

Homepage - Introduction

Introduction

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](#)
- [dbSNP](#)
- [KEGG](#)
- [GO](#) and
- [DrugBank](#)

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

Contact



Document Retrieval

[MORE INFO](#)

Knowledge Discovery

[MORE INFO](#)

Advantages

[MORE INFO](#)

Technology

[MORE INFO](#)

Share



[PRINT](#)

Follow us



[Homepage](#) - Software Services

Software Services

SCAIVIEW Academia

[MORE INFO](#)

SCAIVIEW Neuro

[MORE INFO](#)

SCAIVIEW Animal

[MORE INFO](#)

Belief - BEL network creation

[MORE INFO](#)

Share



[PRINT](#)

Follow us



SCAIVIEW Academia

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

By clicking on the link below for accessing SCAIVIEW Academia, you accept our [Terms and Conditions of Use](#):
Please click here to launch [SCAIVIEW Academia](#)!

Contact



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](#).

Share



PRINT

Follow us



SCAIView Neuro



SCAIView Neuro is funded by the national German project [Neuroallianz](#), 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.
-> [SCAIView Neuro](#)

Contact



Stephan Springstubbe
Fraunhofer SCAI

Phone +49 2241 14-4031
Fax +49 2241 14-2656

-> [Send email](#)



Dr. Marc Jacobs
Fraunhofer SCAI

Phone +49 2241 14-4013
Fax +49 2241 14-2656

-> [Send email](#)

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



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@scai.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 annotation 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 Micro RNA 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 annotation 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 Micro RNA annotation dictionary for pig and is incorporated into SCAIView Animal.

Contact



Prof. Dr. Martin Hofmann-Apitius
Fraunhofer SCAI

Phone +49 2241 14-4103
Fax +49 2241 14-2656

-> [Send email](#)

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



[Homepage](#) · [Software Services](#) · [Belief - BEL network creation](#)

Belief - BEL network creation

Authors: Juliane Fluck, Sumit Madan, Sam Ansari, Justyna Szostak, Julia Hoeng, Marc Zimmermann, Martin Hofmann-Apitius, 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 significant 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](#).

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



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. 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.

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?

Your Query

Show/Hide Overall Query

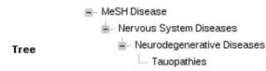
[(MeSH Disease:"Alzheimer Disease")] AND [Human Genes / Proteins:"APP"]

Query Builder

[MeSH Disease:"Alzheimer Disease"]

Alzheimer Disease (MeSH Disease)

Description A degenerative disease of the BRAIN characterized by the insidious onset of DEMENTIA
Synonyms Synonyms are disabled in the academic version.



AND [Human Genes / Proteins:"APP"]

AND

Show Results in:

- Documents
- Documents
- Alzheimer Ontology
- BioMarker Terminology
- Drug Names
- Human Genes / Proteins
- Human MiRNA
- Hypothesis Finder
- MeSH Disease
- Non Normalized MIRNA
- PLIO
- Taxonomy
- VPH

Share

PRINT

Follow us

Knowledge Discovery in SCAIView

The most important feature 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.

Share



PRINT

Follow us



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, dbSNP, KEGG, GO, DrugBank)
- Document visualisation with user defined highlighting
- Export to Excel or Cytoscape
- Programmatic access via an Application Programmers Interface (API)

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



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

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



[Homepage](#) - [First Steps](#)

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 Alzheimers 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!

[QUERY](#) [DOCUMENTS](#) [ENTITY](#) [ANALYSIS](#) [EXPORT](#)

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 Alzheimers 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.

Share



SHARE



TWEET



SHARE



SHARE

[PRINT](#)

Follow us

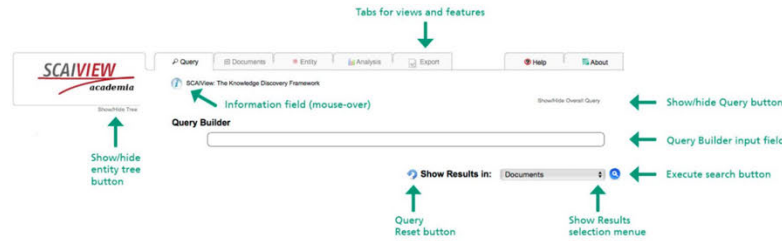


Introduction to the basic SCAIView functions

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 Alzheimers 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!

