



PhyloSuite v2: the development of an all-in-one, efficient and visualization-oriented suite for molecular dating analysis and other advanced features

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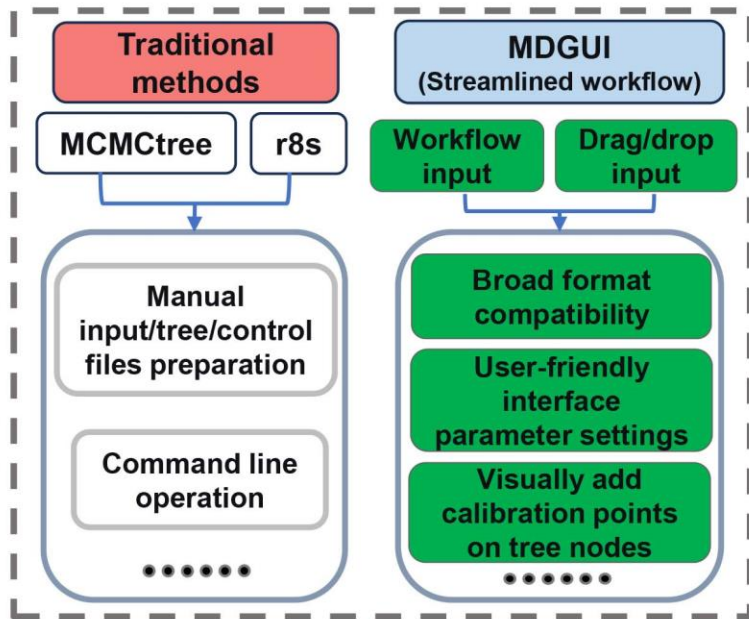
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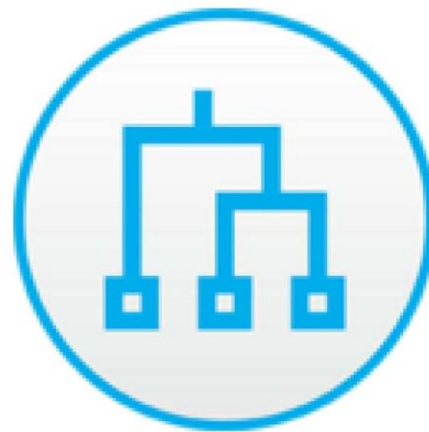


