

Package: TrIdent (via r-universe)

October 1, 2026

Type Package

BiocType Software

Title TrIdent - Transduction Identification

Version 1.5.3

Description The `TrIdent` R package automates the analysis of transductomics data by detecting, classifying, and characterizing read coverage patterns associated with potential transduction events. Transductomics is a DNA sequencing-based method for the detection and characterization of transduction events in pure cultures and complex communities. Transductomics relies on mapping sequencing reads from a viral-like particle (VLP)-fraction of a sample to contigs assembled from the metagenome (whole-community) of the same sample. Reads from bacterial DNA carried by VLPs will map back to the bacterial contigs of origin creating read coverage patterns indicative of ongoing transduction.

License GPL-2

Encoding UTF-8

LazyData false

Imports graphics, utils, stats, dplyr, ggplot2, patchwork, stringr, tidy, roll, nloptr, S4Vectors

biocViews Coverage, Metagenomics, PatternLogic, Classification, Sequencing

URL <https://github.com/jlmaier12/TrIdent>,
<https://jlmaier12.github.io/TrIdent/>

BugReports <https://github.com/jlmaier12/TrIdent/issues>

Suggests BiocStyle, knitr, rmarkdown, kableExtra

VignetteBuilder knitr

Depends R (>= 4.2.0)

Config/roxygen2/version 8.0.0

Config/pak/sysreqs cmake make libicu-dev
Repository https://bioc.r-universe.dev
Date/Publication 2026-09-01 03:19:17 UTC
RemoteUrl https://github.com/bioc/TrIdent
RemoteRef HEAD
RemoteSha a4ee81929e1b8ca622131e6b9b907e4799f62454

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geneSearch	<i>Search for gene annotations on positively classified contigs</i>
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Description

Search contigs classified with TrIdent for gene-annotations that match a provided key-word(s). Outputs read coverage plots for contigs with matching annotations.

Usage

```
geneSearch(  
  TrIdentResults,  
  VLPpiledup,  
  gff,  
  searchCol,  
  keyWords,  
  inPatMat = FALSE,  
  bpRange = 0,  
  saveFilesTo,  
  verbose = TRUE  
)
```

Arguments

- TrIdentResults** The output from 'TrIdent()'.
- VLPpiledup** A .txt file containing mapped sequencing read coverages averaged over 100 bp windows/bins.
- gff** A .gff file imported using Bioc.gff::readGFF that is associated with the whole-community contigs

searchCol	The exact column name (in quotes) in the gff file that you'd like to search for specific 'keyWords'. Commonly annotation, product, gene, or acc columns, for example, however the specific name may change based on annotation tool used. For example: "pfam_desc".
keyWords	The keyWord(s) to search for. Case independent. Searches will return the string that contains the matching keyWord. KeyWord(s) must be in quotes, comma-separated, and surrounded by c() i.e(c("antibiotic", "resistance", "drug"))
inPatMat	TRUE or FALSE. If TRUE, only search for gene-annotations in the pattern-match region. Default is FALSE (i.e search the entire contig for the gene annotation key-words)
bpRange	If 'inPatMat' = TRUE, the user may specify the region (in base pairs) that should be searched to the left and right of the pattern-match region. Default is 0.
saveFilesTo	Optional, Provide a path to the directory you wish to save output to. A folder will be made within the provided directory to store results.
verbose	TRUE or FALSE. Print progress messages to console. Default is TRUE.

Value

list of ggplot objects

Examples

```
data("VLPFractionSamplePileup")
data("TrIdentSampleOutput")
data("gffSample")

patternMatches <- geneSearch(
  TrIdentResults = TrIdentSampleOutput,
  VLPpileup = VLPFractionSamplePileup,
  gff = gffSample,
  searchCol="pfam_desc",
  keyWords=c("toxin", "drug", "resistance", "phage")
)
```

plotTrIdentResults	<i>Plot read coverage graphs of contigs classified as Prophage-like, Sloping, or HighCovNoPattern</i>
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Description

Plot the read coverages of a contig and its associated pattern-match for Prophage-like, Sloping and HighCovNoPattern classifications. Returns a list of ggplot objects.