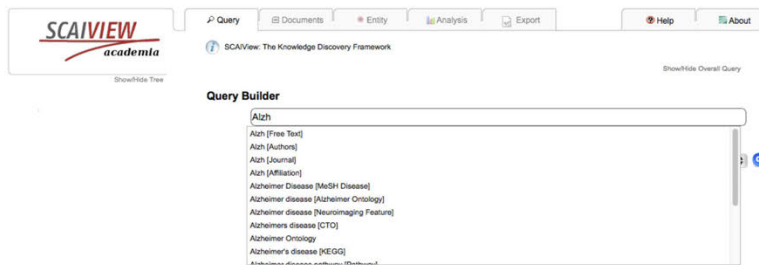


The new SCAIView entry page

Version 0.9.5 has now a new look and improved functionality, and is ready to be used by users without any bioinformatics experts background. All you need is some basic experience with Google. In particular, query building is now supported through auto-completion of typed words which results in rapid building of complex queries and fast retrieval of relevant information. The new Graphical User Interface (GUI) offers several new features (see Graphic 1) including the text input field 'Query Builder' and the selection menu 'Show results in:'.

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.

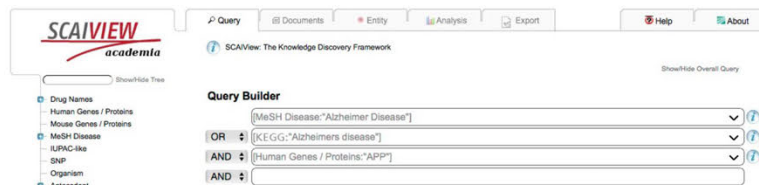


Auto-completion in the Query Builder

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 'Alzh...' activates the auto-completion functionality which suggests all the available classes containing your typed words.

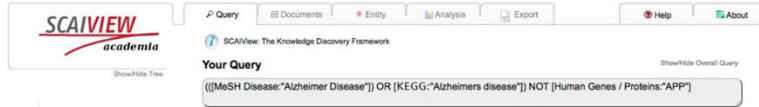
Further Queries

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 connections 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.



Query visualization

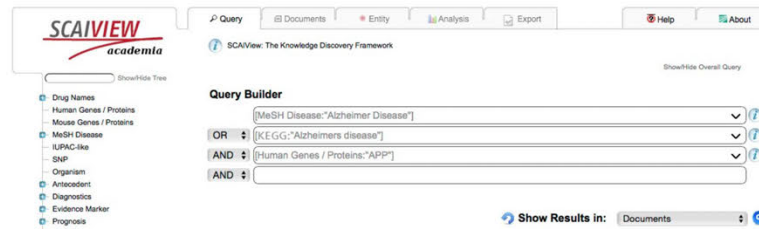
A new feature enables users to visualize the query or copy/paste queries. To use this feature you must choose the "Show/Hide Query" button to get the "Your Query" input field.



SCAView Query visualisation

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.



SCAView Show tree feature

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". SCAView changes automatically to the view / tab, accordingly to your selection. You can go back to the "Query tab" to modify your query.

Share



PRINT

Follow us



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 Alzheimers 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!

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 were selected in your query; e.g. if you select genes from a certain pathway, only those genes are shown. If this box is not activated all genes of the pathway plus all cooccurring entities are shown.
- Select table column: 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. Mouse over the entity shows the corresponding definition. If you select one of these entities you switch to the document view and the document with respect to the selected entity and your query are shown. Selecting the opens the analysis view for this entity in the selected query.
- 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. Mouse over the entity shows the corresponding definition. If you select one of these entities you switch to the document view and the document with respect to the selected entity and your query are shown. Selecting the opens the analysis view for this entity in the selected query.
- For each entity the relevance ranking based on relative entropy is given by default.
- Reference document count states the number of abstracts
- Doc count states the number of abstracts corresponding to your query where the entity is found

The screenshot shows the SCAIView interface with the following elements:

