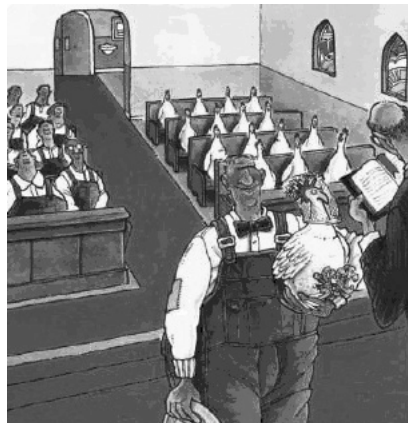


Introduction to BIOINFORMATICS

What is Bioinformatics?

The marriage between biology and informatics



Understanding nature's mute elegant language of living cells is the question of modern molecular biology.

From an alphabet of only four letters representing the chemical subunits of DNA, emerges a syntax of life processes whose most complex expression is man.

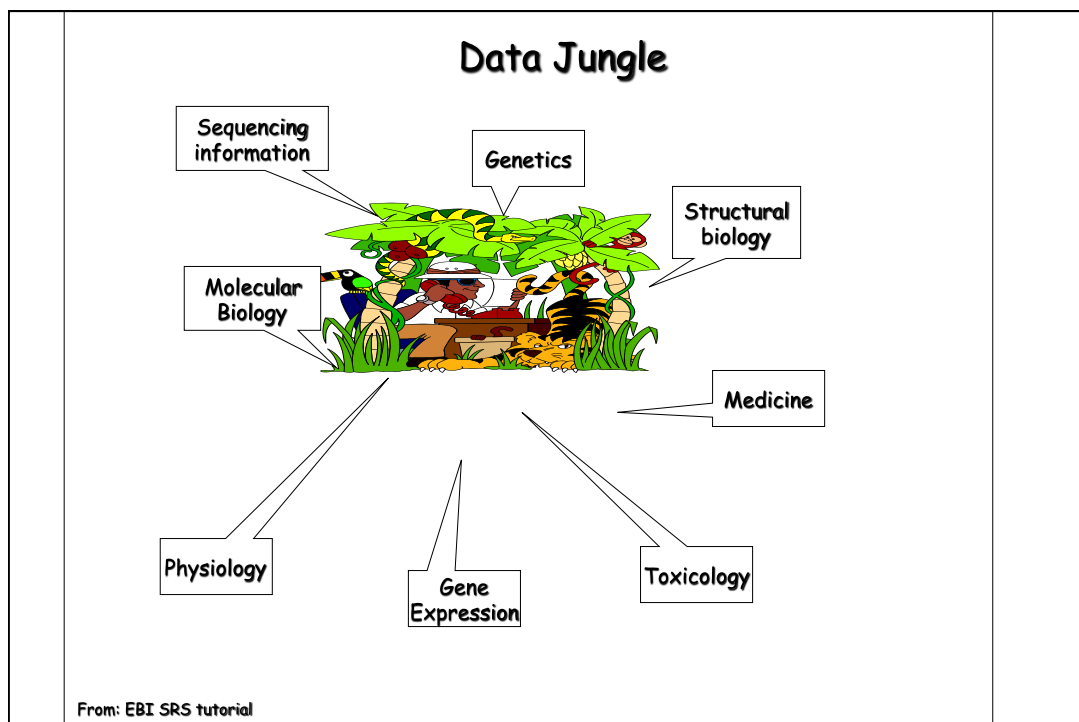
From the National Centre for Biotechnology Information (NCBI), <http://www.ncbi.nlm.nih.gov>

The challenge is in finding new approaches to deal with the volume and complexity of data, and in providing researchers with better access to analysis and computing tools in order to advance understanding of our genetic legacy and its role in health and diseases.

