Chapter 2

Kinds of Ontologies and the Role of Taxonomies

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Kinds of Ontologies and the Role of Taxonomies

An ontology, as we conceive it, is a representational artifact aimed at representing universals, defined classes, and relations among them. We are interested here specifically in the universals, defined classes, and relations discovered by and pertinent to scientific research. In this chapter we discuss in more detail the philosophical background of ontology in general, and introduce some distinctions between kinds of ontologies, including domain ontologies, top-level ontologies, reference ontologies, and application ontologies. We also discuss in more detail the idea of a structured classification or taxonomy.

Philosophical Ontology

Historically, ontology is a branch of philosophy having its origins in ancient Greece in the work of philosophers such as Parmenides, Heraclitus, Plato, and Aristotle. “Ontology” derives from the Greek words *ontos* (meaning “existence” or “being”) and *logos* (meaning “rational account” or “knowledge”). Ontology in this sense is concerned with the study of what is, of the kinds and structures of objects, properties, events, processes, and relations in reality. From the philosophical perspective, ontology seeks to provide a definitive and exhaustive classification of entities in all spheres of being. Philosophers have emphasized in this connection the role of certain basic or preferred types of entities—for example, absolute simples—that are regarded as being truly real, as contrasted with other, less-privileged entities, which are seen as being constructed on their basis.

Contemporary philosophical ontology (sometimes called “analytic metaphysics”) has sometimes allowed the study of entities dealt with by the special sciences (physics, chemistry, biology, psychology, and others), but it still overwhelmingly pursues a more general focus, one directed at providing a description and explanation of the kinds of objects and relations that are common to all scientific domains. Examples of such common or domain-neutral features of reality include unity and plurality; cause and effect; identity, both at a time and across time; compositional structure, determined either via part-whole or member-set relations; spatial and temporal and spatiotemporal location; and so on.

Where the biologist studies cells, the chemist studies molecules, and the physicist studies energy and electrons; the philosophical ontologist, in contrast, is interested in giving an account of what is common to cells, molecules, and electrons (for example, that they are all entities or things that exist as the bearers of certain properties or qualities) and of the relations in which these kinds of entities stand to one another. Such relations may extend across the usual disciplinary boundaries of the special sciences and across granularities, as in the case of relationships between microlevel entities such as atoms or molecules and macrolevel entities such as organisms and planets. The goal of philosophical ontology is at its core to provide a clear, coherent, and rigorously worked-out account of the basic structures of the whole of reality thus conceived.

Philosophical Ontology and Taxonomy

A major feature of philosophical ontology is the classification of different kinds of entities. This involves not only differentiating between basic categories of entities (for example, between *objects* such as a heart, and *processes* such as the beating of a heart), but also recognizing more specific kinds of entities falling under these categories (such as the difference between an individual object, such as a human being, and an aggregate or group of objects, such as a population of human beings). The result is a set of representations of the kinds of objects there are, either in general or in a given field of investigation, organized according to certain principles of classification. The so-called Porphyrian Tree (illustrated in figure 2.1), a version of which was included in an introduction to the work of Aristotle by the Greek philosopher Porphyry, is designed to represent the principle types of things (in Greek the *katēgoriai*) found in reality from the Aristotelian point of view. This idea has been used by thinkers in a variety of disciplines ever since. The Linnaean Taxonomy—first developed by Carl Linnaeus in the eighteenth century to classify living things and still used by biologists today—is based on the Porphyrian Tree, and the idea has been reused in multiple further fields—in the periodic table of the elements, the WHO International Classification of Diseases,1 the Department of Defense Joint Hierarchy of Military Doctrine,2 and many more.

[Insert figure 2.1]

Simple Taxonomies

The Porphyrian Tree is an example of what we have already referred to in chapter 1 as a *hierarchy*: a graph with *nodes* (including *leaves*, the lowest nodes) and *edges* (the lines connecting the nodes), forming *branches* that connect each node (each box in figure 2.1: thing, material substance, etc.) in a path leading upward to the highest node or *root* (see chapter 4 for further details. Nodes are connected by relations of subsumption (where the more general, or parent node, subsumes the less general, or child node).

