Package: copyseparator (via r-universe)

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Type Package

Title Assembling Long Gene Copies from Short Read Data

Version 1.2.0

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Description Assembles two or more gene copies from short-read Next-Generation Sequencing data. Works best when there are only two gene copies and read length >=250 base pairs. High and relatively even coverage are important.

License GPL-2

URL https://github.com/LeiYang-Fish/copyseparator

BugReports https://github.com/LeiYang-Fish/copyseparator/issues

Depends R (>= 3.5.0)

Encoding UTF-8

LazyData TRUE

Imports ape, seqinr, stringr, kmer, DECIPHER, beepr, Biostrings, grDevices, doParallel, foreach, parallel

RoxygenNote 7.2.1

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Repository https://leiyang-fish.r-universe.dev

RemoteUrl https://github.com/leiyang-fish/copyseparator

RemoteRef HEAD

RemoteSha 8046ae63692f7218938abbee9d3db61d3a4a1c22

Contents

`copy_assemble` *copy_assemble*

Description

Assembles a small number of overlapping DNA sequences into their respective gene copies.

Usage

```
copy_assemble(filename, copy_number, verbose = 1)
```

Arguments

`filename`	A fasta alignment of a small number of overlapping DNA sequences (results from "copy_separate") covering the entire length of the target gene. Check the alignment carefully before proceeding.
`copy_number`	An integer (e.g. 2,3, or 4) giving the anticipated number of gene copies. Must be the same value as used for "copy_separate".
`verbose`	Turn on (verbose=1; default) or turn off (verbose=0) the output.

Value

A fasta alignment of the anticipated number of full-length gene copies.

Examples

```
## Not run:
copy_assemble("inst/extdata/combined_con.fasta",2,1)

## End(Not run)
```

copy_detect *copy_detect*

Description

Separates two or more gene copies from a single subset of short reads.

Usage

```
copy_detect(filename, copy_number, verbose = 1)
```

Arguments

filename	A fasta file contains short reads from a single subset generated by "subset_downsize".
copy_number	An integer (e.g. 2,3, or 4) giving the anticipated number of gene copies in the input file.
verbose	Turn on (verbose=1; default) or turn off (verbose=0) the output.

Value

A fasta alignment of the anticipated number of gene copies.

Examples

```
## Not run:
copy_detect("inst/extdata/toysubset.fasta",2,1)

## End(Not run)
```

copy_separate *copy_separate*

Description

Separates two or more gene copies from short-read Next-Generation Sequencing data into a small number of overlapping DNA sequences.

Usage

```
copy_separate(
  filename,
  copy_number,
  read_length,
  overlap = 225,
  rare_read = 10,
  verbose = 1
)
```

Arguments

filename	A fasta file contains thousands of short reads that have been mapped to a reference. The reference and reads that are not directly mapped to the reference need to be removed after mapping.
copy_number	An integer (e.g. 2,3, or 4) giving the anticipated number of gene copies in the input file.
read_length	An integer (e.g. 250, or 300) giving the read length of your Next-generation Sequencing data. This method is designed for read length >=250bp.
overlap	An integer describing number of base pairs of overlap between adjacent subsets. More overlap means more subsets. Default 225.
rare_read	A positive integer. During clustering analyses, clusters with less than this number of reads will be ignored. Default 10.
verbose	Turn on (verbose=1; default) or turn off (verbose=0) the output.

Value

A fasta alignment of a small number of overlapping DNA sequences covering the entire length of the target gene. Gene copies can be assembled by reordering the alignment manually or use the function "copy_assemble".

Examples

```
## Not run:
copy_separate("inst/extdata/toydata.fasta",2,300,225,10,1)

## End(Not run)
```

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copy_validate *copy_validate*

Description

A tool to help identify incorrectly assembled chimeric sequences.

Usage

```
copy_validate(filename, copy_number, read_length, verbose = 1)
```

Arguments

filename	A DNA alignment in fasta format that contains sequences of two or more gene copies (e.g. results from "copy_assemble").
copy_number	An integer (e.g. 2,3, or 4) giving the number of gene copies in the input file.
read_length	An integer (e.g. 250, or 300) giving the read length of your Next-generation Sequencing data.
verbose	Turn on (verbose=1; default) or turn off (verbose=0) the output.

Value

A histogram in pdf format showing the relationships between the physical distance between neighboring variable sites and read length.

Examples

```
## Not run:
copy_validate("inst/extdata/Final_two_copies.fasta",2,300,1)

## End(Not run)
```

---

sep_assem *sep_assem*

Description

Separates two or more gene copies from short-read Next-Generation Sequencing data into a small number of overlapping DNA sequences and assemble them into their respective gene copies.

Usage

```
sep_assem(
  copy_number,
  read_length,
  overlap = 225,
  rare_read = 10,
  core_number = 1,
  verbose = 1
)
```

Arguments

copy_number	An integer (e.g. 2,3, or 4) giving the anticipated number of gene copies in the input file.
read_length	An integer (e.g. 250, or 300) giving the read length of your Next-generation Sequencing data. This method is designed for read length >=250bp.
overlap	An integer describing number of base pairs of overlap between adjacent subsets. More overlap means more subsets. Default 225.
rare_read	A positive integer. During clustering analyses, clusters with less than this number of reads will be ignored. Default 10.
core_number	An integer describing number of cores to use.
verbose	Turn on (verbose=1; default) or turn off (verbose=0) the output.

Value

A fasta alignment of the anticipated number of full-length gene copies.

Examples

```
## Not run:
sep_assem(2,300,225,10,1,1) # all input fasta files in the working directory will be processed

## End(Not run)
```

---

subset_downsize *subset_downsize*

Description

Subdivides the imported read alignment into subsets and then downsizes each subset by deleting those sequences that have too many gaps or missing data.

Usage

```
subset_downsize(filename, read_length, overlap, verbose = 1)
```

Arguments

filename	A fasta file contains thousands of short reads that have been mapped to a reference. The reference and reads that are not directly mapped to the reference need to be removed after mapping.
read_length	An integer (e.g. 250, or 300) giving the read length of your Next-generation Sequencing data. This method is designed for read length >=250bp.
overlap	An integer describing number of base pairs of overlap between adjacent subsets. More overlap means more subsets.
verbose	Turn on (verbose=1; default) or turn off (verbose=0) the output.

Value

A number of overlapping subsets (before and after downsizing) of the input alignment.

Examples

```
## Not run:
subset_downsize("inst/extdata/toydata.fasta",300,225,1)

## End(Not run)
```

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