

Package ‘metabinR’

October 6, 2025

Type Package

Title Abundance and Compositional Based Binning of Metagenomes

Version 1.10.0

biocViews Classification, Clustering, Microbiome, Sequencing, Software

Description Provide functions for performing abundance and compositional based binning on metagenomic samples, directly from FASTA or FASTQ files.
Functions are implemented in Java and called via rJava.
Parallel implementation that operates directly on input FASTA/FASTQ files for fast execution.

License GPL-3

Encoding UTF-8

Language en-US

LazyData false

Depends R (>= 4.3)

Imports methods, rJava

SystemRequirements Java (>= 8)

RoxygenNote 7.3.1

URL <https://github.com/gkanogiannis/metabinR>

BugReports <https://github.com/gkanogiannis/metabinR/issues>

Suggests BiocStyle, cvms, data.table, dplyr, ggplot2, gridExtra,
knitr, R.utils, rmarkdown, sabre, spelling, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

git_url <https://git.bioconductor.org/packages/metabinR>

git_branch RELEASE_3_21

git_last_commit f3a7794

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-10-05

Author Anestis Gkanogiannis [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-6441-0688>>)

Maintainer Anestis Gkanogiannis <anestis@gkanogiannis.com>

Contents

metabinR-package	2
abundance_based_binning	3
composition_based_binning	4
hierarchical_binning	5
Index	7

metabinR-package	<i>metabinR: Abundance and Compositional Based Binning of Metagenomes</i>
------------------	---

Description

Provide functions for performing abundance and compositional based binning on metagenomic samples, directly from FASTA or FASTQ files. Functions are implemented in Java and called via rJava. Parallel implementation that operates directly on input FASTA/FASTQ files for fast execution.

Author(s)

Maintainer: Anestis Gkanogiannis <anestis@gkanogiannis.com> (ORCID)

See Also

- Useful links:
- <https://github.com/gkanogiannis/metabinR>
 - Report bugs at <https://github.com/gkanogiannis/metabinR/issues>

abundance_based_binning

Abundance based binning on metagenomic samples

Description

This function performs abundance based binning on metagenomic samples, directly from FASTA or FASTQ files, by long kmer analysis ($k > 8$). See [doi:10.1186/s1285901611863](https://doi.org/10.1186/s1285901611863) for more details.

Usage

```
abundance_based_binning(
  ...,
  eMin = 1,
  eMax = 0,
  kMerSizeAB = 10,
  numOfClustersAB = 3,
  outputAB = "AB.cluster",
  keepQuality = FALSE,
  dryRun = FALSE,
  gzip = FALSE,
  numThreads = 1
)
```

Arguments

...	Input fasta/fastq files locations (uncompressed or gzip compressed).
eMin	Exclude kmers of less or equal count.
eMax	Exclude kmers of more or equal count.
kMerSizeAB	kmer length for Abundance based Binning.
numOfClustersAB	Number of Clusters for Abundance based Binning.
outputAB	Output Abundance based Binning Clusters files location and prefix.
keepQuality	Keep fastq qualities on the output files. (will produce .fastq)
dryRun	Don't write any output files.
gzip	Gzip output files.
numThreads	Number of threads to use.

Value

A [data.frame](#) of the binning assignments. Return value contains numOfClustersAB + 2 columns.

- read_id : read identifier from fasta header
- AB : read was assigned to this AB cluster index
- AB.n : read to cluster AB.n distance

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

<https://github.com/gkanogiannis/metabinR>

Examples

```
abundance_based_binning(
  system.file("extdata", "reads.metagenome.fasta.gz", package = "metabinR"),
  dryRun = TRUE, kMerSizeAB = 8
)
```

composition_based_binning

Composition based binning on metagenomic samples

Description

This function performs composition based binning on metagenomic samples, directly from FASTA or FASTQ files, by short kmer analysis ($k < 8$). See [doi:10.1186/s1285901611863](https://doi.org/10.1186/s1285901611863) for more details.

