DisCVR: Rapid Viral Diagnostic Tool

Introduction

DisCVR is a viral detection tool which allows the identification of known human viruses in clinical samples from high-throughput sequencing (HTS) data. It uses the *k*-mers approach in which the sample reads are decomposed into *k-mer*s and then matched against a virus *k*-mers database. The built-in database is a list consists of all *k*-mers (*k*=22) that are not low-complexity and only found in the viral genomes but not in the human genome. Each *k*-mer is assigned the taxonomic label of all viral genomes that contain that *k*-mer in the NCBI taxonomy tree. These assignments are made at the species and strains taxonomic level.

DisCVR has a user-friendly Graphical User Interface (GUI) which runs the analysis on the sample and shows the results interactively. It enables the visualisation of the coverage of the virus genomes found in the sample in order to validate the significance of the results. In addition, DisCVR is a generic tool which can be used with other non-human viruses by facilitating the build and use of customised *k*-mers database.

DisCVR is designed to run on machines with low processing capacity and small memory.

System Requirements

- Disk Space: DisCVR.jar requires ~700MB space for installation with the built-in databases. It is recommended to have space for 2x sample size when using DisCVR for classification as the process involves writing temporary files to disk. When building a customised database, the amount of space depends on the size of the viral sequences and the *k* size. For example, extracting *k*-mers of size 32 from the human genomes generates a file that is 80GB in size. If the viral data sequences are 3GB in size, then the minimum disk space needed to build a customised database is 200GB.
- Memory: DisCVR runs efficiently on a machine with 4GB RAM, which is the current standard for PCs. It is much faster on machines with higher RAM such as 8GB RAM. However, the amount of RAM depends on the number of the sequences used and the size of the *k*-mer. The larger the dataset and the *k*-mer, the larger the amount of RAM needed. Therefore, in the case of "out of memory" errors, the Java heap space should be increased.

Installation

- Operating System: DisCVR runs on both Windows and Linux platforms. To use DisCVR, the users need first to download the appropriate folder for their operating system.
- Java: Java (1.8 or above) must be installed and the full path to the jre\bin folder should be included in the system variables. Java can be downloaded from: http://www.oracle.com/technetwork/java/javase/downloads/jre8-downloads-2133155.html
- DisCVR.jar: After downloading the DisCVR zipped folder, it is recommended to use a tool, such as 7-zip, to unzip the Windows OS version and extract all files to a local directory. For Linux and Mac version, open a command prompt and move to the location of the zipped folder. Type the following commands to unzip the folder:

  - tar -xzvf DisCVR_Linux.tar.gz

  This creates a folder, called DisCVR. The contents of DisCVR consists of one jar: *DisCVR.jar* and a *lib* folder which are used to run the classification. The script file: *downloadDataAndRefSeq.sh* and the folders: *bin*, *customisedDB*, and *TestData* which are needed to build a customised database.

  IMPORTANT: The full path to DisCVR directory must NOT contain space nor the dot '.' to avoid conflict with the files naming during the classification process.

- Dependencies: DisCVR uses external libraries such as KAnalyze, for *k*-mers counting, and JFreechart packages, for graphs plotting. It makes use of Tanoti, a Blast-based tool for reference assembly. These are 10 files in total and they are in the *lib* folder. It is important not to alter the *lib* folder or its contents and to ensure that it is in the same path as the jar file.
- If you want to build a customised database, the following NCBI tools and files must be downloaded and installed:
  - The NCBI *eutilities* tools are used to download data. The tools can be found at: (`ftp://ftp.ncbi.nlm.nih.gov/entrez/entrezdirect/`). The full path to the *edirect* folder should be added to the system variables
  - The NCBI *taxdump* files are used for taxonomy information retrieval when building a customised database. The file can be downloaded from (`ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/`). The file taxdump.tar.gz should be downloaded and unzipped. The two files: *names.dmp* and *nodes.dmp* MUST be copied to the customised database folder: *customisedDB* which is in the same path as *DisCVR.jar*.

To test if the tools are installed properly, open a command prompt and type the following:

- To know what Java version is installed: `java -version`
  - ➢ This should state "java version "1.8.0_<some number>"
- To see if Java is added to the path: `java`
  - ➢ If the jre\bin is not added to the path, you will see the following message: "java is not recognized as an internal or external command, operable program or batch file".
- To see if *eutilities* tools is added to the path: `esearch`
  - ➢ This should state "Must supply -db database on command line"

DisCVR Built-in Databases:

DisCVR tool has three virus *k*-mers (*k*=22) databases which are built in DisCVR.jar:

1. Human Hemorrhagic virus dataset (hemorrhagic dataset)
2. Human Respiratory virus dataset (respiratory dataset)
3. Human Pathogenic viruses dataset (pathogenic dataset)

The hemorrhagic and respiratory datasets consist of a list of selected circulating viruses. The pathogenic datatset consist of a list of all human pathogenic viruses identified as biological agents from by the Health and Safety Executive (HSE) in the UK available at: http://www.hse.gov.uk/pubns/misc208.pdf

Both the hemorrhagic and respiratory datasets overlap with the HSE database but are smaller in size and therefore are faster to use in classification.

Moreover, each dataset has a list of viral reference genomes that is associated with the viruses in the database. The reference genomes are used in the validation stage of DisCVR.

Information about the viruses in the databases can be obtained from the **Database** icon on the menu bar from DisCVR GUI. The information includes the virus rank on the taxonomy tree, the number of sequences used in the database build to represent it, and the accession number of its reference genome. Segmented viruses have their reference genome accession number listed in decreasing order of the segment size. The accession numbers of the reference genomes are linked to their webpages on the NCBI which can be viewed by clicking on the reference genome accession.

