



Ontology-based mammography annotation and Case-based Retrieval of breast masses

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ABSTRACT

This paper describes ontology-based annotation of mammography and a Case-based Retrieval approach for breast masses from digital mammography archive. We first present our Mammography Annotation Ontology focusing on its main concepts and relationships, as well as the annotation tool. Then, we propose a model for similarity calculation between breast masses based on their high, mid and low-level features. We use Semantic Query-enhanced Web Rule Language (SQWRL) to process retrieval of similar masses from annotated mammography collection in OWL. We give both retrieving process and results we obtained from experimentations, in detail.

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1. Introduction

Breast cancer is the most general tumor for the women, in Western countries. Some statistics of breast cancer shows that nearly 1 in 8 women in the United States will develop invasive breast cancer over the their lifetime (Breast Cancer Statistics, 2012). But, breast cancer is most treatable when it is early detected. In this sense, a mammography examination, called a mammogram, is the gold standard for breast cancer screening, early detection and diagnosis. So, computer aided diagnosis of breast cancer becomes significant topic for mammography (Keles, Keles, & Yavuz, 2011; Mousa, Munib, & Moussa, 2005; Verma, McLeod, & Klevansky, 2010). The American Cancer Society recommends that women 40 years old and older have an annual mammogram. Mammograms can help detect 85–90% of all breast cancers, even before they are felt like a lump (Mammograms, 2012). Mammography is a specific type of imaging that uses a low dose X-ray system to examine breasts.

Radiology department of an average hospital may produce hundreds of mammograms per day. Thus, annotation and retrieval of mammographic examinations in an acceptable time is important for right diagnosis. In this respect, Hung and Chen propose a Case-based Retrieval (CBR) system for mammographic cases (Hung & Chen, 2006). On the other hand, in recent years, many researches aim to develop ontology-based medical image annotation and retrieval approach to reduce the occurrence of irrelevant resource retrieval in a medical imaging information system. The main goal is

to answer the user queries based on semantic relations that can be inferred from meaningfully between the data items. Hu et al. built a semantically rich system by accommodating image annotation and retrieval services around a rigidly defined ontology for medical images used in breast cancer treatment, in 2003. The aim of the their Breast Cancer Imaging Ontology (BCIO) is to provide a commonly agreed vocabulary with formal definitions that can be used to represent breast X-ray and MRI images, abnormal findings and medical assessments (Hu, Dasmahapatra, Lewis, & Shadbolt, 2003). In 2006, Qi et al. developed a mammography ontology called as Pocket-Ontology. They use ontology-based comparison method for finding groups of diagnosis that radiologists detect using the same analysis process. Their comparison method is based on an edit distance, which is a similarity measurement between two concepts (Qi, Denton, & Zwiggelaar, 2006). Ren and Barnaghi created a framework for medical specialists to be able to annotate digital mammograms, and to retrieve relevant resources based on semantic relations, in 2007 (Ren and Barnaghi, 2007). In 2008, Rubin et al. develop an ontology-based annotation and retrieval framework, which is called Annotation and Imaging Markup (AIM Rubin, Mongkolwat, Kleper, Supekar, & Channin, 2008). Levy et al. perform a SWRL rule on AIM to identify the malignancy of liver lesions, depend on its length (Levy, O'Connor, & Rubin, 2009). Shadbolt et al. developed an ontology-based knowledge management system which is called MIAKT (Medical Imaging with Advanced Knowledge Technologies) for the data that the screening process generates, as well as providing a means for medical staff to investigate, annotate and analyze the using web, in 2004 (Shadbolt, Dasmahapatra, & Hu, 2004).

In this work, we introduce a new Mammography Annotation Tool and ontology-based annotation and retrieval system for breast

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masses with description of high and mid-level features. The system uses SQWRL to process the query using Mammography Annotation Ontology. We perform annotation based on ontology. In other words, all parts of the annotation are stored in an RDF file as concept instances. Then, we use SQWRL to retrieve breast masses examined in digital mammography.

Rest of the paper is organized as follows: the Section 2 presents the basics of ontology-based annotation introducing the annotation tool we develop. Additionally, we provide brief information about our dataset, SWRL and SQWRL. The Section 3 discusses mathematical model of similarity calculation between two breast lesions and implementation of the model with SQWRL query and gives sample retrieval results. The last Section 4 concludes the paper and discusses the future works on this topic.

2. Ontology-based mammography annotation

The representation of complex and detailed medical concepts is a very important task in current medical information systems. Therefore, medical ontologies are developed to solve problems such as when reusing and sharing of patient data, required of semantic-based queries/inference or the transmission of these data.

2.1. Mammography Annotation Ontology (MAO)

In this study we aim to annotate mammograms based on ontology. Therefore, the key part of the system is the Mammography Annotation Ontology (MAO). In development of MAO we used the 3rd edition of BI-RADS (Breast Imaging Reporting and Date System) Mammography Atlas (American College of Radiology, 2012), and used the ontology to annotate any abnormality observed in mammograms. Principally, the MAO provides a shared vocabulary and knowledge that makes annotations understandable and computable by computers. Prominently it makes reasoning of any other information possible and forms a knowledge base.

There is no one correct way or methodology for developing ontologies. Furthermore, ontology development is necessarily an iterative process. While we were developing our ontology we consider the domain covered with intended use of the ontology. We use middle-out strategy as ontology development methodology (Fernández-López, 1999). To achieve this, we choose the base concepts in mammography (i.e. Case, Breast, Image, Abnormality etc.) and some of their basic relationships first. Then, we describe the other necessary concepts (i.e. ROI, 2D Point etc.). Fig. 1 shows major concepts of the MAO with their relationships.

