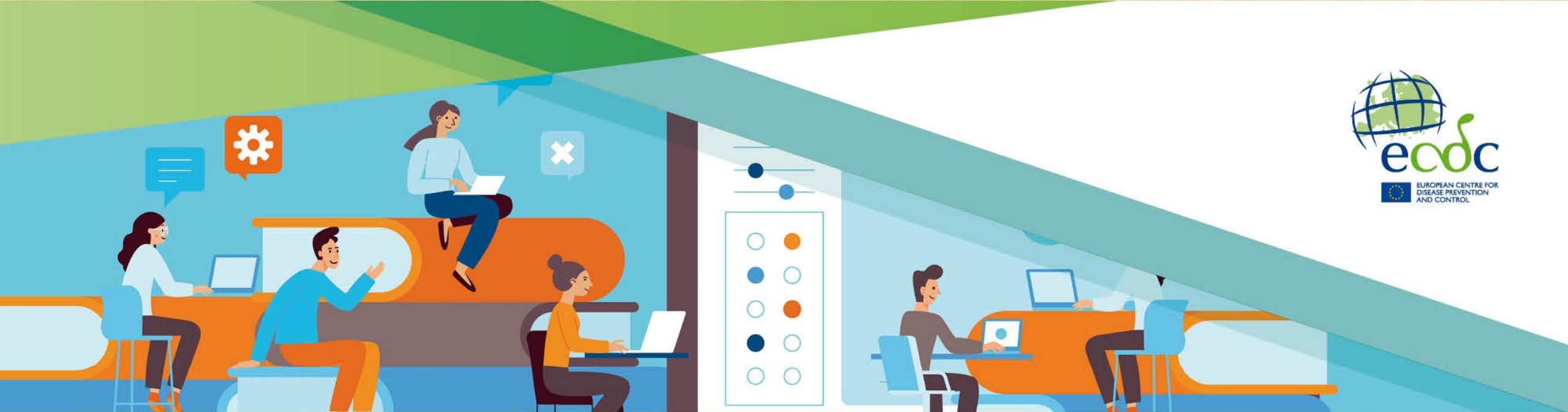




Genomics and epidemiology of polioviruses: How a virus resists eradication

Guided correction of exercise

July 2027

Darlan da Silva Candido, PhD

Wellcome ECA Research Fellow, Imperial College London

Aim and learning objectives

Use genetic sequences to characterise and understand basic aspects of poliovirus spread during outbreaks

Specific learning objectives

At the end of this session, you will be able to:

1. **Understand** how to build your own background dataset.
2. **Generate** your own multiple sequence alignment and perform alignment quality control.
3. **Generate** a maximum likelihood phylogenetic tree.
4. **Root and interpret** a tree using FigTree.
5. **Perform** quality control of phylogenetic analysis.
6. **Build** a microreact project.

Outline

This session consists of the following elements

1. Building a multiple sequence alignment
2. Multiple sequence alignment
3. Maximum likelihood tree
4. Tree visualisation and interpretation
5. Exercise answers
6. Microreact

Building a background dataset

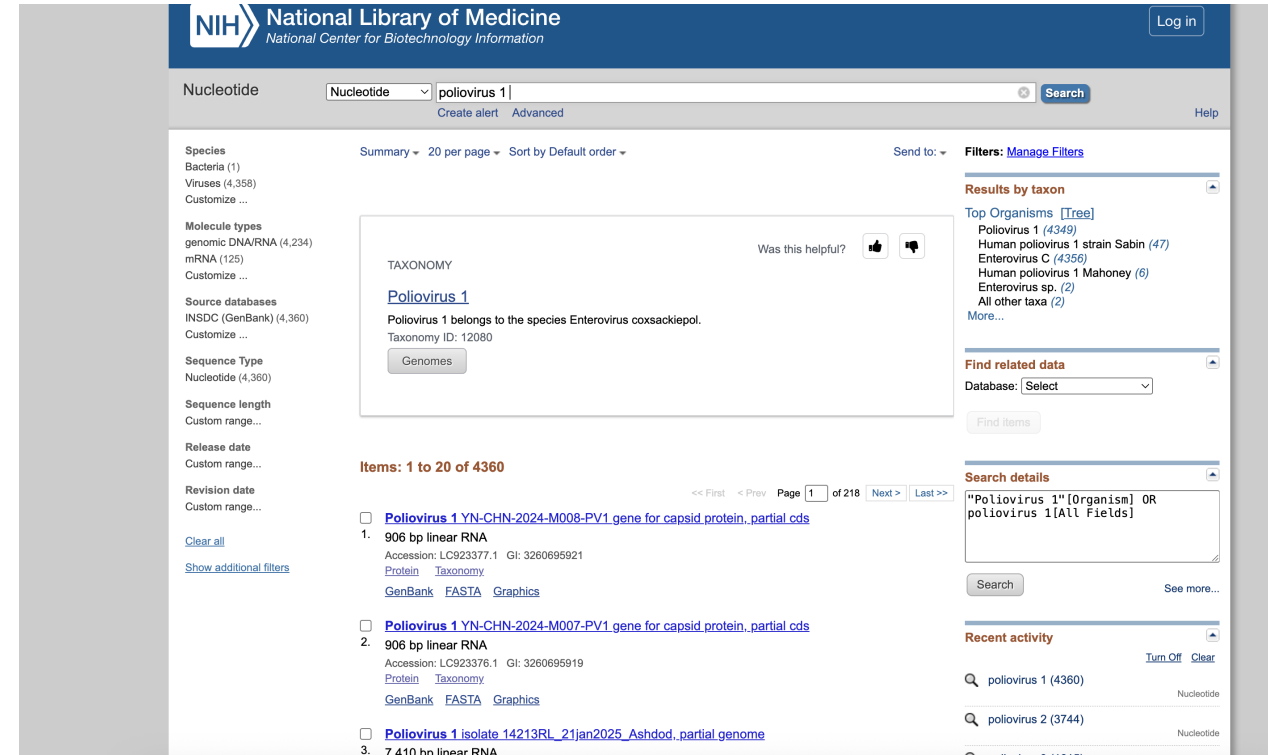
- Go to the main databases that keep sequences of the viruses you are investigating and download the information;
- Remove sequences which might belong to experiments, product development, reference genomes, duplicates or anything that might not represent the process you are trying to investigate.

What is a good background dataset?

- It will depend on the question you are trying to answer
- Representative of the biology and epidemiology of the virus
- Evolutionary, geographically and temporally balanced
- Large enough (No need to be super large and repetitive)
- Good quality sequences (i.e., without lots of gaps, ambiguities, missing information or poor assembling)

Building a background dataset

- Sequences of poliovirus 1, 2 and 3, from different countries and years
- Sabin 1, 2 and 3
- Virus is extremely unlikely to be wild type poliovirus 2 and 3
- Wild type poliovirus 1 diversity more closely related to Pakistan and Afghanistan
- Vaccine viruses are more likely to be Sabin 2
- Your dataset will be limited to the sequences you have access to, i.e., publicly available or that might have been made available to you.



The screenshot shows the NCBI search results for 'poliovirus 1'. The search bar at the top shows 'poliovirus 1' with a search button. Below the search bar, there are filters for 'Nucleotide' and 'Create alert'. The main results area shows a list of items, with the first item being 'Poliovirus 1 YN-CHN-2024-M008-PV1 gene for capsid protein, partial cds'. The results are sorted by 'Default order' and show 1 to 20 of 4360 items. The right sidebar contains 'Results by taxon', 'Find related data', 'Search details', and 'Recent activity'.

NIH National Library of Medicine
National Center for Biotechnology Information

Nucleotide Search

Summary 20 per page Sort by Default order

Species: Bacteria (1), Viruses (4,358), Customize ...