- Navigation Bar:** Includes tabs for Query, Documents, Entity, Analysis, and Export, along with Help and About buttons.
- Header:** SCAIView academia logo and "SCAIVIEW - The Knowledge Discovery Framework".
- Your Query:** A text input field containing the query: "[MeSH Disease:"Alzheimer Disease"] AND [human Genes / Proteins:"APP"]".
- Show Results in:** A dropdown menu currently set to "Human Genes / Proteins".
- Select Table Columns:** A button to customize the table columns.
- Table:** A table with 10 columns: Entity, Relevance, Ref. Doc Count, Doc Count, Date Reported, and Links. It displays 10 rows of results for the query.
- Footer of Table:** "1.830 entities found in 14353 documents, displaying 1 to 10." and pagination controls.

Entity	Relevance	Ref. Doc Count	Doc Count	Date Reported	Links
@APP	██████████	2293	14353	2012-07	HUGO
@PSEN1	██████████	3374	1139	2012-05	HUGO
@BACE1	██████████	1858	973	2012-08	HUGO
@MAPT	██████████	14136	965	2012-04	HUGO
@APOE	██████████	4108	817	2012-05	HUGO
@PSEN2	██████████	2328	425	2012-05	HUGO
@E2F		570	161	2012-03	HUGO
@NCSTN		382	132	2012	HUGO
@ROR1		9680	256	2012-04	HUGO
@ARL2		196	97	2012-04	HUGO

SCAIVIEW Entities View with highlighted entity classes

Share



PRINT

Follow us



Homepage - First Steps

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 Alzheimers 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!

QUERY DOCUMENTS ENTITY ANALYSIS EXPORT

Analysis View: To see the frequencies of all entities over all found abstracts, return to the Entity tab and click on the analysis icon. You will be directed to the Analysis tab where an overview of the entities and their occurrence frequencies in the abstracts is given.

The screenshot displays the SCAIView interface with the 'Analysis' tab selected. It shows a grid of tables for various entity classes. Each table lists entities and their relative frequencies. The classes shown include:

- Human Genes / Proteins** (1,820 entities found)
- Human MDNA** (17 entities found)
- Chemical Compounds** (27 entities found)
- Alzheimer's Disease** (275 entities found)
- Pharmacology / Toxicology** (112 entities found)
- CELL** (160 entities found)
- VEHICLE** (300 entities found)
- Hypothese Finder** (147 entities found)
- Scientific Literature** (520 entities found)
- Diseases** (542 entities found)
- SCAIVIEW** (1,117 entities found)

Analyses View with frequencies of entities for all classes

Share

SHARE
 TWEET
 SHARE
 SHARE

PRINT

Follow us

[Homepage](#) » [Publications](#)

Publications

Publications related to SCAIView

[SCAIVIEW](#) [SCAIVIEW RELATED](#) [NAMED ENTITY RECOGNITION](#) [BELIEF - BEL NETWORK CREATION](#)

SCAIVIEW

Malhotra A, Younesi E, Gurulingappa H, Hofmann-Apitius M. "HypothesisFinder:" a strategy for the detection of speculative statements in scientific text. *PLoS Comput Biol.* 2013;9(7):e1003117. doi: 10.1371/journal.pcbi.1003117 [Link](#)

Younesi E, Toldo L, Müller B, Friedrich CM, Novac N, Scheer A, Hofmann-Apitius M, Fluck J. Mining biomarker information in biomedical literature. *BMC Med Inform Decis Mak.* 2012 Dec 18;12:148. doi: 10.1186/1472-6947-12-148. [Link](#)

Christoph M. Friedrich, Holger Dach, Tobias Gattermayer, Gerhard Engelbrecht, Siegfried Benkner, and Martin Hofmann-Apitius: @neulink: A Service-oriented Application for Biomedical Knowledge Discovery. In *Proceedings of the HealthGrid (2008)*, pp. 165-172. [Link](#)

Martin Hofmann-Apitius, Juliane Fluck, Laura Furlong, Oriol Fornes, Corinna Kolárik, Susanne Hanser, Martin Boeker, Stefan Schulz, Ferran Sanz, Roman Klinger, Heinz-Theodor Mevissen, Tobias Gattermayer, Baldo Oliva, and Christoph M. Friedrich: Knowledge environments representing molecular entities for the virtual physiological human. In: *Philosophical Transactions of The Royal Society A Mathematical, Physical & Engineering Sciences* 366 (2008), Sep, No. 1878, pp. 3091-3110. - [Link](#)

Sudeep Sahadevan, Martin Hofmann-Apitius, Karl Schellander, Dawit Tesfaye, Juliane Fluck and Christoph M. Friedrich: Introducing the potential of text mining to animal sciences. In *J ANIM SCI* jas.2011-4841; published ahead of print June 4, 2012.