In MAO, annotation starts with a Patient class with properties of such as age, patientId etc. The Patient class has at least

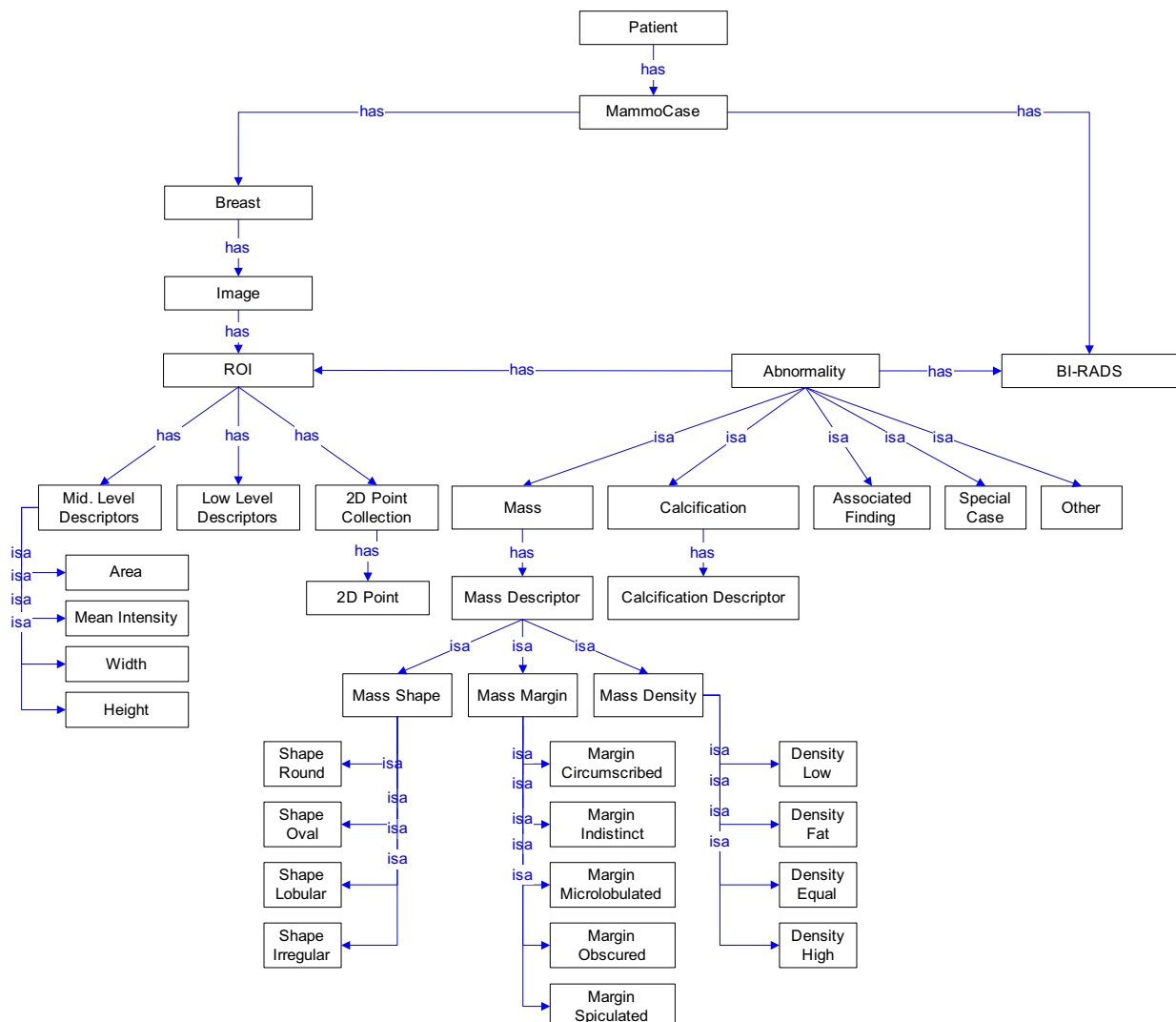


Fig. 1. Major classes and their relationships in Mammography Annotation Ontology (MAO).

one *MammoCase* instance that describes a mammography case having breast and image. Each case has an instance of BI-RADS class, but as a rule, if the case contains one or more abnormality then the BI-RADS score of *MammoCase* is the highest BI-RADS score of all abnormalities within the case.

The *Image* class represents digital images of any modalities such as MRI, CT, mammography etc. Screening mammography generally involves two views of each breast: one from above (Cranial-Caudal view, CC) and the other from oblique or angled views (Mediolateral-Oblique, MLO). Therefore, a typical screening mammography case contains four mammograms, MLO and CC views for two breasts.

The *ROI* class describes a region of interest on an image. The radiologists create or draw a Region of Interest (ROI) by using proper tools in application and we assume that each ROI indicates an abnormality with further information such as computer generated mid and low-level features.

Abnormality class describes an abnormality observed in an image and each *Abnormality* class must have one BI-RADS instance to describe final opinion of the expert about the abnormality and one *ROI* instance, which has mid and low-level features of the abnormality. On the other hand, the class has five subclasses to be able to describe any abnormality in detail. These classes are namely *Mass*, *Calcification*, *Associated_Finding*,

Special_Case and *Other*, where each one has its own *High_Level_Descriptor* class. For example *Mass_Descriptor* class is one of the subclasses of the *High_Level_Descriptor* class and each mass instance must have one from each *Mass_Shape*, *Mass_Margin* and *Mass_Density* class instance.

In Fig. 2, we illustrate a sample mass annotation, which is in the right breast, and annotated by irregular shape, speculated margin, equal density and BI-RADS score 5. The mean intensity value of the mass is 35598.1 in 16bits level and area of the mass is 81765 pixel².