Molecule types: genomic DNA/RNA (4,234), mRNA (125), Customize ...

Source databases: INSDC (GenBank) (4,360), Customize ...

Sequence Type: Nucleotide (4,360)

Sequence length: Custom range...

Release date: Custom range...

Revision date: Custom range...

[Clear all](#)

[Show additional filters](#)

TAXONOMY

[Poliovirus 1](#)

Poliovirus 1 belongs to the species Enterovirus coxsackiepol.

Taxonomy ID: 12080

[Genomes](#)

Was this helpful?

Items: 1 to 20 of 4360

<< First < Prev Page 1 of 218 Next > Last >>

☐ [Poliovirus 1 YN-CHN-2024-M008-PV1 gene for capsid protein, partial cds](#)

1. 906 bp linear RNA
Accession: LC923377.1 GI: 3260695921
[Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

☐ [Poliovirus 1 YN-CHN-2024-M007-PV1 gene for capsid protein, partial cds](#)

2. 906 bp linear RNA
Accession: LC923376.1 GI: 3260695919
[Protein](#) [Taxonomy](#)
[GenBank](#) [FASTA](#) [Graphics](#)

☐ [Poliovirus 1 isolate 14213RL_21jan2025_Ashdod, partial genome](#)

3. 7,410 bp linear RNA

Results by taxon

Top Organisms [Tree](#)

Poliovirus 1 (4349)
Human poliovirus 1 strain Sabin (47)
Enterovirus C (4356)
Human poliovirus 1 Mahoney (6)
Enterovirus sp. (2)
All other taxa (2)
[More...](#)

Find related data

Database:

[Find items](#)

Search details

"Poliovirus 1"[Organism] OR poliovirus 1[All Fields]

[See more...](#)

Recent activity

[Turn Off](#) [Clear](#)

☐ poliovirus 1 (4360) Nucleotide

☐ poliovirus 2 (3744) Nucleotide

☐ poliovirus 3 (1615) Nucleotide

Building a background dataset

	10	20	30
AY184221.1 Sabin 3	g g t a t t g a a g a t t t g a c t t c t g a a g t t g c a		
AY082688.1 Sabin1	g g g t t a g g t c a g a t g c t t g a a a g c a t g a t t t		
Sabin 2	G G A A U U G G U G A C A U G A U U G A G G G G C C G U U		
KR817066.1 Human WPV2 AFP CAM80 Cameroon_NA 1980	G G G C T G G G T G G C T T G A T T G A A G G G G T T A T C		
KR817065.1 Human WPV2 AFP KUW80 Kuwait_NA 1980	G G G C T T G G C A A C T T G A T T G A A G G G G T A G T C		
KR817064.1 Human WPV2 AFP MOR78 Morocco_NA 1978	G G G C T G G G A G A T C T A A T A G A G G G A G T C T T		
HQ286321.1 Human WPV2 AFP IND9911248 India_NA 1999	G G T C T G G G A G A T C T G C T A G A G G C G T G A T T		
HQ286320.1 Human WPV2 AFP CIV9411247 CotedIvoire_NA 1994	G G G T T G G G C G A C T T G A T C G A A G G G G T C A T T		
AF551798.1 Human WPV2 AFP 0297_EGY79 Egypt_NA 1979	G G G C T T G G T G A C T T G A T T G A A G G G G C A G T C		
AF551800.1 Human WPV2 Contact 2203_BAN82 Bangladesh_NA 1982	G G T T T G G G A G A C T T G C T A G A G G G A G T G A T T		
AF551802.1 Human WPV2 AFP 0864_GEO87 Georgia_NA 1987	G G G T T G G G T A A C A T G A T T G A A A G G G C C A T T		
AF551805.1 Human WPV2 AFP 3825_PAK91 Pakistan_NA 1991	G G C C T G G G A G A C C T G C T A G A A G G A G T G A T T		
EU046199_1 Human WPV1 AFP ANG-LUA-KIL-07-003 Angola_Kilamba-Kia	G G T T T G G G C C A G A T G C T T G A G A G T A T G A T T		
EU046210_1 Human WPV1 AFP NAM-KHO-WHK-06-018 Namibia_Windhoel	G G T T T G G G C C A A A T G C T C G A G A G T A T G A T T		
EU046219_1 Human WPV1 AFP RDC-EQT-ING-07-002 DRC_NA 2007	G G T T T G G G C C A A A T G C T C G A G A G T A T G A T T		
JF838288_1 Human WPV1 AFP PV1-RC2010-43 Congo_NA 2010	G G T T T G G G C C A G A T G C T T G A G A G T A T G A T T		
JQ906480_1 Human WPV1 AFP NW_40_07_082_Mardan Pakistan_Mardan 2	G G C T T G G G G C A A A T G C T C G A G A G T A T G A T T		
KC880369_1 Human WPV1 AFP TJK35363 Tajikistan_Bokhtar 2010-04-10	G G T T T G G G C C A G A T G C T C G A G A G C A T G A T T		
KC880380_1 Human WPV1 AFP RUS36815 Russia_Moscow 2010-06-08	G G T T T G G G C C A G A T G C T C G A G A A C A T G A T T		
KC880387_1 Human WPV1 AFP TJK35313 Tajikistan_Varzob 2010-04-12	G G T T T G G G C C A G A T G C T C G A G A G C A T G A T T		
KJ502551_1 Human WPV1 AFP DRC1118832 DRC_NA 2011	G G T T T G G G C C A G A T G A T T G A G A G T A T G A T T		
KU925280_1 Human WPV1 AFP CAE1419303 Cameroon_NA 2014	G G C C T G G G A C A G A T G T T G G A G A A C A T G A T T		
KY162693_1 Human WPV1 NA EQG1419331 EquatorialGuinea_NA 2014-03	G G C C T G G G A C A G A T G T T G G A G A A C A T G A T T		
AM707031.1 Human WPV3 AFP Tz18_92 Tunisia_Tozeur 1992	G G T A T G A T G A T T T G A T A A C T G A G G T G G C A		
AY189884.1 Human WPV3 AFP INDMHBM00113 India_BastiDistrict 2000-0	G G A G T A G A A G A T T T G A T A T C C G A A G T G G C A		
AY221224.1 Human WPV3 AFP AFG0111673 Afghanistan_NA 2001	G G A G T A G A A G A C T T G A T A T C C G A G G T G G C G		
FJ842158.1 Human WPV3 Aseptic_meningitis FIN84-60212 Finland_NA 198	G G G G T G G A T G A T C T G A T A A C T G A G G T G G C G		
GU562882.1 Human WPV3 ? NIE0311205 Nigeria_NA 2003	G G G G T C G A T G A T T T G A T A T C T G A G G T A G C A		
GU562886.1 Human WPV3 ? CHA9911209 Chad_NA 1999	G G G G T C G A T G A T T T G A T A A C C G A G G T A G C A		
HQ286297.1 Human WPV3 AFP INO9511254 Indonesia_NA 1995	G G G G T G G A T G A C T T G A T A A C T G A A G T A G C A		
HQ286301.1 Human WPV3 AFP PAK0911257 Pakistan_NA 2009	G G A G T A G A T G A T C T T A T A A C T G A G G T A A C A		
JN812654.1 Human WPV3 AFP 78_BRA-RN_88 Brazil_RN 1988	G G G G T G G A C G A T C T G A T A A C A G A A G T G G C A		
KU925285.1 Human WPV3 AFP CAE0919310 Cameroon_NA 2009	G G G G T G A T G A C T T G A T A T C T G A G G T A G C A		

Why do we have to align?

