

Package ‘FScanR’

September 12, 2021

Type Package

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

Version 1.2.0

Description 'FScanR' identifies Programmed Ribosomal Frameshift-
ing (PRF) events from BLASTX homolog sequence alignment
between targeted genomic/cDNA/mRNA sequences against the peptide li-
brary of the same species or a close relative.
The output by BLASTX or diamond BLASTX will be used as input of 'FS-
canR' and should be in a tabular format with 14 columns.
For BLASTX, the output parameter should be: -outfmt '6 qseqid sseqid pident length mis-
match gapopen qstart qend sstart send eval bitscore qframe sframe'.
For diamond BLASTX, the output parameter should be: -outfmt 6 qseqid sseqid pi-
dent length mismatch gapopen qstart qend sstart send eval 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_13

git_last_commit 95f349c

git_last_commit_date 2021-05-19

Date/Publication 2021-09-12

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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,  
  evalvalue_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 evalvalue bitscore qframe sframe'
- mismatch_cutoff

Threshold of number of mismatches for BLASTX hits, default 5 (aa)
- evalvalue_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 evalvalue bitscore qframe sframe'.

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

Value

dataframe

Author(s)

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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)
```

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