

**wellcome
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science**

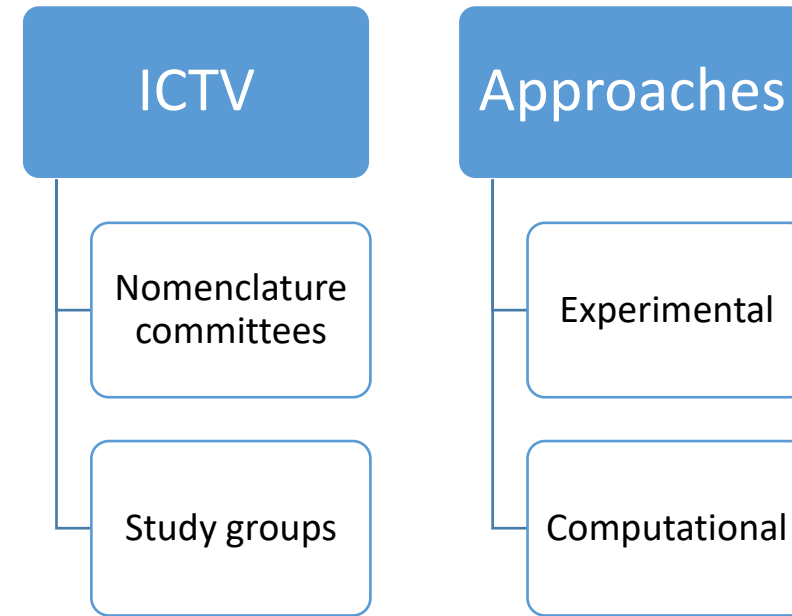
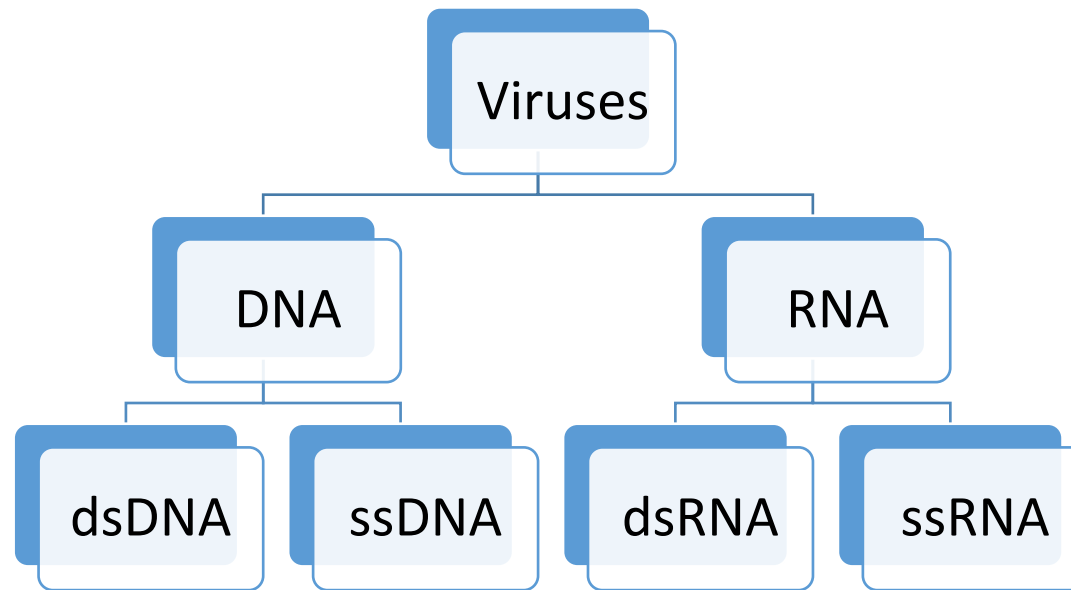


Computational Methods for Typing Viruses

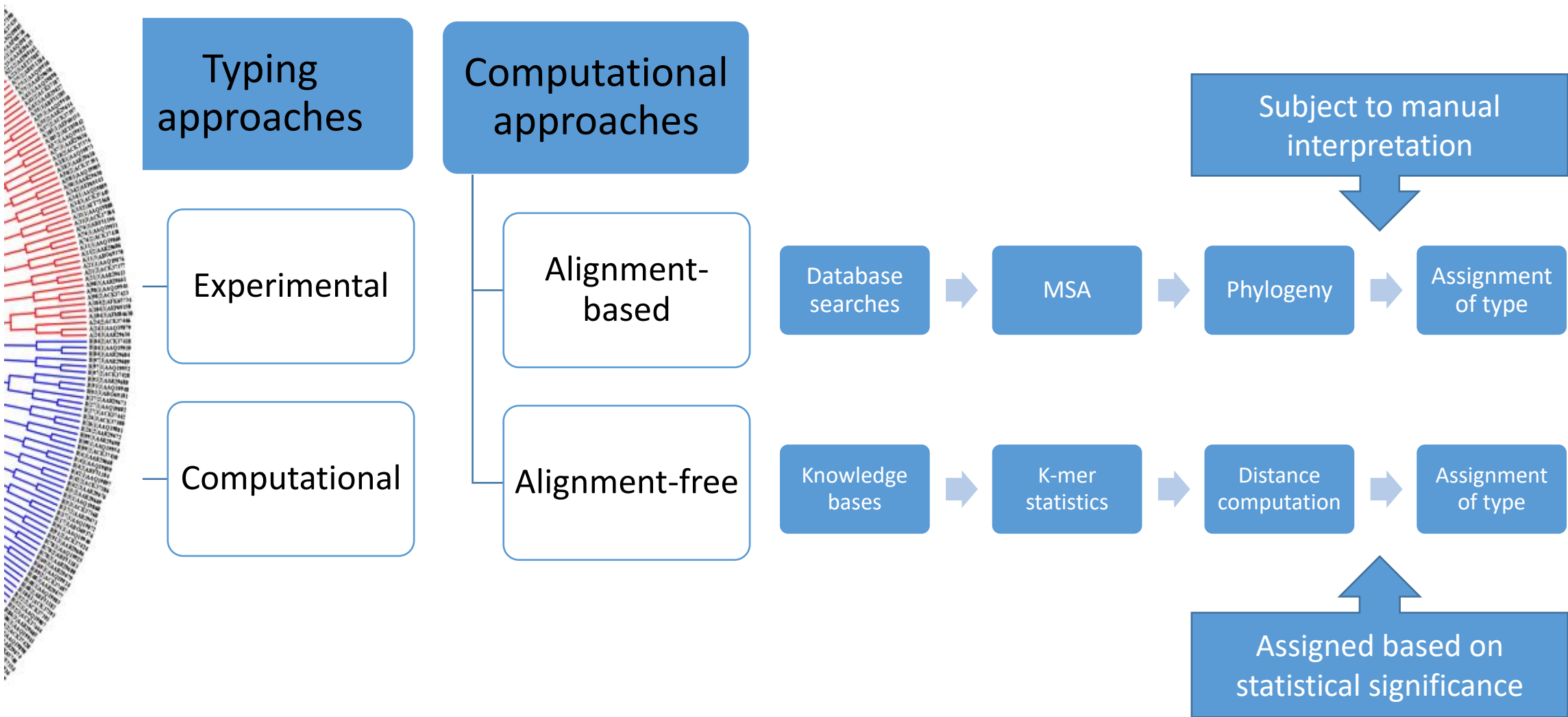
Dr. Urmila Kulkarni-Kale

S. P. Pune University | University of Southeastern Norway | Citadel Precision Medicine
urmila.Kulkarni.kale@gmail.com

Virus Taxonomy & Nomenclature



Viral typing: the starting point for characterization



Virus Typing based on Molecular Phylogeny Analysis : the workflow

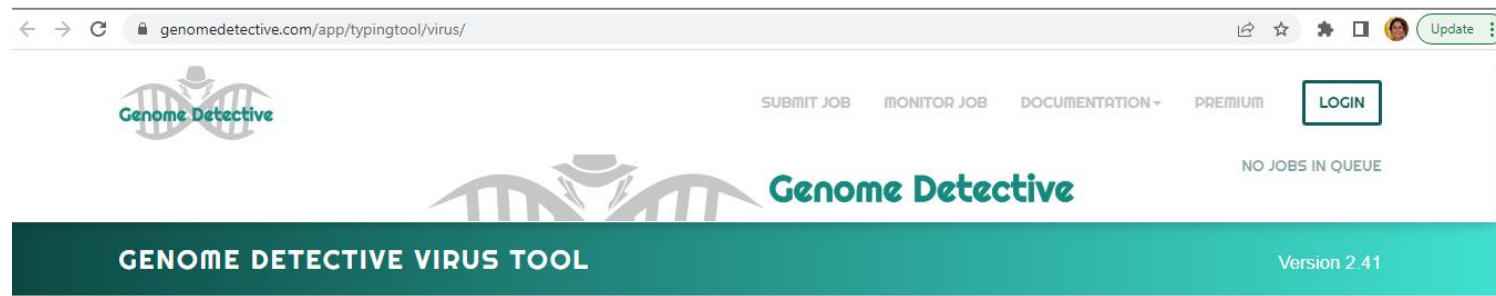
- Define the objective
- Curate a set of reference sequences (known types)
- Carry out Multiple Sequence Alignments
- Undertake phylogenetic analysis:
 - distance-based (NJ: Neighbor-Joining)
 - character-based (MP: Maximum parsimony)
 - Bayesian-based (ML: Maximum likelihood)
- Generate datasets for bootstrapping
- Use clustering method
- Generate consensus tree
- Assess tree topology(ies)
- Analysis of inferred tree(s)
- Assign type to the viral isolate based on proximity to known ones