All the ontologies with which we have to deal in what follows can be viewed as graph-theoretic structures along these lines, consisting of nodes (the terms of the ontology) connected by edges (representing relations). In a taxonomy the nodes are intended to represent types or universals in reality, while the edges represent *is\_a* (which means subtype) relations connecting these types or universals in reality. We use “*is\_a”* to mean “is a subtype of,” defined as follows:3

*A is\_a B* =def. *A* and *B* are types and all instances of type *A* are also instances of type *B*

The basic *is\_a* relations represented by the links connecting lower and higher nodes together form a hierarchical classification of entities. For example, in the Porphyrian Tree we have the following:

*material substance is\_a thing,*

*animate (living) entity is\_a material substance,*

*living entity with sensation is\_a living entity,*

*rational animal is\_a living entity with sensation,*

*human is\_a rational animal.*

We have something similar in the Linnaean taxonomy shown in figure 2.2.

[Insert figure 2.2]

Both the Porphyrian and Linnaean taxonomies are built on the basis of an Aristotelian approach, which in effect conceives the *is\_a* relation as a generalization of the species-genus relationship. In the Porphyrian Tree, *material substance* can be considered both as a species of the genus *thing*, and as a genus with *animate entity* and *nonanimate entity* as its two species. *Animate entity*, similarly, is the genus for both *living entity with sensation* (a species of animate entity) and *living entity without sensation* (another species of animate entity), and so on, down the tree to *human*. Importantly, at each step from a genus to a lower species, the species must be identified in terms of its possession of a *differentia*, some defining characteristic or characteristics that makes the species both more specific than its subsuming genus and serves to set it apart from other species of the same genus. In Porphyry’s taxonomy being a living thing is what makes *animate entity* more specific than *material substance* and also what differentiates it from *nonanimate entity*. Similarly, being rational is what makes *rational animal* more specific than *living entity with sensation* and differentiates it from other *nonrational* types of animals. (As we will discuss in more detail in chapter 4, stating the genus and differentia of a type is a crucial part of providing what we shall refer to as an “Aristotelian definition” of that type. Taxonomies and definitions are closely interconnected in ontology design.)

Classification of the Porphyrian sort is nothing unusual. We are dealing constantly with hierarchical relationships of greater and lesser generality, whether in library catalogs, in restaurant menus, in functional classifications of genes, or in the directory structure used by the operating systems of our computers. Such sorting is a key element in the creation of an ontology, and constructing coherent taxonomies based on explicit and consistent principles of classification —set forth in detail in chapter 4—is one key component of good ontology design.

Formal vs. Material Ontologies

A formal ontology is domain neutral. It contains just those most general terms—such as “object” and “process”—which apply in all scientific disciplines whatsoever. Thus it corresponds to the sort of ontological interest we identified above as predominating among philosophers. A material ontology is domain specific. It contains terms—such as “cell,” or “carburetor”—which apply only in a subset of disciplines.

A formal ontology is a representation of the *categories* of entities and of the relationships within and between them. We here adapt Aristotle’s term “category” and use it to mean: domain-neutral universal. Categories are those universals whose instances are to be found in any domain of reality. Thus categories are also very general universals. The most obvious category is *entity*, meaning: anything that exists in any way. No matter what science one is considering it studies entities, and thus the category *entity* applies to the subject matter of that science. An example of a formal-ontological relation is *part\_of*, since every science is committed to the existence of at least some entities which have or are parts.

A domain ontology, by contrast, consists of representations of the material (meaning: nonformal) universals that are instantiated in some specific domain of reality, such as genetics, anatomy, plant biology, cancer, and so on. Where a formal ontology will contain representations of universals shared by many ontologies, each material ontology will contain representations used in the ontology alone. Thus the universals represented in an ontology of cell biology, for example, will not overlap with those represented in an ontology of cosmology or of architecture. This distinction will prove to be of great significance for the project of ontology design in support of information-driven science.

Domain Ontology

A *domain* is a delineated portion of reality corresponding to a scientific discipline such as cell biology or electron microscopy, or to an area of knowledge or interest such as the Great War or stamp collecting or construction permits. Not everything that is part of an entity within a given domain is also part of that domain. Thus every human being has molecules as parts, but molecules do not form part of the domain of, for example, human geography, or human rights law (an issue that will be treated under the heading of “granularity” in chapter 3). Each domain ontology consists of a *taxonomy* (a hierarchy structured by the *is\_a* relation) together with other relations such as *part\_of*, *contained\_in*, *adjacent\_to*, *has\_agent*, *preceded\_by*, and so forth, along with definitions and axioms governing how its terms and relations are to be understood. A domain ontology is thus a taxonomy that has been enhanced to include more information about the universals, classes, and relations that it represents. A domain ontology provides a controlled, structured representation of the entities within the relevant domain, one that can be used, for example, to annotate data pertaining to entities in that domain in order to make the data more easily accessible and shareable by human beings and processable by computers.

