SIFR annotator: ontology-based semantic annotation of French biomedical text and clinical notes

- **Autor:** Tchechmedjiev, Andon ; Abdaoui, Amine ; Emonet, Vincent ; Zevio, Stella ; Jonquet, Clement
- **Assuntos:** Abstracting and Indexing as Topic ; Analysis ; Artificial Intelligence ; Bioinformatics ; Biological Ontologies ; Computational linguistics ; Computer Science ; Data Analysis ; Document and Text Processing ; France ; Gene Expression Profiling ; Health Records, Personal ; Humans ; Information Storage and Retrieval ; Language processing ; Medical Informatics ; MEDLINE ; Natural language interfaces ; Natural Language Processing ; Semantics ; Software ; Web ; Web applications
- **É parte de:** BMC bioinformatics, 2018, Vol.19 (1), p.405-405, Article 405
- **Descrição:** Despite a wide adoption of English in science, a significant amount of biomedical data are produced in other languages, such as French. Yet a majority of natural language processing or semantic tools as well as domain terminologies or ontologies are only available in English, and cannot be readily applied to other languages, due to fundamental linguistic differences. However, semantic resources are required to design semantic indexes and transform biomedical (text)data into knowledge for better information mining and retrieval. We present the SIFR Annotator (http://bioportal.lirmm.fr/annotator), a publicly accessible ontology-based annotation web service to process biomedical text data in French. The service, developed during the Semantic Indexing of French Biomedical Data Resources (2013-2019) project is included in the SIFR BioPortal, an open platform to host French biomedical ontologies and terminologies based on the technology developed by the US National Center for Biomedical Ontology. The portal facilitates use and fostering of ontologies by offering a set of services -search, mappings, metadata, versioning, visualization, recommendation- including for annotation purposes. We introduce the adaptations and improvements made in applying the technology to French as well as a number of language independent additional features -implemented by means of a proxy architecture- in particular annotation scoring and clinical context detection. We evaluate the performance of the SIFR Annotator on different biomedical data, using available French corpora -Quaero (titles from French MEDLINE abstracts and EMEA drug labels) and CépiDC (ICD-10 coding of death certificates)- and discuss our results with respect to the CLEF eHealth information extraction tasks. We show the web service performs comparably to other knowledge-based annotation approaches in recognizing entities in biomedical text and reach state-of-the-art levels in clinical context detection (negation, experiencer, temporality). Additionally, the SIFR Annotator is the first openly web accessible tool to annotate and contextualize French biomedical text with ontology concepts leveraging a dictionary currently made of 28 terminologies and ontologies and 333 K concepts. The code is openly available, and we also provide a Docker packaging for easy local deployment to process sensitive (e.g., clinical) data in-house (https://github.com/sifrproject).
- **Editor:** England: BioMed Central Ltd
- **Idioma:** Inglês
- **Identificador:** ISSN: 1471-2105; EISSN: 1471-2105; DOI: 10.1186/s12859-018-2429-2; PMID: 30400805
- **Fonte:** PubMed; PubMed Central; SpringerLink E-Journals; DOAJ Directory of Open Access Journals

ODMSummary: A Tool for Automatic Structured Comparison of Multiple Medical Forms Based on Semantic Annotation with the Unified Medical Language System

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- **Autor:** Ebrahimie, Esmaeil
- **Assuntos:** Annotations ; Automation ; Biology and Life Sciences ; Breast cancer ; Care and treatment ; Clinical Coding - methods ; Codes ; Comparative analysis ; Computer and Information Sciences ; Consortia ; Data exchange ; Data models ; Data processing ; Design ; Documentation ; Electronic health records ; Engineering and Technology ; Evaluation ; Experts ; Feedback ; Health informatics ; Humans ; Internet ; Language ; Mechanization ; Medical advice systems ; Medical Records - standards ; Medical Records Systems, Computerized - instrumentation ; Medical research ; Medicine and Health Sciences ; Medicine, Experimental ; Metadata ; Multidisciplinary Sciences ; Ontology ; Patients ; Prostate ; Science & Technology ; Science & Technology - Other Topics ; Semantics ; Social Sciences ; Studies ; Technology application ; Unified Medical Language System ; Usability ; Web Browser