Genome Detective Virus Tool

<http://www.genomedetective.com/app/typingtool/virus/>

- Assigns taxonomic rank at species level to sequences of eukaryotic viruses & phages
- Ranking is subject to availability of reference genomes in RefSeq
- Currently 11140 distinct taxonomic names are assigned based on 14500 reference sequences
- Subtyping tools, for the identification of subspecies, are available for 19 viruses
- Input: NGS short reads (FASTQ); Contigs; Consensus (FASTA)

- Chikungunya Typing Tool
- Coronavirus Typing Tool
- Dengue Typing Tool
- Enterovirus typing tool
- HCV Recombinant Typing Tool
- HHV82 Virus Typing Tool
- HTLV-1 and 2 Typing Tool
- Hepatitis A Virus Genotyping Tool
- Hepatitis B Virus
- Hepatitis E Virus Genotyping Tool
- Human Immunodeficiency Virus Typing Tool
- Measles Virus TypingTool
- MonkeyPox Virus
- Norovirus Typing tool
- Panviral Tool
- Rift Valley Fever Virus
- West Nile Virus
- Yellow Fever Virus Typing Tool
- Zika Virus Typing Tool



Dengue Virus Typing Tool@ Genome Detective



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NO JOBS IN QUEUE



DENGUE VIRUS TYPING TOOL

Version 3.83

How Genome Detective assigns SARS-CoV-2 (the virus that causes COVID-19 disease)

[Read more](#)

DENGUE VIRUS TYPING TOOL

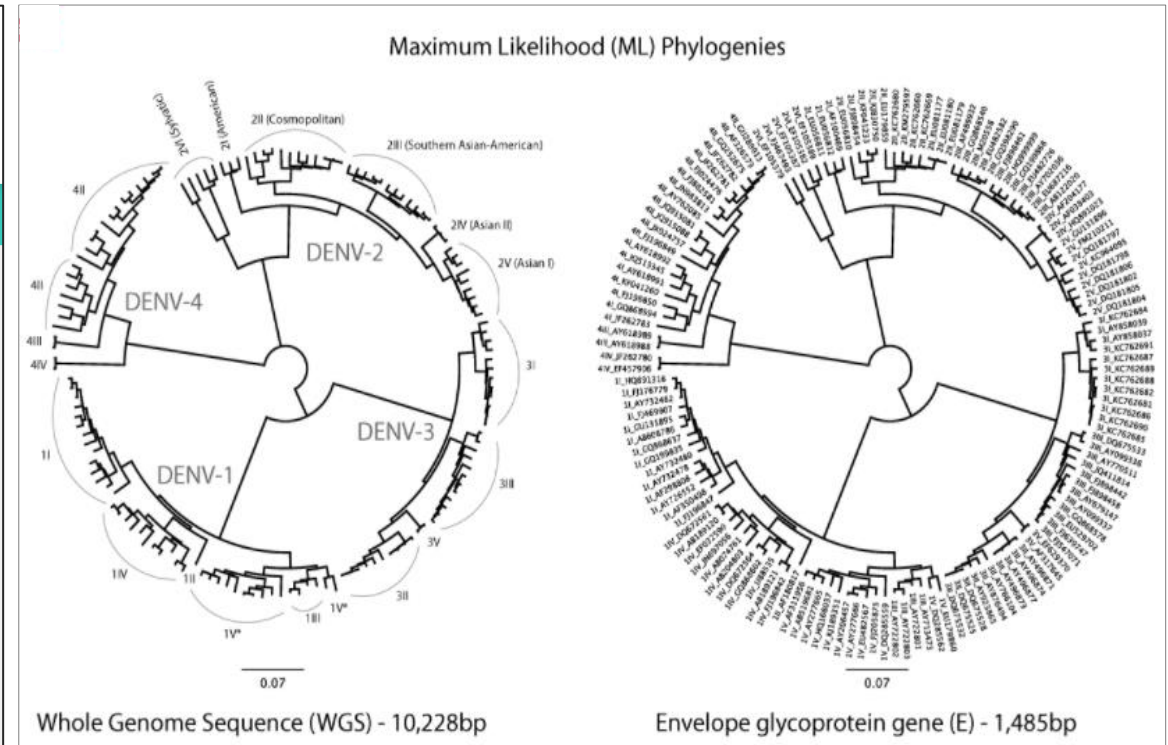
This tool is designed to use Blast and phylogenetic methods in order to identify the Dengue virus serotypes and genotypes of a nucleotide sequence.

Note for batch analysis: The tool accepts up to 2000 sequences at a time.

INPUT

Submit one or more FASTA sequences to be typed individually. If you have raw NGS reads (short reads or long reads), please use the [Genome Detective Virus Tool](#) to assemble first. Subtyping tools will be linked in the results.

[Click here](#) to load some sample data.



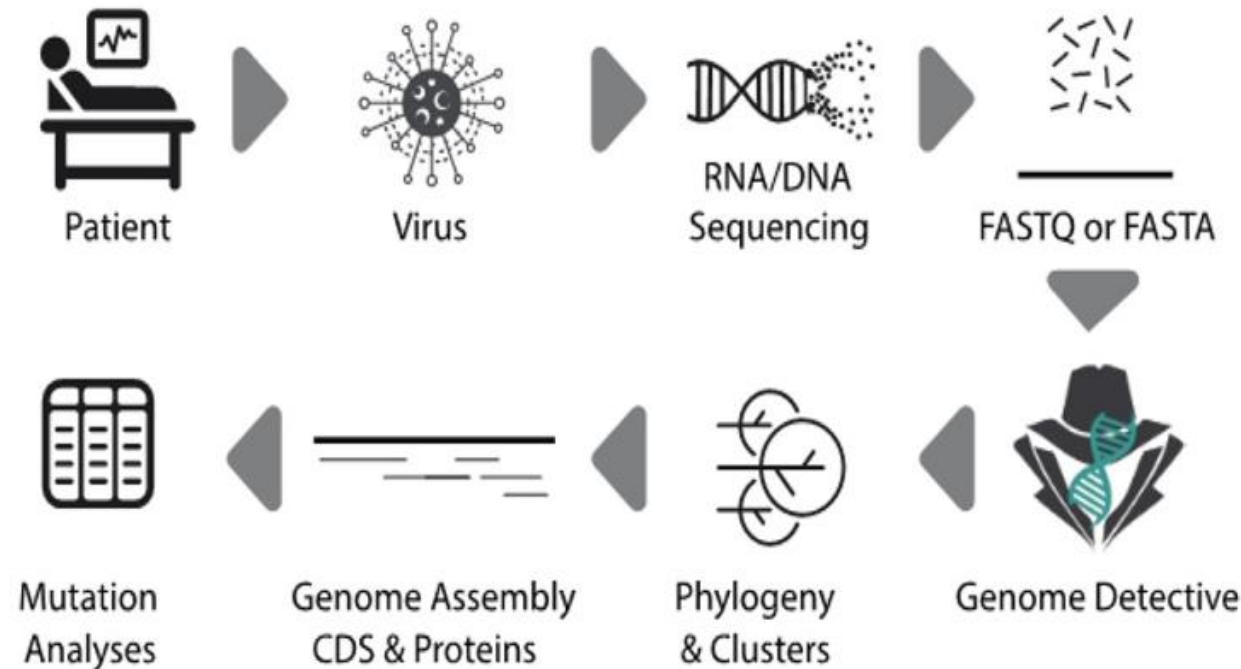
<https://www.genomedetective.com/app/typingtool/dengue/>

Group leader: Dr. Tulio de Oliveira, South Africa

Genome Detective: SARS-CoV-2 Typing Tool

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

Figure 1: Genome Detective Coronavirus Typing Tool assembles genomes from next-generation sequencing (NGS) in FASTAQ



Bioinformatics, Volume 36, Issue 11, June 2020, Pages 3552–3555, <https://doi.org/10.1093/bioinformatics/btaa145>

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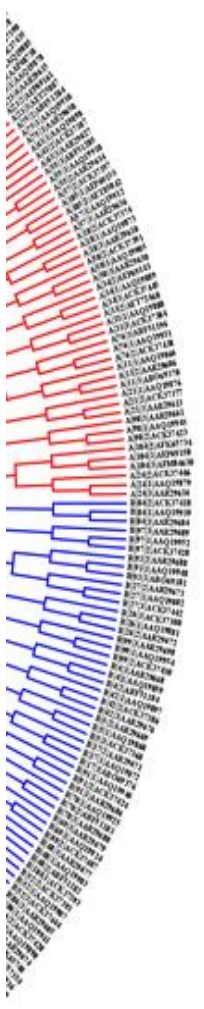


