




1 phylo2vec: a library for vector-based phylogenetic tree 2 manipulation

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10 Summary

11 Phylogenetics is a fundamental component of evolutionary analysis frameworks in biology (Yang,
12 2014) and linguistics (Atkinson & Gray, 2005). Recently, the advent of large-scale genomics and
13 the SARS-CoV-2 pandemic has highlighted the necessity for phylogenetic software to handle
14 large datasets (Attwood et al., 2022; Kapli et al., 2020; Khurana et al., 2024; Kraemer et al.,
15 2025). While significant efforts have focused on scaling optimisation algorithms (De Maio et
16 al., 2023; Sanderson, 2021; Turakhia et al., 2021), visualization (Sanderson, 2022), and lineage
17 identification (McBroome et al., 2024), an emerging body of research has been dedicated to
18 efficient representations of data for genomes (Deorowicz et al., 2023) and phylogenetic trees
19 (Chauve et al., 2025; Penn et al., 2025; Richman et al., 2025). Compared to the traditional
20 Newick format which represents trees using strings of nested parentheses (Felsenstein, 2004),
21 modern tree representations utilise integer vectors to define the tree topology traversal. This
22 approach offers several advantages, including easier manipulation, increased memory efficiency,
23 and applicability to machine learning.

24 Here, we present the latest release of phylo2vec (or Phylo2Vec), a high-performance software
25 package for encoding, manipulating, and analysing binary phylogenetic trees. At its core,
26 the package is based on the phylo2vec (Penn et al., 2025) representation of binary trees,
27 and is designed to enable fast sampling and tree comparison. This release features a core
28 implementation in Rust for improved performance and memory efficiency (Figure 1), with
29 wrappers in R and Python (superseding the original release (Penn et al., 2025)), making it
30 accessible to a broad audience in the bioinformatics community.

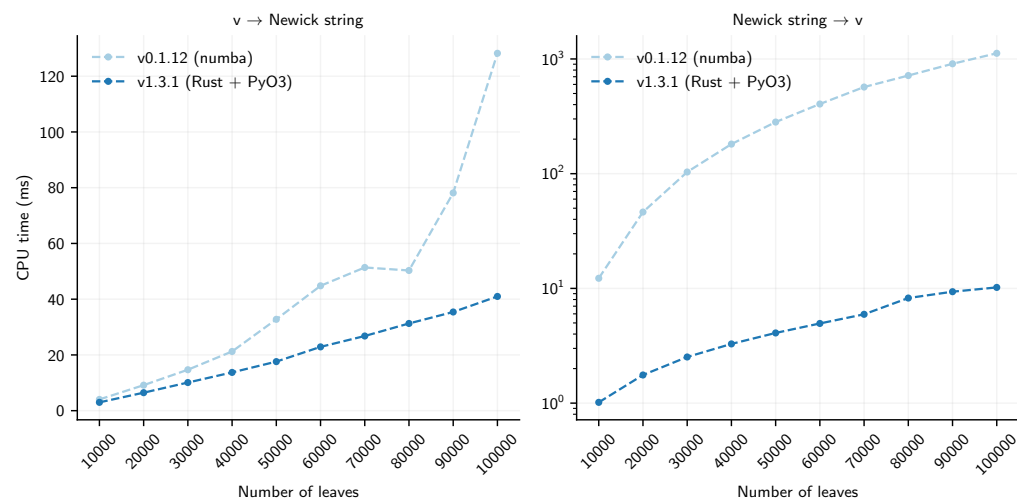


Figure 1: Benchmark times for converting a phylo2vec vector to a Newick string (left) and vice versa (right). Execution time was measured over at least 20 runs per size, comparing Python functions in the latest release (via Rust bindings with PyO3) against the previous release (Penn et al., 2025) based on Numba (Lam et al., 2015). All benchmarks were performed on a workstation equipped with an AMD Ryzen Threadripper PRO 5995WX (64 cores, 2.7 GHz) and 256 GB of RAM.

Statement of need

The purpose of the phylo2vec library is threefold. First, it provides robust phylogenetic tree manipulation in Rust, complementing other efforts such as `light_phylogeny` (Duchemin et al., 2018) for reconciled phylogenies (Nakhleh, 2013), and `rust-bio` (Köster, 2016), which does not yet cover phylogenetics. Second, it complements existing libraries such as `ape` (Paradis & Schliep, 2019) in R, and `ete3` (Huerta-Cepas et al., 2016) and `DendroPy` (Moreno et al., 2024) in Python, by providing fast tree sampling, fast tree comparison and efficient tree data compression (Penn et al., 2025). Third, the phylo2vec representation offers a pathway to using new optimisation frameworks for phylogenetic inference. A notable example is `GradME` (Penn et al., 2023), a gradient descent-based algorithm which uses a continuous relaxation of the phylo2vec representation.

Features

The presented release of phylo2vec addresses optimisation limitations of (Penn et al., 2025) with $\mathcal{O}(n \log n)$ implementations for vector-to-Newick and Newick-to-vector conversions, leveraging Adelson-Velsky and Landis (AVL) trees (Adelson-Velsky & Landis, 1962) and Fenwick trees (Fenwick, 1994), respectively.

New features in the latest release include an extension of the vector representation to support branch length annotations, leaf-level operations (pruning, placement, and MRCA identification), fast cophenetic distance matrix calculation, and various optimisation schemes based on phylo2vec tree representations, notably hill-climbing (Penn et al., 2025) and `GradME` (Penn et al., 2023). We also propose a likelihood function for Bayesian MCMC inference that leverages tree representation similarities with `BEAGLE` (Ayres et al., 2012; Suchard & Rambaut, 2009). Finally, user-friendliness is enhanced with step-by-step demos of phylo2vec's representations and core functions.

Maintenance

A strong focus of this release is to support long-term maintenance through implementing recommended software practices into its project structure and development workflow. The project is structured with a Rust API containing core algorithms with language bindings to avoid tight coupling and enable easy language additions. Additionally, we have established a robust continuous integration (CI) pipeline using GitHub Actions, which features:

- Unit test frameworks for Rust ([cargo](#)), Python ([pytest](#)), and R ([testthat](#) ([Wickham, 2011](#)))
- Benchmarking on the Rust code ([criterion](#)) and its Python bindings ([pytest-benchmark](#))

Lastly, to complement Jupyter Notebook demos, comprehensive documentation is provided using [Jupyter Book](#) and [Read the Docs](#).

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