# Symbolic modeling of structural relationships in the Foundational Model of Anatomy

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**ABSTRACT**

*The need for a sharable resource that can provide deep anatomical knowledge and support inference for biomedical applications has recently been the driving force in the creation of biomedical ontologies. Previous attempts at the symbolic representation of anatomical relationships necessary for such ontologies have been largely limited to general partonomy and class subsumption. We propose an ontology of anatomical relationships beyond class assignments and generic part-whole relations and illustrate the inheritance of structural attributes in the Digital Anatomist Foundational Model of Anatomy. Our purpose is to generate a symbolic model that accommodates all structural relationships and physical properties required to comprehensively and explicitly describe the physical organization of the human body.*

*Keywords: Ontology; Knowledge representation; Spatial reasoning; Mereotopology; Partonomy; Anatomy*

## INTRODUCTION

The main objective of the terminologies correlated by UMLS is to serve as repositories of terms that can be reused with consistency by a variety of applications.[1] In general, most of the current biomedical and educational applications are designed to present hard-coded, didactic information, or they support low-level, look-up functions with no, or at best limited, capabilities for inference. The semantic structure of today's controlled medical terminologies (CMTs) as well as of biomedical ontologies seems adequate for the needs of such contemporary applications. Next-generation applications, however, will have to incorporate increasing levels of intelligence in order to meet the demands of the evolving environment in education, biomedical research and the practice of the various health professions. Such knowledge-based applications call for the representation of much deeper and richer knowledge than that retrievable from today's CMTs and ontologies. Since most of these projects primarily target clinical medicine, they are deficient in basic science concepts necessary to support reasoning. Moreover, since relationships between concepts constitute an important dimension of knowledge, next-generation knowledge sources must model comprehensively not only the concepts but also the relationships that characterize a particular field of basic science. Therefore, there is a need to generate enabling knowledge sources at least in those domains that generalize to diverse fields of education, biomedical research and clinical practice. Anatomy is such a fundamental domain.

We are developing the Foundational Model of Anatomy (FMA)[2-4] as an evolving resource for knowledge-based applications that will require anatomical information. Our intent is that the FMA should serve as a reference ontology for biomedical informatics[4] by furnishing a representation of anatomical entities and relationships necessary for the symbolic modeling of the structure of the human body at the highest level of granularity. The FMA explicitly represents declarative anatomical knowledge currently constrained to the human species in computable form, which should also be understandable by humans. It is intended as a reusable and generalizable resource for any biomedical application that requires anatomical information.

We first give a brief account of the ontological structure of the FMA to put in perspective the modeling of structural relationships in terms of a high level scheme, which we call the Anatomical Structural Abstraction (ASA). We then describe the components of this scheme and their interactions with one another.

## ONTOLOGICAL FEATURES OF THE FMA

The elements of a disciplined modeling approach for establishing the FMA, described in greater detail elsewhere,[4] consist of declared foundational principles, a high level scheme for representing anatomical concepts and relationships, and a knowledge modeling environment that implements the principles and the inheritance of definitional and non-definitional attributes. Of these elements we only comment in this paper on the high level scheme for the FMA and, in the next section, the scheme for the ASA.

The high level scheme of the FMA specifies the concept domain and scope of the symbolic model and defines its main components:

$$\boldsymbol{FMA = (AT, ASA, ATA, Mk)} \qquad (1)$$

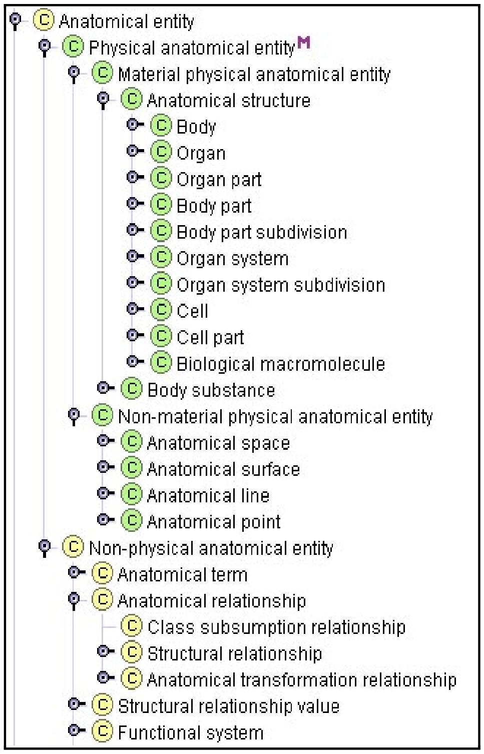


Figure 1. High level classes in the Anatomy Taxonomy (**AT**) displayed in Protégé-2000.

**AT**, the Anatomy taxonomy, assigns anatomical entities as class concepts in an Aristotelian-type hierarchy; **ASA**, the Anatomical Structural Abstraction, includes structural relationships among the entities represented in the **AT** and is the subject of this report; **ATA**, the Anatomical Transformation Abstraction, is based on relationships that describe the morphological and physical transformation of anatomical entities during pre- and postnatal development (not yet instantiated); and **Mk** refers to *Metaknowledge*, which comprises the principles and sets of rules, according to which the relationships are represented in the model's other three component abstractions.

