

An Ontological Framework for Representing Topological Information in Human Anatomy

Takeshi IMAI, Kazuhiko OHE
Graduate School of Medicine,
The University of Tokyo
Tokyo, JAPAN

Emiko SHINOHARA, Masayuki KAJINO,
and Ryota SAKURAI
Dept. of Healthcare Information Management,
The University of Tokyo Hospital
Tokyo, JAPAN

Kouji KOZAKI
The Institute of Scientific and Industrial Research,
Osaka University
Osaka, JAPAN

Riichiro MIZOGUCHI
Research Center for Service Science, School of Knowledge
Science, Japan Advanced Institute of Science and
Technology (JAIST)
Ishikawa, JAPAN

Abstract—Medical ontologies have been a focus of constant attention in recent years as one of the fundamental techniques and knowledge bases for clinical decision support applications. In this paper, we discuss the description framework of our anatomy ontology with a focus on representing topological information, which is required for anatomical reasoning in clinical decision support applications. Our framework has major advantages over preceding studies with respect to: (1) representations of branching sequence; (2) combined representation of relevant knowledge with the use of “*general structural component*”; and (3) cooperation with the disease and abnormality ontologies.

Keywords—*Medical Ontology; Human Anatomy; Topological Information; Clinical Decision Support Application*

I. INTRODUCTION

Physicians use various kinds of knowledge in their clinical decision making. The knowledge can be categorized into two groups: 1) superficial knowledge such as empirical associations between diseases and their manifestations, and 2) deep knowledge such as pathophysiological causal relations or anatomical knowledge. Implementing such deep knowledge in clinical decision support applications, as well as superficial knowledge, has been widely recognized as fundamental in dealing with difficult cases and in supplying satisfactory explanations about inferred results. Since the 1970s, substantial efforts have been made to develop clinical decision support applications by implementing deep knowledge [1][2]. Especially in anatomical reasoning, topological information has been considered important for deep knowledge. For example, topological information, such as “Nerve-X has a branch of Nerve-Y” is needed for inferring that “If Nerve-X is disordered after branching with Nerve-Y, the area innervated by Nerve-Y does not get disturbed.” Ohe et al. proposed a framework to represent such topological information using PROLOG[3][4]. In addition to a nerve system, topological

information about the vascular network is also important for cause-effect reasoning (e.g., which organs will be damaged if upstream vessel-clogging occurs?).

Ontologies are one of the most promising techniques for formally representing and sharing medical knowledge. Several anatomy ontologies or terminologies have thus far been developed, such as the Foundational Model of Anatomy (FMA) [5] and the anatomical component of the Systematized Nomenclature Of MEDicine - Clinical Terms (SNOMED-CT)¹. SNOMED-CT is known as the world’s largest clinical terminology, and includes approximately 30,000 anatomical concepts; however, topological information regarding anatomical entities has not been described. FMA is another important anatomy ontology and is widely recognized as one of the biggest and most sophisticated biomedical ontologies ever developed. It contains more than 30,000 relations regarding topological connections between anatomical entities (e.g., “Abdominal part of esophagus”=(connected_with)=> “cardia of stomach”). However, from the viewpoint of utilizing the ontology for clinical decision support applications, there are several insufficiencies. First, branching sequence information is missing for subsystems such as the cardiovascular and nerve systems, and therefore, it is difficult to use it for cause-effect reasoning based on topological connections, as stated in the vessel-clogging example above. Second, there is some missing information, which would combine relevant knowledge. For example, there is no information that associates the “*articulate_with*” relation between Bone-A and B with Joint-C by which the relation holds. They are defined independently. It is thus difficult to reason about “If Joint X is damaged, which ‘*articulate_with*’ relation between two bones will be affected?” and vice versa.

To tackle these problems, we have developed the application-oriented anatomy ontology from scratch since 2007,

¹ <http://www.ihtsdo.org/snomed-ct> (accessed April,2016)

which constitutes our entire medical ontology together with the disease ontology [6][7] and the abnormality ontology [8] which we also have developed in parallel as a national project. Those ontologies share the same top-level ontology YAMATO [9], and are designed to work together. Diseases are defined as causal chains of clinical disorders, each of which is defined in the abnormality ontology with reference to the anatomical structures described in the anatomy ontology.