Usage

```
plotTrIdentResults(
  VLPpfileup,
  WCPfileup,
  TrIdentResults,
  onlyPlot,
  logScale = FALSE,
  allPlots = FALSE,
  saveFilesTo
)
```

Arguments

VLPpfileup	VLP-fraction pileup file generated by mapping sequencing reads from a sample's ultra-purified VLP-fraction mapped to the sample's whole-community metagenome assembly. The pileup file MUST have the following format: * V1: Contig accession * V2: Mapped read coverage values averaged over 100 bp windows * V3: Starting position (bp) of each 100 bp window. Restarts from 0 at the start of each new contig. * V4: Starting position (bp) of each 100 bp window. Does NOT restart at the start of each new contig.
WCPfileup	A whole-community pileup file generated by mapping sequencing reads from a sample's whole-community mapped to the sample's whole-community metagenome assembly. The pileup file MUST have the following format: * V1: Contig accession * V2: Mapped read coverage values averaged over 100 bp windows * V3: Starting position (bp) of each 100 bp window. Restarts from 0 at the start of each new contig. * V4: Starting position (bp) of each 100 bp window. Does NOT restart at the start of each new contig.
TrIdentResults	Output from 'TrIdentClassifier()'.
onlyPlot	Optional, use to 'only plot' the contigs classified as either "Prophage-like", "Sloping", or "HighCovNoPattern".
logScale	TRUE or FALSE, display VLP-fraction read coverage in log10 scale. Default is FALSE.
allPlots	TRUE or FALSE. Display read coverage patterns for all contigs greater than the length cutoff (default 30 kbp). Default is FALSE. *Warning* This may produce a lot of plots and a very large list object!
saveFilesTo	Optional, Provide a path to the directory you wish to save output to. A folder will be made within the provided directory to store results.

Value

Large list containing ggplot objects

Examples

```
data("VLPFractionSamplePileup")
data("WholeCommunitySamplePileup")
data("TrIdentSampleOutput")
```

```

patternMatches <- plotTrIdentResults(
  VLPpileup = VLPFractionSamplePileup,
  WCPileup = WholeCommunitySamplePileup,
  TrIdentResults = TrIdentSampleOutput
)

```

specializedTransductionID

Identify potential specialized transduction events on contigs classified as Prophage-like

Description

Search contigs classified as Prophage-like for dense read coverage outside of the pattern-match borders that may indicate specialized transduction. Returns a list with the first object containing a summary table and the second object containing a list of plots of with associated specialized transduction search results. If the plot is green, it has been identified as having potential specialized transduction.

Usage

```

specializedTransductionID(
  VLPpileup,
  TrIdentResults,
  specificContig,
  noReadCov = 500,
  specTransLength = 2000,
  logScale = FALSE,
  verbose = TRUE,
  SaveFilesTo
)

```

Arguments

VLPpileup	VLP-fraction pileup file generated by mapping sequencing reads from a sample's ultra-purified VLP-fraction mapped to the sample's whole-community metagenome assembly. The pileup file MUST have the following format: * V1: Contig accession * V2: Mapped read coverage values averaged over 100 bp windows * V3: Starting position (bp) of each 100 bp window. Restarts from 0 at the start of each new contig. * V4: Starting position (bp) of each 100 bp window. Does NOT restart at the start of each new contig.
TrIdentResults	Output from 'TrIdentClassifier()'
specificContig	Optional, Search a specific contig classified as Prophage-like ("NODE_1").
noReadCov	Number of basepairs of zero read coverage encountered before specialized transduction searching stops. Default is 500. Must be at least 100.

specTransLength	Number of basepairs of non-zero read coverage needed for specialized transduction to be considered. Default is 2000. Must be at least 100.
logScale	TRUE or FALSE, display VLP-fraction read coverage in log10 scale. Default is FALSE.
verbose	TRUE or FALSE. Print progress messages to console. Default is TRUE.
SaveFilesTo	Provide a path to the directory you wish to save output to. 'specializedTransductionID()' will make a folder within the provided directory to store results.

