

## Glossary

### Association learning

Techniques that find conjunctive implication rules (associations) that satisfy given criteria. The conventional association algorithms are sound and complete methods for finding all associations that satisfy criteria for minimum support (at least this fraction of the instances must satisfy both sides) and minimum confidence (at least this fraction of instances satisfying the left hand side, or antecedent, must satisfy the right hand side, or consequent).

### Attribute

A quantity describing an instance (feature). An attribute has a domain, which denotes the values that can be taken by an attribute – the attribute's type. The following domain types are common: Nominal (categorical). No relation holds between different values. For example: last name, color. Ordinal. There is a known ordering to the values. Continuous. Subset of real numbers. Integers are usually treated as continuous in machine learning work. Discrete. There is a finite set of values.

### Bioinformatics

The application of computational techniques to biology, in particular molecular biology.

### The Cancer Biomedical Information Grid - Cancer Bioinformatics Infrastructure Objects (caBIG - caBIO)

The caBIO model and architecture is the primary programmatic interface to caCORE. The heart of caBIO is its domain objects, each of which represents an entity found in biomedical research. These domain objects are related to each other, and examining these relationships can bring to the surface biomedical knowledge that was previously buried in the primary data sources (<http://ncicb.nci.nih.gov/core/caBIO>)

### The Cancer Biomedical Information Grid - Cancer Genome Anatomy Project (caBIG - cGAP)

The information in the Mitelman Database of Chromosome Aberrations in Cancer relates chromosomal aberrations to tumor characteristics, based either on individual cases or associations. cGAP has developed five web search tools to help analyze the information within the Mitelman Database (<http://cgap.nci.nih.gov/>)

**Cancer informatics**

Cancer informatics provides both a methodology and practical information tools. Cancer informatics supports a patient-centric record with access to personalized protocols and clinical guidelines supported by and being part of a continuously updated clinical trials system.

**Case-Based Reasoning**

A reasoning paradigm that solves new problems by reusing solutions from past similar problems.

**Classifier**

A system that performs automatic classification.

**Clinical trials and longitudinal studies**

A clinical trial is a scientific study to determine the safety and effectiveness of a treatment or intervention. A longitudinal study is a study in which the same group of individuals is monitored at intervals over a period of time.

**Clustering**

The process of grouping data points into clusters, i.e. a set of data points that are grouped by their proximity in a metric space.

**Collision induced dissociation (CID)**

The fragmentation of ions by collision with inert gas molecules

**Computational biology**

The development of computational tools and efficient algorithms for biology to support data base management, search, analysis and knowledge discovery, mathematical modeling, computer simulation, etc.

**Cytogenetics**

The study of chromosomes and chromosome abnormalities.

**Data mining**

The process of finding useful patterns in data.

**Data model**

A mathematical formalism comprising a notation for describing data and a set of operations used to manipulate that data.

The database of single nucleotide polymorphisms (dbSNP). The database of single nucleotide polymorphisms (<http://www.ncbi.nlm.nih.gov/SNP/>).

**Detection depth**

The number of proteins detected in a proteomics experiment

**Differential in-gel electrophoresis (DIGE)**

Quantitative proteomics by 2-DE based on selective fluorescence labeling of proteins. Protein extracts are labeled with two different fluorophores, combined and separated by 2-DE. Differential excitation of the two fluorophores allows for relative quantification.

**DNA**

The sequencing, identification of genes, analysis of genetic variation and mutation analysis. Technologies include DNA sequencing, phylogenetics, haplotyping and SNP identification.

**Edman sequencing**

A methodology developed by Pehr Edman, also known as Edman degradation. It is the selective, step-by-step removal of the N-terminal amino acid of a protein after selective modification with phenyl isothiocyanate. This step will be repeated to identify stretches of the amino acid sequence.

**Electrospray ionization (ESI)**

A mild ionization form used for biomolecular MS. A liquid containing the analyte of interest is pumped through a narrow column. A high voltage is applied directly to the solvent and a fine aerosol of droplets is sprayed from the end of the column.