As a late comer, our strategy is aimed at leveraging preceding research with the current state-of-the-art ontology engineering theory to make it ontologically sound. In this paper, we discuss the description framework of our anatomy ontology with a focus on representing topological information, which is required for anatomical reasoning in clinical decision support applications.

This paper is organized as follows. In Section II, we introduce topological information in focus and representations in FMA. In Section III, we outline our description framework. In Section IV, we present some examples. And in Section V, we discuss our framework comparing with FMA and give an outline of future work, followed by concluding remarks.

II. TOPOLOGICAL INFORMATION REGARDING HUMAN ANATOMY AND ITS REPRESENTATION IN FMA

A. Topological information for clinical decision support applications

Topological connections exist in almost every place in the human body: not only in subsystems (e.g., vascular network, alimentary system, nerve system and so on,) but also in adjacency among different types of anatomical entities such as organ, soft tissue, tendon, skin, peritoneum, etc. Most of all, connections in subsystems can be considered important since they are tightly related to functions provided by the subsystem, such as transporting blood, transmitting electrochemical nerve impulses, propagating physical force and so on. Therefore, for the use in clinical decision support applications, we have to distinguish various types of those connections, that is, a simple “connected_to” relation cannot cover all variations.

In addition, from a viewpoint of availability for clinical applications, branching sequence information is indispensable for several situations: (1) topological simulation (e.g., guiding introduction of a catheter); (2) cause-to-effects reasoning (e.g., “If a dissection is localized in the area of arch of aorta, stomach or liver would not be damaged”); and (3) effects-to-cause reasoning (e.g., estimating the area of nerve damage from patient’s manifestations, such as disorders occurred only in “biceps” and “pronator teres”).

B. Representations of topological connections in FMA

FMA is one of the most famous medical ontologies in the domain of anatomy. It contains approximately 75,000 classes, over 120,000 terms and more than 2.1 million relationship instances from over 168 relationships types.² Among those relationship types, 31 were related to the representations of

² <http://sig.biostr.washington.edu/projects/fm/AboutFM.html> (accessed April 2016)

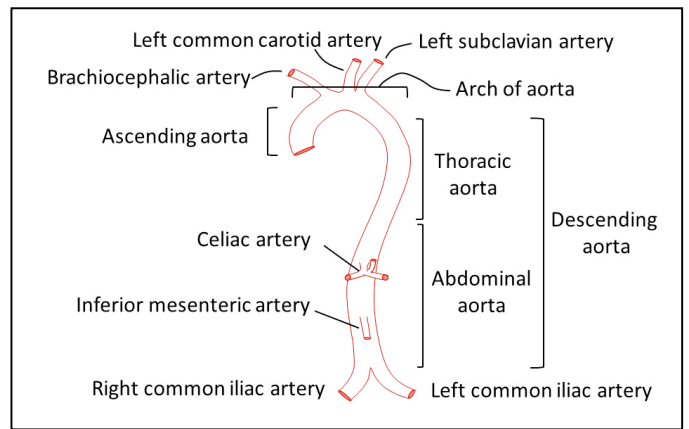


Fig.1 Vascular connections among aorta and downstream arteries

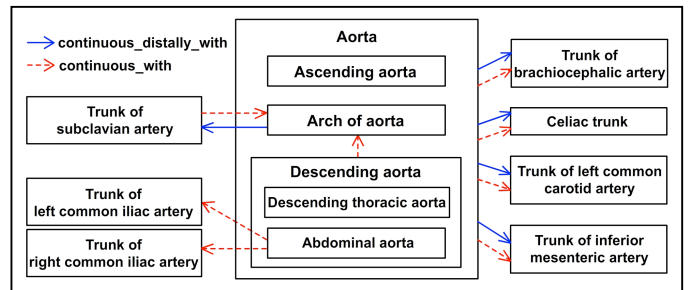


Fig.2 Representation of vascular connections in FMA

topological connections³. Seven types of relations are defined as subordinate concepts of “connected_to”, such as “continuous_with”, “attaches_to”, “articulates_with” and so on. Four types are defined as subordinate concepts of “regional_part”, such as “tributary_of” and “branch”. Other relations such as “nerve_supply” and “proximal_to” are defined independently.