DisCVR Classification

The DisCVR GUI can be used to carry out a single sample classification. To launch the DisCVR GUI, either double click on *DisCVR.jar*, or open a command prompt and type the following commands:

```
cd full/path/to/DisCVR folder

java –jar full/path/to/DisCVR.jar
```

Command 1: to move to DisCVR directory and launch the GUI

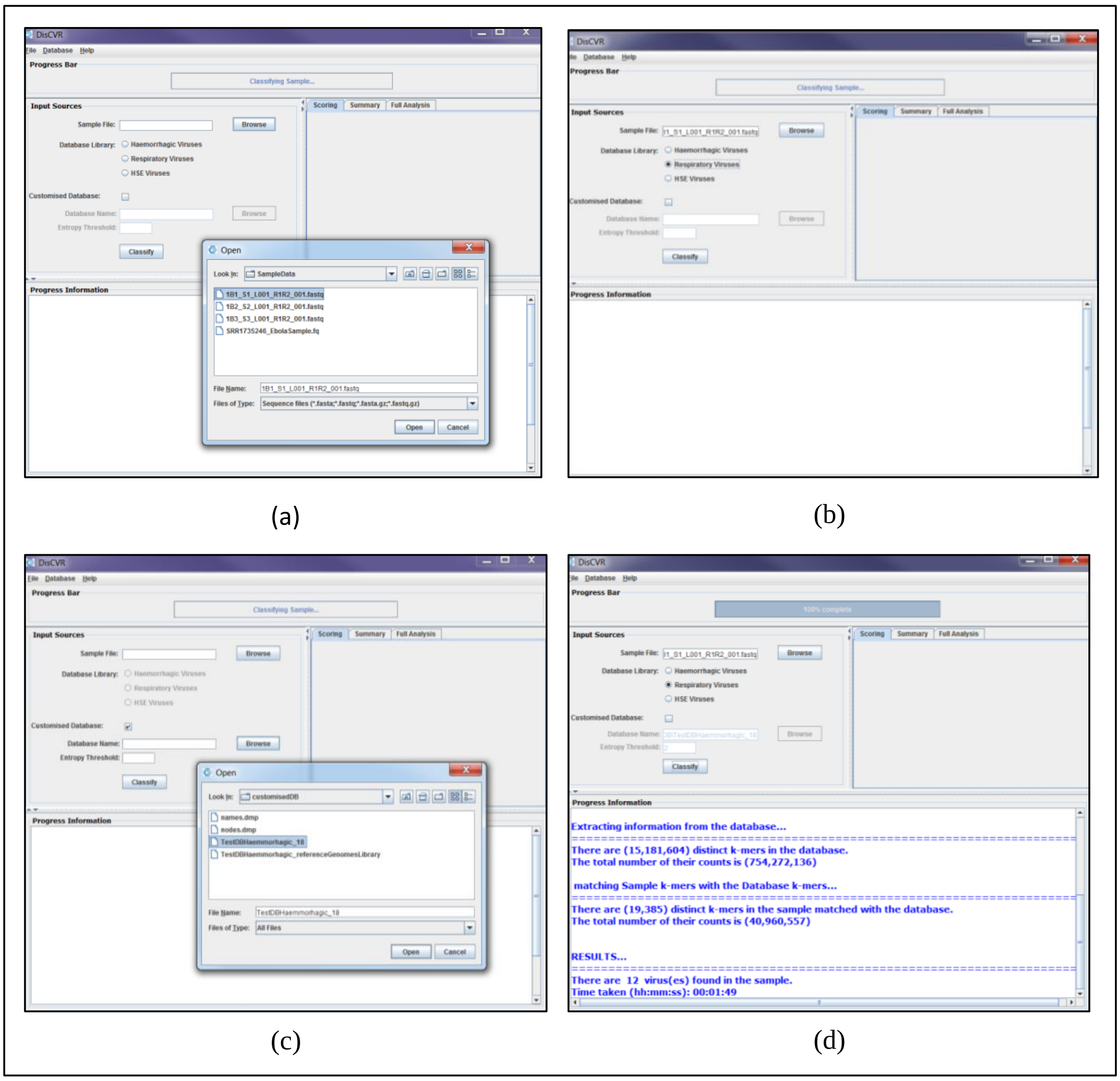
Once DisCVR is launched, there are 4 panels in the graphical interface:

1. Progress Bar: shows the progression of the classification process.
2. Input Sources: allows the user to choose the sample file and a *k*-mers database for classification.
3. Classification Results: shows the classification output in three sub-panels
4. Progress Information: updates the user about classification output.

To start a classification process, the user needs to first select the sample file they wish to investigate. Currently, DisCVR supports .fasta, .fa, .fastq, and .fq formats. It allows for the selection of one file hence, for paired-end files, it is recommended to concatenate both files. The second step is to choose the database for the classification. The default setting is to select one of the three built-in databases. This sets the *k*-mer size to 22 and removes all sample *k*-mers with entropy ≤ 2.5. On the other hand, if the user chooses to use a customised database for the classification, then the box next to the **Customised Database** label must be checked. The fields for this selection are then activated for the user to upload the customised database file which MUST be in the *customisedDB* folder that is in the same path as *DisCVR.jar*. The *k*-mer size for the classification is extracted from the database name and the threshold to filter out low-entropy *k*-mers from the sample should be entered in its corresponding field. The entropy threshold should be the same value used in the build of the customised database which is recommended to be in the range of [0, 3.0]. If the users choose not to specify a value for the entropy threshold then the default value, 2.5, is displayed in the field and used in the classification.

Once, the database library is selected, the user clicks the classify button to start the classification process.