2.2. Mammography Annotation Tool

We designed and develop an annotation tool, Mammography Annotation Tool (MAT), to annotate mammograms. MAT allows radiologists to examine four images in total, CC and MLO projection of the right and left breasts, for a typical mammography case. During this examination, the radiologists mark and annotate the abnormalities on images by using a variety of tools, which are easily done by clicking on it, and can also add the breast type. MAT stores all annotations in XML format, which is then easily converted into OWL format. The annotation file can also produce classical radiology reports in natural language, or to any other desired format. We developed MAT using C++ programming language with

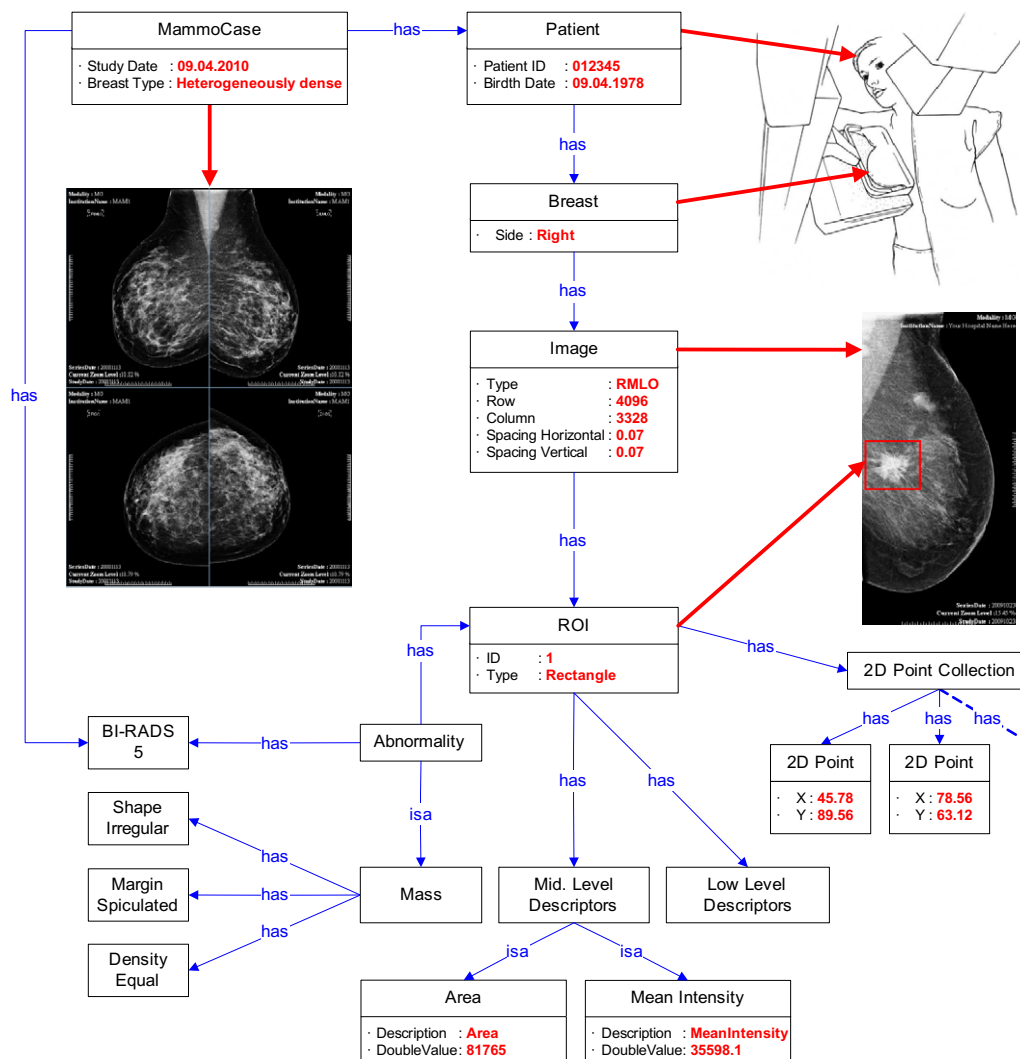


Fig. 2. Annotation of mammograms with MAO.

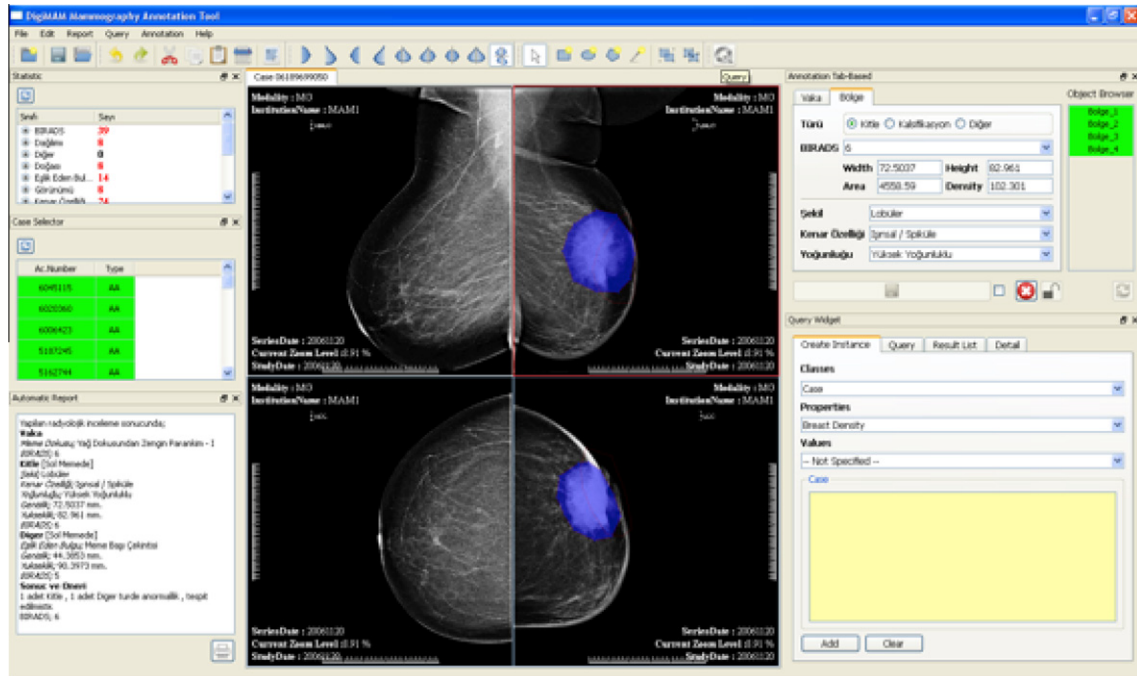


Fig. 3. Mammography Annotation Tool.