From the National Centre for Biotechnology Information (NCBI), <http://www.ncbi.nlm.nih.gov>

Essentially, Bioinformatics has three components

- The creation of databases allowing the storage and management of large biological data sets.
- The development of algorithms and statistics to determine relationships among members of large data sets.
- The use of these tools for the analysis and interpretation of various types of biological data, including DNA, RNA and protein sequences, protein structures, gene expression profiles, and biochemical pathways



Factors that made bioinformatics so important

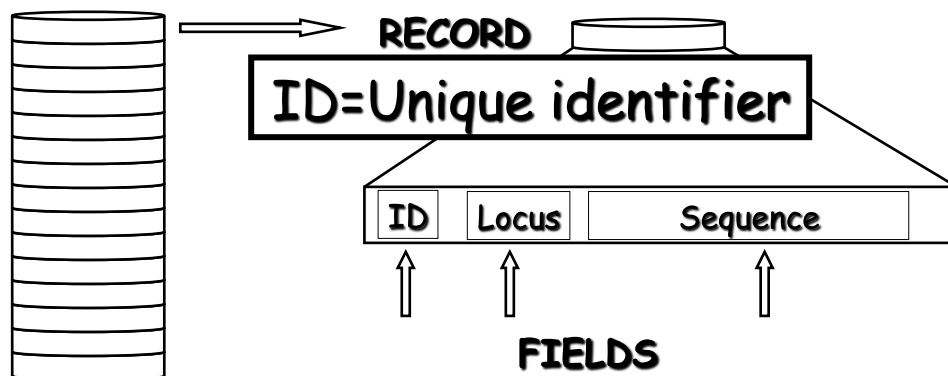
- **Rapid and cheap techniques for DNA sequencing**
- **The development of powerful computers**
- **Internet and the Wide World Web**

DATA SOURCES FOR DATABASES

- **Direct scientific submission**
- **Genome sequencing labs and groups**
- **Scientific literature**
- **Patent applications**

DATABASE: a collection of data that has a regular structure and that is organized in such a way that a computer can easily find and retrieve information.

A database is generally a collection of **RECORDS**, available through specific entries, each of which contains one or more **FIELD**.



Data Resources at NCBI

Databases: Primary and Derivative

Primary Databases

- Archival submissions of experimental results
- Database staff organize but don't add additional information