Introduction



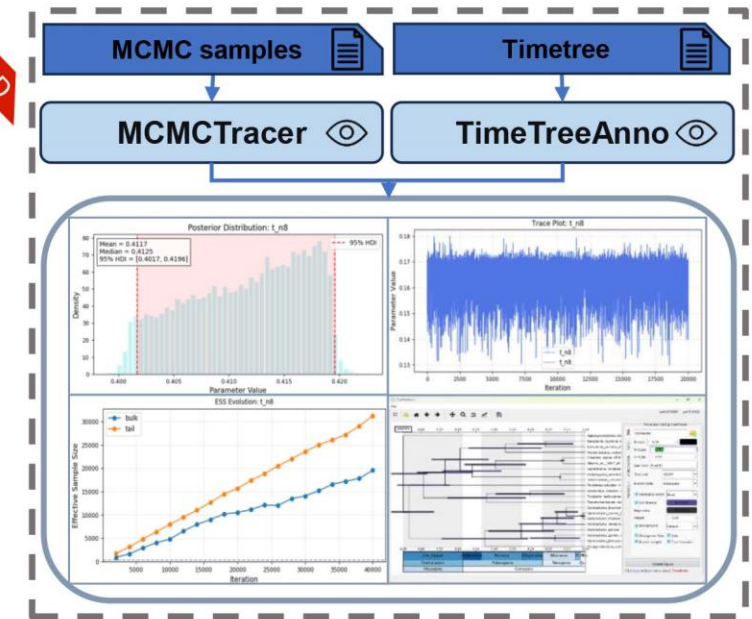
Easy configuration

Molecular Dating Suite

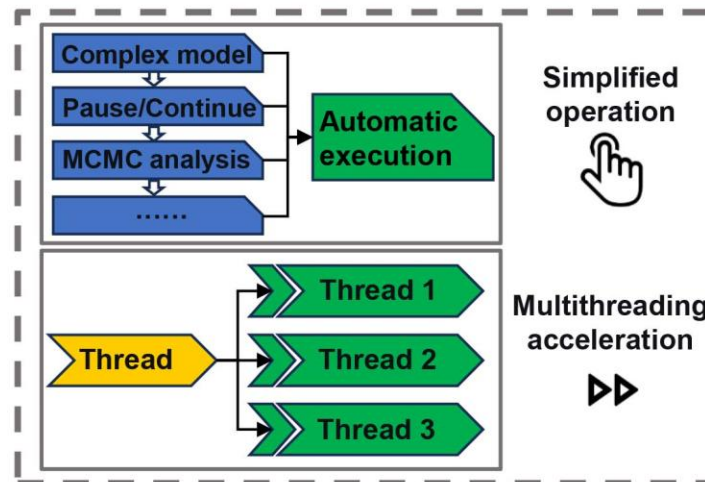


PhyloSuite v2

INTEGRATED



Visualization



Simplification & Acceleration



Highlights

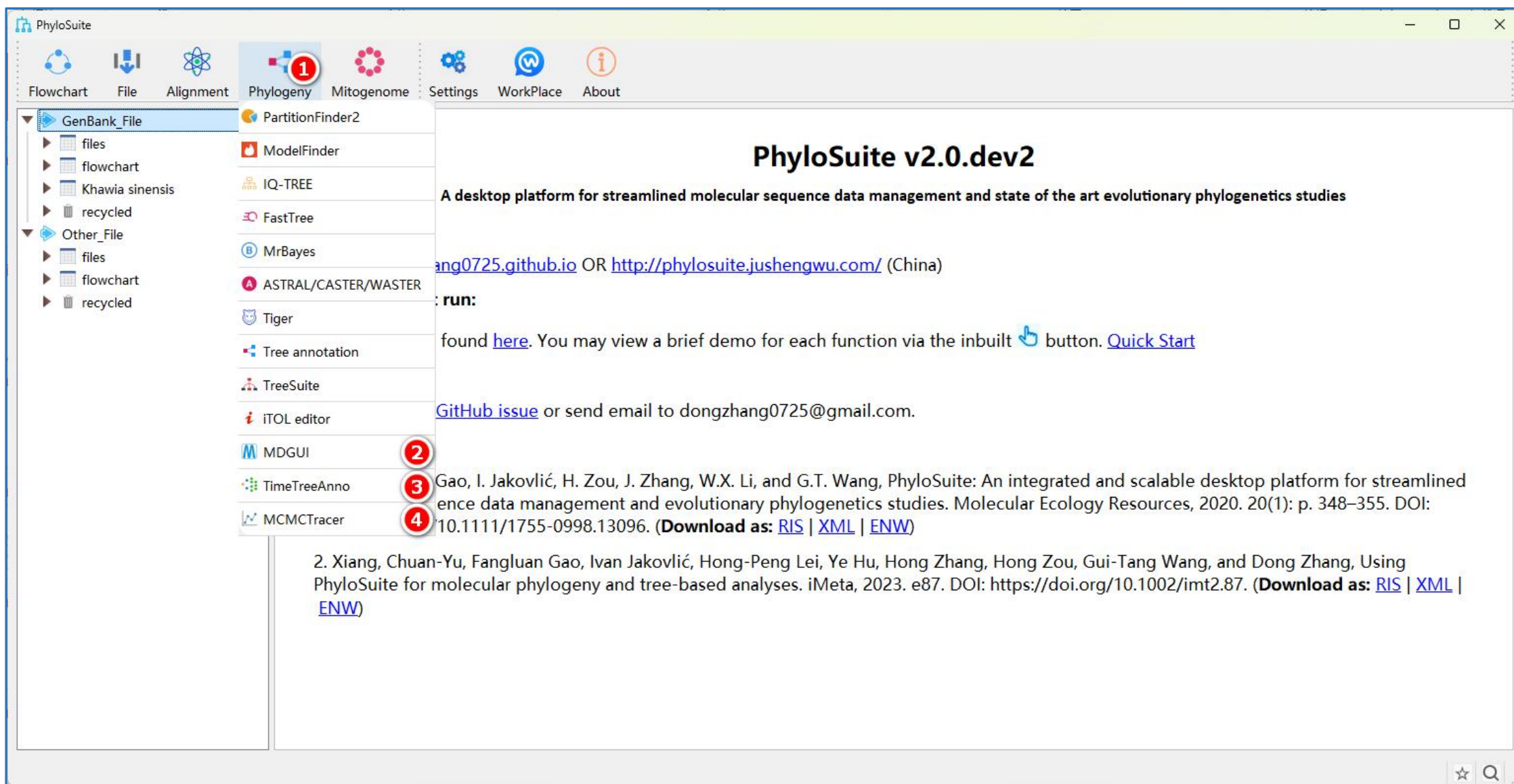


Figure 1. Main interface of PhyloSuite v2 and the entry point of the molecular dating suite

[PhyloSuite official website](#)