There are 4 stages in the classification process and the progress bar is updated after the completion of each stage. Messages in relation to the output of each stage are displayed in the progress information panel. This includes the number of reads in the sample, the number of distinct *k*-mers and their total counts in the database and the sample file, the number of sample *k*-mers after removing single copies and low entropy *k*-mers, and the number of classified *k*-mers and their total counts. The final message shows the number of viruses with classified *k*-mers found in the sample and the time taken to finish the classification process. Figure 1 shows screenshots of the sample classification process using the DisCVR GUI.



```
Extracting information from the database...
====================================================================
There are (15,181,604) distinct k-mers in the database.
The total number of their counts is (754,272,136)

 matching Sample k-mers with the Database k-mers...
====================================================================
There are (19,385) distinct k-mers in the sample matched with the database.
The total number of their counts is (40,960,557)


RESULTS...
====================================================================
There are  12  virus(es) found in the sample.
Time taken (hh:mm:ss): 00:01:49
```

Figure 1: Screenshots of a sample classification process using DisCVR GUI. First (a) sample file is uploaded, the *k*-mers database is then selected either from (b) the DisCVR database library or (c) the user customised database. The classification results are displayed in (d).

Classification Output

At the end of the classification process, the progress information panel states the number of viruses with matched *k*-mers to the database. Detailed information about the classification results are displayed on the centre panel.

The classification results panel consists of three sub-panels: Scoring, Summary, and Full Analysis. Once the classification is completed, a bar chart showing up to three viruses is displayed on the scoring panel. These are the viruses with the most number of classified distinct *k*-mers found in the sample. The chart shows for each virus, the number of distinct *k*-mers that are specific to the virus as well as the number of shared *k*-mers with other viruses in the sample, which are referred to as non-specific *k*-mers. The Summary panel gives a list of the viruses found in the sample along with their number of specific and non-specific distinct *k*-mers. The Full Analysis panel shows a table with taxonomic and detailed information about the viruses with classified *k*-mers from the sample. The results are uploaded on the table such that the first row shows the virus with the highest number of *k*-mers found in the sample. However, the users can click on any column heading to sort out the results in the table according to the information in the column. The full analysis table consists of 8 columns:

1. Virus Name: the scientific name for the virus taking from the NCBI *names.dmp* file.
2. Taxa ID: the taxonomy identification for the virus in the NCBI taxonomy tree.
3. Virus Rank: the rank of the virus according to the NCBI *nodes.dmp* file.
4. Total counts of *k*-mers in DB: the total counts of *k*-mers that represent the virus in DisCVR's database.
5. No. of distinct Classified *k*-mers: the number of distinct *k*-mers that represent the virus in the sample after removing single copies and low entropy *k*-mers and matched with the *k*-mers database.
6. (%) of distinct Classified *k*-mers: the percentage of distinct classified *k*-mers that represent the virus in the sample.
7. Total counts of Classified *k*-mers: the total number of *k*-mers that represent the virus in the sample; some distinct *k*-mers can occur in the reads multiple times.
8. (%) of total classified *k*-mers: the percentage of the total number of *k*-mers that represent the virus in the sample's total number of *k*-mers.

The table can be saved as .csv file from the File icon on the GUI tool bar. Figure 2 shows screenshots of the classification results sub-panels.

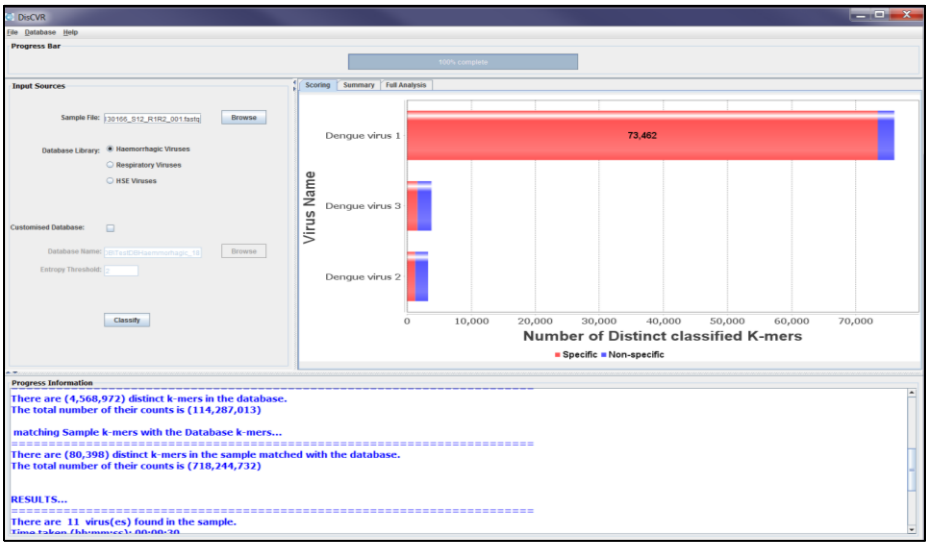
Output Validation

DisCVR allows the validation of the classification output using the reference-assembly technique to assess significance of matches. During the build of the virus *k*-mers database in DisCVR, a library that contains the complete reference genomes of some of the viruses, which are represented by *k*-mers in the database, is generated. The tool allows two validations using the extracted reference genome library:

1. *k*-mer Assembly: maps all classified *k*-mers to a reference genome.
2. Read Assembly: maps all sequence reads to a reference genome using Tanoti (a BLAST-guided aligner).

The validation takes place from the Full Analysis panel when the user right-click on the virus, which they wish to validate. A list with two items: *k*-mer Assembly and Read Assembly appears and once the user makes a selection, the reference-assembly starts. When the alignment is finished, a line graph showing the coverage and depth of the sequence data in the sample is displayed. A full coverage of the reference genome indicates strong evidence for the presence of the virus in the sample. The graphs can be saved as a PNG file for future reference. Figure 3 shows an example of the validation stage and its outputs.

