

Phylogeny: construction, visualization and interpretation



February 2023

Erkison Ewomazino Odih
SEQAFRICA, University of Ibadan, Nigeria
University of Copenhagen, Denmark

Outline

- Phylogeny inference from SNPs
- Phylogenetic tree construction
- Phylogenetic tree interpretation
- Phylogenetic tree visualization – Microreact

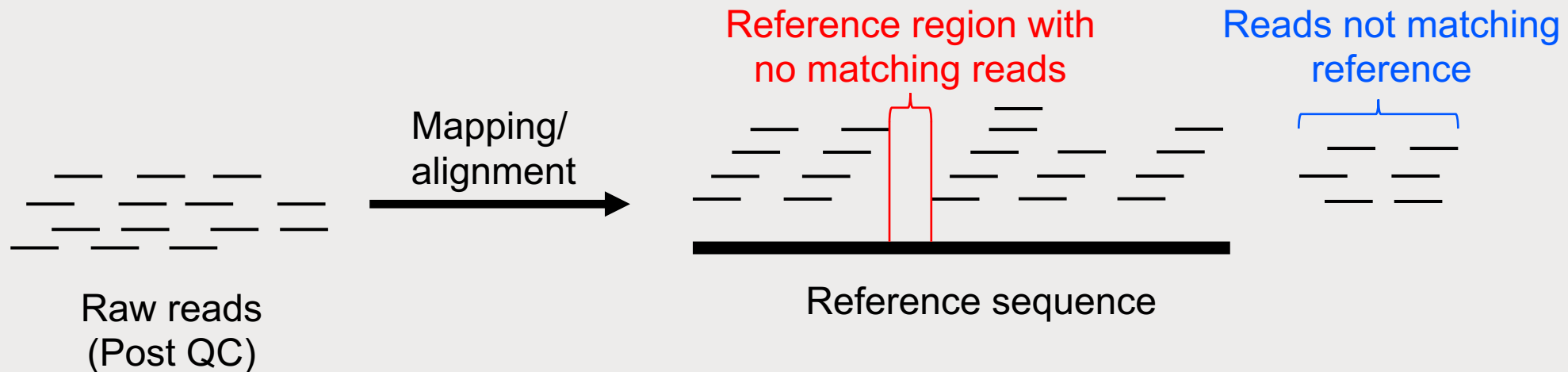
Phylogeny

- Phylogeny represents the evolutionary relationships and relatedness between a group of organisms.
- Inferred from single nucleotide polymorphisms (SNPs)
- SNPs are allelic nucleotide variants at given positions in the genome.
- For phylogeny analyses, SNPs are assumed to be:
 - Independent
 - Random

Inferring phylogeny from SNPs – Overview

1. Select reference and map reads to reference

- The closer the reference to the sample data, the better.

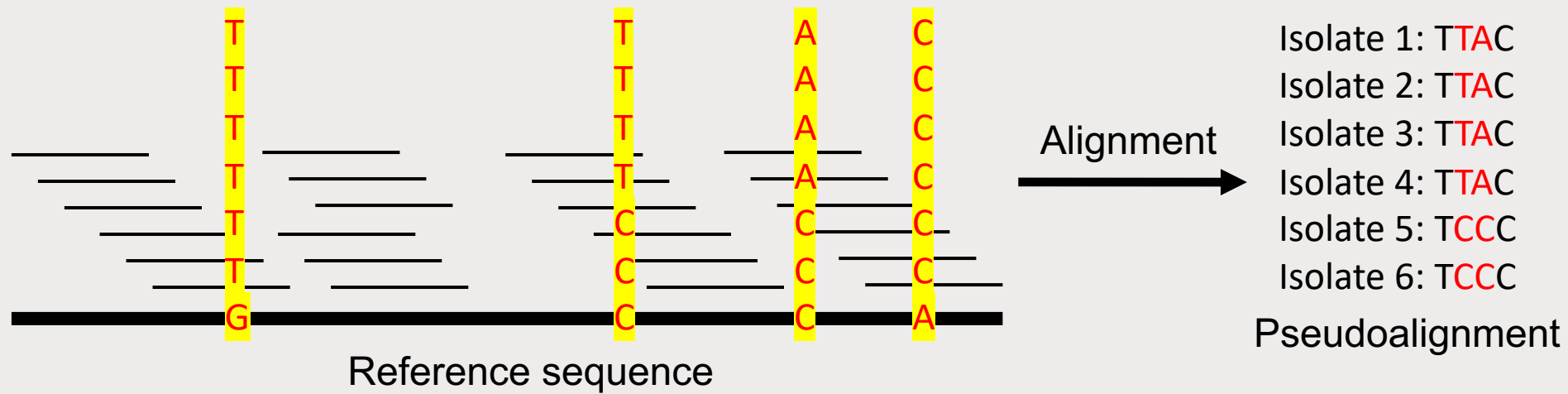


Software: BWA mem, samtools, Mauve...