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



[Homepage](#) - Publications

Publications

Publications related to SCAIView

SCAIVIEW SCAIVIEW RELATED NAMED ENTITY RECOGNITION BELIEF - BEL NETWORK CREATION

SCAIVIEW related

Younesi E, Hofmann-Apitius M. Biomarker-guided translation of brain imaging into disease pathway models. *Sci Rep.* 2013 Nov 29;3:3375. doi: 10.1038/srep03375 [Link](#)

Harsha Gurulingappa, Bernd Müller, Martin Hofmann-Apitius, and Juliane Fluck: A Semantic Platform for Information Retrieval from E-Health Records. In The Twentieth Text REtrieval Conference (TREC 2011) Proceedings, Gaithersburg, Maryland, USA, November 2011. - [Link](#)

Harsha Gurulingappa, Bernd Müller, Martin Hofmann-Apitius, and Juliane Fluck: Information Retrieval Framework for Technology Survey in Biomedical and Chemistry Literature. In The Twentieth Text REtrieval Conference (TREC 2011) Proceedings, Gaithersburg, Maryland, USA, November 2011. - [Link](#)

Harsha Gurulingappa, Bernd Müller, Roman Klinger, Heinz-Theo Mevissen, Martin Hofmann-Apitius, Christoph M. Friedrich, and Juliane Fluck: Prior Art Search in Chemistry Patents based on Semantic Concepts and Co-citation Analysis. In The Nineteenth Text REtrieval Conference (TREC 2010) Proceedings, Gaithersburg, Maryland, USA, November 2010. - [Link](#)

Bernd Müller, Roman Klinger, Harsha Gurulingappa, Heinz-Theodor Mevissen, Martin Hofmann-Apitius, Juliane Fluck, and Christoph M. Friedrich: Abstracts versus Full Texts and Patents: A Quantitative Analysis of Biomedical Entities. In Proceedings of the 1st IRF Conference, Lecture Notes in Computer Science. Springer, 2010. - [Link](#)

Harsha Gurulingappa, Bernd Müller, Roman Klinger, Heinz-Theo Mevissen, Martin Hofmann-Apitius, Juliane Fluck, and Christoph M. Friedrich: Patent Retrieval in Chemistry based on semantically tagged Named Entities. In The Eighteenth Text REtrieval Conference (TREC 2009) Proceedings, Gaithersburg, Maryland, USA, November 2009. - [Link](#)

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



Homepage - Publications

Publications

Publications related to SCAIView

- SCAIVIEW
- SCAIVIEW RELATED
- NAMED ENTITY RECOGNITION**
- BELIEF - BEL NETWORK CREATION

Named Entity Recognition

Corinna Kolářik, Roman Klinger, and Martin Hofmann-Apitius: Identification of Histone Modifications in Biomedical Text for Supporting Epigenomic Research. *BMC Bioinformatics*, 10(S28), January 2009. Proceedings of the Asia Pacific Bioinformatics Conference (APBC). - [Link](#)

Roman Klinger, Corinna Kolářik, Juliane Fluck, Martin Hofmann-Apitius, and Christoph M. Friedrich: Detection of IUPAC and IUPAC-like Chemical Names. *Bioinformatics*, 24(13):i268-i276, 2008. Proceedings of the International Conference Intelligent Systems for Molecular Biology (ISMB). - [Link](#)

Roman Klinger, Laura I. Furlong, Christoph M. Friedrich, Heinz Theodor Mevissen, Juliane Fluck, Ferran Sanz, and Martin Hofmann-Apitius: Identifying gene specific variations in biomedical text. *Journal of Bioinformatics and Computational Biology*, 5(6):1277-1296, December 2007. - [Link](#)

