**Evolview, an online visualization and management tool for customized and annotated phylogenetic trees**

**Abstract**

**Introduction**

The phylogenetic tree is a powerful tool for displaying evolutionary relationships among different species. Several algorithm methods (including ML, MP and NJ) can be used in phylogenetic tree constructions according to different cases. In order to figure out the topology of phylogenetic trees, researchers have developed much tree visualization software, such as TreeView, MEGA, iTol and etc. But users cannot customize phylogenetic trees and attaching annotations when using the above software, let alone manage both of them. In 2012, we developed an online tree visualization tool, which we called Evolview. Unlike other software, Evolview allows users administrate phylogenetic trees and attaching annotations interactively. Additionally, users can share data with their friends. Recently we have updated Evolview, and the new version adds several annotation datasets including leaf label decoration, group labels, dot plot and heatmap. Each new annotation dataset will endow more meaningful information for the phylogenetic tree.

**Features**

**New dataset types**

* 1. New dataset type I: leaf label decorations

We added a new annotation type in Evolview, which we called leaf label decorations. It was usually used for dividing the same group species of the phylogenetic tree into subgroups. Leaf label decorations provide 4 different labels (star, tick, rectangle and roundness) and 2 styles (full and empty) for users to choose. The users can choose any color to decorate labels by modifying the RGB code of annotation files. To annotate the species more precisely, more than one lead label decorations can be added for the same species in the phylogenetic tree, which is helpful to supply more information in one phylogenetic tree.

* 1. New dataset type II: group labels

Secondly, a new kind of annotation type in Evolview that we added is group labels. A main feature of phylogenetic tree is to classify the species by following Linnaeus’s binomial nomenclature so that the evolutionary status can be determined for a new species. The evolutionary level of species can be easily identified by using group labels. Evolview provides 5 kinds of visualization styles of group labels and supply the circular mode. In addition, different kinds of styles can be combined in one phylogenetic tree.

* 1. New dataset type III: dot plot

Another new annotation we added in Evolview is Dot plot. Dot plot is a variant of bar chart and it is similar with leaf labels. The difference between dot plot and leaf label is that dot plot can the reflect variation degree of a particular attribute for one species. For example, warinner’s paper used dot plot dataset to represent targeted 16S rRNA hypervariable regions in phylogenetic tree, fig 1B. We reconstructed the phylogenetic tree and added the dot plots annotation using Evolview. The Evolview generated figure can achieve as the same effect as the original image. Each species can be annotated by more than one dot plot types.

* 1. New dataset IV: Heatmap

Heatmap is usually used in gene expression analysis to imply the expression correlationship among samples. In phylogenetics, heatmap also can reflect the correlationship of some properties for each species in the phylogenetic tree. In Hornsby’s paper, they used heatmap annotations to figure out the strength of the ELISA signal of each anti-SCAN domain Fabs by using Evolview. The heatmap annotation has a great potential role in the annotation of phylogenetics, such as dispensable or unique genes of each bacterial strain in pan genomics analysis.

3 Summaries and Outlook

In this new version, we mainly update the annotation system of Evolview by adding several new annotation types. The new annotation types can help users explain more complex informations of the phylogenetic trees. In future, we will continue this project to make further update to meet the need of broad users.