- **É parte de:** PloS one, 2016, Vol.11 (10), p.e0164569-e0164569
- **Descrição:** Introduction Medical documentation is applied in various settings including patient care and clinical research. Since procedures of medical documentation are heterogeneous and developed further, secondary use of medical data is complicated. Development of medical forms, merging of data from different sources and meta-analyses of different data sets are currently a predominantly manual process and therefore difficult and cumbersome. Available applications to automate these processes are limited. In particular, tools to compare multiple documentation forms are missing. The objective of this work is to design, implement and evaluate the new system ODMSummary for comparison of multiple forms with a high number of semantically annotated data elements and a high level of usability. Methods System requirements are the capability to summarize and compare a set of forms, enable to estimate the documentation effort, track changes in different versions of forms and find comparable items in different forms. Forms are provided in Operational Data Model format with semantic annotations from the Unified Medical Language System. 12 medical experts were invited to participate in a 3-phase evaluation of the tool regarding usability. Results ODMSummary (available at https://odmtoolbox.uni-muenster.de/summary/summary.html) provides a structured overview of multiple forms and their documentation fields. This comparison enables medical experts to assess multiple forms or whole datasets for secondary use. System usability was optimized based on expert feedback. Discussion The evaluation demonstrates that feedback from domain experts is needed to identify usability issues. In conclusion, this work shows that automatic comparison of multiple forms is feasible and the results are usable for medical experts.
- **Editor:** SAN FRANCISCO: Public Library Science
- **Idioma:** Inglês
- **Identificador:** ISSN: 1932-6203; EISSN: 1932-6203; DOI: 10.1371/journal.pone.0164569; PMID: 27736972
- **Fonte:** Web of Science - Social Sciences Citation Index - 2016 from WEB OF SCIENCE; PubMed; PubMed Central; DOAJ Directory of Open Access Journals

Formal and relational concept analysis for fuzzy-based automatic semantic annotation

- **Autor:** De Maio, C. ; Fenza, G. ; Gallo, M. ; Loia, V. ; Senatore, S.
- **Assuntos:** Annotations ; Applied sciences ; Artificial Intelligence ; Computer Science ; Computer Science, Artificial Intelligence ; Computer science; control theory; systems ; Computer systems and distributed systems. User interface ; Data analysis ; Data processing. List processing. Character string processing ; Descriptions ; Exact sciences and technology ; Fuzzy ; Fuzzy logic ; Hotels & motels ; Information systems. Data bases ; Knowledge ; Legacy ; Logic ; Machines ; Manufacturing ; Mathematical analysis ; Mathematical models ; Mechanical Engineering ; Memory organisation. Data processing ; Multimedia ; Ontology ; Processes ; Science & Technology ; Semantic web ; Semantics ; Software ; Technology
- **É parte de:** Applied intelligence (Dordrecht, Netherlands), 2014, Vol.40 (1), p.154-177
- **Descrição:** Semantic annotation is at the core of Semantic Web technology: it bridges the gap between legacy non-semantic web resource descriptions and their elicited, formally specified conceptualization, converting syntactic structures into knowledge structures, i.e., ontologies. Most existing approaches and tools are designed to deal with manual or semi-/automatic semantic annotation that exploits available ontologies through the pattern-based discovery of concepts. This work aims to generate the automatic semantic annotation of web resources, without any prefixed ontological support. The novelty of our approach is that, starting from web resources, content with a high-level of abstraction is obtained: concepts, connections between concepts, and instance-population are identified and arranged into an ex-novo ontology. The framework is designed to process resources from different sources (textual information, images, etc.) and generate an ontology-based annotation. A data-driven analysis reveals the data and their intrinsic relationships (in the form of triples) extracted from the resource content. On the basis of the discovered semantics, corresponding concepts and properties are modeled, allowing an ad hoc ontology to be built through an OWL-based coding annotation. The benefit of this approach is the generation of knowledge structured in a quite automatic way (i.e., the human support is restricted to the configuration of some parameters). The approach exploits a fuzzy extension of the

mathematical modeling of Formal Concept Analysis and Relational Concept Analysis to generate the ontological structure of data resources.
- **Editor:** Boston: Springer US
- **Idioma:** Inglês
- **Identificador:** ISSN: 0924-669X; EISSN: 1573-7497; DOI: 10.1007/s10489-013-0451-7
- **Fonte:** Web of Science - Science Citation Index Expanded - 2014 from WEB OF SCIENCE; SpringerLink E-Journals

Towards a new approach for video database semantic annotation

- **Autor:** Dali Youcef, Lamia Fatiha ; Ghomari, Abdelghani ; Kazi Tani, Mohammed Yassine
- **Assuntos:** Annotations ; Conferences ; Feature extraction ; Indexing ; Knowledge representation ; Low level ; Manuals ; MPEG7 ; Ontologies ; Semantics ; semi-automatic annotation ; Transform coding ; Video annotation ; XML
- **É parte de:** 2014 Science and Information Conference, 2014, p.1030-1033
- **Descrição:** Video database annotation has become the area field of interest recently, where several methods and techniques emerge. Regarding manual annotation as seriously time-consuming and automatic ones as large-scale of video unsatisfied, our topic of interest belongs to the semi-automatic annotation, where a little set of video is annotated manually and this will be propagated to the entire databases. We try to consider annotation able to exploit unconsidered concepts to help for improving annotation and XML performance. Our approach takes the low level descriptors' MPEG7 file added to the ontology's lexicon as input, and defines concepts of high level as output. Hence, an annotated video database is created.
- **Editor:** The Science and Information (SAI) Organization
- **Idioma:** Inglês
- **Identificador:** ISBN: 0989319334; ISBN: 9780989319331; EISBN: 0989319318; EISBN: 9780989319317; EISBN: 0989319326; EISBN: 9780989319324; DOI: 10.1109/SAI.2014.6918316
- **Fonte:** IEEE Electronic Library (IEL) Conference Proceedings