Organize sites/positions that are homologues (if the organisms or genes or regions are homologues, so are their nucleotides)

To perform evolutionary/phylogenetics analysis – homology assumption (population history)

So...sequence alignments try to maximize similarities;

recover historical information

<i>Bonobo</i>	-	t	t	t	t	t	t	c	t	t	t	t	t	g	t	t	c	a	a	c	g	t	t	t	-	t	g	a	c	t	g	g	a	a	a	g	a	a	g	a	t	t	a	c	-
<i>Chimp</i>	-	t	t	t	t	t	t	c	t	t	t	t	t	g	t	t	c	a	a	c	g	t	t	t	-	t	g	a	c	t	g	g	a	a	a	g	a	a	g	a	t	t	a	c	c
<i>Human</i>	t	t	t	t	t	t	t	c	t	t	t	t	t	g	t	t	c	a	a	c	g	t	t	t	t	t	g	a	c	t	g	g	a	a	a	g	a	a	g	t	t	t	c	c	-
<i>Gorilla</i>	t	t	t	t	t	t	t	c	t	t	t	t	t	g	t	t	c	a	a	c	g	t	t	t	-	t	g	a	c	t	g	g	a	a	a	g	a	a	g	t	t	t	c	c	-

Multiple sequence alignment

Algorithms: Progressive /iterative; Hidden Markov Model

For multiple sequences

These methods differ in speed, accuracy, and their approach to minimizing errors caused by distant evolutionary relationships

Progressive: Build the alignment once by progressively adding sequences or groups of sequences

Iterative: Repeatedly improve an existing alignment (usually progressively generated)

Feature	Progressive	Iterative
Speed	Very Fast	Moderate
Accuracy	Low to Moderate	High
Error Handling	Propagates errors	Corrects errors
Best Use Case	Large datasets	Refinement/Medium set
Example	ClustalW	MUSCLE, MAFFT

Multiple sequence alignment

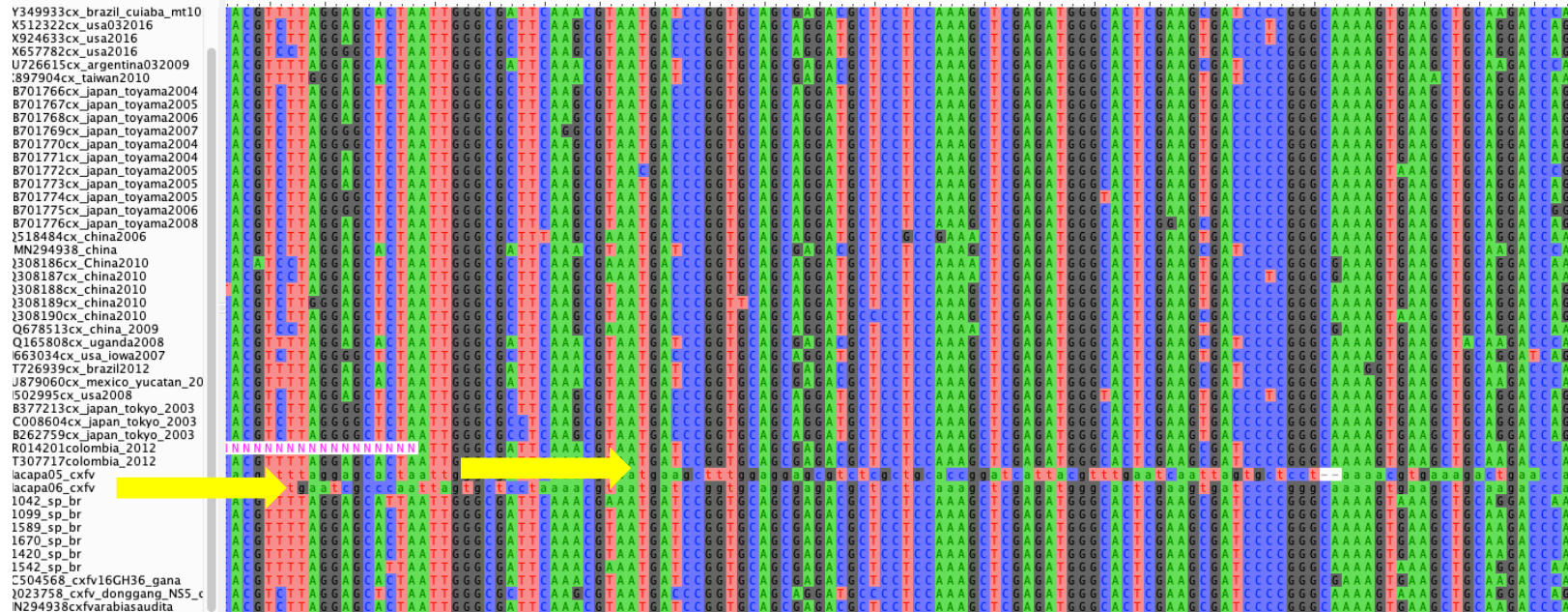
mafft -auto Background_dataset.fasta > align_Background_dataset.fasta

```
Last login: Tue Jul 14 16:12:20 on ttys001
(base) ddasilva@IC-P2PF9XL450 ~ % cd /Users/ddasilva/Dropbox/Mac/Desktop/ECDC_training/Class/Alignments
(base) ddasilva@IC-P2PF9XL450 Alignments % mafft --auto Background_dataset.fasta > align_Background_dataset.fasta
outputhat23=16
treein = 0
compacttree = 0
stacksize: 8176 kb
generating a scoring matrix for nucleotide (dist=200) ... done
All-to-all alignment.
tbfast-pair (nuc) Version 7.490
alg=L, model=DNA200 (2), 2.00 (6.00), -0.10 (-0.30), noshift, amax=0.0
0 thread(s)

outputhat23=16
Loading 'hat3.seed' ...
done.
Writing hat3 for iterative refinement
generating a scoring matrix for nucleotide (dist=200) ... done
Gap Penalty = -1.53, +0.00, +0.00
tbtree = 1, compacttree = 0
Constructing a UPGMA tree ...
  30 / 33
done.

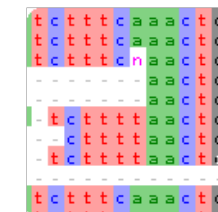
Progressive alignment ...
STEP   32 /32
done.
tbfast (nuc) Version 7.490
alg=A, model=DNA200 (2), 1.53 (4.59), -0.00 (-0.00), noshift, amax=0.0
1 thread(s)
```

