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BLAST & FASTA

WHAT IS A DATABASE?

- A database is a computerized archive used to store and organize data in such a way that information can be retrieved easily via a variety of search criteria.
- Each record, also called an entry, should contain a number of fields that hold the actual data items.
- **Types of databases:**
- 1- Flat files.
- 2- Relational
- 3- Object oriented.

Flat files databases using a single table as in a flat file database.

Relational databases use a set of tables to organize data.

Each table, also called a *relation*, is made up of columns and rows. Columns represent individual fields and rows represent values in the fields of records.

One of the problems with relational databases is that the tables used do not describe complex hierarchical relationships between data items.

To overcome the problem,

Object-oriented databases have been developed that store data as objects, the object-oriented database system is more flexible.

To facilitate the access and retrieval of data, sophisticated computer software programs for organizing, searching, and accessing data have been developed, they are called

database management systems.

These systems contain not only raw data records but also operational instructions to help identify hidden connections among data records.

Depending on the types of data structures, these database management systems can be classified into two types:

1- Relational database management systems.

2- Object-oriented database management systems.

Biological databases:

Current biological databases use all three types of database structures: flat files, relational, and object oriented.

Pubmed:

It is biomedical literature database and one of the accessible data bases, which contains abstracts and in some cases the full text articles fromnearly 4,000 journals.

Pubmed:

An important feature of PubMed is the retrieval of information based on medical subject headings (MeSH) terms.

<u>MeSH system</u> consists of a collection of more than 20,000 controlled and standardized vocabulary terms used for indexing articles.

In other words, it is a the saurus that helps convert search keywords into standardized terms to describe a concept.

By doing so, it allows "smart" searches in which a group of accepted synonyms are employed so that the user not only gets exact matches, but also related matches on the same topic that otherwise might have been missed.

Pubmed:

Another way to broaden the retrieval is by using the "Related Articles" option.

PubMed uses a word weight algorithm to identify related articles with similar words in the titles, abstracts, and MeSH. By using this feature, articles on the same topic that were missed in the original search can be retrieved.

Several Selected PubMed Tags and Their Brief Descriptions				
Tag	Name	Description		
AB	Abstract	Abstract		
AD	Affiliation	Institutional affiliation and address of the first author and grant numbers		
AID	Article identifier	Article ID values may include the PII (controlled publisher identifier) or doi (digital object identifier)		
AU	Author	Authors		
DP	Publication date	The date the article was published		
JID	Journal ID	Unique journal ID in the National Library ofMedicine's catalog of books, journals, and audiovisuals		
LA	Language	The language in which the article was published		
PL	Place of publication	Journal's country of publication		
PT	Publication type	The type of material the article represents.		
SO	Source	Composite field containing bibliographic information		
ТА	Journal title abbreviation	Standard journal title abbreviation		
TI	Title	The title of the article		
VI	Volume	Journal volume		
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	PMID: 20198908 [PubMed - indexed for MEDLINE] Related articles	Titles with your search terms
2.	[The level of TNF-alpha secretion of PBMC in patients with chronic hepatitis C and nonalcoholic fatty liver] Dong Y, Zhang HF, Zhu SS, Chen H, Li J, Cheng Y. Zhonghua Shi Yan He Lin Chuang Bing Du Xue Za Zhi. 2009 Apr;23(2):109-11. Chinese. PMID: 20104750 [PubMed - indexed for MEDLINE] Related articles	 Pegylated interferon and ribavirin combination therapy for chror [Scand J Gastroenterol. 2008] Clinical course of pregnant women with chronic hepatitis C virus i [Dig Liver Dis. 2001] Use of PEG-interferon alfa-2a plus ribavirin as treatment for chror [Pediatr Blood Cancer. 2004]
	Helicobacter species DNA in liver and gastric tissues in children and	» See more
3.	adolescents with chronic liver disease. Casswall TH, Németh A, Nilsson I, Wadström T, Nilsson HO. Scand J Gastroenterol. 2010;45(2):160-7.	111 free full-text articles in PubMed Central
	Related articles	Review Update on autoimmune hepatitis. [World J Gastroenterol. 2009]
4.	[Gene polymorphism of transforming growth factor beta1 (TGF-beta1) in the pathogenesis and clinical course of chronic hepatitis in children]	Review Hepatitis B immunization strategies: timing is everything. [CMAJ. 2009] Vitamin E treatment for children with chronic

