## Bioinformatics introduction

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# Bioinformatics introduction: Genomics, proteomics and the Central Dogma of Molecular Biology

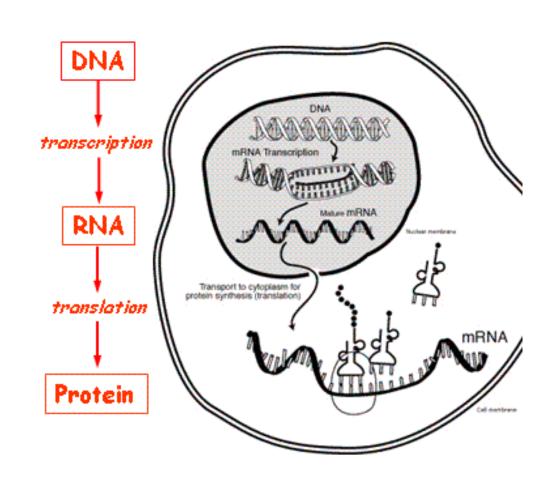
- Discoveries concerning the structure and function of DNA have revolutionized biology, dating from the work of Watson, Crick, Wilkins & Franklin in 1950s.
- Double helix, complementary strands, A-T, G-C base pairs.
- DNA (deoxyribonucleic acid) is the informatics basis of (1) heredity and (2) physiology.
- The "central dogma" concerns the flow of *information*.
- The "Code of Life" is software!



# Bioinformatics introduction: The Central Dogma of Molecular Biology

The central dogma of molecular biology: the coded genetic information in DNA is transcribed into messenger RNA (mRNA) containing programs for translation (synthesis) to particular proteins.

Exceptions to the rule: now known as a result of genomic discoveries in recent years (gene regulation, alternative splicing, post-translational modification, epigenetics).



From NIH-NCBI online course: Molecular Biology Review

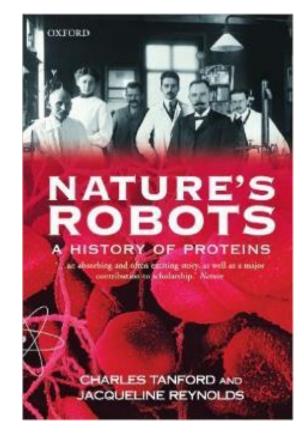
## Bioinformatics introduction: Genomics and proteomics

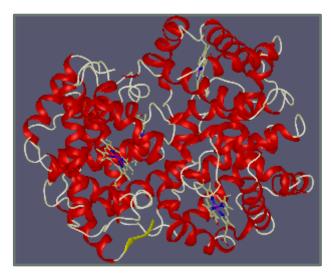
### Glossary of terms

bioinformatics	The science of collecting and analyzing complex biological data such as genetic codes.
gene	Unit of heredity. Section of DNA which is expressed as a molecular gene product, typically a protein.
genotype	genetic pattern
genome	full genetic code of an organism
proteome	full protein set of an organism
genomics	study of genomes and their interrelationships, including cross- species
proteomics	study of proteomes and their interrelationships, including cross- species
phenotype	observable physical trait

## Bioinformatics introduction: Proteins are nature's robots

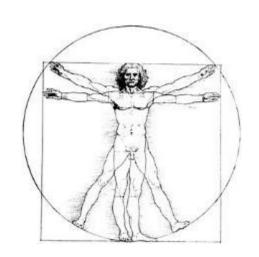
- Proteins govern *all* physiological functions
  - Actin & myosin (muscle)
  - Lipase, amylase (digestive enzymes)
  - Hemoglobin (02)
  - Rhodopsin (light receptor)
  - Gustducin (taste receptor)
  - Antibodies (immune system)
- Proteins interact and regulate
  - Highly connected biological network

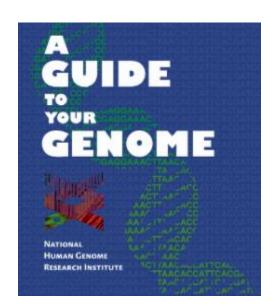




## Bioinformatics introduction: Human Genome Project and its offspring

- Human Genome Project (HGP), \$3B, 1990-2003.
- Offspring:
  - Fully\* sequenced genome (\*some restrictions apply)
  - Identified genes (~20k)
  - Variations (SNPs) and disease associations
  - Cross-species associations
  - ENCODE Project: Encyclopedia of (functional)
     DNA Elements
  - NHGRI, National Human Genome Research Institute
  - Many, many datasets





## Bioinformatics introduction: Genomic data example: Gene Ontology

"The Gene Ontology (GO) project is a collaborative effort to address the need for consistent descriptions of gene products across databases. Founded in 1998, the project began as a collaboration between three model organism databases, <a href="FlyBase">FlyBase</a> (Drosophila), the <a href="Saccharomyces Genome Database">Saccharomyces Genome Database</a> (SGD) and the <a href="Mouse Genome Database">Mouse Genome Database</a> (MGD). The GO Consortium (GOC) has since grown to incorporate many databases, including several of the world's major repositories for plant, animal, and microbial genomes. The <a href="GO Contributors">GO Contributors</a> page lists all member organizations.

