

# The Importance of Biological Databases in Biological Discovery

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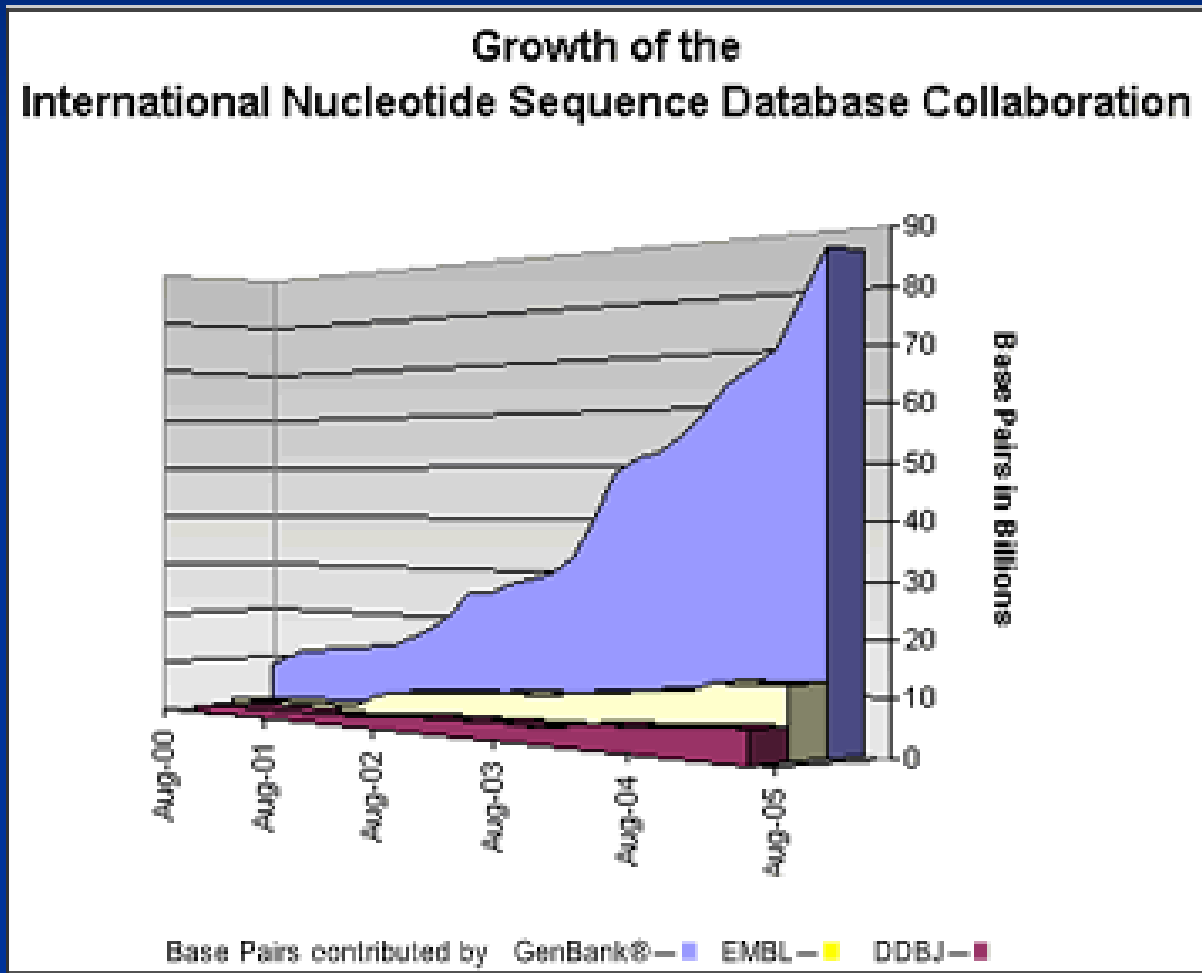
The database that most biologists are familiar with is GenBank.

## ■ GenBank

-is the annotated collection of all publicly available *DNA* and *protein* sequences.

-is maintained by NCBI (National Center for Biotechnology) at NIH (National Institute of Health).

- -represents a collaborative effort between NCBI, EMBL (European Molecular Biology Laboratory) and DDBJ (DNA Data Bank of Japan)



<http://www.ncbi.nlm.nih.gov/Genbank/>

- GenBank® is the NIH genetic sequence database, an annotated collection of all publicly available DNA sequences (*Nucleic Acids Research 2007 Jan 1;35(Database issue):D16-20*).
- There are approximately 65,369,091,950 bases in 61,132,599 sequence records in the *traditional GenBank divisions* and 80,369,977,826 bases in 17,960,667 sequence records in the *WGS division* as of August 2006.

