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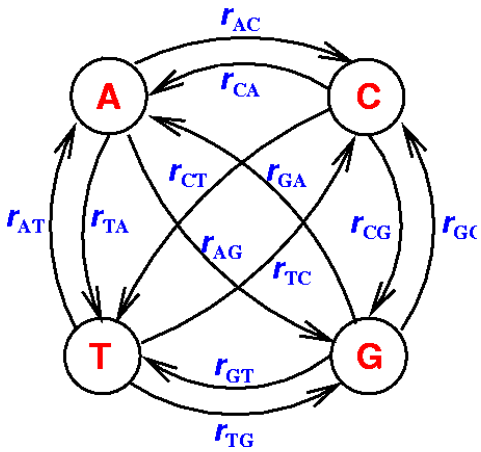
Research Institute for Medicines

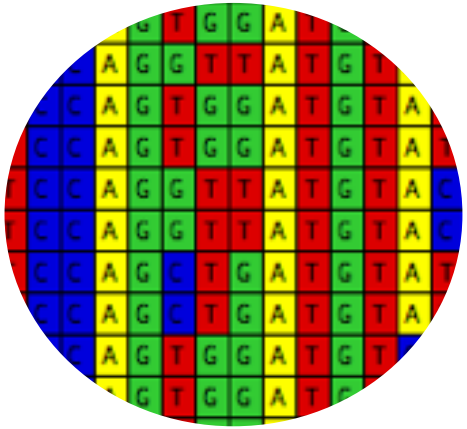
LISBOA
UNIVERSIDADE DE LISBOA

FACULDADE DE FARMÁCIA
Universidade de Lisboa

PATHOGEN MULTIOMICS AND BIOINFORMATICS

Module 5: Introduction to Phylogenetics and Public Health II





Ifeanyi Ezeonwumelu

30.06.2021

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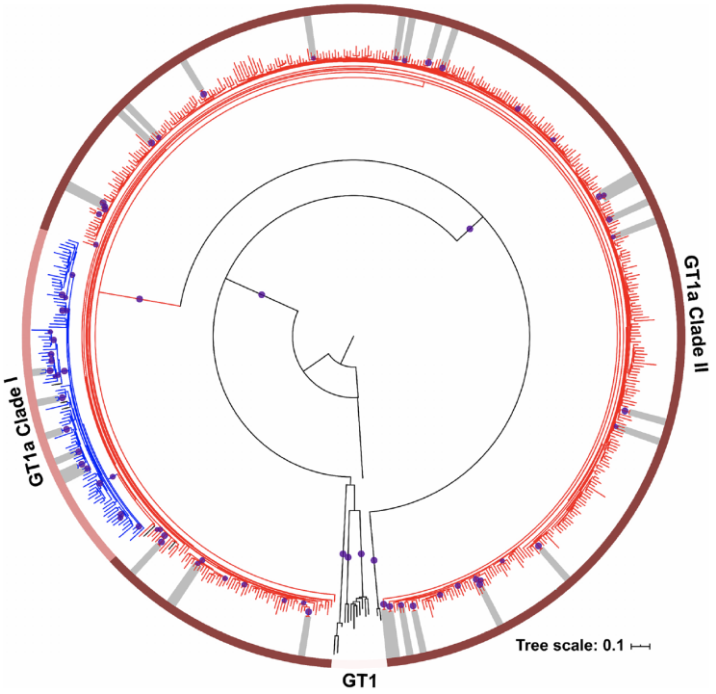
Phylogeography Practice Session: Case study