Figure 2.3 represents a small section of a domain ontology for lipids (note its explicitly taxonomic structure).4 A lipid is defined in this ontology as a hydrophobic or amphipathic small molecule, and this is consistent with the classification shown in the figure, where we can see that “*lipid is\_a small molecule*.” Notice that these researchers have not only chosen to classify various subtypes of lipids—for example, *LC lipoxins*, *LC hepoxilins*, and *LC cluvalones*—but have chosen to do this within a more general schema that is rooted in the class *biological entity*.

[Insert figure 2.3]

Domain Ontology and Taxonomy

The basic role of taxonomic classification in ontology has already been introduced. Here we discuss this issue in more detail as it relates specifically to domain ontologies. We have seen examples of taxonomies already. What we have called a *taxonomy* is a representational artifact that is organized hierarchically with nodes representing universals or classes and edges which represent the *is\_a* or subtype relation. Where simple taxonomies are organized in terms of the basic *is\_a* relation only, *ontologies* are organized also by other relations, such as *parthood.* For example, a domain ontology for cell biology might include information such as

*nucleus is\_a intracellular membrane-bounded organelle,*

*Golgi apparatus part\_of plasma cell,*

*hindbrain nucleus part\_of hind brain,*

and so on. This feature of ontologies is illustrated in figure 2.4 for the case of the Foundational Model of Anatomy. The solid arrows pointing vertically in the diagram represent the *is\_a* relationship, while the dotted arrows moving horizontally across the bottom of the diagram represent the *part\_of* relationship.

[Insert figure 2.4]

Similarly, figure 2.5 presents the beginnings of an ontology in the domain of biomedical ethics. What both of these ontologies have in common is that they explicitly represent multiple different kinds of relationships (in addition to species-genus hierarchies organized by the *is\_a* relation) obtaining among the universals and classes that they represent. These additional relationships are indicated in the legend inside the rounded rectangle in figure 2.5.

[Insert figure 2.5]

Along the same lines, the periodic table of the elements is a tabular representation of a taxonomic classification encoding relations such as

*lithium is\_a alkali metal,*

*flourine is\_a halogen,*

and so on. But chemists also recognize other relationships that exist between the elements, which can be represented in a corresponding domain ontology. For example, from the Chemical Entities of Biological Interest (ChEBI) ontology:

*fusicoccin has\_role toxin,*

*water has\_role amphiprotic solvent,*

*atom has\_part electron*,5

and so on.

Definition, Taxonomy, Ontology

So far we have stressed the role of taxonomies (*is\_a* hierarchies) and of the representation of other relations (such as *part\_of*) among universals as essential features of an ontology. As we shall discuss in more detail in chapter 4, explicit and clear definitions of the terms in an ontology are essential also. Indeed, all ontologies, as we understand them here, consist of (1) a central backbone taxonomy, in which all the nodes of the ontology are linked together via *is\_a* relations, together with (2) further relations defined between the nodes of the ontology. In addition, each node consists of (3) a term along with, when necessary, (4) synonyms for the term, and crucially (5) a definition of the term that makes use of the Aristotelian genus and differentia structure.

Definitions are perhaps the most important component of ontologies, since it is through definitions that an ontology draws its ability to support consistent use across multiple communities and disciplines, and to support computational reasoning. Definitions also constrain the organization of the ontology. Simply put, every term in an ontology (with the exception of some very general terms) must be provided with a definition, and the definition should be formulated through the specification of how the instances of the universal represented by the relevant term are differentiated from other instances of the universal designated by its parent term.

The resultant regimentation makes possible simple inferences. For example, from

*COPI vesicle coat is\_a protein complex,*

and

*protein complex is\_a macromolecular complex,*

we can infer that

*COPI vesicle is\_a macromolecular complex.*

From

*MRI image output preceded\_by MRI test,*

and

*MRI test preceded\_by referral,*

we can infer that

*MRI image output preceded\_by referral.*

The power to make such inferences also allows the ontology to be used for error checking by allowing us to test at any given stage in its development whether its definitions and relations are consistent. If we use the ontology to annotate a body of data—to create what is sometimes called a “knowledgebase”—then we can use the result also as a tool to detect certain sorts of errors in our data (as described in chapter 8). And because a domain ontology is relatively independent of the specific data-collection goals of specific groups of researchers, it can also be used to advance the sharing of data among multiple communities of researchers, and to support retrieval of data that might otherwise be masked by the use of labels that are obscure or undefined.