# The growth of GenBank

- Human Genome Project
- Other systematic sequencing projects
  - accumulation of sequence data

# NCBI & Boolean Search

## ■ Entrez homepage of NCBI

is not a database itself but rather the interface through which all of its component databases can be accessed and traversed.

<http://www.lib.berkeley.edu/TeachingLib/Guides/Internet/Boolean.pdf>

**Boolean logic**

**From Wikipedia, the free encyclopedia**

The screenshot displays the NCBI Entrez search interface. At the top, there are navigation tabs for 'HOME', 'SEARCH', 'SITE MAP', 'PubMed', 'All Databases', 'Human Genome', 'GenBank', 'Map Viewer', and 'BLAST'. Below these is a search bar with the text 'Search across databases' and a search term 'P53'. To the right of the search bar are buttons for 'GO', 'CLEAR', and 'Help'. The main content area shows a grid of search results for various databases, each with a count, an icon, and a brief description. The results are as follows:

Count	Database	Description
41638	PubMed	biomedical literature citations and abstracts
12312	PubMed Central	free, full text journal articles
19	Site Search	NCBI web and FTP sites
731	Books	online books
357	OMIM	online Mendelian Inheritance in Man
none	OMIA	Online Mendelian Inheritance in Animals
8739	Nucleotide	sequence database (includes GenBank)
3990	Protein	sequence database
14	Genome	whole genome sequences
107	Structure	three-dimensional macromolecular structures
none	Taxonomy	organisms in GenBank
303	SNP	single nucleotide polymorphism
1240	Gene	gene-centered information
512	HomoloGene	eukaryotic homology groups
none	PubChem Compound	unique small molecule chemical structures
96	PubChem Substance	deposited chemical substance records
none	Genome Project	genome project information
286	UniGene	gene-oriented clusters of transcript sequences
17	CDD	conserved protein domain database
421	3D Domains	domains from Entrez Structure
558	UniSTS	markers and mapping data
29	PopSet	population study data sets
130266	GEO Profiles	expression and molecular abundance profiles
100	GEO DataSets	experimental sets of GEO data
294	Cancer Chromosomes	cytogenetic databases
1	PubChem BioAssay	bioactivity screens of chemical substances
13	GENSAT	gene expression atlas of mouse central nervous system
1597	Probe	sequence-specific reagents

# KEGG (Kyoto Encyclopedia of Genes and Genomes)

- a widely-used compendium of biochemical pathways that has practical use in the modeling of expression data and in understanding higher-order cellular processes.

### 3. Useful links & tools- Glossary

- [Bioinformatics Glossary;](#)
- [Genome Glossary NCBI;](#)
- [-Omes and -omics glossary](#)



