

**Viral Bioinformatics 2024**  
**Topics: MSA, Phylogeny, Virus Typing & Recombination detection**  
**Hands-on exercises**

**Multiple Sequence Alignments:**

1. **Module Developers & Assistants:** Dr. Urmila Kulkarni-Kale & Mr. Sanket Limaye

2. **Learning outcomes:**

At the end of the session, participants are expected to understand –

- sequence alignment concepts, pairwise sequence alignment (local and global), multiple sequence alignment algorithms, and their applications in virus bioinformatics.
- fundamentals of sequence analysis, the basis of scoring matrices, the importance of gap penalties, etc.
- the steps in the MAFFT algorithm, familiarity with sequence input/output formats, how to carry out MSA, interpretation of results, etc.

3. **Background (MSA):**

Multiple sequence alignment (MSA) is one of the most frequently used bioinformatics techniques for aligning nucleotide and protein sequences. MSA often serves as a starting point for analyzing viral sequences to identify regions of similarity/differences and indicate potential functional, structural, and evolutionary relationships. Several algorithms and software tools are available for MSA, of which MAFFT will be discussed in detail using a case study.

4. **Key resources:**

MAFFT publication: Katoh et al., 2009; DOI: [10.1007/978-1-59745-251-9\\_3](https://doi.org/10.1007/978-1-59745-251-9_3)

Phylogeny review: Chao et al., 2022; DOI: [10.3390/biom12040546](https://doi.org/10.3390/biom12040546)

Lecture on MSA overview & MAFFT: To be shared.

Software: [MAFFT for Linux - a multiple sequence alignment program \(cbrc.jp\)](http://mafft.cbrc.jp/alignment/software/)

MAFFT documentation & help:

<https://mafft.cbrc.jp/alignment/software/manual/manual.html>

5. **Method:**

Case study: Perform multiple genome alignment of Dengue Virus serotype 4 (DENV4) isolates (DENV4\_seq.fas) using MAFFT. What is the percentage of identical sites in the alignment? Save the genome alignment in fasta and Clustal formats.

Input dataset:

MSA\_phylogeny\_RDP\1\_mafft\input\ DENV4\_seq.fas

Output files:

MSA\_phylogeny\_RDP\1\_mafft\output\ DENV4\_aln.fas and DENV4\_clustal\_aln.fas

**Commands:**

For fasta format:

mafft DENV4\_seq.fas > DENV4\_aln.fas

For clustal format

```
mafft --clustalout DENV4_seq.fas > DENV4_clustal_aln.fas
```

For identifying the conserved nucleotides:

```
grep -o "*" DENV4_aln.fas | wc -l
```

### **Molecular Phylogeny and virus typing:**

1. **Module Developers & Assistants:** Dr. Urmila Kulkarni-Kale & Mr. Sanket Limaye

2. **Learning outcomes:**

At the end of this session, participants are expected to develop an understanding of –

- concepts in phylogeny and evolution.
- various methods for phylogenetic analysis.
- tree visualization and interpretation.
- Various approaches for serotyping and genotyping of virus isolates.

3. **Background (Phylogeny and typing):**

Molecular phylogeny analyses are performed not only to carry out basic research, such as understanding the genetic diversity of viruses, tracking the spread of viral diseases, and studying the evolution and diversification of viruses, but also for translation research to design drugs and vaccines.

Typing virus isolates is an essential prerequisite for many downstream analyses. Computational approaches for typing involve phylogenetic analysis of the isolates with unknown types and the known ones (reference set). The type is assigned based on clustering proximity of the unknown with the known, which demands human interventions. On the other hand, alignment-free approaches automate the typing process and circumvent a few limitations of alignment-based MPA. An overview of typing methods and a few case studies will be presented.

#### **Phylogeny**

Phylogeny publication: [Link to PDF](#)

Lecture on Phylogeny and typing: To be shared

Software:

o IQ-Tree: [Getting Started \(iqtree.org\)](http://iqtree.org/);

o Figtree: [Releases · rambaut/figtree \(github.com\)](https://github.com/rambaut/figtree)

IQ-Tree documentation & help: <http://www.iqtree.org/doc/Quickstart>

#### **Typing**

Webserver: Genome Detective (DENGUE VIRUS TYPING TOOL):

<https://www.genomedetective.com/app/typingtool/dengue/>

RTD-based Dengue Typer Server: The URL is to be shared.