Multiple sequence alignment



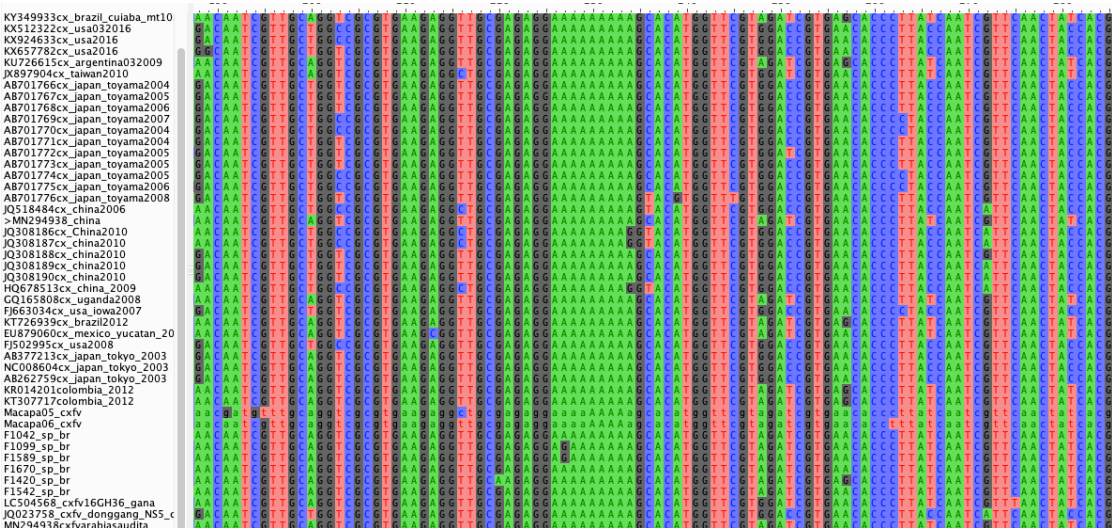
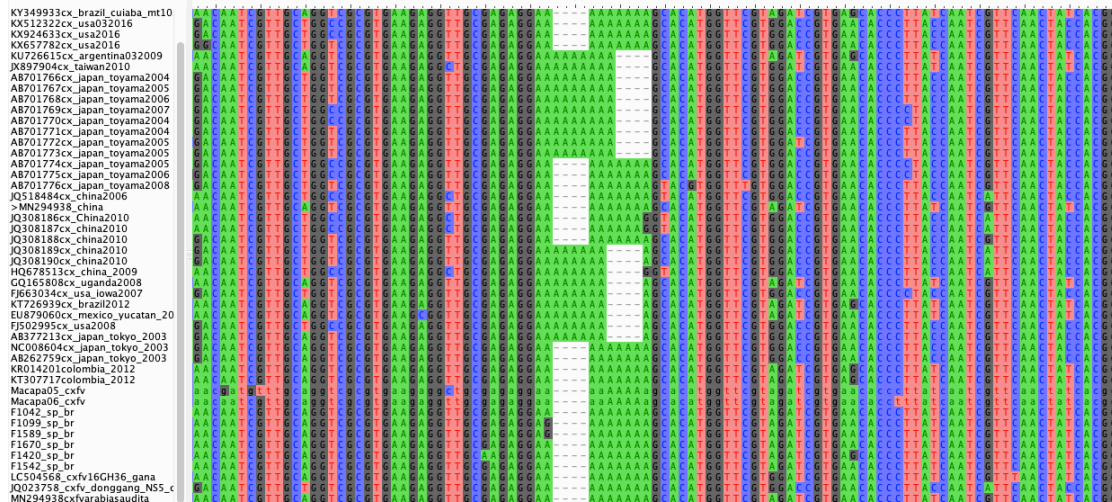
ALIVIEW

- ✓ Assembly issues (low coverage?)
- ✓ Reverse-complement genome
- ✓ Other region /same virus
- ✓ Same region/ Other virus

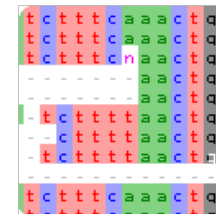


<https://github.com/AliView/AliView>

Multiple sequence alignment



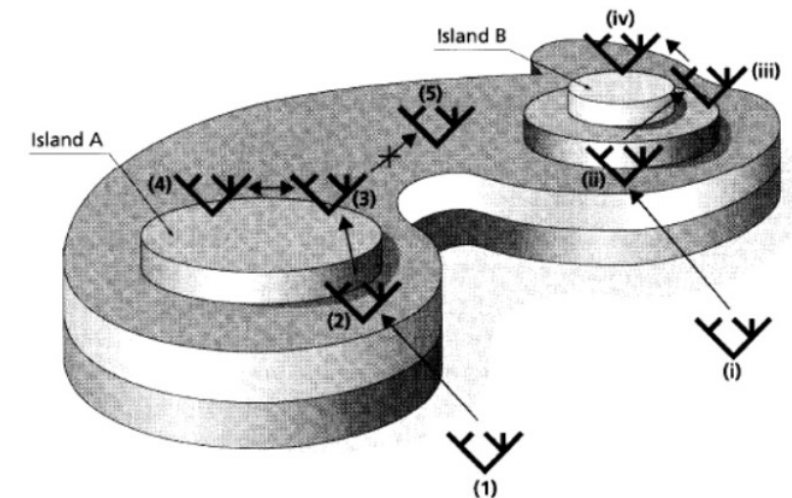
ALIVIEW



<https://github.com/AliView/AliView>

Inferring the tree

	Tree evaluation	Step-wise clustering
Character state	Parsimony Maximum Likelihood (ML) Bayesian inference	
Distance matrix	Fitch-Margoliash	UPGMA Neighbour-joining (NJ)



Note: In step-wise addition, one can get stuck in a local sub-optimal tree peak.

Maximum parsimony

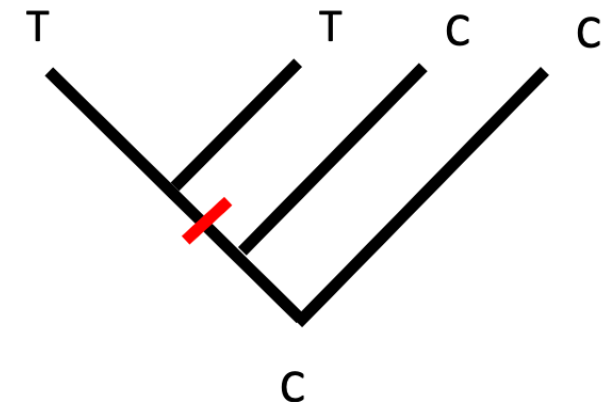
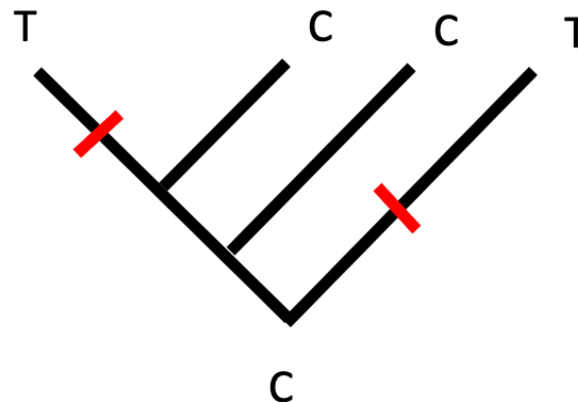
Key idea: *simplest explanation is the best*

Optimizes algorithmically for identifying the tree that requires the least number of mutations

Limitations:

- It does not explicitly incorporate molecular evolution models
- No statistical consistency
- Can't estimate rates and dates

1	2	3
T	A	G
T	A	G
C	A	G
C	A	G



Superimposed mutations (multiple hits)