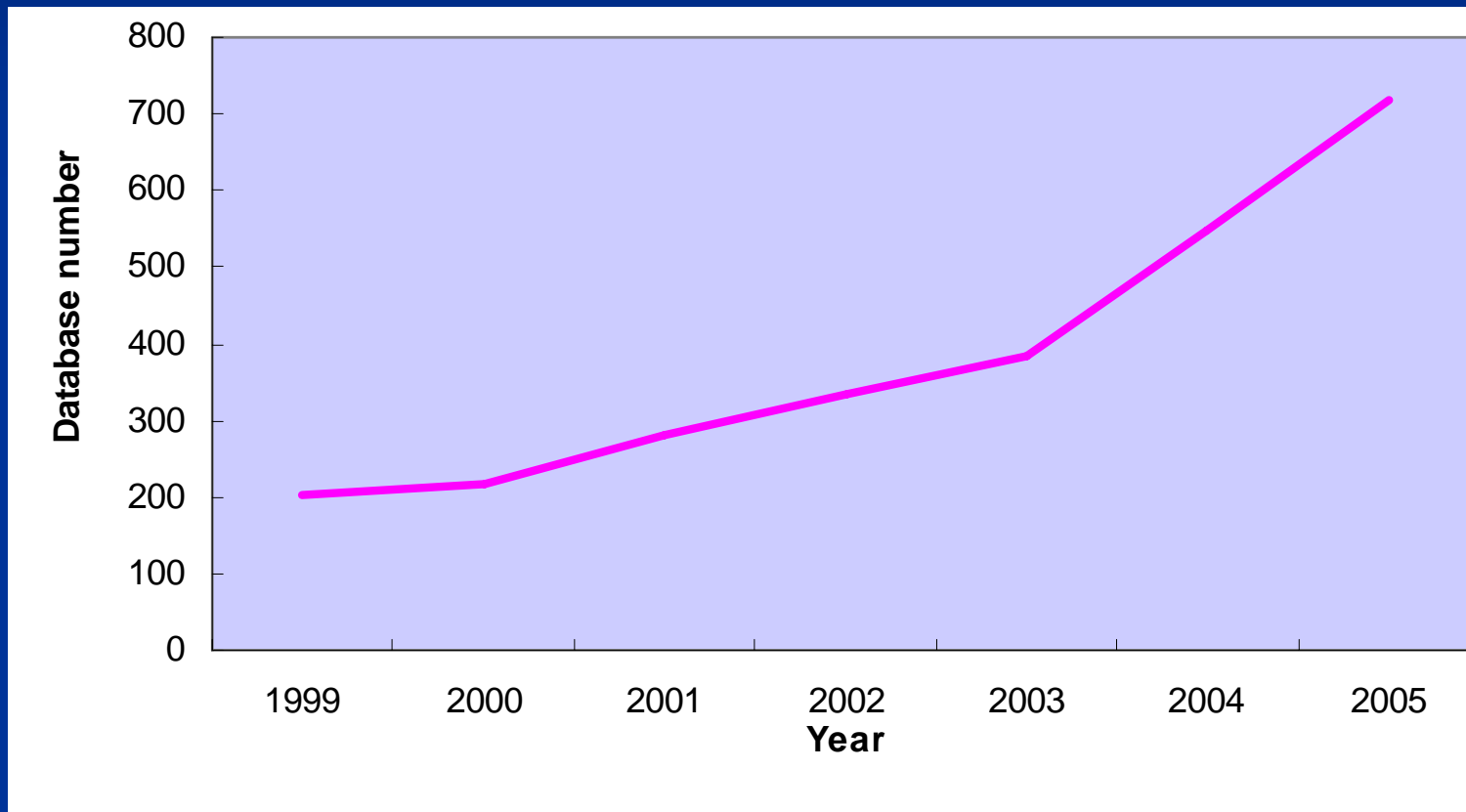
# Biological databases

- Like any other database
  - Data organization for optimal analysis
- Data is of different types
  - Raw data (DNA, RNA, protein sequences)
  - Curated data (DNA, RNA and protein annotated sequences and structures, expression data)

# Characteristics of biological data

- **Complex** → **Thoughtful data modeling**  
Data types range from sequences, 3-dimensional structures, pathways, images, text, and a wide variety of annotation.
- **Heterogeneous** → **Universal schema**  
storage format, management, and access vary widely
- **Dynamic** → **Flexible designing**  
contents and schema change routinely and rapidly (twice/year)
- **Inconsistent** → **Ontology**  
lack standards at the ontology level
  - **Controlled vocabulary for consistent naming for biomedical terms within and between databases**
  - **Data models for modeling or abstraction of biological system and processes**