4. **Method:**

- A. Use the genome alignment of DENV4 isolates and generate a whole-genome phylogenetic tree with the help of IQTREE. Select the best nucleotide substitution model that fits the data using ModelSelector. Reconstruct maximum likelihood-based phylogeny with 1000 bootstrap replicates using the Ultrafast method available in IQTREE. What are the number of invariant sites and parsimoniously informative sites? Which nucleotide model best fits the data

provided? Using the consensus tree, find the clusters where Indian isolates are observed. Also, check if the isolates of the same genotype cluster together.

Input dataset: \MSA\_phylogeny\_RDP\2\_iqtree\input\ DENV4\_aln.fas

Output files: \MSA\_phylogeny\_RDP\2\_iqtree\output\

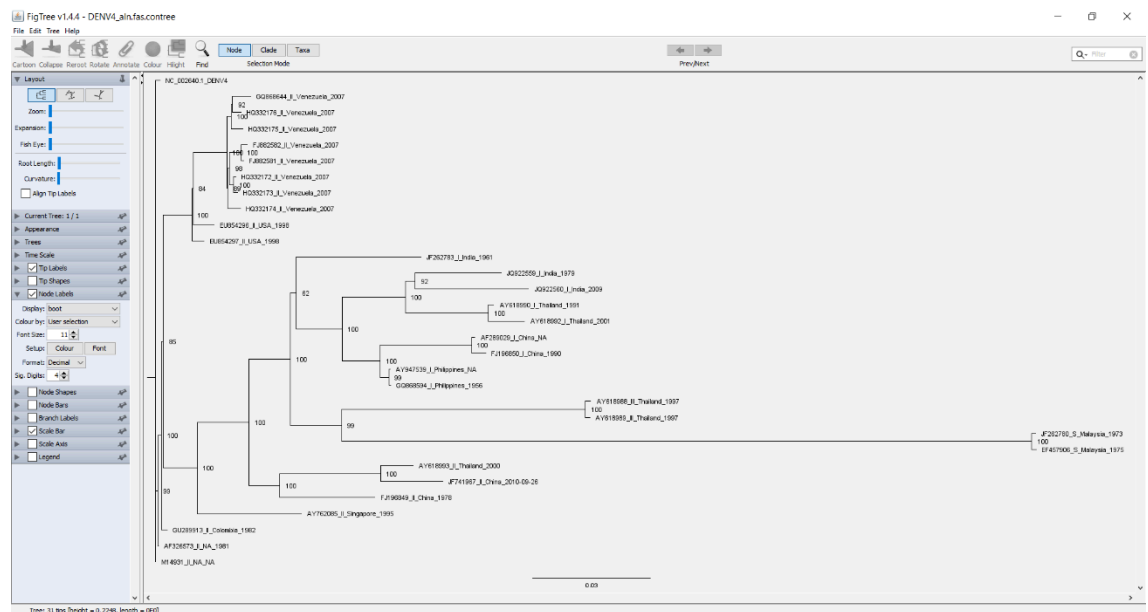
### Commands:

#### IQTREE

iqtree -s DENV4\_aln.fas -bb 1000

#### Figtree

Open “.contree” file > select node labels > select “Display: bootstrap”



B. Perform genotyping of the unknown DENV4 isolates using the methods mentioned below. Observe if the methods assign different genotypes to both the isolates.

- View the “DENV4\_genotyping\_aln.contree” file in Figtree software and assign genotypes to the two isolates (DENV4\_A and DENV4\_B) based on the clustering pattern.

Input dataset:

\MSA\_phylogeny\_RDP\4\_test\ DENV4\_genotyping\_aln.contree

Use the file “DENV4\_unknown.fas” as input to the DENGUE VIRUS TYPING TOOL available at the GENOME DETECTIVE web server and assign genotypes to the two isolates (DENV4\_A and DENV4\_B).

URL: <https://www.genomedetective.com/app/typingtool/dengue/>

Input dataset: \MSA\_phylogeny\_RDP\4\_test\ DENV4\_unknown.fasta

## **Recombination Detection:**

1. **Module Developers & Assistants:** Dr. Urmila Kulkarni-Kale & Mr. Sanket Limaye

2. **Learning outcomes:**

At the end of the session, participants are expected to develop an understanding of –

- various methods available for recombination detection
- why and how to carry out recombination analysis

3. **Background (Recombination Detection):**

A recombination event occurs when genetic material from two or more viruses mixes during replication. It is one of the major driving forces behind virus diversification and the emergence of novel strains.

4. **Key resources (Recombination Detection):**

RDP4 publication: <https://academic.oup.com/ve/article/1/1/vev003/2568683>

Lecture on Recombination: To be shared.