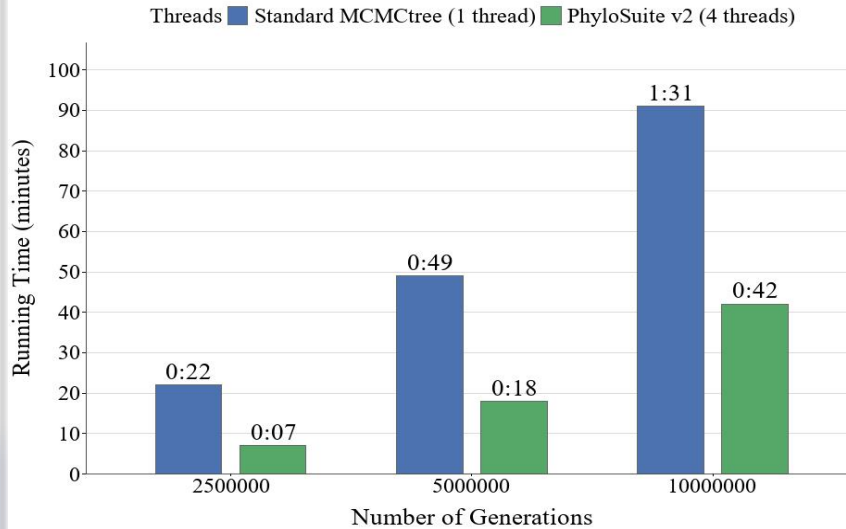
[Molecular dating analysis tutorials](#)

Highlights

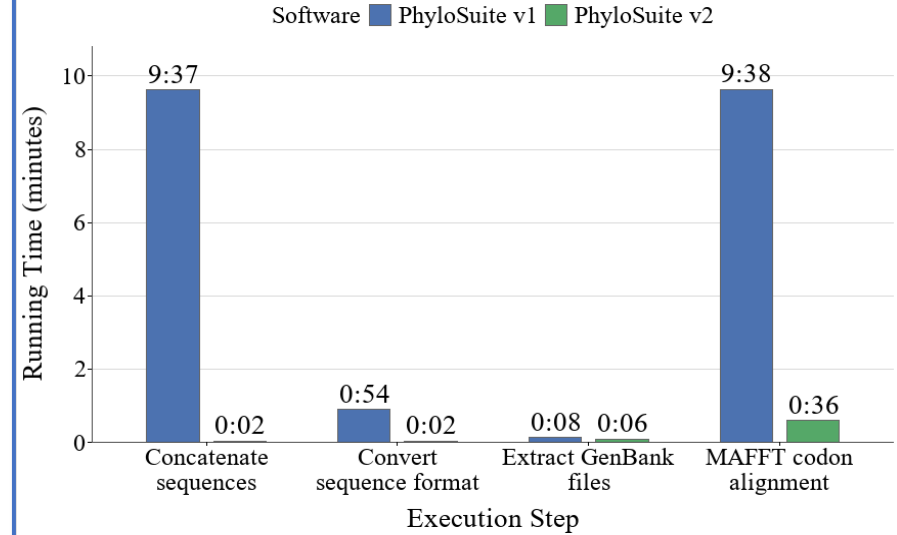
Test datasets and computer configurations

- 41 species
- 374,157 sites
- Ultra 5 125H
32G

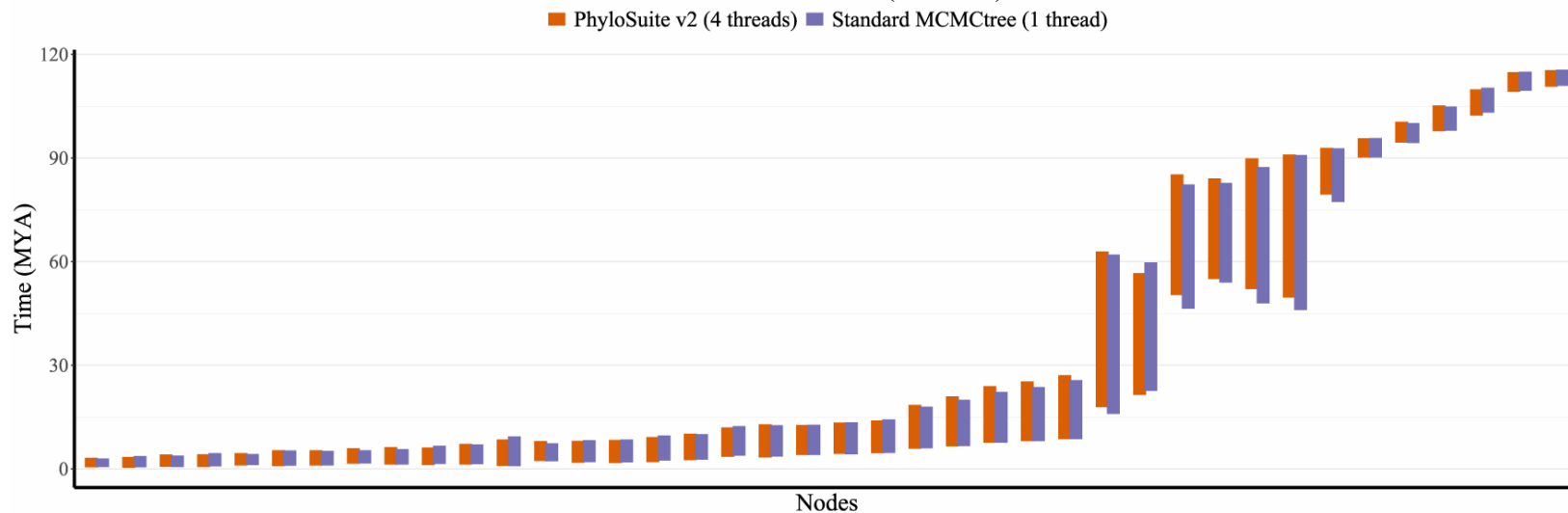
Comparison of time consumption of molecular dating analyses between PhyloSuite v2 (4 threads) and standard MCMCtree (1 thread) (hour:minute).