# The growth of public domain bio-databases

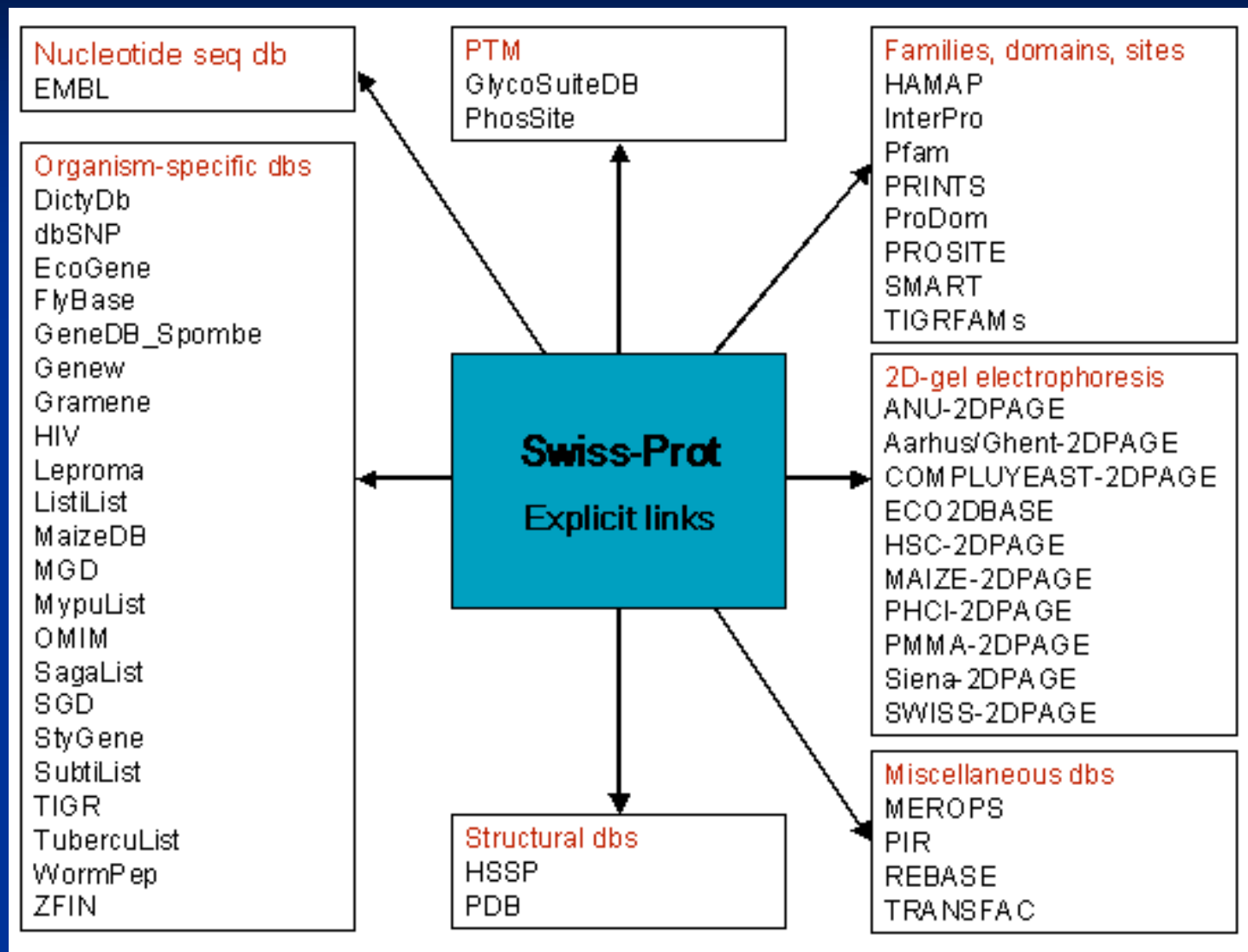


(The Molecular Biology Database Collection from *Nucleic Acids Research*)

# Three main tendencies of bio-databases

- Database proliferation
  - Dozens to hundreds at the moment
- In the next 5 years biological data analysis will be trifurcated
  - Bio-webs : remote data analysis and mining
  - Bio-grids : transparent high-end computing
  - Bio-semantic webs : biological knowledge
- More and more scientific discoveries result from inter-database analysis and mining

# Cross-references



# Gene Ontology database-1

“The Gene Ontology (GO) project seeks to provide a set of *structured vocabularies* for *specific biological domains* that can be used to describe gene products in any organism.”

## **A few key points:**

GO is a “structured” vocabulary, which is really a specialized type of a “controlled” vocabulary.

