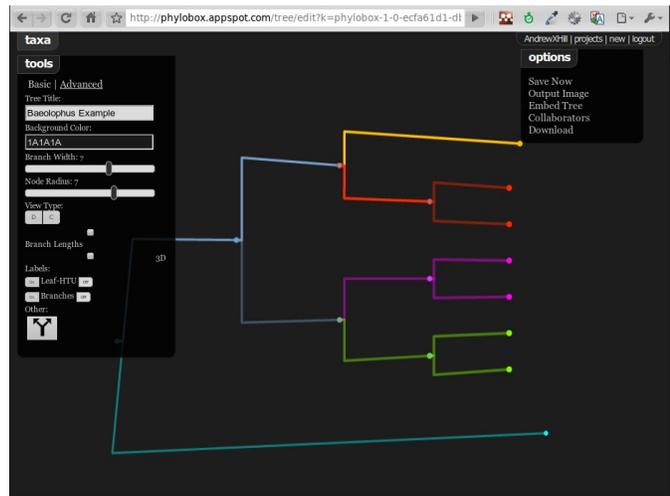


## PhyloBox

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PhyloBox is a tool to allow researchers to go from phylogeny to publication quality images and web publishable widgets in a minimum number of steps. While still in early development, we plan to support many of the same tools as Mesquite. Unlike many phylogeny interfaces in the past, PhyloBox has been designed to take advantage of the modern web browser. PhyloBox uses JavaScript and HTML freeing the user from any need for an applet (Java), browser plug-in (Flash), or desktop application. PhyloBox represents a significant shift away from the traditional phylogenetic methods in four main areas: editing and collaboration, visualization, publication, and philosophy.

*Editing and collaboration:* The editing workflow is simple, 1) Upload a phylogeny. 2) Edit (see figure to right). 3) Save or Publish. We have tried to simplify upload, and while we currently only support phyloXML files, we are also expanding support. Editing is done *in the browser* with a growing library of tools to change the look and display of the tree, including branch coloring, clade display toggling, re-rooting, and drawing method (e.g. dendrogram, cladogram, circular cladogram, etc.). When users finish editing, they can save trees to their *existing Google account*, without the need for further user registration. Furthermore, they can invite, through a simple dialog, any other user to edit the same tree. We give all users a *Project Manager* where they can see all projects they own or are collaborating on. The original user is always maintained as the original author of the tree.



*Visualization.* Drawing phylogenies on the web has never been a trivial task. PhyloBox has pushed the envelope, supporting thousands of nodes rendered –with movement in 3D– directly in the web browser. We are supporting and refining dendrogram, cladogram, and circular versions of each variation. Users can change variables such as offset on the screen, angular velocity of the tree spin, branch and node width and radius, all in real time. Our engine has been designed to support multiple trees on in the same visualization in the near future. We have been actively developing this technology using the Frost et al. (2006) Amphibia tree found on the phyloXML.org website with little noticeable slowdown on a modern laptop, while further improvements need to be made for the limited resources of other technologies (e.g. the iPad). See that example here, <http://phylobox.appspot.com/tree/edit?k=phylobox-1-0-b6c5201d-b7d0-4e60-8ee5-480811cd2221>

*Publication.* PhyloBox has been designed to support a diversity of members of the community. For the individual user we make publication easy; the user can output images, embed images directly from our site, or embed our widget on their webpage. Our widget is an exciting advancement in web publication of phylogenies, giving users a YouTube-like plug-in to display phylogenies on their webpage or blog. Furthermore it gives your readers the ability to re-publish the widget on their own websites. The widget gives a reader the view of the phylogeny through a small portal and also features a *fullscreen* button for expanded viewing. To see a working example and a description of many more features, see our accompanying blog post at <http://biodivertido.blogspot.com>. We are developing our API and services so that a PhyloBox widget can be programmatically added to, say EOL or TreeBase pages.

*Philosophy.* PhyloBox supports a feature we call forking. When you publish a tree on the web you will always be recorded as the original author. Next, a reader of your website may think that the data could be displayed more effectively in a different way; they simply *fork* your tree, creating a new version that they can edit and republish. We always keep a record of your original authorship and a record of all those that have contributed along the way.

While PhyloBox is a relatively new project (<2 months old), we have packed many exciting features into our service. Our 3D rendering of very large trees in the web browser is only one step in a long list of benchmarks for our project. Soon, we will give users to ability to render multiple trees in the same space. From there the visualization and analysis potential increases greatly. We hope that through the iEvoBio visualization challenge we can spread our idea, gather feedback, and further PhyloBox development to meet many needs of the community.

PhyloBox can be found at <http://phylobox.appspot.com>

Code can be found at <http://code.google.com/p/phylobox/>