A given site may change more than once over evolutionary timescales

This is particularly the case for rapidly evolving organisms

AATCGCCCGTACGA

AAGCGCCCATACGA

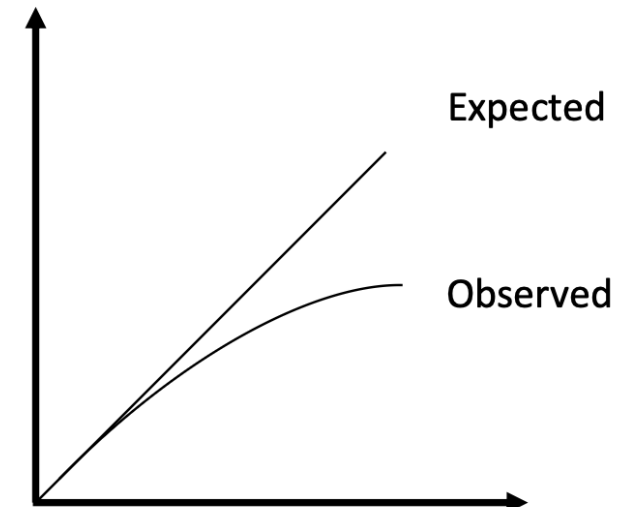
Observed mutations: 3

AATCGCCCGTACGA

A T T

AAGCGCCCATACGA

Actual mutations: 7



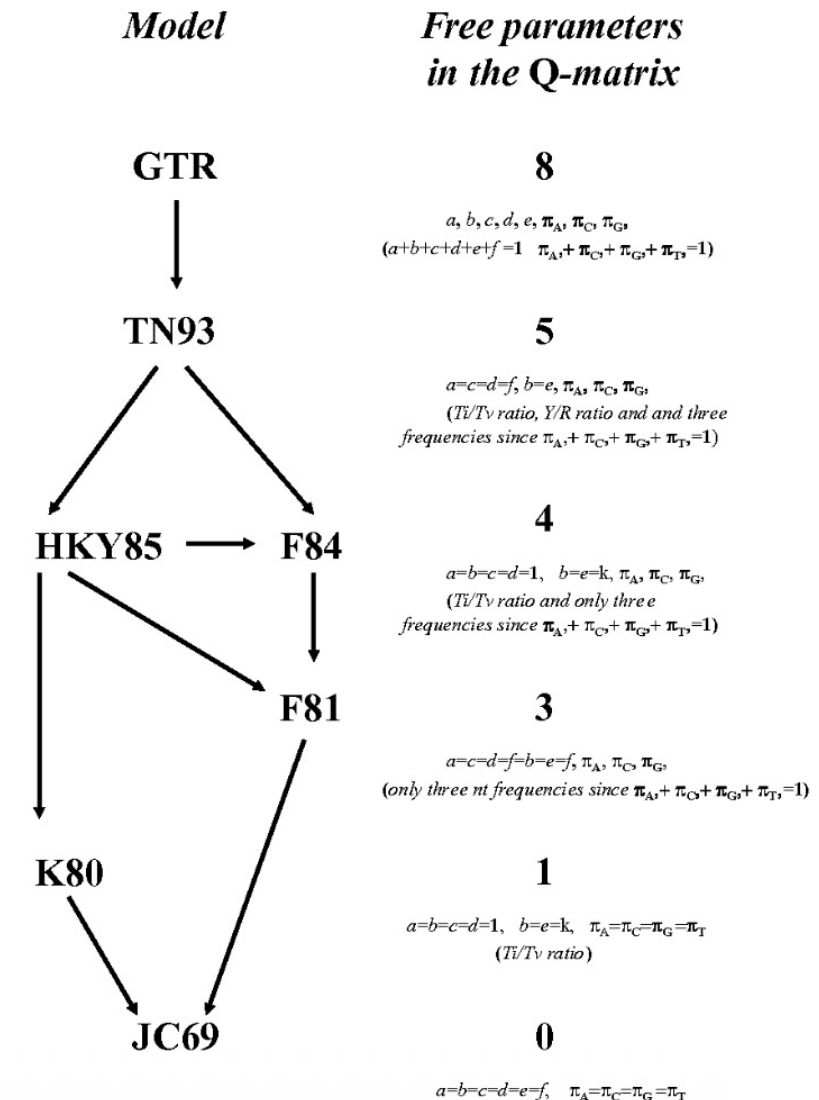
Nucleotide substitution models



Substitution models were proposed
to account for unobserved mutations
for phylogenetic inference

Multiple models exist, from the most
simple to the most complex

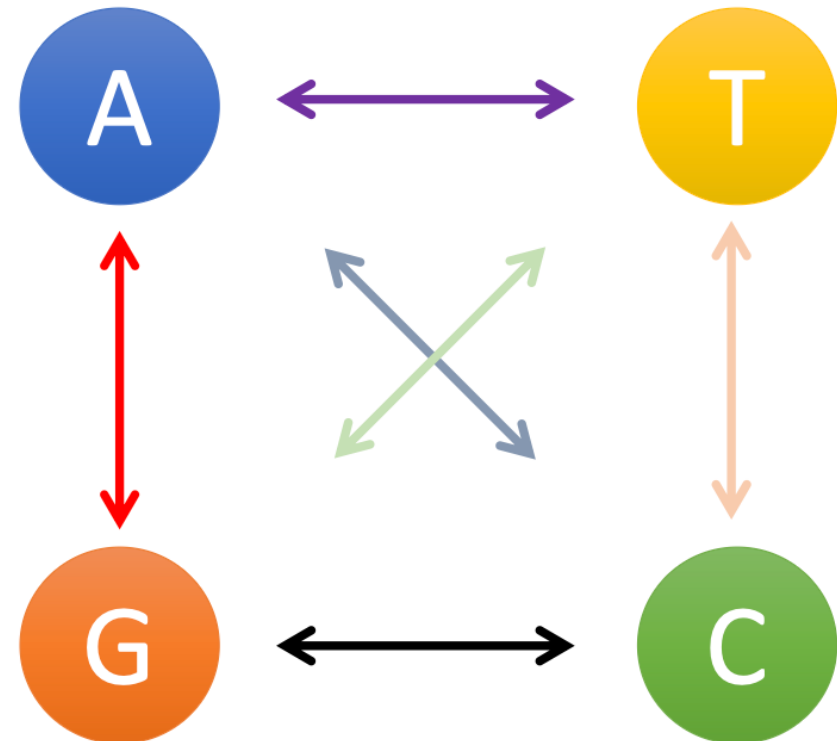
Hierarchical nature



Nucleotide substitution models

General time reversible (GTR)

- All rates are different
- Unequal base frequencies



Maximum-likelihood

A standard method in statistical inference

Key idea: *to calculate the probability of the data, given a hypothesis* (model and parameters)

ML conceptually:

- Compute the likelihood of possible outcomes given a set of parameters for a model
- The best estimate is the set of parameter values that maximize the likelihood (maximum likelihood estimate)

P (data | hypothesis)

In phylogenetics

- Data: multiple sequence alignment
- Probabilistic model: phylogenetic likelihood function
- Parameters: topology, branch lengths, nucleotide frequencies, substitution rates

P (alignment | tree)

Maximum-likelihood with IQ-TREE

IQ-TREE 2 edited_align_Background_dataset.fasta -B 1000 -alrt 1000 -m MFP

```
Last login: Sun Jul 19 11:57:06 on ttys001
cd %
(base) ddasilva@IC-P2PF9XL450 ~ % cd /Users/ddasilva/Dropbox/Mac/Desktop/ECDC_training/Class/Tree
(base) ddasilva@IC-P2PF9XL450 Tree % /Users/ddasilva/Dropbox/Mac/Downloads/iqtree-2.2.0-MacOSX/bin/iqtree2 -s edited_align_Background_dataset.fasta -B 1000 -alrt 1000 -m MFP
IQ-TREE multicore version 2.2.0 COVID-edition for Mac OS X 64-bit built Jun 1 2022
Developed by Bui Quang Minh, James Barbetti, Nguyen Lam Tung,
Olga Chernomor, Heiko Schmidt, Dominik Schrempf, Michael Woodhams, Ly Trong Nhan.

Host: IC-P2PF9XL450 (SSE4.2, 64 GB RAM)
Command: /Users/ddasilva/Dropbox/Mac/Downloads/iqtree-2.2.0-MacOSX/bin/iqtree2 -s edited_align_Background_dataset.fasta -B 1000 -alrt 1000 -m MFP
Seed: 865943 (Using SPRNG - Scalable Parallel Random Number Generator)
Time: Sun Jul 19 12:22:11 2026
Kernel: SSE2 - 1 threads (10 CPU cores detected)

HINT: Use -nt option to specify number of threads because your CPU has 10 cores!
HINT: -nt AUTO will automatically determine the best number of threads to use.

Reading alignment file edited_align_Background_dataset.fasta ... Fasta format detected
Reading fasta file: done in 0.00196099 secs using 95.97% CPU
Alignment most likely contains DNA/RNA sequences
Constructing alignment: done in 0.000980139 secs using 76.42% CPU
Alignment has 33 sequences with 909 columns, 449 distinct patterns
449 parsimony-informative, 20 singleton sites, 440 constant sites
WARNING: Some sequence names are changed as follows:
GU562882.1|Human|WPV3|?|NIE0311205|Nigeria_NA|2003 -> GU562882.1|Human|WPV3|_|NIE0311205|Nigeria_NA|2003
GU562886.1|Human|WPV3|?|CHA9911209|Chad_NA|1999 -> GU562886.1|Human|WPV3|_|CHA9911209|Chad_NA|1999

Analyzing sequences: done in 2.59876e-05 secs using 88.5% CPU
```