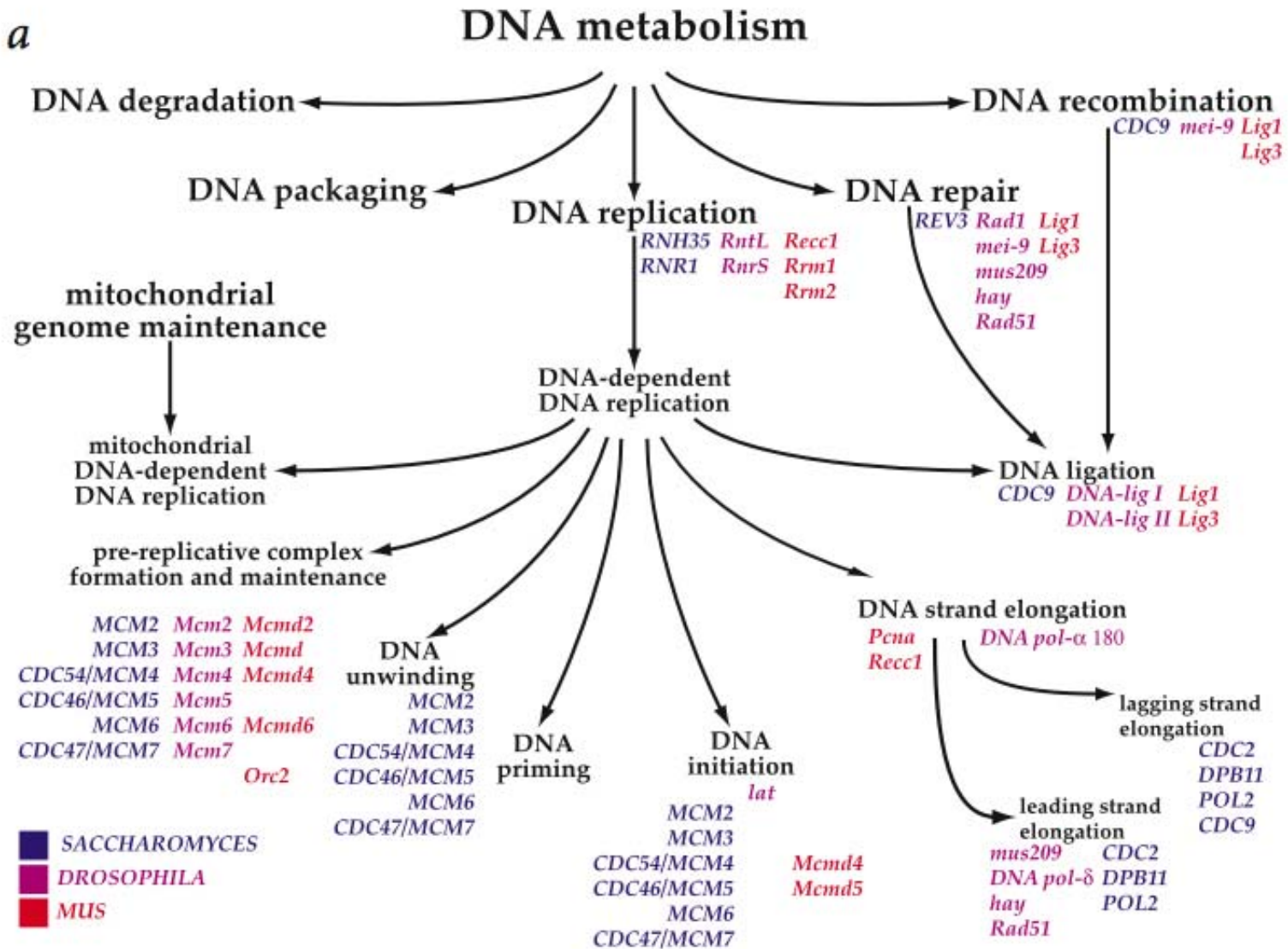
# Gene Ontology database-2

The ontologies in GO are intended to describe three biological areas, “molecular function”, “biological processes” and “cellular components”.

GO was originally developed through the collaboration of the members of *three model organism projects*: SGD, the *Saccharomyces* Genome database; FlyBase, the *Drosophila* genome database; and MGD/GXD, the Mouse Genome Informatics databases.