In FMA, various types of connections between anatomical entities are represented using combinations of those relations. For example, Fig.1 illustrates the simplified model of vascular connections among the aorta and the downstream arteries, and Fig.2 shows how such topological connections are represented in FMA⁴. In Fig.2, arrows show connections between arteries (“continuous_with” and “continuous_distally_with”), and the nested boxes show “has_regional_part” relations among those entities. Following the path from “ascending aorta” to “descending aorta,” however, we observe some problems: (1) there are some missing connections between arteries (e.g., “ascending aorta” and “arch of aorta”); and (2) branching sequence information is also missing (i.e., four arteries on the right of Fig.2 are branched from “aorta” at the same time).

The first problem can easily be resolved using a later auditing process; however, the second problem is crucial for clinical decision support applications that utilize topological information based on an anatomy ontology. Branching

³ <https://sites.google.com/a/imai.am/suppl/icbo2016>

⁴ Based on FMA v3.2.1 on the Bioportal Web Site <http://bioportal.bioontology.org/ontologies/FMA> (accessed April 2016)

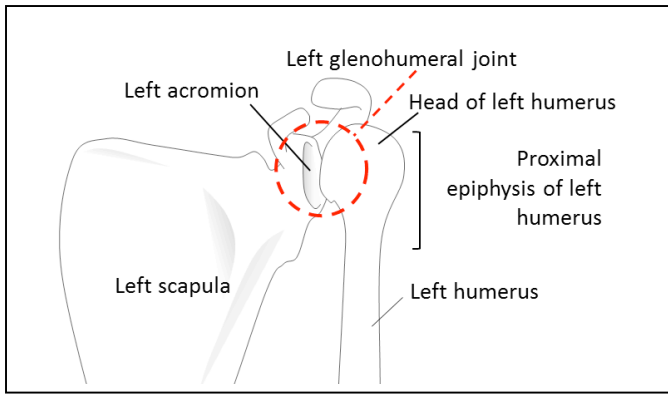


Fig. 3 Simplified model of the left glenohumeral joint

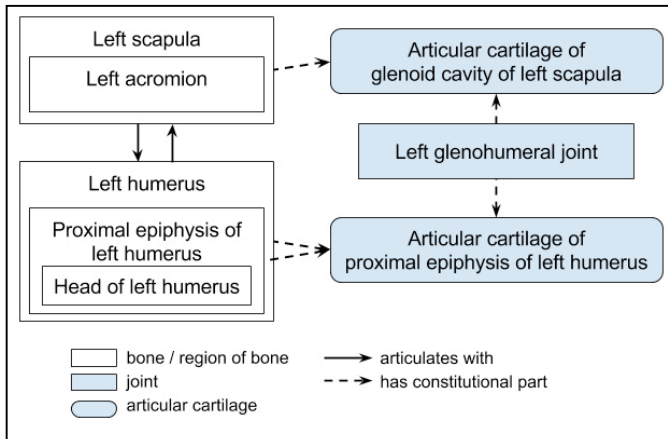


Fig. 4 Representation of the joint in FMA

sequence is indispensable for cause-effect reasoning (e.g., “Which organs will be damaged if upstream vessel-clogging occurs?”) as well as for answering some anatomical questions regarding positional relationships (e.g., “Which branches are located in the arch of aorta?”). Branching sequence is thus important not only for the cardiovascular system but also for some other subsystems of the human body that consist of “branching,” such as the nerve system, the respiratory system, and so on.

Other major examples of topological information relate to the musculoskeletal system and the alimentary system. They are fundamental subsystems of the human body, and it may seem much easier to model the topological information of those subsystems (e.g., connections between digestive canals) since they do not consist of branching. However, it is not as straightforward as it appears, especially for modeling “joints.” Fig. 3 illustrates the simplified model of the “left glenohumeral joint”, and Fig. 4 shows how such topological information is represented in FMA. The “left glenohumeral joint” is that which connects the two bones: the “left scapula” and “left humerus.” In FMA, the joint and the two bones share the same cartilage as a constitutional part – “articular cartilage of glenoid cavity of left scapula” and “articular cartilage of proximal epiphysis of left humerus” – and this is the only information by which we can associate the joint with each bone. There are also direct links (“articulates with”) between the two bones, which are defined independently from the joint. The problem here is that the links between the two bones

(“articulates with”) are not directly associated with the joint. In other words, there is some missing information, which would combine relevant knowledge.