(a)



Sample File: 130166_S12_R1R2_001.fastq

Database Library: [✓ Haemorrhagic Viruses] Respiratory Viruses HSE Viruses

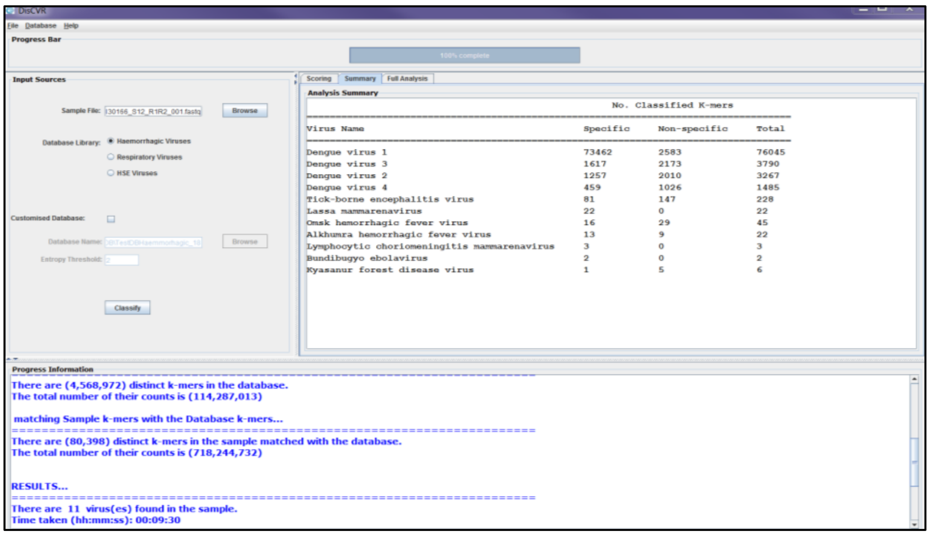
Customised Database: ☐

Database Name: DB\TestDBHaemmorhagic_18

Entropy Threshold: 2

```
==========================================================================
There are (4,568,972) distinct k-mers in the database.
The total number of their counts is (114,287,013)

 matching Sample k-mers with the Database k-mers...
==========================================================================
There are (80,398) distinct k-mers in the sample matched with the database.
The total number of their counts is (718,244,732)


RESULTS...
==========================================================================
There are  11  virus(es) found in the sample.
```

(b)



Sample File: 130166_S12_R1R2_001.fastq

Database Library: [✓ Haemorrhagic Viruses] Respiratory Viruses HSE Viruses

Customised Database: ☐

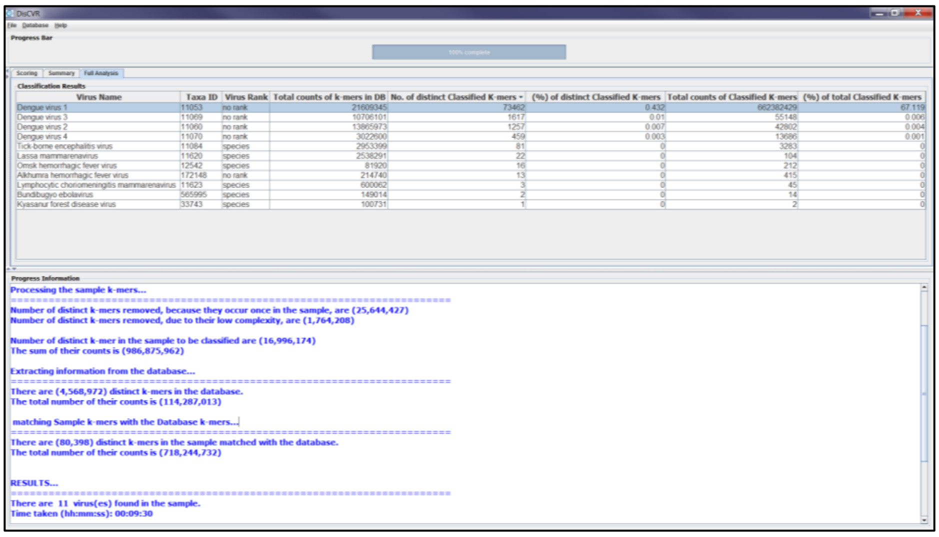
Database Name: DB\TestDBHaemmorhagic_18

Entropy Threshold: 2

```
                                                No. Classified K-mers
---------------------------------------------------------------------------------------
Virus Name                                      Specific     Non-specific     Total
---------------------------------------------------------------------------------------
Dengue virus 1                                  73462        2583             76045
Dengue virus 3                                  1617         2173             3790
Dengue virus 2                                  1257         2010             3267
Dengue virus 4                                  459          1026             1485
Tick-borne encephalitis virus                   81           147              228
Lassa mammarenavirus                            22           0                22
Omsk hemorrhagic fever virus                    16           29               45
Alkhumra hemorrhagic fever virus                13           9                22
Lymphocytic choriomeningitis mammarenavirus     3            0                3
Bundibugyo ebolavirus                           2            0                2
Kyasanur forest disease virus                   1            5                6
```

```
==========================================================================
There are (4,568,972) distinct k-mers in the database.
The total number of their counts is (114,287,013)

 matching Sample k-mers with the Database k-mers...
==========================================================================
There are (80,398) distinct k-mers in the sample matched with the database.
The total number of their counts is (718,244,732)


RESULTS...
==========================================================================
There are  11  virus(es) found in the sample.
Time taken (hh:mm:ss): 00:09:30
```

(c)

