Semantic Web 0 (2013) 1–0
IOS Press

Using the relation ontology Metarel for modelling Linked Data as multi-digraphs

Editor(s): Mikel Egaña Aranguren, Technical University of Madrid (UPM), Spain; Michel Dumontier, Carleton University, Ottawa, Canada; Jesualdo Tomás Fernández Breis, University of Murcia (UM), Spain
Solicited review(s): Carlos Aranda, Pontificia Universidad Católica de Chile; Matt-Mouley Bouamrane, University of Glasgow, Scotland; one anonymous reviewer

Ward Blondé [a,c,*], Erick Antezana [b], Vladimir Mironov [b], Stefan Schulz [c], Martin Kuiper [b] and Bernard De Baets [a]

[a] *Department of Mathematical Modelling, Statistics and Bioinformatics, Ghent University, Coupure links 653, 9000 Gent, Belgium, Europe.*
E-mail: {ward.blonde,bernard.debaets}@ugent.be
[b] *Department of Biology, Norwegian University of Science and Technology, Realfagbygget DU1-111, Høgskoleringen 5, Trondheim, Norway, Europe.*
E-mail: {erick.antezana,vladimir.mironov,martin.kuiper}@bio.ntnu.no
[c] *Institute for Medical Informatics, Statistics and Documentation, Medical University of Graz, Auenbruggerplatz 2, 8036 Graz, Austria, Europe.*
E-mail: {ward.blonde,stefan.schulz}@medunigraz.at

Abstract.

The Semantic Web standards OWL and RDF are often used to represent biomedical information as Linked Data, however, the OWL/RDF syntax, which combines both, was never optimised for querying. By combining two formal paradigms for modelling Linked Data, namely multi-digraphs and Description Logic, many precise terms for relations have emerged that are defined in the Metarel relation ontology. They are especially useful in Linked Data and RDF knowledge bases that 1) rely on SPARQL querying and 2) require semantic support for chains of relations.

Metarel-described multi-digraphs were used for knowledge integration and reasoning in three RDF knowledge bases in the domain of genome biology: BioGateway, Cell Cycle Ontology and Gene Expression Knowledge Base. These knowledge bases integrate both data, like Kegg, and ontologies, like Gene Ontology, in the same RDF graphs. Their libraries with biomedically relevant SPARQL queries show the practical benefits of this semantic paradigm. In addition to the management of RDF stores, this paper describes how Metarel can be used for remodelling Linked Data as SPARQL-friendly and semantically rich multi-digraphs. Metarel can be downloaded from http://www.semantic-systems-biology.org/metarel.

Keywords: Linked Data, RDF, relations, Description Logics, SPARQL, rules

1. Introduction

Hosted by the Semantic Systems Biology (SSB) platform, Metarel is an ontology for class-level relations on the Semantic Web, that matured over the last five years [1]. Its support for direct relations between classes has successfully complemented the Web Ontology Language (OWL) [2], which uses relations between individuals at the level of its syntactic representation in the Resource Description Framework (RDF) [3].

Three integrated RDF knowledge bases, BioGateway [4], Cell Cycle Ontology (CCO) [5] and Gene

---

[*] Corresponding author. E-mail: ward.blonde@ugent.be.

Expression Knowledge Base (GeXKB) [6], have used Metarel for integration and reasoning. Their resulting RDF model is a multi-digraph (MDG), which has appeared to be very manageable and intuitive for writing and executing biomedically relevant queries in the SPARQL Protocol and RDF Query Language (SPARQL) [7,8].

The rising popularity of the Linked Data paradigm urges to broaden the scope of Metarel as a bridge between semantically rich knowledge in OWL, and semantically poor triples that were published in various manners on the Web. Two new use cases are described in this paper: the translation of the OWL/RDF syntax towards MDGs and the semantic enrichment of Linked Data through annotations with Metarel's vocabulary. They complement the use case of managing RDF stores through Metarel-described MDGs.

After an overview of the scientific background of Linked Data and the Semantic Web in Section 2, Metarel's three use cases are explained in Section 3. The theoretical basis of Metarel, including its relation to the currently standardised vocabulary of the Semantic Web, is given in Section 4. After that, in Section 5, the practical work of integrating resources from the genomic domain as Linked Data through Metarel is summarised. Sections 6 and 7 contain a discussion and the conclusions.

2. Background

After the World Wide Web and the Semantic Web, the paradigm of Linked Data is the latest concept created by Tim Berners-Lee [9,10]. By the use of the HyperText Transfer Protocol (HTTP), Internationalised Resource Identifiers (IRI) and RDF, Linked Data is a further extension of the Semantic Web. The emphasis on browsability and HTTP links is an attempt to upgrade the Semantic Web from a series of separate RDF boxes to a cross-linked web that integrates with any type of data.

RDF and its standard query language SPARQL are central technologies for the Semantic Web that connect IRIs in a set of triples. Linked Data is data that is formatted in RDF for which the IRIs are dereferenceable through HTTP by web browsers and query services, which means that a representation can be retrieved for the IRI. Hence, Linked Data effectively integrates two types of resource retrieval: the first over the classical untyped web links through HTTP, and the second over typed links in the form of RDF triples through SPARQL. Linked Data graphs are called browsable if the lookup of any IRI node retrieves a recursive description of the node. This is done by returning all the triples in which the node is a subject or an object and by describing also all the blank nodes that are retrieved. An update language called SPARQL 1.1 Update (SPARUL) [11], that can be used for modifying Linked Data through inferences from queries, is in the process of becoming a W3C recommendation.

The advantages of Linked Data for the management of large amounts of information and data have been acknowledged by the biomedical community [12]. The Health Care and Life Science Interest Group of the W3C (HCLS IG) has facilitated the research on RDF and Linked Data through the development and integration of large-scale biomedical knowledge bases that are accessible through SPARQL endpoints. Such web resources, like Bio2RDF [13], OBO Foundry ontologies [14], DrugBank [15] and many others, are often interconnected and constitute a substantial part of W3C's Linking Open Data (LOD) project cloud [16]. SPARQL, the query language of RDF, can be used to query links within the LOD cloud, thereby integrating answers from large biomedical resources with more popular resources like DBpedia [17] and W3C wordnet [18].

Many of the largest biomedical data resources are to be found in the genomic domain. UniProtKB [19] is a high-quality database about proteins, which is maintained by the UniProt Consortium. Their system for uniquely identifying types of proteins and genes through IRIs has been the basis for more specialised data resources. The Gene Ontology Annotations (GOA) [20] connect UniProt-identified protein types to classes of functions, biological processes and cellular locations in the Gene Ontology (GO) [21]. Enzymatic pathways, which elucidate how series of protein interactions are coordinated into the realisation of biological functions, are described in the Kyoto Encyclopedia of Genes and Genomes (KEGG) [22]. Some databases annotate genomic knowledge from well-studied organisms, like NCBI Gene ID [23], or from literature, like IntAct [24] for molecular interactions. All these large genomic databases are part of the LOD cloud.

