examples**

```r
maps <- getScoreMaps()
```

**JohnsonKinaseAnnotation**

*Get file path to local cache of annotation data for kinase PWMs*

**Description**

Internal cache accessor function.

**Usage**

```r
JohnsonKinaseAnnotation(metadata=FALSE)
```
Arguments
metadata

When 'metadata=FALSE' the full resource is loaded, when 'metadata=TRUE' just the metadata are displayed.

Value
A character vector with the file path to the local cache of the annotation data.

See Also
Use getKinaseAnnotation() to load the data.

Examples
anno <- JohnsonKinaseAnnotation()

JohnsonKinaseBackgroundQuantiles
Get file path to local cache of background score quantiles

Description
Internal cache accessor function.

Usage
JohnsonKinaseBackgroundQuantiles(metadata=FALSE)

Arguments
metadata

When 'metadata=FALSE' the full resource is loaded, when 'metadata=TRUE' just the metadata are displayed.

Value
A character vector with the file path to the local cache of background score quantiles.

See Also
Use getScoreMaps() to load the score mapping functions.

Examples
quants <- JohnsonKinaseBackgroundQuantiles()
JohnsonKinaseBackgroundScores

*Get file path to local cache of background scores*

**Description**

Internal cache accessor function.

**Usage**

JohnsonKinaseBackgroundScores(metadata=FALSE)

**Arguments**

- **metadata**
  
  When `metadata=FALSE` the full resource is loaded, when `metadata=TRUE` just the metadata are displayed.

**Value**

A character vector with the file path to the local cache of the background scores.

**See Also**

Use `getBackgroundScores()` to load the data.

**Examples**

```r
scores <- JohnsonKinaseBackgroundScores()
```

---

JohnsonKinasePWM

*Get file path to local cache of kinase PWM data*

**Description**

Internal cache accessor function.

**Usage**

JohnsonKinasePWM(metadata=FALSE)

**Arguments**

- **metadata**
  
  When `metadata=FALSE` the full resource is loaded, when `metadata=TRUE` just the metadata are displayed.
processPhosphopeptides

Value
A character vector with the file path to the local cache of the PWM data.

See Also
Use getKinasePWM() to load the data.

Examples
data <- JohnsonKinasePWM()

Description
Process phospho-peptides to a common format used for PWM matching

Usage
processPhosphopeptides(
sites,
onlyCentralAcceptor = TRUE,
allowPhosphoPriming = TRUE
)

Arguments
sites Character vector with phospho-peptides
onlyCentralAcceptor Process only the central phospho-acceptor residue?
allowPhosphoPriming Allow phospho-acceptors at non-central positions? These should be indicated by the lower case letters s, t or y.

Details
Phosphorylated residues are recognized either by lower case letters (s, t or y) or the phosphorylated residue is followed by an asterisk (S*, T* or Y*).

If a peptide reports several phosphorylated residues, parameter onlyCentralAcceptor allows for two processing options: (1) By default, only the central phospho-acceptor of each phospho-peptide is considered. Here central is defined as the left-closest position to floor(nchar(site)/2)+1. (2) All phospho-acceptors are considered as central in which case the phospho-peptide is replicated and aligned for each of its phosphorylated residues. In this case the output sites are not in parallel to the input peptides.
In both cases, non-central phospho-acceptors are indicated by lower case letters (s, t, or y). These residues enable phospho-priming of the site. If phospho-priming is disabled (parameter `allowPhosphoPriming`) these residues are converted to upper case letters.

If a site does not follow the phosphorylation patterns described above, the central residue defined by position `floor(nchar(site)/2)+1` is considered the default phospho-acceptor site.

The input sites are truncated and/or padded such that the processed sites are of width 10 and have the central phospho-acceptor surrounded by 5 upstream and 4 downstream residues, as required for PWM matching.

A warning is raised if the central phospho-acceptor is not serine or threonine, as these sites are not covered by the Johnson PWMs.

**Value**

A tibble with columns: sites, processed, acceptor

**Examples**

```r
procSites <- processPhosphopeptides(c("SAGLLS*DEDC", "RtEKGS*N", "EKGDSN__"))
```

---

**scorePhosphosites**  
*Match kinase PWMs to processed phosphosites*

**Description**

`scorePhosphosites` takes a list of kinase PWMs and a vector of processed phosphosites as input and returns a matrix of match scores per PWM and site.

**Usage**

```r
scorePhosphosites(
  pwms,
  sites,
  scoreType = c("lod", "percentile"),
  BPPARAM = BiocParallel::SerialParam()
)
```

**Arguments**

- **pwms**  
  List with kinase PWMs as returned by `getKinasePWM`.

- **sites**  
  A character vector with phosphosites. Check `processPhosphopeptides` for the correct phosphosite format.

- **scoreType**  
  Log2-odds score or percentile rank.

- **BPPARAM**  
  A `BiocParallelParam` object specifying how parallelization should be performed.
scorePhosphosites

Details

The match score is either the log2-odds score (lod) or the percentile rank (percentile) in the background score distribution.

Value

A numeric matrix of size length(sites) times length(pwms).

See Also

getKinasePWM for getting a list of kinase PWMs, processPhosphopeptides for the correct phosphosite format, and getScoreMaps for mapping PWM scores to percentile ranks

Examples

score <- scorePhosphosites(getKinasePWM(), c("TGRRHTLAEV", "LISAVSPEIR"))
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