SCAIView's key features are:

- A user-friendly search environment with a query builder supporting semantic queries with biomedical entities
- Fast and accurate search and retrievals, based on the newest technologies of semantic search engines
- Visualization and ranking of the most relevant entities and documents
- Exportation of the search results in various file formats

Documents are retrieved by precisely formulated questions using ontological representations of biomedical entities. The entities are embedded in searchable hierarchies and span from genes, proteins, accompanied single-nucleotide polymorphisms to chemical compounds and medical terminologies. SCAIView supports the selection of the suitable entities by an autocompletion functionality and a knowledge base for each entity. This includes a description of the entity, structural information, pathways and links to relevant biomedical databases like

- EntrezGene
- KEGG
- DTDNA and
- WormBase

SCAIView represents the search results using a color-coded highlighting of the different entity-classes, statistical search results and various ranking functions.
Software Services

SCAIView Academia
SCAIView Neuro
SCAIView Animal
Belief - BEL network creation

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SCAIView Academia

SCAIView Academia is a designated scientific SCAIView version for the research community. Extended functionality is available in the commercial version.

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Please click here to launch SCAIView Academia.

Terminologies in SCAIView Academia

Alzheimer Disease Ontology (ADO)
Alzheimer Disease Ontology is an interoperable and standardized semantic framework that enables semantic search in scientific text and is able to capture both established and scattered knowledge existing in Alzheimer’s disease domain. The Alzheimer Disease Ontology is incorporated into SCAIView Academia.

BioMarker Terminology
The BioMarker Terminology is incorporated into SCAIView Academia.

Drug Names
The Drug Names Terminology is incorporated into SCAIView Academia.

Hypothesis Finder
The Hypothesis Finder allows detection, systematic collation and analysis of published speculative statements in a specific context. The Hypothesis Finder Terminology is incorporated into SCAIView Academia.
SCAIView Neuro is funded by the national German project Neuralliance, a research cooperation in conjunction with the Pharmaceuticals Initiative for Germany, financed by the Federal Ministry of Education and Research through the contract no. 0315603B.
The animal distribution of SCAIView

SCAIView Animal
SCAIView Animal is a SCAIView version specialized for the Animal domain. The searchable documents are from the Medline veterinary corpus. This version is currently deactivated. Please contact Prof. Dr. Martin Hofmann-Apitius (martin.hofmann-apitius(at)scsiai.fraunhofer.de) for further information.

Terminologies in SCAIView Animal
Cattle terminology
The Cattle terminology is a gene and protein annotations dictionary for cattle and is incorporated into SCAIView Animal.

Cattle Orthologue terminology
The Cattle Orthologue terminology is a gene and protein annotations dictionary for cattle generated from orthologue human and mouse genes and is incorporated into SCAIView Animal.

Preimplantation terminology
The Preimplantation terminology is generated from key developmental stages associated with cattle preimplantation period and is incorporated into SCAIView Animal.

Cattle MicroRNA terminology
The Cattle MicroRNA terminology is a MicroRNA annotation dictionary for cattle and is incorporated into SCAIView Animal.

Pig terminology
The Pig terminology is a gene and protein annotations dictionary for pig and is incorporated into SCAIView Animal.

Pig Orthologue terminology
The Pig Orthologue terminology is a gene and protein annotations dictionary for pig generated from orthologue human and mouse genes and is incorporated into SCAIView Animal.

Pig MicroRNA terminology
The Pig MicroRNA terminology is a MicroRNA annotation dictionary for pig and is incorporated into SCAIView Animal.
Belief - BEL network creation

Authors: Juliane Fluck, Sumit Madan, Sam Ansari, Justyna Szostak, Julia Hoeng, Marc Zimmermann, Martin Hofmann-Apifius, Manuel C. Peitsch

Abstract: In order to extract networks for systems biology from the literature an UIMA based extraction workflow using various named entity recognition processes and different relation extraction methods has been composed. The Unstructured Information Management architecture (UIMA) is a Java-based framework that allows assembling complicated workflows from a set of NLP components. The new system is processing scientific articles and is writing the open access biological expression language (OpenBEL) as output. OpenBEL is a machine and human readable language with defined knowledge statements that can be used for knowledge representation, causal reasoning, hypothesis generation, and assembling causal biological network models to enable reliable quantification of perturbations within these networks. In order to curate the automatically derived OpenBEL statements, our workflow integrates a curation interface that provides access to BEL statements generated by text mining and that integrates supporting information to facilitate manual curation. By using the semi-automated curation pipeline, expert time to model relevant causal relationships in BEL could be significantly reduced. In this paper the UIMA workflow and the key features of the curation interface are described.

By clicking on the link below for accessing the BELIEF pipeline, you accept our Terms and Conditions of Use. The BELIEF pipeline can be tested here.
Document retrieval strategies

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. 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
- 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?

Your Query

\[\text{MeSH Disease: "Alzheimer Disease"} \land \text{Human Genes / Proteins: "APP"}\]

**Search builder**

- **MeSH Disease: "Alzheimer Disease"**
  - **Description:** A degenerative disease of the brain characterized by the insidious onset of dementia.
  - **Synonyms:** Synonymy is a function that maps the text to the MeSH term.
  - **Tree:** Tree concept refers to the hierarchical structure of the MeSH terms.