Inferring phylogeny from SNPs – Overview

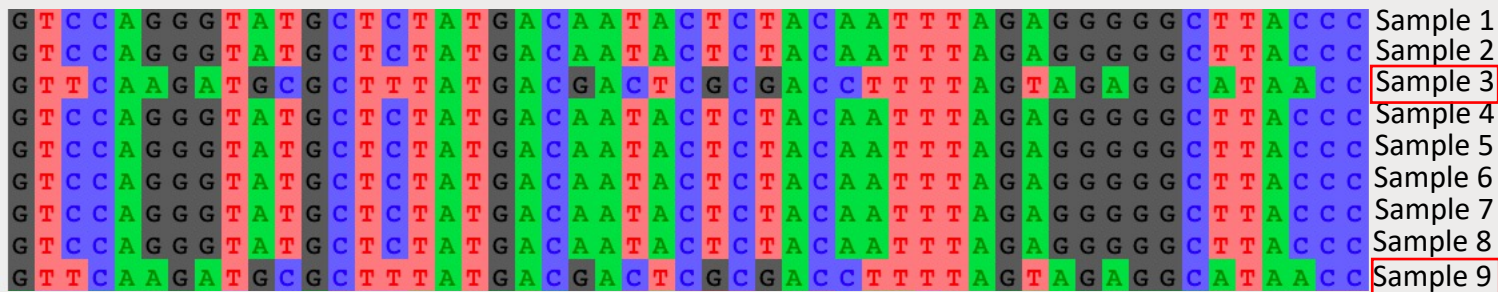
4. Concatenate filtered SNPs to create pseudogenomes and a pseudoalignment.

- Constructed from only shared positions in all genomes and reference



Inferring phylogeny from SNPs – Overview

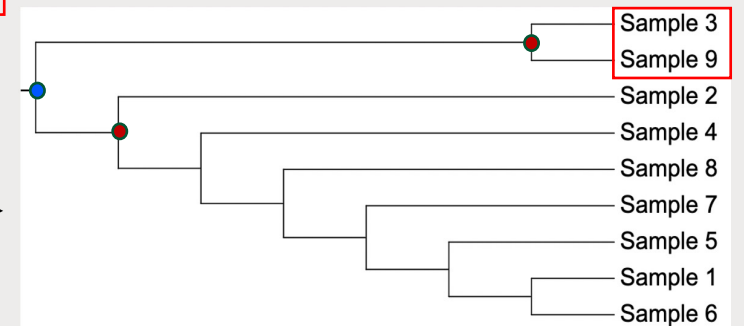
5. Construct phylogenetic tree from pseudoalignment using chosen method and algorithm.