Suppose that a dislocation occurs in the joint whereby the two bones are not damaged but only the connection between the two is broken. This would mean that an abnormality has occurred in the joint. In FMA, this can be modeled as the breaking of the “articulates with” relations; however, based on the relations in Fig. 4, this breaking cannot be directly associated with the abnormality of the joint and vice versa. Even if we assume that anatomical entities that share the same entity are connected, it is difficult to infer that the joint is associated with the “articulates with” relation since we cannot distinguish various functional types of such topological connections – transporting something, propagating signals or forces, and so on. For example, the “left ventricle” and “right atrium” can also be seen as connected using the same mechanism because they share the same entity “cardiac endomysium”; but it should be clearly distinguished from the case of the joint.

III. PROPOSED FRAMEWORK

In this section, we present some important features of our description framework to tackle the problems stated in Section II, mainly focusing on the representation of topological information. We used YAMATO as the top-level ontology, and all anatomical entities are defined under “organ in general.” Please see more details of the general features and upper-level structures in the cited papers [10][11].

A. Class constraint, role and role holder

Our basic framework for defining concepts is to describe their components, each of which has a class constraint and a role played in the context of defining the concept. The entity that plays a role in the context is called a “role holder.” Fig. 5 shows an example of concept definition in our framework with the use of the ontology editor Hozo⁵. In the definition of the “esophagus,” the entity constrained by a “wall-like structure” class and plays the “wall of esophagus role” in such a context is the role holder “wall of esophagus”, where “p/o” stands for a “part-of” link and “a/o” for an “attribute-of” link.

B. Representation of commonality and specificity

1) General structural components

Many organs share common structural components. For example, a “tubular structure” can be found in both the blood vessel and the esophagus. To represent such a commonality, we introduced “general structural components” and defined many general components as subordinate concepts, such as “tubular structure,” “cavity-like structure,” and “wall-like structure,” to name a few. Then, “tubular structure” was used as a class constraint in each definition of “blood vessel” or “esophagus.” The properties specific to each organ can be defined additionally or by specialization of the properties inherited from the common structural component. This mechanism is useful not only for the compact representation

⁵ <http://www.hozo.jp/> (accessed April 2016)

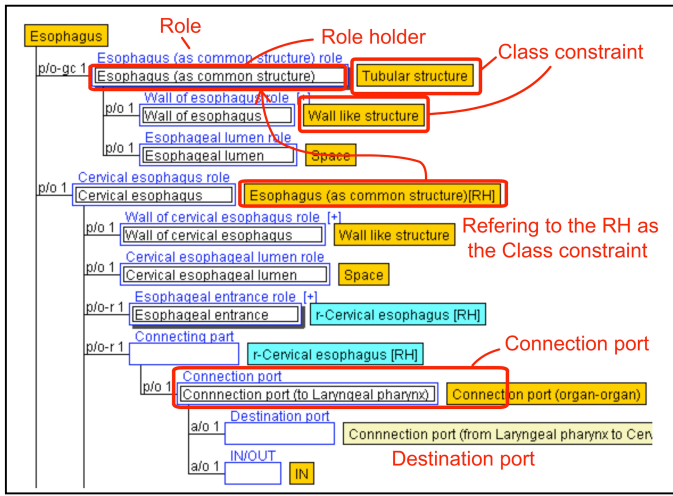


Fig.5 Class constraint, Role and Role holder

of properties, which are shared among many organs, but also for reasoning about the consequent dysfunction and the treatment. For example, the “tubular structure” has a potential malfunction of arctation, which will cause “a failure in supply” downstream. A possible treatment (e.g., “widening operations”) can also be shared among tubular structures (e.g., “blood vessel” and “esophagus.”)

2) Representation of laterality

To represent commonality and specificity for the entities that exist in both left and right sides of the human body, we utilized the same idea as that in “general structural component.” In defining the “right upper limb” and “left upper limb,” we first defined the “upper limb,” which is an abstraction of both and includes the common structures. Then, we defined the left and right upper limbs, with the “upper limb” referred to as a class constraint. The same mechanism was used to represent similar cases, such as the fingers, ribs and so on.