Top-Level Ontology

The use of domain ontologies is becoming increasingly common in many branches of science in reflection of the increasing need to use computers for the handling of scientific data. However, the very success of the ontology-based approach has brought with it the Tower of Babel problems discussed in the Introduction. Multiple groups of researchers are creating incompatible domain ontologies focused on their specific local needs, resulting in new information siloes, with all the problems of inaccessible and nonsharable data, and nonoptimal use of resources, that this brings.

It is above all to counteract this tendency that we promote a strategy focusing on the need to define, first, those terms in an ontology which refer to universals—terms which together form the shared vocabulary of scientists in the relevant domain—and to use these terms as our starting point for developing definitions of terms representing the multiple different sorts of lower-level universals and of defined classes needed for application purposes by different sub-communities of scientists. We believe that insisting that definitions for ontology terms be created in this way can help to ensure the consistent development of ontologies across multiple communities of researchers in much the same way that insisting that all medical students share a common knowledge of the basic biomedical sciences helps to ensure that they are able to communicate with each other as they acquire different sorts of specialist knowledge.6

But all Aristotelian definitions need a starting point—some parent (genus) in relation to which the child (species) term can be defined, and this starting point is, given what was said earlier, in every case the root node of the ontology in question.7 But how can we ensure that the many different ontologies that we will need for the many different domains will be developed in consistent fashion? How can we ensure that the different ontology-building communities will employ comparable and mutually understandable definitions? The answer, we believe, is to ensure that all domain ontologies share a common top-level formal ontology in terms of which their respective root nodes can be defined. This common top level would in effect provide the shadow parent terms needed in order to initiate the process of creating Aristotelian definitions, and thereby provide the common overarching framework needed for consistency.

Where a *domain ontology* is constructed as a representation of a basic set of universals pertinent to a single scientific domain, a *top-level* ontology is a highly general representation of categories and relations common to all such domains. For example, if *cellular division* is a universal in one domain ontology, and *cancer development* is a universal in another domain ontology, then a top-level ontology will include a category such as *process*, which subsumes both of these. Whereas domain ontologies help to integrate and make available information pertinent to a given area, top-level ontologies help to integrate and organize information across different domains.

Our proposal is that domain ontologies be constructed by downward population, using the mechanism of Aristotelian definitions, from a common top level. Experience has shown that in the absence of this common top level, the domain ontologies developed by different groups—for example, the anatomy ontologies developed by different communities of mouse, rat, or human biologists—will be developed in relative isolation from each other. This will make the sharing of annotated information based on these ontologies a difficult and time-consuming task and it will contribute further to the problem of data siloes. Use of a shared top-level by different groups of ontology developers will also increase the flexibility of training; it will allow more effective governance and quality assurance of ontology development; and it will promote the degree to which multiple different groups of ontology developers and users can inspect and critique and help to improve their respective bodies of work.

Semantic Interoperability

One central goal of the annotation of data using ontologies is to enable what is called “semantic interoperability” between heterogeneous computer systems, defined as the ability of two or more such systems to exchange information in such a way that the meaning of the information generated by any one system can be automatically interpreted by each receiving system accurately enough to produce results useful to its end users. The use of a common top-level ontology for describing the data generated by information systems increases the likelihood that these conditions will be capable of being met. It can also assist in advancing the degree to which information systems that use it can support formal reasoning. Thus, where a domain ontology assists in organizing the data of a particular domain to make that data understandable, accessible, and computer tractable, a top-level ontology assists in organizing the data of multiple domain ontologies in a way that promotes the degree to which the information systems using these ontologies will be semantically interoperable.