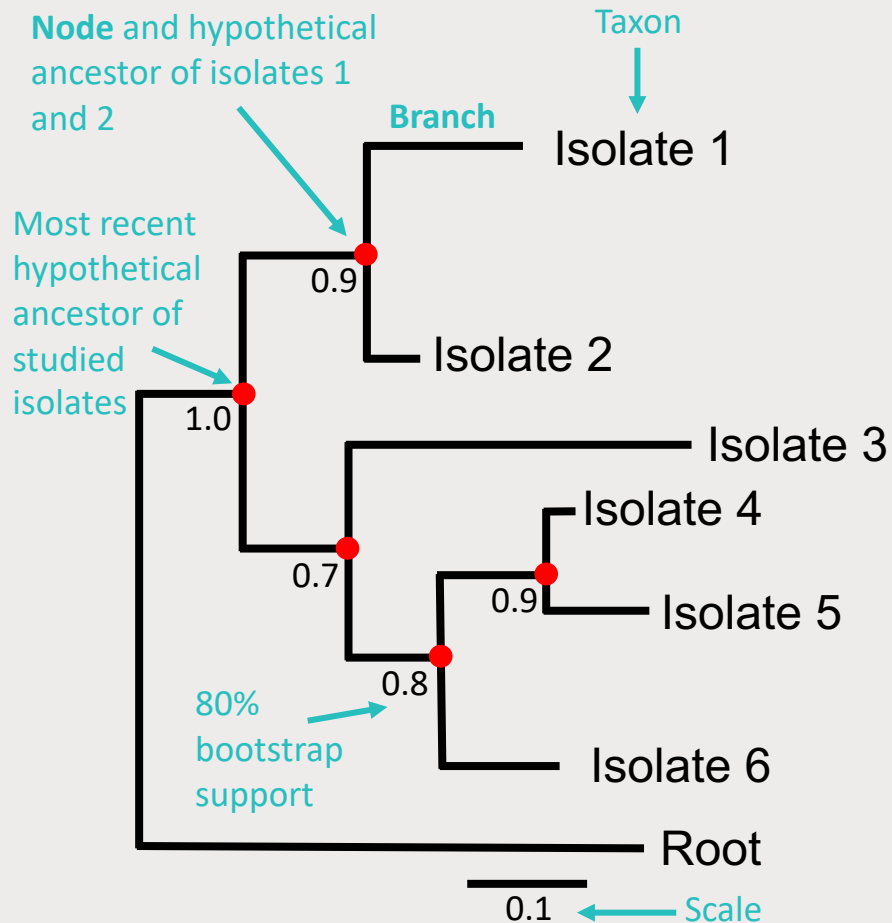
Pseudoalignment

Tree
construction

Software: IQ-Tree, FastTree, RaxML

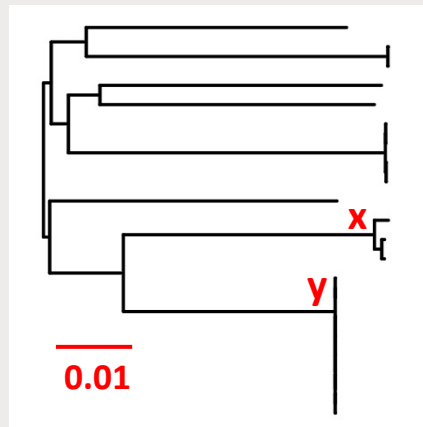
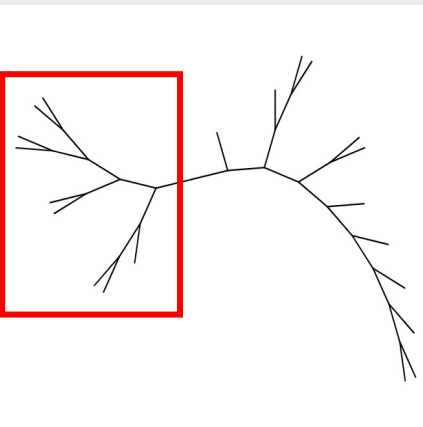
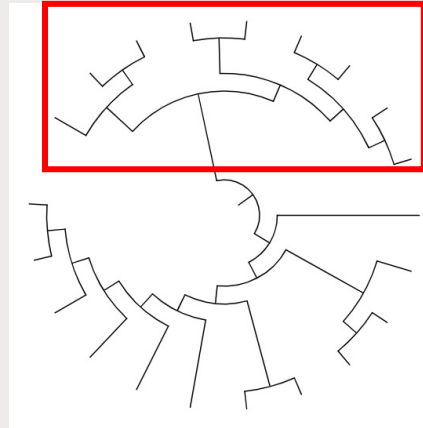
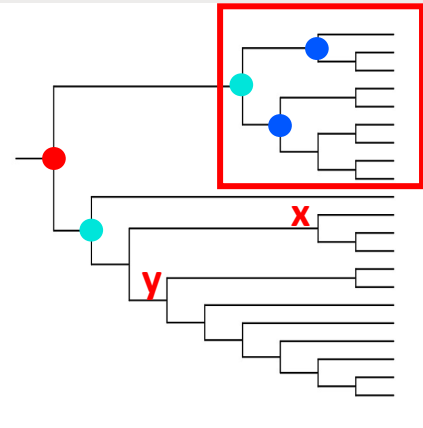


