



The screenshot displays the SCAIView interface. On the left, the 'Entity View' shows a hierarchical tree of biomedical entities, with 'SERPINA1: serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1' highlighted. The main area shows a table of search results with columns for 'Entity', 'Relative Entropy', 'KEGG Pathway', 'Ref. Count', 'Doc. Count', and 'Date Reported'. A magnifying glass highlights the 'PLAT' entity. On the right, the 'Document View' shows a list of search results, with the first document titled '1. Endothelial nitric oxide synthase polymorphism (-786T->C) and increased risk of angio vasospasm after aneurysmal subarachnoid hemorrhage' highlighted.

- 1 Entity View with aggregated resultsets and linkout possibilities.
- 2 Document View: entity types are highlighted in different colours, linkouts possible.

Fraunhofer Institute for Algorithms and Scientific Computing SCAI

Schloss Birlinghoven 1
53757 Sankt Augustin
Germany

Contact

Dr. Marc Jacobs
phone +49 2241 14-4013
marc.jacons@scai.fraunhofer.de
www.scai.fraunhofer.de/scaiview

Distribution

scapos AG
phone +49 2241 14-4400
www.scapos.com

KNOWLEDGE DISCOVERY AND SEMANTIC SEARCH IN SCIENTIFIC LITERATURE

Situation

SCAIView is an advanced search engine and addresses questions of interest to general biomedical researchers. Most of the information is given as unstructured text (publications, text fields in databases).

Advanced retrieval technology allows answering complex queries such as:

- Which genes/proteins are related to a certain context (e.g. disease/pathway/epigenetics)?
- Give me an overview of relevant biomedical concepts in my subcorpus.
- Which drugs are relevant for this context?
- To which diseases is my gene associated?
- Which chromosomes show linkage to the disease?
- Which variations are mentioned in the context of the disease and could they be found in dbSNP?

- What other diseases are possibly co-occurring with my relevant disease?

SCAIView allows for full text and biomedical concept searches with large biomedical terminologies and outstanding text mining technologies.

Document Retrieval

The documents are retrieved via free text queries in combination with semantic or ontological search of biomedical entities of interest. The biomedical entities are embedded in searchable hierarchies and span from genes, proteins, accompanied SNPs to chemical compounds and medical terminology.

With ontological Filtering, it is possible to restrict the result to a subset; e.g. genes on a KEGG pathway or in a Cytoband region.

Textual information

by **SCAI**. Control of **SCAI** protein levels by **SCAI** may represent a versatile mechanism for fine-tuning of the expression of this key regulatory kinase by different cellular signals.

Results
SCAI associates with **CREB** and this process is facilitated by β -arrestin stimulation and β -arrestin1

SCAI is rapidly degraded by the proteasome pathway in response to **RAAR** agonist stimulation, whereas the turnover of the **CREB** kinase is not, which factor kinase activity is severely impaired (Ponka et al., 1999). We have also reported that **SCAI** turnover is dependent on β -arrestin function, and that overexpression of either β -arrestin1 or β -arrestin2 is able to promote **SCAI** proteolysis (Ponka et al., 2001), thus suggesting that these adaptor molecules may recruit some of the factors needed for **SCAI** ubiquitination and proteasome degradation. Interestingly, β -arrestins interact with **SCAI**, bringing this process to the plasma membrane **SCAI** complex, where **SCAI** triggers ubiquitination of β -arrestin1 and β -arrestin2 (Glorioso et al., 2002; Wang et al., 2002). **SCAI** is also part of activated **CREB** complexes, and the possibility that **SCAI** could act as a **SCAI** ubiquitin ligase. Consistent with this idea, we find that endogenous **SCAI** and **SCAI** are associated to **SCAI** cells, as shown by immunoprecipitation experiments using either anti-**SCAI** or anti-Mds1 antibodies (Supplementary Data and Supplementary Figure S1A). This suggests that both proteins can be found in the same molecular complex at steady-state conditions in cells.

We have previously shown that agonist stimulation of **RAAR** decreases **SCAI** half-life times of cells (Dodd conditions)

Figure 1 **SCAI** is involved in **CREB** degradation - A. Schem et al.

Figure 2 **SCAI** is involved in **CREB** degradation - B. Schem et al.

Figure 3 **SCAI** is involved in **CREB** degradation - C. Schem et al.

PDF icon and ADOBE logo.

Normalization

Chemical structure of a molecule with multiple hydroxyl groups.

Entrez Gene logo

UniProt logo

Tree icon

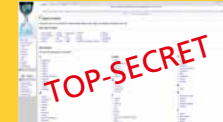
Experimental data



Pathway/Interaction Databases



Proprietary knowledge



3

Knowledge Discovery

The most important feature of any Knowledge Discovery tool or search engine is the ranking according to relevance of the results. For this we use a technique named relative entropy. Even if some proteins like insulin are mentioned quite often in the context of a search, it will be ranked low if it is not mentioned over-proportional in your specific query result set.

The other property of real Knowledge Discovery, novelty detection, could be shown in several biomedical applications.

Example

In a review on the "Genetics of intracranial aneurysms"¹, 18 associated genes are mentioned. A query with SCAIView for "intracranial aneurysm AND MESH: genetics" with the selection of human genes/proteins leads to the retrieval of 122 genes with top ranked hits contained in the experts review. Even new associated genes not described in the review have been found.

Successful uptake of the SCAIView information via an Application Programmers Interface for pediatric diseases in the EU project Health-e-Child could be demonstrated at HealthGrid 2009.

Advantages

- Superior text mining technology based on approximative search and machine learning
- Support for confidence information (adjustment of precision/recall)
- Combination of full text, semantic and ontology search
- Very fast retrieval from large corpora and relevance ranking of retrieved results
- Support of large resultsets (e.g. 1 Mio hits)
- Relevance ranking on aggregated entity search results
- Overview of found terminology in defined sub corpora
- Links to relevant biomedical databases (e.g. EntrezGene, dbSNP, KEGG, GO, DrugBank)
- Document visualization with user defined highlighting
- Export to Excel or Cytoscape
- Programmatic access via an Application Programmers Interface (API)

Technology

The selected biomedical entities are found by an approximate search algorithm implemented in the Fraunhofer-Gesellschaft information extraction tool ProMiner®, which additionally disambiguates synonyms of entities to unique identifiers in public available entity databases.

ProMiner has been evaluated as one of the best tools regarding protein and gene detection at the 2004 and 2007 BioCreAtiVe contest.

Additionally, non-enumerable entities like IUPAC names are found by a machine learning-based ProMiner plugin².

For improved performance of the retrieval engine, a highly optimized multi-threaded search engine is used.

Requirements

Client

- Firefox > 2.0
- Internet Explorer > 6.0

Server

- Minimum RAM: ≥ 2 GB
- Operating System: Linux, Windows XP, Windows 7, Solaris
- Application Server: Tomcat > 5.5
- Multi-Core processors: Recommended for near linear performance scale-up

1 Krschek, B.; Inoue, I.: The genetics of intracranial aneurysms. Journal of Human Genetics, 2006, 51, 587-594.

2 Klinger, R.; Kolárik, C.; Fluck, J.; Hofmann-Apitius, M.; Friedrich, C. M.: Detection of IUPAC and IUPAC-like chemical names. Bioinformatics, 2008, 24, i268-i276.