Figure 1 shows a portion of the **AT** to illustrate some of its the high level classes, including anatomical relationships.

Our previous reports[2,3,5-10] are primarily concerned with the classification of physical anatomical entities (material objects, body substances, spaces, surfaces, lines and points), which constitutes the **AT**. In this communication our objective is to illustrate the importance of anatomical relationships among these entities for the symbolic modeling of structural knowledge, a dimension unique to anatomy among the biomedical sciences.

## ANATOMICAL STRUCTURAL ABSTRACTION

### *High Level Scheme*

Many treatises on mereotopology make extensive reference to human anatomy[11,12] but they all stop short of implementing in a comprehensive system the theories they propose and illustrate. Since the purpose of the FMA is to represent the physical organization (i.e., anatomical structure) of the human body, we have implemented more than a million of explicit structural relationships in the FMA. This knowledge base population task was guided by the specification of knowledge elements that describe this organization in terms of structural relationships and physical properties. We conceptualized these knowledge elements as the high level scheme of the **ASA**, which consists of two taxonomies that complement the **AT** and a number of interacting networks made up of different classes of relationships.[3,13]

$$ASA = (Dt, PPt, Bn, Pn, , SAn) \qquad (2)$$

**Dt**, Dimensional taxonomy, is a type hierarchy which represents dimensional entities of zero to three dimensions and shape classes of 3D entities, and distinguishes between real and virtual dimensional entities. **PPt**, Physical Properties taxonomy, describes physical state properties of anatomical entities, such as mass, temperature, viscosity and density, which determine or affect the structural organization of anatomical entities. Both taxonomies are represented in terms of which the Boundary network (**Bn**), Partonomy network (**Pn**) and Spatial Association network (**SAn**) may be described at an abstract level. Elaboration of **PPt** is beyond the scope of this paper and is discussed in the context of the symbolic representation of physiologic function as an extension of the FMA[14]. The subsequent sections explain and illustrate the interacting networks.

***Boundary Network***

Although parthood relationships predominate in anatomical reasoning and knowledge representation, the specification of boundaries is prerequisite for the demarcation of parts. The practical application of boundary information is critical in the segmentation of images and volumetric datasets, tasks that the FMA supports[5]. We define a boundary as a `Non-material physical anatomical entity`[*] of two or fewer dimensions that delimits or demarcates anatomical entities from one another that are of one dimension higher than the bounding entity. Thus the FMA specifies the `Internal surface of stomach` (a 2D entity) as the boundary of the `Cavity of stomach` (a 3D entity), as well as that of the `Wall of stomach` (3D). Should it become desirable for educational applications, for instance, to accept `Wall of stomach` as the boundary of the cavity, the appropriate modifications would need to be introduced in the particular application ontology derived from the FMA reference ontology.

We model the relationship between bounded and bounding entities by the inverse relations -*bounds*- and -*bounded by*-. The boundary network arises by a progression along the boundaries of an entity in a decreasing order of dimension: `Right ventricle` (3D) -*bounded by*- `Surface of right ventricle` (2D) -*bounded by*- `Line of right coronary sulcus, Line of anterior interventricular sulcus, Line of posterior interventricular sulcus` (1D) -*bounded by*- `Crux of heart, Apex of heart` (0D). The boundary network of the `Right ventricle`, moreover, also interacts with the **Bn** of the `Left ventricle` and `Right atrium`.

Modeling of anatomical boundaries presents a complex challenge in terms of fiat and real boundaries defined by Smith[11], which we have not yet implemented in the FMA. We distinguish between real and virtual boundaries. A real boundary of an anatomical structure corresponds to its surface, which is a `Non-material physical anatomical entity` in the AT. A virtual boundary is a `Non-physical anatomical entity`, such as the imaginary plane that demarcates the esophagus from the stomach (`Plane of gastoesophageal junction`), or the `Plane of pelvic inlet`, which demarcates the abdominal cavity from the pelvic cavity.

***Partonomy Network***

Although some knowledge modelers may regard an entity's boundary as a kind of parthood, we make a distinction between boundary and parthood. In the FMA, parthood relations are allowed only for entities of the same dimension. For example, `Cavity of stomach` (3D entity) -*has part*- `Cavity of pyloric antrum` (3D entities); `Internal surface of stomach` -*has part*- `Internal surface of pyloric antrum` (2D entities). Such a generic part relation suffices for describing spaces, surfaces

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[*] Classes represented in the **AT** appear in the text in `New Courier` font.

and lines, as well as body substances (e.g., blood, semen), but greater specificity is called for when representing the parts of anatomical structures. Based on the work of Winston et al.[15] several authors have proposed a classification of parts, but cognates of the generic part relation are implemented, apart from the FMA, only in the anatomy (common reference) module of GALEN[16]. We have elaborated on such earlier proposals and developed a taxonomy of part-whole relationships[17] for guiding the representation of anatomical parts in the FMA. In addition we have defined distinct partitions for decomposing anatomical structures, and also enhanced the specificity of parthood by attributing part relations[17.]