Phylogenetic tree interpretation



- **Taxa** are on the tree tips/leaves
- **Nodes**: hypothetical taxa ancestors
- **Branches** connect nodes and taxa
- **Topology**: branching structure of a tree
- **Clade**: taxa sharing a unique common ancestor
- **Bootstraps**: proportion of multiple replicate trees supporting each node.
- **Root**: more distantly related to all taxa on the tree; tells direction of evolution

Phylogenetic tree interpretation

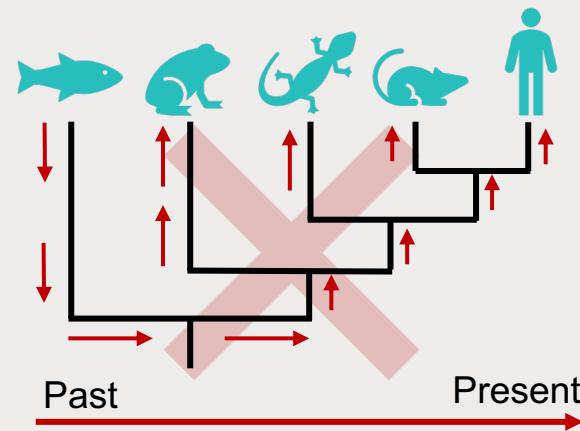


Reading phylogenetic trees

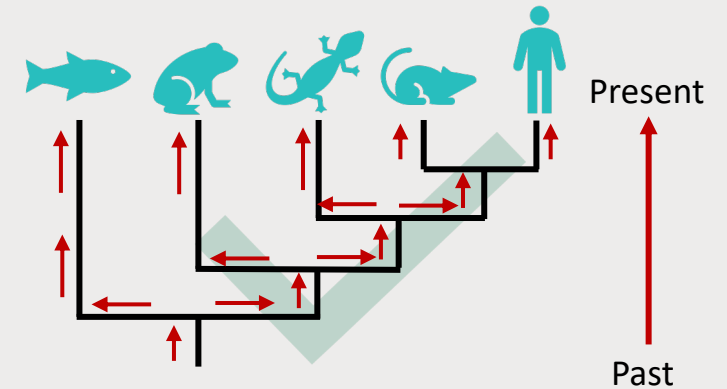
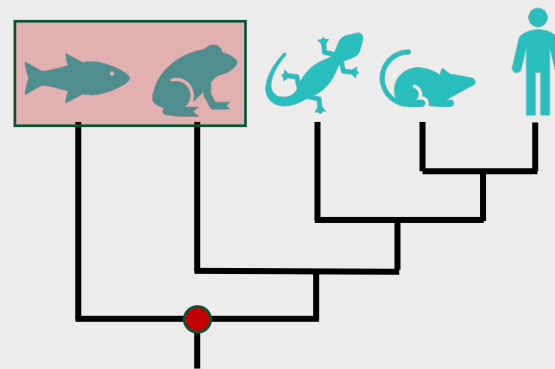
- Trees depict branching history; topology most important.
- Different orientations, same topology.
- Unless otherwise indicated, branch lengths are meaningless; avoid inferring temporal information that is not shown
- Branch lengths, when indicated, reflect the amount of evolutionary change as well as the passage of time.

Phylogenetic tree interpretation: Misconceptions

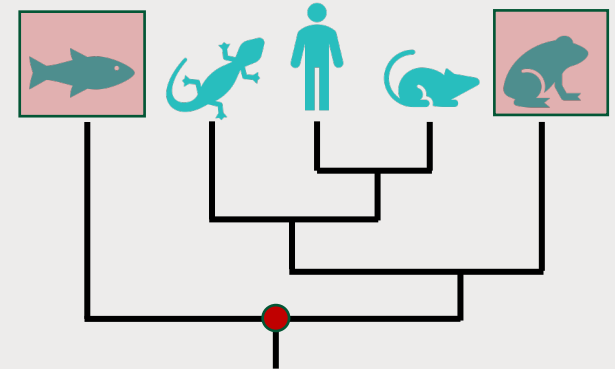
1. Evolutionary timeline flows from tips/leaves