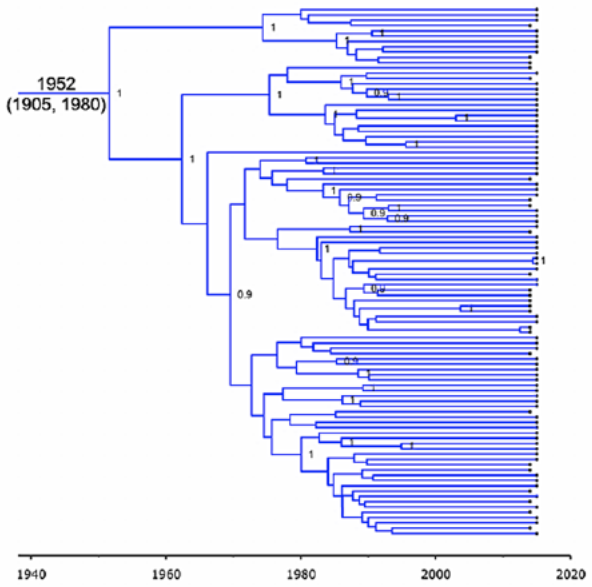
SCIENTIFIC REPORTS
nature research

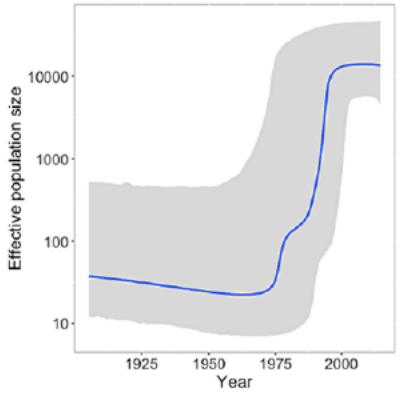
Check for updates

Epidemic history and baseline resistance to NS5A-specific direct acting drugs of hepatitis C virus in Spain

Claudia Palladino[1,4], Ifeanyi Jude Ezeonwumelu[1,4], Irene Mate-Cano[2], Pedro Borrego[1], Paula Martínez-Román[2], Sonia Arca-Lafuente[2], Salvador Resino[2], Nuno Taveira[1,3] & Verónica Briz[2]







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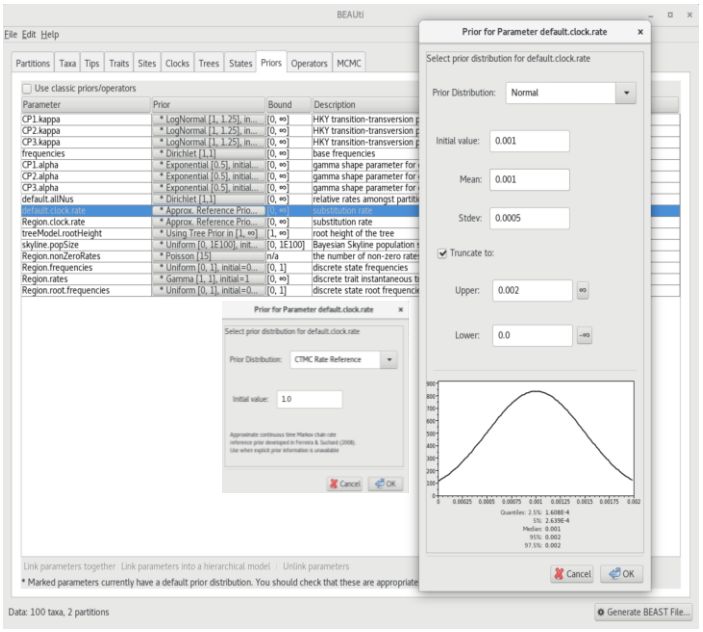
BEAUti and the BEAST

The BEAST package contains a suite of programmes for computing Bayesian Evolutionary Analysis and Trees Sampling.



BEAUti | Bayesian Evolutionary Analysis Utility:

This program is used to import data (*FASTA* & *NEXUS*), design the analysis, and generate the BEAST control (*XML*) file.

BEAST | Bayesian Evolutionary Analysis Sampling Trees:

This is the main program that takes as input, ***XML*** files generated by BEAUti and performs the analysis.

https://beast.community/index.html
https://github.com/beast-dev/beast-mcmc

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BEAST: Output Analysis

LogCombiner | This is a utility program that will combine log & tree files from different runs and reduce the sampling frequency (thin them).

TreeAnnotator | This is a post-analysis program that will produce a summary tree from the output of BEAST. Takes as input .tree files to generate a Maximum clade credibility tree.

Not included in the BEAST package but indispensable in BEAST Output Analysis

Tracer:
A graphical program for exploring the output of BEAST, diagnosing problems, and summarizing the results.

FigTree:
A graphical program for viewing trees, displaying summary information from TreeAnnotator and generating publication-ready figures.

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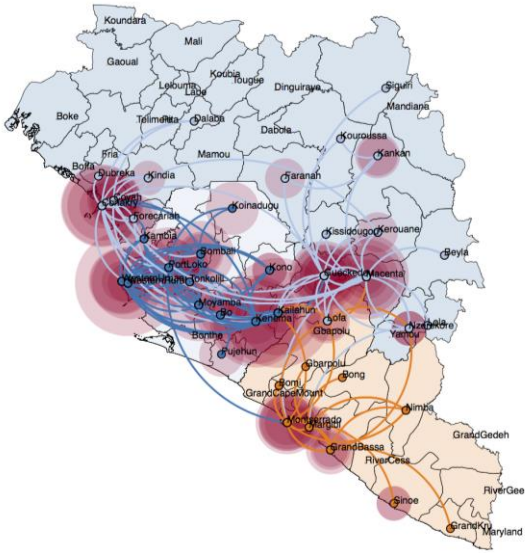
SpreaD3: Time-scaled Phylogreography