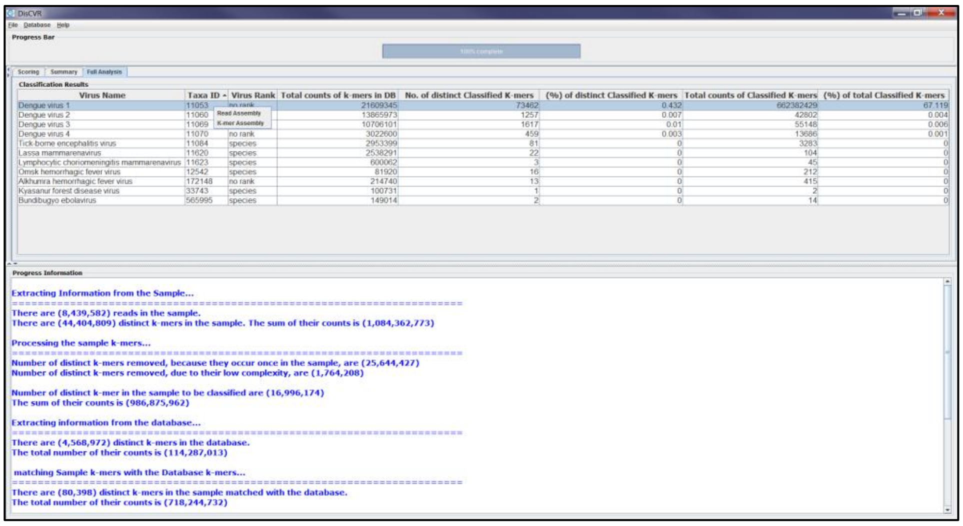


Virus Name	Taxa ID	Virus Rank	Total counts of k-mers in DB	No. of distinct Classified K-mers	(%) of distinct Classified K-mers	Total counts of Classified K-mers	(%) of total Classified K-mers
Dengue virus 1	11053	no rank	21609345	73462	0.432	662382429	67.119
Dengue virus 3	11069	no rank	10706101	1617	0.01	55148	0.006
Dengue virus 2	11060	no rank	13865973	1257	0.007	42802	0.004
Dengue virus 4	11070	no rank	3022600	459	0.003	13686	0.001
Tick-borne encephalitis virus	11084	species	2953399	81	0	3283	0
Lassa mammarenavirus	11620	species	2538291	22	0	104	0
Omsk hemorrhagic fever virus	12542	species	81920	16	0	212	0
Alkhumra hemorrhagic fever virus	172148	no rank	214740	13	0	415	0
Lymphocytic choriomeningitis mammarenavirus	11623	species	600062	3	0	45	0
Bundibugyo ebolavirus	565995	species	149014	2	0	14	0
Kyasanur forest disease virus	33743	species	100731	1	0	2	0

```
Processing the sample k-mers...
==========================================================================
Number of distinct k-mers removed, because they occur once in the sample, are (25,644,427)
Number of distinct k-mers removed, due to their low complexity, are (1,764,208)

Number of distinct k-mer in the sample to be classified are (16,996,174)
The sum of their counts is (986,875,962)

Extracting information from the database...
==========================================================================
There are (4,568,972) distinct k-mers in the database.
The total number of their counts is (114,287,013)

 matching Sample k-mers with the Database k-mers...
==========================================================================
There are (80,398) distinct k-mers in the sample matched with the database.
The total number of their counts is (718,244,732)


RESULTS...
==========================================================================
There are  11  virus(es) found in the sample.
Time taken (hh:mm:ss): 00:09:30
```

Figure 2: Screenshots showing sample classification output on the results sub-panels. The (a) scoring panel shows the three viruses with the highest number of matched k-mers, (b) the summary panel, and (c) the full analysis panel with detailed information about the viruses found in the sample.

(a)



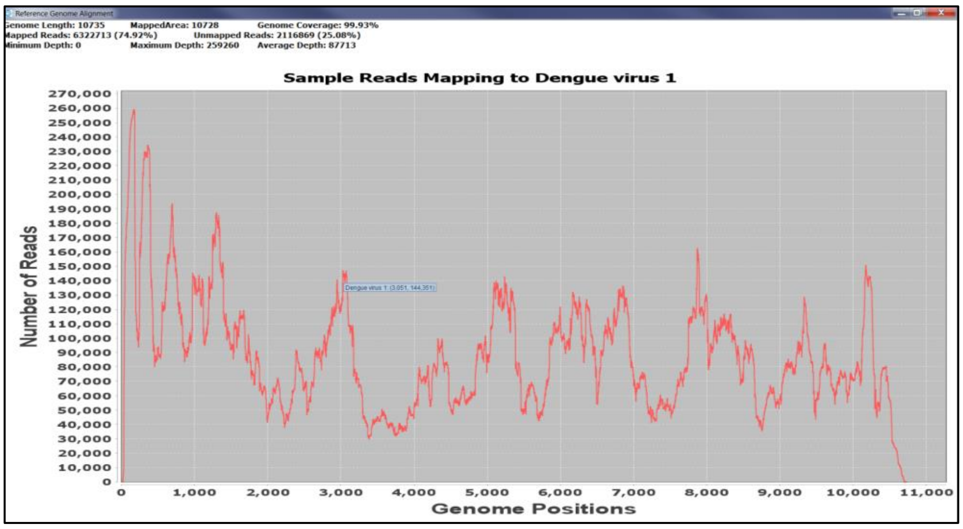
Classification Results

Virus Name	Taxa ID	Virus Rank	Total counts of k-mers in DB	No. of distinct Classified K-mers	(%) of distinct Classified K-mers	Total counts of Classified K-mers	(%) of total Classified K-mers
Dengue virus 1	11053	no rank	21609345	73462	0.432	662382429	67.119
Dengue virus 2	11060		13865973	1257	0.007	42802	0.004
Dengue virus 3	11069		10706101	1617	0.01	55148	0.006
Dengue virus 4	11070	no rank	3022600	459	0.003	13686	0.001
Tick-borne encephalitis virus	11084	species	2953399	81	0	3283	0
Lassa mammarenavirus	11620	species	2538291	22	0	104	0
Lymphocytic choriomeningitis mammarenavirus	11623	species	600062	3	0	45	0
Omsk hemorrhagic fever virus	12542	species	81920	16	0	212	0
Alkhumra hemorrhagic fever virus	172148	no rank	214740	13	0	415	0
Kyasanur forest disease virus	33743	species	100731	1	0	2	0
Bundibugyo ebolavirus	565995	species	149014	2	0	14	0