2. Related species have proximal leaves



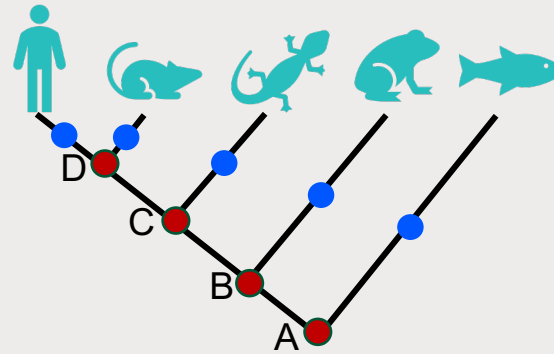
Evolution is not linear but nested



Relationships are inferred from common ancestry, not leaf proximity

Phylogenetic tree interpretation: Misconceptions

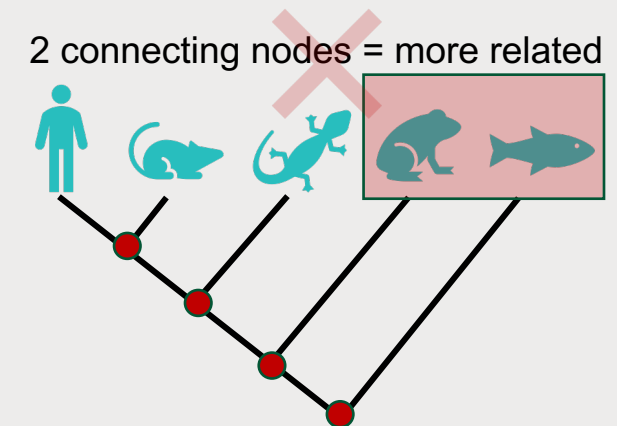
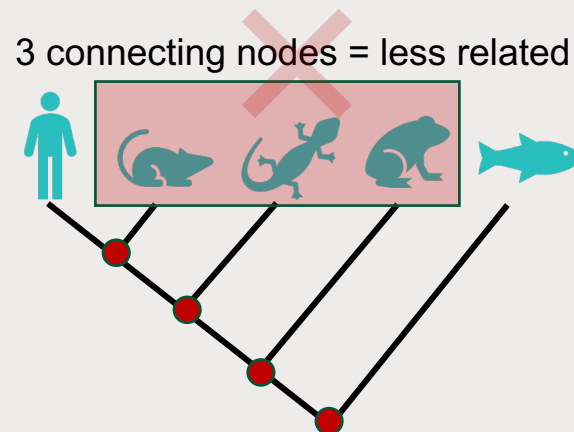
3. Genetic change occurs only at nodes



Fact:

- Changes accumulate in taxa over time and are present along branches
- Nodes simply represent (hypothetical) common ancestors between taxa
- - Shared ancestor; divergence event
- - Unique ancestor

4. Related species have fewer connecting nodes



Phylogenetic tree visualisation: Microreact

- A flexible, interactive software/web application for easy visualization of datasets consisting of a combination of trees, maps, timelines, and associated metadata.
- Input:
 - Data file: Comma separated values (.csv) format; can contain a combination of textual metadata, locations and dates.
 - Optional tree file: Newick (.nwk) format.
- Output: interactive tree, map, timeline, and table.

Phylogenetic tree visualisation: Microreact

Sample data file

id	latitude	longitude	Country	Country__colour	Country__shape	Pedalism
Bovine	46.227638	2.213749	France	Red	square	Four
Gibbon	15.870032	100.992541	Thailand	Green	circle	Two
Orangutan	-0.589724	101.3431058	Sumatra	Blue	circle	Two
Gorilla	1.373333	32.290275	Uganda	#CC33FF	circle	Two
Chimp	-0.228021	15.827659	Congo	Orange	circle	Two
Human	55.378051	-3.435973	UK	#CCFF33	circle	Two
Mouse	40.463667	-3.74922	Spain	#00FFFF	square	Four

<https://microreact.org/instructions>

- **Mandatory column**

id – unique identifier for each data row

- **Optional columns**

latitude, **longitude** – geographic columns

year, **month**, **day** – temporal columns

<custom-name> – other metadata

<column-name>__colour – specify colour

<custom-name>__shape – specify shape

Phylogenetic tree visualisation: Microreact

Data file (.csv)