GO is one of the few OBO ontologies that was accepted by OBO's review panel. Also the PRotein Ontology (PRO) [25], Chemical entities of biological entities (CHEBI) [26] as well as three other ontologies, have reached this status. Many other interesting ontologies, both OBO and OWL formatted, are

OBO candidates, like the Sequence Ontology [27] or OBO ontologies of interest, like the NCBI organismal classification (NCBITaxon) [23]. All the OBO ontologies together form a great body of knowledge and can be used for annotating biomedical data. The OBO Foundry provides a uniform method for identifying ontology classes through IRIs that start with http://purl.obolibrary.org/obo, an OWL/RDF export and a SPARQL endpoint in the Ontobee [28] system.

The semantics of links, as (chains of) RDF triples between RDF resources, can be described with the language constructs of W3C's standards OWL and RDF(S) [29]. According to their language specifications two different semantic contexts are distinguished. The first is *Direct Semantics* (DS) [30], which suits Description Logic (DL) [31] based dialects of OWL, such as OWL DL and OWL EL [32]. This semantics subscribes to the set-theoretical DL semantics and assumes a strict distinction between individuals (also called instances) and classes, (*e.g.* those referred to by proper names in natural language, such as Belgium, the year 2012, Tim Berners-Lee) and classes (referred to by general nouns like country, year, human). The second semantic context, called *RDF-Based Semantics* (RBS) [33], supports Linked Data that is represented in OWL Full or RDF(S). Here the same symbol may be used for denoting an individual or class (or it is just left open whether something is an individual or a class). On the one hand this allows more flexibility, whereas it precludes, on the other hand, a solid semantic foundation such as given by DL, and a clear ontological commitment as advocated by the Applied Ontology community. As a consequence, the truth value of logical expressions in OWL Full or RDF(S) cannot be unambiguously decided. To cite an example: The OWL full expression *Mitochondrium hasPart Membrane* does not make clear whether all mitochondria have membranes, or whether all membranes are parts of mitochondria. In contrast, the OWL DL axiom *Mitochondrium subClassOf hasPart some Membrane* clearly states that each individual mitochondrium has some membrane as part.

DLs are decidable fragments of First Order Logic (FOL) and have become increasingly adopted as the foundation of life sciences and healthcare related ontologies [34]. Terminologies like SNOMED CT [35], OpenGalen [36] and many OBO ontologies have been engineered or converted into OWL dialects. There has been a clear preference for the less expressive variant OWL EL due to its polynomial time reasoning performance [37,38].

An important restriction of Direct Semantics is its dependence on description logics syntax and semantics, which allows only individual-level relations (so called object properties), apart from the operators *SubClassOf* and *EquivalentTo*, which relate two classes, and *Type*, which relates an individual with a class it is member of. To use an object property in a DL axiom at the class level requires the use of quantifiers like 'some' and 'all'. In spite of its *Direct* Semantics, relations between classes in OWL profiles are *indirect* when expressed in the standard Semantic Web syntax OWL/RDF. The relation ontology Metarel, which is described in this paper provides a means to clarify the meaning of direct relation arcs in the form of a single RDF triple. In the above example this means that *Mitochondrium hasPart Membrane* is further specified as hasPart_all-some, in order to express the same meaning as in *Mitochondrium subClassOf hasPart some Membrane*.

The description of links in graphs was explored in so-called 'semantic networks' in the decades preceding the development of DL in the nineties [39,40]. Semantic problems with such networks were discussed by Woods in [41]. The research on semantic networks has evolved into two directions; the axiom-based DL on the one hand and the graph-based RDF on the other. RDF(S) provides some notions derived from DL, like *rdfs:Class*, *rdf:type*, *rdfs:domain* and *rdfs:range*, for annotating RDF data. However, it is not based on individuals but on *rdf:resource*, which may be both individual or class. Because of this, it has not overcome the problems reported by Woods. Metarel is similar in scope as RDF(S), but seeks maximal compatibility with DL.

3. Metarel's use cases

There are several ways in which Metarel can facilitate the publishing of Linked Data, and the management of Linked Data through SPARQL and SPARUL. Three use cases are explained here:

- the representation of SPARQL-friendly knowledge expressions that are translations of the standard OWL/RDF syntax,
- the semantic enrichment of existing Linked Data, and
- the semi-automated management of RDF stores that use Metarel.

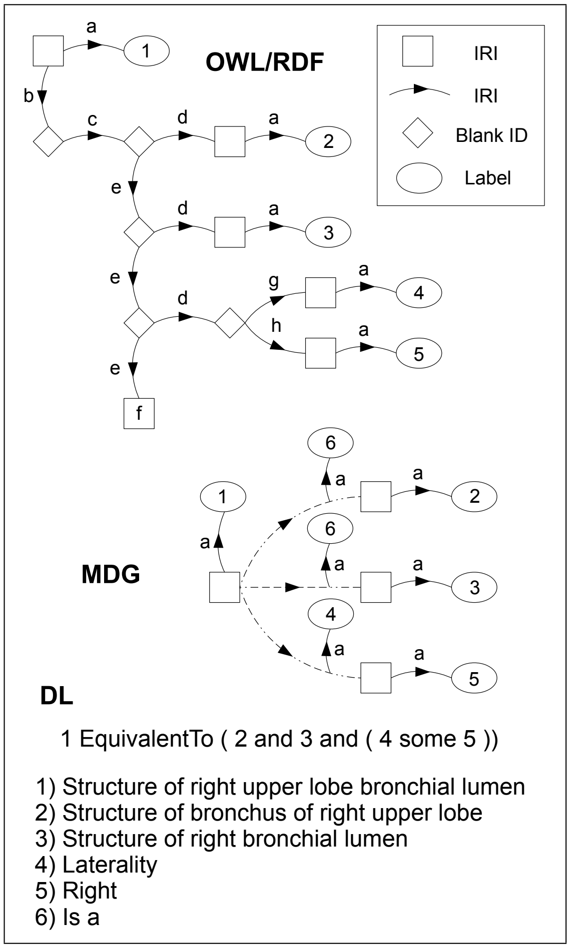

Fig. 1. A fully defined class in SNOMED CT, expressed in OWL/RDF (top) and an MDG (bottom). Standardised IRIs that are used represent label (a), equivalent class (b), intersection of (c), first (d), rest (e), nil (f), on property (g) and some values from (h). Empty boxes are numerical identifiers. The dashed IRIs in the MDG model can be described with Metarel in order to facilitate support for inferences from inverses, transitivity, chains and super-relations.

3.1. Use case 1: converting OWL/RDF to MDGs

The OWL/RDF syntax was engineered as a communication format that represents OWL faithfully and that can easily be serialised. However, its modelling constructs make it hard, both programmatically and computationally, to query OWL/RDF through SPARQL. This is where Metarel comes to aid. Through extra language constructs in Metarel, large parts of OWL can be extracted into an MDG, which is a SPARQL-friendly section of RDF that is also suited for visualisation [42].