**Elaboration of Part Relations**

When we address partonomy pertaining to instances of the class `Anatomical structure`, specifications must be introduced in the generic part-whole relationship because anatomical structures can be and have been decomposed based on several different contexts. The taxonomy of anatomical part relations, shown in Figure 2, illustrates such contexts. For instance, the stomach can be decomposed into its fundus, body and pyloric antrum (to name but a few of such parts), in one context and, as already mentioned, into its wall and cavity, in another context. We regard the former as a spatial partition into "*regional*" parts, whereas the latter is a compositional partition into "*constitutional*" parts. Constitutional parts are genetically determined, whereas regional parts are defined not only by genetically regulated developmental processes (e.g., lobe of lung, cortex of kidney, finger), but also by arbitrary landmarks or coordinates, such as used for demarcating the thoracic and abdominal parts of the aorta and the fundus of the stomach from adjacent parts of the corresponding wholes.

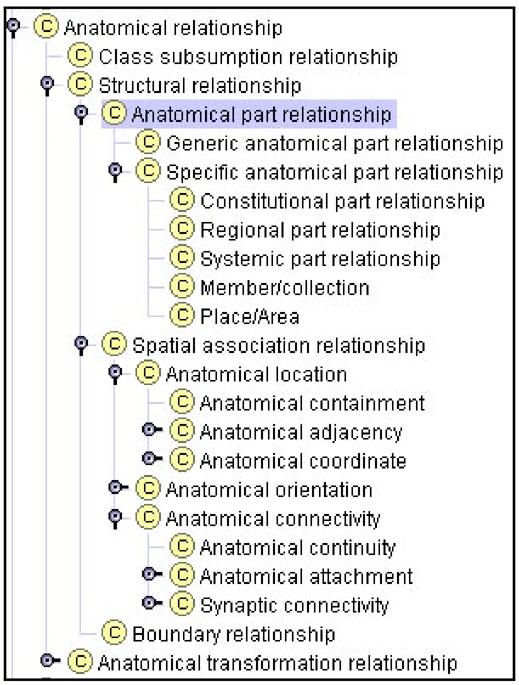

Figure 2. Classes of anatomical part-whole relationships represented in Protégé-2000.

As illustrated in Figure 3, we represent this distinction by associating the attributes *anatomical* or *arbitrary* with regional parts, and do so for anatomical structures at all levels in the **AT**. Figure 4 applies this scheme to the stomach. Furthermore, these attributes provide the basis for the different views of regional partitions, as in the case of the liver, where its traditional partition into lobes based on *arbitrary* landmarks constitutes an arbitrary kind of regional view, while another partition based on the distribution of the tributaries of the hepatic veins or branches of the hepatic artery constitutes an *anatomical* regional view. Both views, and in the case of some other organs, more than two such views, are current in clinical and educational discourse.

Although inherent 3D shape is a defining attribute of instances of the class `Anatomical structure`, the nature of continuities established between anatomical structures is such that certain parts of one structure overlap or become shared by another. The tracheobronchial tree and right and left lungs each meet the definition of `Organ`. However, since a part of the tracheobronchial tree is embedded in the right and left lungs, a distinction needs to be made between the parts of the tree that are shared and unshared. Instances of the class that form branching trees (e.g., `Vascular tree`, `Neural tree`) and serous sacs (e.g., `Pleural sac`, `Peritoneal sac`) always share some of their parts with instances of another organ subclass. The attributes *shared* and *unshared* can be associated with constitutional as well as with regional parts and these attributes can specify partonomic relationships at any level of the **AT.**

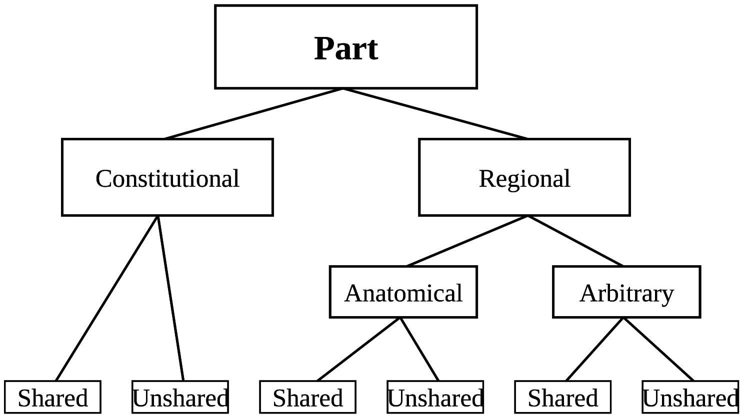


Figure 3. Taxonomy of part-whole relationships for subclasses of `Anatomical structure`.

Figure 3 illustrates these meronymic enhancements that are accordingly inherited by the concepts subsumed by the class `Anatomical structure`.