**Epidemiology and population studies**

Epidemiological and population research studies investigate the incidence, distribution, and control of disease in a population.

**Evidence-based medicine (EBM)**

The integration of best research evidence with clinical expertise and patient values.

**Functional genomics**

The exploration and analysis of gene function. Technologies include microarray, ChIP, and network analysis.

**The Gene Ontology (GO)**

The GO is a controlled vocabulary of biological processes, functions and localizations. (<http://www.geneontology.org/>).

**Information-based medicine**

Integration of healthcare, life sciences, and information technology with the goal to deliver relevant information to researchers and clinicians in real time, support acquisition, integration, analysis, visualization and interpretation of complex data.

**Isotope coded affinity tags (ICAT)**

A chemical isotope label for quantitative proteomics. The reagent specifically reacts with cysteine SH-side chains.

**Isotope coded protein label (ICPL)**

A chemical isotope label for quantitative proteomics. The reagent specifically reacts with lysine NH<sub>2</sub>-side chains.

**Kyoto Encyclopedia of Genes and Genomes (KEGG)** KEGG is a suite of databases and associated software covering the information about the genes, proteins, chemical compounds and reactions, and molecular pathways (<http://www.genome.ad.jp/kegg/kegg2.html>).

**Knowledge discovery**

A (nontrivial) process of identifying valid, novel, potentially useful, and ultimately understandable patterns in data.

**Knowledge management**

The representation, organization, acquisition, creation, use and evolution of knowledge in its many forms.

**Laser capture microdissection (LCM)**

A methodology for the isolation of selected cells from solid tissue with a low power laser beam.

**Mascot**

Commercially available search algorithm from Matrix Science.

**Mass spectrometer (MS)**

An instrument used to measure the mass-to-charge ratio ( $m/z$ ) of ions in the gas phase.

**Liquid chromatography mass spectrometry (LC-MS)**

The coupling of liquid chromatography with mass spectrometry

**Matrix-assisted laser desorption/ionization (MALDI-TOF-MS)**

A mild ionization form used for biomolecular MS. An analyte is mixed with a matrix molecule and crystallized on top of a sample target plate. A pulsing laser is used to ionize both the analyte of interest and the matrix molecule.

**Surface-enhanced laser desorption ionization time-of-flight mass spectrometry (SELDI-TOF-MS)**

A variation of MALDI-TOF-MS. The sample target plate is coated with different chromatography resins (e.g. ion exchange, reverse phase etc.) to minimize the

sample complexity. The systems were commercially introduced by CIPHERGEN Biosystems.

#### Tandem mass spectrometry (MS/MS)

First the mass of an ion is determined by MS, then individual ions are isolated and fragmented by collision induced dissociation and the m/z of each fragmentation peak is determined. The result is a tandem mass spectrum (MS/MS)

#### Medical informatics

Medical information science involves using system-analytic tools to develop algorithms for management, process control, decision-making, and scientific analysis of medical knowledge. Medical informatics comprises the theoretical and practical aspects of information processing and communication, based on knowledge and experience derived from processes in medicine and health care.

#### Metabolomics

Large-scale detection of small molecular metabolites.

#### Model

A characterization of relationships between input and output variables.

#### Multidimensional protein identification technology (MudPIT)

The on-line separation of peptides by two-dimensional chromatography followed by mass spectrometry

#### mzXML

An open, generic XML representation of mass spectrometry data (<http://sashimi.sourceforge.net/software.html>).

#### OMSSA

The Open Mass Spectrometry Search Algorithm (OMSSA) is available from the NCBI.

**Ontology Web language (OWL)** A semantic markup language for creating and sharing ontologies on the World Wide Web. OWL has been developed as an extension of RDF (Resource Description Framework). It is derived from the DAML+OIL Web Ontology language and is a collaborative development endorsed by the W3C (<http://www.w3.org/TR/2004/REC-owl-ref-20040210/>).