SPARQL has become one of the most used technologies of the Semantic Web. A SPARQL-friendly format is therefore very desirable. The MDG format proposed here is very suited for querying in SPARQL, because it prefers direct links instead of chains of blank nodes. Only a few triples are required in a query pattern about terms T1 and T2. The following query pattern describes the relation between T1 and T2 in both directions:

```
{T1 ?p1 T2.
?p1 rdfs:label ?pred1.}
UNION
{T2 ?p2 T1.
?p2 rdfs:label ?pred2.}
```

Generic queries of this type over graphs in the OWL/RDF syntax cannot be created with SPARQL. For example, classes that are defined through a set of many different necessary and sufficient conditions, will have a long chain of blank nodes between the node for the class and nodes for terms that appear in the conditions (see Figure 1). This chain has often side chains of different types and sizes for each condition. Such RDF-expressed class definitions correspond to many different patterns of chains, a bit similar to molecules in organic chemistry. The exploration of the chains should therefore happen through programming languages like Java in combination with SPARQL.

Whereas browsing OWL/RDF could still be achieved with a combination of SPARQL and Java, normal querying through SPARQL cannot be done. This can be understood by considering the two models represented in Figure 1 in more detail. Imagine a health care specialist who wants to investigate the occurrence of injuries on the right side of the body, versus the left side. Her count for the number of right-sided injuries could happen on the MDG model with a SPARQL pattern of about three lines:

```
?Injury rdf:type Injury.
?Injury findingSite ?AnatomicalStructure.
?AnatomicalStructure laterality Right.
```

The same approach cannot be followed in OWL/RDF, because there are no direct links between anatomical structures and their laterality, nor any fixed chains of links with a standardised structure.

3.2. Use case 2: semantically enriching Linked Data

Metarel can be used to annotate Linked Data that does not distinguish individuals from classes in a consequent manner. First of all, Metarel assumes the presence of an MDG, as depicted in Figure 2. Consider

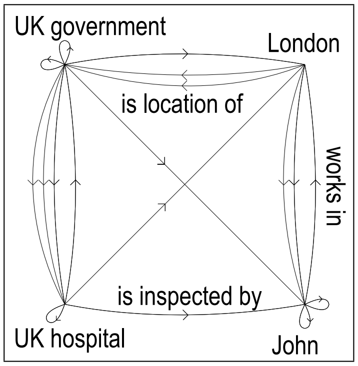

Fig. 2. An MDG about people, cities and UK institutes. Three of the four nodes represent individuals. UK hospital, however, refers to the class of all the hospitals in the UK.

three IRI spaces prefixed by pref1 to pref3. The following three triples form a little part of the MDG in this figure:

```
pref1:John pref1:worksIn pref2:London.
pref3:UKHosp pref3:inspecBy pref1:John.
pref2:London pref3:isLocationOf pref3:UKGov.
```

The IRIs used in the triples are supposed to have labels, in triples like *pref1:John rdfs:label 'John'*. The combination of the MDG with the labels is highly browsable with SPARQL. When this Linked Data was crawled and assembled in an RDF graph called `http://crawled_LOD_MDG`, then the following simple SPARQL query, containing only two triple patterns, is all that is required for describing a node as specified by Berners-Lee in [10]:

```
PREFIX pref1:<http://people_space1/>
SELECT *
WHERE {
  GRAPH <http://crawled_LOD_MDG> {
     {pref1:John ?p1 ?o.}
     UNION
     {?s ?p2 pref1:John.}
 }
}
```

Such MDGs may not always have a strong ontological commitment. In order to improve the semantics of the MDG for consistency checking and reasoning, every IRI for a node should be defined as either an individual or a class:

```
pref1:John   rdf:type owl:Thing.
pref2:London rdf:type owl:Thing.
pref3:UKGov  rdf:type owl:Thing.
pref3:UKHosp rdf:type owl:Class.
```

The distinction between individuals and classes is important information for the creation of consistent ontologies, and it can be the basis for a further conversion to OWL. However, relations that are used between classes or between individuals and classes, like pref3:inspecBy, do not have a straightforward interpretation with respect to algebraic properties like transitivity and inverse. A clearer interpretation exists for relations between individuals, on the basis of which most relations between classes can be defined [14]. Only pref1:worksIn and pref3:isLocationOf can be interpreted as such in Figure 2. For pref3:inspecBy a new IRI is needed, for example in an IRI space pref4. The Metarel vocabulary can be used to connect the original IRI with the new IRI:

```
pref4:inspecBy rdf:type owl:ObjectProperty.
pref3:inspecBy mrl:isBasedOn pref4:inspecBy.
pref3:inspecBy rdf:type mrl:AllSomeRelation.
```

When the graph `http://crawled_LOD_MDG` is used as a merger to contain all these triples, a valid representation in DL-based OWL dialects can easily be created with SPARUL rules. The following rule translates arcs of relations that hold from an individual to a class, into OWL DL:

```
PREFIX rdf:<http://www.w3.org/1999/02/22-rdf-
syntax-ns#>
PREFIX owl:<http://www.w3.org/2002/07/owl#>
PREFIX mrl:<http://www.metarel.org/>
INSERT INTO GRAPH <http://crawled_OWL_DL> {
    ?individual ?obj_property  _:bnode.
    _:bnode     rdf:type       ?class.
}
WHERE {
 GRAPH <http://crawled_LOD_MDG> {
    ?individual ?pred          ?class.
    ?individual rdf:type       owl:Thing.
    ?class      rdf:type       owl:Class.
    ?pred       rdf:type mrl:AllSomeRelation.
    ?pred       mrl:isBasedOn  ?obj_property.
 }
}
```

Whereas the LOD_MDG graph in this example can be used for SPARQL querying, the OWL_DL graph can be used for consistency checking and fully automated reasoning.

3.3. Use case 3: managing RDF stores

Metarel has an RDF format, *metarel.rdf*, which can be loaded into RDF stores. The whole architecture for the usage of Metarel can be seen in Figure 3. Relations that are used in Linked Data have to be annotated with terms in Metarel, in order to enable the inferencing of

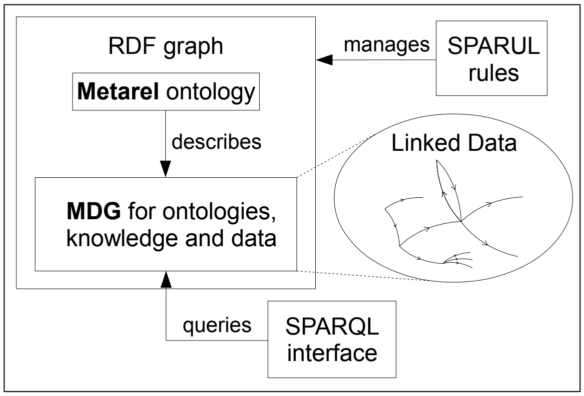

Fig. 3. By merging Linked Data, *metarel.rdf* and annotated relations in a single RDF graph, SPARUL rules can infer direct links as RDF triples that can be queried through SPARQL.

new, direct links that support SPARQL queries. The rules for creating such inferences have to be specified in SPARUL, which works natively on RDF.

The set of triples in *metarel.rdf* plus a set of triples that are annotations of relations with IRIs in *metarel.rdf*, is called a Metarel ontology. The SPARUL update queries will operate over a merger of the Metarel ontology and MDG-modelled Linked Data. SPARQL queries that support a user interface will typically only address the latter.