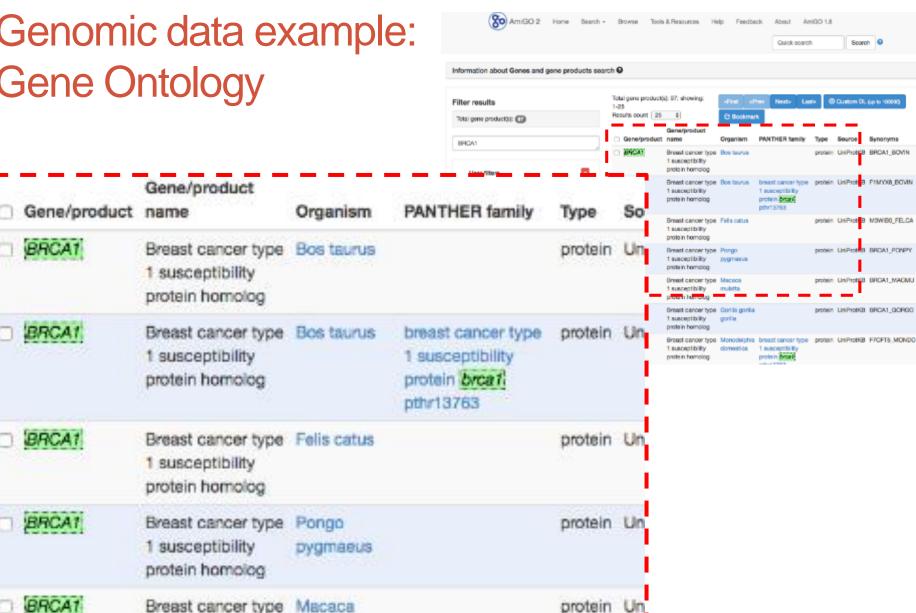
The GO project has developed three structured ontologies that describe gene products in terms of their associated **biological processes**, **cellular components and molecular functions** in a species-independent manner. There are three separate aspects to this effort: first, the development and maintenance of the ontologies themselves; second, the annotation of gene products, which entails making associations between the ontologies and the genes and gene products in the collaborating databases; and third, the development of tools that facilitate the creation, maintenance and use of ontologies."

From http://geneontology.org documentation

### Bioinformatics introduction:

Genomic data example: Gene Ontology

1 susceptibility



mulatta

Search 0

## Bioinformatics introduction: Genomic data example: OMIM, Online Mendelian Inheritance in Man

"Online Mendelian Inheritance in Man (OMIM®) is a continuously updated catalog of human genes and genetic disorders and traits, with particular focus on the molecular relationship between genetic variation and phenotypic expression. It is thus considered to be a phenotypic companion to the Human Genome Project. OMIM is a continuation of Dr. Victor A. McKusick's Mendelian Inheritance in Man, which was published through 12 editions, the last in 1998. OMIM is currently biocurated at the McKusick-Nathans Institute of Genetic Medicine, The Johns Hopkins University School of Medicine."

# Bioinformatics introduction: Genomic data example: OMIM, Online Mendelian Inheritance in Man

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Contributors

Creation Date

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\*113705

BREAST CANCER 1 GENE; BRCA1

HGNC Approved Gene Symbol: BRCA1

Cytogenetic location: 17q21.31 Genomic coordinates (GRCh38): 17:43,044,294-43,125,482

(from NCBI)

#### Gene-Phenotype Relationships

Location	Phenotype	Phenotype	Inheritance	Phenotype
		MIM number	(in progress)	mapping key
17q21.31	{Breast-ovarian cancer, familial, 1}	604370	AD, Mu	3
	{Pancreatic cancer, susceptibility to, 4}	614320		3

#### TEXT

#### Description

BRCA1 plays critical roles in DNA repair, cell cycle checkpoint control, and maintenance of genomic stability. BRCA1 forms several distinct complexes through association with different adaptor proteins, and each complex forms in a mutually exclusive manner (Wang et al., 2009).

#### Cloning and Expression

Miki et al. (1994) identified cDNA sequences corresponding to the BRCA1 gene by positional cloning of the region on 17q21 implicated in familial breast-ovarian cancer