Genbank

dbEST

dbSNP

Probe

Derivative Databases

- Curated/expert review
- Computationally derived
- Combinations

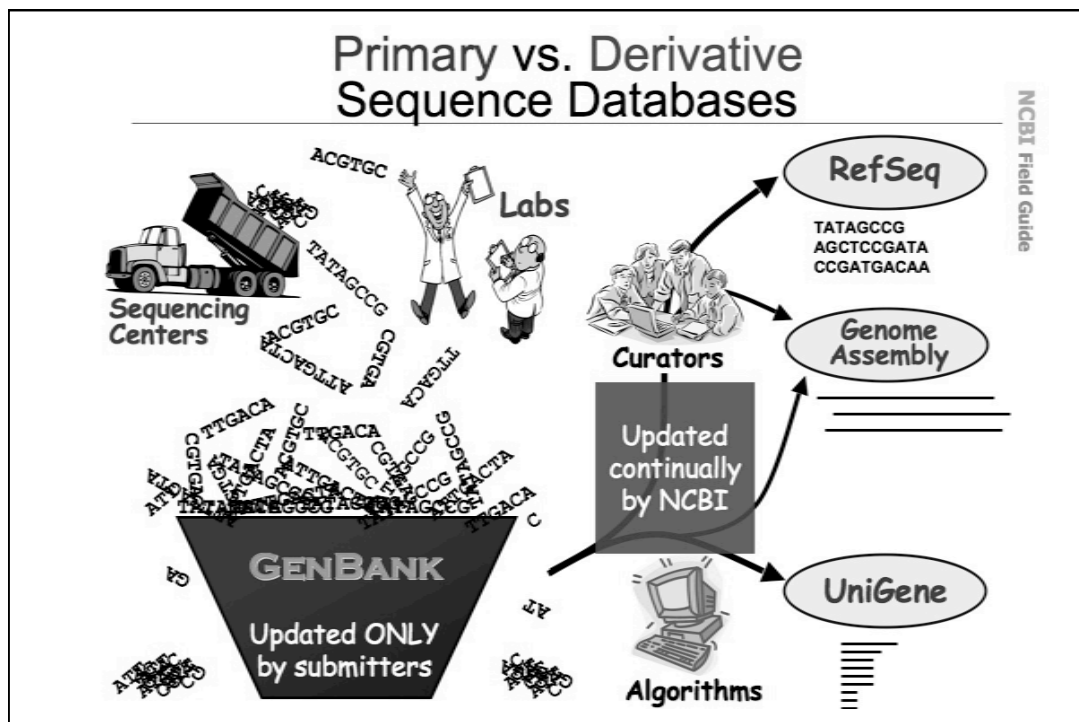
Refseq

Genomes

UniGene

UniSTS

Homologene



■ Bioinformatics Developers

They develop tools for bioinformatics

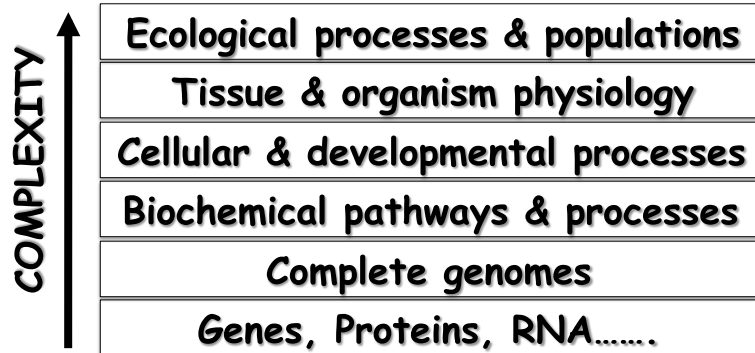
- Experts in Mathematics, Statistics and Informatics
- Computational biologists

