GICAS: towards a web–based integration of bioinformatics resources

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Abstract

Key bioinformatics programs and databanks are now maintained by professionals using unix–operated computer systems. Most end users of biofinformatics are working with personal computers, using the web to access these remote resources, despite the CGI protocol's desperate statelessness. This makes it unsuitable for production environments in which communication between people is essential.

We developed a prototype of a web server dedicated to bioinformatics, using Itasca, a distributed object database management system. Our system allows the users to perform elementary operations, like databank query trough SRS, BLAST requests, logical operations on sets of data, and several web presentations of results.

Our experimental server has three major features: (i) It implements the CGI protocol; (ii) It keeps track of the users' data on the server side; (iii) It records the users' actions to progressively build a knowledge base. The latter allows the users to replay at any time their former actions, or to gather them to build a macro command. Our system is thus continuously enriched by the users' actions and, in this way, certain users, especially expert ones, can easily transmit their knowledge to others under a readily accessible web form.