- **AND:** Human Genes / Proteins: "APP"

**Show Results in:**

- Documents
- Alzheimer Ontology
- Disease/Pathway
- Drug Names
- Human Genes / Proteins
- Human miRNA
- Hypothesis Finder
- MeSH Disease
- Non Normalized mRNAs
- PLIO
- Taxonomy
- XMIR

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Knowledge Discovery in SCAIView

The most important features of any Knowledge Discovery tool or any search engine is the ranking according to relevance of the results. For this we use a technique termed 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.
Advantages

SCAIView is an efficiently implemented software which implies all the advantages of a web-based technology. The following list shows an overview of the main technological and the content related advantages of SCAIView:

- 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 result sets (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, doiME, KEGG, GO, DrugBank)
- Document visualization with user defined highlighting
- Export to Excel or Cytoscape
- Programmable access via an Application Programmers Interface (API)
Technology of SCAIView

Technological backgrounds

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 2006 BioCreative contest. Additionally non-enumerable entities like IUPAC names are found by a machine learning based ProMiner® plugin.

SCAIView client requirements

- Current versions of any browser like Internet Explorer, Safari, Google Chrome, Firefox, and Opera

SCAIView Server requirements

- Minimum RAM: 2GB more is better
- Operating System: Linux, Windows XP, Windows 7, Solaris
- Overview of found terminology in defined sub corpora
- Application Server: Tomcat > 6
- Multi-Core processors: Recommended for near linear scaleup
Introduction to the basic SCAIView functions

Most of the current biomedical knowledge from these large text collections is present in unstructured scientific text (journal publications, text fields in databases, e.g. more than 20 Mio. Documents in PubMed). SCAIView provides users with full text and biomedical concept search capabilities, which are supported by large biomedical terminologies and ontologies, processed together with outstanding text mining technologies. Using machine learning and dictionary-based Named Entity Recognition (NER), SCAIView identifies information about genes, drugs, SNPs and other Life Science entities in MEDLINE abstracts and extracts this information.

SCAIView uses a multi-threaded Lucene Index to allow semantic and ontological search on unstructured (text) data. Complex queries such as “what drugs are mentioned in the context of Alzheimer’s disease?” or “what genes are co-mentioned with Diabetes and are on the insulin signalling pathway?” can be asked in a user-friendly, intuitive way.

Please follow the following pages of the “First Steps” to get in touch with SCAIView!
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First Query
In the Query Builder you type in your search terms. You can use any term you want with a ‘full text’ search in the knowledge space. This feature behaves like a normal Google search function and results in a list of all occurrences of that search term in the literature. In addition, SCAIView 0.9.5 provides an auto-completion function to suggest a list of classes.

Further Queries
After editing a search term into the “Query Builder” input field, SCAIView automatically gives you an additional empty input field, to edit further query terms. You can select, in which logical (Boolean) concatenation this new search term has to be evaluated. The standard search operation is a Boolean AND connection shown on the left hand side of the search box. The combination can be changed to OR and NOT through the drop down menu. You can add or delete terms to your query. To delete a search term the minus button on the right hand side can be used.

The user is free to select the free-text search (select first entry in the column) or to select any class provided by the autocompletion window. The auto-completion function includes all synonyms of the search dictionaries and suggests the classes to be selected. The class search is more intelligent in a sense that it uses domain specific terms and synonyms, and sub-classes thereby generating more specific results. Typing a disease-specific term like ‘Alzheimer’s’ activates the auto-completion functionality which suggests all the available classes containing your typed words.
Query visualization

A new feature enables users to visualize the query or copy/paste queries. To use this feature you must choose the "Show/Hide Query" button to get the 'Your Query' input field.

Selection of classes from Search tree

All annotated classes are visualized in the tree on the left hand side of the interface. In the entry page the tree is hidden and can be visualized by clicking the 'Show/Hide Overall Query' button. The tree can be used to browse within the different classes. If a class is selected it will be added to the Query Builder as additional search class. The Class tree offers a search field, which helps to find concepts in the tree structure.

Show Results in

The selection menu 'Show results in' gives the possibility to select the search results in direct document visualization (show documents or overview pages about specific entities such as genes, drugs or diseases. Depending on your setting in the 'Show Results in' selection menu, the results of your query will be shown in the "Document view" or "Entity view". SCAIView changes automatically to the view/tab, accordingly to your selection. You can go back to the "Query tab" to modify your query.
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If you choose a specific dictionary or ontology in the 'Show Results in' selection menu, e.g. 'Human Genes / Proteins', your query will result in a list of relevant entities (Figure 8). SCAIView changes automatically to the tab 'Entity' view.

In this tab you have several information and options:

- You can switch back to another flag
- Your Query is shown
- You can select another view in Show Results
- Show only those entities which where selected in your query, e.g. if you select genes from a certain pathway, only those genes are shown.
- Select table columns: select your entity specific configuration of the entity view
- The number of all relevant entities
- A list which is shown pagewise of all these entities relevant for your query in arbitrary direction using the scroll buttons 'Next' and 'Last' or select a page of interest.
- Reference document count states the number of abstracts
- Doc count states the number of abstracts corresponding to your query where the entity is found

SCAIView Entities View with highlighted entity classes
Introduction to the basic SCAIView functions

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Publications related to SCAIView

SCAIView


Publications related to SCAIVew

Publications related to SCAIView

Named Entity Recognition


Publications related to SCAIView


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