Table 1

Distribution of the lesions according to their types in DEMS.

Lesion types	Case count	Lesion count	Total annotation count
Mass	116	136	260
Calcification	121	146	278
Special Case	19	20	32
Associated Finding	65	97	146
Other	10	13	23

QT framework (QT, 2012) with a cross-platform support. Fig. 3 depicts a sample screen shot of the MAT.

2.3. Dataset

In this work, we use DEMS (DEMS, 2012) dataset containing 485 mammographic cases where 255 of them contain one or more abnormality and 260 mass annotations in total. Each case has four images of standard views (i.e. CC and MLO). An expert radiologist, who is one of the authors of this paper, annotated each case in two phases using the MAT.

In Tables 1 and 2, *Case Count* column shows the number of unique mammographic case contains related lesion type/property/value. *Lesion Count* column shows the number of unique lesion marked with related lesion/property/value. *Total Annotation Count* is the number of annotation instances totally created for related lesion/property/value. For instance, in Table 2, total number of cases containing lobular shaped mass is 28. On the other hand, the total number of lobular shaped mass is 29 since a case contains more than one mass with lobular shape. And finally, totally 57 annotation instances are created to describe all these 29 masses. *Total Annotation Count* is higher than *Lesion Count* because mostly a lesion is seen in two different mammograms and both of them are annotated individually even they are the same lesion. This is because; mid and low-level features are different although the high-level interpretation of the lesion is same.

Table 2

High-level features of masses in DEMS.

BI-RADS	Case count	Lesion count	Total annotation count
2	23	27	50
3	26	29	55
4A	9	9	18
4B	6	6	12
4C	10	10	19
5	37	39	75
6	14	16	31
<i>Shape</i>			
Round	21	27	50
Lobular	28	29	57
Irregular	56	59	113
Oval	21	21	40
<i>Margin</i>			
Circumscribed	44	52	98
Microlobular	5	5	9
Obscured	16	16	31
Indistinct	22	26	49
Spiculated	37	37	73
<i>Density</i>			
High	51	62	119
Equal/isodense	55	59	111
Low/not fat containing	3	3	6
Fat containing radiolucent	11	12	24

2.4. Semantic Query-Enhanced Web Rule Language (SQWRL)

SQWRL is built on the Semantic Web Rule Language (SWRL), which is an expressive OWL-based rule language. SWRL makes possible to write inference rules and this provides more powerful deductive reasoning capabilities than OWL alone. Semantically, SWRL is built on the same description logic foundation as OWL and provides similar strong formal guarantees when performing inference (SWRL, 2012). For example, as we mentioned before if a mammographic case contains one or more abnormality then

```

MammoCase(?case) ∧ hasBreast(?case, ?breast) ∧ hasImage(?breast,
?image) ∧ hasROI(?image, ?roi) ∧ hasAbnormality(?roi, ?mass) ∧
    hasBirads(?mass, ?birads) ∧ sortIndex(?birads, ?sortIdx) *
sqwrl:makeSet(?setBirads, ?sortIdx) ∧ sqwrl:groupBy(?setBirads,
    ?case) * sqwrl:max(?maxIndex, ?setBirads) ∧
    swrlb:equal(?maxIndex, ?sortIdx)
    →
    hasBirads(?case, ?birads)

```

Fig. 4. SWRL Rule to Infer and Set BI-RADS Score of a MammoCase.

```

Mass(?mass) ∧ hasROI(?mass, ?roi) ∧ hasMidLevelDescriptor(?roi,
    ?meanIntensity) ∧ description(?meanIntensity,
    ?desMeanIntensity) ∧ swrlb:equal(?desMeanIntensity,
    "MeanIntensity") ∧ doubleValue(?meanIntensity,
    ?meanIntensityValue) * sqwrl:makeSet(?setMeanIntensity,
    ?meanIntensityValue) * sqwrl:max(?maxMeanIntensityValue,
    ?setMeanIntensity)
    →
    sqwrl:select(?maxMeanIntensityValue)

```

Fig. 5. SQWRL rule to retrieve maximum mean intensity value of the masses.

the highest BI-RADS score of the masses in that case is assigned as the BI-RADS score of the case. So, following SWRL rule, Fig. 4, infers and sets BI-RADS score of a particular mammographic case (MammoCase) according to the BI-RADS score of its abnormalities.

On the other hand, SQWRL takes a standard SWRL rule. Both of them have an antecedent part, which is referred to as the body, and

a consequent part, which is referred to as the head. Differently, SQWRL replaces the rule consequent with a retrieval specification for retrieving knowledge from OWL by providing SQL-like operations (SQWRL, 2012). For example, the following SQWRL rule, Fig. 5, retrieves maximum mean intensity value in all mass instances.

Table 3
Similarity matrixes for high-level features of the masses.