In our opinion, accurate and comprehensive representation of the structural organization of the body requires the level of specificity we are implementing in the FMA for partonomic relations. Indeed, all these knowledge elements are explicitly or implicitly embedded in scholarly treatises of anatomy, as well as in anatomical discourse. An ontological representation of parthood, however, also demands that clear distinctions be made between part relations and other relations, such as boundary and containment (see below).

**Distinction of Part and Other Structural Relations**

In addition to boundary, containment relations, included in the Spatial Association network, may also be conflated with partonomic relations. While context in natural language usually circumvents confusion and ambiguity, we believe both boundary and containment need to be distinguished explicitly in an anatomical reference ontology. Therefore we have formulated two rules, which enforce these distinctions[17].

As already illustrated in the sections on the boundary and partonomy networks, the rule of *Dimensionality Consistency* distinguishes between boundary and partonomy relationships in the FMA. The rule of *Containment/Part Distinction* constrains the *-contains-* relationship to the class

| Constitutional part \ Regional part | Fundus | Body | Antrum |
|---|---|---|---|
| Wall | Wall of fundus of stomach | Wall of body of stomach | Wall of antrum of stomach |
| Cavity | Cavity of fundus of stomach | Cavity of body of stomach | Cavity of antrum of stomach |

Figure 4. Table columns represent the *arbitrary* regional parts of the stomach and table rows, the constitutional parts.

Anatomical space, and its inverse, *-contained-in-*, to Body substance and Anatomical structure. Therefore, in accord with this rule, the following are valid assertions: Tibialis anterior *-contained in-* Anterior compartment of leg; Anterior compartment of leg *-part of-* Leg; Tibialis anterior *-part of-* Leg. Although this example suggests transitivity across containment and part relations, another example negates such an assumption: Urine *–contained in-* Cavity of urinary bladder; Cavity of urinary bladder *–part of-* Urinary bladder; but Urine *-part of-* Urinary bladder is an invalid assertion. Thus, in anatomical context, keeping containment and part relations independent of one another, serves the purpose of specificity and clarity.

***Spatial Association network***

In addition to boundary and parthood, the FMA also represents topological relationships that are important for describing the structure of the body. These relations constitute the Spatial Association network (**SAn**) component of the ASA, which itself consists of a number of subnets corresponding to the descendants of the Spatial association relationship class shown in Figure 2. The descendants of this relationship class represent three topological axes or viewpoints in terms of which anatomical spatial associations may be conceptualized:

***SAn = (Location, Orientation, Connectivity)*** *(3)*

**Location.** Topology deals extensively with location, and the relation *-has location-* is used ubiquitously to describe the positioning of not only anatomical structures relative to one another, but also to associate disease processes with anatomical entities that they affect (e.g., hepatitis *-has location-* liver). However, the modeling of the structural arrangement of anatomical entities in the body calls for greater specificity. Therefore the relation *-has location-*, as such, is not used in the FMA at all; rather it serves as the type for three specific location relationships, which are explicitly implemented in the model (Figure 2). We specify location relationships between anatomical entities as *Containment*, *Adjacency* or *Qualitative coordinate*. For the current purpose enough has been said about containment in relation to its conflation with the part relation; here we elaborate on adjacency and qualitative coordinates.

**Adjacency.** We consider anatomical entity A to be adjacent to entity B if A and B have no overlapping (shared) boundaries and parts, and no other anatomical entity is interposed between them. The adjacency relationship is symmetrical and is valid for entities of the same dimension. Using an example first as an approximation to illustrate the relationship: lung *-adjacent to-* diaphragm; inferior surface of lung *-adjacent to-* superior surface of diaphragm. The modeling in the FMA is more accurate than this assertion implies; it takes into account the interposition of the pleural sac between the lung and the diaphragm: Right lung *-surrounded by-* Right pleural sac; Basal part of right pleural sac *-adjacent to-* Basal part of right lung, Right dome of diaphragm.

The example illustrates a number of challenges for modeling adjacency relationships: 1. Adjacency may be viewed at different levels of granularity in different contexts: the first approximation hides a number of inaccuracies and ontological inconsistencies, although it may be acceptable for the representation of anatomical knowledge at an elementary and crude

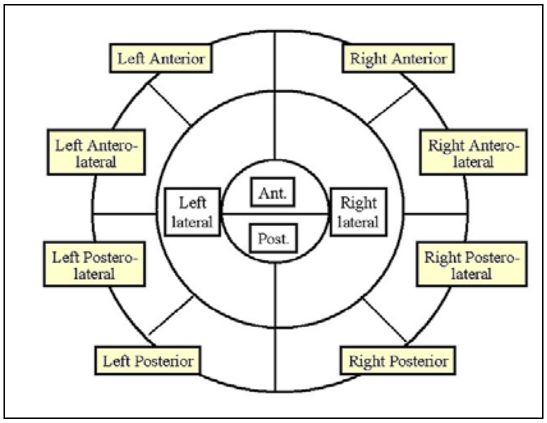

Figure 5. Qualitative radial coordinate system for the **Dt** shape class 'conventional cylinder'.