Semantic Annotation Pattern for Coding and Its Application in Component Development

- **Autor:** Mendes d'Araujo Costa, Taluna ; Santanche, A.
- **Assuntos:** anotação semântica ; dcc ; Java ; ontologia ; Ontologies ; OWL ; Resource description framework ; Semantics ; Software ; XML
- **É parte de:** 2011 Fifth Brazilian Symposium on Software Components, Architectures and Reuse, 2011, p.71-80
- **Descrição:** Source code annotations have an important role in software development. Structured annotations - those that follow building schemes - provide extra semantics to the code and are suitable for the automatization of complementary development tasks. There are recent initiatives towards interrelating annotations and ontologies, expanding their expressiveness and interoperability. In this paper we propose a new strategy based on meta-annotations to support structured annotations implicitly related to ontologies. It systematizes and simplifies the process of semantically annotating code, since programmers can use annotations without knowing details of the involved ontologies. This strategy was successfully applied in the development of components according to the Digital Content Component (DCC) model, enabling to automatize the production of semantic descriptions and interfaces for components, optimizing the development process.
- **Editor:** IEEE
- **Idioma:** Inglês
- **Identificador:** ISBN: 9781467302081; ISBN: 1467302082; EISBN: 9780769546261; EISBN: 0769546269; DOI: 10.1109/SBCARS.2011.16
- **Fonte:** IEEE Electronic Library (IEL) Conference Proceedings

Semantics-driven annotation of patient-specific 3D data: a step to assist diagnosis and treatment of rheumatoid arthritis

- **Autor:** Banerjee, Imon ; Agibetov, Asan ; Catalano, Chiara Eva ; Patané, Giuseppe ; Spagnuolo, Michela
- **Assuntos:** Arthritis ; Artificial Intelligence ; Care and treatment ; Computer Graphics ; Computer Science ; Image Processing and Computer Vision ; Indexing ; Original Article ; Rheumatoid factor ; Semantics
- **É parte de:** The Visual computer, 2016, Vol.32 (10), p.1337-1349
- **Descrição:** In the digital era, patient-specific 3D models (3D-PSMs) are becoming increasingly relevant in computer-assisted diagnosis, surgery training on digital models, or implant design. While advanced imaging and reconstruction techniques can create accurate and detailed 3D models of patients' anatomy, software tools that are able to fully exploit the potential of 3D-PSMs are still far from being satisfactory. In particular, there is still a lack of integrated approaches for extracting, coding, sharing and retrieving medically relevant information from 3D-PSMs and use it concretely as a support to diagnosis and treatment. In this article, we propose the SemAnatomy3D framework, which demonstrates how the ontology-driven annotation of 3D-PSMs and of their anatomically relevant features (parts of relevance) can assist clinicians to document more effectively pathologies and their evolution. We exemplify the idea in the context of the diagnosis of rheumatoid arthritis of the hand district, and show how feature extraction tools and semantic 3D annotation can provide a rich characterization of anatomical landmarks (e.g., articular facets, prominent features, ligament attachments) and pathological markers (erosions, bone loss). The core contributions are an ontology-driven part-based annotation method for the 3D-PSMs and a novel automatic localization of erosion and quantification of the OMERACT RAMRIS erosion score. Finally, our results have been compared against a medical ground truth.
- **Editor:** Berlin/Heidelberg: Springer Berlin Heidelberg
- **Idioma:** Inglês
- **Identificador:** ISSN: 0178-2789; EISSN: 1432-2315; DOI: 10.1007/s00371-016-1226-z
- **Fonte:** SpringerLink E-Journals

SPARQL Queries over Source Code

- **Autor:** Setzu, Mattia ; Atzori, Maurizio
- **Assuntos:** Coding Tools ; Data mining ; Java ; Ontologies ; Resource description framework ; Semantic Annotation ; Semantics ; Software ; Software Engineering ; SPARQL
- **É parte de:** 2016 IEEE Tenth International Conference on Semantic Computing (ICSC), 2016, p.104-106
- **Descrição:** We introduce a framework to extract and parse Java source code, serialize it into RDF triples by applying an appropriate ontology and then analyze the resulting structured code information by using standard SPARQL queries. We present our experiments on a sample of 134 Java repositories collected from Github, obtaining 17 Million triples about methods, input and output types, comments, and other source code information. Experiments also address the scalability of the framework. We finally provide examples of the level of expressivity that can be achieved with SPARQL by using our proposed ontology and semantic technologies.
- **Editor:** IEEE
- **Idioma:** Inglês
- **Identificador:** EISBN: 9781509006625; EISBN: 1509006621; DOI: 10.1109/ICSC.2016.65; CODEN: IEEPAD
- **Fonte:** IEEE Electronic Library (IEL) Conference Proceedings