Usage

```
composition_based_binning(
  ...,
  kMerSizeCB = 4,
  numOfClustersCB = 5,
  outputCB = "CB.cluster",
  keepQuality = FALSE,
  dryRun = FALSE,
  gzip = FALSE,
  numOfThreads = 1
)
```

Arguments

...	Input fasta/fastq files locations (uncompressed or gzip compressed).
kMerSizeCB	kmer length for Composition based Binning.
numOfClustersCB	Number of Clusters for Composition based Binning.
outputCB	Output Composition based Binning Clusters files location and prefix.
keepQuality	Keep fastq qualities on the output files. (will produce .fastq)
dryRun	Don't write any output files.
gzip	Gzip output files.
numOfThreads	Number of threads to use.

Value

A `data.frame` of the binning assignments. Return value contains `numOfClustersCB + 2` columns.

- `read_id` : read identifier from fasta header
- `CB` : read was assigned to this CB cluster index
- `CB.n` : read to cluster `CB.n` distance

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

<https://github.com/gkanogiannis/metabinR>

Examples

```
composition_based_binning(  
  system.file("extdata", "reads.metagenome.fasta.gz", package = "metabinR"),  
  dryRun = TRUE, kMerSizeCB = 2  
)
```

`hierarchical_binning` *Hierarchical (ABxCB) binning on metagenomic samples*

Description

This function performs hierarchical binning on metagenomic samples, directly from FASTA or FASTQ files. First it analyzes sequences by long kmer analysis ($k > 8$), as in [abundance_based_binning](#). Then for each AB bin, it guesses the number of composition bins in it and performs composition based binning by short kmer analysis ($k < 8$), as in [composition_based_binning](#). See [doi:10.1186/s1285901611863](https://doi.org/10.1186/s1285901611863) for more details.

Usage

```
hierarchical_binning(  
  ...,  
  eMin = 1,  
  eMax = 0,  
  kMerSizeAB = 10,  
  kMerSizeCB = 4,  
  genomeSize = 3e+06,  
  numOfClustersAB = 3,  
  outputC = "ABxCB.cluster",  
  keepQuality = FALSE,  
  dryRun = FALSE,  
  gzip = FALSE,  
  numOfThreads = 1  
)
```

Arguments

<code>...</code>	Input fasta/fastq files locations (uncompressed or gzip compressed).
<code>eMin</code>	Exclude kmers of less or equal count.
<code>eMax</code>	Exclude kmers of more or equal count.
<code>kMerSizeAB</code>	kmer length for Abundance based Binning.
<code>kMerSizeCB</code>	kmer length for Composition based Binning.
<code>genomeSize</code>	Average genome size of taxa in the metagenome data.
<code>numOfClustersAB</code>	Number of Clusters for Abundance based Binning.
<code>outputC</code>	Output Hierarchical Binning (ABxCB) Clusters files location and prefix.
<code>keepQuality</code>	Keep fastq qualities on the output files. (will produce .fastq)
<code>dryRun</code>	Don't write any output files.
<code>gzip</code>	Gzip output files.
<code>numOfThreads</code>	Number of threads to use.

Value

A [data.frame](#) of the binning assignments. Return value contains `numOfClustersAB` + 2 columns.

- `read_id` : read identifier from fasta header
- `ABxCB` : read was assigned to this ABxCB cluster index
- `ABxCB.n` : read to cluster ABxCB.n distance

Author(s)

Anestis Gkanogiannis, <anestis@gkanogiannis.com>

References

<https://github.com/gkanogiannis/metabinR>

Examples

```
hierarchical_binning(
  system.file("extdata", "reads.metagenome.fasta.gz", package = "metabinR"),
  dryRun = TRUE, kMerSizeAB = 4, kMerSizeCB = 2
)
```

Index

* **internal**

metabinR-package, [2](#)

abundance_based_binning, [3](#), [5](#)

composition_based_binning, [4](#), [5](#)

data.frame, [3](#), [5](#), [6](#)

hierarchical_binning, [5](#)

metabinR (metabinR-package), [2](#)

metabinR-package, [2](#)