

GetEmpiricalXML

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R Markdown

GetEmpiricalXML allows the user to remove substitution, clock and tree parameters from a beauti XML and instead run a trait analysis using a previously inferred posterior sample of phylogenetic trees.

The benefit of this approach is to reduce run-time, allowing proper inference of the phylogenetic tree before starting a trait analysis.

The script runs a command line application as follows:

```
python3 GetEmpiricalXML.py path/to/originalfile.xml path/to/empiricaltrees.tree
```