	Gap/Ambiguity	Composition	p-value
1 AY184221.1 Sabin	0.99%	passed	71.72%
2 AY082688.1 Sabin1	0.33%	passed	80.41%
3 Sabin_2	0.66%	passed	69.14%
4 KR817066.1 Human WPV2 AFP CAM80 Cameroon_NA 1980	0.66%	passed	98.21%
5 KR817065.1 Human WPV2 AFP KUW80 Kuwait_NA 1980	0.66%	passed	90.95%
6 KR817064.1 Human WPV2 AFP MOR78 Morocco_NA 1978	0.66%	passed	93.54%
7 HQ286321.1 Human WPV2 AFP IND9911248 India_NA 1999	0.66%	passed	92.21%
8 HQ286320.1 Human WPV2 AFP CIV9411247 CotedIvoire_NA 1994	0.66%	passed	95.14%
9 AF551798.1 Human WPV2 AFP 0297_EGY79 Egypt_NA 1979	0.66%	passed	83.15%
10 AF551800.1 Human WPV2 Contact 2203_BAN82 Bangladesh_NA 1982	0.66%	passed	77.59%
11 AF551802.1 Human WPV2 AFP 0864_GEO87 Georgia_NA 1987	0.66%	passed	99.42%

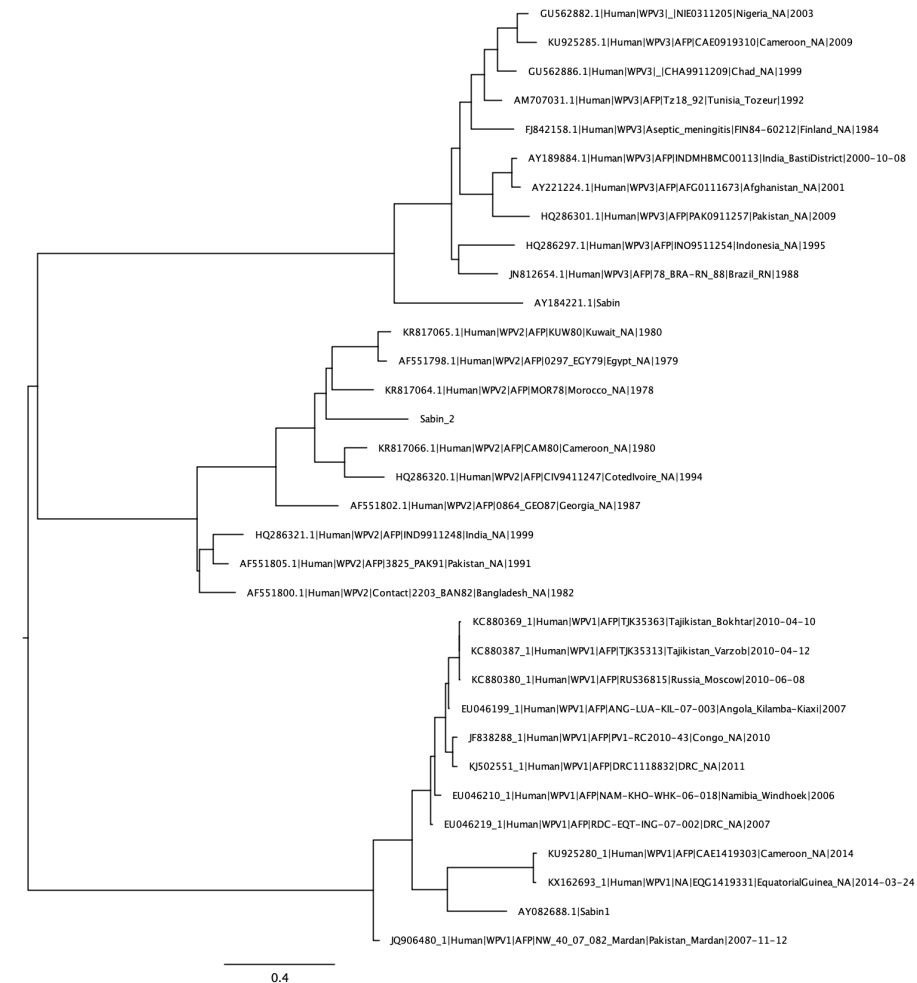
Maximum-likelihood with IQ-TREE

edited_align_Background_dataset.fasta.bionj
edited_align_Background_dataset.fasta.ckp.gz
edited_align_Background_dataset.fasta.contree
edited_align_Background_dataset.fasta.iqtree
edited_align_Background_dataset.fasta.log
edited_align_Background_dataset.fasta.mldist
edited_align_Background_dataset.fasta.model.gz
edited_align_Background_dataset.fasta.splits.nex
edited_align_Background_dataset.fasta.treefile



Open tree in FigTree

Does this tree make sense?



Add our sequences of interest

- Add your sequence of interest to the main alignment
- Perform the previous steps again