Workflow

Reference dataset: 431 WGS – aligned using MUSCLE codon alignment, manual edits for CDS boundaries

Input: NGS data (1Gb) or 2000 assembled genomes;
Formats: FSATQ/FASTA

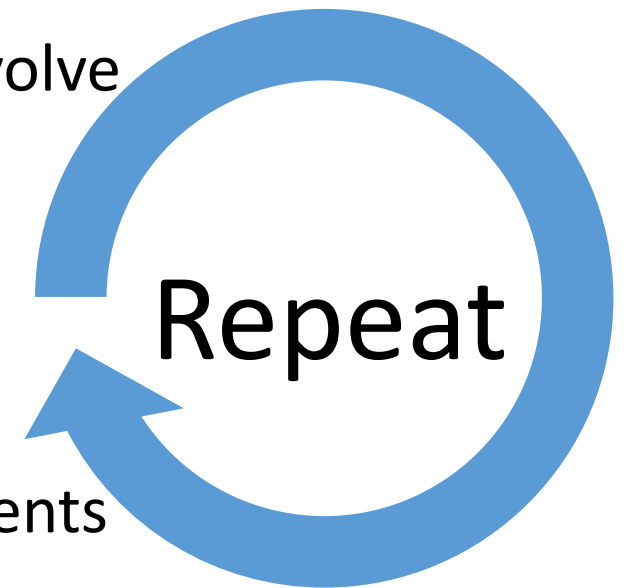
Processes: Species identification, phylogeny construction (ML – PhyML & Bayesian – MrBayes), cluster identification, ADA alignment to identify novel mutations



Alignment-free phylogeny and Viral typing: Algorithm & server developments @ SPPU

Molecular Phylogeny Analysis (MPA): Caveats

- Heuristic appeal in sequence alignment algorithm
- Positions of IN-DELs in MSA impact model of evolution
 - Errors in alignment increases as sequence similarity decreases
- Assumption of character-based methods: sites evolve independently
- Different methods result into different trees
 - Becomes a matter of interpretation
- Size of data in post-genomic era
- Computational complexity and memory requirements
- Time requirements



Designed Novel Approach: Alignment-free

Based on the concept of Return Time Distribution (RTD)

- Accounts for frequency of K-mers and their return times
- Performs equally well in varying levels of sequence similarity
- Fast & accurate with high sensitivity & specificity

Computing RTD for 'A' (k=1)

Return Time (RT): Time required for the reappearance of particular state without its appearance in between.

CTACAACTTTGCGGGTAGCCGGAACATTGTGAATGCGGTGAACA

1-1-0-10-5-0-0-1-5-0-7-0-1 Return times for 'A'

RTD for 'A' in above sample sequence

Return time for A (X)	Frequency (F)
0	5
1	4
5	2
7	1
10	1

Parameters of RTD for 'A'

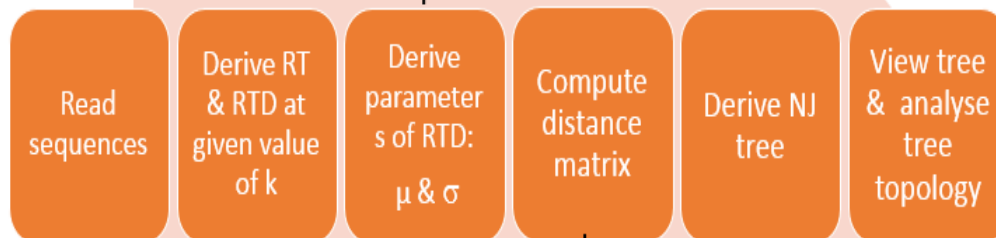
$$\mu(A) = 2.38 \text{ and } \sigma(A) = 3.27$$

Similarly, we can compute μ and σ of RTDs of T, G and C, for k=1.

[illegible]

The frequency distribution of all such observed RT is termed as RTD of that nucleotide

Numeric vector of size $2 \cdot 4^k$
comprising of μ and σ of 4^k possible RTDs



$$D_{ij} = (\sum [G_{ir\mu} - G_{jr\mu}]^2 + \sum [G_{ir\sigma} - G_{jr\sigma}]^2)^{1/2}$$

Sequence data

Computation of RTDs and their parameters

K=1

OTUs	$\mu(A)$	$\sigma(A)$	$\mu(T)$	$\sigma(T)$	$\mu(G)$	$\sigma(G)$	$\mu(C)$	$\sigma(C)$
Species_A	2.398438	3.214566	5.111111	5.559165	2.436508	2.505537	2.991786	3.7152
Species_B	2.398438	3.214566	5.111111	5.559165	2.436508	2.505537	2.991786	3.7152
Species_C	2.398438	3.214566	5.111111	5.559165	2.436508	2.505537	2.991786	3.7152
Species_D	2.398438	3.202391	5.027397	5.541803	2.436508	2.558919	2.936937	

$$D_{ij} = (\sum [G_{ir\mu} - G_{jr\mu}]^2 + \sum [G_{ir\sigma} - G_{jr\sigma}]^2)^{1/2}$$

Euclidean distance function

4	1	2	3	4
Species_A	0			
Species_B	25.3147	0		
Species_C	121.397	126.03067	0	
Species_D	125.3595	114.35555	24.62971	