4. Metarel's theoretical basis

4.1. MDGs in RDF

Metarel supports the RDF model in the form of multi-digraphs (MDG), where the terms are represented as nodes and the predicates between the terms as arcs (See Figure 2). Digraphs are graphs with directed arcs, whereas MDGs also allow multiple arcs between two nodes. MDGs have similarities with RDF graphs, such as nodes and arrows between the nodes, however, for the ensuing explanation, it is important to know that every MDG can be expressed as an RDF graph, but not every RDF graph is an MDG. Indeed, an RDF predicate can also be used as a subject or an object in an RDF triple, which is not allowed in MDGs.

The vocabulary in Metarel is based on relations, which have relation couples as instances. A relation couple is something that holds between two terms. Each instantiation of a relation by a relation couple is represented by a directed relation arc. In RDF as MDG, every relation arc corresponds to an RDF triple by using the two terms of the relation couple as subject and object in the triple, and by using the relation as predicate. Different RDF triples with different predicates for describing the same relation couple are allowed, as long as each separated triple provides a meaningful description by itself. Typed links, as defined by Berners-Lee in [9], correspond to relation arcs.

(S,P,O)	M:	relation arc
	R:	triple
	L:	typed link
P	M:	relation
	R:	predicate
	O:	property
	A:	relation
(S,O)	M:	relation couple
	A:	couple

Table 1

The terminology in Metarel (M) compared with terminology in RDF (R), OWL (O), Linked Data (L) and algebra (A). They are compared on the basis of a generic Subject-Predicate-Object structure, as used in RDF.

'Relation' in Metarel corresponds to 'predicate' in RDF, 'property' in OWL Full, and simply 'relation' in algebra. In the context of Metarel, relations are binary. An overview of the terminology can be seen in Table 1.

The formal aspects of RDF and MDGs can be combined with Metarel as follows:

- **RDF:** Graphs consist of a set of triples that give an order to three RDF terms. The first, called subject term, can be an IRI or a blank node, the second, called predicate term, is an IRI and the third, called object term, is an IRI, a blank node or a literal. The rdfs-label, *e.g.* 'nucleus', of a subject term as IRI, *e.g.* 'obo:GO_0005634', is expressed as a literal in the object term that is combined through 'rdfs:label' in the predicate term.
- **MDG:** Graphs are labelled, directed multigraphs that allow multiple self-loops. Both the nodes and arcs carry labels, but the label for each node should be unique within the MDG.

Metarel describes $\mathcal{M}$-graphs, which are Linked Data graphs that have the following properties:

- $\mathcal{M}$ has the structure of an MDG. The MDG nodes are ontology terms that are either individuals or classes, and they correspond to subject and object nodes of RDF triples. IRIs appear as MDG labels.
- An RDF triple in $\mathcal{M}$ corresponds to a directed arc in the MDG.

- A relation couple between two ontology terms S and O is unique and directed. The terms are related by exactly one multi-arc which is the aggregation of all directed arcs that have S as subject node and O as object node in $\mathcal{M}$. This multi-arc provides a description of the relation couple.
- Relation couples that bear semantic and/or logical similarities instantiate the same relation. *E.g.* the relation couple between John's heart and John's body shares the property of parthood with the relation couple between Austria and Europe. Both instantiate a relation 'is part of' , which is identified by an IRI.
- The typing of a relation couple between S and O, by a relation R, is expressed by a single RDF triple $S\ R\ O$ in $\mathcal{M}$. If S and/or O is a class, then the logical meaning of R may express a FOL quantification over arcs between instances of S and O. The classification of relations by their quantification method happens in a Metarel ontology outside $\mathcal{M}$.
- Relations have properties like reflexivity, transitivity, symmetry, super-, sub-, chained and inverse relations. These properties are also described in a Metarel ontology outside $\mathcal{M}$.

4.2. Metarel's ontological vocabulary

For describing $\mathcal{M}$-graphs, Metarel uses an ontological vocabulary that has the above-described notion of relation as a basis. This vocabulary can be used in inference systems and rule systems, like a library of SPARUL queries, which manipulate $\mathcal{M}$-graphs. Some language constructs that equate with constructs in OWL are not recommended to be used. They are introduced for clarity and for comparison with OWL in the next section.

The aim of Metarel's ontological vocabulary is to describe relations, like 'all are part of some', 'is integral part of', 'some are located in some' or 'contains at all times'. This description provides a semantics for the relations in terms of which other relations can be inferred from them. Broken down to logics they often summarize complex expressions. This approach is especially useful for relations that are based on individual-relations, which are well understood in DL and/or FOL.

A relation between individuals is called 'individual-relation', a relation between classes 'class relation', a relation between an individual and a class 'individual-class relation' and a relation between a class and an individual 'class-individual relation'.

An 'individual-based relation' is a relation that may relate classes, but that adheres strictly to first-order quantifications based on individual-relations between instances of these classes. A subclass of 'individual-based relation' is 'all-some class relation'. When *e.g.* the IRI rel_ont:class_level_part_of is described in a Metarel ontology as an all-some class relation, and it is used in the RDF triple 'nucleus is part of cell', then it means that every nucleus is part of some cell. Some other examples (subclasses) of individual-based relations are 'all-all class relation' (e.g. 'ABC computer *all are connected to all* CDE printer'), 'some-some class relation' (e.g. 'bird *some eat some* fish') and 'tight class relation' (e.g. 'heart *is integral part of* body', meaning that every heart is part of some body and every body has some heart as part).

The IRI rel_ont:class_level_part_of is a class relation that is based on an individual-relation, *e.g.* obo:is_part_of. The first one inherits certain algebraic properties, like transitivity, from the latter. This connection is a metarelation called 'is based on', between the class relation and the individual-relation, which enables to propagate algebraic properties like transitivity to the class level. Every relation can also be annotated explicitly, using multiple inheritance, as a 'transitive relation' (e.g. *is part of*), a 'symmetric relation' (e.g. *is connected to*) or a 'reflexive relation' (e.g. *is same as*).

Class relations that are based on a pair of inverse individual-relations can be related with 'is reciprocal of'. On the class level, assuming 'all-some' semantics, *is part of* is not the inverse of *has part*. For example, 'beard is part of face' may hold in the sense 'all beards are part of some face', but 'face has part beard' does not hold in the sense 'all faces have part some beard'.

In order to support relations between IRIs that are not clearly either individuals or classes, some more generic relations like 'subject-object relation' and 'subject-data relation', are also defined as direct subclasses of 'relation', which is the most generic class in this hierarchy. At this level relations can also be annotated as being temporally qualified. In this way relation arcs can be created that hold at all times during the existence of the subject, or only at some time (e.g. 'biological cell *all at all times contains some* water molecule'). The addition of more specialised types of relations in Metarel are under consideration, especially with respect to probabilistic associations and default interpretations. This would enable to express that 'hu-

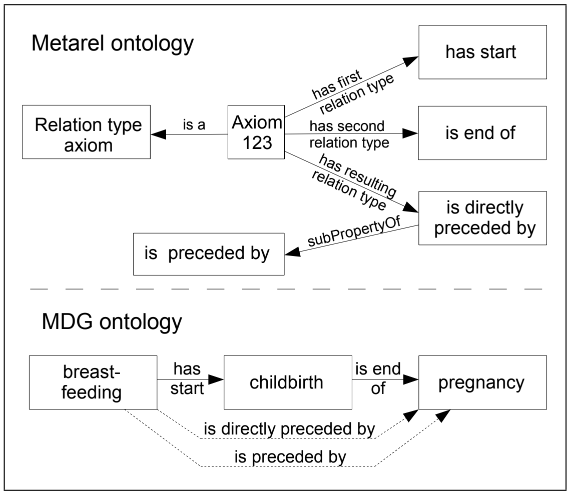

Fig. 4. Two class relation arcs 'is directly preceded by' and 'is preceded by' can be directly inferred on the class level from the metarelations between class relations in the Metarel ontology.

man *has part* hair', considering that some people are in fact bald.