# Biological Process Ontology

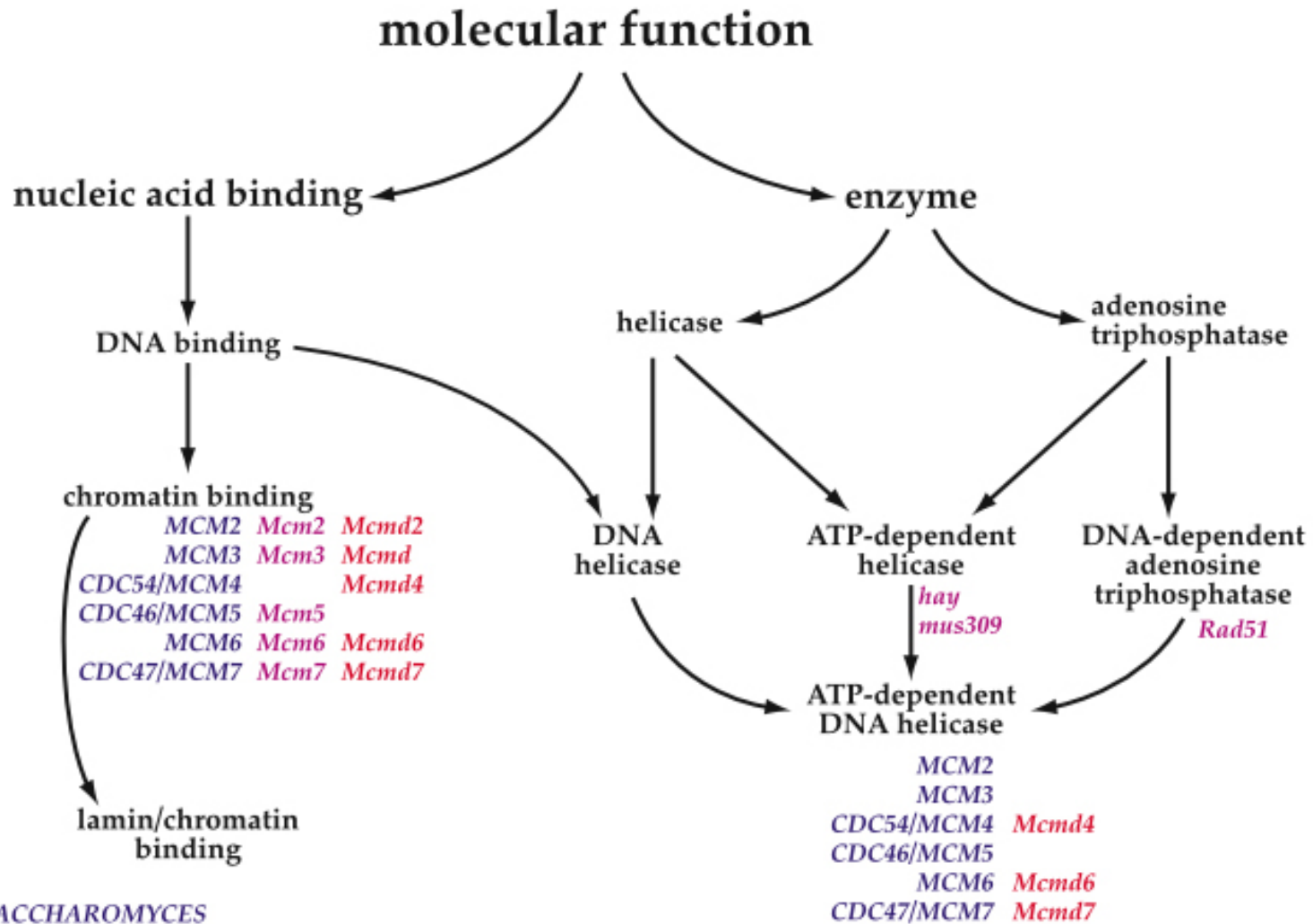
a





# Molecular Function Ontology

b



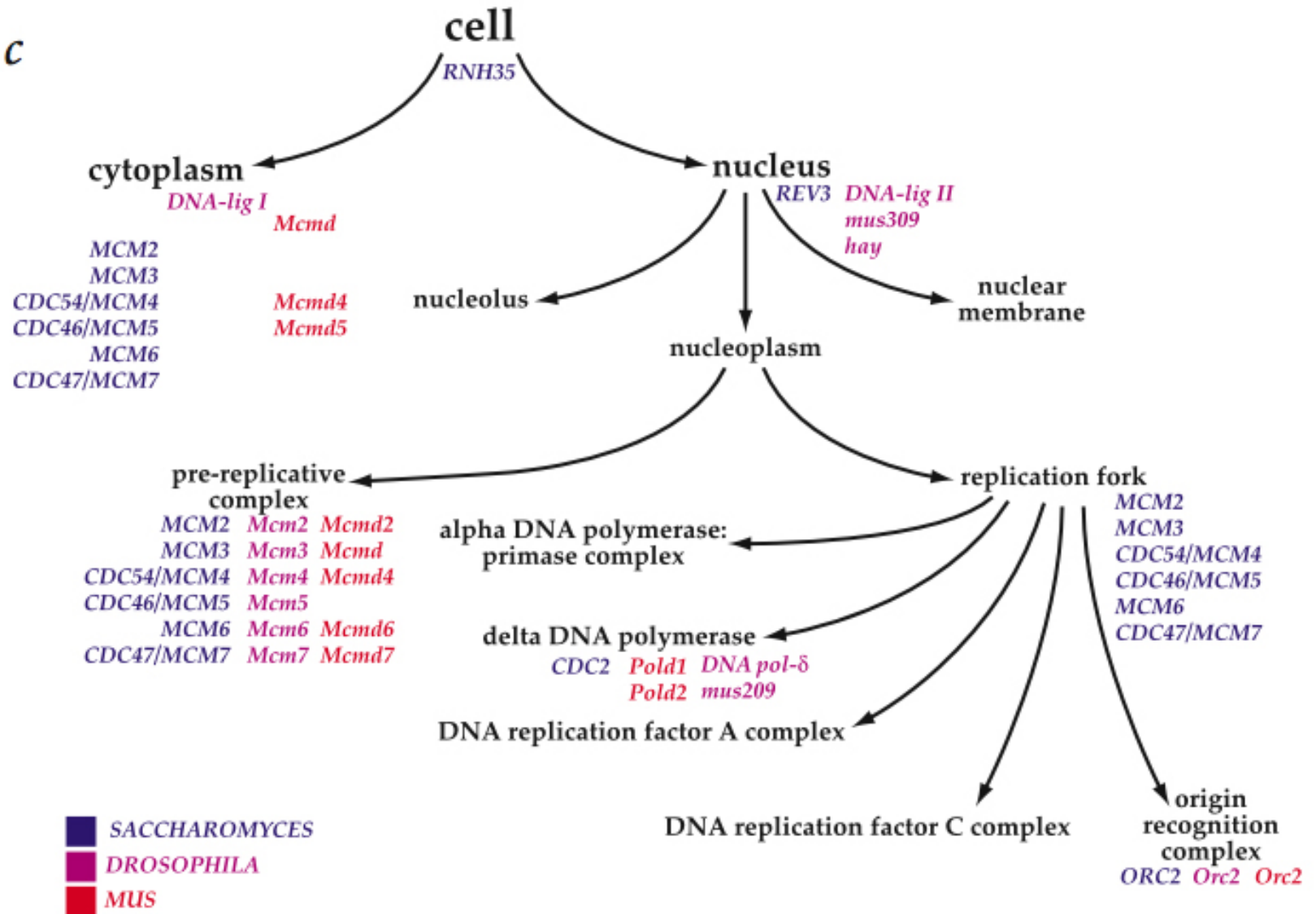
■ SACCHAROMYCES

■ DROSOPHILA

■ MUS

# Cellular Component Ontology

c



# The CANCER GENOME ANATOMY PROJECT

- The Gene Ontology Browser (GO Browser) classifies human and mouse genes by molecular function, biological process, and cellular component.

# What GO is Not

1. GO is **not** a way to unify biological databases. Sharing nomenclature is a step toward unification, but is not, in itself, sufficient.
2. GO is **not** a dictated standard, mandating nomenclature across databases. Groups participate because of self-interest and cooperate to arrive at a **consensus**.
3. GO does **not** define homologies between gene products from different organisms. The use of the GO results in shared annotations for gene products from different organisms, and this may reflect an evolutionary relationship, but the shared annotation is in itself not sufficient for such a determination.