Distance matrix

Neighbor-joining Clustering algorithm

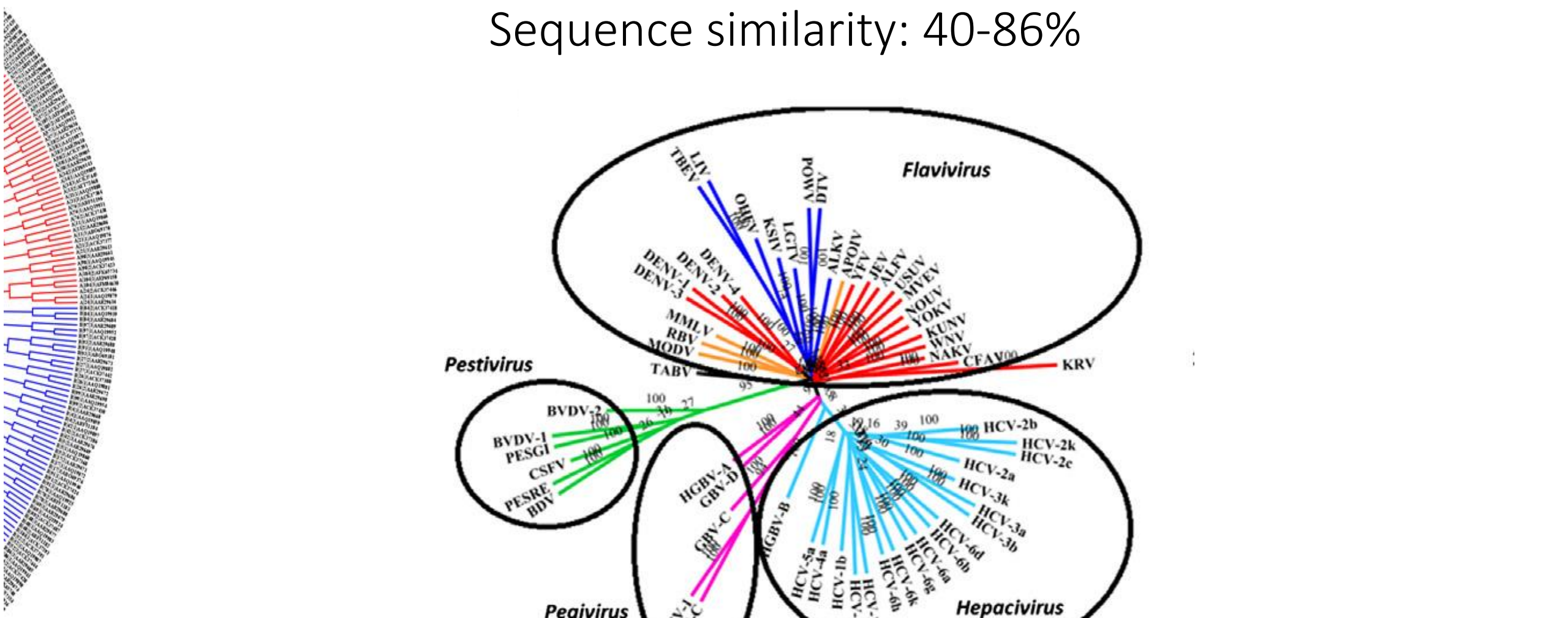
Phylogenetic tree

Sequence similarity: 40-86%

The phylogenetic tree illustrates the evolutionary relationships between several virus families. The main cluster is **Flavivirus**, which includes viruses like TBEV, DENV-1, DENV-2, DENV-3, MMLV, RBV, MODV, TABV, ALK, APOIV, JEV, ALFV, USUV, MVEV, NOUV, YOKV, KUNV, WNV, NAKV, CFAV, and KRV. Other families shown are **Pestivirus** (BVDV-1, BVDV-2, PESGI, CSFV, PESRE, BDV), **Peavivirus** (HGBV-A, GBV-D, GBV-C, GBV-E), and **Hepacivirus** (HCV-2a, HCV-2b, HCV-2c, HCV-3a, HCV-3b, HCV-3c, HCV-3d, HCV-3e, HCV-3f, HCV-3g, HCV-3h, HCV-3i, HCV-3j, HCV-3k, HCV-3l, HCV-3m, HCV-3n, HCV-3o, HCV-3p, HCV-3q, HCV-3r, HCV-3s, HCV-3t, HCV-3u, HCV-3v, HCV-3w, HCV-3x, HCV-3y, HCV-3z, HCV-3aa, HCV-3ab, HCV-3ac, HCV-3ad, HCV-3ae, HCV-3af, HCV-3ag, HCV-3ah, HCV-3ai, HCV-3aj, HCV-3ak, HCV-3al, HCV-3am, HCV-3an, HCV-3ao, HCV-3ap, HCV-3aq, HCV-3ar, HCV-3as, HCV-3at, HCV-3au, HCV-3av, HCV-3aw, HCV-3ax, HCV-3ay, HCV-3az, HCV-3ba, HCV-3bb, HCV-3bc, HCV-3bd, HCV-3be, HCV-3bf, HCV-3bg, HCV-3bh, HCV-3bi, HCV-3bj, HCV-3bk, HCV-3bl, HCV-3bm, HCV-3bn, HCV-3bo, HCV-3bp, HCV-3bq, HCV-3br, HCV-3bs, HCV-3bt, HCV-3bu, HCV-3bv, HCV-3bw, HCV-3bx, HCV-3by, HCV-3bz, HCV-3ca, HCV-3cb, HCV-3cc, HCV-3cd, HCV-3ce, HCV-3cf, HCV-3cg, HCV-3ch, HCV-3ci, HCV-3cj, HCV-3ck, HCV-3cl, HCV-3cm, HCV-3cn, HCV-3co, HCV-3cp, 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HCV-3gx, HCV-3gy, HCV-3gz, HCV-3ha, HCV-3hb, HCV-3hc, HCV-3hd, HCV-3he, HCV-3hf, HCV-3hg, HCV-3hh, HCV-3hi, HCV-3hj, HCV-3hk, HCV-3hl, HCV-3hm, HCV-3hn, HCV-3ho, HCV-3hp, HCV-3hq, HCV-3hr, HCV-3hs, HCV-3ht, HCV-3hu, HCV-3hv, HCV-3hw, HCV-3hx, HCV-3hy, HCV-3hz, HCV-3ia, HCV-3ib, HCV-3ic, HCV-3id, HCV-3ie, HCV-3if, HCV-3ig, HCV-3ih, HCV-3ii, HCV-3ij, HCV-3ik, HCV-3il, HCV-3im, HCV-3in, HCV-3io, HCV-3ip, HCV-3iq, HCV-3ir, HCV-3is, HCV-3it, HCV-3iu, HCV-3iv, HCV-3iw, HCV-3ix, HCV-3iy, HCV-3iz, HCV-3ja, HCV-3jb, HCV-3jc, HCV-3jd, HCV-3je, HCV-3jf, HCV-3jg, HCV-3jh, HCV-3ji, HCV-3jj, HCV-3jk, HCV-3jl, HCV-3jm, HCV-3jn, HCV-3jo, HCV-3jp, HCV-3jq, HCV-3jr, HCV-3js, HCV-3jt, HCV-3ju, HCV-3jv, HCV-3jw, HCV-3jx, HCV-3jy, HCV-3jz, HCV-3ka, HCV-3kb, HCV-3kc, HCV-3kd, HCV-3ke, HCV-3kf, HCV-3kg, HCV-3kh, HCV-3ki, HCV-3kj, HCV-3kl, HCV-3km, HCV-3kn, HCV-3ko, HCV-3kp, HCV-3kq, HCV-3kr, HCV-3ks, HCV-3kt, HCV-3ku, HCV-3kv, HCV-3kw, HCV-3kx, HCV-3ky, HCV-3kz, HCV-3la, HCV-3lb, HCV-3lc, HCV-3ld, HCV-3le, HCV-3lf, HCV-3lg, HCV-3lh, HCV-3li, HCV-3lj, HCV-3lk, HCV-3ll, HCV-3lm, HCV-3ln, HCV-3lo, HCV-3lp, HCV-3lq, HCV-3lr, HCV-3ls, HCV-3lt, HCV-3lu, HCV-3lv, HCV-3lw, HCV-3lx, HCV-3ly, HCV-3lz, HCV-3ma, HCV-3mb, HCV-3mc, HCV-3md, HCV-3me, HCV-3mf, HCV-3mg, HCV-3mh, HCV-3mi, HCV-3mj, HCV-3mk, HCV-3ml, HCV-3mm, HCV-3mn, HCV-3mo, HCV-3mp, HCV-3mq, HCV-3mr, HCV-3ms, HCV-3mt, HCV-3mu, HCV-3mv, HCV-3mw, HCV-3mx, HCV-3my, HCV-3mz, HCV-3na, HCV-3nb, HCV-3nc, HCV-3nd, HCV-3ne, HCV-3nf, HCV-3ng, HCV-3nh, HCV-3ni, HCV-3nj, HCV-3nk, HCV-3nl, HCV-3nm, HCV-3nn, HCV-3no, HCV-3np, HCV-3nq, HCV-3nr, HCV-3ns, HCV-3nt, HCV-3nu, HCV-3nv, HCV-3nw, HCV-3nx, HCV-3ny, HCV-3nz, HCV-3oa, HCV-3ob, HCV-3oc, HCV-3od, HCV-3oe, HCV-3of, HCV-3og, HCV-3oh, HCV-3oi, HCV-3oj, HCV-3ok, HCV-3ol, HCV-3om, HCV-3on, HCV-3oo, HCV-3op, HCV-3oq, HCV-3or, HCV-3os, HCV-3ot, HCV-3ou, HCV-3ov, HCV-3ow, HCV-3ox, HCV-3oy, HCV-3oz, HCV-3pa, HCV-3pb, HCV-3pc, HCV-3pd, HCV-3pe, HCV-3pf, HCV-3pg, HCV-3ph, HCV-3pi, HCV-3pj, HCV-3pk, HCV-3pl, HCV-3pm, HCV-3pn, HCV-3po, HCV-3pp, HCV-3pq, HCV-3pr, HCV-3ps, HCV-3pt, HCV-3pu, HCV-3pv, HCV-3pw, HCV-3px, HCV-3py, HCV-3pz, HCV-3qa, HCV-3qb, HCV-3qc, HCV-3qd, HCV-3qe, HCV-3qf, HCV-3qg, HCV-3qh, HCV-3qi, HCV-3qj, HCV-3qk, HCV-3ql, HCV-3qm, HCV-3qn, HCV-3qo, HCV-3qp, HCV-3qq, HCV-3qr, HCV-3qs, HCV-3qt, HCV-3qu, HCV-3qv, HCV-3qw, HCV-3qx, HCV-3qy, HCV-3qz, HCV-3ra, HCV-3rb, HCV-3rc, HCV-3rd, HCV-3re, HCV-3rf, HCV-3rg, HCV-3rh, HCV-3ri, HCV-3rj, HCV-3rk, HCV-3rl, HCV-3rm, HCV-3rn, HCV-3ro, HCV-3rp, HCV-3rq, HCV-3rr, HCV-3rs, HCV-3rt, HCV-3ru, HCV-3rv, HCV-3rw, HCV-3rx, HCV-3ry, HCV-3rz, HCV-3sa, HCV-3sb, HCV-3sc, HCV-3sd, HCV-3se, HCV-3sf, HCV-3sg, HCV-3sh, HCV-3si, HCV-3sj, HCV-3sk, HCV-3sl, HCV-3sm, HCV-3sn, HCV-3so, HCV-3sp, HCV-3sq, HCV-3sr, HCV-3ss, HCV-3st, HCV-3su, HCV-3sv, HCV-3sw, HCV-3sx, HCV-3sy, HCV-3sz, HCV-3ta, HCV-3tb, HCV-3tc, HCV-3td, HCV-3te, HCV-3tf, HCV-3tg, HCV-3th, HCV-3ti, HCV-3tj, HCV-3tk, HCV-3tl, HCV-3tm, HCV-3tn, HCV-3to, HCV-3tp, HCV-3tq, HCV-3tr, HCV-3ts, HCV-3tt, HCV-3tu, HCV-3tv, HCV-3tw, HCV-3tx, HCV-3ty, HCV-3tz, HCV-3ua, HCV-3ub, HCV-3uc, HCV-3ud, HCV-3ue, HCV-3uf, HCV-3ug, HCV-3uh, HCV-3ui, HCV-3uj, HCV-3uk, HCV-3ul, HCV-3um, HCV-3un, HCV-3uo, HCV-3up, HCV-3uq, HCV-3ur, HCV-3us, HCV-3ut, HCV-3uu, HCV-3uv, HCV-3uw, HCV-3ux, HCV-3uy, HCV-3uz, HCV-3va, HCV-3vb, HCV-3vc, HCV-3vd, HCV-3ve, HCV-3vf, HCV-3vg, HCV-3vh, HCV-3vi, HCV-3vj, HCV-3vk, HCV-3vl, HCV-3vm, HCV-3vn, HCV-3vo, HCV-3vp, HCV-3vq, HCV-3vr, HCV-3vs, HCV-3vt, HCV-3vu, HCV-3vv, HCV-3vw, HCV-3vx, HCV-3vy, HCV-3vz, HCV-3wa, HCV-3wb, HCV-3wc, HCV-3wd, HCV-3we, HCV-3wf, HCV-3wg, HCV-3wh, HCV-3wi, HCV-3wj, HCV-3wk, HCV-3wl, HCV-3wm, HCV-3wn, HCV-3wo, HCV-3wp, HCV-3wq, HCV-3wr, HCV-3ws, HCV-3wt, HCV-3wu, HCV-3wv, HCV-3ww, HCV-3wx, HCV-3wy, HCV-3wz, HCV-3xa, HCV-3xb, HCV-3xc, HCV-3xd, HCV-3xe, HCV-3xf, HCV-3x