Metarel also contains semantic rules, which are generalised from the individual-level to the class level. Figure 4 shows an example of a chain rule for relations at the class level. Blank nodes, like Axiom123 in the figure, remain outside the MDG model. They can be exploited for creating inferences with SPARUL.

4.3. Metarel in the Semantic Web

The IRIs used for Metarel are human readable, which is important for the maintenance of a library of SPARUL rules. For example, the term 'relation' is identified as follows:

http://www.metarel.org/Relation

Such IRIs will be abbreviated here through the prefix *mrl*, like mrl:Relation. The IRIs, which are provided by *metarel.rdf*, can be used for annotating relations in MDG-modelled Linked Data. Also newly created relations, that are necessary for fitting in the MDG, are described by annotations with Metarel terms. This happens through the predicates rdf:type, rdfs:subPropertyOf and through the metarelation mrl:isBasedOn.

In order to avoid the usage of Metarel vocabulary that is already standardised by OWL, RDF or RDF(S), equivalence statements are created in metarel.rdf with *owl:sameAs*, as shown in Table 2. However, the correspondence of the terminology in Metarel with the terminology in OWL and RDF is a complicated issue, because the two semantic contexts that exist for Semantic Web resources, DS and RBS, provide different meanings for the same language constructs, like owl:ObjectProperty and – ironically – even owl:sameAs.

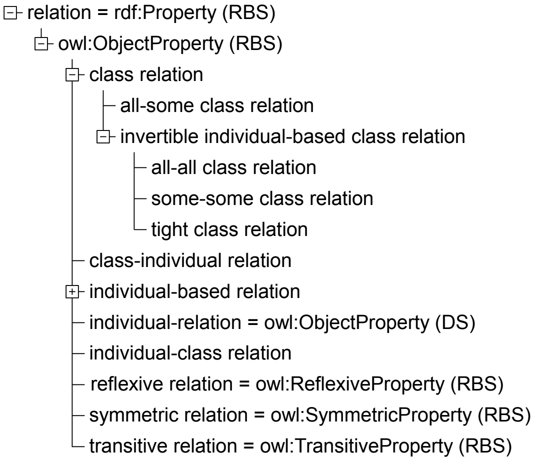
- relation = rdf:Property (RBS)
  - owl:ObjectProperty (RBS)
    - class relation
      - all-some class relation
      - invertible individual-based class relation
        - all-all class relation
        - some-some class relation
        - tight class relation
    - class-individual relation
    - individual-based relation
    - individual-relation = owl:ObjectProperty (DS)
    - individual-class relation
    - reflexive relation = owl:ReflexiveProperty (RBS)
    - symmetric relation = owl:SymmetricProperty (RBS)
    - transitive relation = owl:TransitiveProperty (RBS)

Fig. 5. Relation types in Metarel provide unambiguous meaning for language constructs that have a different logical meaning in the RDF-based Semantics and the Direct Semantics of OWL.

The hierarchy underneath the term 'relation' in Metarel is shown in Figure 5. Equations of terms in Metarel with terms in OWL and RDF are indicated, both for RBS and DS. The figure shows that Metarel has more affiliation with RBS, since four terms equate with RBS interpreted language constructs and only one for DS. The terminology of Metarel has the virtue of distinguishing the RBS and DS meanings more precisely, because class relations are object properties in the RBS sense, but not in the sense of DS. Instead, object properties in DS equate to individual-relations in Metarel.

By this equation of the vocabulary, an inference system like SPARUL can convert some sections of DS-interpreted OWL profiles bidirectionally to Linked Data in the form of an MDG, described by Metarel. RBS-interpreted resources can be semantically enhanced through Metarel.

5. Practical implementations

Metarel currently supports three integrated RDF knowledge bases: BioGateway [4], CCO [5] and GeXKB [6], whose original RDF data files were created with ONTO-PERL [43]. All of them have

mrl:SubjectDataRelation	owl:DatatypeProperty
mrl:SubjectObjectRelation	owl:ObjectProperty
mrl:Relation	rdf:Property
mrl:ReflexiveRelation	owl:ReflexiveProperty
mrl:SymmetricRelation	owl:SymmetricProperty
mrl:TransitiveRelation	owl:TransitiveProperty

Table 2

IRIs in *metarel.rdf* (left column) that are explicitly equalised to RBS-interpreted IRIs in OWL and RDF (right column) with owl:sameAs statements.

SPARQL endpoints for querying, and both CCO and GeXKB are available in BioPortal [44], which interlinks them with other resources that are published as Linked Data. These three knowledge bases all contain ontologies and data that is annotated with ontologies in the domain of genomics. The IRI-identified data entities derive from the databases Gene Ontology Annotations, Kegg pathways, IntAct, UniProtKB and NCBI Gene ID, as well as from the output of TurboOrtho [45], a multi-threaded C++ implementation of the OrthoMCL algorithm [46]. All these data entities were interpreted as classes of proteins, genes, biological pathways, protein interactions or protein orthologs. They were annotated to the Gene Ontology, the Molecular Interactions ontology and NCBI Taxonomy, either as subclasses or as having a relation to a class in these ontologies.

BioGateway has also included all the OBO candidate ontologies that are accessible via the OBO Foundry, both OBO formatted and OWL ontologies, as well as the Basic Formal Ontology (BFO) [47]. The RDF stores for CCO and GeXKB use the Semanticscience Integrated Ontology (http://code.google.com/p/semanticscience/wiki/SIO) as upper level ontology.

The IRI-identified entities in all these resources, both ontologies and data, represent classes exclusively. The database approach of managing large numbers of genomic data entities as instances of a few classes, leads to class descriptions that are semantically flawed and it cannot be used in the presence of OBO ontologies. Therefore the three knowledge bases BioGateway, CCO and GeXKB, have all used the same set of 365 Metarel-annotated relations, which were extracted from the OBO formatted ontologies into a file called Biorel.owl [7]. Biorel contains only individual-relations and could be validated as OWL 2 DL. A merger of Biorel and Metarel, called BioMetarel, contains the necessary class relations and propagates the semantic properties from the individual-level to the class level. The addition of BioMetarel as a separate RDF graph in the stores, has enabled to execution of a set of iterated SPARUL queries, thereby creating relational closures for reflexivity, transitivity, priority over subsumption, super-relations and mixed relation chains. This is where Metarel interlinks datasets that use the same entities through a massive inference of relation arcs (the typed links).

