Comparative analyses of biomolecules

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Vasudeva Ginjala

Abstract

The BMERC website provides a platform for searching DNA, RNA and protein sequence databases and performing bioinformatic analyses.

Content

The BMERC website provides a platform for searching DNA, RNA and protein sequence databases and performing bioinformatic analyses. The center itself provides research support in both the development and application of computational biology and bioinformatics methods in biology. The website distributes non-commercial software and support-information for developers and the scientific community. The site's long-term goal is to provide full-genome identification and domain dissection.

There are many useful computational analysis tools, which are interlinked. Among the protein analysis tools are the protein structure prediction server, which is used for prediction of protein secondary structure and protein folding classes. The protein domain profile analysis interface maintains a library of 'functional domain profiles' created by clustering and alignment of proteins with known functional and/or structural similarity. The user can search their query sequence against this library. The website also maintains a database of all completely sequenced genomes, the Cross Genome Analysis (CGA) server, which may be queried using the center's BLAST interface or by searching annotation data. Information is maintained and stored relating to the comparison of each genome against all other sequences in the BMERC database, SWISS-PROT, PDB and other public databases. This is useful for extracting similar sequences from related organisms and is an aid to studies of molecular evolution, gene regulation and developmental genetics. A CGA report for any sequence includes its protein sequence, annotation, any functional domain profiles that it matches and the top two BLAST matches in other organisms. Wherever possible the BMERC site provides links to the appropriate tools or reports within the site allowing the user to generate a coherent collection of information about a query from the BMERC records and external sites. Options are always provided for saving reports. BMERC is powered by a relational database (MySQL) that responds quickly and allows large amounts of data to be compared. The center has also developed a number of perl modules and tools for computational biology, many of which are available to download from the FTP site.

There are links to other databases (for example, FlyBase, AceDB), links to related departments and graduate programs in bioinformatics at Boston University, and links to online scientific journals.

Navigation

The site is fairly small and one cannot easily get lost, as every page has a link back to the home page. There is an excellent site map. The search engine is helpful in finding information on the web pages or in the database and search results are clearly labeled. The server is quite fast so there is no delay in loading, and the responsiveness is quite good. All pages can be printed, including those of the database.

Reporter's comments

Timeliness

At the time of reporting, the site had last been modified on 31 May 2000.

Wish list

It would be good to see a separate introduction page on the home page explaining how to use the database and the other resources on-site.

Related websites

Similar genome-wide analyses can be performed at FlyBase, AceDB and the *Saccharomyces* genome database.

Table of links

BioMolecular Engineering Research Center (BMERC)

FlyBase

AceDB

Saccharomyces genome database

References

1. BioMolecular Engineering Research Center (BMERC).

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