

CompPhy2: a flexible and real time collaborative web platform for editing and comparing phylogenies

Floréal Cabanettes, Jean-François Dufayard, Vincent Berry, Vincent Lefort, Frédéric F. de Lamotte, Anne-Muriel Arigon Chifolleau

▶ **To cite this version:**

Floréal Cabanettes, Jean-François Dufayard, Vincent Berry, Vincent Lefort, Frédéric F. de Lamotte, et al.. CompPhy2: a flexible and real time collaborative web platform for editing and comparing phylogenies. 2018. hal-01885401

HAL Id: hal-01885401
https://hal.science/hal-01885401

Preprint submitted on 1 Oct 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NoDerivatives 4.0 International License

Bioinformatics
doi.10.1093/bioinformatics/xxxxxx
Advance Access Publication Date: Day Month Year
Manuscript Category

OXFORD

Subject Section

CompPhy2: a flexible and real time collaborative web platform for editing and comparing phylogenies

Floréal Cabanettes [1], Jean-François Dufayard [2], Vincent Berry [1], Vincent Lefort [1], Frédéric de Lamotte [3] and Anne-Muriel Arigon Chifolleau [1,*]

[1]LIRMM, UMR 5506 - CNRS Université de Montpellier, Montpellier, France
[2]CIRAD, UMR AGAP, F- 34398 Montpellier, France
Univ Montpellier, CIRAD, INRA, Montpellier SupAgro, Montpellier, France and
[2]AGAP, Univ Montpellier, CIRAD, INRA, Montpellier SupAgro, Montpellier, France.

*To whom correspondence should be addressed.

Associate Editor: XXXXXXX

Received on XXXXX; revised on XXXXX; accepted on XXXXX

Abstract

Summary: CompPhy2 is a real time collaborative web platform for visualization, comparison and annotation of phylogenetic trees with a responsive user friendly interface. It is the only phylogenetic web platform allowing several users to work synchronously or asynchronously on a same dataset. CompPhy2 brings new features such as side by side comparison, tree annotation, custom display, supertree inference, ...

Availability: CompPhy2 is available at http://www.atgc-montpellier.fr/compphy and does not require user registration.

Contact: chifolleau@lirmm.fr

1 Introduction

Online collaborative and real-time tools are widely used in various domains for projects involving remote partners. In the last twenty years, web technologies have enabled the development of such tools to jointly edit office documents. However, only few such tools exist in scientific domains, but prior to the introduction of the CompPhy website [10], no collaborative tool was available to process phylogenies. CompPhyâŁ™s purpose is to fulfill this gap in the phylogeny domain. Although a large number of studies and projects in evolutionary biology and systematics involve collaborations between scientists from different institutes, or between students, most existing tools for visualizing and comparing phylogenies offer single-user access or focus on high-level features for a single tree (TreeView [Page, 2002], TreeDyn [Chevenet *et al*., 2006], Dendroscope [Huson *et al*., 2007], Archeopteryx [Han *et al*., 2009], FigTree [Rambaut, 2016], iTOL [Letunic *et al*., 2011], EvolView [Zhang *et al*., 2012] and PhyloIO [Robinson *et al*., 2016]).

To fulfill this gap, we have introduced CompPhy in 2014, a web platform providing a collaborative approach to store, edit, visualize, compare phylogenetic trees [Fiorini *et al*., 2014]. This platform allows multiple users to manage shared phylogenetic trees stored on a common server. The access can be done synchronously, when several partners edit and discuss data or trees at the same time, or asynchronously, partners then accessing the work of others done since their last access. CompPhy is a unique tool that combines tree comparison operations such as restricting two trees to their common taxa, automatically swapping branches to match leaves of two trees, the computation of consensus trees and supertrees. The web platform provides two ways to handle trees: either by choosing two trees for a detailed visualization side by side, or in batch mode by operations on several hundred trees. Finally, it offers an interface with the usual editing features of trees, such as leaf or sub-tree coloring, annotation management, subtree swapping and re-rooting.

CompPhy introduced several key features. Data are stored online on a secured platform and all collaborators have access to an always up-to-date dataset, avoiding data loss or desynchronisation between partners. Since CompPhy is a web platform, it does not require any installation, a web

© The Author 2015. Published by Oxford University Press. All rights reserved. For permissions, please e-mail: journals.permissions@oup.com

Version preprint

Comment citer ce document :
Cabanettes, F. (Co-premier auteur), Dufayard, J.-F., Berry, V. (Collaborateur), Lefort, V. (Collaborateur), De Lamotte Guéry, F. (Co-dernier auteur), Arigon Chifolleau, A.-M. (Auteur de correspondance) (2018). CompPhy2: a flexible and real time collaborative web platform for editing and comparing phylogenies . Bioinformatics, In Press, 1-3.

browser is enough. The real time approach facilitates collaborative works between remote partners. This makes it also appropriate for teaching. Students can easily work in groups, lecturers can share data, perform phylogenetic analyses in real time and show phylogenetic trees to students or give them assignments on the platform. Finally, the side by side tree comparaison is useful to visually highlight tree differences or common parts and customize each tree by annotating it. It opens the door to a visual comparison of trees inferred from different hypothesis or analyses.

