Package 'HextractoR'

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Type Package

Title Integrated Tool for Hairping Extraction of RNA Sequences

Version 1.4

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Description Simple and integrated tool that automatically extracts and folds all hairpin sequences from raw genome-wide data. It predicts the secondary structure of several overlapped segments, with longer length than the mean length of sequences of interest for the species under processing, ensuring that no one is lost nor inappropriately cut.

License Apache License 2.0

Encoding UTF-8

LazyData true

Imports seqinr, parallel, doParallel, foreach,

NeedsCompilation no

RoxygenNote 6.1.1

Repository CRAN

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HextractoR *HextractoR: Integrated Tool for Hairping Extraction of RNA Sequences*

Description

To preprocess a genome, you need a file containing the raw genome in fasta format. To run HExtractor, simply call the main function. This function creates 2 files in the "out" folder and automatically names them.

Usage

```
HextractoR(input_file, min_valid_nucleotides = 500, window_size = 160,
  window_step = 30, only_sloop = T, min_length = 60, min_bp = 16,
  trim_sequences = T, margin_bp = 6, blast_evalue = 1,
  identity_threshold = 90, nthreads = 4, nworks = 4,
  filter_files = { })
```

Arguments

input_file	filename of the fasta file to proccess
min_valid_nucleotides	Each input sequence must have this quantity of valid nucleotides (not 'N') to be processed.
window_size	Number of bases in the windows.
window_step	Window step. This number defines indirectly the overlap: window_overlap=window_size-window_step
only_sloop	Only extract single loop sequence.
min_length	Minimum sequence length. Shorter sequences are discarded.
min_bp	Minimum number of base-pairs that must form a sequence.
trim_sequences	Use some heuristics to trim the hairpins.
margin_bp	When the sequence is trimmed, at least min_bp+margin_bp base-pairs are left.
blast_evalue	e-value used in blast to match the extracted sequences with the sequences from the filter files.
identity_threshold	Identity threshold used to match sequences with the sequences from the filter files.
nthreads	Allows using more than one thread in the execution.
nworks	Split each sequence in nworks to use less RAM memory.
filter_files	Fasta files with known sequences to separate the output stems.

Value

A list with the path of the output files and the result of the proccessing of each sequence (if it was succesful or failed)

Examples

```
# Small example without filter files
library(HextractoR)
# First we get the path of the example FASTA file
fpath <- system.file("Example_tiny.fasta", package="HextractoR")
# To run HextractoR, simply call the main function
HextractoR(input_file = fpath)
# Other example with filter files and bigger input file
fpath1 <- system.file("Example_human.fasta", package="HextractoR")
fpath2 <- system.file("Example_pre-miRNA.fasta", package="HextractoR")
HextractoR(input_file = fpath1, filter_files = {fpath2})
# This function creates 2 files in the working directory and automatically
# names them.
```

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