While for representing subsystems of male/female human body (e.g., cardiovascular system of the male/female human body, etc), we first defined the subsystem of the human body including the common structures only in both male and female, and then we defined the subsystem of male/female body as a subordinate concept.

C. Representation of partiality and collectivity

We also introduced variations of the “part-of” link because the normal “part-of” is insufficient to cover various cases.

1) p/o-gc (general component)

“Esophagus” can be divided into the “cervical esophagus,” “thoracic esophagus” and “abdominal esophagus,” and they share the same structure (“esophagus.”) To represent the situation, we introduced the “p/o-gc” link. In Fig. 5, the “esophagus” has the common structure, the “esophagus (as common structure),” which is used as a class constraint to define each part of the esophagus. In this way, “p/o-gc” is used to define a general component that can be referred to within the context of concept definition.

2) p/o-r (region)

“Esophageal entrance” is certainly a regional part of the “esophagus,” but it cannot be considered a structural component of the esophagus. “p/o-r” is a mechanism for assigning the name for a specific region of an anatomical entity that cannot be considered a structural component, such as “gastric angle” in the definition of “stomach.”

3) p/o-w (whole)

“Esophagus” can also be divided into “upper esophagus,” “mid-esophagus,” and “lower esophagus,” depending on the perspective. “p/o-w” is used to define another partition of the anatomical entity from a different perspective.

D. Representation of topological information

1) Connection port

To represent topological connections, we introduced the “connection port,” an imaginary port that exists in the “connecting part” of an anatomical entity. Each connection is represented as a cross-reference of connection ports. In Fig. 5, the “cervical esophagus” has a connecting part that has a “connection port (from the cervical esophagus to the laryngeal pharynx).” In the definition of “laryngeal pharynx,” a connection port in the inverse direction also exists. Each “connection port” refers to the other as the “destination port.” The types of connection can be distinguished by the class constraint (i.e., subtypes of “connection port.”)

By introducing this mechanism, we can distinguish a physical abnormality of an anatomical entity from an abnormality of a connection that the entity has, such as the dislocation example stated in Section II.

2) Branching structure

To represent branching sequence, we also introduced the general structural component called “branching structure.” If “artery X” has branches of “artery Y” and “Z,” as shown in Fig. 6, we place the “branching structure” (blue circle) at each point of branching, and, thus, “artery X” is subsequently divided into “artery X: part1,” “artery X: part2,” and so on. Each connection is also defined as a cross-reference of “connection ports,” as explained previously. This mechanism was applied to human body subsystems that consist of “branching,” such as the cardiovascular system, nerve system, and respiratory system, and so on.

IV. EXAMPLES

According to the framework described in the previous section, we have developed the anatomy ontology from scratch since 2007. This ontology constitutes our entire medical ontology together with the disease ontology [6][7] and the abnormality ontology [8], which we have also developed in parallel as a national project. The anatomy ontology consists of approximately 150,000 concepts in total, which includes

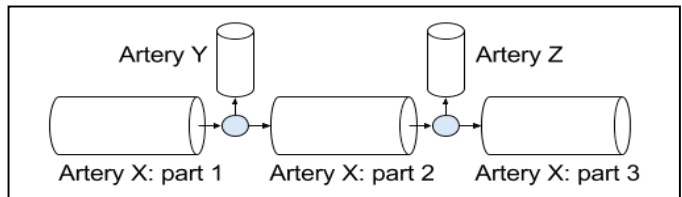


Fig.6 Branching structures

73,000 connection ports. In this section, we highlight the representation of topological information, and show the following two representative examples: A) cardiovascular system and B) musculoskeletal system.

A. Cardiovascular System

Fig. 7 illustrates the topological information of the cardiovascular system in our ontology, with arteries around the “aorta” taken as an example for comparison with FMA. The blue node represents an artery branched from the “aorta” whereas the red node represents a component of the entire “aorta”, divided by “branching structures”. These components of the aorta, such as “aorta-part1,” “aorta-part2,” and so on, are further organized by part-of relation and constitute larger components, such as the “arch of aorta” and “thoracic aorta.”