Juliane Fluck, Heinz-Theodor Mevissen, Holger Dach, Marius Oster, and Martin Hofmann-Apitius: ProMiner: recognition of human gene and protein names using regularly updated dictionaries. In: Proceedings of the Second BioCreative Challenge Evaluation Workshop (2007), pp. 149-251. - [Link](#)

Share



PRINT

Follow us



[Homepage](#) » [Publications](#)

Publications

Publications related to SCAIView

SCAIVIEW	SCAIVIEW RELATED	NAMED ENTITY RECOGNITION	BELIEF - BEL NETWORK CREATION
--------------------------	----------------------------------	--	---

Ansari, S.; Szostak, J.; Madan, S.; Fluck, J.; Talikka, M.; Iskandar, A.; De Leon, H.; Hofmann-Apitius, M.; Peitsch, M.; Hoeng, J.; (2015) **A semi-automated curation workflow to construct biological networks from unstructured information**. The Journal of Biological Databases and Curation (DATABASE)

Fluck, J.; Madan, S.; Ansari, S.; Szostak J.; Hoeng, J.; Zimmermann, M.; Hofmann-Apitius, M.; Peitsch, M.; (2014) **BELIEF - A semiautomatic workflow for BEL network creation**. 6th International Symposium on Semantic Mining in Biomedicine (SMBM 2014), Aveiro, Portugal.

Fluck, J.; Klenner, A.; Madan, S.; Ansari, S.; Bobic, T.; Hoeng, J.; Hofmann-Apitius, M.; Peitsch, M.; (2013) **BEL networks derived from qualitative translations of BioNLP Shared Task annotations**. The Association for Computational Linguistics (ACL) Sofia 2013.

Share



SHARE



TWEET



SHARE



SHARE

[PRINT](#)

Follow us



[Homepage](#) > [Contact](#)

Contact



Fraunhofer Institute for Algorithms and Scientific Computing SCAI

Schloss Birlinghoven 1
53757 Sankt Augustin
Germany
Phone +49 2241 14-4300
Fax +49 2241 14-2460

[-> Contact form](#)

Useful links and documents

[-> Travel directions Schloss Birlinghoven, Sankt Augustin](#)

Share



SHARE



TWEET



SHARE



SHARE

[PRINT](#)

Follow us



[Homepage](#) · [Terms and Conditions](#)

Terms and Conditions

By using the BELIEF software service offered on this website you agree to the following:

The BEL statements generated by BELIEF according to your input are licensed under the Creative Commons Attribution-ShareAlike 4.0 International License. To view a copy of this license, visit <http://creativecommons.org/licenses/by-sa/4.0/>.

By using the Website, its Services, or Website Contents, User declares to have read and understood and will comply with the following terms and conditions at all times during its use.

USER RIGHTS AND DUTIES, RESTRICTIONS ON USE

FRAUNHOFER SCAI RIGHTS AND DUTIES

WARRANTY, LIABILITY, INDEMNIFICATION

TERMINATION

MISCELLANEOUS

User Rights and Duties, Restrictions on use

- 1. Non-commercial Purposes:** Use of the Website, Website Contents and Services as whole or in parts is only granted non-exclusively and for non-commercial purposes. Non-commercial purposes in the sense of this agreement shall mean internal research and academic purposes, and exclude, without limitation, any use, as part of, or in any way in connection with, a product or service which is sold, offered for sale, licensed, leased, loaned, or rented.

User agrees not to access or use the Website, Website Contents or Services for any other purpose than personal and non-commercial use solely as permitted by the normal functionality of the Website or Services offered thereon.
- 2. Third Party Content:** The Services include the SCAIView search engine which uses third party content, such as the United States National Library of Medicine (NLM) Database for search and text mining purposes. It is the sole responsibility of the User to ensure that it has obtained any relevant third party permissions for its intended use of any such third party content.
- 3. User may:**

 - access the Website in order to use the Services to search, retrieve, display, download, and otherwise use Content in compliance with these terms and conditions;
 - electronically save and print out retrieved information of the Website Content;
 - display, download, print any part or parts of the resource for the purpose of promotion of the Website Content;
 - publicly perform the Website Content as part of an academic presentation at a seminar, conference, workshop, or other such similar professional and non-commercial activity.
- 4. User may not and may not authorize any third party to:**