NCBI (National center for biotechnology information) also maintains a taxonomy database that contains the names and taxonomic positions of over 100,000 organisms with at least one nucleotide or protein sequence represented in the GenBank database.

GenBank

GenBank is the most complete collection of annotated nucleic acid sequence data for almost every organism. The content includes genomic DNA, mRNA, cDNA, ESTs, high throughput raw sequence data, and sequence polymorphisms.

There is also a **GenPept database** for protein sequences, the majority of which are conceptual translations from DNA sequences, although a small number of the amino acid sequences are derived using peptide sequencing techniques.

There are two ways to search for sequences in GenBank:

- One is using text-based keywords similar to a PubMed search.
- The other is using molecular sequences to search by sequence similarity using BLAST.
- **GenBank Sequence Format:**
- The search output for sequence files is produced as flat files for easy reading. The resulting flat files contain three sections
- (Header, Features, and Sequence entry)



The accession number

- It is a unique number assigned to a piece of DNA when it was first submitted to GenBank and is permanently associated with that sequence.
- This is the number that should be cited in publications.
- It has two different formats: two letters with five digits or one letter with six digits.

Basic Local Alignment Search Tool BLAST

Basic Local Alignment Search Tool, or BLAST

BLAST, is an algorithm for comparing primary biological sequence information, such as the amino-acid sequences of different proteins or the nucleotides of DNA sequences.

BLAST search enables a researcher to compare a query sequence with a library or database of sequences, and identify library sequences that resemble the query sequence above a certain threshold.

BLAST program was designed by Stephen Altschul, Warren Gish, Webb Miller, Eugene Myers, and David J. Lipman at the NIH and was published in the Journal of Molecular Biology in 1990.

Different types of BLASTs are available according to the query sequences.

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BLAST: Basic Local Alignment Search Tool

blast.ncbi.nlm.nih.gov/

The **Basic Local Alignment Search Tool** (**BLAST**) finds regions of local similarity between sequences. The program compares nucleotide or protein sequences to ...

Align two or more - Protein BLAST: ***search ... - Nucleotide BLAST Rat - sequences

Nucleotide BLAST: Search nucleotide databases using a nucleotide

blast.ncbi.nlm.nih.gov/Blast.cgi?...blastn...BlastSearch...

No BLAST database contains all the sequences at NCBI. BLAST databases ...

BLAST - Wikipedia, the free encyclopedia

en.wikipedia.org/wiki/BLAST

In bioinformatics, **Basic Local Alignment Search Tool**, or **BLAST**, is an algorithm for comparing primary biological sequence information, such as the amino-acid ... Process - Output - Input - Background

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a nucleotide database using a nucleotide query <i>Algorithms</i> : blastn, megablast, discontiguous megablast
<u>protein blast</u>	Search protein database using a protein query <i>Algorithms:</i> blastp, psi-blast, phi-blast
<u>blastx</u>	Search protein database using a translated nucleotide query
<u>tblastn</u>	Search translated nucleotide database using a protein query
<u>tblastx</u>	Search translated nucleotide database using a translated nucleotide query

Input:

Input sequences are in **FASTA** or <u>Genbank</u> format and weight matrix.

FASTA format is a text-based format for representing either nucleotide sequences or peptide sequences, in which nucleotides or amino acids are represented using single-letter codes. The format also allows for sequence names and comments to precede the sequences. The format originates from the FASTA software package, but has now become a standard in the field of bioinformatics. A sequence in FASTA format begins with a single-line description, followed by lines of sequence data. The description line is distinguished from the sequence data by a greater-than (">") symbol in the first column.

