

27. MicrobialTREE: A user friendly tool for bacterial taxonomy navigation.

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MicrobialTree program is a user friendly tool designed to facilitate the browsing of NCBI bacterial taxonomic data. The program allows the navigation along the taxonomy tree corresponding to bacteria and archaea. The tool is based on the construction of an XML file representing the tree structure using as source data the text files available at the NCBI taxonomy database. In addition, the user can customize each taxonomic entry with personal annotations and links to appropriate URLs. These capabilities allow the users to organize research data around the framework of the taxonomic tree.

The majority of the taxonomic elements, even considering all organisms, correspond to bacteria and archaea. Prokaryotic organisms have a very complex taxonomic classification because there is an immense diversity of species. The management of these thousands of taxonomy elements can be difficult but it is required for developing many tasks. Hence a tool allowing an easy navigation across this large taxonomic tree would be very useful. We have developed a visual interactive tool that includes the taxonomy of bacteria and archaea and allow the user to manage the taxonomic data.

Working with microorganisms, the need of organizing the information around the taxonomic tree is extremely frequent. To cover this need we have incorporated to the program the capability of establishing associations between taxonomic elements and text data and/or URL addresses. Thus, the user can organize their research data (sequences, epidemiology data, experimental data, bibliographic data or any other textual data) around the taxonomic classification of prokaryotic organisms.

In addition, the taxonomic tree would be a very appropriate framework to organize interesting URLs. MicrobialTree program takes the data from the NCBI taxonomic database and using a Java program generates an XML file from the text files available at <ftp://ftp.ncbi.nih.gov/pub/taxonomy/>. As we thought that the taxonomic framework could be an appropriate organizer of information for the microbiologist, we have programmed the following functionalities:

The possibility of the definition of a set of URLs linked to any of taxonomic node. These URLs can be classified according a set of Keywords.

The possibility of store textual information linked to any taxonomic node. This textual information can also be classified by means of the set of keywords.

A textual search system that retrieves the nodes fulfilling searching criteria

MicrobialTREE will be available at our web site <http://www.era7.com/MicrobialTREE/>