TTOP : A System for Phylogenetic Tree Editing and Evolutionary Annotation of Genes

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Keywords: evolution, annotation, phylogenetic tree, XML, Java

1 Introduction

We have developed a tool called TTOP (stand for "Tree Topology Operation Tool"). TTOP has applications both in phylogenetic tree editing and in the annotation of the evolutionary characteristics of genes. Evolutionary annotation is the process which associates genes with certain events which may have taken place during evolution of those genes e.g. duplication events, deletion events, and functional specialization of genes.

The chief advantage of the phylogenetic trees created using TTOP is that they are totally customizable. Also any tree can be saved in either a multi-tree editable format or a single-tree picture format. TTOP has been incorporated into the gene annotation system used in the H-invitational project. The TTOP system is highly interoperable as is based on Java technology. The TTOP can be used on any OS platform which has Java installed.

2 Features of TTOP

The main functionality of the tool is illustrated in Fig. 1. What follows is a brief description of the defining characteristics of the tool.

2.1 Flexible and User Friendly Topological Operation

The tool has functions such as varying the out-group, complete rotation/flap group of branches, compression/expansion of any branch or group of branches. Suspected speciation and gene duplication events may also be recorded on a tree. Under TTOP, the topology of a tree may be altered with a couple of mouse clicks but the bootstrap values and the length for the tree branches are retained. Undo and Redo commands have been incorporated into TTOP to make the editing process both easier and less fraught.

2.2 Reflective and Intuitive Character Editing Interface

The function of find and replace was also added to arrange the information about annotation easily. For example, the numerical search of branch length/bootstrap value and the text search and replace of taxa can be performed. The added functionality created by the addition of these commands allows the user to edit large complex trees in a more effective manner.

2.3 Output Formats : JBIRC, SVG and Newick Standard

JBIRC format is a TTOP specific format for saving trees in a multi-tree editable format. This multi-tree format lets the user store related trees together and manage large projects with greater efficiency. Trees may be flattened into single-tree format images also. In addition to PS and GIF formats, individual trees can be saved in SVG/XML picture format. SVG format has the advantages of relatively low kilobyte size and being in editable character format rather than binary format as in PS or GIF. Due to its functionality SVG may be considered to be the optimal picture format for the exchange of phylogenetic tree information between researchers. In addition, TTOP can save output trees using the Newick standard format.

2.4 High Flexibility of Dealing with Any Kind of Trees

TTOP can be used to show both rooted and unrooted trees. The tool can also display trees which contain negatively scored branches and multifurcated nodes (Fig.3). TTOP automatically selects either rooted or unrooted based upon the particular dataset. The user may create/alter the rooting point for either a rooted or unrooted tree.

Table 1: Feature list.

I/O settings	Options
Input	Newick standard JBIRC format (compressed)
Output	JBIRC format, Newick format
Graphic output (print)	GIF, PostScript, SVG (Print adjustable: the graphic size, the number of pages)
Window configuration	(Recordable)

Editing	Contents
Topological change	Rotation, Swapping, Compress, Outgroup selection, Collapse
Character editing	Taxa name
Drawing tree	Rectangle, Radial
Adjustment	Enlarge, Reduce, Ratio of length & width, Font change
Show value	Branch length, Bootstrap probability

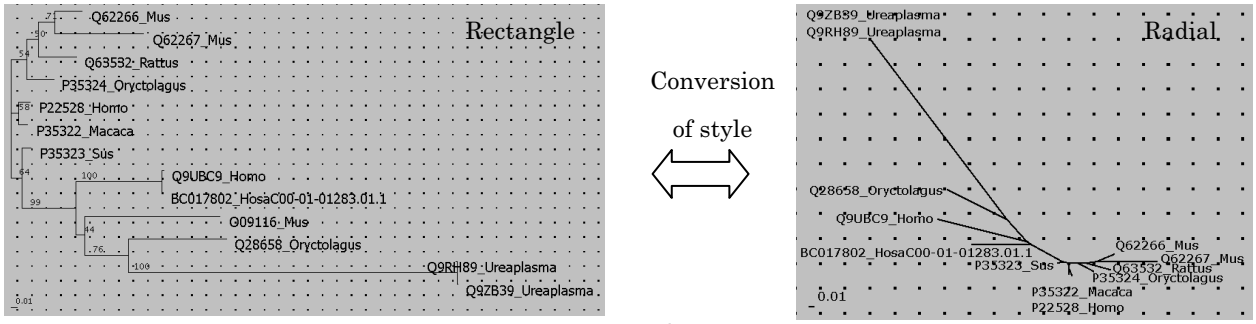

Figure 1: Tree style coversion.

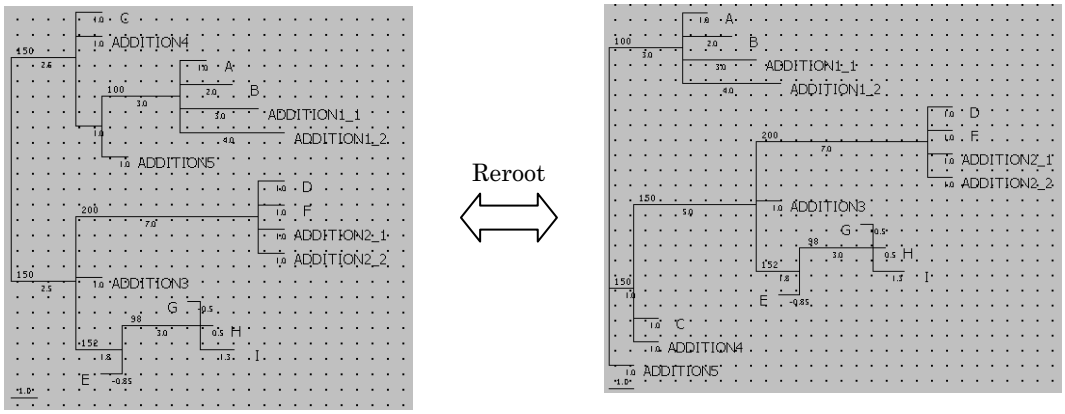

Figure 2: Representation of trees with negative branches and multifurcated nodes.

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