

CAPRI: a new web interface for sequence analysis programs

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Many widely used sequence analysis tools, such as Blast, FastA or even packages like EMBOSS or GCG, were originally developed on unix or other operating systems based on a command line interface. More recently the introduction of more user-friendly graphic interfaces such as SeqWeb, W2H or Pise, allowed a larger number of researchers easy access to such tools. Although these represent an important achievement, still access to the programs is limited by the need for installing an X server, which usually requires significant computer resources, or constrained within the one-page/one program approach used by PISE and other web based interfaces, which is good for use of a single program, but inefficient to deal with a larger number of simple tasks on a given sequence as one would do in a typical desktop application.

Here we report the development of CAPRI (Common Application Program Remote Interface), a new interface tool, used in our site to create a single consistent access model to a large number of sequence analysis tools. The system is accessed through a web browser, but the interface is organized to accurately mimic a typical desktop application, where the user selects the sequence and uses a number of menus to access the various functions. Users are not required to install any special plugin or other software on their machine, apart from a recent browser, and have full access to the processing power and the databases available on the remote server.

The program was originally derived from PISE (C. Letondal, *Bioinformatics*, 17(1), 2001, pp 73-82), with which it nicely coexist on the same server, sharing the same XML program descriptions and the program definition objects, and was completely developed in Perl, apart from a few simple client-side Javascript routines. Unlike PISE it is based on a single CGI, which is able to produce pages designed for DNA or protein sequences. The web pages may contain one, two or more sequences, and automatically recognize the number of sequences used and change the menus accordingly. When more information is necessary to run a program, an intermediate page, organized as a typical dialog box, is displayed. Linking a program for which a PISE XML is available only takes a few minutes, and of course, it is always possible to write a new XML description if it is not already available. At the moment CAPRI includes most programs from the EMBOSS package, Blast, FastA and ClustalW.