level; the second one describes the arrangement of the related entities without ignoring elements of reality that may not be meaningful to some users, and this is the objective of the FMA; 2. Adjacency assertions must be constrained to anatomical entities subsumed by the same **AT** subclasses of `Anatomical structure`, which specify levels of structural organization: `Biological macromolecule`, `Cell part`, `Cell`, `Tissue`, `Organ part`, `Organ`, which correspond to the granular partitions of the body proposed by Bittner and Smith[18]. Thus, organs: `Right lung`, `Right pleural sac`; organ parts: `Basal part of right pleural sac`, `Basal part of right lung`, `Right dome of diaphragm`; 3. Adjacency relationships must be qualified by such descriptors as -*surrounded by*- and its inverse -*surrounds*-, or by qualitative anatomical coordinates that describe vectors of directionality, illustrated by the following example.

The esophagus, or a part of it, inherits its shape from the **Dt** class `Conventional hollow cylinder`. This shape specifies the set of adjacency relationships that is allowed for this shape class. Figure 5 shows these relationships graphically in terms of a qualitative radial coordinate system. In Figure 6 the qualitative coordinate system for cylinder is superimposed and centered on the esophagus in a section of the male Visible Human at the level of the eighth thoracic vertebra. In Figure 7 the adjacencies of `T8 part of the esophagus` are represented symbolically in terms of these qualitative coordinates. Although some of these adjacency relationships remain constant, others change from one vertebral level to the next. The AT of the FMA represents each vertebral level of the esophagus as a discrete subzone, which permits the symbolic modeling of the changing adjacency relationships of the esophagus as it "passes" from the neck to the abdomen.

It deserves mention that the qualitative coordinates anterior, posterior, lateral, mentioned in Figures 5 and 7, as well as others (e.g., superior, inferior) are standard directional terms defined in relation to the orientation of the body in the so called "*anatomical position*"; they remain constant regardless of the position the body assumes.

The spatial knowledge captured by the adjacency relationships shown in Figure 7 is of importance to a student dissecting the esophagus for the first time and also to a surgeon planning to remove a lymph node adjacent to the esophagus through a mediastinoscope. The FMA can provide knowledge of adjacency relationships appropriate for applications developed for each of these types of users. Moreover,

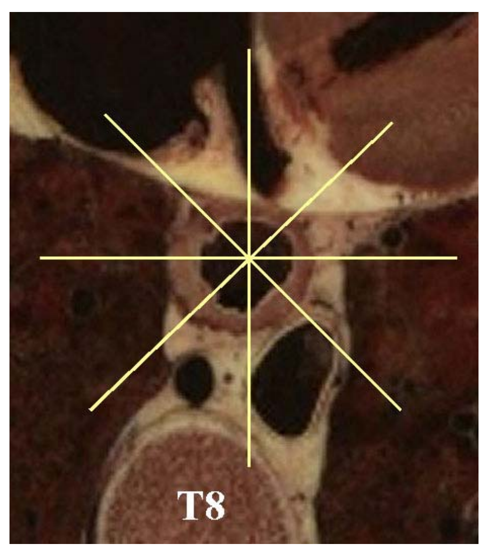

Figure 6. Coordinate system of conventional cylinder superimposed on T8 part of esophagus.

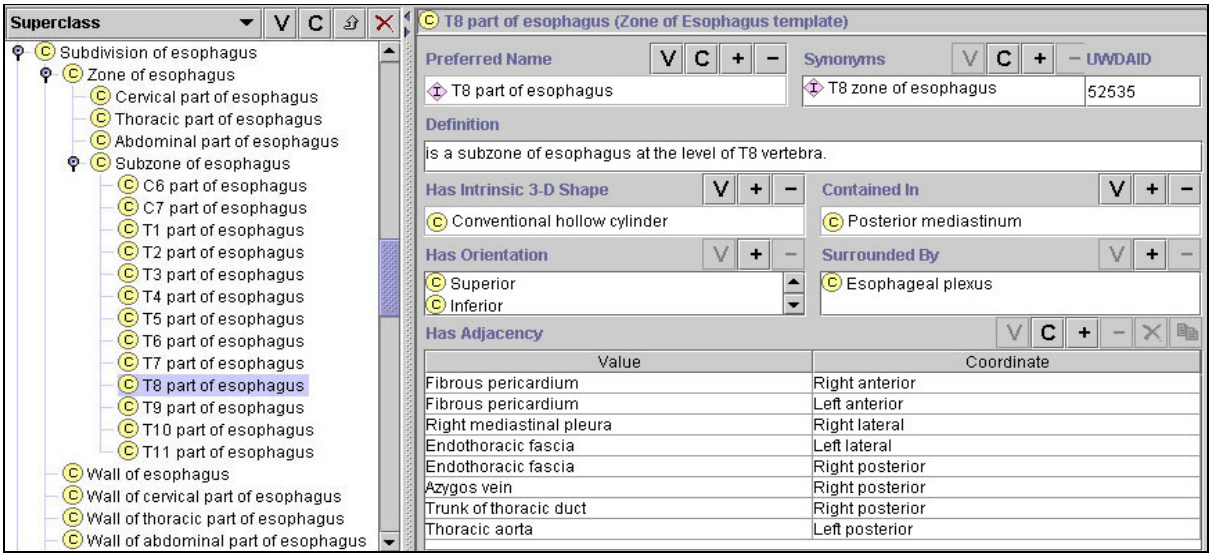

Figure 7. Frame-based representation in Protégé-2000 of `T8 part of esophagus` in **At** in the left pane and its attributes in the right pane.

since we can represent inverse values for these relationships, and make inferences based on their transitivity, the FMA could support inference required for answering user-generated spatial queries at different levels of complexity.