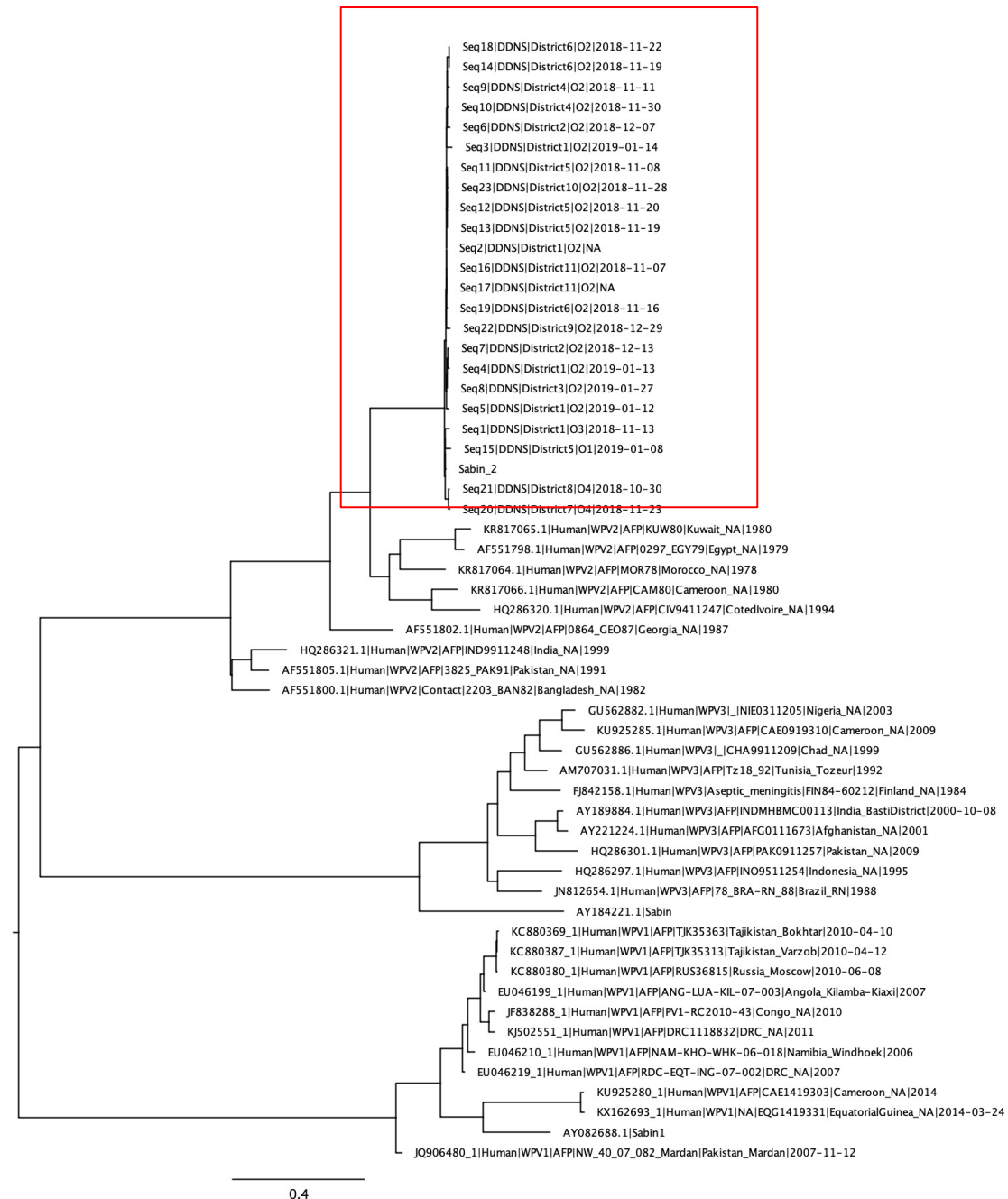
Answer the questions

Question 1. What is the serotype of the sequences of interest?

Answer: Poliovirus 2

Question 2: Are these sequences wild-type or vaccine-derived?

Answer: Vaccine



0.4

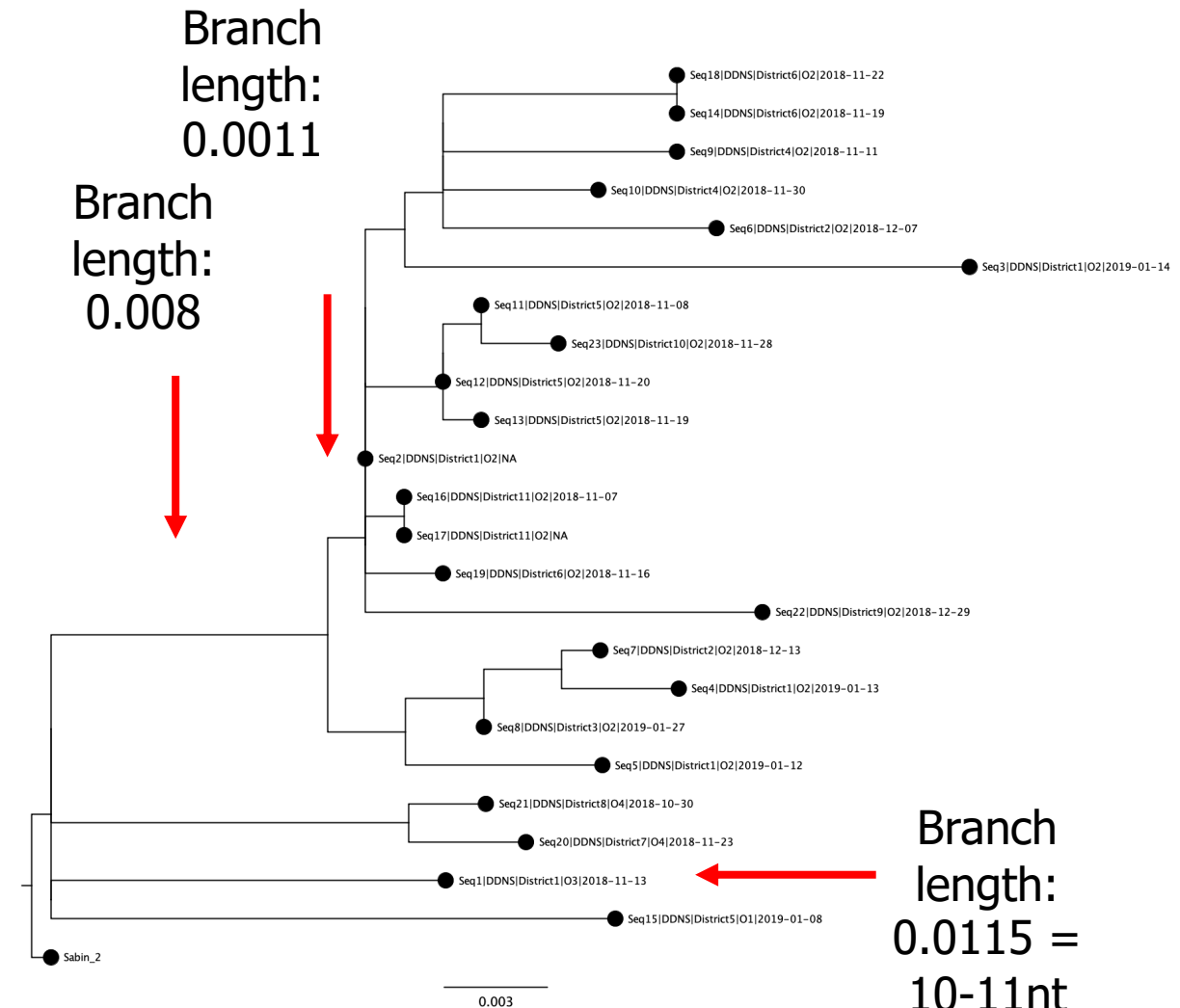
Answer the questions

Question 3: Are these sequences Sabin-like or VDPVs?

Answer: VDPVs (≥ 6 nt from Sabin)

Question 4: How many different emergence groups do these sequences belong to?