External Links	
▶ Genome	
▶ DNA	
▶ Protein	
▼ Gene Info	
BioGPS	
Ensembl	
GeneCards	
Gene Ontology	
KEGG	
NCBI Gene	
UCSC	
Clinical Resources	
▶ Variation	
Animal Models	
Cell Lines	
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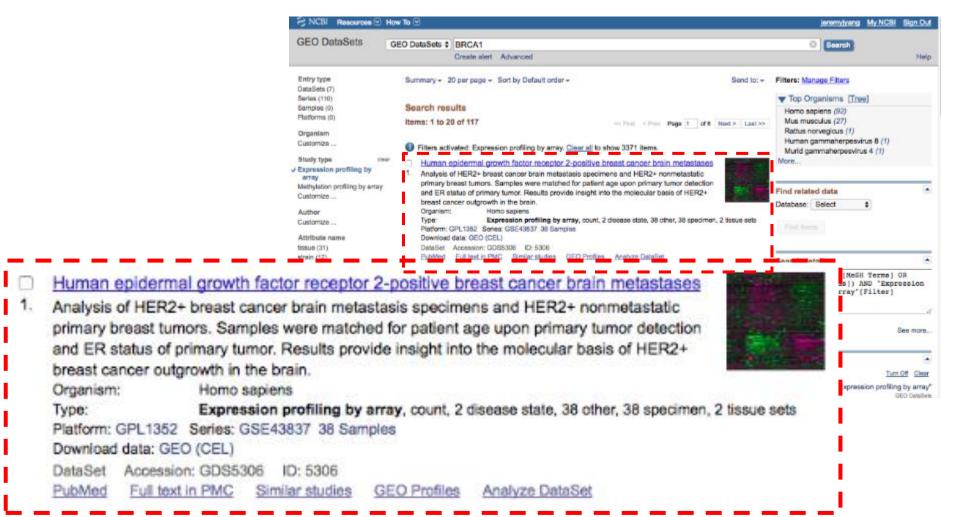
## Bioinformatics introduction: Genomic data example: GEO, Gene Expression Omnibus

"GEO is an international public repository that archives and freely distributes microarray, next-generation sequencing, and other forms of high-throughput functional genomics data submitted by the research community.

The three main goals of GEO are to:

- 1.Provide a robust, versatile database in which to efficiently store high-throughput functional genomic data.
- 2.Offer simple submission procedures and formats that support complete and well-annotated data deposits from the research community.
- 3. Provide user-friendly mechanisms that allow users to query, locate, review and download studies and gene expression profiles of interest."

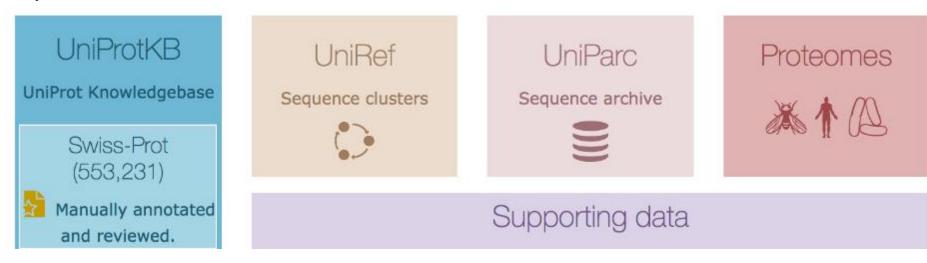
## Bioinformatics introduction: Genomic data example: GEO, Gene Expression Omnibus



## Bioinformatics introduction: Proteomic data example: UniProt



"The mission of <u>UniProt</u> is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information."

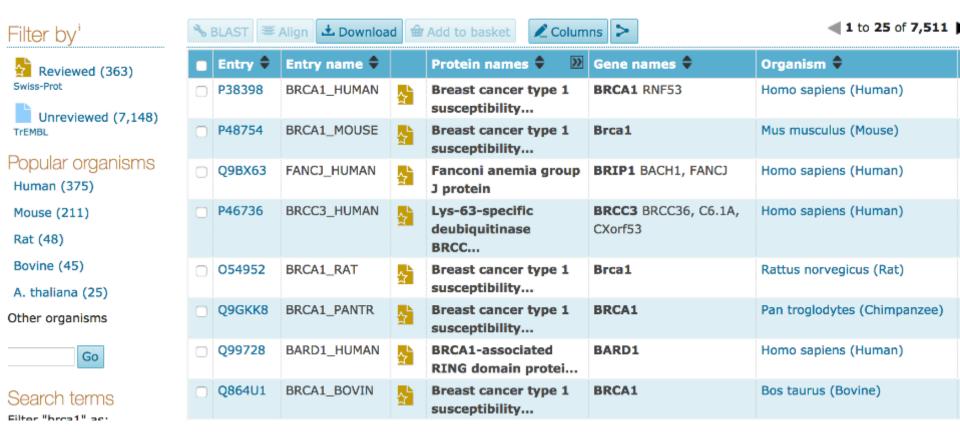


From UniProt, http://www.uniprot.org/

# Bioinformatics introduction: Proteomic data example: UniProt

#### UniProtKB results

About UniProtl



From UniProt, http://www.uniprot.org/

# Bioinformatics introduction: Take home messages

- Bioinformatics concerns the structure and function of biomolecules: DNA, RNA and proteins
- DNA is the basis of (1) heredity and (2) physiology.
- The "central dogma" concerns the flow of information.
- The "Code of Life" is software!
- Bioinformatics involves very big data.
- We can learn about life (physiology) and disease (pathology) from bioinformatics.
- Data Science very applicable!