Mass shape, (sim _s)	Round	Oval	Lobular	Irregular		
Round	1	0.8	0.8	0.4		
Oval	0.8	1	0.6	0		
Lobular	0.8	0.6	1	0.6		
Irregular	0.4	0	0.6	1		
Mass margin, (sim ^M)	Circumscribed	Microlobulated	Obscured	Indistinct	Spiculated	
Circumscribed	1	0.6	0.5	0.4	0.2	
Microlobulated	0.6	1	0.5	0.6	0.3	
Obscured	0.5	0.5	1	0.8	0.7	
Indistinct	0.4	0.6	0.8	1	0.8	
Spiculated	0.2	0.3	0.7	0.8	1	
Mass density, (sim ^D)	High	Equal	Low	Fat		
High	1	0.5	0.2	0		
Equal	0.5	1	0.7	0.6		
Low	0.2	0.7	1	0.9		
Fat	0	0.6	0.9	1		
BI-RADS, (sim ^B)	3	4A	4B	4C	5	6
3	1	0.8	0.8	0.8	0.6	0.4
4A	0.8	1	1	1	0.8	0.6
4B	0.8	1	1	1	0.8	0.6
4C	0.8	1	1	1	0.8	0.6
5	0.6	0.8	0.8	0.8	1	0.8
6	0.4	0.6	0.6	0.6	0.8	1

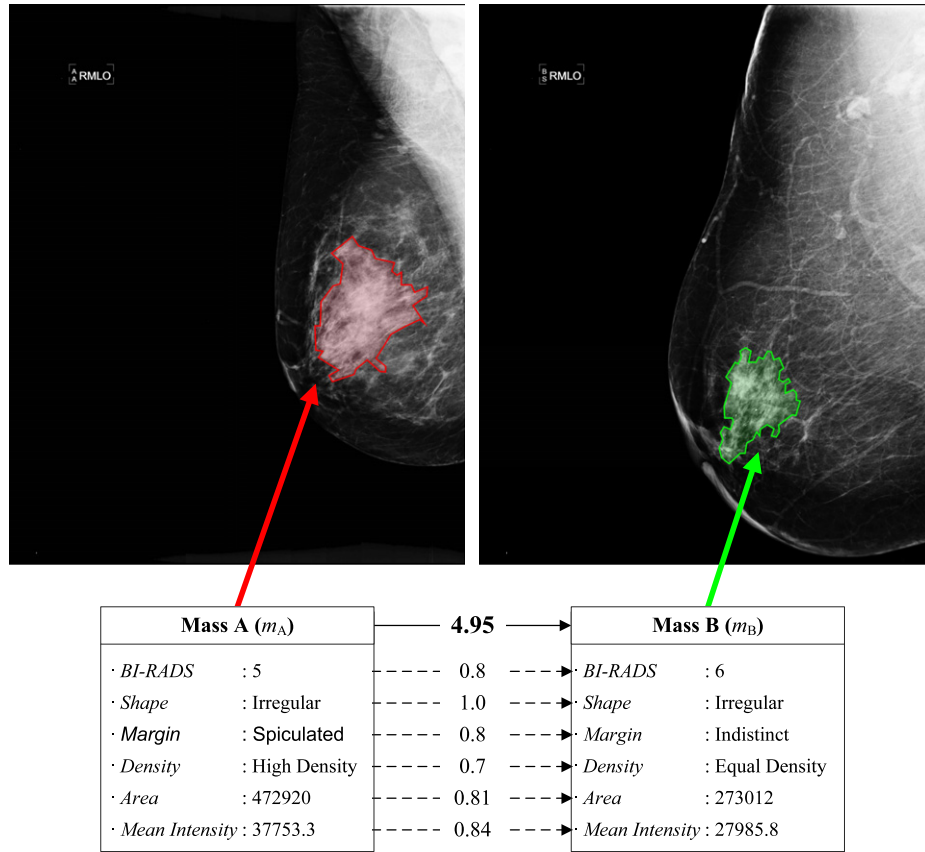


Fig. 6. Sample similarity calculation for masses A and B.

```

<owl:AnnotationProperty rdf:ID="AnnoMassDensityHighEqual">
<rdfs:domain rdf:resource="#DensityHigh"/>
<rdfs:range rdf:resource="#DensityEqual"/>
<rdfs:label rdf:datatype="http://www.w3.org/2001/XMLSchema#string">
0.5
</rdfs:label>
<rdf:type rdf:resource="http://www.w3.org/2002/07/owl#ObjectProperty"/>
</owl:AnnotationProperty>

```

Fig. 7. Sample annotation property for Classes DensityHigh and DensityEqual.

3. Reasoning

In Case-based Retrieval systems, the similarity calculation between two items is inevitable, thus, we explain the similarity calculation of masses in detail. However, system can be easily extended to any other type of abnormalities (e.g. Calcification, Associated Finding etc.). In MAO, we have modeled as each mass may have three types of features: high, mid and low-level features. Low and mid-level descriptors are directly associated with its ROI instance and calculated automatically. On the other hand, experts directly assign high-level features to mass.

Let us assume that we have a database of masses, each described with a set of descriptors. More formally, a mass database, M , is defined as follows:

$$M = \{m_1, m_2, \dots, m_n\} \quad (1)$$

Furthermore, each mass is defined with a set of features: high, mid and low-level. For a given arbitrary mass, m_i , is defined as follows:

$$m_i = \{F_i^H, F_i^M, F_i^L\} \quad (2)$$

where the terms F_i^H , F_i^M and F_i^L denotes high, mid and low-level features of the mass m_i , respectively. High-level features are semantically meaningful labels describing an entity. For example, value of high-level features describing the shape of a mass can be *round*, *oval*, *lobular* or *irregular*. Furthermore, high-level features are expected to set by experts, in our study. Secondly, mid-level features are descriptor, which are generally computed by computers and can be interpreted by both computers and humans. Typical mid-level features are *area*, *length* or *average intensity* of a mass etc. The third, low-level features are extracted by computers and generally represented as a vector numbers. Additionally, low-level features are not semantically meaningful by human. It requires an intensive processing to make interpretable by human. Formally, each type of feature may be defined with a different set of sub attributes.