■ Bioinformatics Users

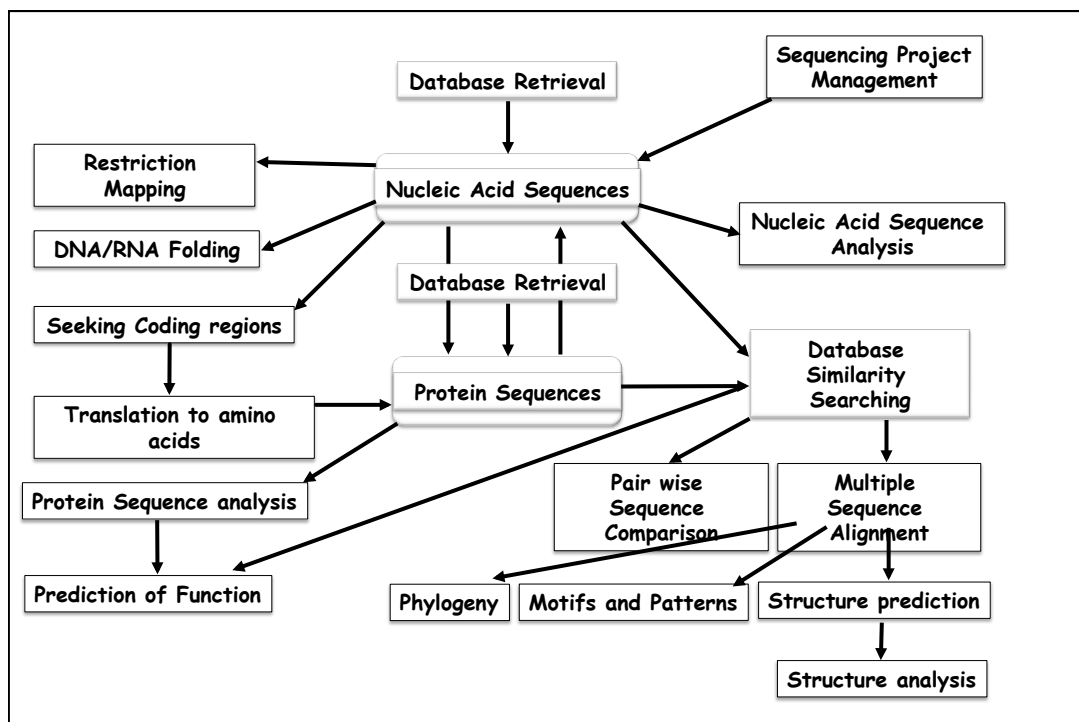
They use the tools of bioinformatics

- Researchers (Biologists, Biotechnologist,...)

Biological complexity



Introduction to Bioinformatics: www.bioinformatics.com/courses.com/bioinform



**Sites where the integration among databases
and between databases and software
is developed**

- **USA**
NCBI (National Center for Biotechnology Information)
- **Europe**
EBI (European Bioinformatics Institute, Hinxton, UK)
- **Japan**
NIG (National Institute of Genetics)

Biological database history

1965

M. Dayhoff *et al.* published "Atlas of Protein Sequences and Structures"

1982

EMBL started the DNA sequence collection

1983

Genbank started the DNA sequence collection

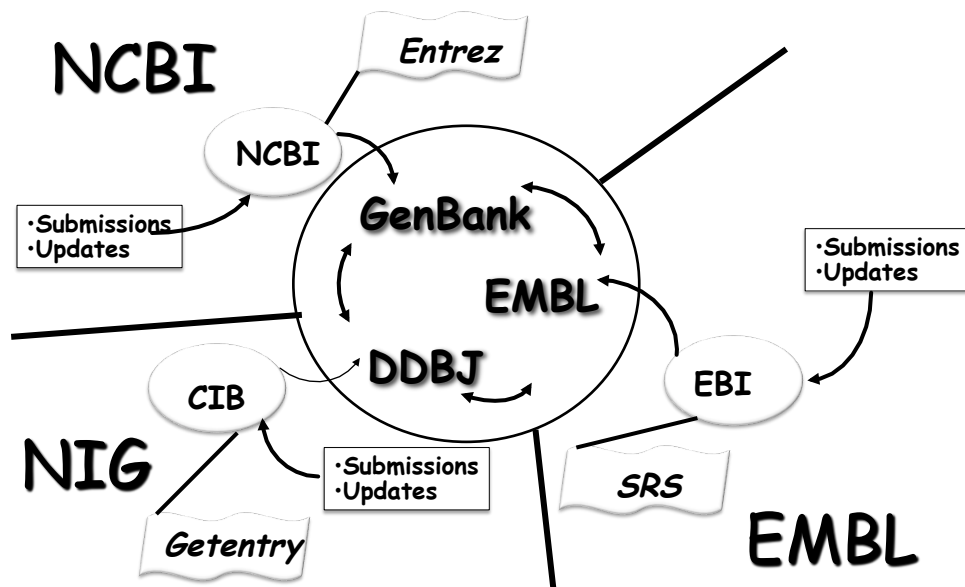
1984

DNA sequence databases of Japan

1988

Embl/GenBank/DDBJ agreed on common format for data elements

The International Sequence Database Collaboration



[http://](http://dccb.dbbj.ac.jp/) **DDBJ** DNA Data Bank of Japan

Accession DNA Protein AIDBS Taxonomy Site Search
Accession numbers
DDBJ UniProt PDB DAD PRF Patent [more](#) Go

HOME Submission How to Use Search/Analysis FTP/WebAPI Report/Statistics Contact Us [RSS](#) [Japanese](#)

About DDBJ
How to Use
Q and A

Sequence Submission
SAKURA
Mass Submission
Data Updates
DDBJ Sequence Read Archive
DDBJ Trace Archive