Examples of relation arcs are protein A *interacts with* protein B, *participates in* process C, *is located in* location D, and process C *negatively regulates* process E. Useful and responsive queries require the precomputed inference that protein A *regulates* process E, which is achieved through a combination of the SPARUL closures. The results of the reasoning were positively evaluated in the three RDF stores, which all have libraries of biomedically relevant SPARQL queries. 158 million inferred relation arcs were created in BioGateway, the largest of the stores. Queries can now optionally be launched over the inferred RDF graphs, resulting in more complete answers.

6. Discussion

The combination of Ontology and DL has brought an end to the problems that were reported by Woods in [41] some decades ago. A universally accepted distinction of terms in either individual or class, as provided by Ontology, combined with decidable logics like OWL DL, has solved the most common ambiguities in semantic networks. OBO ontologies, expressed in the RDF syntax of OWL DL, form a good example of a modern semantic network with a clear interpretation. Metarel supports this solution by exploring to what extent multi-digraphs, free of blank nodes, can be built on top of these foundations.

Many semantic formalisms have used graphical elements like dots, boxes, ovals and arcs, including Topic Maps [48], Conceptual Graphs [49] and Peirce's existential graphs [50]. Two problems remain unsolved for most of these systems. Firstly, they do not distinguish identifiers from labels properly, since IRIs were not standardised until recently. Secondly, they have attempted to provide a semantic foundation to the graphs by translations to undecidable logics, FOL in particular. That undecidable logics cannot support a well-understood reasoning process has remained an uninteresting theoretical result until real-life applications were developed in computer science two decades ago. In the Semantic Web, RDF and OWL Full can be used to model FOL syntactically.

	OWL DL	RDF(S)	Metarel
High expressivity	✓		
Defined classes	✓		
Decidable reasoning	✓		✓
SPARQL friendliness		✓	✓
Low number of IRIs	✓	✓	

Table 3

MDGs annotated with Metarel, compared to RDF-expressed OWL DL and RDF(S). Advantages are checked for each of the three RDF models. MDGs are less expressive and require more IRIs for distinguishing many types of relations, but they can be queried more easily.

Metarel's usage of relations between classes was inspired by OBO's Relationship Ontology [51], which asserts relations between classes with tags and natural language definitions. Some relations, like 'is integral part of', had to be reengineered to the individual-relation 'is part of' for translation to OWL DL. Metarel can annotate it as a tight class relation, whereas most others translate to all-some relations.

Although Metarel provides a vocabulary for relations in an ontological framework, it is not a logic. The vocabulary can be used as a basis to specify logics, like *e.g.* the Class-Relationship Logic of Nilsson [52]).

Metarel attempts to annotate MDGs in such a way that it can be translated to DL. A faithful translation in the other direction, from an expressive DL into an MDG, however, is not possible. Metarel currently does not bring the expressivity of MDGs beyond primitive classes and quantifiers like 'all' and 'some'. Decidable reasoning about logic constructs like number restriction, domain and ranges, but most importantly, fully-defined classes, can only be handled in DLs.

An interesting approach for querying DL in OWL/RDF is delivered by SPARQL-DL [53]. However, this extension of SPARQL may require a greater knowledge of Description Logic and it has not specified a SPARQL-friendly RDF format for storing - and thus querying - reasoned inferences. Metarel could be complementary to such a technology for querying highly expressive DL through SPARQL.

There is another improvement that modern semantic technologies have achieved in comparison with the semantic networks from the past. More performant computers and the virtually unlimited number of identifiers that can be created through IRIs have facilitated more detailed distinctions between closely related entities. Modern semantics distinguish *e.g.* Tim, the length of Tim, a measurement of the length of Tim, the numerical value of the length of Tim and the measurement unit that suits the numerical value of the length of Tim. Metarel benefits from this evolution by proposing closely related distinctions between relations, like 'is part of' as individual-relation, as all-some relation and as a relation that holds at some time. These relations need a different IRI and need to be treated differently during management and reasoning processes. This increased number of IRIs implies a clear drawback compared to the architecture that was engineered for both OWL and RDF(S). Metarel has its value as a combination of decidability and SPARQL-friendly querying. The advantages and drawbacks of Metarel are compared with RDF(S) and RDF-expressed OWL DL in Table 3.

Linked Data relies on RDF graphs that are browsable. For being browsable, query systems should be able to follow chains of links over blank nodes automatically. It is not clear how this can be achieved with SPARQL alone, without the need for a procedural language like Java. Since RDF/MDG does not contain any blank nodes, it is highly browsable and it can be queried by SPARQL without any additions. Metarel works very well together with this recent evolution in the Semantic Web.

7. Conclusion

The use of MDGs, annotated with terms about relations in Metarel, enables a bridge between graph-based representations like RDF and DL-based representations like OWL. It complements the standard OWL/RDF syntax, which contains all the information encoded by OWL, by providing an RDF format that is less expressive, but highly queryable through SPARQL. This makes MDGs very suited to express Linked Data. Browsing to related concepts can happen with a single, generic SPARQL query instead of requiring procedural techniques to browse over chains of blank nodes.

Metarel can also facilitate interesting solutions for materialising logical inferences from OWL as RDF triples. Its use of primitive classes and existential restriction is not very expressive, but provides decidable reasoning unlike RDF(S), OWL Full and other formalisms that use the RDF-Based Semantics. Transitivity, super-properties and chain rules may often be sufficient to support semantic queries within large biomedical datasets like Gene Ontology Annotations. The success of this approach was proven on different integrated biomedical knowledge bases.

References

[1] W. Blondé, E. Antezana, B. De Baets, V. Mironov, and M. Kuiper, "Metarel: an Ontology to support the inferencing of Semantic Web relations within Biomedical Ontologies," in *Proc. of the International Conference on Biomedical Ontologies (ICBO)*, pp. 79–82, University at Buffalo, NY, USA, 2009.

[2] G. Schreiber and M. Dean, "OWL Web Ontology Language Reference," W3C Recommendation, W3C, 2004, Retrieved on 16 April 2012. `http://www.w3.org/TR/2004/REC-owl-ref-20040210/`.

[3] E. Miller and F. Manola, "RDF Primer," W3C Recommendation, W3C, 2004, Retrieved on 16 April 2012. `http://www.w3.org/TR/2004/REC-rdf-primer-20040210/`.

[4] E. Antezana, W. Blondé, M. Egaña, A. Rutherford, R. Stevens, B. De Baets, V. Mironov, and M. Kuiper, "BioGateway: a semantic systems biology tool for the life sciences," *BMC Bioinformatics*, vol. 10 Suppl 10, no. Suppl 10, pp. S11+, 2009.

[5] E. Antezana, M. Egaña, W. Blondé, A. Illarramendi, I. Bilbao, B. De Baets, R. Stevens, V. Mironov, and M. Kuiper, "The Cell Cycle Ontology: An application ontology for the representation and integrated analysis of the cell cycle process," *Genome Biology*, vol. 10, no. 5, pp. R58+, 2009.

[6] A. Venkatesan, V. Mironov, and M. Kuiper, "Towards an integrated knowledge system for capturing gene expression events," in *Proceedings of the 3rd International Conference on Biomedical Ontology, KR-MED Series, Graz, Austria* (R. Cornet and R. Stevens, eds.), vol. 897 of *CEUR Workshop Proceedings*, pp. 85–90, CEUR-WS.org, 2012.