Figures 5 and 6 invite comment about the relative usefulness of geometric and qualitative coordinates for representing such structural attributes as location and adjacency. The relationships expressed in terms of qualitative coordinates could be derived from the quantitative geometric matrix of the Visible Human data set, for example. These geometric coordinates, however, would have to be expressed as qualitative coordinates in order to make them intelligible in anatomical discourse. Geometric coordinates are valid only for one instance, whereas anatomical qualitative coordinates describe relationships that hold true in all members of a species. Only those structures can be referenced by geometric coordinates that are visible with a particular imaging modality. Qualitative coordinates, on the other hand, can describe the relationship of invisible structures to visible ones, as illustrated in Figure 7 by the esophageal plexus, fibrous pericardium and mediastinal pleura; none of these structures can be identified in the image of the anatomical section. Moreover, inference required for reasoning about structural relationships within the body must make use of qualitative coordinates. Therefore, the symbolic representation of location relationships in terms of qualitative coordinates is an important component of the FMA.

In summary, location of an anatomical structure may be described in terms of containment (e.g., `Right lung` -*contained in*- `Right half of thoracic cavity`); adjacency (e.g., `Right lung` -*surrounded by*- `Right pleural sac`) and qualitative anatomical coordinates, such as those illustrated for `T8 part of the esophagus.`

**Orientation.** Since a defining attribute of entities subsumed by the class `Anatomical structure` is inherent shape, their orientation within the body can be specified, largely in terms of shape and the qualitative coordinates of their parts or boundaries that demarcate them from other structures. Figure 8 illustrates orientation information entered in the FMA for the `Esophagus`, the shape of which is the dimensional entity `Hollow cylinder`. The

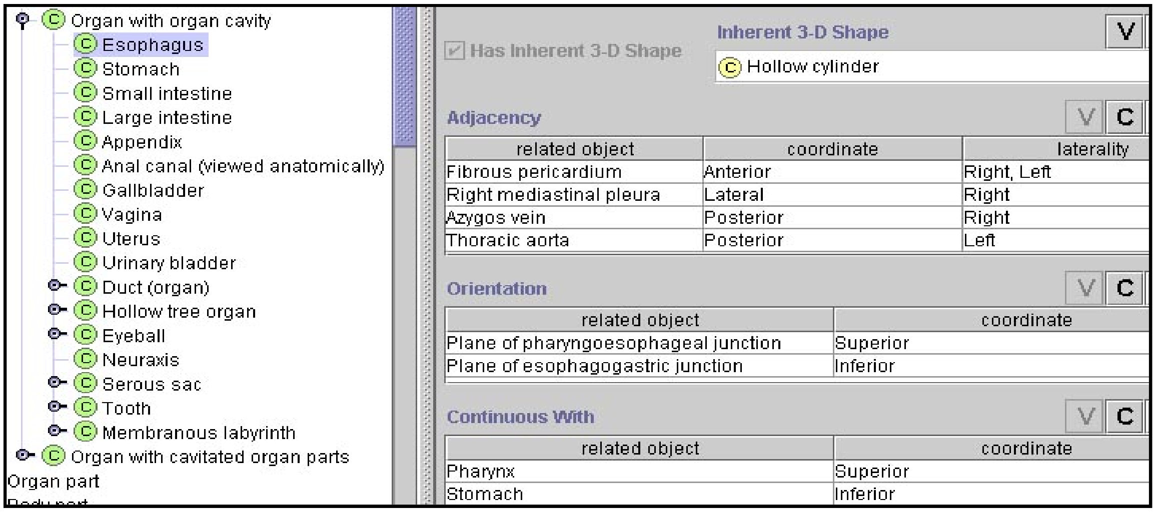

Figure 8. Spatial Association network (SAn) slots *–adjacency-*, *-orientation-* and *–continuous with-* in the frame of the `Esophagus` displayed in Protégé-2000.

orientation of the esophagus is defined by the virtual `Plane of pharyngoesophageal junction` and `Plane of gastroesophageal junction`, which demarcate the esophagus from the pharynx and the stomach respectively. The orientation of the esophagus is specified by the qualitative coordinates superior and inferior for these two planes, respectively, which serve as coordinate and vector reference in the context of the human anatomical position. In other instances, it is necessary to declare right or left laterality coordinates. For example, in describing the orientation of the cone-shaped `Heart`, we use `Apex of heart` and `Base of heart` as the entities of reference and specify their location by qualitative coordinates (inferior and left lateral for the apex and posterior for the base). Orientation is treated much less specifically in conventional anatomical discourse than in geometric modeling. However, there is a need for coordinating symbolic modeling in the FMA with geometric modeling and this will require, for example, that we define axes of anatomical structures for specifying orientation also in the FMA.