Progress Information

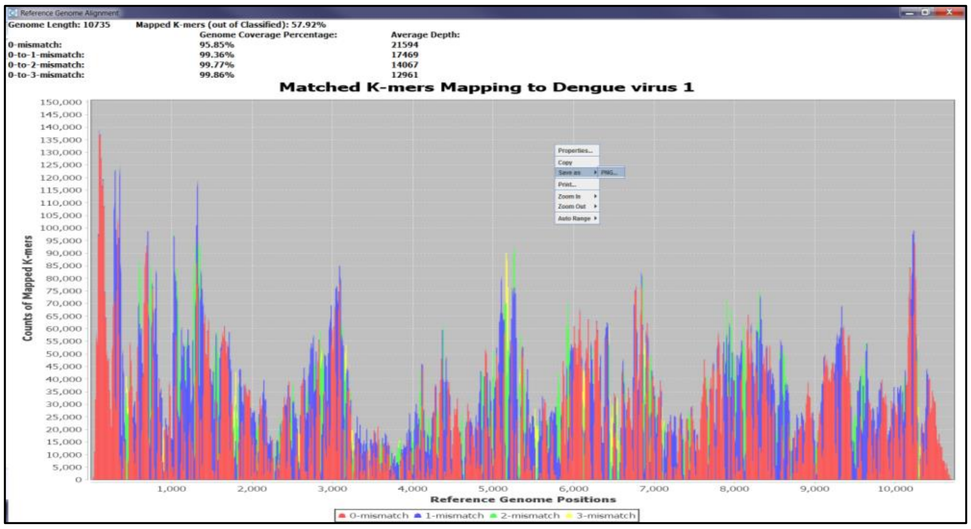
```
Extracting Information from the Sample...
========================================================================
There are (8,439,582) reads in the sample.
There are (44,404,809) distinct k-mers in the sample. The sum of their counts is (1,084,362,773)

Processing the sample k-mers...
========================================================================
Number of distinct k-mers removed, because they occur once in the sample, are (25,644,427)
Number of distinct k-mers removed, due to their low complexity, are (1,764,208)

Number of distinct k-mer in the sample to be classified are (16,996,174)
The sum of their counts is (986,875,962)

Extracting information from the database...
========================================================================
There are (4,568,972) distinct k-mers in the database.
The total number of their counts is (114,287,013)

 matching Sample k-mers with the Database k-mers...
========================================================================
There are (80,398) distinct k-mers in the sample matched with the database.
The total number of their counts is (718,244,732)
```

(b)



```
Genome Length: 10735        MappedArea: 10728         Genome Coverage: 99.93%
Mapped Reads: 6322713 (74.92%)        Unmapped Reads: 2116869 (25.08%)
Minimum Depth: 0            Maximum Depth: 259260     Average Depth: 87713
```

(c)



```
Genome Length: 10735       Mapped K-mers (out of Classified): 57.92%
                           Genome Coverage Percentage:      Average Depth:
0-mismatch:                95.85%                           21594
0-to-1-mismatch:           99.36%                           17469
0-to-2-mismatch:           99.77%                           14067
0-to-3-mismatch:           99.86%                           12961
```

Figure 3: Screenshots showing how to assess the significance of matches from the sample classification results. (a) right-clicking on a row from the Full Analysis table provides a pop-up list of choices to start reference assembly. (b) Right-clicking on a graph e.g. Read-Assembly graph shows the number of reads at a certain reference genome position. (c) Right-clicking on a graph e.g. *k*-mer assembly allows the users to save it as a PNG file.

DisCVR Command Line

DisCVR can be used to classify multiple samples at once using the command line. In this case, a folder is generated containing the results for each sample in a separate .csv file. The results consist of information about the reads in the sample and the full analysis of matched *k*-mers. The following commands show an example of using DisCVR to classify multiple files. The user needs to generate a java executable first before running the SampleClassification program on all the sample files.

```
javac -d ./bin src/model/*.java src/utilities/*.java
src/tanotipackage/*.java
java -cp ./bin model.SampleClassification <samples folder> <k>
<file format> <Database name> <database option> <entropy
threshold>
```

- `<samples folder>`: is the full path to the folder which contains sample files to be classified.
- `<k>`: is the *k*-mer size.
- `<file format>`: is the format of the sample files e.g. fastq
- `<database name>`: is the name of the database to be used in the classification. If DisCVR's built-in database to be used then use *HaemorrhagicVirusDB*, *RespiratoryVirusDB*, or *HSEVirusDB*. In case of a customisedDB, the full path to the database file must be provided.
- `<database option>`: if it is one of DisCVR's database then use *BuiltInDB* and if it is a customised database file then use *customisedDB*.
- `<entropy threshold>`: is the threshold to use to remove low-entropy *k*-mers.

command 2: to run DisCVR using command lines to classify multiple clinical samples.

Using the command line, DisCVR allows the validation of the classification results only when a customised database file is used in the classification. Users need to provide the taxonomy ID for the virus reference genome and the reference genomes file which is generated during the build of the database. In addition, only read assembly validation is available through command line because users have no access to the matched *k*-mers at the end of the process. The validation output does not show a graph of the reference genome alignment. Instead, it prints out at the command prompt a summary of the coverage and depth of the reads in relation to the reference genome. The following commands execute the read assembly validation from the command line.

```
javac -d ./bin src/model/*.java src/utilities/*.java
src/tanotipackage/*.java
java -cp ./bin model.ReferenceGenomeAlignment <taxID>
<reference_Genome file> <sample file> <database option>
```

- `<taxID>`: is the taxonomy ID for the virus whose reference genome will be used in the alignment.
- `<reference_Genome file>`: is the full path to the reference genome library in the customised database.
- `<input file>`: is the sample file to be investigated.
- `<database option>`: it must be *customisedDB*.

command 3: to run read assembly validation in DisCVR using command lines.