As shown in the figure, the branching sequence is well represented through the introduction of “branching structures” compared with the representation in FMA shown in Fig. 2. Moreover, it is also useful for answering some anatomical questions regarding positional relationships (e.g., “Which branches are located in the arch of the aorta?”).

B. Musculoskeletal System

We defined the “general joint structure” as a general structural component to describe each joint. Fig. 8 shows the representation of the glenohumeral joint in our ontology, which is constrained by the “general joint structure.” In the definition of the joint, two participating bones and cartilages are defined in reference to the original definitions as class constraint. Each bone, “scapula” or “humerus”, has a connection to the “glenohumeral joint” (“bone-joint connection”) and the connection between two bones (“bone-

bone connection,” the same as “articulate_with” relation in FMA) is defined in the context of the joint.

The dislocation example in Section II can then be naturally represented as the abnormality that occurred in the “destination port” in the “bone-joint” or “bone-bone” connection. Clearly, the connection is associated with the joint because the “destination port” is a slot that the joint has. Moreover, “even if the connection is broken, the two bones are not damaged physically” because the “destination port” is defined with the use of “a/o (attribute-of)” link.

To describe muscles and tendons, we also introduced the “compound component of the muscle and tendon” as a general structural component similar to “joint”. Finally, the musculoskeletal system was defined as a collection of such

