

Package ‘pfamAnalyzeR’

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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	<i>Determine domain isotype</i>
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Description

Determine domain isotype

Usage

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

Arguments

pfamRes	A data frame with pfam augmented 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 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/hmmsearch>.

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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