Collaborative System for Semantic Annotation of Audiovisual Contents - Applications in the Context of Brazilian Independent Culture

- **Autor:** Rolim, L ; Osorio, A ; Avila, I

- **Assuntos:** audiovisual annotation ; Collaboration ; Cultural differences ; information discovery ; knowledge based semantic indexing ; Materials ; OWL ; semantic web ; social media retrieval ; Transform coding
- **É parte de:** 2010 Brazilian Symposium on Collaborative Systems II - Simposio Brasileiro de Sistemas Colaborativos II, 2010, p.1-4
- **Descrição:** This work presents an architecture that supports collaborative semantic annotation for audiovisual (AV) contents on the web. The main goal is to propose a semantically oriented infrastructure to organize audiovisual material produced by Brazilian points of culture and independent producers so as to optimize the searches made by community TV broadcasters, schools, film societies and internauts. The collaboration will rely on a content annotation scheme, designed to stimulate both consumers and producers to enrich the overall content description by incorporating viewpoints and meanings associated to relevant scenes, regions and objects present in the production. The proposed architecture is based on technologies for AV content description, such as MPEG-7, semantic web concepts and the Ontology Web Language (OWL). This work considers that collaborative approaches, along with the on-going efforts in expanding the coverage of Internet broadband access in Brazil, will foster the dissemination of the digital technologies in the production and recording of cultural manifestations, allowing artists and entities to publish and distribute in a more effective way their cultural patrimony over the Internet.
- **Editor:** IEEE
- **Idioma:** Inglês
- **Identificador:** ISBN: 9781424484461; ISBN: 1424484464; EISBN: 9780769542409; EISBN: 0769542409; DOI: 10.1109/SBSC-II.2010.10
- **Fonte:** IEEE Electronic Library (IEL) Conference Proceedings

OmniSearch: a semantic search system based on the Ontology for MIcroRNA Target (OMIT) for microRNA-target gene interaction data

- **Autor:** Huang, Jingshan ; Gutierrez, Fernando ; Strachan, Harrison J ; Dou, Dejing ; Huang, Weili ; Smith, Barry ; Blake, Judith A ; Eilbeck, Karen ; Natale, Darren A ; Lin, Yu ; Wu, Bin ; Silva, Nisansa de ; Wang, Xiaowei ; Liu, Zixing ; Borchert, Glen M ; Tan, Ming ; Ruttenberg, Alan
- **Assuntos:** Biomedical ontology ; Computational Biology - methods ; Data annotation ; Data integration ; Epistasis, Genetic - genetics ; Gene Ontology ; microRNA ; MicroRNAs - genetics ; Non-coding RNA ; Ontology development ; Semantic search ; Semantics ; SPARQL query ; Target gene ; User-Computer Interface
- **É parte de:** Journal of biomedical semantics, 2016, Vol.7 (1), p.25-25, Article 25
- **Descrição:** As a special class of non-coding RNAs (ncRNAs), microRNAs (miRNAs) perform important roles in numerous biological and pathological processes. The realization of miRNA functions depends largely on how miRNAs regulate specific target genes. It is therefore critical to identify, analyze, and cross-reference miRNA-target interactions to better explore and delineate miRNA functions. Semantic technologies can help in this regard. We previously developed a miRNA domain-specific application ontology, Ontology for MIcroRNA Target (OMIT), whose goal was to serve as a foundation for semantic annotation, data integration, and semantic search in the miRNA field. In this paper we describe our continuing effort to develop the OMIT, and demonstrate its use within a semantic search system, OmniSearch, designed to facilitate knowledge capture of miRNA-target interaction data. Important changes in the current version OMIT are summarized as: (1) following a modularized ontology design (with 2559 terms imported from the NCRO ontology); (2) encoding all 1884 human miRNAs (vs. 300 in previous versions); and (3) setting up a GitHub project site along with an issue tracker for more effective community collaboration on the ontology development. The OMIT ontology is free and open to all users, accessible at: http://purl.obolibrary.org/obo/omit.owl. The OmniSearch system is also free and open to all users, accessible at: http://omnisearch.soc.southalabama.edu/index.php/Software.
- **Editor:** England: BioMed Central
- **Idioma:** Inglês
- **Identificador:** ISSN: 2041-1480; EISSN: 2041-1480; DOI: 10.1186/S13326-016-0064-2; PMID: 27175225
- **Fonte:** PubMed; PubMed Central; SpringerLink E-Journals; DOAJ Directory of Open Access Journals

