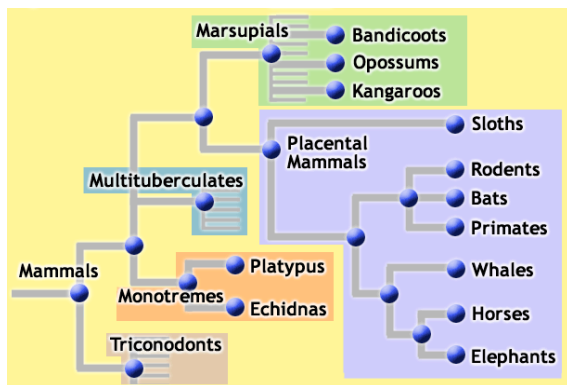


# Information Architecture of the Tree of Life Project

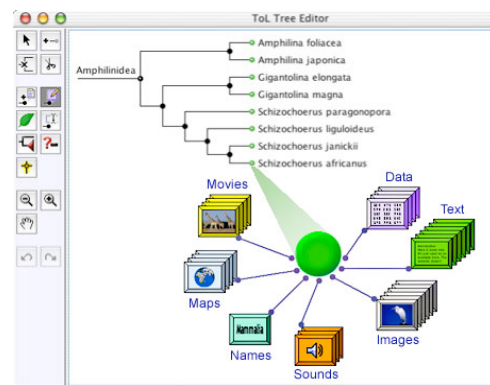
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The architecture and navigational structure of the Tree of Life Project (<http://tolweb.org>) is based upon phylogenetic relationships between the organisms it catalogues and describes. This structure is achieved via a *node-based information architecture*. Nodes are branching points in the phylogenetic hierarchy of life. Each node represents a particular group of organisms, including all descendents of a common ancestor, and descendent nodes correspond to smaller subgroups of the group represented by the parent node.

Materials contained in the Tree of Life database (e.g., text, images, maps, sounds, movies, etc.) are treated as objects that are attached to individual nodes following a hierarchical schema: nodes deep in the Tree of Life have objects attached that apply to large, more inclusive groups of organisms, e.g., ALL plants, ALL fungi, ALL mammals, etc., while nodes higher up in the tree own objects that apply to smaller, less inclusive groups, e.g., individual species.



Nodes in the tree



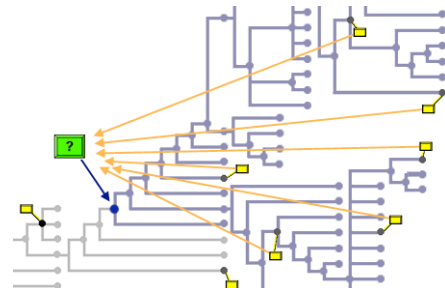
Tol Editor plus some objects that could be attached to a node

Tree of Life contributors enter materials into the Tree of Life database using *Tol Editor*, a custom Java application currently in the final testing phase. *Tol Editor* has two main components: a graphical *Tree Editor* that allows authors to build the phylogenetic tree for their group and a *Node Data Editor* for each individual node in the tree, which lets authors attach a variety of different objects.

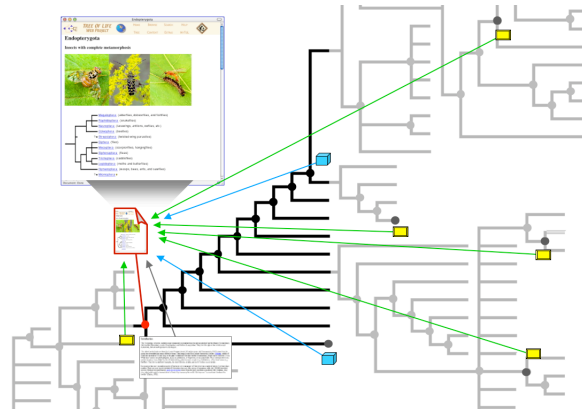
In addition to objects that are native to the Tree of Life collection, other collections and databases will have the opportunity to introduce phylogenetic structure into their holdings by linking items relevant to particular groups of organisms to the Tree of Life system.

Tree of Life data (both native and imported or linked from other projects) can then be made available to a variety of different *requestors*, e.g., other databases, analytical tools, and web browsers.

For example, another database project, e.g., one focusing on mammals, could request the structure of the entire mammal branch of the Tree of Life. In addition, it could retrieve all of the objects of a particular class (e.g., pictures of mammal teeth, sound recordings, etc.) that are attached to nodes in the mammal branch. The requested objects can then be harvested from the Tree of Life database and returned to the requestor.

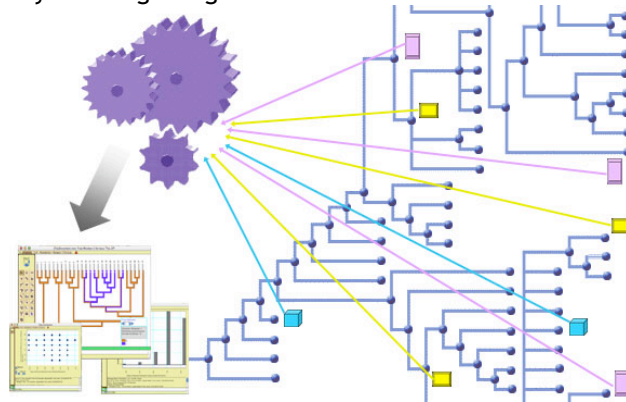


Tree of Life web pages are a special class of objects; each page will be put together when the user requests it, by combining a selection of materials attached to a particular node and its descendants. For example, to create a web page for a particular group of insects, one would harvest text sections and other objects that are attached to the node for this group, providing information about the characteristics of the group as a whole. This material would then be supplemented by additional objects harvested from descendent nodes, e.g., images of representative species that illustrate what organisms in the group look like.



A particular page object contains a specification of other objects to be harvested together and formatted into the page to be presented to the web browser. Exactly which objects are to be harvested and presented on a page will be determined by page object templates. The Tree of Life web site offers a number of prebuilt page object templates, and visitors to the site will soon have the option to modify these templates according to their own preferences.

Objects attached to nodes in the Tree of Life are suitable not only for display and illustration; they can also be used to analyze patterns of biological diversity across the phylogeny. By integrating with existing analysis programs (e.g., Mesquite, <http://mesquiteproject.org>), the Tree of Life Project will provide its visitors with the opportunity to conduct exploratory studies online, using tools available on the Tree of Life website. Both professional and student researchers will then be able to trace the distribution of characteristics across branches of the tree of life and to ponder forces that may have shaped the observed diversity of living things.



The phylogenetic tree of life provides the underpinnings for much of the modern, comparative life sciences, both theoretical and applied, and it is therefore the ideal framework for the organization of biological knowledge. The Tree of Life Project presents this tree as an integrated whole, and the project's node-based information architecture allows the retrieval of phylogenetically structured data for a variety of different purposes, enabling researchers, teachers, and students to explore patterns and explanations of biological diversity in an appropriately synthetic, evolutionary framework.