Performance optimizations and speed improvements in PhyloSuite v2 (new) compared to v1 (old) across different functions (minute:second).



Comparison of node divergence times and confidence intervals between PhyloSuite v2 (4 threads) and standard MCMCtree (1 thread).



Overview of PhyloSuite v2

The molecular dating suite of PhyloSuite v2 consists of three main modules: MDGUI, TimeTreeAnno, and MCMCTracer.

MDGUI

Input

Alignment: Input alignment with FASTA/NEXUS/PHYLP/PAML formats

Treefile: The tree should be NEWICK format

seqtype: nucleotides

☐ Enabling tip-dating analyses Add calibration points in tree Species:

Click [here](#) to learn more about **MCMCTree**

MCMCTree r8s

MCMCTree.ctl parameters setting

MCMC run: burin: 5% sampfreq: 10 nsample: 20000

☐ RootAge: > 0.00 < 0.00

clock: independent rates

usedata: approximate likelihood FAST

rgene_gamma: 2.00 20.00 1.00

model: AUTO

kappa_gamma: 6.00 2.00

Program for generating Hessian matrix: IQ-TREE for all sequences (more models)

BDparas: 1.00 1.00 0.00 conditional

print: everything

Threads: 2 ☒ Repeat for convergence

sigma2_gamma: 1.00 10.00 1.00

alpha: 0.50 ncatG: 5

alpha_gamma: 1.00 1.00

☐ Using mixture models

Preview/Edit configurations MCMCTracer

Continue Previous Analysis Summarize MCMC samples and infer time tree

Run: Start Stop

Progress: 0%

Show log

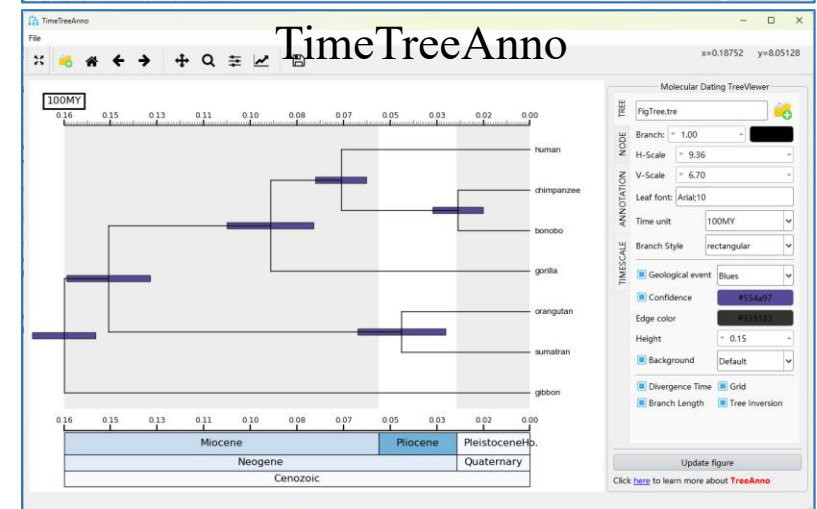
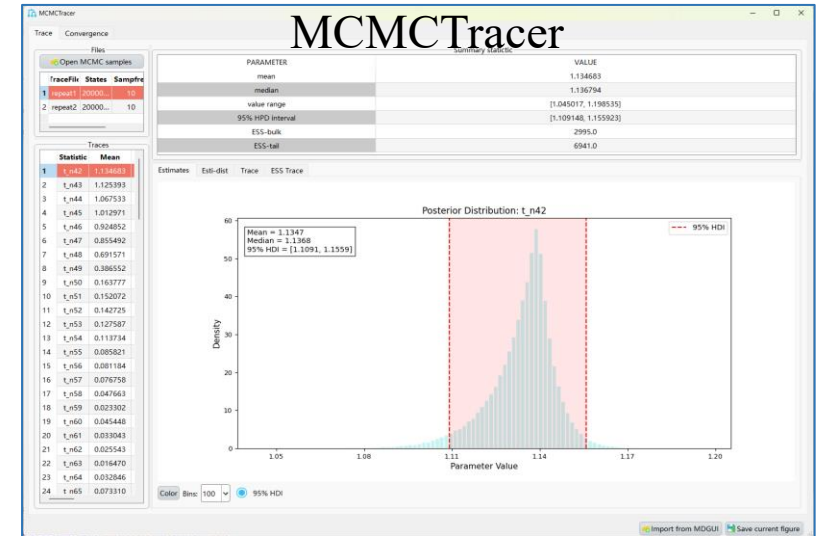


