

# Package ‘FScanR’

October 14, 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 evaluate bitscore qframe sframe'.

For diamond BLASTX, the output parameter should be: -outfmt 6 qseqid sseqid pi-  
dent length mismatch gapopen qstart qend sstart send evaluate 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

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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,
  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)
```

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