## PHEIO, A NOVEL PHYLOGENETIC EDITOR TO ADD PHYLOGENETIC RELATIONSHIPS TO NCBI TAXONOMY TREE

Velloso H, Pena IA and Ortega JM

Lab. Biodados ICB UFMG Belo Horizonte MG Brazil

We developed PHEIO (PHylogenetic EdItOr), a visual phylogenetic tree editor. PHEIO is developed in Java and uses MySQL as its database. PHEIO loads NCBI taxonomy database into a local server and allows the user to create and edit taxon groups, thus turning taxonomy relationships into phylogenetic ones. PHEIO can read input files containing a list of taxon names and traces the path back to the root for each taxon, than it mounts and shows a user-friendly graphical phylogenenic tree. PHEIO also allows the users to create their own taxons in PHEIO database. PHEIO lets the user to expand a tree branch, allowing one to insert into the visible tree all the child nodes of that specific branch. PHEIO also allows the user to remove a node from the visible tree. When the user selects a taxon in the visible tree, PHEIO shows information about that taxon, such as scientific name, rank, tax id, user observations and the distance of a node to the tree root. PHEIO also provides a taxon search system. Finally, PHEIO has a user registry system, so different users can access the program and register their activities. Bacterial evolutionary trees were used as a model. In conclusion, the user friendly interface combined with a powerful database allows one to apply phylogenetic relationships to automated evolutionary analysis.