#### Outlier

An example pattern that is not representative of the majority of observed data.

#### Peptide mass fingerprint

Proteins are digested with sequence specific enzymes. The collection of resulting peptide ions can be used as an identifier of the unknown protein.

**Proteome**

The complete set of proteins expressed by an organism

**Proteomics**

Large-scale identification, characterization and quantification of proteins involved in a particular pathway, organelle, cell, tissue, organ or organism that can be studied in concert to provide accurate and comprehensive data about that system. Technologies include protein interaction models, high-throughput protein analysis and modeling.

**Expression proteomics**

Detection of every protein expressed in a given biological system.

**Functional proteomics**

Global detection of protein-protein interactions.

**Proteomics of posttranslational modifications**

Detection of posttranslational protein modifications by mass spectrometry. The ultimate goal is to detect every modification, changes in its relative abundance and its exact localization on each protein.

**Structural proteomics**

The determination of the exact three-dimensional structure of every protein.

**Proteomics investigation strategy for Mammals (PRISM)**

An analysis strategy for mammalian proteins by LC-MS. Mammalian tissue is fractionated into discrete organelle fractions. Proteins are analyzed by MudPIT profiling, generated spectra are statistically validated and high confidence proteins are automatically mapped against the Gene Ontology annotation scheme.

**Resource Description Framework (RDF)**

A language for representing information about resources in the World Wide Web. It is intended for representation of metadata about Web resources, such as the title or author of a web page (<http://www.w3.org/TR/2004/REC-rdf-primer-20040210/#intro>).

**Reactome**

Reactome covers biological pathways ranging from the basic processes of metabolism to high-level processes such as hormonal signaling, with a special emphasis on human data (<http://www.reactome.org/>).

**Systems Biology Markup Language (SBML)** A format designed to enable the exchange of biochemical network models between different software packages (<http://www.sbml.org/docs/>).

**SEQUEST**

Commercially available search algorithm from Thermo Finnigan. The original code was developed by Yates and colleagues.

**Silica-bead perfusion technique**

Selective isolation of plasma membranes by coating with colloidal cationic silica beads

**Snap-frozen**

Quick freeze of tissue/cells by placing them immediately in liquid nitrogen or isopentane-dry ice.

**Simple Object Access Protocol (SOAP)**

An XML based protocol for encoding of application defined data types from a number of different languages, and remote procedure calls and responses. SOAP enables different programs running on different computers to communicate with one another.

**Stable Isotope Labeling with Amino acids in Cell culture (SILAC)**

An isotope labeling strategy for proteins in cell culture for quantitative proteomics. The cell culture growth medium is supplemented with an essential nutrient (e.g. an amino acid) in either the light or heavy isotopic version.

**Systems biology**

Scientific approach that uses quantitative systems-level experimentation to systematically identify and characterize molecules and molecular interactions that define cellular pathways, tissues, organs and organisms, and applies computational biology tools to integrate, analyze, visualize, and model experimental data.

**Therapeutics**

The treatment of cancer by remedial agents or methods.

**Tissue Micro Array (TMA)**

A platform for high throughput analysis and examination of a large number of tumor cases on a single histology slide and having been subjected to a specific stain. In TMA, small (6-15 mm diameter) cores of formalin fixed and paraffin embedded tissue are arrayed into a single paraffin block.

**Transcriptomics**

Global detection of mRNA

**Two-dimensional gel electrophoresis (2-DE)**

Separation of proteins by gel electrophoresis in two dimensions. In the first dimension proteins are separated by isoelectric point. In the second dimension proteins are separated based on molecular mass.

**Xenograft**

Growth of cells/tissues in organism/animal of different species, e.g. human tumor cells in immune deficient mice.

**X!Tandem**

An open-source proteomics search algorithm available from the Global Proteome Machine Organization (<http://www.thegpm.org>)

**Extensible Markup Language (XML)**

A flexible and adaptable information identification format ([www.xml.org](http://www.xml.org)).



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