Figure 2. Interface of the molecular dating suite in PhyloSuite v2



Overview of PhyloSuite v2

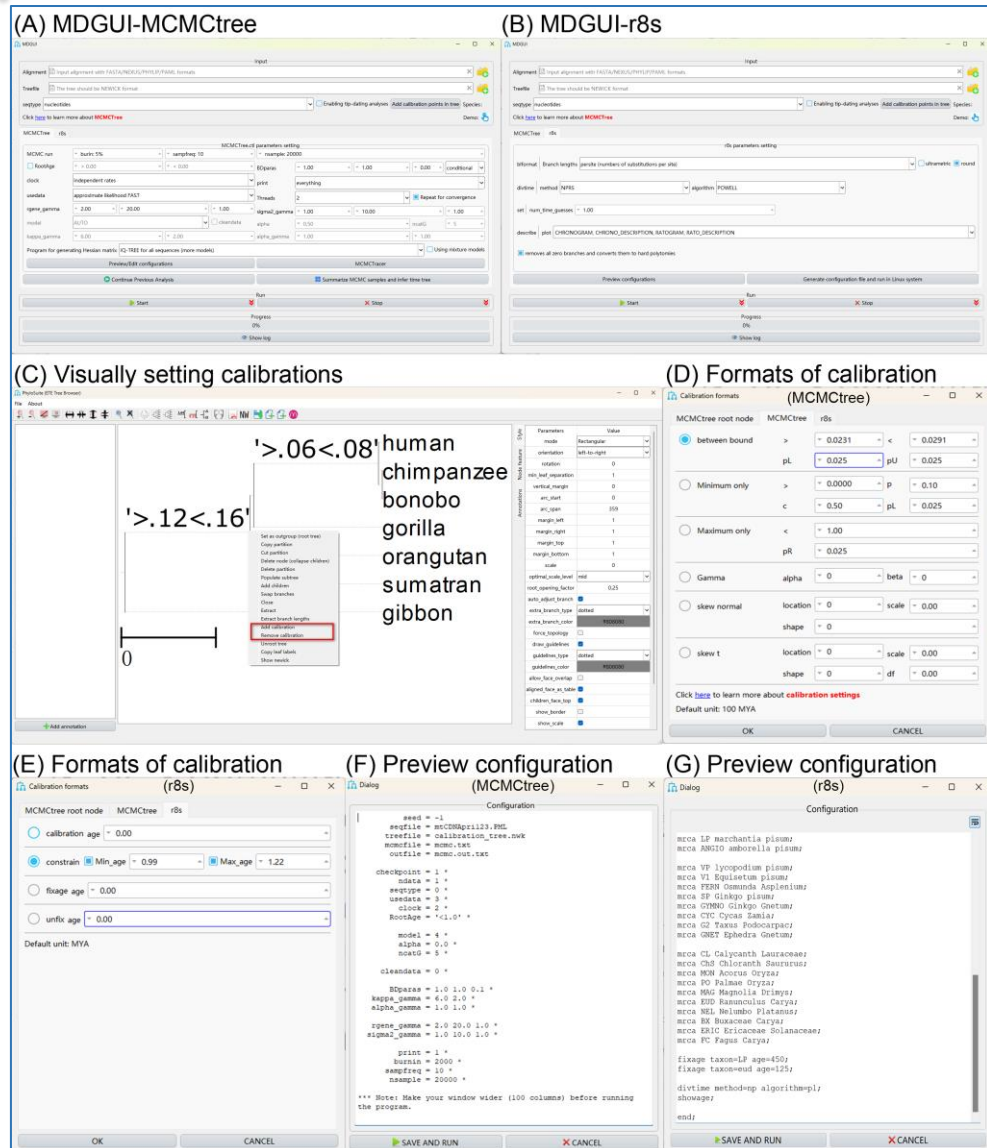


Figure 3. The interface and main functions of the molecular dating suite – MDGUI – in PhyloSuite.