$$F_i^H = \{f_i^{\text{Shape}}, f_i^{\text{Margin}}, f_i^{\text{Density}}, f_i^{\text{Bi-rads}}\} \quad (3)$$

$$F_i^M = \{f_i^{\text{Area}}, f_i^{\text{MeanIntensity}}\} \quad (4)$$

so, by using Eqs. (3) and (4), we can represent the m_i as follows,


```

Mass(?m-q) ∧ ID(?m-q, ?id-q) ∧ swrlb:equal(?id-q, "A") ∧ Mass(?m-r) ∧
  tbox:notequalto(?m-q, ?m-r) ∧ hasROI(?m-q, ?roi-q) ∧
  hasMidLevelDescriptor(?roi-q, ?midArea-q) ∧ description(?midArea-q,
    ?desArea-q) ∧ swrlb:equal(?desArea-q, "Area") ∧ doubleValue(?midArea-q,
    ?valArea-q) ∧ hasMidLevelDescriptor(?roi-q, ?midMeanIntensity-q) ∧
    description(?midMeanIntensity-q, ?desMeanIntensity-q) ∧
    swrlb:equal(?desMeanIntensity-q, "MeanIntensity") ∧
    doubleValue(?midMeanIntensity-q, ?valMeanIntensity-q) ∧ hasROI(?m-r, ?roi-r)
  ∧ hasMidLevelDescriptor(?roi-r, ?midArea-r) ∧ description(?midArea-r,
    ?desArea-r) ∧ swrlb:equal(?desArea-r, "Area") ∧ doubleValue(?midArea-r,
    ?valArea-r) ∧ hasMidLevelDescriptor(?roi-r, ?midMeanIntensity-r) ∧
    description(?midMeanIntensity-r, ?desMeanIntensity-r) ∧
    swrlb:equal(?desMeanIntensity-r, "MeanIntensity") ∧
    doubleValue(?midMeanIntensity-r, ?valMeanIntensity-r) ∧ hasMassShape(?m-q,
    ?ds-q) ∧ hasMassMargin(?m-q, ?dm-q) ∧ hasMassDensity(?m-q, ?dd-q) ∧
    hasBirads(?m-q, ?db-q) ∧ abox:hasClass(?ds-q, ?cs-q) ∧ abox:hasClass(?dm-q,
    ?cm-q) ∧ abox:hasClass(?dd-q, ?cd-q) ∧ abox:hasClass(?db-q, ?cb-q) ∧
    hasMassShape(?m-r, ?ds-r) ∧ hasMassMargin(?m-r, ?dm-r) ∧
    hasMassDensity(?m-r, ?dd-r) ∧ hasBirads(?m-r, ?db-r) ∧ abox:hasClass(?ds-r,
    ?cs-r) ∧ abox:hasClass(?dm-r, ?cm-r) ∧ abox:hasClass(?dd-r, ?cd-r) ∧
    abox:hasClass(?db-r, ?cb-r) ∧ tbox:isProperty(?ap-s) ∧
    tbox:isAnnotationProperty(?ap-s) ∧ tbox:isInDomainOf(?cs-q, ?ap-s) ∧
    tbox:isInRangeOf(?cs-r, ?ap-s) ∧ rdfs:hasLabel(?ap-s, ?lb-s) ∧
    StringToDoble(?s2d-s) ∧ stringValue(?s2d-s, ?str-s) ∧ swrlb:equal(?str-s,
    ?lb-s) ∧ doubleValue(?s2d-s, ?sv-s) ∧ tbox:isProperty(?ap-m) ∧
    tbox:isAnnotationProperty(?ap-m) ∧ tbox:isInDomainOf(?cm-q, ?ap-m) ∧
    tbox:isInRangeOf(?cm-r, ?ap-m) ∧ rdfs:hasLabel(?ap-m, ?lb-m) ∧
    StringToDoble(?s2d-m) ∧ stringValue(?s2d-m, ?str-m) ∧ swrlb:equal(?str-m,
    ?lb-m) ∧ doubleValue(?s2d-m, ?sv-m) ∧ tbox:isProperty(?ap-d) ∧
    tbox:isAnnotationProperty(?ap-d) ∧ tbox:isInDomainOf(?cd-q, ?ap-d) ∧
    tbox:isInRangeOf(?cd-r, ?ap-d) ∧ rdfs:hasLabel(?ap-d, ?lb-d) ∧
    StringToDoble(?s2d-d) ∧ stringValue(?s2d-d, ?str-d) ∧ swrlb:equal(?str-d,
    ?lb-d) ∧ doubleValue(?s2d-d, ?sv-d) ∧ tbox:isProperty(?ap-b) ∧
    tbox:isAnnotationProperty(?ap-b) ∧ tbox:isInDomainOf(?cb-q, ?ap-b) ∧
    tbox:isInRangeOf(?cb-r, ?ap-b) ∧ rdfs:hasLabel(?ap-b, ?lb-b) ∧
    StringToDoble(?s2d-b) ∧ stringValue(?s2d-b, ?str-b) ∧ swrlb:equal(?str-b,
    ?lb-b) ∧ doubleValue(?s2d-b, ?sv-b) ∧ swrlb:add(?templ, ?sv-s, ?sv-m) ∧
    swrlb:add(?temp2, ?sv-d, ?sv-b) ∧ swrlb:add(?sumHigh, ?templ, ?temp2) *
    sqwrl:makeSet(?setmidArea-q, ?valArea-q) ∧ sqwrl:makeSet(?setmidArea-r,
    ?valArea-r) ∧ sqwrl:makeSet(?setmidMeanIntensity-q, ?valMeanIntensity-q) ∧
    sqwrl:makeSet(?setmidMeanIntensity-r, ?valMeanIntensity-r) *
    sqwrl:union(?setUnionArea, ?setmidArea-q, ?setmidArea-r) ∧
    sqwrl:union(?setUnionMeanIntensity, ?setmidMeanIntensity-q,
    ?setmidMeanIntensity-r) ∧ sqwrl:max(?maxArea, ?setUnionArea) ∧
    sqwrl:max(?maxMeanIntensity, ?setUnionMeanIntensity) ∧
    swrlb:subtract(?subArea, ?valArea-q, ?valArea-r) ∧ swrlb:abs(?absArea,
    ?subArea) ∧ swrlb:divide(?divArea, ?absArea, ?maxArea) ∧
    swrlb:subtract(?simResArea, 1, ?divArea) ∧ swrlb:subtract(?subMeanIntensity,
    ?valMeanIntensity-q, ?valMeanIntensity-r) ∧ swrlb:abs(?absMeanIntensity,
    ?subMeanIntensity) ∧ swrlb:divide(?divMeanIntensity, ?absMeanIntensity,
    ?maxMeanIntensity) ∧ swrlb:subtract(?simResMeanIntensity, 1,
    ?divMeanIntensity) ∧ swrlb:add(?sumMid, ?simResArea, ?simResMeanIntensity) ∧
    swrlb:add(?sumSim, ?sumHigh, ?sumMid)
    →
    sqwrl:select(?m-q, ?m-r, ?cs-q, ?cs-r, ?cm-q, ?cm-r, ?cd-q, ?cd-r, ?sumHigh,
    ?valArea-q, ?valArea-r, ?valMeanIntensity-q, ?valMeanIntensity-r, ?sumMid,
    ?sumSim) ∧ sqwrl:orderByDescending(?sumSim)