However, the first version of CompPhy suffered from several drawbacks: a non-smooth process when several partners edited trees simultaneously, several tree edit operations had to be performed in non-intuitive ways and finally only few annotations could be put in regards of the trees. We thus developed a new version, that aims to improve the existing functionalities and to add new ones, in particular to answer the needs of the biologist users from feedback we had.

2 Features

CompPhy2 offers a friendly and responsive interface developed with D3.js [Bostock *et al*., 2011]. A user can easily create a project to gather phylogenetic trees and invite collaborators to cooperate on CompPhy2. Once a project is created, several actions are available, including :

- importing trees (Newick, NEXUS and NHX format), all trees are available online at anytime and can be visualized via thumbnails;
- importing annotations in a tabular format to visualize them next to the trees;
- visualizing and manipulating imported phylogenetic trees on the main CompPhy2 page;
- export trees in various formats.

The main CompPhy2 page is divided into three areas (see Figure 1). The area at the top ("Tree Collections 1/2" in Figure 1) displays a list of imported trees, that can be splitted into two collections. From the thumbnail pictures of the trees in these collections, the user easily selects trees to be sent to the central workbench (allowing side by side display of two trees) for close inspection, comparison, annotation or discussion purposes. CompPhy2 accommodates big trees by automatically collapsing some selected subtrees.

The workspaces in the central area ("Workbenches" in Figure 1) provide a set of features for editing and comparing two trees. Within a project, each user can take control of desired trees. Thus, the other project collaborators can see in live the changes made to these trees. They can also manipulate other trees. A set of relevant tools is available between the two workspaces:

- to customize the tree display (branch color and thickness, subtree coloring, subtree masking by a collapse operation, nodes swapping);
- to set up the zoom applicable to the displayed trees;
- several tree comparison features: consensus trees computation, distance between the two trees topologies, or automatic branch rotating. The methods implemented in these tools comply with the state of art [Fiorini *et al*., 2014].

In each workspace, users can edit tree annotations ("Side annotationsâŁž in Figure 1) and manually edit the tree in Newick format (" Manual newick editing " in Figure 1).

The box at the bottom of the page ("Miscellaneous tools" in Figure 1) contains project management tools and tools that can be simultaneously applied to a bunch of trees, including renaming trees or taxa, re-rooting trees based on a specific out-group and inferring supertrees. For the latter operation, CompPhy uses the phylogenomics services provided by the ATGC platform (http://www.atgc-montpellier.fr/). Finally, a lateral toolbar

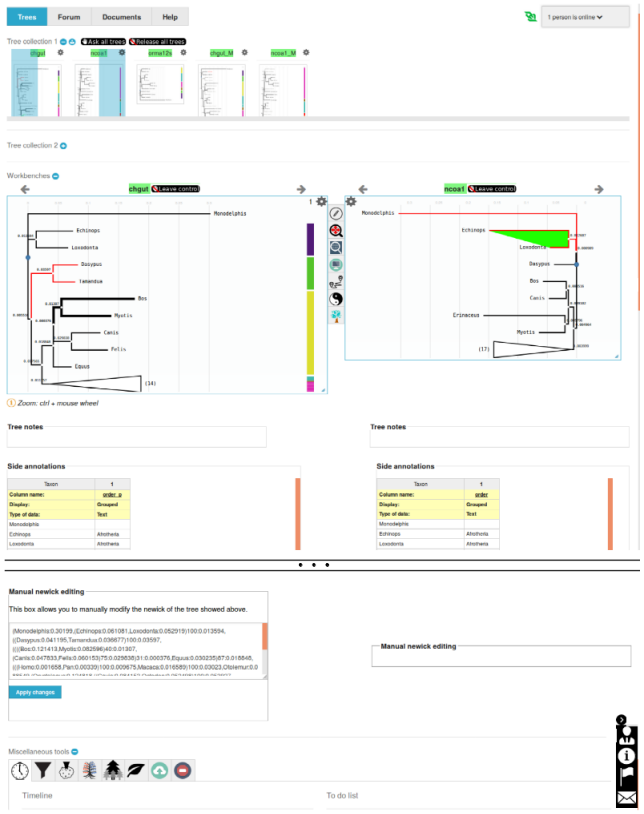


Fig. 1. CompPhy2âŁ™s interface. The main page has three areas: tree collections ("Tree collection 1 and 2"), workspaces ("Workbenches") and an area containing tools for processing tree sets and managing the project ("Miscellaneous tools").

facilitates collaborative aspects. It allows a user to quickly have access to notifications and queries waiting to be answered (such as control requests) or to modify certain user parameters applicable to the project. An instant messenger is also available to facilitate the real time collaboration.