Search
getentry
ARSA

DDBJ : DNA Data Bank of Japan
DDBJ (DNA Data Bank of Japan) is one of the three databases that constitute DDBJ/EMBL/GenBank International Nucleotide Sequence Database, which was established through cooperative work with EBI in Europe and NCBI in the USA. Photo: S. Naito

Hot Topics
Aug. 23, 2010 The NCBI RefSeq data was released in the mirror
Jul. 2, 2010 Release of new fission yeast GSS 113,551 entries and EST 101,079 entries
[More](#)

Maintenance
Aug. 2, 2010 (Aug. 10-11) NIG supercomputer (supernig) services temporary down
[More](#)

DDBJ getentry -- Data retrieval by accession numbers etc -- [HELP](#) [Japanese Page](#)

NEW [\[Inquiry Form to Forward Your Question/Request to the Submitter of the DDBJ Entry\]](#) **Notice** Accept only DDBJ (INSDC) data.
[Caution] Revision of DDBJ flat file format: Deletion of E-mail address, phone and fax numbers

ID : Accession Number

DNA DATABASE : ☒ DDBJ / GenBank / EMBL output format : Flat file (DDBJ)

Protein DATABASE : ☐ UniProt ☐ PDB ☐ DAD ☐ PRF ☐ Patent output format : default

Result : [www](#) E-mail Address :

[PMQ](#) [Links](#) [Careers](#)

International Nucleotide Sequence Database Collaboration ☒ DDBJ exchanges data via the [SINET3](#) computer network.

DDBJ DNA Data Bank of Japan [DDBJ banner images](#)

Cell Innovation [Cell Innovation Program Portal site \(in Japanese\)](#)

EMBL-EBI

EB-eye Search

All Databases

Enter Text Here

Go

Reset ?

Advanced Search

Give us feedback

Databases

Tools

EBI groups

Training

Industry

About Us

Help

Site Index

Data Resources & Tools

ENA

UniProt

ArrayExpress

Ensembl

InterPro

PDB

Genomes

Nucleotide Sequences

Protein Sequences

Macromolecular Structures

Small Molecules

Gene Expression

Molecular Interactions

Reactions & Pathways

Protein Families

Enzymes

Literature

Taxonomy

Ontologies

Patent Resources

Downloads

Web Services

European Bioinformatics Institute

About the EBI

Research

PhD Studies

Training

Industry Support

Group & Team Leaders

EBI Funders

User Support

EBI Mission

People

Events at the EBI

Genome Campus Events

How to Find us

Jobs

EBI Hosted Project Websites

1000 Genomes

BioCatalogue

BioSapiens

E-MeP

EGA

ELKRI

EMBRACE

EMERALD

ENFIN

FELICS

IMPACT

INSDC

LRG

SLING

Microme

SPINE

SYBARIS

SYMBIOmatics

Events

Conference: Bridging the Gap in Biomedical Genetics

27-29 October 2010

more

Registration closes 8 October 2010

EBI Open Day

02 Nov 2010

more

Registration closes 4 October 2010

Hands-on training at EBI - Joint EBI-Wellcome Trust Proteomics workshop

13-17 December 2010

more

Registration closes 30 August 2010- 12 noon (GMT)

Research Highlights

High resolution insights to the regulation of transcript processing in eukaryotic cells

July 05, 2010

A paper in Nature Structural and Molecular Biology released online today finally ends speculation on whether a protein involved in splicing regulation functions as a repressor or facilitator of splicing. It does both! The study, authored by researchers from EMBL, EBI, Cambridge and Slovenia, used a new high-resolution technique to pinpoint the precise transcript binding positions of the protein... more

Latest News

1000 Genomes Project Releases Data from Pilot Projects

June 21, 2010

The 1000 Genomes Project, an international public-private consortium to build the most detailed map of human genetic variation to date, announces the completion of three pilot projects and the deposition of the final resulting data in freely available public databases for use by the research community... more

NCBI: The National Center for Biotechnology Information

Map of the United States

Bethesda, Maryland

Photograph of the NCBI building in Bethesda, Maryland, with a large tree in the foreground.