Total = $0.0091 \text{ subst/site} \times \sim 900 = 8-9 \text{ nt}$



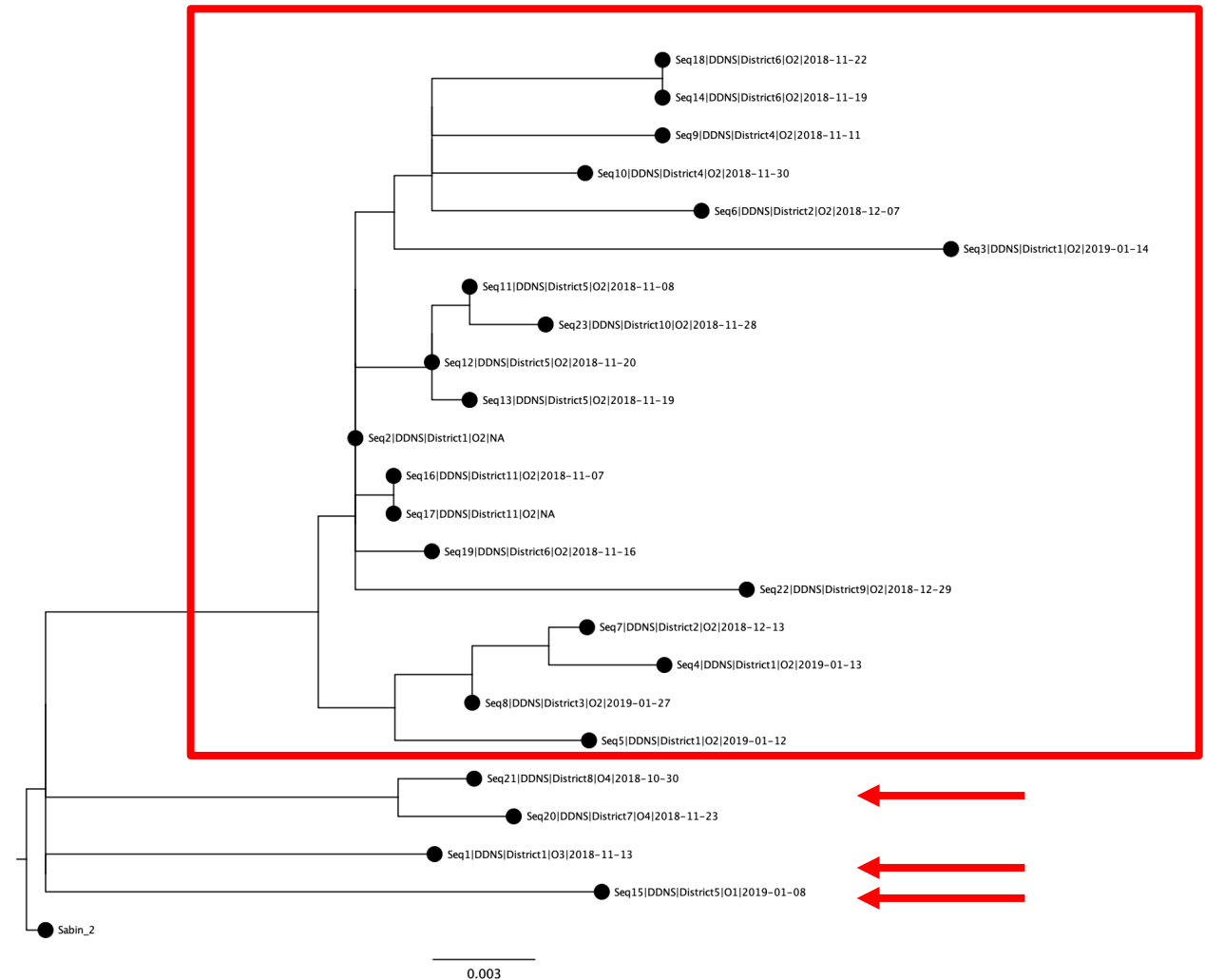
Answer the questions

Question 3: Are these sequences Sabin-like or VDPVs?

Answer: VDPVs (≥ 6 nt from Sabin)

Question 4: How many different emergence groups do these sequences belong to?

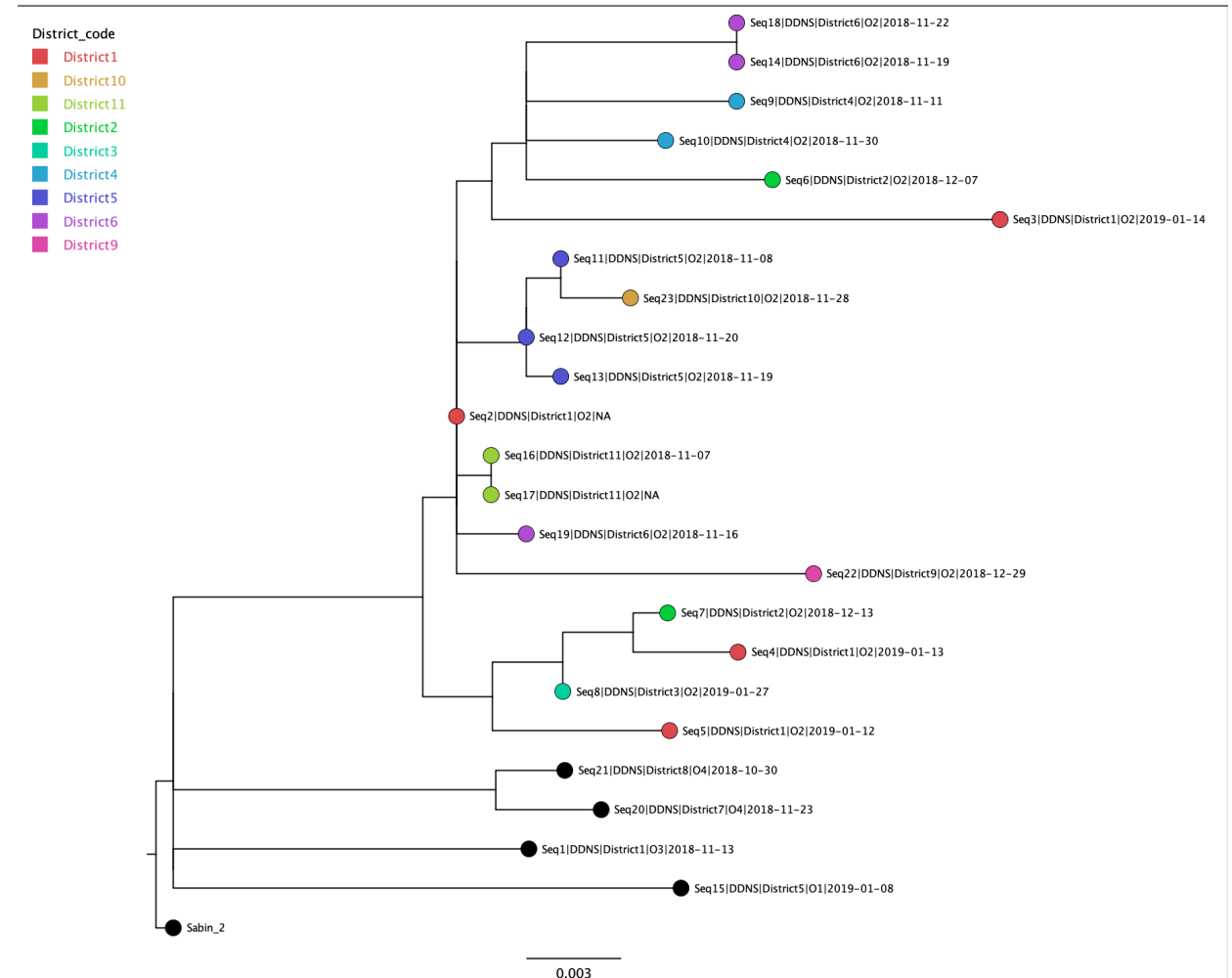
Answer: 4



Answer the questions

Question 5: How geographically intermixed was the observed spread?

Fairly good mixing with sequences from District 1 present in several clusters



Microreact

1. Drop the rooted tree saved as Newick and the CSV file with metadata information onto <https://microreact.org/upload>



Recommended material to explore further

- **Foundations**

Lemey P, Salemi M, Vandamme A-M (eds.). **The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing.**

Page RDM, Holmes EC. **Molecular Evolution: A Phylogenetic Approach.**

- **Applications of genomic epidemiology**

Dudas G, Carvalho LM, Rambaut A, Bedford T. **Virus genomes reveal factors that spread and sustained the Ebola epidemic.** *Nature*. 2017.

Lemey P, Rambaut A, Bedford T, et al. **Unifying viral genetics and human transportation data to predict the global transmission dynamics of human influenza H3N2.** *PLOS Medicine*. 2014.

Candido DS, Claro IM, de Jesus JG, et al. **Evolution and epidemic spread of SARS-CoV-2 in Brazil.** *Science*. 2020.

Dudas G, Carvalho LM, Rambaut A, Bedford T, et al. **MERS-CoV spillover at the camel–human interface.** *eLife*. 2018.

- **Poliovirus case studies**

Candido D, et al. **Genomic epidemiology of circulating vaccine-derived poliovirus transmission in the Democratic Republic of the Congo.** *Nature Microbiology*. 2026.

Jørgensen D, et al. **Genomic epidemiology of poliovirus transmission using environmental and clinical surveillance.** *Nature Communications*. 2025.

References

Genomic epidemiology

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