The word following the ">" symbol is the identifier of the sequence, and the rest of the line is the description (both are optional).

There should be no space between the ">" and the first letter of the identifier. It is recommended that all lines of text be shorter than 80 characters. The sequence ends if another line starting with a ">" appears; this indicates the start of another sequence. A simple example of one sequence in FASTA format: >gi|18203677|sp|Q9ZGE9|BCHN MERVERENGCFHTFCPIASVAWLHRKIKDSFFLIVGTHTCAHFIQTALDVMVYAHSRFGFAVLEESDLVS ASPTEELGKVVQQVVDEWHPKVIFVLSTCSVDILKMDLEVSCKDLSTRFGFPVLPASTSGIDRSFTQGED AVLHALLPFVPKEAPAVEPVEEKKPRWFSFGKESEKEKAEPARNLVLIGAVTDSTIQQLQWELKQLGLPK VDVFPDGDIRKMPVINEQTVVVPLQPYLNDTLATIRRERRAKVLSTVFPIGPDGTARFLEAICLEFGLDT SRIKEKEAQAWRDLEPQLQILRGKKIMFLGDNLLELPLARFLTSCDVQVVEAGTPYIHSKDLQQELELLK ERDVRIVESPDFTKQLQRMQEYKPDLVVAGLGICNPLEAMGFTTAWSIEFTFAQIHGFVNAIDLIKLFTK PLLKRQALMEHGWAEAGWLE

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Click the "Blast!" button at the bottom to submit your sequence data.

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Submitted at	Mon Nov 3 01:01:00 2008		
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This screen will come up next. Finally (sometimes after a lengthy wait), a new window will appear showing any "hits" your sequence made. The results will be color coded and annotated

Method of search:

Using a heuristic method, BLAST finds similar sequences, not by comparing either sequence in its entirety, but rather by locating short matches between the two sequences.

This process of finding initial words is called seeding. It is after this first match that BLAST begins to make local alignments. While attempting to find similarity in sequences, sets of common letters, known as words, are very important.

- For example, suppose that the sequence contains the following stretch of letters, GLKFA.
- If a <u>BLASTp</u> was being conducted under default conditions, the word size would be 3 letters.
- In this case, using the given stretch of letters, the searched words would be GLK, LKF, KFA.
- Once both words and neighborhood words are assembled and compiled, they are compared to the sequences in the database in order to find matches. The threshold score T determines whether or not a particular word will be included in the alignment.

Output:

BLAST output can be delivered in a variety of formats. These formats include <u>HTML</u>, <u>plain text</u>, and <u>XML</u> formatting.



The bars show what places along your sequence are similar to other published sequences; the colors indicate how many bases were involved in homology determination.

Descriptions

Legend for links to other resources: U UniGene 🔲 GEO G Gene Structure M Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

Accession	Description	Max score	Total score	Query coverage	- value	Max ident	Links
EU557008.1	Uncultured bacterium clone C56 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	
EU557006.1	Uncultured bacterium clone C59 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	
EU557004.1	Uncultured bacterium clone C62 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	
EU557001.1	Uncultured bacterium clone C66 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	
EU557000.1	Uncultured bacterium clone C72 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	
EU556999.1	Uncultured bacterium clone C75 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	
EU556998.1	Uncultured bacterium clone C80 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	
EU556996.1	Uncultured bacterium clone C99 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	
EU285587.1	Enterococcus faecalis strain C19315led5A 16S ribosomal RNA gene, partial s	946	946	98%	0.0	97%	
EU547775.1	Enterococcus faecalis strain IJ-07 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	_
AB362599.1	Enterococcus faecalis gene for 16S rRNA, partial sequence, strain: NRIC 011	946	946	98%	0.0	97%	
EF653454.1	Enterococcus faecalis strain 47/3 16S ribosomal RNA gene, partial sequence	946	946	98%	0.0	97%	
EF608536.1	Uncultured bacterium clone PCD-8 16S ribosomal RNA gene, partial sequenc	946	946	98%	0.0	97%	
AM697463.1	Uncultured bacterium partial 16S rRNA gene. isolate BF0001D078	946	946	98%	0.0	97%	OR THE THE OWNER OF THE OWNER