Knowledge-assisted semantic video object detection

- **Autor:** Dasiopoulou, S. ; Mezaris, V. ; Kompatsiaris, I. ; Papastathis, V.-K. ; Strintzis, M.G.
- **Assuntos:** Bandwidth ; Color ; Computer vision ; Context modeling ; Devices ; Engineering ; Engineering, Electrical & Electronic ; Enrichment ; Homogeneity ; Image coding ; Independent component analysis ; Knowledge representation ; Knowledge-assisted analysis ; Mathematical models ; Multimedia ; multimedia ontologies ; Networks ; Object detection ; Ontologies ; Science & Technology ; Semantic Web ; Semantics ; Studies ; Technology ; Transcoding ; video analysis
- **É parte de:** IEEE transactions on circuits and systems for video technology, 2005, Vol.15 (10), p.1210-1224
- **Descrição:** An approach to knowledge-assisted semantic video object detection based on a multimedia ontology infrastructure is presented. Semantic concepts in the context of the examined domain are defined in an ontology, enriched with qualitative attributes (e.g., color homogeneity), low-level features (e.g., color model components distribution), object spatial relations, and multimedia processing methods (e.g., color clustering). Semantic Web technologies are used for knowledge representation in the RDF(S) metadata standard. Rules in F-logic are defined to describe how tools for multimedia analysis should be applied, depending on concept attributes and low-level features, for the detection of video objects corresponding to the semantic concepts defined in the ontology. This supports flexible and managed execution of various application and domain independent multimedia analysis tasks. Furthermore, this semantic analysis approach can be used in semantic annotation and transcoding systems, which take into consideration the users environment including preferences, devices used, available network bandwidth and content identity. The proposed approach was tested for the detection of semantic objects on video data of three different domains.
- **Editor:** PISCATAWAY: IEEE
- **Idioma:** Inglês
- **Identificador:** ISSN: 1051-8215; EISSN: 1558-2205; DOI: 10.1109/TCSVT.2005.854238; CODEN: ITCTEM
- **Fonte:** Web of Science - Science Citation Index Expanded - 2005 from WEB OF SCIENCE™; IEEE Electronic Library (IEL) Journals

PheneBank: a literature-based database of phenotypes

- **Autor:** Pilehvar, Mohammad Taher ; Bernard, Adam ; Smedley, Damian ; Collier, Nigel
- **Autor:** Wren, Jonathan
- **Assuntos:** AcademicSubjects ; Algorithms ; Applications Notes ; Data Mining ; Humans ; Phenotype ; Rare Diseases ; SCI01060 ; Software
- **É parte de:** Bioinformatics, 2022, Vol.38 (4), p.1179-1180
- **Descrição:** Abstract Motivation Significant effort has been spent by curators to create coding systems for phenotypes such as the Human Phenotype Ontology, as well as disease–phenotype annotations. We aim to support the discovery of literature-based phenotypes and integrate them into the knowledge discovery process. Results PheneBank is a Web-portal for retrieving human phenotype–disease associations that have been text-mined from the whole of Medline. Our approach exploits state-of-the-art machine learning for concept identification by utilizing an expert annotated rare disease corpus from the PMC Text Mining subset. Evaluation of the system for entities is conducted on a gold-standard corpus of rare disease sentences and for associations against the Monarch initiative data. Availability and implementation The PheneBank Web-portal freely available at http://www.phenebank.org. Annotated Medline data is available from Zenodo at DOI: 10.5281/zenodo.1408800. Semantic annotation software is freely available for non-commercial use at GitHub: https://github.com/pilehvar/phenebank. Supplementary information Supplementary data are available at Bioinformatics online.
- **Editor:** England: Oxford University Press
- **Idioma:** Inglês

- **Identificador:** ISSN: 1367-4803; EISSN: 1460-2059; EISSN: 1367-4811; DOI: 10.1093/bioinformatics/btab740; PMID: 34788791
- **Fonte:** PubMed; PubMed Central; Alma/SFX Local Collection

Semantic composition of optimal process service plans in manufacturing with ODERU