Value

Large list containing two objects

Examples

```
data("VLPFractionSamplePileup")
data("TrIdentSampleOutput")

specTransduction <- specializedTransductionID(
  VLPpileup = VLPFractionSamplePileup,
  TrIdentResults = TrIdentSampleOutput
)

specTransductionNODE62 <- specializedTransductionID(
  VLPpileup = VLPFractionSamplePileup,
  TrIdentResults = TrIdentSampleOutput,
  specificContig = "NODE_62"
)
```

TrIdentClassifier	<i>Classify contigs as Prophage-like, Sloping, HighCovNoPattern, and NoPattern</i>
-------------------	--

Description

Performs all the pattern-matching and summarizes the results into a list. The first item in the list is a table consisting of the summary information of all the contigs that passed through pattern-matching (i.e. were not filtered out). The second item in the list is a table consisting of the summary information of all contigs that were classified via pattern-matching. The third item in the list contains the pattern-match information associated with each contig in the previous table. The fourth object in the list is a table containing the contigs that were filtered out prior to pattern-matching. The fifth item is the windowSize used for the search.

Usage

```

TrIdentClassifier(
  VLPpileup,
  WCPileup,
  windowSize = 1000,
  minBlockSize = 10000,
  maxBlockSize = Inf,
  minContigLength = 30000,
  minSlope = 0.001,
  minSlopeSize = 20000,
  minHCNPRatio = 2,
  VLPReads,
  WCReads,
  verbose = TRUE,
  searchMethod = "grid",
  DirectMaxEval = 100,
  globalLocal = "local",
  SaveFilesTo
)

```

Arguments

VLPpileup	VLP-fraction pileup file generated by mapping sequencing reads from a sample's ultra-purified VLP-fraction mapped to the sample's whole-community metagenome assembly. The pileup file MUST have the following format: * V1: Contig accession * V2: Mapped read coverage values averaged over 100 bp windows * V3: Starting position (bp) of each 100 bp window. Restarts from 0 at the start of each new contig. * V4: Starting position (bp) of each 100 bp window. Does NOT restart at the start of each new contig.
WCPileup	A whole-community pileup file generated by mapping sequencing reads from a sample's whole-community mapped to the sample's whole-community metagenome assembly. The pileup file MUST have the following format: * V1: Contig accession * V2: Mapped read coverage values averaged over 100 bp windows * V3: Starting position (bp) of each 100 bp window. Restarts from 0 at the start of each new contig. * V4: Starting position (bp) of each 100 bp window. Does NOT restart at the start of each new contig.
windowSize	The number of basepairs to average read coverage values over. Options are 100, 200, 500, 1000 ONLY. Default is 1000.
minBlockSize	The minimum size (in bp) of the Prophage-like block pattern. Default is 10000. Must be at least 1000.
maxBlockSize	The maximum size (in bp) of the Prophage-like block pattern. Default is NA (no maximum).
minContigLength	The minimum contig size (in bp) to perform pattern-matching on. Must be at least 25000. Default is 30000.
minSlope	The minimum slope value to test for sloping patterns. Default is 0.001 (i.e minimum change of 10x read coverage over 100,000 bp).

<code>minSlopeSize</code>	The minimum width of sloping patterns. Default and absolute minimum is 20,000 bp.
<code>minHCNPRatio</code>	The minimum VLP:WC ratio value used for HighCovNoPattern classifications. Default is 2. (i.e the median VLP-fraction coverage must be at least 2x the median WC read coverage to be classified as HighCovNoPattern).
<code>VLPReads</code>	Optional, the number of VLP-fraction reads used for mapping and creation of pileup.
<code>WCReads</code>	Optional, the number of WC reads used for mapping and creation of pileup.
<code>verbose</code>	TRUE or FALSE. Print progress messages to console. Default is TRUE.
<code>searchMethod</code>	Search method to use. Either "grid" for the original grid search or "direct" for DIRECT global optimization.
<code>DirectMaxEval</code>	Maximum number of DIRECT evaluations to make. Default is 100. Default is 100.
<code>globalLocal</code>	Use global or local DIRECT search. Local search makes the DIRECT algorithm more efficient for contigs without multiple potential read coverage patterns. Default is local.
<code>SaveFilesTo</code>	Optional, Provide a path to the directory you wish to save output to. A folder will be made within the provided directory to store results.

Value

Large list containing 5 objects

Examples

```
data("VLPFractionSamplePileup")
data("WholeCommunitySamplePileup")

TrIdent_results <- TrIdentClassifier(
  VLPPileup = VLPFractionSamplePileup,
  WCPileup = WholeCommunitySamplePileup
)
```

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