Package 'FScanR'

May 9, 2023

Type Package

Title Detect Programmed Ribosomal Frameshifting Events from mRNA/cDNA BLASTX Output

Version 1.10.0

Description 'FScanR' identifies Programmed Ribosomal Frameshifting (PRF) events from BLASTX homolog sequence alignment between targeted genomic/cDNA/mRNA sequences against the peptide library of the same species or a close relative.
The output by BLASTX or diamond BLASTX will be used as input of 'FScanR' and should be in a tabular format with 14 columns.
For BLASTX, the output parameter should be: -outfmt '6 qseqid sseqid pident length mismatch gapopen qstart qend sstart send evalue bitscore qframe sframe'.
For diamond BLASTX, the output parameter should be: -outfmt 6 qseqid sseqid pident length mismatch gapopen qstart qend sstart send evalue bitscore qframe qframe.

License Artistic-2.0

Encoding UTF-8

LazyData true

Depends R (>= 4.0)

Imports stats

Suggests knitr, rmarkdown

VignetteBuilder knitr

BugReports https://github.com/seanchen607/FScanR/issues

biocViews Alignment, Annotation, Software

RoxygenNote 7.1.1

git_url https://git.bioconductor.org/packages/FScanR

git_branch RELEASE_3_17

git_last_commit 0f596d9

git_last_commit_date 2023-04-25

Date/Publication 2023-05-09

Author Xiao Chen [aut, cre] (<https://orcid.org/0000-0001-5059-8846>)

Maintainer Xiao Chen <seanchen607@gmail.com>

R topics documented:

FScanR *FScanR*

Description

'FScanR' identifies Programmed Ribosomal Frameshifting (PRF) events from BLASTX homolog sequence alignment between targeted genomic/cDNA/mRNA sequences against the peptide library of the same species or a close relative.

Usage

```
FScanR(
  blastx_output,
  mismatch_cutoff = 5,
  evalue_cutoff = 1e-05,
  frameDist_cutoff = 10
)
```

Arguments

`blastx_output`	Input file with 14 columns in tab-delimited format, output from BLASTX using parameters: -outfmt '6 qseqid sseqid pident length mismatch gapopen qstart qend sstart send evalue bitscore qframe sframe'
`mismatch_cutoff`	Threshold of number of mismatches for BLASTX hits, default 5 (aa)
`evalue_cutoff`	Threshold of E-value for BLASTX hits, default 1e-5
`frameDist_cutoff`	Threshold for gap size (bp) to detect frameshifting between BLASTX hits of same mRNA/cDNA sequence, default 10 (nt)

Details

The output by BLASTX or diamond BLASTX will be used as input of 'FScanR' and should be in a tabular format with 14 columns.

For BLASTX, the output parameter should be: -outfmt '6 qseqid sseqid pident length mismatch gapopen qstart qend sstart send evalue bitscore qframe sframe'.

For diamond BLASTX, the output parameter should be: -outfmt 6 qseqid sseqid pident length mismatch gapopen qstart qend sstart send evalue bitscore qframe qframe.

Value

dataframe

Author(s)

Xiao Chen

References

1. X Chen, Y Jiang, F Gao, W Zheng, TJ Krock, NA Stover, C Lu, LA Katz & W Song (2019). Genome analyses of the new model protist Euplotes vannus focusing on genome rearrangement and resistance to environmental stressors. Molecular Ecology Resources, 19(5):1292-1308. <https://doi.org/10.1111/1755-0998.13023>

Examples

```
test_data <- read.table(system.file("extdata", "test.tab", package = "FScanR"), header=TRUE, sep="\t")
FScanR(test_data)
```

Index