- **Autor:** Mazzola, Luca ; Kapahnke, Patrick ; Klusch, Matthias
- **Assuntos:** Annotations ; Automation ; Automobile industry ; Automotive engineering ; Business process engineering ; Business process reengineering ; Cloud computing ; Coding ; Composition ; Cost analysis ; Human error ; Industrial applications ; Manufacturing ; Multiple objective analysis ; Ontology ; Optimization ; Problem solving ; Semantic web ; Semantics ; Value engineering
- **É parte de:** International journal of Web information systems, 2018, Vol.14 (4), p.495-523
- **Descrição:** Purpose The need to flexibly react to changing demands and to cost-efficiently manage customized production even for lot size of one requires a dynamic and holistic integration of service-based processes within and across enterprises of the value chain. In this context, this paper aims at presenting ODERU, the authors' novel pragmatic approach for automatically implementing service-based manufacturing processes at design and runtime within a cloud-based elastic manufacturing platform. Design/methodology/approach ODERU relies on a set of semantic annotations of business process models encoded into an extension of the business process model and notation (BPMN) 2.0 standard. Leveraging the paradigms of semantic SOA and XaaS, ODERU integrates pattern-based semantic composition of process service plans with QoS-based optimization based on multi-objective constraint optimization problem solving. Findings The successful validation of ODERU in two industrial use cases for maintenance process optimization and automotive production in the European project CREMA revealed its usefulness for service-based process optimization in general and for significant cost reductions in maintenance in particular. Originality/value ODERU provides a pragmatic and flexible solution to optimal service composition with the following three main advantages: full integration of semantic service selection and composition with QoS-based optimization; executability of the generated optimal process service plans by an execution environment as they include service assignments, data flow (variable bindings) and optimal variable assignments; and support of fast replanning in a single model and plan.
- **Editor:** Bingley: Emerald Group Publishing Limited
- **Idioma:** Inglês
- **Identificador:** ISSN: 1744-0084; EISSN: 1744-0092; DOI: 10.1108/IJWIS-05-2018-0038
- **Fonte:** Emerald

Exploiting tourism destinations' knowledge in an RDF-based P2P network

- **Autor:** Kanellopoulos, Dimitris N. ; Panagopoulos, Alkiviadis A.
- **Assuntos:** Adaptability ; Applied sciences ; Coding, codes ; Computer Science ; Computer Science, Hardware & Architecture ; Computer Science, Interdisciplinary Applications ; Computer Science, Software Engineering ; Design ; Destination Management Systems ; Distributed RDF repositories ; Documentation ; Exact sciences and technology ; Information, signal and communications theory ; Interconnected networks ; Management ; Networks and services in france and abroad ; Organization and planning of networks (techniques and equipments) ; P2P ; Peer to peer computing ; Science & Technology ; Semantic Web ; Signal and communications theory ; Standardization ; Systems, networks and services of telecommunications ; Technology ; Telecommunications ; Telecommunications and information theory ; Teleprocessing networks. Isdn ; Travel industry ; Valuation and optimization of characteristics. Simulation
- **É parte de:** Journal of network and computer applications, 2008, Vol.31 (2), p.179-200
- **Descrição:** Destination Management Systems (DMS) is a perfect application area for Semantic Web and P2P technologies since tourism information dissemination and exchange are the key-backbones of tourism destination management. DMS should take advantage of P2P technologies and semantic web services, interoperability, ontologies and semantic annotation. RDF-based P2P networks allow complex and extendable descriptions of resources instead of fixed and limited ones, and they provide

query facilities against these metadata instead of simple keyword-based searches. The layered adaptive semantic-based DMS (LA_DMS) and Peer-to-Peer (P2P) project aims at providing semantic-based tourism destination information by combining the P2P paradigm with Semantic Web technologies. In this paper, we propose a metadata model encoding semantic tourism destination information in an RDF-based P2P network architecture. The model combines ontological structures with information for tourism destinations and peers.

- **Editor:** LONDON: Elsevier Ltd
- **Idioma:** Inglês
- **Identificador:** ISSN: 1084-8045; EISSN: 1095-8592; DOI: 10.1016/j.jnca.2006.03.003
- **Fonte:** Web of Science - Science Citation Index Expanded - 2008 from WEB OF SCIENCE™; Elsevier ScienceDirect Journals

The Core Ontology for Multimedia

- **Autor:** Franz, Thomas ; Troncy, Raphaël ; Vacura, Miroslav
- **Autor:** Schenk, Simon ; Troncy, Raphael ; Huet, Benoit ; Troncy, Raphaël ; Schenk, Simon ; Huet, Benoit
- **Assuntos:** core ontology for multimedia (COMM) ; DOLCE ontology ; MPEG-7
- **É parte de:** Multimedia Semantics, 2011, p.145-161
- **Editor:** Chichester, UK: Wiley
- **Idioma:** Inglês
- **Identificador:** ISBN: 0470747005; ISBN: 9780470747001; EISBN: 1444341561; EISBN: 1119970237; EISBN: 9781444341560; EISBN: 9781119970231; DOI: 10.1002/9781119970231.ch9
- **Fonte:** Wiley-Blackwell Online Books - All Titles (includes Withdrawn titles)

2327: Prescription opioid dependence in Western New York: Using data analytics to find an answer to the opioid epidemic