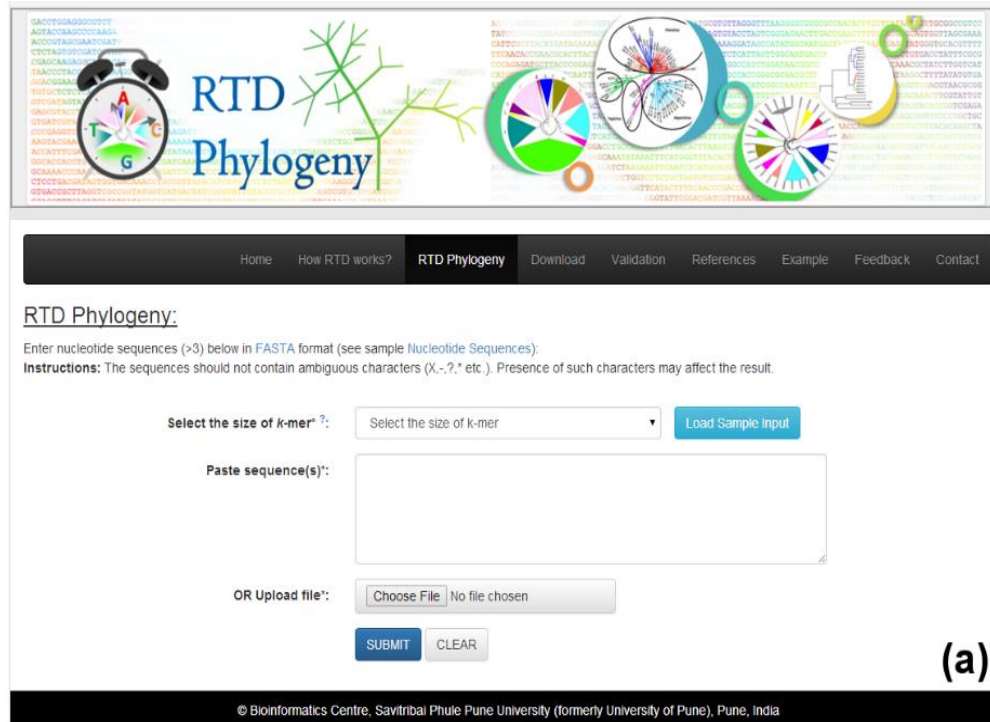
Sequence similarity: 40-86%

The phylogenetic tree illustrates the evolutionary relationships between several virus families. The Flavivirus family is the largest and most diverse, with members like DENV-1, DENV-2, DENV-3, DENV-4, MMLV, RBV, MODV, TABV, and KRV. The Pestivirus family includes BVDV-1, BVDV-2, CSFV, PESRE, and BDV. The Peavivirus family includes HGBV-A, HGBV-B, HGBV-C, and HGBV-D. The Hepacivirus family includes HCV-2a, HCV-2b, HCV-2c, HCV-3a, HCV-3b, HCV-3c, HCV-3d, HCV-3e, HCV-3f, HCV-3g, HCV-3h, HCV-3i, HCV-3j, HCV-3k, HCV-3l, HCV-3m, HCV-3n, HCV-3o, HCV-3p, HCV-3q, HCV-3r, HCV-3s, HCV-3t, HCV-3u, HCV-3v, HCV-3w, HCV-3x, HCV-3y, and HCV-3z.



RTD Phylogeny: alignment-free phylogeny server

<http://bioinfo.unipune.ac.in/RTD/Home.html>



The image shows the RTD Phylogeny web interface. At the top, there is a header with the text "RTD Phylogeny" and a logo featuring a clock and a tree. Below the header is a navigation bar with links: Home, How RTD works?, RTD Phylogeny, Download, Validation, References, Example, Feedback, and Contact. The main content area is titled "RTD Phylogeny:" and contains instructions: "Enter nucleotide sequences (>3) below in FASTA format (see sample Nucleotide Sequences):" and "Instructions: The sequences should not contain ambiguous characters (X, -, ?, * etc.). Presence of such characters may affect the result." There are two input methods: "Select the size of k-mer" with a dropdown menu and a "Load Sample Input" button, and "Paste sequence(s):" with a text area. Below these is an "OR Upload file:" section with a "Choose File" button and a "No file chosen" status. At the bottom are "SUBMIT" and "CLEAR" buttons. The footer contains the copyright information: "© Bioinformatics Centre, Savitribai Phule Pune University (formerly University of Pune), Pune, India".

RTD Phylogeny:

Enter nucleotide sequences (>3) below in FASTA format (see sample Nucleotide Sequences):

Instructions: The sequences should not contain ambiguous characters (X, -, ?, * etc.). Presence of such characters may affect the result.

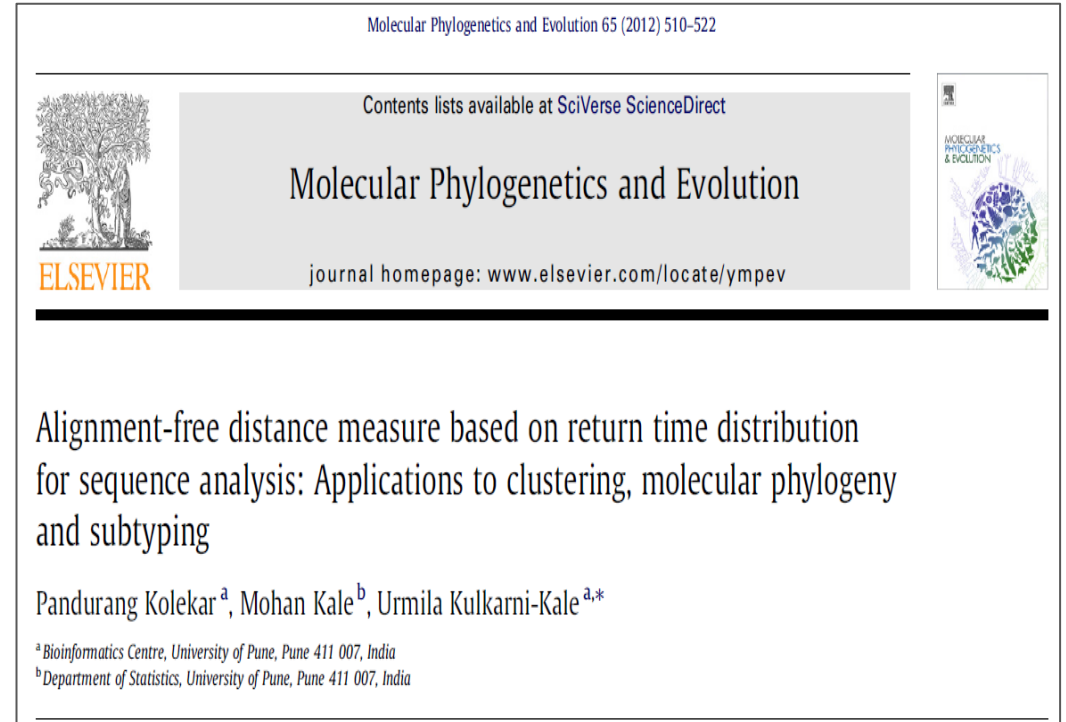
Select the size of k-mer:

Paste sequence(s):

OR Upload file: No file chosen

(a)

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The image shows the cover of the journal "Molecular Phylogenetics and Evolution". At the top, it says "Molecular Phylogenetics and Evolution 65 (2012) 510–522". Below this is a navigation bar with "Contents lists available at SciVerse ScienceDirect". The journal title "Molecular Phylogenetics and Evolution" is prominently displayed. Below the title is the journal homepage: "journal homepage: www.elsevier.com/locate/ympev". The Elsevier logo is on the left, and a small tree diagram is on the right. The bottom section contains the text "Alignment-free distance measure based on return time distribution for sequence analysis: Applications to clustering, molecular phylogeny and subtyping" and the authors "Pandurang Kolekar^a, Mohan Kale^b, Urmila Kulkarni-Kale^{a,*}". Footnotes provide the affiliations: ^aBioinformatics Centre, University of Pune, Pune 411 007, India and ^bDepartment of Statistics, University of Pune, Pune 411 007, India.

