

Easy - TreePruner: A Simple software for Pruning Phylogenetic Trees

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Abstract

Phylogenetic trees are essential tools for visualizing evolutionary relationships among species, yet their construction often requires specialized computational expertise. To address this challenge, we present Easy-TreePruner, a user-friendly software designed to streamline the pruning of large phylogenetic trees. This tool allows researchers, including those without advanced training in evolutionary biology, to efficiently extract subtree structures from comprehensive phylogenetic datasets (e.g., A Global Phylogeny of Birds) by specifying target species. The software supports intuitive input operations and outputs simplified trees for further analysis or publication. Easy-TreePruner is developed for Windows systems and is publicly available under an open-source license.

Introduction

Phylogenetic trees are branching diagrams that reconstruct evolutionary relationships among species. They depict shared ancestral lineages and diversification events, thereby representing the divergence history of biological taxa. In these trees, nodes correspond to common ancestors, while branch lengths serve to quantify evolutionary distance or time.

Essentially, a phylogenetic tree is a visual representation of the relationships between different organisms, illustrating the path through evolutionary time from a common ancestor to various descendants. Its scope of application is wide - ranging: it can represent relationships spanning the entire history of life on Earth, all the way down to individuals within a single population.

However, constructing phylogenetic trees for multiple species is no easy task. For instance, when we need to build a phylogenetic tree for certain species, complex calculation methods are required. This poses a significant challenge for researchers who are not specialized in evolutionary studies. When they intend to create a phylogenetic tree for different species, they are likely to need a simple method to do so.

To address this need, we have developed a visualization software called Easy - TreePruner, which is designed for the construction and visualization of phylogenetic trees.

Usage

Open tree pruner.exe (Fig. 1). For example, if you want to construct a subtree from A GLOBAL PHYLOGENY OF BIRDS (<https://birdtree.org/>), first select the input files (full tree data), then choose the output file location. Next, in the "Species to Keep" box, enter the species' Latin names or paste them using Ctrl + V. After clicking "start analysis", please wait patiently for the analysis to complete (Fig. 2). The subset tree will then be output. We recommend running this software on the Windows 11 system.



Fig. 1. Icon of the software.

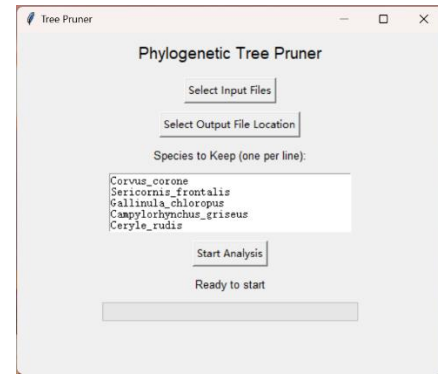


Fig. 2. Software operation interface.

Software Availability

You can download and use the software from this link: <https://github.com/PanshuaiFei/Easy--TreePruner-A-Simple-software-for-Pruning-Phylogenetic-Trees>

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