Choice of Top-Level Ontology

There are already a number of top-level ontologies in existence that are being used in just the way described here. For example, domain ontologies that comprise the Open Biomedical Ontologies (OBO) Consortium are now using Basic Formal Ontology (BFO) as the standard top-level ontology to assist in the integration of biomedical data and information derived from a variety of different sources. Other examples of top-level ontologies include the Descriptive Ontology for Linguistic and Cognitive Engineering (DOLCE) and the Standard Upper Merged Ontology (SUMO). We will provide a detailed introduction to BFO in chapters 5 and 6. One major advantage of the BFO framework is that over 130 public-domain ontologies, thus far primarily in the biological and biomedical domains, have been developed on the basis of BFO, so that the data annotated using terms derived from the BFO framework is orders of magnitude more comprehensive, both in terms of variety of domains and in terms of size of the datasets involved, than either DOLCE or SUMO.

Both DOLCE and SUMO have their advantages, however. DOLCE is defined as a “Domain Ontology for Linguistic and Cognitive Engineer.”8 It is from the point of view of numbers of users a very successful upper-level ontology, and it has been applied in a number of projects in biology and social science. DOLCE and BFO in fact grew out of a common philosophical orientation, and thus BFO overlaps with parts of DOLCE’s top level. In contrast to BFO, which focuses on the universals in reality, DOLCE relies on an ontology of possible worlds, and thus includes in its coverage domain putative objects of mythology and fiction. SUMO, too, has proved to have considerable value as an upper-level ontology for certain purposes.9 It should be noted, however, that SUMO is not a top-level ontology in the sense that this term is used here. This is because it contains, for example, biological terms (“protein,” “crustacean,” “body-covering,” “fruit-Or-vegetable”), and this means that it cannot cleanly support the strategy of downward population that has proved so useful to scientists in the case of BFO. Table 2.1 provides a summary of the different meanings of the term ‘ontology’ that have been surveyed thus far.

[Insert Table 2.1]

Application vs. Reference Ontology

Where the distinction between domain ontologies and top-level ontologies has to do with the generality of subject matter, we now need to introduce also a distinction between *application ontologies* and *reference ontologies*, which has to do with the goal or purpose for which an ontology is designed.

An *application* ontology is an ontology that is created to accomplish some specified local task or application. For example, the Situational Awareness and Preparedness for Public Health Incidents Using Reasoning Engines (SAPPHIRE) utilizes an application ontology that classifies unexplained illnesses that exhibit flu-like symptoms and sends this information to the Centers for Disease Control and Prevention.

A *reference* ontology, by contrast, is an ontology that is meant to be a canonical, comprehensive representation of the entities in a given domain that is developed to encapsulate established knowledge of the sort that one would find in a scientific textbook. The Foundational Model of Anatomy (FMA), Gene Ontology (GO), Cell Ontology (CL), and Protein Ontology (PRO) are examples of reference ontologies in this sense.

Portions of multiple existing reference ontologies can be reused in an application ontology, which will typically also contain new ontology content created to address its specific local purpose.

The OBO Foundry (http://obofoundry.org) initiative has embraced the goal of creating a library of semantically interoperable reference ontologies devoted to representing different domains of scientific investigation in such a way that elements of this library could be used and reused for particular application ontology purposes.

Conclusion

In this chapter, we have introduced some basic distinctions between kinds of ontologies. We have explained what a taxonomy is, and discussed the central role that taxonomies play in ontologies. Indeed, it is not going too far to say that an ontology just *is* a very sophisticated type of taxonomy. At this point, our survey of the basic theoretical components needed to make sense out of ontology design is complete. For most ontology designers, the goal will be to build a functional domain ontology, and in the next two chapters we turn to some specific recommendations that are applicable to this process.

Further Reading on Top-Level and Domain Ontology

<bok>Simons, Peter M. Parts: A Study in Ontology. Oxford: Oxford University Press, 1997.</bok>

<edb>Smith, Barry. “Ontology.” In Blackwell Guide to the Philosophy of Computing and Information, ed. Luciano Floridi, 155–166. Oxford: Blackwell, 2003.</edb>

Further Reading on Taxonomy and Classification

<edb>Jansen, Ludger. “Classifications.” In Applied Ontology: An Introduction, ed. Katherine Munn and Barry Smith, 159–172. Frankfurt: Ontos Verlag, 2008.</edb>

<edb>Smith, Barry. “The Logic of Biological Classification and the Foundations of Biomedical Ontology.” In Invited Papers from the 10th International Conference in Logic Methodology and Philosophy of Science, ed. Dag Westerståhl, 505–520. London: King’s College Publications, 2005.</edb>

Figure 2.1

The Porphyrian Tree

Figure 2.2

A partial Linnaean taxonomy

Figure 2.3

Section of a taxonomic classification from a lipid ontology

Figure 2.4

Fragment from the Foundational Model of Anatomy ontology

*Source:* C. Rosse and J. L. V. Mejino Jr., “The Foundational Model of Anatomy Ontology,” in *Anatomy Ontologies for Bioinformatics: Principles and Practice*, vol. 6, ed. Albert Burger, Duncan Davidson, and Richard Baldock (London: Springer, 2007), 59–117.