**Connectivity.** Among anatomical structures only cells floating free in blood and other body substances or locked in the lacunae of hyaline cartilage can be considered unconnected to other structures. Even cells that move about in loose connective tissue, or on epithelial surfaces, or through epithelia form adhesions with the substrates on or through which they move. With the few notable exceptions, all anatomical structures are connected to one another through a variety of continuities and junctions. Connections exist horizontally and vertically across all levels of structural organization or granular partitions, which accounts for the material integrity of the human body or that of any biological organism. Perhaps the greatest attention has been paid to inter- and intracellular junctions, which, like junctions at higher levels, have a specific structure that distinguishes them from one another. Therefore in the FMA, we classify these junctions as anatomical structures, rather than relationships. In this section we are concerned with the connectivity relationship, rather than the material entities that establish the physical connection between two or more structures.

As in the case of location, we consider connectivity a relation type or class and explicitly implement in the FMA only its cognates: *Continuity*, *Attachment* and *Synaptic connectivity*.

**Continuity**. We regard continuity as a symmetrical connectivity relationship between two or more anatomical entities asserted by the relationship -*continuous with*-. We regard A as -*continuous with*- B if no real boundary exists between corresponding constitutional parts of A and B. For example, in these terms, continuity exists between a main arterial, venous and nerve trunk on the one hand, and their respective branches on the other. We also sanction the assertion `Esophagus` -*continuous with*- `Stomach`, because constitutional parts of their wall (mucosa, submucosa, muscularis) are not demarcated by a real boundary. `Esophagus` and `Stomach` qualify as different organs because of the distinct structural attributes they exhibit in terms of shape and the characteristic arrangement of their constitutional parts (the structure and morphology of their mucosa and organizational pattern of muscle layers in their wall).

As illustrated in Figure 8, we attribute each continuity relationship with a qualitative coordinate, in order to distinguish continuities with more than one structure. Such attributed continuities also need to be declared between regional parts of an organ, which may or may not be associated with a structural change in the constitutional parts of its different regions. For example, we need to assert that continuity exists between the fundus and the body of the stomach, but there is no continuity between the fundus and the pyloric antrum, all of which are regional parts of the stomach. The FMA does not accommodate negation or disjunction; therefore the lack of continuity with an entity must be inferred from its absence among the values of the -*continuous with*- slot in the frames of two entities.

Continuity between arbitrary regional parts of an anatomical structure may be taken for granted. However even such continuities need to be explicitly represented, since it needs to be asserted that the thoracic part of the esophagus is continuous *superiorly* with its cervical part, and continuous *inferiorly* with the abdominal part of the esophagus. Listing continuities without their attributes would omit an element of structural knowledge.

The FMA also represents continuities between anatomical spaces, surfaces and lines as well as between anatomical structures. The modeling of these continuities, however, presents less of a challenge than that of anatomical structures.

**Attachment.** We regard attachment as an asymmetrical connectivity relationship between two or more anatomical entities asserted by the inverse relationships -*attached to*- and -*receives attachment of*-, which are constrained to selected subclasses of `Anatomical structure`. We regard A as attached to B, and B as receiving the attachment of A, if A and B are subsumed by different subclasses of `Anatomical structure` and if A intermingles at least one of its constituent parts with a constituent part of B. For example, the patellar ligament [subclass of `Ligament(organ)`] is attached to a narrow area along the lower margin of the patella and to a tuberosity at the upper end of the tibia [the two bones are subsumed by subclasses of `Bone(organ)`]. All these anatomical structures have their own real boundaries, but at its proximal and distal ends, the stout ligament comes into intimate contact with circumscribed areas of each bone, where extensions of its collagen fiber bundles (so called Sharpey's fibers) penetrate the bone and intermingle with each bone's own matrix. The ligament may be separated from the bone only by severing Sharpey's fibers.

Similar attachments occur between membranes and bones (e.g., the circumference of the tympanic membrane is attached to bones of the skull forming the external auditory meatus), membranes and viscera (e.g., visceral pleura is attached to the lung proper intermingling its loose connective tissue on its non-serous surface with the fibrous stroma of the lung), and also between muscles and bones.

Muscle attachments are qualified with respect to whether the bone to which they attach moves or remains stable in the normal course of the muscle's action. Therefore, each site of a muscle's attachment is attributed as either the origin or the insertion .

**Synaptic connectivity.** We regard synaptic connectivity as a specialized attachment relationship occurring in neural and neuromuscular synapses. It is also implemented as an attributed relationship that identifies the connection between the parts of synapsing structures like the axon and the dendrite or the neuromuscular junction.

