Sequence analysis with CAPRI, a web-desktop application - (session: Others)

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CAPRI (Common Application Program Remote Interface) is a new interface tool, developed in our laboratory and used in our site to create a single consistent access model to a large number of sequence analysis tools. The tool uses any web browser to accurately reproduce the behaviour of a typical desktop application, where the user sees a sequence or other type of document in a window and chooses from a number of menus the various functions.that need to be applied. The menus work exactly as in a standard interactive Mac or Windows application and allow only the options which are relevant to the type of data selected, hiding or disabling the rest.This mechanism allows to present the user with a large number of programs, when needed, but to keep the interface clean otherwise. The linked programs are always easily identified, and the original documentation is made readily available.

Document windows may represent DNA pages containing one, two or more sequences. The page automatically recognizes the number of sequences used and changes the menus accordingly, for example activating all pairwise sequence alignment programs only when in two-sequence mode. A protein window behaves similarly, but provides protein analysis tools. A typical dialog box is used to gather additional information from the user when options are available in the underlying program. Standard 'File' and Edit' menus are also implemented, but being a server based program, files may be loaded or saved either from the local client or from the remote file system. Additional options from the 'File' menu allow direct retrieval of data from EMBL or other databases.

The program is based on the concept of a virtual 'application memory', kept on the server, which stores all the information relative to the 'running' application, including sequence data and user preferences, but is able to access the user directory for data storage and retrieval. All databases and other centrally mantained data are seen by the user as part of the application. Large sequences are only kept on the server, thus allowing analysis of very large ones without delay even from a remote location. The program uses an object model to link external programs as modules. It is able to interface with PISE (C. Letondal, Bioinformatics, 17(1), 2001, pp 73-82), with which it nicely coexists on the same server, sharing the same XML program descriptions and the program definition objects. CAPRI is mainly developed in Perl, and uses client-side Javascript routines. At the moment CAPRI includes most programs from the EMBOSS package, Blast, FastA and ClustalW.

Current work on the project is aimed to further expand the number of linked programs, as well as to introduce new page types for dealing with other biological data.