```

Fig. 8. The SQWRL rule to retrieve similar masses for a given mass.

$$m_i = \left\{ \left\{ f_i^{\text{Shape}}, f_i^{\text{Margin}}, f_i^{\text{Density}}, f_i^{\text{Bi-rads}} \right\}, \left\{ f_i^{\text{Area}}, f_i^{\text{MeanIntensity}} \right\}, f_i^L \right\} \quad (5)$$

where f_i^{Area} and $f_i^{\text{MeanIntensity}}$ are double values and they are calculated by using pixel values of the mass and,

$$f_i^{\text{Shape}} \in \{\text{Round, Oval, Lobular, Irregular}\},$$

$$f_i^{\text{Margin}} \in \{\text{Circumscribed, Microlobulated, Obscured, Indistinct, Spiculated}\},$$

$$f_i^{\text{Density}} \in \{\text{Low, Fat, Equal, High}\},$$

$$f_i^{\text{Bi-rads}} \in \{3, 4A, 4B, 4C, 5, 6\}.$$

In this study, we have included only high and mid-level features into similarity score calculation between to masses, m_x , m_y . The similarity function is given in Eq. (6)

$$S(m_x, m_y) = S^H(m_x, m_y) + S^M(m_x, m_y) \quad (6)$$

where S^H denotes the high-level similarity score while S^M denotes mid-level similarity score of the masses. In detail,

$$S^H(m_x, m_y) = \text{sim}^S(f_x^{\text{Shape}}, f_y^{\text{Shape}}) + \text{sim}^M(f_x^{\text{Margin}}, f_y^{\text{Margin}}) + \text{sim}^D(f_x^{\text{Density}}, f_y^{\text{Density}}) + \text{sim}^B(f_x^{\text{Bi-rads}}, f_y^{\text{Bi-rads}}) \quad (7)$$

where the similarity functions sim^S , sim^M , sim^D and sim^B use Table 3. The arguments of these functions denote row and column of the

Table 4

Sample mass queries with their results.

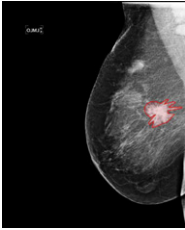
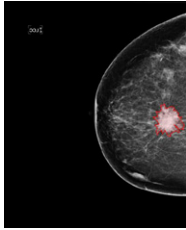
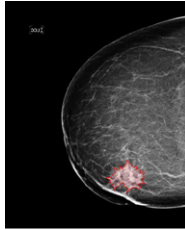

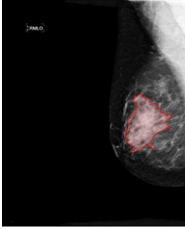
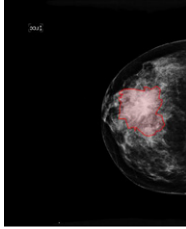
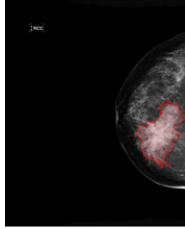

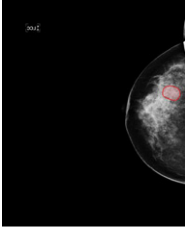
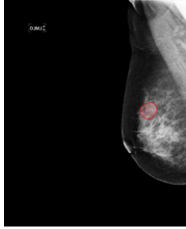
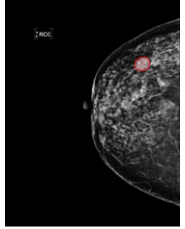

Query-A	Result-A.1	Result-A.2	Result-A.3
			
Query-B	Result-B.1	Result-B.2	Result-B.3
			
Query-C	Result-C.1	Result-C.2	Result-C.3
			

table. The table is similarity matrixes for each high-level property (i.e. shape, margin and density), its values are empirically set within a range of 0.0 and 1.0. Here, the value of 1.0 means that the features are identically similar while 0.0 indicates no similarity

$$S^M(m_x, m_y) = sim^A(m_x, m_y) + sim^{Mi}(m_x, m_y) \quad (8)$$

where $sim^A(m_x, m_y)$ and $sim^{Mi}(m_x, m_y)$ are functions to calculate similarity score between the masses m_x and m_y , depends on their Area and Mean Intensity values, respectively. In detail,

$$sim^A(m_x, m_y) = 1 - \frac{|f_x^{Area} - f_y^{Area}|}{\maxArea} \quad (9)$$

$$sim^{Mi}(m_x, m_y) = 1 - \frac{|f_x^{MeanIntensity} - f_y^{MeanIntensity}|}{\maxMeanIntensity} \quad (10)$$

where f_x^{Area} and f_y^{Area} are area, $f_x^{MeanIntensity}$ and $f_y^{MeanIntensity}$ are mean intensity values of masses m_x and m_y , respectively. \maxArea and \maxMeanIntensity denotes the maximum area and mean intensity values in all over masses, which are calculated automatically.

