Topic: **Genomics, Evolution and Phylogeny**

ARPA: AUTOMATIC RECONSTRUCTION OF PHYLOGENOMIC ANALYSIS

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Due the explosive growth of genomic data, molecular phylogenetic reconstruction has been seriously affected by the advance and development of different algorithms. We have developed an automatic system for the reconstruction of phylogenetic trees. Our ARPA pipeline integrates different phylogenetic algorithms using programs considered as the most useful. ARPA is a web-based platform for phylogenetic analyses of molecular data. Phylogenetic techniques used include alignment trimming, branch length optimization, evolutionary model testing and distance, maximum parsimony, maximum likelihood and Bayesian methods. Tools included in ARPA cover a wide yet selected range of programs such as PHYLIP, PAUP, PHYML, WEIGHBOR, TREE-PUZZLE, RAXML, GARLI and MRBAYES. ARPA pipeline can be used for phylogenetic analyses of single or multiple/concatenated genes, in DNA or amino acid data. The pipeline was developed using two options, one to be used locally through command lines and other to be used through a Web interface. The command line structure and the algorithms executed by the Web interface were developed using the Python programming language. The ARPA graphic interface for the Web was developed as part of a free software solution. Its structure uses the Linux operating system Ubuntu 8.04 and the Web server Apache 1.3. The pages were developed using HTML 4.0. Javascript 1.2 was used as the language for validations in the customer's machine and Ajax technology (lib effects.js) for a user friendly interface. Web Interface was developed to be compatible with the Internet Explorer (IE) 6 and Firefox 1.5 browsers. ARPA pipeline and interface are hosted at FIOCRUZ and will be available at: http://arpa.biowebdb.org. They will be integrated to ProtozoaDB (http://protozoadb.biowebdb.org) and Stingray (http://stingray.biowebdb.org/) database systems. One direction for future development is to enable the automated reconstruction of 'species tree' using several and more robust phylogenomics approaches. Also, we plan to follow the recommended standards for minimum information about a phylogenetic analysis (MIAPA). Supported by: CNPq, FAPERJ, IOC/FIOCRUZ