 - copy, reproduce, distribute or otherwise exploit any Website Content for any other purpose than non-commercial purposes without the prior written consent of Fraunhofer SCAI the respective owners, or licensors of the Website Content;
 - sell, resell, or otherwise distribute or make available any part or parts of the Website, Website Content or Services in any manner or in any medium to any third party unless explicitly allowed under these terms and conditions;
 - circumvent, disable or otherwise interfere with any security related features of the Website, Website Content, Service or features that (i) prevent or restrict use of or copying of the Content or (ii) enforce limitations on the use of the Website, Service, or the Website Content accessible via the Service;
 - remove, obscure or modify copyright notices, text acknowledging, or other means of identification or disclaimers as they may appear without prior written permission of Fraunhofer SCAI or, where third party content is concerned without such permission;
 - use Website Content in published books, in CD ROMs or in any other electronic format that is to be marketed and published for which revenue is received as a result;
 - affect or compromise the functionalities of the Website or Service;
 - alter or modify any part of the Website, Website Content or any Service;
 - upload third party's content without its explicit permission;
 - upload content which is not free from licensing restrictions;
 - User agrees not to collect or harvest any personal data of any user of the Website or any Service.
- 5. User acknowledges that all copyrights, patent rights, trademarks, database rights, trade secrets and other intellectual property rights relating to the Website, Services or Website Content which is not third party content, are the property of Fraunhofer SCAI and that this agreement does not assign or transfer any right, title or interest therein to User except for the right to use the Website Content in accordance with the terms and conditions of this agreement.**

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



Homepage » Terms and Conditions

Terms and Conditions

By using the BELIEF software service offered on this website you agree to the following:

The BEL statements generated by BELIEF according to your input are licensed under the Creative Commons Attribution-ShareAlike 4.0 International License. To view a copy of this license, visit <http://creativecommons.org/licenses/by-sa/4.0/>.

By using the Website, its Services, or Website Contents, User declares to have read and understood and will comply with the following terms and conditions at all times during its use.

USER RIGHTS AND DUTIES, RESTRICTIONS ON USE FRAUNHOFER SCAI RIGHTS AND DUTIES WARRANTY, LIABILITY, INDEMNIFICATION TERMINATION MISCELLANEOUS

Fraunhofer SCAI Rights and Duties

1. Fraunhofer SCAI provides access to the Website, Website Content and Services to User in compliance with these Terms and Conditions. This granting of access cannot be construed to stipulate a right of the User to claim access to any Services. Fraunhofer SCAI reserves the right to discontinue the Website and/or stop providing the Services, or any features within it at its sole discretion and without prior notice.
2. Fraunhofer SCAI reserves the right to modify or supplement these Terms and Conditions at any time. Accordingly, User shall check the Website from time to time as each User will be bound by any such revisions.
3. In the event that Fraunhofer SCAI becomes aware of a violation of these Terms and Conditions by User and where such violation consists in or results in a breach of criminal law, Fraunhofer SCAI reserves the right to inform the competent authorities hereof.

Share



PRINT

Follow us



[Homepage](#) » [Terms and Conditions](#)

Terms and Conditions

By using the BELIEF software service offered on this website you agree to the following:

The BEL statements generated by BELIEF according to your input are licensed under the Creative Commons Attribution-ShareAlike 4.0 International License. To view a copy of this license, visit <http://creativecommons.org/licenses/by-sa/4.0/>.

By using the Website, its Services, or Website Contents, User declares to have read and understood and will comply with the following terms and conditions at all times during its use.

