

Package ‘viromeBrowser’

April 7, 2021

Type Package

Title Virome Sequencing Analysis Result Browser

Version 1.1.0

Description Experiments in which highly complex virome sequencing data is generated are difficult to visualize and unpack for a person without programming experience. After processing of the raw sequencing data by a next generation sequencing (NGS) processing pipeline the usual output consists of contiguous sequences (contigs) in fasta format and an annotation file linking the contigs to a reference sequence. The virome analysis browser app imports an annotation file, a corresponding fasta file containing the annotated contigs and a alignment file in BAM format of the sequence reads aligned to the contigs. It facilitates browsing of annotations in multiple files and allows users to select and export specific annotated sequences from the associated fasta files. Various annotation quality thresholds can be set to filter contigs from the annotation files. Further inspection of selected contigs can be done in the form of automatic open reading frame (ORF) detection. Separate contigs and/or separate ORFs can be downloaded in nucleotide or amino acid format for further analysis.

Depends R (>= 3.4)

Imports shiny (>= 1.3.2), shinyWidgets, ggplot2, shinydashboard, DT, rbokeh, Biostrings, Rsamtools, data.table, markdown, stringr, shinycssloaders

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Encoding UTF-8

RoxygenNote 7.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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viromeBrowser	<i>Launch the Virome Browser</i>
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Description

An application for viewing virome annotation files

The viromeBrowser package provides a single function to launch the virome browser shiny app

Usage

```
viromeBrowser(
  host = getOption("shiny.host", "127.0.0.1"),
  port = getOption("shiny.port", 3838)
)
```

Arguments

host	The host ip address, 127.0.0.1 or "localhost" by default.
port	The host port, 3838 by default.

viromeBrowser functions

```
viromeBrowser()
```

Examples

```
viromeBrowser()
```

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