SpreaD3 | (Spatial Phylogenetics Reconstruction of Evolutionary Dynamics using Data-Driven Documents (D3)):

A package for analysis and visualisation of pathogen phylodynamic reconstructions

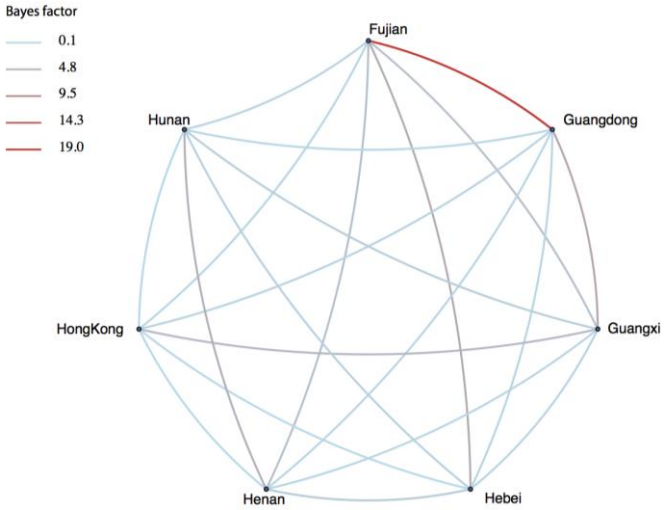
Input:

- .mcc tree files & region.rates.log files (BEAST-BSSVS)
- .geoJSON file (map locations)
- Geographical coordinates text files



Output:

- Interactive visualizations of spatio-temporal phylogenies
- Bayes factor analysis for epidemic migrations



https://rega.kuleuven.be/cev/ecv/software/SpreaD3_tutorial

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Phylogeography Practice Session II: OUTLINE

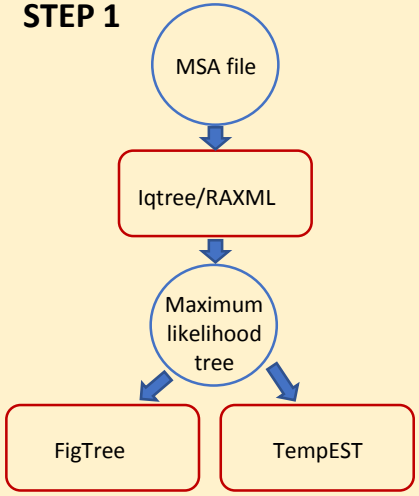
Session I

Session II

TempEST v1.5.3; FigTree v1.4.3; IQ-Tree v2; MEGA X

SpreaD3 v0.9.6

STEP 1



IqTree:

- ML tree

FigTree:

- Tree visualization

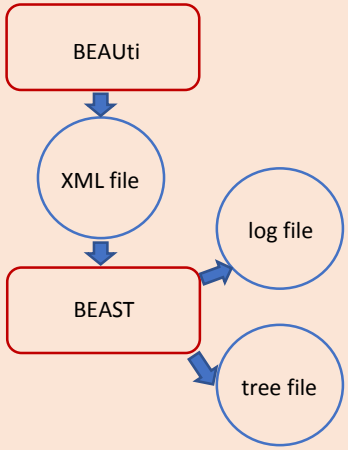
ClusterPicker:

- Transmission Clusters

TempEST:

- Remove outliers
- Determine Molecular clock likelihood

STEP 2



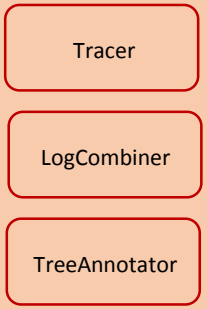
BEAUTi:

- Define data partitions, select models and define priors
- Decision on best Model/prior selection: specify MLE

BEAST:

- Bayesian Inference (MCMC)

STEP 3



Tracer:

- Check for convergence of MCMC, visualize log files, summarize data.

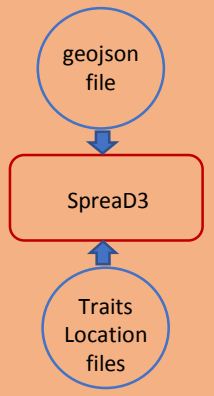
LogCombiner:

- Combine output files

TreeAnnotator:

- Summarize tree files to Maximum clade credibility trees

STEP 4



spreaD3:

- Spatiotemporal visualization
- BF for location transitions

BEAST v1.10 package