- **Autor:** Sinha, Shyamashree ; Burstein, Gale ; Leonard, Kenneth E. ; Murphy, Timothy ; Elkin, Peter
- **Assuntos:** Addictions ; Age groups ; Biomedical Informatics ; Buprenorphine ; Data processing ; Drug abuse ; Drug overdose ; Epidemiology ; Ethnicity ; Health Informatics ; Heroin ; Hispanic Americans ; Informatics ; Language ; Methadone ; Minority & ethnic groups ; Naloxone ; Narcotics ; Natural language processing ; Ontology ; Opioids ; Overdose ; Pain ; Patients ; Phenotyping ; Population studies ; Semantics
- **É parte de:** Journal of clinical and translational science, 2017, Vol.1 (S1), p.15-15
- **Descrição:** OBJECTIVES/SPECIFIC AIMS: Dependence and abuse of prescription opioid pain medication has substantially increased over the last decade. The consistent rise in opioid dependence contributes to the rising prescription drug overdose deaths over the last decade. The study of the distribution and determinants of opioid dependence among patients who are treated with chronic pain medications prescribed by their healthcare providers would aid in answering some key questions about potential abuse and overdose on opioids. The descriptive epidemiology of opioid dependence would help in identifying the vulnerable age group, race, ethnicity, and type of opioid pain medications that more commonly result in dependence. METHODS/STUDY POPULATION: We implemented an Observational Medical Outcomes Partnership/Observational Health Data Sciences and Informatics (OMOP/OHDSI) database, to hold structured EHR data from our Allscripts patient records. We also created a high-throughput phenotyping, natural language processing system that can parse 7,000,000 clinical notes in 1.5 hours. This runs as a web service and provides a modular component based NLP system. After the full semantic parse, we match the content against any number of ontologies. For each match we tag it as either a positive, negative, or uncertain assertion. We then perform automated compositional expressions. The codes are stored in a Berkley database (BDB) NOSQL database and the compositional expressions are stored in Neo4J (a graph database) and Graph DB (a triple store). This flexibility allows rapid retrieval of complex questions in real time. The High-Throughput Phenotyping (HTP) Natural Language Processing (NLP) Subsystem (HTP-NLP) is software that produces, given biomedical text, semantic annotations of the text. The semantic annotations identify

conceptual entities—their attributes, the relations they have with other entities and the events they participate in, as expressed in the input text. The conceptual entities, relations, attributes, and events identified are specified by various knowledge representations (KRs) as documented in Coding Sources. Examples of coding sources are medical terminologies [eg, SNOMED CT, RxNorm, LOINC and open biomedical ontologies (OBO) foundry ontologies, eg, gene ontology (GO), functional model of anatomy, OBI, and others]. The annotation results may be displayed or output in formats suitable for further processing. Entity identified is assigned a truth value from 0 to 1. Values from the text are assigned to entities from ontologies such as SNOMED CT. The retrospective analysis of EHR data from local clinic patients was performed using queries on the problem list, demographic data, and medication list of all the patients in the database. The OMOP/OHDSI database was collected from Allscripts EHRs from 2010 to 2015. This common data model helps in the systematic analysis of disparate observational databases of clinic records from the primary care and family medicine clinics in Western New York region. The database contained 212,343 patient records that were parsed and deidentified. Specific research IDs were assigned to each of the patient records and stored in a secure firewall device for data analytics. The entire 212,343 records were queried for opioid dependence from the ICD-9 and 10 diagnostic codes and SNOMED CT codes mapped to both the clinical notes and the problem list for each patient based on the mapped ICD and SNOMED CT codes. In total, 1356 patients were identified as to having opioid dependence. The records were stratified into 7 age groups from age 18 to 28 and ending with age 79–89 years. RESULTS/ANTICIPATED RESULTS: Of the 212,343 patients in the database 1356 patients revealed opioid dependence on the problem list, ICD9-10 codes and prescription opioid pain medication with or without Buprenorphine and Naloxone (Suboxone) in the medication list. The prevalence of opioid dependence in the clinic population was 0.64% (95% CI: 0.61%–0.67%) over a 5-year period. The 7,000,000 patient records generated 750,000,000 SNOMED CT codes (on average 107 codes per record). The highest numbers of opioid dependence were seen in the 29 to 38 years' age group. That comprised 39.38% (95% CI: 36.78%–41.98%) of the total opioid dependent population but accounted for only 2.03% of whole clinic population in this age group (95% CI: 1.86% to 2.2%). The subjects were then stratified by race and ethnicity. There were 1005 patients with opioid dependence, in the non-Hispanic population (total number 108,402). Among the White non-Hispanic or Latino population with opioid dependence, 41.33% (95% CI: 38.27%–44.39%) were 29–38 years old. The next common age group among the White Non-Hispanic opioid dependent subjects was 19–28 years, comprising of 22.48% (95% CI: 19.88%–25.08%) of the total number of White non-Hispanic or Latino opioid dependent population. Among the total clinic population Hispanics comprise 51.24%, but they comprise only 2.58% (95% CI: 1.74%–3.42%) of the total opioid dependent population. The non-Hispanic population comprise 51.05% of total clinic population while the percent of people who are opioid dependent is 83.26% (95% CI: 83.04%–83.48%) of the total 1356 opioid dependent population.
DISCUSSION/SIGNIFICANCE OF IMPACT: The trends of opioid dependence among the clinic population in the study indicate that the prevalence is more in a certain section of the population. The predominance is among the non-Hispanic White population in the 19–38 years of age. The prevalence in younger age implies that the complications related to opioid dependence would be there for a longer duration of time. The prevalence of dependence in this clinic population would be rising if this trend continues. Interventions at curbing prescription opioid dependence is necessary for the vulnerable population. The findings suggest that a broad based approach is necessary to address this problem. The distribution of opioid dependence in this patient population indicate the need for special attention to these specific age group and race ethnicities. The young age of many of the addicted patients demonstrate the risks of legitimate opioid prescriptions in leading this age group towards addiction and implies the need for routine screening for substance abuse. The evidence of complications of opioid overdose among long-term opioid users and risk of abuse with other agents including illicit agents makes the need for an approach that uses real-time interventions in addition to effect long-term improvement in addiction rates. A potentially cost-effective approach to implement monitoring programs and clinical decision support tools would be to develop inter operable linkage from the EHRs to the state Department of Healths' prescription monitoring programs.