Molecular Phylogenetics and Evolution 65 (2012) 510–522

Contents lists available at SciVerse ScienceDirect

Molecular Phylogenetics and Evolution

journal homepage: www.elsevier.com/locate/ympev

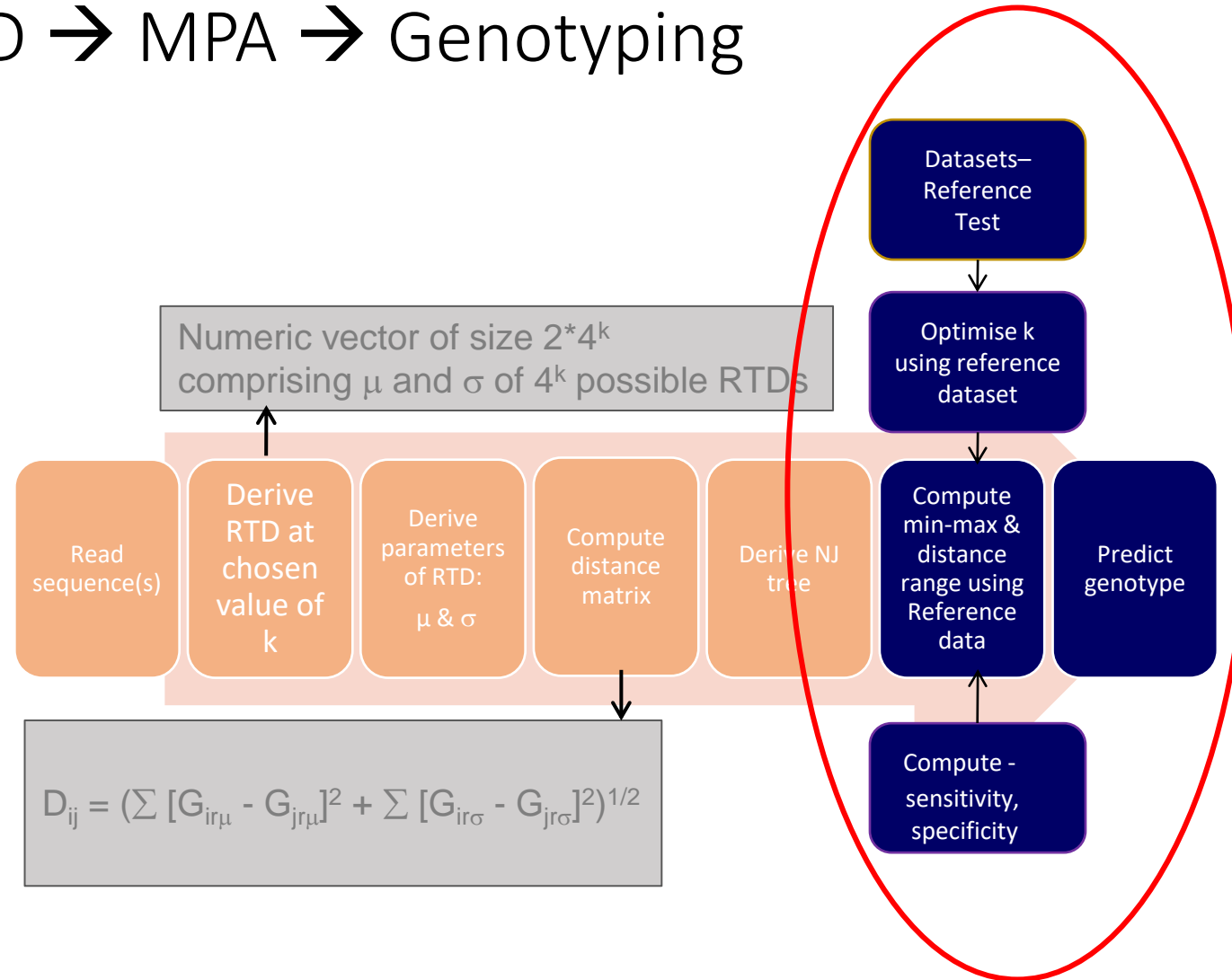
Alignment-free distance measure based on return time distribution for sequence analysis: Applications to clustering, molecular phylogeny and subtyping

Pandurang Kolekar^a, Mohan Kale^b, Urmila Kulkarni-Kale^{a,*}

^aBioinformatics Centre, University of Pune, Pune 411 007, India

^bDepartment of Statistics, University of Pune, Pune 411 007, India

RTD → MPA → Genotyping



Genotyping of *Mumps viruses*

Genus *Rubulavirus* | family *Paramyxoviridae*

et al. Immunome Research 2011, 7:3:4
www.immunome-research.net/



SEARCH

Open Access

Genotyping of Mumps viruses based on SH gene: Development of a server using alignment-free and alignment-based methods

Prang S Kolekar¹, Mohan M Kale², Urmila Kulkarni-Kale^{1*}

Abstract

Mumps is an acute infectious childhood disease caused by mumps virus (MuV), a member of genus Rubulavirus, family Paramyxoviridae. Based on the genetic variability in small hydrophobic (SH) genes, current MuVs have been divided into twelve confirmed genotypes designated as A-L and one proposed genotype, M. Despite successful vaccination program, a few genotypes are observed to co-circulate in the vaccinated population. Furthermore, lack of cross protection between different genotypes is evident and hence, as a part of epidemiological surveillance, WHO has recommended genotyping of MuV. Currently genotyping is carried out using molecular phylogeny analysis (MPA) of SH genes and no genotyping server is available for MuV. The present study reports development of a genotyping server for the

- Known genotypes: 15
- Input : **SH gene**
- Optimum k=4
- Sensitivity : 98.95%*
- Specificity : 100%
- *Annotation error in GenBank

MuV Genotyping Server

[Home](#) [Blast Search](#) [Phylogeny](#) [RTD based genotyping](#) [Combined analysis](#) [Datasets](#) [Validation](#) [References](#) [Examples](#) [Contact Us](#)

Description of the server:

Mumps Virus (MuV) genotyping server assigns genotype to query sequence(s) of small hydrophobic (SH) gene. The server uses two conventional methods viz., BLAST, molecular phylogeny analysis (MPA) and a novel method based on Return Time Distribution (RTD), which is developed in-house.

[Go to Combined analysis based genotyping \(by BLAST, Phylogeny and RTD\)](#)

[Go to BLAST-based genotyping](#)

[Go to Phylogeny-based genotyping](#)

[Go to RTD-based genotyping](#)

Citation information:

Kolekar PS, Kale M, Kulkarni-Kale U: Genotyping of Mumps viruses based on SH gene: Development of a server using alignment-free and alignment-based methods. Immunome Res. 2011. 7(3):1-7. [PMID: 22126822]

Also Visit:

[CEP : Conformational Epitope Prediction Server](#)

[AgAbDb : Antigen Antibody Interaction Database](#)

[VPS : Viral Protein Structure Resource](#)



Mumps virus genotyping server has been developed at [Bioinformatics Centre, University of Pune](#), funded by [Department of Biotechnology](#), Government of India under Centre of Excellence (CoE) grant.

