Package: TrIdent (via r-universe)

June 13, 2026

Type Package

BiocType Software

Title TrIdent - Transduction Identification

Version 1.4.0

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, tidyr, roll

biocViews Coverage, Metagenomics, PatternLogic, Classification, Sequencing

RoxygenNote 7.3.3

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/testthat/edition 3

Config/pak/sysreqs make libicu-dev

Repository https://bioc-release.r-universe.dev

Date/Publication 2026-04-28 13:04:09 UTC

RemoteUrl https://github.com/bioc/TrIdent

RemoteRef RELEASE_3_23

RemoteSha 57933f33587a2284aff832fd5145b8bbd2ce27de

Contents

`plotTrIdentResults` *Plot read coverage graphs of contigs classified as Prophage-like, Sloping, or HighCovNoPattern*

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(
  VLPpileup,
  WCpileup,
  TrIdentResults,
  onlyPlot,
  logScale = FALSE,
  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.
`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.
`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 specialzied 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` *Classify contigs as Prophage-like, Sloping, HighCovNoPattern, and NoPattern*

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,
  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).
`minSlopeSize`	The minimum width of sloping patterns.Default and absolute minimum is 20,000 bp.
`minHCNPRatio`	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).
`VLPReads`	Optional, the number of VLP-fraction reads used for mapping and creation of pileup.
`WCReads`	Optional, the number of WC reads used for mapping and creation of pileup.
`verbose`	TRUE or FALSE. Print progress messages to console. Default is TRUE.
`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 5 objects

Examples

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

TrIdent_results <- TrIdentClassifier(
  VLPpileup = VLPFractionSamplePileup,
  WCpileup = WholeCommunitySamplePileup
)
```

Index