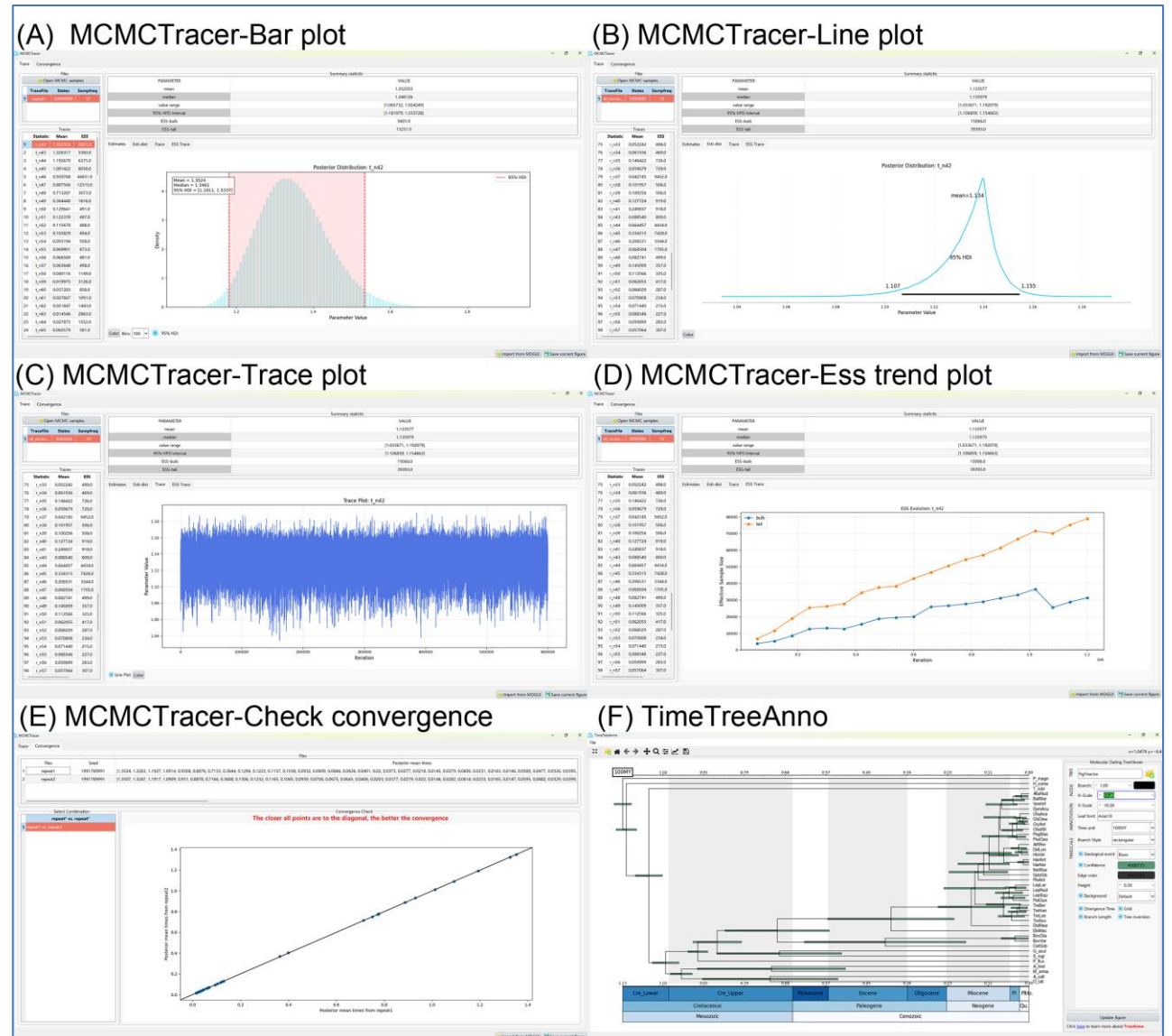


Figure 4. The interface of MCMCTracer and TimeTreeAnno.