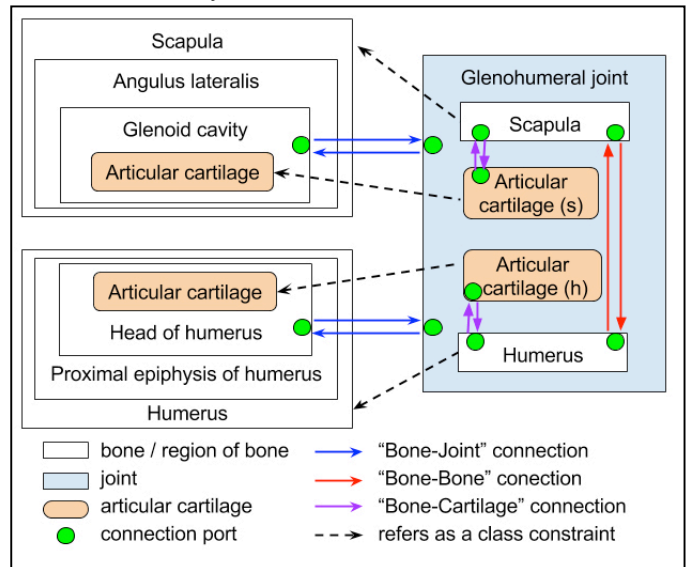


Fig.8 Representation of the glenohumeral joint in our ontology

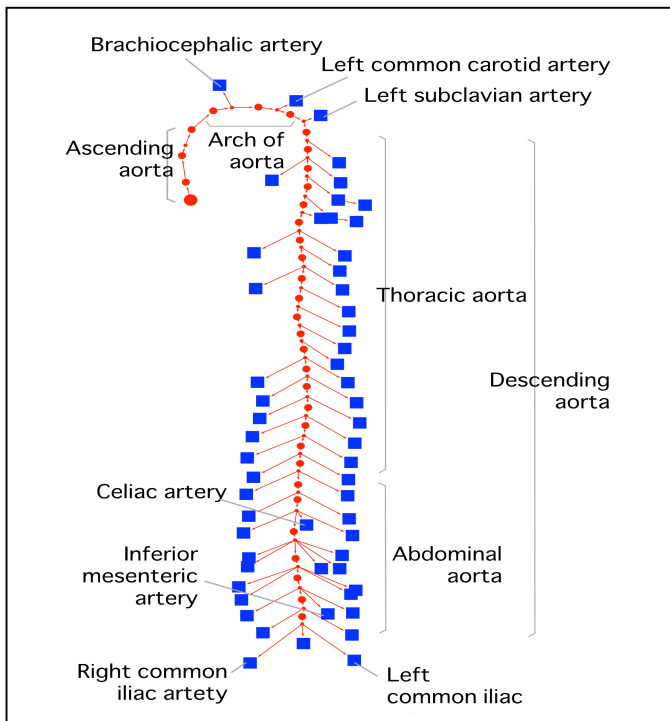


Fig.7 Topological information of arteries around the aorta

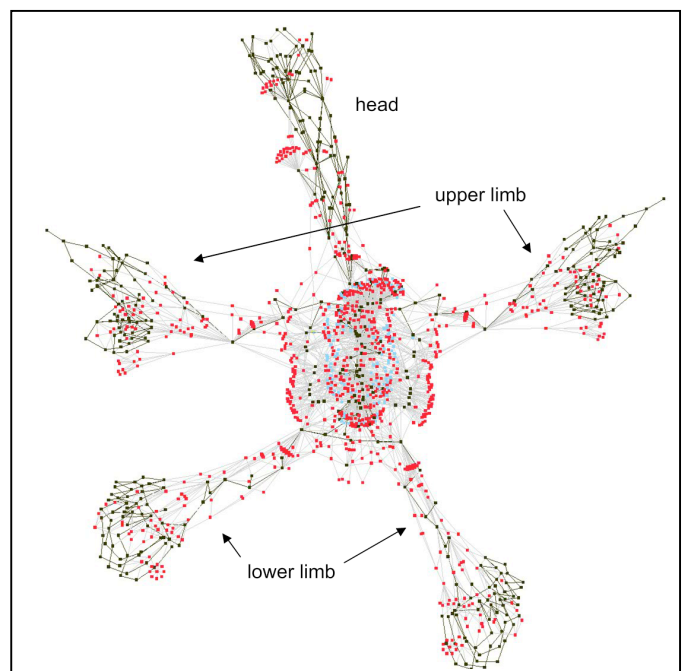


Fig.9 Topological information of musculoskeletal system

joints, muscles, tendons, and bones.

Fig. 9 shows the topological information of the musculoskeletal system in the entire human body, as drawn in Cytoscape⁶, where the black nodes represent the bones, the red nodes represent the muscles and the blue nodes represent the cartilages.

V. DISCUSSION

A. Important features of our description framework

As stated in Section II, previous research on anatomical ontologies has several insufficiencies from the viewpoint of utilizing these ontologies for clinical decision support applications. Our description framework works well for such a problem. First, with the introduction of “*branching structures*,” the branching sequence was well represented in our framework; such will be useful for cause-effect reasoning based on topological connections. Second, in FMA, no information associates the “*articulate with*” relation between Bone A and B with Joint C by which the relation holds. In our framework, “*general structural components*” play an important role in combining relevant knowledge. The connection between two bones was represented in association with the joint through the introduction of the “*general joint structure*” and “*connection port*,” which also enables us to distinguish the physical abnormality of an anatomical entity from that of a connection that the entity has.

The anatomy ontology was designed to work with the disease ontology[6][7] and the abnormality ontology[8], which we have developed in parallel. Diseases are defined as causal chains of clinical disorders, each of which is defined in the abnormality ontology with reference to the anatomical structures described in the anatomy ontology. It represents another important feature of our framework.

B. Limitations and future directions

This study has several limitations. First, anatomical structures related to anomaly were outside the scope of this study. For example, the several types of anatomic variations of the portal vein are common knowledge. For these cases, we selected the most common structure. Anatomical structures related to a fetus, the early development stage, and congenital abnormality were also excluded because we focused on the common and normal structures. Describing the detailed structures of the brain and the topological information of capillary blood vessels was difficult too, so they were outside of the scope or abstracted as “*capillary system*.” Second, the topological information of the integumentary system is currently not fully represented in our ontology. It is considered as another important issue related to topological information because it includes many fiat boundaries.

Extending our target to such anatomical systems is an important direction of our future work, which will increase the availability of the ontology and its applicability to clinical decision support systems. Currently, our ontology is available only in Japanese; however, we are now planning to develop the

English version and make it available via the Bioportal website, which is also an important direction of our future work.

VI. CONCLUDING REMARKS

In this paper, we discussed the description framework of our anatomy ontology, with a focus on representing topological information, which is required for anatomical reasoning in clinical decision support applications. Our framework has major advantages over those in previous studies in terms of the representation of branching sequence, combined representation of relevant knowledge with the use of “*general structural components*,” and cooperation with the disease and abnormality ontologies.

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⁶ <http://www.cytoscape.org/>