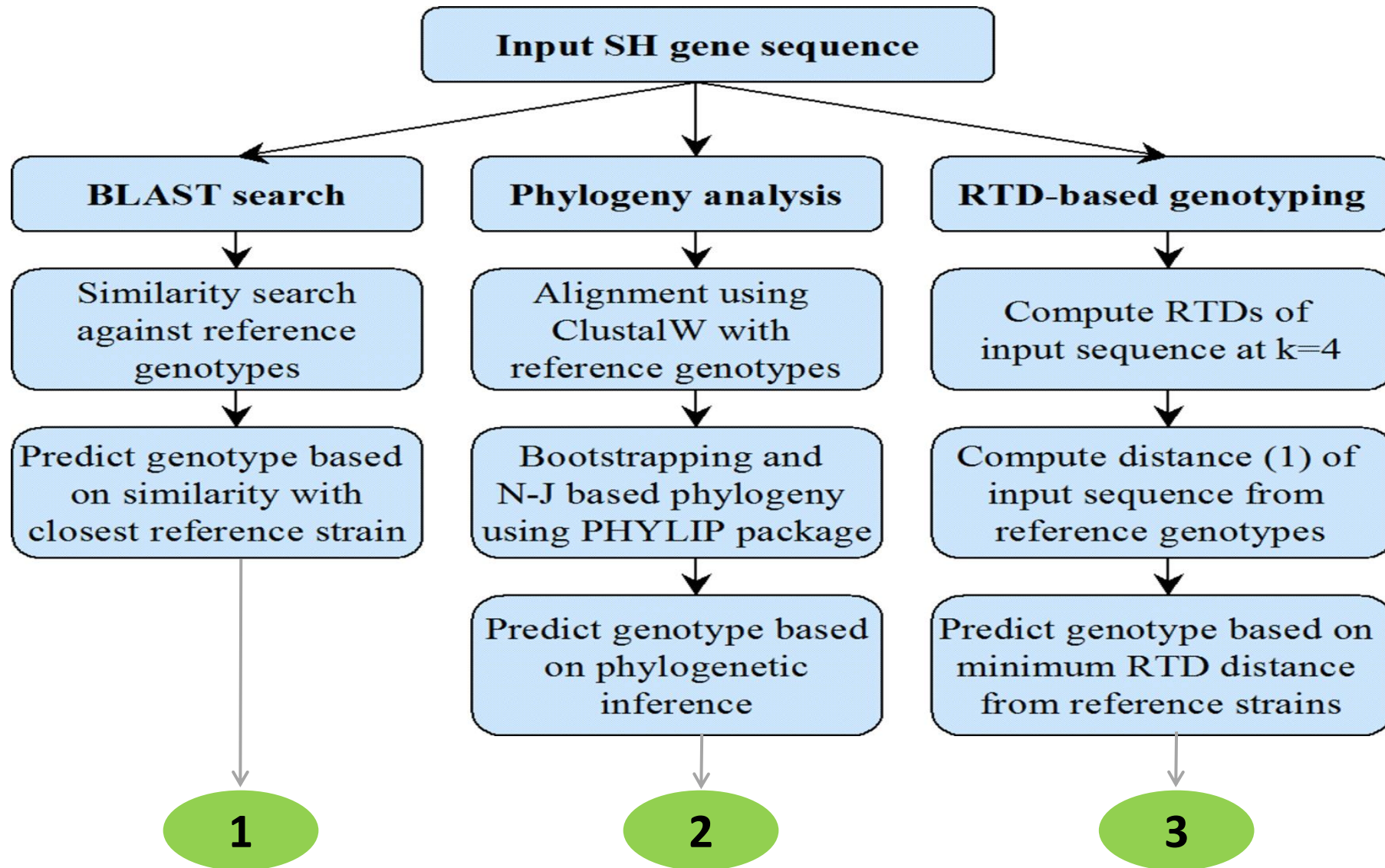


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Available at:

<http://bioinfo.net.in/muv/homepage.html>

How Mumps Genotyping server works



Dengue viruses : Serotypes & Genotypes

Dengue virus (DENV):

Genus: *Flavivirus*; family: *Flaviviridae*

Single-stranded positive sense RNA virus

Simple genome: ~10.5Kb; 3 structural and 7 non-structural genes

Four distinct '**serotypes**': DENV-1, DENV-2, DENV-3 and DENV -4

Each serotype is further divided into phylogenetically distinct '**genotypes**'

Dengue virus serotype 1

- Genotype I
- Genotype II
- Genotype III
- Sylvatic

MS under preparation

Dengue virus serotype 2

- American
- Asian-I
- Asian-II
- Asian/American
- Cosmopolitan
- Sylvatic

Waman et al., 2016

Dengue virus serotype 3

- Genotype I
- Genotype II
- Genotype III
- Genotype IV
- Genotype V

Waman et al., 2017

Dengue virus serotype 4

- Genotype I
- Genotype II
- Genotype II
- Sylvatic

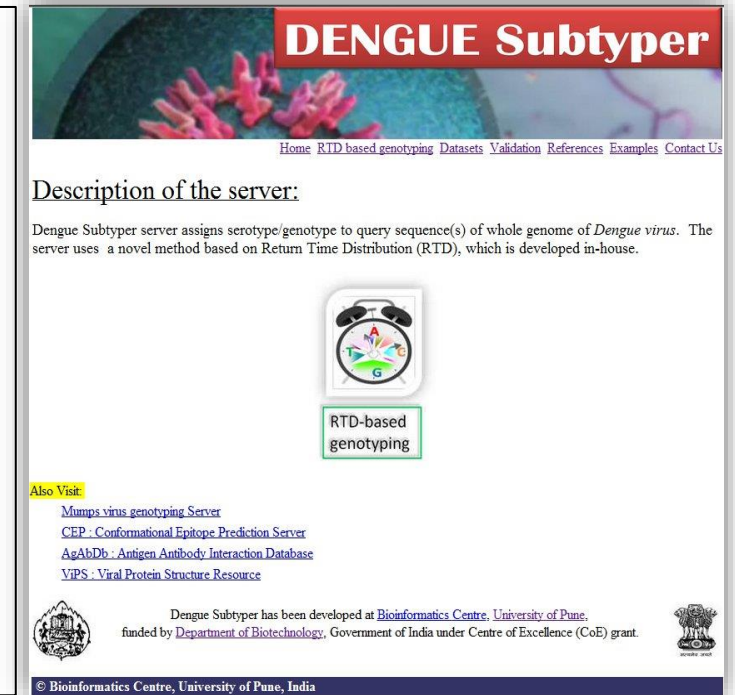
Waman et al., 2016

Subtyping of *Dengue viruses*

Genus *Flavivirus* | Family *Flaviviridae*



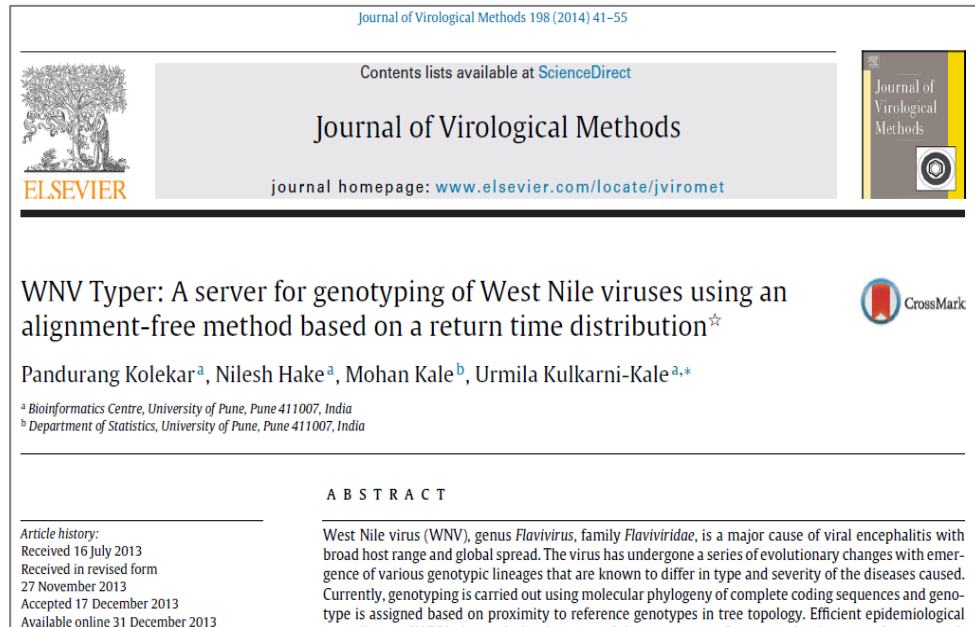
- Input : **Whole genome**
- Optimum k=5
- Reference dataset: 57
- Test dataset: 371
- Sensitivity : 100%
- Specificity : 100%
- Kolekar et al (2012) Mol Phyl Evol . 65(2):510-22.



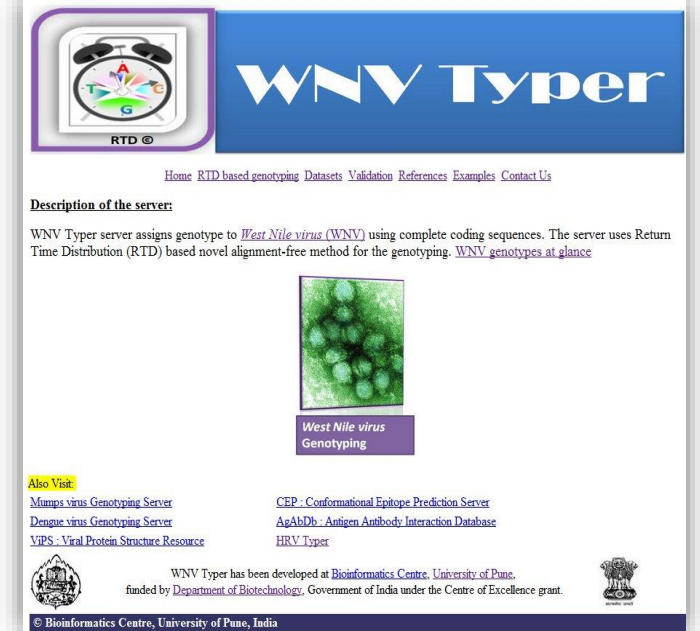
Available at:
<http://bioinfo.net.in/dengue/homepage.html>