Software: **Recombination (RDP4 software):** [RDP home page \(uct.ac.za\)](http://uct.ac.za)

- a. Download and install **RDP4.101** (we use and prefer the **Windows** version; the link for the Linux version is available on the same page)
- b. Version 4.101 is more stable than RDP5.55

RDP4 documentation and help: <http://web.cbio.uct.ac.za/~darren/RDP4Manual.pdf>

5. **Method:**

A. Use the genome alignment of DENV4 isolates and detect the recombination events using the RDP4 program. Select the p-value cutoff and threshold of the minimum number of methods that positively detect a recombination event. List the number of recombination events that were detected. How many of them were considered significant? From the significant recombination hits obtained, report the major parent and minor parent along with the breakpoints of the sequences.

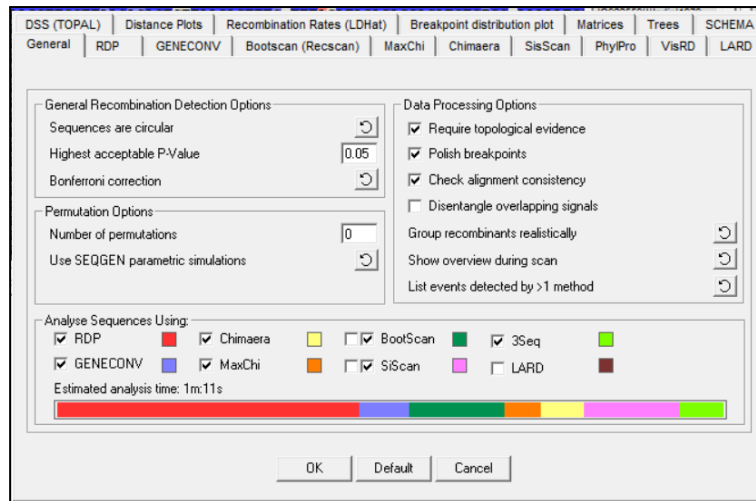
Input dataset: \MSA\_phylogeny\_RDP\3\_RDP4\input\ DENV4\_aln.fas

Output files: \MSA\_phylogeny\_RDP\3\_RDP4\output\ DENV4\_RDP.csv

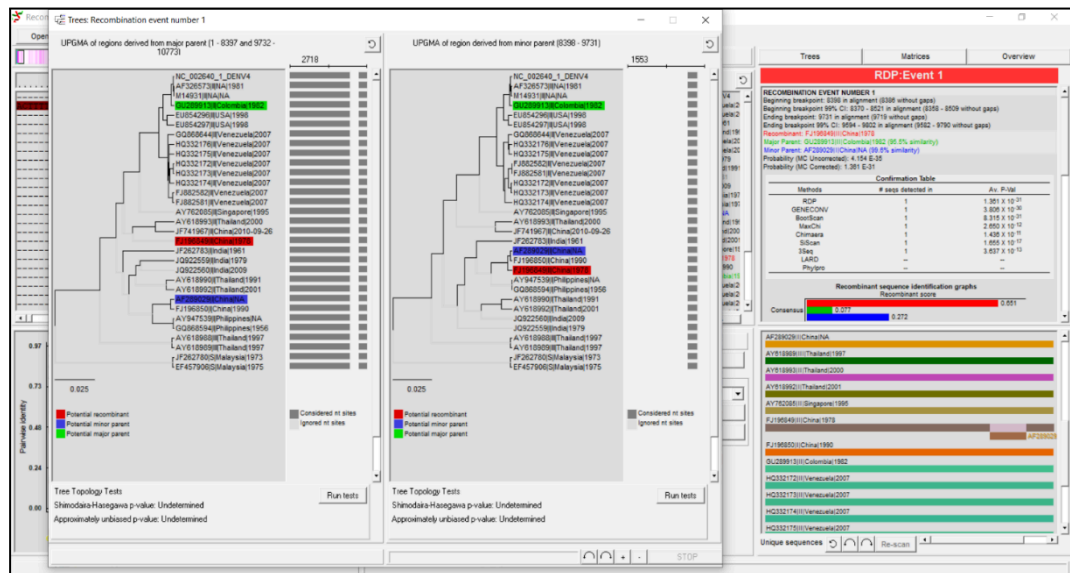
**Commands:**

**RDP4**

Open the alignment file > Set the “Highest acceptable P-value” > Select “ List events detected by > 3 ” > Select the different scanning methods > RUN



Select the “Overview” in the top right corner > Select an event > Select the “Recombination info” tab.



Save the results as “.rdp” and .csv file.