Workflow of molecular dating analysis

PhyloSuite v2: Molecular dating suite workflow

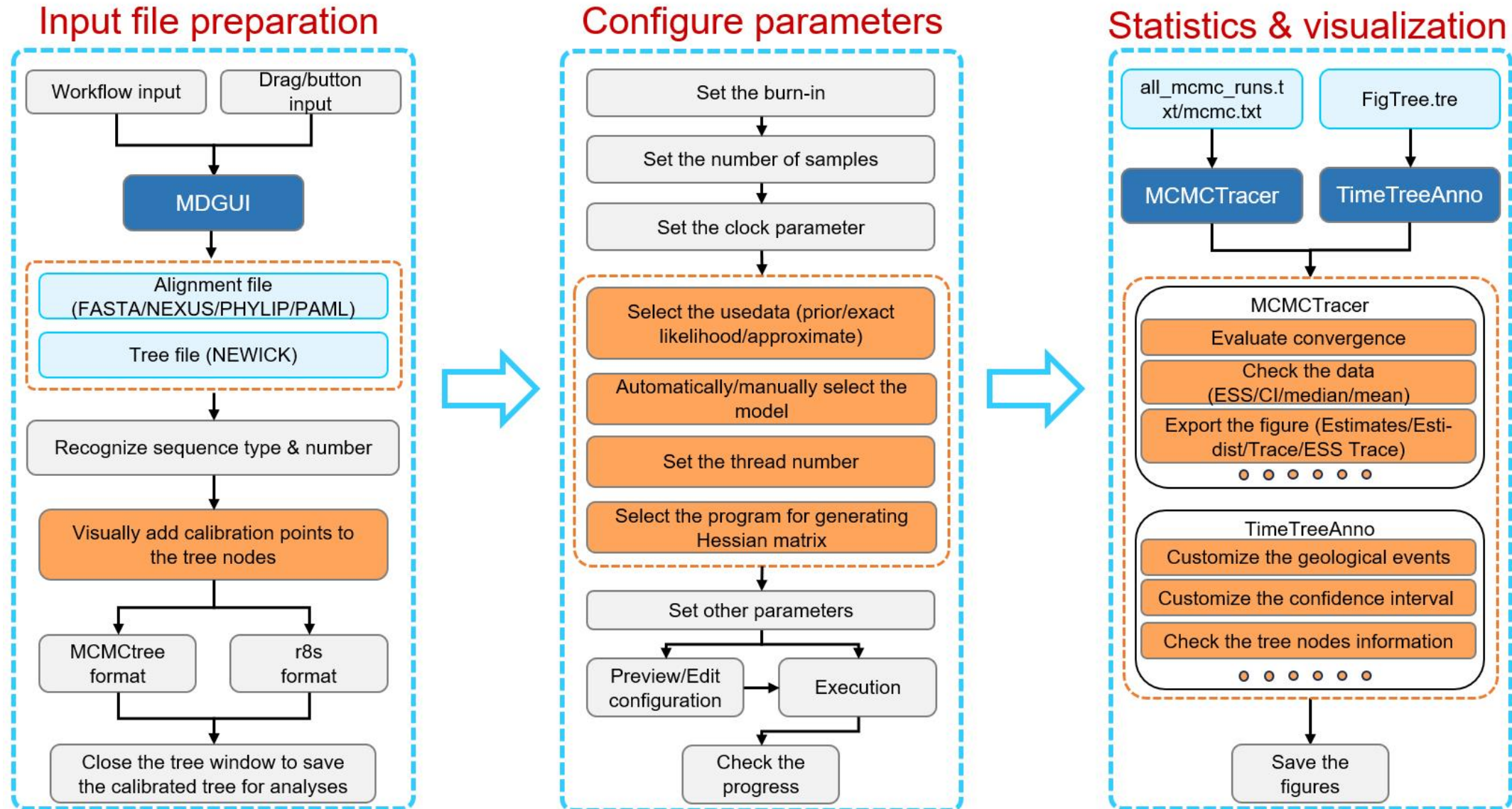
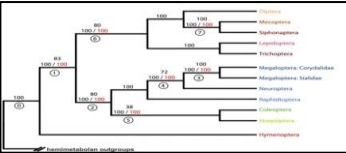


Figure 5. Workflow of molecular dating analysis in PhyloSuite v2



Case: Workflow of molecular dating using nuclear genome data

sequence1: TATGGAATG...
sequence2: TAGAATG...
sequence3: TCTATGATG...
.....