Clicking on a "gi" link at the beginning of any line will take you to the GenBank accession page for a sequence showing similarity to yours. There you can find a wealth of information about the published sequence to which yours showed some homology. > <u>gb EU285587.1</u> Enterococcus faecalis strain C19315led5A 16S ribosomal RNA gene, partial sequence Length=1456

Score = 946 bits (512), Expect = 0.0
Identities = 550/566 (97%), Gaps = 12/566 (2%)
Strand=Plus/Plus

Query	1	CGGTCGAGC-TGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCC	59
Sbjct	893	CGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCC	952
Query	60	TTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGGACAAAGTGACAGGTGGTGCATGGT	119
Sbjct	953	TTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGACAAAGTGACAGGTGGTGCATGGT	1012
Query	120	TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATT	179
Sbjct	1013	TGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATT	1072
Query	180	GTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGACTGCCGGTGACAAACCGGAGGAA	239
Sbjct	1073	GTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGACTGCCGGTGACAAACCGGAGGAA	1132
Query	240	GGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAAT	299
Sbjct	1133	GGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAAT	1192
Query	300	GGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGCAAATCTCTTAAAGCTTCTCTCAG	359
Sbjct	1193	GGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGCAAATCTCTTAAAGCTTCTCTCAG	1252
Query	360	TTCGGATTGGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGCGGATC	419
Sbjct	1253	TTCGGATTG-CAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGCGGATC	1311
Query	420	AGCACGCCGCGGTGAATACGTTGCCGGGGCCTTGTACACACCGCCCGTCACACCACGAGA	479
Sbjct	1312	AGCACGCCGCGGTGAATACGTTCCCGGG-CCTTGTACACACCGCCCGTCACACCACGAGA	1370
Query	480	GTTTGTAACACCCGAAGTCGG-GAGGTACCCTTTT-GGAGC-A-CCGCCTTAGGTGG-AT	534
Sbjct	1371	GTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTTTGGAGCCAGCC	1430
Query	535	AGATGAT-GGGGTGA-GTTC-TAACA 557	

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Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a nucleotide database using a nucleotide query <i>Algorithms</i> : blastn, megablast, discontiguous megablast
<u>protein blast</u>	Search protein database using a protein query <i>Algorithms:</i> blastp, psi-blast, phi-blast
<u>blastx</u>	Search protein database using a translated nucleotide query
<u>tblastn</u>	Search translated nucleotide database using a protein query
<u>tblastx</u>	Search translated nucleotide database using a translated nucleotide query

Basic BLAST

Choose a BLAST program to run.

nucleotide blast

Search a **nucleotide** database using a **nucleotide** query *Algorithms*: blastn, megablast, discontiguous megablast

<u>protein blast</u>

Search **protein** database using a **protein** query *Algorithms:* blastp, psi-blast, phi-blast

Nucleotide blast:

compares a nucleotide query sequence to nucleotide database.

protien blast:

compares a protien query sequence to protein sequence database.

blastx Search protein database using a translated nucleotide query

tblastn | Search translated nucleotide database using a protein query

tblastx Search **translated nucleotide** database using a **translated nucleotide** query

blastx:

compares a nucleotide query sequence translated in all reading frames against a protein sequence database.

tblastn:

Compares a protein query sequence against a nucleotide sequence database dynamically translated in all reading frames.

tblastx:

Compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

Conversion of sequence format:

Readseq < Sequence Format Conversion < EMBL-EBI www.ebi.ac.uk/Tools/sfc/readseq/



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