Genotyping of *West nile viruses*

Genus *Flavivirus* | Family *Flaviviridae*



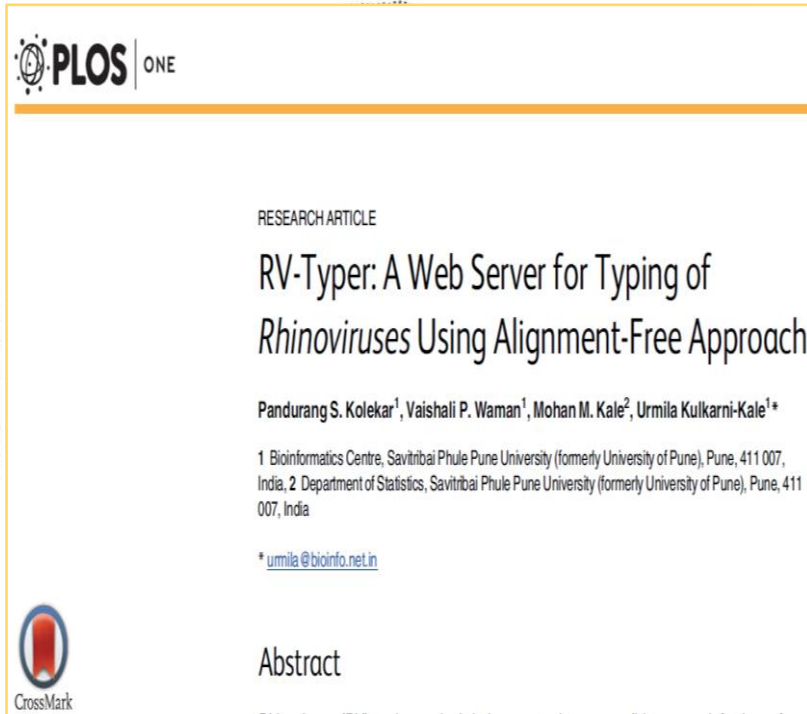
- Input : **Whole genome**
- Optimum k=7
- Reference dataset: 61
- Test dataset: 566
- Sensitivity : 100%
- Specificity : 100%



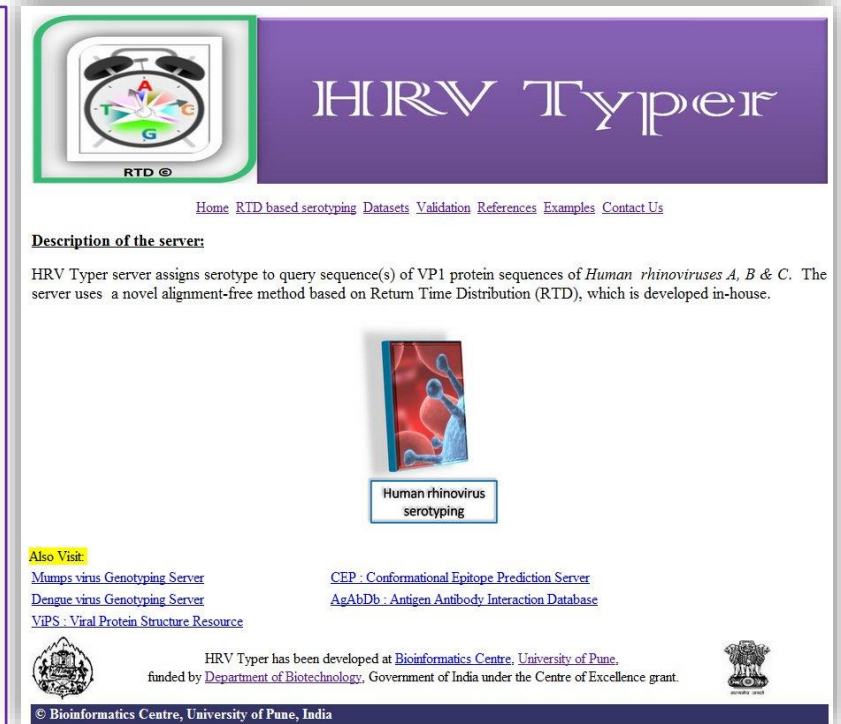
Available at:
<http://bioinfo.net.in/wnv/homepage.html>

Genotyping of *Human rhinoviruses*

Genus Enterovirus | Family *Picornaviridae*

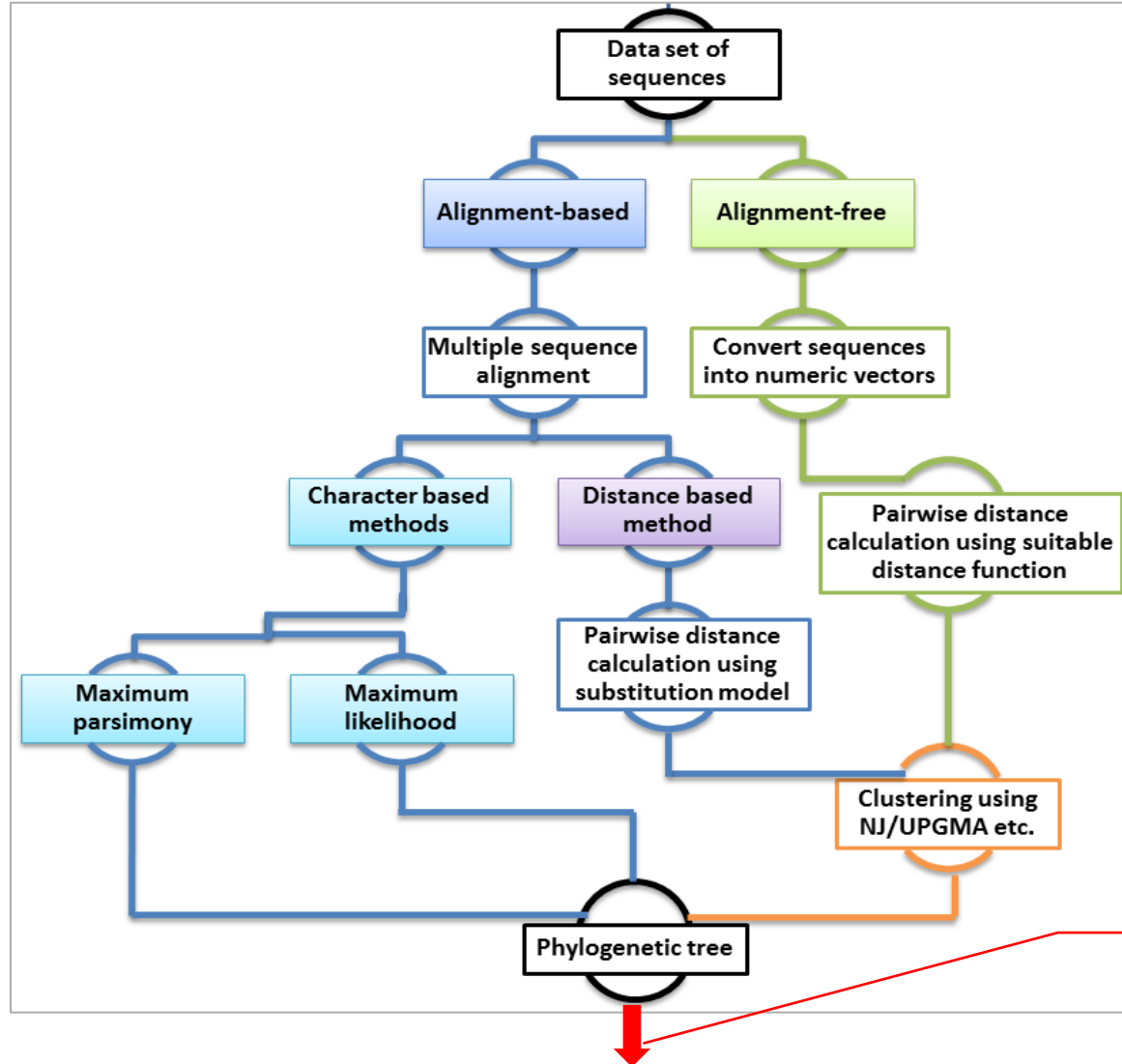


- Input : **VP1 protein**
- Optimum k=1
- Reference dataset: 432
RV-A (238), -B (83) and
-C (111)
- Test dataset: 218
- Sensitivity : 100%
- Specificity : 100%



Available at:
<http://bioinfo.net.in/hrv/homepage.html>

Molecular Phylogeny Approaches for Viral Typing



Alignment-free Phylogeny:

- Quick computations
- High accuracy
- Works equally well with sequences having similarity in the range of 25-99%
- Uses BLOCK-Bootstrap

Knowledge-based Servers for Viral Typing

Assign geno- /serotype based on clustering proximity of unknown with known

RTD for Clustering, Molecular Phylogeny, Genotyping, Serotyping & Multi-Locus Sequence Typing