Created by US Congress in 1988, NCBI is part of the National Library of Medicine at National Institutes of Health.

10



The National Center for Biotechnology Information (NCBI)

- **Created as a part of the National Library of Medicine in 1988**
 - Establish public databases
 - Research in computational biology
 - Develop software tools for sequence analysis
 - Disseminate biomedical information
- **Tools: BLAST(1990), Entrez (1992)**
- **GenBank (1992)**
- **Free MEDLINE (PubMed, 1997)**
- **Other databases: dbEST, dbGSS, dbSTS, MMDB, OMIM, UniGene, GeneMap, Taxonomy, CGAP, SAGE, Gene, RefSeq**

http://www.ncbi.nlm.nih.gov

National Center for Biotechnology Information

NCBI Resources How To

National Center for Biotechnology Information Search All Databases

Resources

NCBI Home

- All Resources (A-Z)
- Literature
- DNA & RNA
- Proteins
- Sequence Analysis
- Genes & Expression
- Genomes
- Maps & Markers
- Domains & Structures
- Genetics & Medicine
- Taxonomy
- Data & Software
- Training & Tutorials

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

More about the NCBI | Mission | Organization | Research | RSS

Genome Reference Consortium

Formed to improve human and mouse reference assemblies, GRC will fix loci misrepresented in reference assembly, fill remaining gaps, and make alternate representations of complex loci.

1 2 3 4

Popular Resources

- PubMed
- PubMed Central
- Bookshelf
- BLAST
- Gene
- Nucleotide
- Protein
- GEO
- Conserved Domains
- Structure
- PubChem

NCBI News

November and December 2004 News

How To...