[USER RIGHTS AND DUTIES, RESTRICTIONS ON USE](#)[FRAUNHOFER SCAI RIGHTS AND DUTIES](#)[WARRANTY, LIABILITY, INDEMNIFICATION](#)[TERMINATION](#)[MISCELLANEOUS](#)

Warranty, Liability, Indemnification

- Services and Website Content are provided "as is". Fraunhofer makes no representation or warranty (express, implied, oral or written) including, but not limited to, any and all implied warranties of title, quality, performance, merchantability or fitness for a particular purpose.
- Fraunhofer does not warrant or make any representation that the functions contained in the Services or Website will be accurate, reliable, suitable for certain purpose, uninterrupted or error-free, that defects will be corrected, or that the Website, the Service, or the servers that make the Website Content available, are free of viruses or other harmful components.
- User agrees that it is solely responsible for any breach of its obligations under the General Terms of Use and for the consequences resulting thereof.
- Fraunhofer, its legal representatives and employees expressly disclaim any liability beyond willful intent and gross negligence with respect to the Website, Service and Website Content or any part thereof, including, but not limited to, errors or omissions contained therein, libel, defamation, infringements of rights of publicity, privacy, trademark rights, infringements of any other third party intellectual property rights, moral rights, or the disclosure of confidential information. Except in cases of willful intent and gross negligence, Fraunhofer, its legal representatives and employees shall not be liable for any direct, indirect, consequential or incidental damages (including damages for loss of business profits, business interruption, loss of business information, and the like) arising out of the use or inability to use Website, Services, or Website Content even if Fraunhofer SCAI has been advised of the possibility of such damages.
- Fraunhofer accepts no liability for any loss suffered or incurred by the User or any third party as a result of their reliance on the Website, Services or Website Contents. User acknowledges that use of or reliance on the Website, Services or Website Contents is at User's sole risk.
- It is the sole responsibility of the User to ensure that it has obtained any relevant third party permissions for its intended forms of use of third party content. User shall be responsible for any and all damages, liabilities, claims, causes of action, legal fees and costs incurred by User in defending against any third party claim of intellectual property rights infringements or threats of claims thereof with respect of the use of third party content.
- The above limitations of liability do not affect Fraunhofer's, its legal representatives' and employees' liability for personal injuries, death of a person, willful intent, or gross negligence.
- User agrees to indemnify, defend and hold Fraunhofer SCAI harmless from and against any and all claims, losses, liability, costs and expenses (including attorneys' fees) incurred by Fraunhofer SCAI in connection with or arising out of User's breach of these Terms of Use.

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



Homepage » Terms and Conditions

Terms and Conditions

By using the BELIEF software service offered on this website you agree to the following:

The BEL statements generated by BELIEF according to your input are licensed under the Creative Commons Attribution-ShareAlike 4.0 International License. To view a copy of this license, visit <http://creativecommons.org/licenses/by-sa/4.0/>.

By using the Website, its Services, or Website Contents, User declares to have read and understood and will comply with the following terms and conditions at all times during its use.

USER RIGHTS AND DUTIES, RESTRICTIONS ON USE FRAUNHOFER SCAI RIGHTS AND DUTIES WARRANTY, LIABILITY, INDEMNIFICATION **TERMINATION** MISCELLANEOUS

Termination

1. Fraunhofer SCAI shall have the right to terminate this agreement forthwith if User has materially breached any of its obligations under this agreement or if Fraunhofer SCAI is required to do so by law.

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us



[Homepage](#) » [Terms and Conditions](#)

Terms and Conditions

By using the BELIEF software service offered on this website you agree to the following:

The BEL statements generated by BELIEF according to your input are licensed under the Creative Commons Attribution-ShareAlike 4.0 International License. To view a copy of this license, visit <http://creativecommons.org/licenses/by-sa/4.0/>.

By using the Website, its Services, or Website Contents, User declares to have read and understood and will comply with the following terms and conditions at all times during its use.

USER RIGHTS AND DUTIES, RESTRICTIONS ON USE

FRAUNHOFER SCAI RIGHTS AND DUTIES

WARRANTY, LIABILITY, INDEMNIFICATION

TERMINATION

MISCELLANEOUS

Miscellaneous

1. If any of the provisions of this agreement should be held as invalid, the validity of the remaining provisions shall not be affected. Invalid provisions shall be replaced by valid provisions formulated in such a way that the intended purpose will largely be achieved.
2. The agreement and any additions or amendments shall be in writing; additions and amendments must be marked as such. Any waiver of these formal requirements shall be in writing.
3. This License shall be governed and construed in accordance with the laws of Germany. The application of the United Nations Convention on Contracts for the International Sale of Goods (CISG) is expressly excluded.

Share



SHARE



TWEET



SHARE



SHARE

PRINT

Follow us