[7] W. Blondé, V. Mironov, A. Venkatesan, E. Antezana, B. De Baets, and M. Kuiper, "Reasoning with bio-ontologies: using relational closure rules to enable practical querying," *Bioinformatics*, vol. 27, no. 11, pp. 1562–1568, 2011.

[8] E. Prud'hommeaux and A. Seaborne, "SPARQL Query Language for RDF." W3C Recommendation, 2008, Retrieved on 16 April 2012. `http://www.w3.org/TR/rdf-sparql-query/`.

[9] C. Bizer, T. Heath, and T. Berners-Lee, "Linked Data - The Story So Far," *International Journal on Semantic Web and Information Systems (IJSWIS)*, vol. 5, no. 3, pp. 1–22, 2009.

[10] T. Berners-Lee, "Linked Data," tech. rep., 2006, Retrieved on 17 April 2012. `http://www.w3.org/DesignIssues/LinkedData.html`.

[11] A. Seaborne, G. Manjunath, C. Bizer, J. Breslin, S. Das, I. Davis, S. Harris, K. Idehen, O. Corby, K. Kjernsmo, and B. Nowack, "SPARQL Update, A language for updating RDF graphs," W3C Member Submission, 2008, Retrieved on 16 April 2012. `http://www.w3.org/Submission/SPARQL-Update/`.

[12] K.-H. Cheung, E. Prud'hommeaux, Y. Wang, and S. Stephens, "Semantic Web for Health Care and Life Sciences: a review of the state of the art," *Briefings in Bioinformatics*, vol. 10, no. 2, pp. 111–113, 2009.

[13] F. Belleau, M. Nolin, N. Tourigny, P. Rigault, and J. Morissette, "Bio2RDF: Towards a mashup to build bioinformatics knowledge systems," *Journal of Biomedical Informatics*, vol. 41, no. 5, pp. 706–716, 2008.

[14] B. Smith, M. Ashburner, C. Rosse, J. Bard, W. Bug, W. Ceusters, L. J. Goldberg, K. Eilbeck, A. Ireland, C. J. Mungall, N. Leontis, P. Rocca-Serra, A. Ruttenberg, S.-A. Sansone, R. H. Scheuermann, N. Shah, P. L. Whetzel, and S. Lewis, "The OBO Foundry: coordinated evolution of ontologies to support biomedical data integration," *Nature Biotechnology*, vol. 25, no. 11, pp. 1251–1255, 2007.

[15] D. S. Wishart, C. Knox, A. C. C. Guo, D. Cheng, S. Shrivastava, D. Tzur, B. Gautam, and M. Hassanali, "DrugBank: a knowledgebase for drugs, drug actions and drug targets," *Nucleic Acids Research*, vol. 36, no. Database issue, pp. D901–906, 2008.

[16] E. Meij, M. Bron, L. Hollink, B. Huurnink, and M. de Rijke, "Mapping queries to the Linking Open Data cloud: A case study using DBpedia," *Web Semantics*, vol. 9, no. 4, pp. 418–433, 2011.

[17] S. Auer, C. Bizer, G. Kobilarov, J. Lehmann, R. Cyganiak, and Z. Ives, "DBpedia: A Nucleus for a Web of Open Data The Semantic Web," in *Proceedings of 6th International Semantic Web Conference, 2nd Asian Semantic Web Conference (ISWC+ASWC)*, vol. 4825 of *Lecture Notes in Computer Science*, (Berlin, Heidelberg), pp. 722–735, Springer, 2007.

[18] M. V. Assem, A. Gangemi, and G. Schreiber, "Conversion of WordNet to a standard RDF/OWL representation," in *5th edition of the International Conference on Language Resources and Evaluation (LREC), Genoa, Italy*, 2006.

[19] The Uniprot Consortium, "The Universal Protein Resource (UniProt) in 2010," *Nucleic Acids Research*, vol. 38, no. Suppl. 1, pp. D142–D148, 2010.

[20] E. Camon, M. Magrane, D. Barrell, D. Binns, W. Fleischmann, P. Kersey, N. Mulder, T. Oinn, J. Maslen, A. Cox, and R. Apweiler, "The gene ontology annotation (GOA) project: implementation of GO in SWISS-PROT, TrEMBL, and InterPro," *Genome Research*, vol. 13, no. 4, pp. 662–672, 2003.

[21] M. Ashburner, C. A. Ball, J. A. Blake, D. Botstein, H. Butler, J. M. Cherry, A. P. Davis, K. Dolinski, S. S. Dwight, J. T. Eppig, M. A. Harris, D. P. Hill, L. Issel-Tarver, A. Kasarskis, S. Lewis, J. C. Matese, J. E. Richardson, M. Ringwald, G. M. Rubin, and G. Sherlock, "Gene ontology: tool for the unification of biology. The Gene Ontology Consortium," *Nature Genetics*, vol. 25, no. 1, pp. 25–29, 2000.

[22] M. Kanehisa and S. Goto, "KEGG: Kyoto encyclopedia of genes and genomes," *Nucleic Acids Research*, vol. 28, no. 1, pp. 27–30, 2000.

[23] E. W. W. Sayers, T. Barrett, D. A. A. Benson, S. H. H. Bryant, K. Canese, V. Chetvernin, D. M. M. Church, M. Dicuccio, R. Edgar, S. Federhen, M. Feolo, L. Y. Y. Geer, W. Helmberg, Y. Kapustin, D. Landsman, D. J. J. Lipman, T. L. L. Madden, D. R. R. Maglott, V. Miller, I. Mizrachi, J. Ostell, K. D. D. Pruitt, G. D. D. Schuler, E. Sequeira, S. T. T. Sherry, M. Shumway, K. Sirotkin, A. Souvorov, G. Starchenko, T. A. A. Tatusova, L. Wagner, E. Yaschenko, and J. Ye, "Database resources of the National Center for Biotechnology Information," *Nucleic Acids Research*, vol. 37, no. Database issue, pp. D5–15, 2009.

[24] S. Kerrien, Y. Alam-Faruque, B. Aranda, I. Bancarz, A. Bridge, C. Derow, E. Dimmer, M. Feuermann, A. Friedrichsen, R. Huntley, C. Kohler, J. Khadake, C. Leroy, A. Liban, C. Lieftink, L. Montecchi-Palazzi, S. Orchard, J. Risse, K. Robbe, B. Roechert, D. Thorneycroft, Y. Zhang, R. Apweiler, and H. Hermjakob, "IntAct—open source resource for molecular interaction data," *Nucleic Acids Research*, vol. 35, pp. D561–D565, Jan. 2007.

[25] D. Natale, C. Arighi, W. Barker, J. Blake, T. C. Chang, Z. Hu, H. Liu, B. Smith, and C. Wu, "Framework for a protein ontol-

ogy," *BMC Bioinformatics*, vol. 8, no. Suppl 9, pp. S1+, 2007.

[26] P. de Matos, A. Dekker, M. Ennis, J. Hastings, K. Haug, S. Turner, and C. Steinbeck, "ChEBI: a chemistry ontology and database," *Journal of Cheminformatics*, vol. 2, no. Suppl 1, pp. P6+, 2010.

