Package ‘pfamAnalyzeR’

April 25, 2025

Type Package

Title Identification of domain isotypes in pfam data

Version 1.9.0

Description Protein domains is one of the most import annoation of proteins we have with the Pfam database/tool being (by far) the most used tool. This R package enables the user to read the pfam prediction from both webserver and stand-alone runs into R. We have recently shown most human protein domains exist as multiple distinct variants termed domain isotypes. Different domain isotypes are used in a cell, tissue, and disease-specific manner. Accordingly, we find that domain isotypes, compared to each other, modulate, or abolish the functionality of a protein domain. This R package enables the identification and classification of such domain isotypes from Pfam data.

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Depends R (>= 4.3.0), readr, stringr, dplyr

Imports utils, tibble, magrittr

Encoding UTF-8

LazyData false

RoxygenNote 7.2.1

Suggests BiocStyle, knitr, rmarkdown

VignetteBuilder knitr

biocViews AlternativeSplicing, TranscriptomeVariant, BiomedicalInformatics, FunctionalGenomics, SystemsBiology, Annotation, FunctionalPrediction, GenePrediction, DataImport

BugReports `https://github.com/kvittingseerup/pfamAnalyzeR/issues`

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`analyse_pfam_isotypes` *Determine domain isotype*

Description

Determine domain isotype

Usage

```
analyse_pfam_isotypes(pfamRes, fracCutoff = 0.1)
```

Arguments

`pfamRes`	A data frame with pfam augmneted with indel and truncation info (as produced by `augment_pfam`).
`fracCutoff`	The fraction of a protein domain that must be affected before classifying it a truncation or indel.

Value

The data.frame with the Pfam results now augmented with info about domain domain isotype

Examples

```
### Load pfam data
pfamResultFile <- system.file("extdata/pfam_results.txt", package = "pfamAnalyzeR")
pfamRes <- read_pfam(pfamResultFile)

### Augment the pfam data
pfamRes <- augment_pfam(pfamRes)

### Predict domain isotype
pfamRes <- analyse_pfam_isotypes(pfamRes)
```

`augment_pfam` *Augment pfam domains with truncation/indel calculations*

Description

Augment pfam domains with truncation/indel calculations

Usage

```
augment_pfam(pfamRes)
```

Arguments

`pfamRes`	A data frame with pfam results as produced by `read_pfam`.

Value

The data.frame with the Pfam results now augmented with info on trunkation and indel sizes

Examples

```
### Load pfam data
pfamResultFile <- system.file("extdata/pfam_results.txt", package = "pfamAnalyzeR")
pfamRes <- read_pfam(pfamResultFile)

### Augment the pfam data
pfamRes <- augment_pfam(pfamRes)
```

`pfamAnalyzeR` *Read in and analyze pfam domains isotypes*

Description

Read in and analyze pfam domains isotypes

Usage

```
pfamAnalyzeR(path, fracCutoff = 0.1)
```

Arguments

`path`	A string indicating the full path to the Pfam result file
`fracCutoff`	The fraction of a protein domain that must be affected before classifying it a truncation or indel.

Value

The data.frame with the Pfam results now augmented with info about domain structural variation

Examples

```
### Predict domain isotypes in pfam results
pfamResultFile <- system.file("extdata/pfam_results.txt", package = "pfamAnalyzeR")
pfamRes <- pfamAnalyzeR(pfamResultFile)
```

`read_pfam` *Read Pfam file into R*

Description

Read Pfam result file file into R. Supports both result files from local and web-server

Usage

```
read_pfam(path)
```

Arguments

`path`	A string indicating the full path to the Pfam result file

Details

The pfam webserver can be found at `https://www.ebi.ac.uk/Tools/hmmer/search/hmmscan`.

Value

A data.frame with the Pfam results

Examples

```
pfamResultFile <- system.file("extdata/pfam_results.txt", package = "pfamAnalyzeR")
pfamRes <- read_pfam(pfamResultFile)
```

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