Two connection modes are available: a user can create a project while remaining anonymous (its data are not saved) or create an account (its data are then preserved). In the later mode, a user can share projects with others and beneficiate from the collaborative features to coordinate multiple accesses to the project by several partners at the same time.

3 Conclusion

CompPhy was a first step toward: a collaborative web platform in phylogeny. CompPhy2 improves significantly the first version and marks a major breakthrough. It presents new features and great enhancements of existing ones. The main developments concern the interactivity and the fluidity of the interface as well as the collaborative aspects. For the latter, the granularity is particularly refined to allow management at each tree. This online platform is available through a simple web browser and offers solutions to modern problems by facilitating collaborative work in phylogeny domain. CompPhy2âŁ™s interface was entirely re-implemented taking advantages of new technologies to present a modern, reactive and user-friendly interface. In 2014, CompPhy was integrated the ATGC platform (processing more than 25000 hours of computation per month), which coordinates the bioinformatics services activities in the South of France for the French Institute of Bioinformatics (IFB). CompPhy2 is been in production on the ATGC platform since 2017.

Version preprint

Comment citer ce document :
Cabanettes, F. (Co-premier auteur), Dufayard, J.-F., Berry, V. (Collaborateur), Lefort, V. (Collaborateur), De Lamotte Guéry, F. (Co-dernier auteur), Arigon Chifolleau, A.-M. (Auteur de correspondance) (2018). CompPhy2: a flexible and real time collaborative web platform for editing and comparing phylogenies . Bioinformatics. In Press. 1-3.

Funding

This work benefited from a grant from the French state managed by the French National Research Agency under an Investment for the Future program through the LabEx NUMEV (reference ANR-10-LABX-20).

References

Page, R. D. (2002) Visualizing phylogenetic trees using TreeView, *Curr Protoc Bioinformatics*, **Chapter 6**.

Chevenet, F., Brun, C., Banuls, A. L., Jacq, B. and Christen, R. (2006) TreeDyn: towards dynamic graphics and annotations for analyses of trees, *BMC Bioinformatics*, **7**.

Huson; D.H., Richter, D.C., Rausch, C., Dezulian, T., Franz, M. and Rupp, R. (2007) Dendroscope: An interactive viewer for large phylogenetic trees, Bioinformatics, **8**.

Han, M. V. and Zmasek, C. M. (2009) phyloXML: XML for evolutionary biology and comparative genomics, *BMC BMC Bioinformatics*, **10**.

Rambaut, A. (2016) [http://tree.bio.ed.ac.uk/software/figtree/].

Letunic, I. and Bork, P. (2011) Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy, *Nucleic Acids Res*, **39**.

Zhang, H., Gao, S., Lercher, M. J., Hu, S. and Chen, W. H. (2012) EvolView, an online tool for visualizing, annotating and managing phylogenetic trees, *Nucleic Acids Res*, **40**.

Robinson, O., Dylus, D. and Dessimoz, C. Phylo.io: interactive viewing and comparison of large phylogenetic trees on the web. arXiv:1602.04258 [q-bio] (2016).

Bostock M., Ogievetsky V. and Heer J. (2011) D3 Data-Driven Documents, *IEEE Transactions on Visualization and Computer Graphics*, **17**.

Fiorini, N., Lefort, V., Chevenet, F., Berry, V. and Chifolleau, A.-M. A. (2014) CompPhy: a web-based collaborative platform for comparing phylogenies, *BMC Evolutionary Biology*, **14**, 253.

Version preprint

Comment citer ce document :
Cabanettes, F. (Co-premier auteur), Dufayard, J.-F., Berry, V. (Collaborateur), Lefort, V. (Collaborateur), De Lamotte Guéry, F. (Co-dernier auteur), Arigon Chifolleau, A.-M. (Auteur de correspondance) (2018). CompPhy2: a flexible and real time collaborative web platform for editing and comparing phylogenies . Bioinformatics. In Press, 1-3.