[27] M. Bada and K. Eilbeck, "Efforts toward a More Consistent and Interoperable Sequence Ontology," in *Proc. of the International Conference on Biomedical Ontologies, Graz, Austria* (R. Cornet and R. Stevens, eds.), vol. 897 of *CEUR Workshop Proceedings*, pp. 67–71, CEUR-WS.org, 2012.

[28] Z. Xiang, C. Mungall, A. Ruttenberg, and Y. He, "Ontobee: A Linked Data Server and Browser for Ontology Terms," in *Proc. of the 2nd International Conference on Biomedical Ontologies (ICBO)* (O. Bodenreider, M. Martone, and A. Ruttenberg, eds.), pp. 279–281, University at Buffalo, NY, USA, 2011.

[29] R. V. Guha and D. Brickley, "RDF Vocabulary Description Language 1.0: RDF Schema," W3C Recommendation, W3C, 2004, Retrieved on 16 April 2012. `http://www.w3.org/TR/2004/REC-rdf-schema-20040210/`.

[30] P. F. Patel-Schneider, B. Motik, and B. C. Grau, "OWL 2 Web Ontology Language Direct Semantics," W3C recommendation, W3C, 2009, Retrieved on 16 April 2012. `http://www.w3.org/TR/2009/REC-owl2-direct-semantics-20091027/`.

[31] F. Baader, D. Calvanese, D. L. McGuinness, D. Nardi, and P. F. Patel-Schneider, *The Description Logic Handbook: Theory, Implementation and Applications*. New York, NY, USA: Cambridge University Press, 2nd ed., 2010.

[32] B. Motik, A. Fokoue, I. Horrocks, Z. Wu, C. Lutz, and B. C. Grau, "OWL 2 Web Ontology Language Profiles," W3C recommendation, W3C, 2009, Retrieved on 16 April 2012. `http://www.w3.org/TR/2009/REC-owl2-profiles-20091027/`.

[33] M. Schneider, "OWL 2 Web Ontology Language RDF-Based Semantics," W3C recommendation, W3C, 2009, Retrieved on 16 April 2012. `http://www.w3.org/TR/2009/REC-owl2-rdf-based-semantics-20091027/`.

[34] E. Antezana, M. Kuiper, and V. Mironov, "Biological knowledge management: the emerging role of the Semantic Web technologies," *Briefings in Bioinformatics*, vol. 10, no. 4, pp. 392–407, 2009.

[35] S. Schulz, R. Cornet, and K. Spackman, "Consolidating SNOMED CT's ontological commitment," *Applied Ontology*, vol. 6, no. 1, pp. 1–11, 2011.

[36] A. L. Rector, J. E. Rogers, P. E. Zanstra, E. Van Der Haring, and Openg, "OpenGALEN: open source medical terminology and tools," *Proceedings of the Annual Symposium of the American Medical Informatics Association (AMIA)*, 2003.

[37] F. Baader and B. Morawska, "Unification in the description logic el," *Logical Methods in Computer Science*, vol. 6, no. 3, 2010.

[38] R. Hoehndorf, M. Dumontier, A. Oellrich, S. Wimalaratne, D. Rebholz-Schuhmann, P. Schofield, and G. V. Gkoutos, "A common layer of interoperability for biomedical ontologies based on OWL EL," *Bioinformatics*, vol. 27, no. 7, pp. 1001–1008, 2011.

[39] A. M. Collins and E. F. Loftus, "A Spreading Activation Theory of Semantic Processing," *Psychological Review*, vol. 82, no. 6, pp. 407–428, 1975.

[40] J. F. Sowa and A. Borgida, *Principles of semantic networks : explorations in the representation of knowledge*. Morgan Kaufmann, San Mateo, Calif., 1991.

[41] W. Woods, "What's in a Link: Foundations for Semantic Networks," in *Representation and Understanding* (D. Bobrow and A. Collins, eds.), Language, Thought and Culture: Advances in the Study of Cognition, Academic Press, New York, San Francisco, London, 1975.

[42] J. Abello and J. Korn, "MGV: a system for visualizing massive multidigraphs," *Transactions on Visualization and Computer Graphics*, vol. 8, no. 1, pp. 21–38, 2002.

[43] E. Antezana, M. Egaña, B. De Baets, M. Kuiper, and V. Mironov, "ONTO-PERL: An API for supporting the development and analysis of bio-ontologies," *Bioinformatics*, vol. 24, no. 6, pp. 885–887, 2008.

[44] N. F. Noy, N. H. Shah, P. L. Whetzel, B. Dai, M. Dorf, N. Griffith, C. Jonquet, D. L. Rubin, M.-A. A. Storey, C. G. Chute, and M. A. Musen, "BioPortal: ontologies and integrated data resources at the click of a mouse," *Nucleic acids research*, vol. 37, no. Web Server issue, pp. W170–W173, 2009.

[45] O. Ekseth, B. Lindi, M. Kuiper, and V. Mironov, "TurboOrtho – a high performance alternative to OrthoMCL," in *European Conference on Computational Biology, Ghent, Belgium*, vol. Comparative genomics, phylogeny and evolution, poster B-12, 2010.

[46] L. Li, C. J. Stoeckert, and D. S. Roos, "OrthoMCL: identification of ortholog groups for eukaryotic genomes," *Genome Res.*, vol. 13, pp. 2178–2189, Sep 2003.

[47] B. Smith and W. Ceusters, "Ontological realism: A methodology for coordinated evolution of scientific ontologies," *Applied Ontology*, vol. 5, no. 3-4, pp. 139–188, 2010.

[48] A. Kawtrakul, C. Yingsaeree, and F. Andres, "A framework of NLP based information tracking and related knowledge organizing with topic maps," in *12th International Conference on Applications of Natural Language to Information Systems, Paris, France*, vol. 7022 of *Lecture Notes in Computer Science*, pp. 272–283, Springer, 2007.

[49] G. Amati and I. Ounis, "Conceptual graphs and first order logic," *The Computer Journal*, vol. 43, pp. 1–12, Jan. 2000.

[50] D. D. Roberts, *The Existential Graphs of Charles S. Peirce*. Approaches to Semiotics, Mouton & Co. N.V., Publishers, The Hague, 1973.

[51] B. Smith, W. Ceusters, B. Klagges, J. Kohler, A. Kumar, J. Lomax, C. Mungall, F. Neuhaus, A. Rector, and C. Rosse, "Relations in biomedical ontologies," *Genome Biology*, vol. 6, no. 5, 2005.

[52] J. F. Nilsson, "Querying Class-Relationship Logic in a Metalogic Framework," in *Flexible Query Answering Systems - 9th International Conference, Ghent, Belgium,* (H. Christiansen, G. D. Tré, A. Yazici, S. Zadrozny, T. Andreasen, and H. L. Larsen, eds.), vol. 7022 of *Lecture Notes in Computer Science*, Springer, 2011.

[53] E. Sirin and B. Parsia, "SPARQL-DL: SPARQL Query for OWL-DL," in *3rd OWL: Experiences and Directions Workshop (OWLED), Innsbruck, Austria* (C. Golbreich, A. Kalyanpur, and B. Parsia, eds.), CEUR Workshop Proceedings, CEUR-WS.org, 2007.