- 41 species
- 374,157 sites

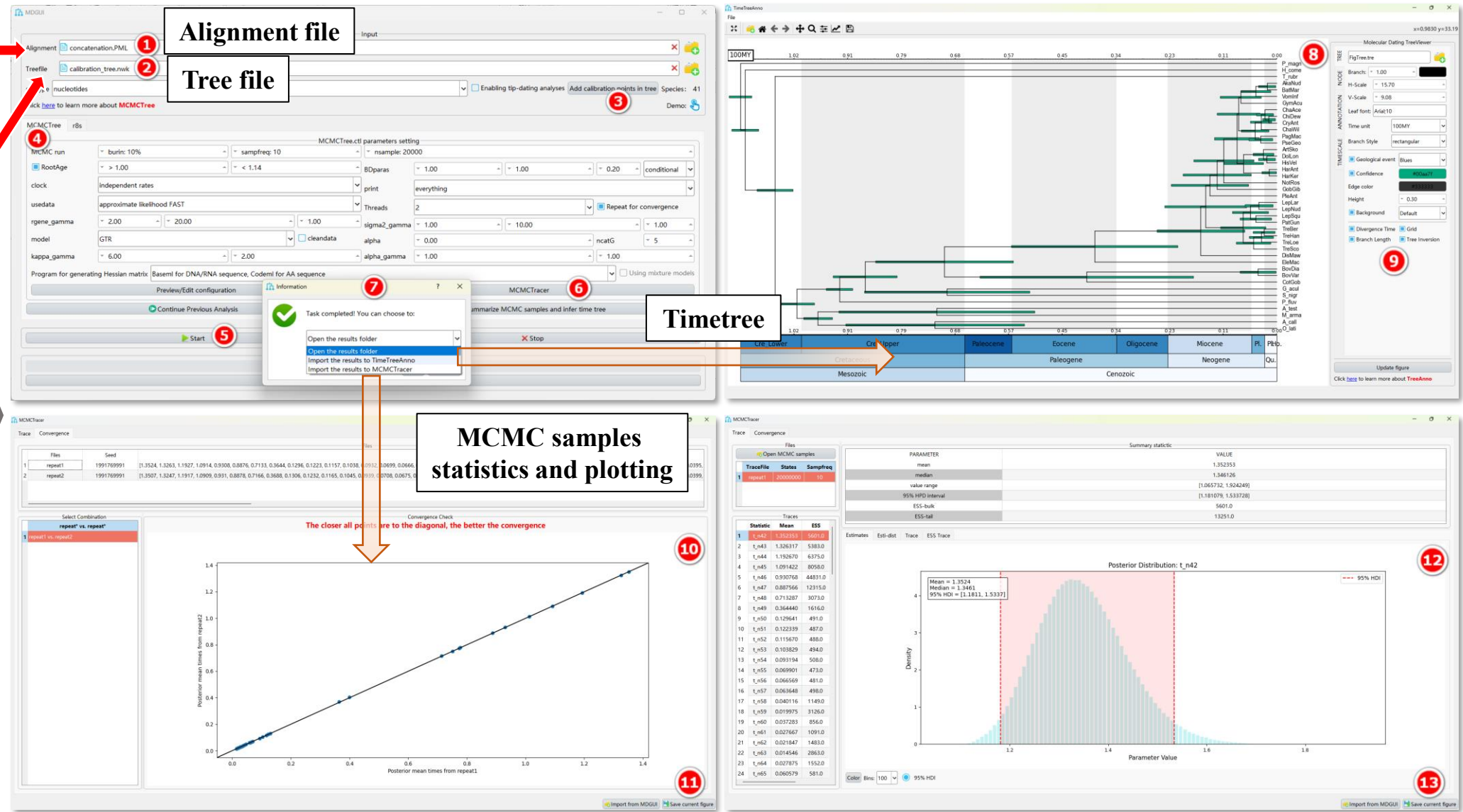


Figure 6. Performing molecular dating analysis using the PhyloSuite v2 platform



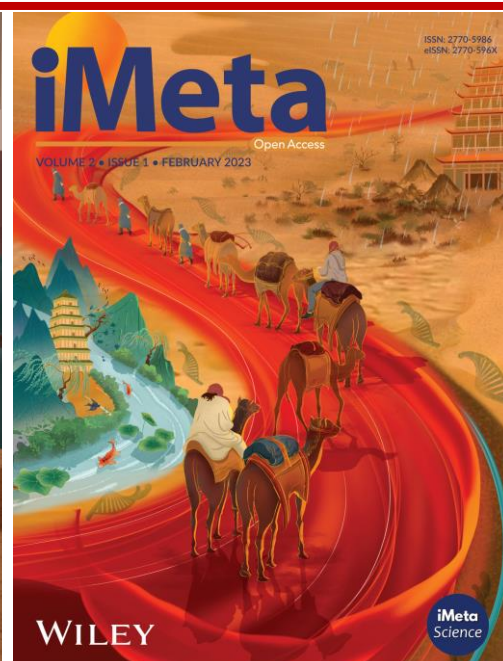
Summary

- ❑ In this study, we introduce the newly designed and integrated molecular dating suite in PhyloSuite (v2): MDGUI, TimeTreeAnno, and MCMCTracer.
- ❑ The suite provides drag-and-drop operation, automatic import of upstream results, and direct visual setting of calibration points on tree nodes; supports extensive file formats and all substitution models available in IQ-TREE; offers multithreading acceleration, pause/continue analysis, and real-time results summarization; and enhances visualization support for molecular dating trees, Tracer-like result plots, and interactive MCMC convergence assessment.
- ❑ PhyloSuite v2 enhances gene duplication handling, codon concatenation, and IQ-TREE integration for speed, and delivers high-resolution interface optimizations with extensive bug fixes.
- ❑ Website: <http://phylosuite.jushengwu.com/dongzhang0725.github.io/>
Tutorials: <http://phylosuite.jushengwu.com/dongzhang0725.github.io/PhyloSuite-demo/Molecular-dating-analysis/>

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