Figure 2.5

Section of a domain ontology for clinical trials in biomedical ethics

*Source*: David Koepsell, Robert Arp, Jennifer Fostel, and Barry Smith, “Creating a Controlled Vocabulary for the Ethics of Human Research: Towards a Biomedical Ethics Ontology,” *The Journal of Empirical Research on Human Research Ethics* 4 (2009): 43–58.

Table 2.1

Review of three meanings of “ontology”

Philosophical Ontology

• The study of what is, of the kinds and structures of objects, properties, events, processes, and relations in every area of reality (metaphysics). Results in ontologies, descriptions, or theories of what exists, as representational artifacts.

• Has roots in ancient Greece in the work of philosophers such as Parmenides, Heraclitus, Plato, and Aristotle

• Example: the Porphyrian Tree

Material or Domain Ontology

• A structured representation of the entities and relations existing within a particular domain of reality such as medicine, geography, ecology, or law

• A graph-theoretic structure whose nodes are linked by the subtype relation (thereby forming a taxonomy) and by other relations

• Goal: to support knowledge sharing and reuse

• Examples: Gene Ontology (GO), Foundational Model of Anatomy (FMA), Environment Ontology (EnvO), Chemical Entities of Biological Interest (ChEBI), and many others.

Formal or Top-Level Ontology

• Upper-level ontology that assists in making communication between and among domain ontologies possible by providing a common ontological architecture

• Goal: the calibration of interoperable domain ontologies into larger networks

• Examples: Basic Formal Ontology (BFO), Descriptive Ontology for Linguistic and Cognitive Engineering (DOLCE), Standard Upper Merged Ontology (SUMO)

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1. World Health Organization, “International Classification of Diseases (ICD),” accessed August 5, 2014, <http://www.who.int/classifications/icd/en/>.

2. U.S. Army, “Joint Doctrine Hierarchy,” accessed August 5, 2014, [http://usacac.army.mil/cac2/doctrine/CDM pages/cdm\_joint heirarchy.html](http://usacac.army.mil/cac2/doctrine/CDM%20pages/cdm_joint%20heirarchy.html).

3. Defined classes may also stand in the *is\_a* relation to each other, as we will briefly discuss in chapter 7.

4. H-S. Low, C. J. O. Baker, A. Garcia, and M. R. Wenk, “An OWL-DL Ontology for Classification of Lipids,” in *Proceedings of the International Conference on Biomedical Ontology* (ICBO 2009) (Buffalo, NY: NCOR, 2009), 3–7, accessed December 18, 2014, <http://icbo.buffalo.edu/2009/Proceedings.pdf>.

5. See <http://www.ebi.ac.uk/chebi/>, accessed June 16, 2011.

6. Cornelius Rosse, Anand Kumar, Jose Leonardo V. Mejino, Daniel L. Cook, Landon T. Detwiler, and Barry Smith, “A Strategy for Improving and Integrating Biomedical Ontologies,” in *Proceedings of AMIA Symposium* (Washington, DC: AMIA, 2005), 639–643.

7. We assume for the sake of simplicity that each ontology has a single root node. The Gene Ontology has three distinct roots, but is for this reason best conceived as a collection of three ontologies; see One Ontology . . . or Three? under “Ontology Structure,” accessed August 5, 2014, [http://geneontology.org/page/ontology-structure](http://www.geneontology.org/page/ontology-structure).

8. Aldo Gangemi, Nicola Guarino, Claudio Masolo, Alessandro Oltramari, Luc Schneider, “Sweetening Ontologies with DOLCE,” in *Knowledge Engineering and Knowledge Management: Ontologies and the Semantic Web*, vol. 2473, ed. Nicola Guarino (Berlin: Springer-Verlag, 2002), 166–181.

9. Ian Niles and Adam Pease, “Towards a Standard Upper Ontology,” in *Proceedings of the International Conference on Formal Ontology in Information Systems* (FOIS) (New York: ACM Digital Press, 2002), 2–9.

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