The included figures which illustrate various relationships that in aggregate constitute the ASA are all based on Protégé-2000, the frame-based ontology authoring and editing environment[19]. The next section enlarges on aspects of this implementation, which is a critical element of the disciplined modeling process through which we have and continue to populate the Foundational Model of Anatomy.

## IMPLEMENTATION

We consider the evolution of the FMA from an earlier controlled vocabulary and elaborate in some detail about the representation of attributes and relationships using the Protégé-2000 modeling environment.

***UWDA and FMA.*** In its initial iteration the FMA was called the University of Washington Digital Anatomist (UWDA) vocabulary and was developed as an anatomical enhancement of UMLS[1]. Populating the UWDA we were less concerned with the richness of anatomical relationships than with the comprehensiveness of the classification of anatomical entities. The authoring tool we developed was designed to generate parallel hierarchies (directed acyclic graphs) based on *is-a*, *part-of*, *branch-of* and *tributary-of* relationships. As we populated subclasses of `Organ part` in the *is-a* hierarchy, for example, we also aligned the concepts along the transitive *part-of* relationship in another hierarchy. However, such a link-centric view and representation of anatomy proved to be inadequate once we began to appreciate the complexity of relationships that were necessary for comprehensively describing the anatomy of the body. The need for such a comprehensive, reusable resource led to formulating the FMA as an ontology of the physical organization (structure) of the human body.

Close to 70,000 FMA concepts are still accessible through the UWDA vocabulary of UMLS, providing a comprehensive controlled terminology for macroscopic, microscopic and neuro-anatomy. Our current work entails the instantiation of the **ASA** networks of these concepts. The association of such multi-dimensional relationships with anatomical concepts called for a node-centric view of anatomy, which was beyond the capacity of the link-centric representation we implemented. The frame-based knowledge acquisition system Protégé-2000[19] has the requisite expressivity and scalability for comprehensively modeling anatomical relationships encompassed by the **ASA**. The same will be true for **ATA** relationships, once we begin the implementation of developmental transformations.

### *Modeling the ASA in Protégé-2000*

Protégé-2000 has been adapted to meet current and evolving needs of the FMA[19]. It is being enhanced by customized active user-interface components as we encounter new challenges in modeling[20].

We regard the FMA as an ontology of concepts and relationships which are represented as frames in Protégé-2000. These frames are data structures, which, through their slots, specify the types of information to be associated with a concept in the **AT**. The values for some of these slots are derived from the **AT** and others from two additional taxonomies: the Dimensional taxonomy (**Dt**) and Physical Properties taxonomy (**PPt**). A fourth taxonomy, the 'Anatomical entity metaclass' hierarchy assures the selective inheritance of the attributes of the entities represented in the **AT**. The 'Anatomical entity metaclass' hierarchy provides templates for all the **AT** classes. Each template is a frame composed of a set of slots; each slot corresponds to a defining or associative attribute manifested by the entities subsumed by a particular **AT** class. The templates become elaborated by new attributes that are introduced as slots when a new class in the **AT** subsumes entities that exhibit the new attribute.

The frames of **AT** classes are assigned as instances of metaclasses (or templates) and therefore inherit the templates slots of their respective metaclasses, These slots now become own slots of the instances of classes, the values of which are unique to the instances.

## DISCUSSION

The Foundational Model of Anatomy is the largest and most comprehensive ontology for the anatomy domain, which encompasses in one continuous information space anatomical structures at all levels of biological organization from macromolecules to cells, tissues, organs, organ systems and body regions. Our purpose in this communication is to illustrate the implementation of a theory expressed by the high level schemes of the FMA and its **ASA** component. This theory concerns the computable symbolic representation of the structural and topological arrangement of the body's constituents. We have emphasized the critical role such relationships play in the modeling of this arrangement. They provide the basis on which spatial reasoning (inference) can be supported[21,22].

The FMA continues to evolve, in particular through the instantiation of its **ASA** component, the main topic of this communication. Although the FMA and **ASA** model a broad segment of declarative structural knowledge in great detail, there remain numerous gaps that must still be filled and other areas that must be refined. However, we consider the most significant feature of the FMA to be not so much its contents as its semantic structure. This structure, reflected in the high level conceptualization coupled with the practical implementation of the ontology, was established through an evolving disciplined approach to populating the knowledge base[4].

A salient feature of our approach is the deliberate constraining of the modeling to a structural context. Structure provides the foundation for all other types of biological information. We believe that the logical and consistent organization of biological structure is a prerequisite for the representation of other biological fields. Therefore we regard the FMA as a *reference ontology* for biological structure. By this assertion we mean that in its "native" format the FMA may not precisely meet the needs of any particular user group. However, developers of applications designed to address particular problems and tasks should be able to filter and derive from the FMA the anatomical information they need. With this motivation in mind, we provide access to the FMA through the Internet and make it available to those whose need for anatomical information goes beyond the mere reuse of anatomical terms.[23]

We believe that even more important is the role the FMA can play as a reference ontology for other disciplines and domains by providing a template for other symbolic models. First examples of such a use of the FMA are the anatomy of non-human species[24] and physiological function[14]. It is our hope that ontology developers in other domains will follow.

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