Fig. 6 shows sample similarity calculation between two masses, Mass A (m_A) and Mass B (m_B). Where,

$$m_A = \{\{Irregular, Spiculated, High, 5\}, \{472920, 37753.3\}\},$$

$$m_B = \{\{Irregular, Indistinct, Equal, 6\}, \{273012, 27985.8\}\} \text{ and}$$

$$S(m_A, m_B) = 4.95.$$

3.1. Reasoning with SQWRL

We use OWL and SQWRL to retrieve similar masses for a given mass query. We process SQWRL rules with Jess rule engine (Jess

Rule Engine, 2012) in SWRLTab of Protégé (Protégé Ontology Editor, 2012). To be able to perform SQWRL rule for retrieval, we also store high-level similarity matrixes in the MAO. To do this, we defined object type owl:AnnotationProperty between each Mass_Descriptor class and use *rdfs:range* and *rdfs:domain* tags of owl:AnnotationProperty to store row and column of our similarity matrix, shown in Table 3. *rdfs:label* tag of owl:AnnotationProperty stores the similarity score in string format, and converted into float while calculation. Fig. 7 shows OWL syntax of a sample owl:AnnotationProperty between DensityHigh and DensityEqual classes, where similarity score is equal to 0.5 as shown in Table 3.

To retrieve similar masses for a given query, we run the SQWRL rule given in Fig. 8. Where variable ?m-q denotes querying mass instance and ?m-r denotes all other mass instances different from the query mass in the ontology (*tbox:notEqualTo*(?m-q, ?m-r)). As we mentioned in Eq. (6), total similarity score between two masses is sum of their high-level and mid-level similarity scores. So the antecedent part of the rule consist of two main parts, one for calculation high-level similarity score (?sumHigh) and the other part for mid-level similarity score (?sumMid) calculation.

To obtain the high-level similarity score we process owl:AnnotationProperty's for each high-level feature of the masses (i.e. *tbox:isAnnotationProperty*(?ap-s) where ?ap-s denotes the owl:AnnotationProperty for high-level feature Shape). As a result of calculation high-level similarity score (?sumHigh), we sum similarity values of each high-level feature of mass (*swrlb:add*(?templ, ?sv-s, ?sv-m) \wedge *swrlb:add*(?temp2, ?sv-d, ?sv-b) \wedge *swrlb:add*(?sumHigh, ?templ, ?temp2), where; ?sv-s, ?sv-m, ?sv-d and ?sv-b denotes similarity values for mass high-level features Shape, Margin, Density and BI-RADS, respectively). On the other hand, to calculate mid-level similarity score (?sumMid) between the masses, first we calculate maximum

Area and Mean Intensity values ($?maxArea$ and $?maxMeanIntensity$) depend on the all mass instances in the MAO. Then, we perform Eq. (9) and (10) for the normalization process (i.e. calculation of sim^A in the Eq. (9); `swrlb:subtract(?subArea, ?valArea-q, ?valArea-r) ^ swrlb:abs(?absArea, ?subArea) ^ swrlb:divide(?divArea, ?absArea, ?maxArea) ^ swrlb:subtract(?simResArea, 1, ?divArea)`, where, $?valArea-q$ and $?valArea-r$ denotes Area value of the query and retrieved masses, respectively and $?simResArea$ denotes result value of the function sim^A). Finally, by summing $?sumHigh$ and $?sumMid$, we obtain result similarity score ($?sumSim$) between the mass (`swrlb:add(?sumSim, ?sumHigh, ?sumMid)`). We sort descending the result set according to $?sumSim$ value to list most similar masses on the top of the result list.

To test our approach, we processed a list of queries. Table 4 shows the results of three sample queries. In Query-A and Query-B, all high-level features of the query masses are equal. Both of the queries mass has irregular shape, spiculated margin, high density and BI-RADS 5. But there is a significant difference between their mid-level features, where area of the mass in the Query-B is larger than Query-A. Therefore, when we look at the query results, we can see that, the size of the masses in result list of the Query-A is smaller than the masses in result list of Query-B. In other words, mid-level feature helps to rank result set, effectively. And we query a mass with oval shape, circumscribed margin, equal density and BI-RADS 2 in Query-C. Table 4 shows the similar cases to all queries.

4. Conclusion

In this work, we introduce Mammography Annotation Ontology (MAO) and Mammography Annotation Tool (MAT) based on the MAO. Then, we present a similar mass retrieval system based on their high, mid-level features. And we show how ontology-based similar mass retrieval is processed in SQWRL for a given query mass and we obtain meaningful results.

We have evaluated the proposed approach with DEMS which is a fully-annotated digital mammography dataset. We used Protégé with Jess Rule engine to process SQWRL. However, the time performance of the tool is far to be used in a large mass collection. As the number of instance is increased, it negatively affects the execution time of SQWRL rules processing in Protégé environment. It definitely needs more efficient implementations of the SQWRL engine for processing such a complex rules.

In future, we plan to include more mid-level features into system. Beside that, we want to include and integrate low-level features into reasoning phase. This may also requires an extension of SWRL to be able to handle low-level features vectors effectively and efficiently. And we hope that the number of built-in functions

in SWRL and SQWRL will be increased with efficient processing of them.

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