+/-

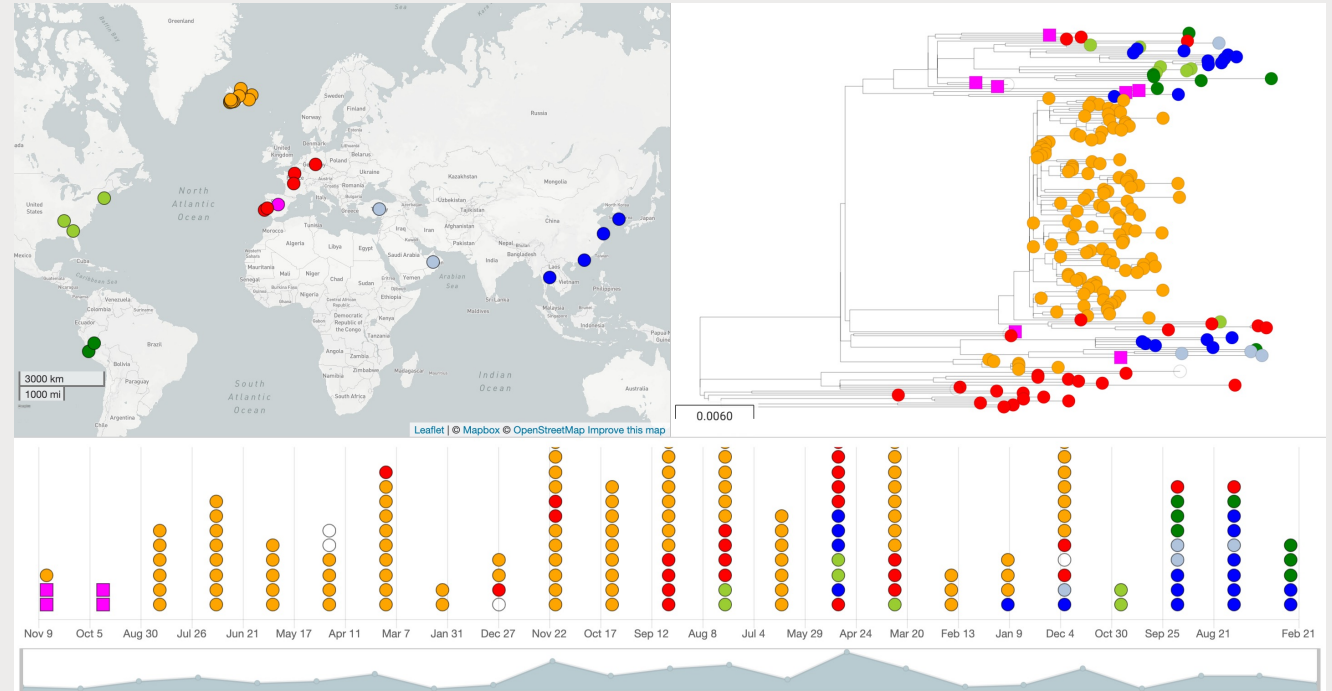


Tree file (.nwk)



Web application

<https://microreact.org>



Source: <https://microreact.org/project/N1TRn11L>

Microreact benefits

- Powerful visualization and data exploration
- Visualization can be shared as a permanent web link among collaborators.
- The web link can be embedded within publications to enable readers to explore and download the data.
- Simple and easy-to-use, yet powerful

Microreact demo



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Edited by:

Spyros Pourmaras,
National and Kapodistrian University
of Athens, Greece

Reviewed by:

Nabil Karah,
Umeå University, Sweden
Konstantina Dafopoulou,
University Hospital of Larissa, Greece

Rectal Colonization and Nosocomial Transmission of Carbapenem-Resistant *Acinetobacter baumannii* in an Intensive Care Unit, Southwest Nigeria

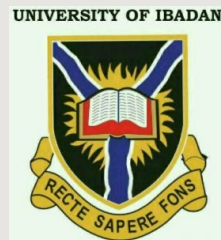
Erkison Ewomazino Odih^{1,2*†}, Emmanuel Oladayo Irek^{3†}, Temitope O. Obadare³, Anderson O. Oaikhena¹, Ayorinde O. Afolayan¹, Anthony Underwood^{4,5}, Anthony T. Adenekan⁶, Veronica O. Ogunleye⁷, Silvia Argimon^{4,5†}, Anders Dalsgaard², David M. Aanensen^{4,5}, Iruka N. Okeke¹ and A. Oladipo Aboderin^{8*}

¹ Department of Pharmaceutical Microbiology, Faculty of Pharmacy, Obafemi Awolowo University, Ile-Ife, Nigeria

Thank you



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This programme is being funded by the UK Department of Health and Social Care.
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