

Resource Summary Report

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Mining On-Line Expert on MedLine

RRID:SCR_001848

Type: Tool

Proper Citation

Mining On-Line Expert on MedLine (RRID:SCR_001848)

Resource Information

URL: <http://medmole.cineca.it/>

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Description: MedMOLE improves the comprehension of microarray experimental results by grouping co-regulated genes on the basis of the informational content of MEDLINE documents. The tool relies on two components: a gene name extractor and a mining algorithm. The name extractor is based on existing dictionaries of gene names and aliases. The mining algorithm analyses the co-occurrences of words in the selected documents in order to automatically interpret the context, identify where the gene names appear, and map documents/genes into functional classes. DNA microarray technology is a high throughput method for gaining information on gene function. This large amount of data can be analyzed to identify groups of genes that share common expression characteristics, but the obtained results provide little information regarding the presence of functional biological correlations of genes within clusters. The published literature, on the other hand, provides a potential source of information to assist in interpretation of clustering results. We have developed a tool (MedMOLE) that improves the comprehension of microarray experimental results by grouping co-regulated genes on the basis of the informational content of MEDLINE documents. The tool relies on two components: a gene name extractor and a mining algorithm. The name extractor is based on existing dictionaries of gene names and aliases. The mining algorithm analyses the co-occurrences of words in the selected documents in order to automatically interpret the context, identify where the gene names appear, and map documents/genes into functional classes. Microarray transcriptional profiling is a powerful tool used in the study of transcriptional control mechanisms. An important point in the analysis of microarray data is the identification of hidden correlations between the differentially expressed genes generated upon some kind of cell stimulus. Functional annotation is an important topic for microarray data mining, however this is quite limited for complex organisms (e.g. *H. sapiens*, *M. musculus*) where a limited number of genes are well characterized and annotated. However, functional data are rapidly accumulating in the scientific literature and most of them are collected by MEDLINE, a database that contains over 11,000,000 biomedical journal citations. A microarray analysis usually generates few hundred of

differentially expressed genes and, after statistical validation of the data and transcription profiles clustering, biologists try to identify genes functionally correlated by scientific literature analysis. Even if some tools have been recently developed to simplify information extraction on the MEDLINE database, reading every article requires too much time and labor. Therefore, it is necessary to have some kind of intelligent information extracting system that recognizes gene names inside the texts. The analysis of text documents (e.g. MEDLINE abstracts) can be approached by two different points of view: text mining and information extraction (I.E.). The former aims at the automatic identification of groups of documents that share the same patterns of words, and thus refer to the same topic or theme. The latter aims at providing a structured representation of the textual information and requires a pre-definition of entities and relationships to be looked for inside texts. Thus while the text mining algorithms are general purpose, the information extraction algorithms are specific to the application. Furthermore, the text mining approach is explorative and enables the discovery of new concepts and relations while information extraction only extracts those elements that have already been defined. These two approaches can be integrated: information extraction tools generate databases that can be analyzed using data mining techniques, and, on the other side, text mining tools might take advantage of specific domain information extracted using I.E. techniques. MedMOLE takes advantage of text mining techniques, and simplifies the extraction of functional knowledge by literature abstracts directly/indirectly related to differentially expressed genes identified by microarray technology. Sponsors: This work was partially supported by PRIN 2001 and FIRB 2002 grants.

Synonyms: MedMOLE

Resource Type: software application, production service resource, service resource, data analysis service, analysis service resource, software resource, text-mining software

Keywords: experimental, extractor, function, functional, gene, algorithm, cell, characteristic, class, dna, informational, literature, mechanism, medline, medline interfaces, microarray, mining, organism, stimulus, technology, transcriptional

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Mining On-Line Expert on MedLine

Resource ID: SCR_001848

Alternate IDs: nif-0000-21258

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260818T043134+0000

Ratings and Alerts

No rating or validation information has been found for Mining On-Line Expert on MedLine.

No alerts have been found for Mining On-Line Expert on MedLine.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Tomo S, et al. (2017) Uncommon oral manifestation of lichen sclerosus: critical analysis of cases reported from 1957 to 2016. Medicina oral, patologia oral y cirugia bucal, 22(4), e410.