Customised Database

DisCVR allows the users to build their own customised database from a list of viruses that are of interest. This section explains the steps to generate the users customised database files. Refer to the Installation section to ensure the required tools are downloaded and installed properly before proceeding to customise your *k*-mers database. The NCBI files, i.e. *names.dmp* and *nodes.dmp*, must be copied to the *customisedDB* folder. The NCBI website (https://www.ncbi.nlm.nih.gov) is used for downloading the data. The following table lists all the files and parameters needed to build a customised database.

Table 1: Files and parameters needed to build DisCVR's customised database

Input File	A file containing information about the set of viruses to build the database from
NCBI Taxdump Files	Two files (*names.dmp* and *nodes.dmp*) to be downloaded into the *customisedDB* folder
Host genomes file	A fasta file containing the host DNA sequences
Entropy threshold	A number in the range [0,3] to act as a low-complexity threshold
Data Location	The path to the folder containing the data to build the database from
Name of the database	The given name to the customised database. This should be a single word that does NOT contain (_)
K size	The length of *k*-mers to be used in the build of the database.
Number of threads	The number of threads to use during the build of the database.
File counter	The number of virus files to process at one time during the build of the database.

The process starts by providing a list of the viruses of interest and the information of their complete genomes, if they exist. This input is a tab-delimited file which contains the taxonomy ID of the virus and the accession number for its reference sequence. In DisCVR, the three built-in databases use only human viral sequences at the species and subspecies levels on the taxonomy tree. However, the customised-database does not require the viruses to be of a particular rank in the taxonomy tree nor the host to be human. In addition, the input file should not have duplicate taxonomy IDs but multiple taxonomy IDs in the list can have the same reference sequence. Table 2 shows an example of the input file.

IMPORTANT: the accession number of the virus reference sequence MUST be the exact accession number provided in the header of the reference sequence.

There are three steps to build the customised database which must be executed sequentially:

1. Data Download; which involves obtaining the data required to build the two database files.
2. Generating the reference genome library file using the information of the reference sequences.
3. Generating the virus *k-mer*s database from the downloaded sequences.

Table 2: An example of the input file for the customised database builds stage. Left column shows an example of a line in the input file. Right column explains the components of the line.

`121791  NC_002728.1`	The virus taxonomy ID is followed by the accession number of the virus's reference sequence.
`499556  NC_010563.1,NC_010562.1`	It is a segmented virus. The accession numbers for the reference sequences segments are comma-separated and listed in order so that the first segment is the largest.
`11598`	Only the virus taxonomy ID is provided because the virus does not have a reference sequence.

1. Data Download

The first step in building the database is to obtain the viral sequences for the viruses of interest. The script *downloadDataAndRefSeq.sh* uses the *eutilities* tools to download the data from the NCBI using the following command:

```
bash downloadDataAndRefSeq.sh <taxIDs_List> <outputDir>
```

- `<taxIDs_List>`: the input file which contains the virus taxonomy IDs and their reference sequence information.
- `<outputDir>`: the name of the directory for the downloaded data.

Command 4: Bash command to download the data needed to build the database files

After executing the script, the output directory will have two sub-directories:

i. ***DataSeq*** which contains the data to be used to build the virus *k-mer*s file, and
ii. ***RefSeq*** which contains the data to create the reference sequence library file.

Each file in both directories includes in its name the taxonomy ID (taxID) of the virus whose data is contained in the file. The ***DataSeq*** directory has two corresponding files for each taxID:

i. Virus_taxID.fa is a fasta file which contains all complete and partial viral sequences for the virus with the taxID, and
ii. Virus_taxID_Info which contains information for the sequences in the corresponding fasta file. The first line states the number of sequences found on NCBI for the taxID followed by information for each sequence. This includes Accession number, title, gi header, update date, length of the sequence, the subtype, and strain.

Similarly, the ***RefSeq*** directory contains files for each taxID which has information of its reference sequence in the input file. The files which are called Virus_taxID_RefSeq.fa are fasta files that contain one or more sequences (in the case of segmented viruses). Information files are used to identify segmented viruses, in the case of ***RefSeq***, and to filter out shared sequences, in the case of ***DataSeq***.

IMPORTANT: ensure that the files in both RefSeq and DataSeq folders are NOT empty. If any of the file are empty, re-run the data download script with an input file that contains only the information for the taxIDs with empty files.

2. Database Files Generation

Java programs are used to generate the two files in the database. These Java programs are found in the folder called 'bin'.

2.1 Reference Genome Library

The reference genome library file is used in the validation stage of DisCVR and it contains the reference sequences for the viruses in the input file. The reference sequences are identified in the input file by their accession numbers and the corresponding sequences are downloaded in the ***RefSeq*** directory. The Java program *GenomesLibrary* is used to generate the reference genome library using the following command:

```
java –cp ./bin customdatabase.GenomesLibrary <taxIDs_List>
<database_Name> <RefSeq_Dir>
```

```
➢ <taxIDs_List>: the input file which contains the virus
  taxonomy IDs and their reference sequence information.
➢ <database_Name>: is the name to be given to the customised
  database
➢ < RefSeq_Dir >: is the full path of the RefSeq folder which
  contains all downloaded data for the reference sequences.
```

Command 5: Java command to generate the reference genome library file.

The output file is called: databaseName_referenceGenomesLibrary and it is in the ***RefSeq*** folder. Each line in the file consists of a virus taxonomy ID, the header, and the sequence of its complete genome. The delimiter "@" is used to separate the three components. In the case where the reference sequence is a concatenation of multiple segments, the headers are separated by a comma and the sequences are separated by a sequence, 300 in length, of the letter N. For the viruses which share the same reference sequence (i.e. species level and their sublevels are assigned the same reference sequence) then their taxonomy IDs are separated with a pipe sign "|".

The output file MUST be copied to the *customisedDB* folder to be used for DisCVR's validation when using the customised *k*-mers database.

2.2 Virus *k*-mers database

The last step to build the customised database is to generate the file which contains the virus *k-mer*s. In the generation of DisCVR's built-in database files, a filtering step was used to remove shared sequences between a virus and its ancestors in the taxonomy tree. This is an optional step which can be used in the build of the customised database to reduce redundancy in the data and to increase virus specificity.

