## Informatica Biomedica

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Informatica Biomedica: Lezione 16

Bionformatics Archives and Information Retrieval The archives

fonte essenziale: A- M- Lesk, Introduction to Bioinformatics, Oxford University Press, 3rd Ed- (2008)

#### Contents

Bionformatics Archives and Information Retrieval The archives

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annotating the compilation of biological information in a form most useful to support research-

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▶ Nucleic acid sequences, including whole-genome projects

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- Publications

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The nucleic acid sequence databases, as distributed, are collections of entries.

Each entry has the form of a text file containing data and annotations for a single contiguous sequence-

Many entries are assembled from several published papers reporting overlapping fragments of a complete sequence.

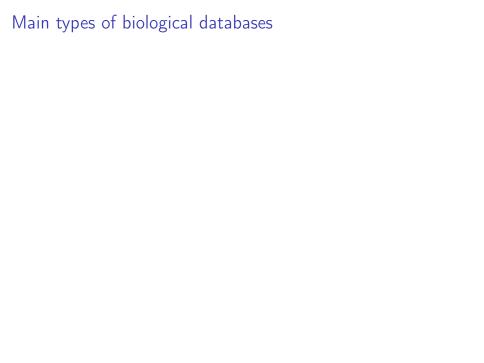
### Entries have a life history

Because of the desire on the part of the user community for rapid access to data, new entries are made available before completion of annotation and checking-

#### Entries mature through the classes:

 ${\sf Unannotated} \to {\sf Preliminary} \to {\sf Unreviewed} \to {\sf Standard}$ 

Rarely, an entry dies; a few have been removed when they are determined to be erroneous.



► Genome databases and genome browsers

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- Protein sequence databases

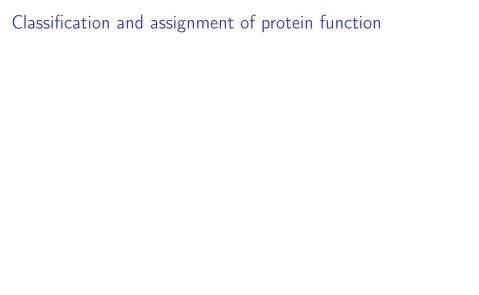
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- Databases of structures
- Classifications of protein structures

## Main types of biological databases

- Genome databases and genome browsers
- Protein sequence databases
- Databases of protein families
- Databases of structures
- Classifications of protein structures
- Accuracy and precision of protein structure determinations



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- Bibliographic databases
- Surveys of molecular biology databases and servers

Access to databases in molecular biology

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► ENTREZ

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- ► The Protein Identification Resource (PIR)
- ► ExPASy-Expert Protein Analysis System