

Bioinformatics glossary based Database of Biological Databases: DBD

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Abstract

Database of Biological/Bioinformatics Databases (DBD) is a collection of 1669 databases and online resources collected from NAR Database Summary Papers (<http://www.oxfordjournals.org/nar/database/a/>) & Internet search engines. The database has been developed based on 437 keywords (Glossary) available in <http://falcon.roswellpark.org/labweb/glossary.html>. Keywords with their relevant databases are arranged in alphabetic order which enables quick accession of databases by researchers. Database description provides brief information about the database with a link to main web page. DBD is available online and can be accessed at <http://www.biodbs.info>.

Keywords: Databases, biological databases, bioinformatics databases, bioinformatics glossary

Introduction

Molecular biology has witnessed an information explosion in the last two decades as a consequence of development of rapid DNA sequencing techniques. The concomitant progress in computer based technologies has enabled molecular biologists in general and bioinformaticists in particular to cope with this information deluge. Information from various sources explicitly presented in the form of biological databases is generally maintained by many institutions. They vary widely in their content, format and access method [Kihler 2004]. Biological data are being deposited in a database and the need for data analysis has made molecular biology databases vital tools for research. Although several databases are reported in literature, many researchers are not aware of their availability and these databases were not effectively utilized (Ajay Babu et al. 2005).

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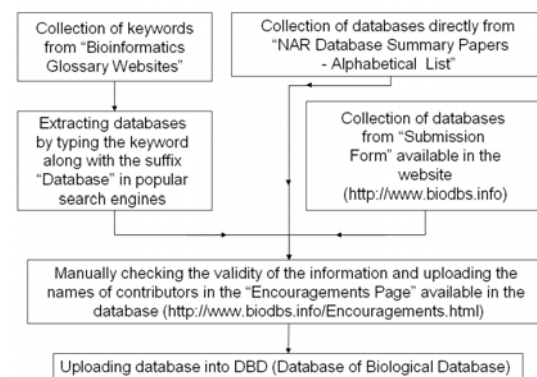
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Databases of Biological Databases such as **DOD** – Database of Databases (<http://www.progenebio.in/DoD/DoD.htm>), **MetaBase** - The Database of Biological Database (<http://biodatabase.org>) and **The Molecular Biology Database Collection – Updates** (Baxevanis 2000), published annually by journal entitled “Nucleic Acids Research” help researchers to identify and correlate important queries beside providing a common platform for various molecular biology databases. Databases in DOD, Metabase & others have been grouped into categories as conceived by the respective authors. For instance, DOD has grouped 719 databases into 14 major categories (Galperin 2005) while Metabase has grouped 1119 databases into 21 categories.

The uniqueness of the present DBD is the alphabetic listing of all databases based on technical terms (keywords) viz. <http://falcon.roswellpark.org/labweb/glossary.html>. This facilitates very quick access to the desired databases.

Figure 1: Structure of DBD (Database of Biological Databases)



Steps involved in construction of DBD (Figure 1)

- Extraction of suitable keywords from bioinformatics glossary website <http://falcon.roswellpark.org/labweb/glossary.html>.
- Typing the keyword along with the suffix “Database” in popular search engines like <http://www.google.com>, <http://www.yahoo.com> etc.

Table 1: Alphabetical listing of the number of keywords with the total number of databases linked to DBD (Database of Biological Database)

Alphabets	Total keywords	Total number of databases	Some major keywords with total number of database linked to DBD
A	16	64	Alignment – 8, Alternative Splicing – 22, Annotation – 12, Agricultural – 4
B	20	68	Bacterial – 8, Bacillus – 6, Binding – 6, Biochemical Pathway – 9, Biological databases listing - 11
C	48	88	Caenorhabditis elegans – 5, Cancer – 14, Chromosome – 9, Cytogenetics – 3, Cluster - 4
D	33	76	Disease – 12, Domain – 9, Drosophila -15, DNA – 18
E	25	86	<i>E.coli</i> – 14, Enzyme – 16, Eukaryotic – 8, EST – 11, Expression databases – 5, EBI – 3, Evolution - 3
F	12	19	Fish – 3, Fly -3, Functional Genomics - 4
G	15	77	Genome – 38, Gene & Gene Expression – 16, Genetics – 7, Germ - 6
H	25	93	HIV – 21, Homologous & Homology – 17, Human – 18, <i>Haemophilus</i> – 3, Higher taxon - 5
I	23	56	Inhibitor - 10, Intron – 6, Isotope - 4
J	Nil	Nil	Nil
K	4	4	Kinases – 1, KEGG - 1
L	9	32	Ligand – 23, Liver proteome - 1
M	41	258	Motif - 10, Metabolic Pathway - 11, Microarray - 22, Microbial - 15, Mitochondrial - 25, Mouse - 30, Mutation - 40
N	11	34	NMR - 5, Nucleic - 4, Nucleotide - 6
O	11	38	Oligo – 38, Organelles - 7, Ortholog - 9
P	52	297	Parasite – 10, Pathway - 12, PCR - 8, Peptide - 34, Phenotype - 9, Plant - 5, Plasmid - 10, Primer - 10, Probe - 13, Promoter – 15, Protease - 12, Protein - 53, Proteome - 18
Q	3	11	QSAR - 6, Quantitative trait loci - 4
R	19	113	Radiation hybrid - 6, Rat - 20, Retrovirus - 5, RNA - 39, Ribosomal – 7, Rice - 17
S	34	132	Sanger - 4, Sequence - 44, Signal Transduction - 8, SNP - 16, Species - 5, Structure - 13, Synapse - 3
T	19	47	Taxonomy - 3, Transcript - 5, tRNA - 3, Transgenic - 3, Tumor - 9, Tree - 3
U	3	7	Unigene - 4, UniProt - 2
V	5	31	Variation - 9, Virus - 16, Vector - 4
W	3	4	Worm - 2
X	3	4	X chromosome - 2, <i>Xenopus laevis</i> - 1
Y	2	25	Yeast - 23
Z	1	5	<i>Zea mays</i> - 5