Obtain the full text of an article

NCBI Resources How To

National Center for Biotechnology Information

Search All Databases

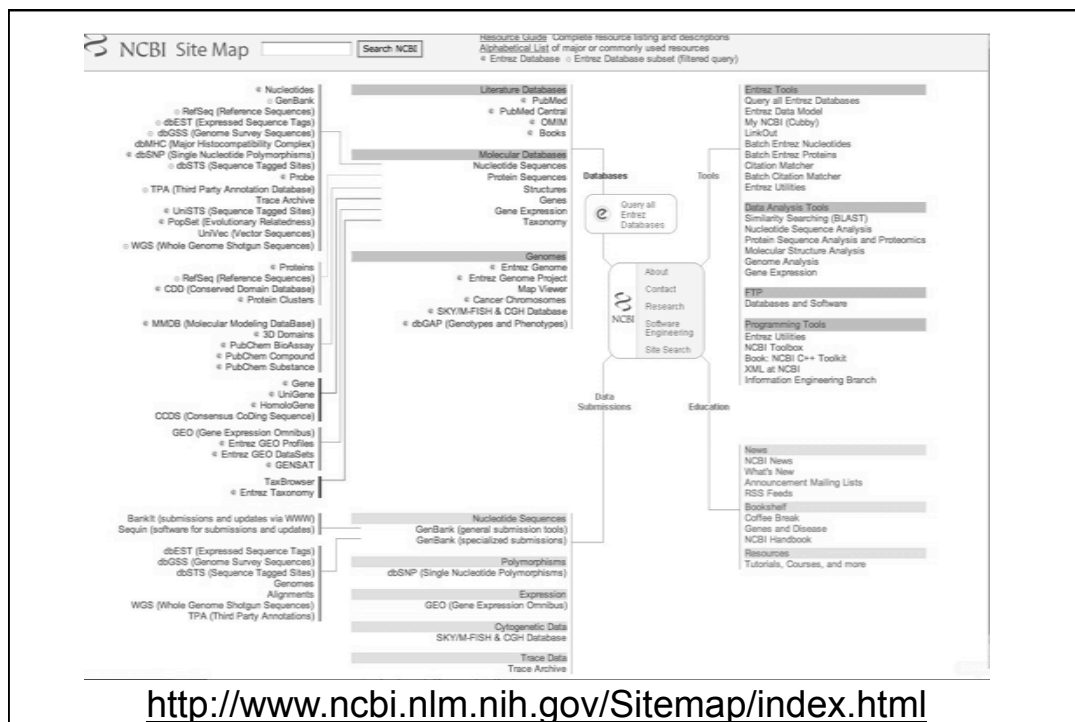
Entrez, The Life Sciences Search Engine

PubMed All Databases Human Genome GenBank Map Viewer BLAST

Search across databases GO Clear Help

Welcome to the Entrez cross-database search page

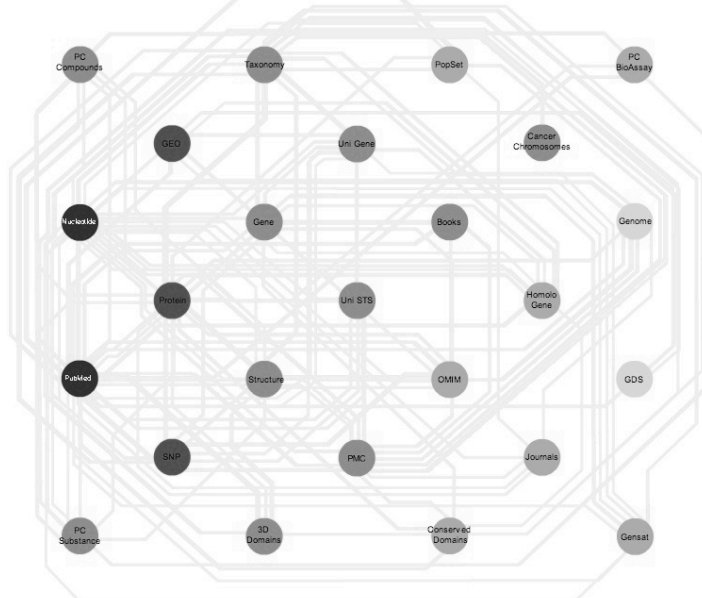
PubMed: biomedical literature citations and abstracts	Books: online books
PubMed Central: free, full text journal articles	OHIM: online Mendelian Inheritance in Man
Site Search: NCBI web and FTP sites	OHIA: online Mendelian Inheritance in Animals
Nucleotide: Core subset of nucleotide sequence records	dbGaP: genotype and phenotype
EST: Expressed Sequence Tag records	UniGene: gene-oriented clusters of transcript sequences
GSS: Genome Survey Sequence records	CDD: conserved protein domain database
Protein: sequence database	3D Domains: domains from Entrez Structure
Genomes: whole genome sequences	UniSTS: markers and mapping data
Structure: three-dimensional macromolecular structures	PopSet: population study data sets
Taxonomy: organisms in GenBank	GEO Profiles: expression and molecular abundance profiles
SNP: single nucleotide polymorphism	GEO DataSets: experimental sets of GEO data
Gene: gene-centered information	Cancer Chromosomes: cytogenetic databases
SRA: Short Read Archive	PubChem BioAssay: bioactivity screens of chemical substances
BioSystems: Pathways and systems of interacting molecules	PubChem Compound: unique small molecule chemical structures
HomoloGene: eukaryotic homology groups	PubChem Substance: deposited chemical substance records
GENSAT: gene expression atlas of mouse central nervous system	Protein Clusters: a collection of related protein sequences
Probe: sequence-specific reagents	Peptidome: HS/MS proteomic experiments
Genome Project: genome project information	
Journals: detailed information about the journals indexed in PubMed and other Entrez databases	MeSH: detailed information about NLM's controlled vocabulary
NLM Catalog: catalog of books, journals, and audiovisuals in the NLM collections	



Databases connections

<http://www.ncbi.nlm.nih.gov/Database/datamodel/index.html>

Entrez databases and the connections between them



<http://www.ncbi.nlm.nih.gov/Database/datamodel/index.html>