2.2.1 *Data Filtering (Optional)*

The filtering process removes shared sequences from the ancestors' data. For example, if sequences are found in both the strain and the species levels, then they are removed from the sequences at the species level. It is recommended to keep a copy of the data in the ***DataSeq*** directory before executing this step to avoid loss of data. The NCBI dump files (i.e. *names.dmp* and *nodes.dmp*) are used in this step and they MUST be included in the *customisedDB* folder. The Java program *DataSequences* is used to filter the downloaded sequences using the following commands:

```
mkdir <DataSeq_filtered>
cp -r <DataSeq_Dir> <DataSeq_filtered>
java –cp ./bin customdatabase.DataSequences <DataSeq_Dir>
<genomes_file> <database_Name>
```

```
➢ < DataSeq_Dir>: is the full path for the DataSeq folder
  which contains the viruses' data (fasta and Info files).
➢ <DataSeq_filtered>: is the full path for the folder which
  contains the filtered data.
➢ <genomes_file>: is the full path for the
  referenceGenomeLibrary which is generated from the previous
  step.
➢ <database_Name>: is the name to be given to the customised
  database.
```

Command 6: Java command to remove common sequences from the downloaded data

After executing the program, the sequence files (i.e. fasta files) for the viruses which are ranked at a higher taxonomic level to other sequences in the ***DataSeq*** directory are modified, if they contain shared sequences. The output file: databaseName_lineageID.txt shows, per line, the taxID of a virus followed by the taxIDs of higher taxonomic level. In addition, a file which contains summary information about the viruses in the database such as their rank in the taxonomy tree and the number of sequences per virus, after filtering, is generated. The file is called: databaseName_DataInformation.csv.

Finally, an output file called: databaseName_allSeqData is generated and it contains all the sequences, after filtering, from all the data files in the directory. The three output files can be found in the ***DataSeq*** directory.

2.2.2 *k-mers database file*

The final step in the customised database build is to generate the virus *k-mer*s database file from the downloaded viral sequences. In this step, *k-mer*s from the viral sequences and from the host genomes are extracted. Low entropy and host *k-mer*s are then removed from the virus *k-mer*s. The remaining set of virus *k-mer*s are assigned the taxIDs of all the viruses which are represented by these *k*-mers. Table 3 shows an example of the virus *k-mer* database file.

Table 3: An example of the virus *k*-mers database file. Each line contains a *k*-mer of size 18, the number of times it occurs in the viral sequence, and a list of taxIDs of the viruses which the *k*-mer is extracted from. The last number in the line indicates whether the *k*-mer occurs in a single virus (e.g. 1) or in multiple related viruses (e.g. 2).

```
AAAAACAAGAATGGACAC    2     11620 1
AAAAACAATGGGCTCTAT    5     1980486 1980491 2
```

The virus *k*-mers database file is generated by using the following command and it is saved to the *customisedDB* folder.

```
java -cp ./bin customdatabase.KmersDatabaseBuild <DataSeq_Dir>
<host_file> <kmersDB_file> <k_size> <num_threads>
<entropy_threshold> <files_counter>
```

- `<DataSeq_Dir>`: full path to the directory which contains a copy of the downloaded data (fasta files).
- `<host_file>`: full path to the host genomes fasta file.
- `<kmersDB_file>`: name to be given to the customised *k-mer*s database file.
- `<k_size>`: *k*-mer size.
- `<num_threads>`: number of threads to use when counting *k-mer*s from the virus files. We recommend using 2
- `<entropy_threshld>`: entropy threshold to filter out low-entropy *k-mer*s. Use 0 to omit this option.
- `<files_counter>`: number of data files to process at once during taxonomy labelling. It is recommended to use 10 to optimise memory use.

Command 7: Java command to build the virus *k*-mers database file

An Example

This section shows an example of the whole process to create the customised *k*-mers database files. The NCBI dump files: *names.dmp* and *nodes.dmp* must be downloaded from the NCBI into the *customisedDB* folder before starting the process. In addition, the *lib* folder must be in the same directory as the *customisedDB* folder. The input files provided in the *TestData* are used in this example. There are two input files:

1. miniDB_sample.txt: contains information of the viruses used to build the *k*-mers database.
2. HumanGenomesTest.fa: contains an example of the host sequences

The process starts by downloading the data from the NCBI and generating the reference genome file. Filtering of shared sequences is then applied on a copy of the viral sequences. The last step is creating the virus *k*-mers database with *k* size equals to 18 and 0 entropy threshold. The number of threads to count *k*-mers is 2 and the number of files to process at once is 10. The given name for the customised database files in this example is “miniDB_sample”. Command 8 lists all the sequential command lines needed to build the database.

```
bash downloadDataAndRefSeq.sh ./TestData/miniDB_sample.txt
./TestData/miniDB_sample/
```

```
mkdir ./TestData/miniDB_sample/DataSeq_filtered
```

```
cp -r ./TestData/miniDB_sample/DataSeq/*
./TestData/miniDB_sample/DataSeq_filtered
```

```
java -cp ./bin customdatabase.GenomesLibrary
./TestData/miniDB_sample.txt miniDB ./TestData/miniDB_sample/RefSeq/
```

```
cp ./TestData/miniDB_sample/RefSeq/miniDB_referenceGenomesLibrary
./customisedDB/
```

```
java -cp ./bin customdatabase.DataSequences
./TestData/miniDB_sample/DataSeq_filtered
./TestData/miniDB_sample/RefSeq/miniDB_referenceGenomesLibrary miniDB
```

```
java -cp ./bin customdatabase.KmersDatabaseBuild
./TestData/miniDB_sample/DataSeq_filtered/
./TestData/HumanGenomesTest.fa miniDB_Kmers_18 18 2 0 10
```

Command 8: A list of all commands to generate DisCVR's customised database files.