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[A semantic approach to approximate service retrieval]

- **Autor:** Toch, Eran ; Gal, Avigdor ; Reinhartz-Berger, Iris ; Dori, Dov
- **Assuntos:** Computer Science ; Computer Science, Information Systems ; Computer Science, Software Engineering ; ontology ; Science & Technology ; semantic web ; service retrieval ; Technology ; Web service
- **É parte de:** ACM transactions on Internet technology, 2007, Vol.8 (1), p.2-es
- **Descrição:** Web service discovery is one of the main applications of semantic Web services, which extend standard Web services with semantic annotations. Current discovery solutions were developed in the context of automatic service composition. Thus, the "client" of the discovery procedure is an automated computer program rather than a human, with little, if any, tolerance to inexact results. However, in the real world, services which might be semantically distanced from each other are glued together using manual coding. In this article, we propose a new retrieval model for semantic Web services, with the objective of simplifying service discovery for human users. The model relies on simple and extensible keyword-based query language and enables efficient retrieval of approximate results, including approximate service compositions. Since representing all possible compositions and all approximate concept references can result in an exponentially-sized index, we investigate clustering methods to provide a scalable mechanism for service indexing. Results of experiments, designed to evaluate our indexing and query methods, show that satisfactory approximate search is feasible with efficient processing time.
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- **Fonte:** Web of Science - Science Citation Index Expanded - 2008 from WEB OF SCIENCE; ACM Digital Library Complete

[PheneBank: a literature-based database of phenotypes]

- **Autor:** Pilehvar, Mohammad Taher ; Bernard, Adam ; Smedley, Damian ; Collier, Nigel
- **Assuntos:** Algorithms ; Data Mining ; Humans ; Phenotype ; Rare Diseases ; Software
- **Descrição:** MOTIVATION: Significant effort has been spent by curators to create coding systems for phenotypes such as the Human Phenotype Ontology, as well as disease-phenotype annotations. We aim to support the discovery of literature-based phenotypes and integrate them into the knowledge discovery process. RESULTS: PheneBank is a Web-portal for retrieving human phenotype-disease associations that have been text-mined from the whole of Medline. Our approach exploits state-of-the-art machine learning for concept identification by utilizing an expert annotated rare disease corpus from the PMC Text Mining subset. Evaluation of the system for entities is conducted on a gold-standard corpus of rare disease sentences and for associations against the Monarch initiative data. AVAILABILITY AND IMPLEMENTATION: The PheneBank Web-portal freely available at http://www.phenebank.org. Annotated Medline data is available from Zenodo at DOI: 10.5281/zenodo.1408800. Semantic annotation software is freely available for non-commercial use at GitHub: https://github.com/pilehvar/phenebank. SUPPLEMENTARY INFORMATION: Supplementary data are available at Bioinformatics online. Medical Research Council (grant MR/M025160/1).
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[2327]

- **Autor:** Shyamashree Sinha ; Gale Burstein ; Kenneth E. Leonard ; Timothy Murphy ; Peter Elkin
- **É parte de:** Journal of clinical and translational science, 2018, Vol.1, p.15-15
- **Descrição:** OBJECTIVES/SPECIFIC AIMS: Dependence and abuse of prescription opioid pain medication has substantially increased over the last decade. The consistent rise in opioid dependence contributes to the rising prescription drug overdose deaths over the last decade. The study of the distribution and determinants of opioid dependence among patients who are treated with chronic pain medications prescribed by their healthcare providers would aid in answering some key questions about potential abuse and overdose on opioids. The descriptive epidemiology of opioid dependence would help in identifying the vulnerable age group, race, ethnicity, and type of opioid pain medications that more commonly result in dependence. METHODS/STUDY POPULATION: We implemented an Observational Medical Outcomes Partnership/Observational Health Data Sciences and Informatics (OMOP/OHDSI) database, to hold structured EHR data from our Allscripts patient records. 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