

Package ‘flipflop’

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Title Fast lasso-based isoform prediction as a flow problem

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Description Flipflop discovers which isoforms of a gene are expressed in a given sample together with their abundances, based on RNA-Seq read data.

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LazyLoad yes

Imports methods, Matrix, IRanges, GenomicRanges

Suggests

Depends R (>= 2.10.0)

NeedsCompilation yes

biocViews Bioinformatics, RNAseq

BuildVignettes true

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flipflop

*Estimate isoform compositions and abundances***Description**

This function takes count data (RNA-seq alignment in SAM format) for a given gene as input and estimates which isoforms of the gene are most likely to have generated this set of counts. It is based on a Poisson likelihood penalized by an l_1 norm as explained in Bernard et al., 2013.

Usage

```
flipflop(data.file, out.file="FlipFlop_output.gtf", annot.file="", paired=FALSE,
         frag=400, std=20, minReadNum=40, minFragNum=20, minCvgCut=0.25, verbose=0,
         verbosepath=0, max_isoforms=10, use_TSSPAS=0, cutoff=5, BICcst=50,
         isolasso.instance="", NN="")
```

Arguments

data.file	Input alignment file in SAM format.
out.file	Output gtf data file storing the structure of the transcripts which are found to be expressed together with their abundances in FPKM.
annot.file	Optional annotation file in BED format. If given exon boundaries will be taken from the annotations
paired	Boolean for paired-end reads. If FALSE your reads will be considered as single-end reads. Default FALSE
frag	Mean fragment size. Only used if paired is set to TRUE. Default 400.
std	Standard deviation of fragment size. Only used if paired is set to TRUE. Default 20.
minReadNum	[Pre-processing] The minimum number of clustered reads to output. Default 40. If you give an annotation file it will be the minimum number of mapped reads to process a gene.
minFragNum	[Pre-processing] The minimum number of mapped read pairs to process a gene. Only used if paired is TRUE. Default 20.
minCvgCut	[Pre-processing] The fraction for coverage cutoff, should be between 0-1. A higher value will be more sensitive to coverage discrepancies in one gene. Default 0.25.
verbose	Verbosity. Default 0 (little verbosity). Put 1 for more verbosity.
verbosepath	Verbosity of the optimization part. Default 0 (little verbosity). Put 1 for more verbosity.
max_isoforms	Maximum number of isoforms given during regularization path. Default 10.
use_TSSPAS	Do we restrict the candidate TSS and PAS sites. 1 is yes and 0 is no. Default 0 i.e each exon can possibly starts or ends an isoform.

cutoff	For paired-end reads do not report isoforms whose expression level is less than cutoff percent of the most expressed transcripts. Not active is paired is FALSE. Default 5.
BICcst	Constant used for model selection with the BIC criterion. Default 50.
isolasso.instance	Input file directly from IsoLasso. If non empty, the data.file and annot.file fields are ignored.
NN	Total number of mapped fragments. This field is only necessary if you give isolasso.instance.

Value

A `list` with the following elements:

transcripts	A list storing the structure of the expressed isoforms. The list is a <code>GRangesList</code> object from the <code>GenomicRanges</code> package. Rows correspond to exons. On the left hand side each exon is described by the gene name, the chromosome, its genomic position on the chromosome and the strand. Transcripts are described on the right hand side. Every transcript is a binary vector where an exon is labelled by 1 if it is included in the transcript.
abundances	A list storing the abundances of the expressed isoforms in FPKM unit. Each element of the list is a vector whose length is the number of expressed transcripts listed in the above 'transcripts' object.
timer	A vector with the computation time in seconds for each gene.

Author(s)

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Examples

```
## Load the library
library(flipflop)

## Alignment data file in SAM format
data.file <- system.file(extdata/vignette-sam.txt, package=flipflop)

## Run flipflop
ff.res <- flipflop(data.file=data.file,
                  out.file=FlipFlop_output_example.gtf)

## Names of the result list returned by flipflop
names(ff.res)

## Structure of the expressed isoforms for the first gene
## Rows correspond to exons, with chromosome, genomic position and strand information for each exon
## The metadata columns correspond to the expressed transcripts
transcripts <- ff.res$transcripts[[1]]
print(transcripts)
```

```
## Abundances in FPKM of the expressed isoforms for the first gene
## The length of the vector corresponds to the number of transcripts listed in the transcripts object.
## Each element of the vector is the estimated abundance of the corresponding transcript.
abundances <- ff.res$abundances[[1]]
print(abundances)
```

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