

BIOWWW: a pool of specialised databases and algorithms for the analysis of biosequences

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The determination of nucleic acids and protein sequences, made ever easier and faster by modern technologies and instruments, has allowed considerable progress in biomedical research. Nowadays exponential growth in the number of amino acid and protein sequences needs computer-based technologies and tools for their management and analysis. Furthermore, suitable network infrastructures are also instrumental for researchers to access these data from the PC on their desk and analyse them with specific algorithms.

To this purpose we have developed a WEB interface (BioWWW) which allows to access different specialised databases and biosequence analysis methods developed within the research activities of the Italian EMBnet node and of other EU funded projects.

Products presently available under BioWWW are the following:

- MmtDB, a metazoan mitochondrial DNA variant database;
- KEYnet, a hierarchically structured database classifying genes and proteins according to their function;
- UTRdb, a non-redundant database of untranslated 5' and 3' sequences of mRNA from eukaryotes;
- PLMItRNA, a higher plant mitochondrial tRNA genes and molecules database.
- WORDUP, an algorithm to determine statistically significant oligonucleotides in isofunctional sequence collections;
- CODONTREE, a programme for the analysis of codon usage in protein coding genes;
- PATSCAN, a programme to identify complex patterns in nucleotide and amino acid sequences.

The site BioWWW (<http://bio-www.ba.cnr.it:8000/BioWWW/#AMMTDB>) is constantly updated as new programs and databases are made available by our research group.