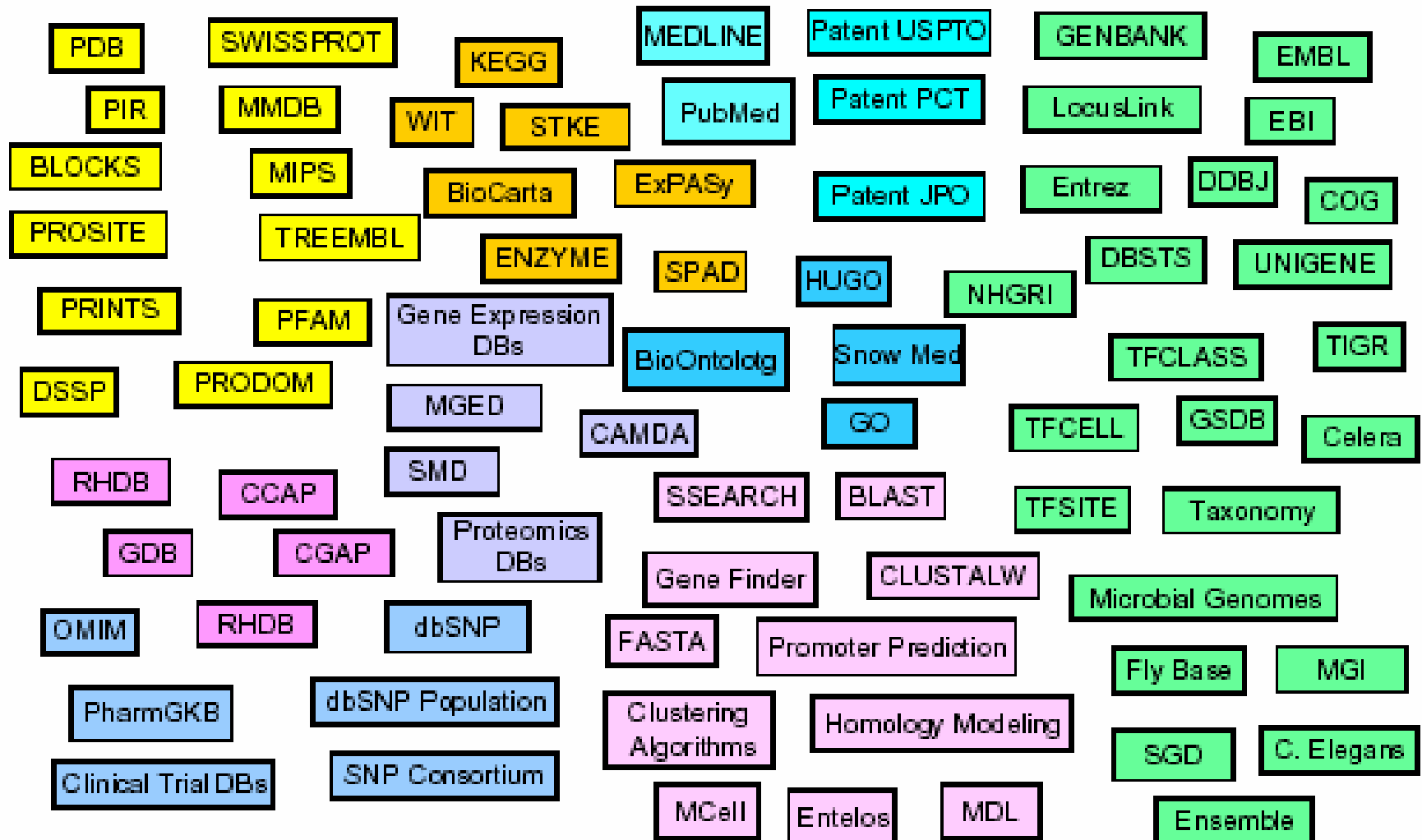
# Knowledge discovery in databases

- **Data mining** is a technique to discover hidden information in large databases. This information, e.g. trends and patterns, can be used to build predictive models.
- **Example:** extracting predictive information of gene expression from genome sequence databases.

# Bio-databases: a short word on problems

- Even today we face some key limitations
  - **There is no standard format**
    - Every database or program has its own format
  - **There is no standard nomenclature**
    - Every database has its own names
  - **Data is not fully optimized**
    - Some datasets have missing information without indications of it
  - **Data errors**
    - Data is sometimes of poor quality, erroneous, misspelled

# Swimming in Data Sources



# The Molecular Biology Database Collection: 2007 update

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## ABSTRACT

The NAR online Molecular Biology Database Collection is a public resource that contains links to the databases described in this issue of *Nucleic Acids Research*, previous NAR database issues, as well as a selection of other molecular biology databases that are freely available on the web and might be useful to the molecular biologist. The 2007 update includes 968 databases, 110 more than the previous one. Many databases that have been described in earlier issues of NAR come with updated summaries, which reflect recent progress and, in some instances, an expanded scope of these databases. The complete database list and summaries are available online on the *Nucleic Acids Research* web site <http://nar.oxfordjournals.org/>.

## NAR Database Categories List

- Nucleotide Sequence Databases
- RNA sequence databases
- Protein sequence databases
- Structure Databases
- Genomics Databases (non-vertebrate)
- Metabolic and Signaling Pathways
- Human and other Vertebrate Genomes
- Human Genes and Diseases
- Microarray Data and other Gene Expression Databases
- Proteomics Resources
- Other Molecular Biology Databases
- Organelle databases
- Plant databases
- Immunological databases



# Nucleic Acids Research




Database & server issues

#### 4. Bioinformatics Journal list



**BMC  
Bioinformatics**

**BMC  
Genomics**

 **BMC  
Medical Informatics and Decision Making**

**ALGORITHMS FOR  
MOLECULAR BIOLOGY**