A Workflow for Improving Medical Visualization of Semantically Annotated CT-Images

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Abstract. RadLex and Foundational Model of Anatomy (FMA) ontologies represent anatomic and image characteristics, and they are commonly used to annotate and describe contents of medical images independently of the image acquisition method (e.g., CT, MR, or US). We present ANISE, a framework that implements workflows to combine these ontologies and image characteristics into Transfer Functions (TFs) that map volume density values into optical properties. Semantics encoded in the image annotations is exploited by reasoning processes to improve accuracy of TFs and the quality of the resulting image.

1 Introduction

In the Life and Health Sciences domains large ontologies have been defined, e.g., SNOMED[3], MesH[4], RadLex[5], and Foundational Model of Anatomy (FMA) [9]. These ontologies are commonly applied to encode scientific knowledge through annotations of concepts, e.g., MeSH terms have been used by curators to annotate and describe PubMed[6] publications and clinical trials published at the Clinical Trials website[7]. Knowledge encoded in these annotations as well as the properties derived from reasoning tasks are used to recovery or discovery properties of the annotated concepts. In this paper we propose a workflow to annotate medical images with terms from RadLex and FMA, and illustrate the benefits of exploiting these annotations during image visualization. We aim at enriching transfer functions (TFs) with semantics encoded in these annotations and provide more precise renderings of the volumetric data of a medical image.

A transfer function (TF) maps density values of volumetric data or voxel into optical properties (e.g., opacity and color) used by rendering algorithms to produce a final image. TFs allow to pre-classify different tissues in an image, and

[3] http://www.nlm.nih.gov/research/umls/Snomed/snomed_mail.html
[4] http://www.nlm.nih.gov/mesh
[5] http://www.rsna.org/radlex/
[6] http://www.ncbi.nlm.nih.gov/pubmed
[7] http://clinicaltrials.gov/

they are based on existing characterizations of the organs that relate a medical image acquisition modality, a tissue, and a density range [7]. Nevertheless, some tissues belonging to different organs may have overlapped densities, and specifying a TF will normally require a robust segmentation technique and specialized segmentation processes to produce a precise tissue classification able to distinguish tissues with overlapped densities. Recently, the problem of tissue classification by semantically annotating volumetric data has gained attention in the literature [2, 3, 5, 8]. Rautek et al. [8] present a fuzzy rule-based system that maps volumetric attributes to visual styles; rules are defined by users without representing special knowledge about the rendering technique. Gerl et al. [5] overcomes this limitation and propose a rule-based system for semantic shader augmentation; this system automatically adds rule-based rendering functionality to static visualization mappings in a shader program. Although both systems rely on rule-based systems to characterize TFs, they do not exploit knowledge encoded in ontologies to improve the quality of the visualization process. Möller et al. [6] present a technique for annotating and searching medical images using ontological semantic concepts for retrieving images from a Picture Archiving and Communication System (PACS); ontologies as FMA and RadLex are used to retrieve data, however, they are not exploited during visualization or tissue classification from the image data. Although applications of semantic annotations have been illustrated, nothing is said about the benefits of using these annotations and the encoded semantics during the definition of TFs.

We present ANISE (an ANatomIc SEmantic annotator), a framework for specifying TFs based on semantic annotations. TFs are based on pre-elaborated semantic annotations of volumetric data which are validated against existing medical ontologies. ANISE relies on a customized reasoner to infer the bounding boxes which contain organs or tissues of a given sub-volume area, as well as its main properties, e.g., density and opacity. Knowledge encoded in the ontologies contribute to characterize and locating tissues by applying specific organ selection algorithms; thus, voxels that are not part of the organ of interest are not considered during the classification process.

This paper contains four additional sections. Section 2 describes ANISE and Section 3 illustrates the ANISE workflow. Section 4 discusses the observed results, and we conclude in Section 5 with an outlook to future work.

2 Architecture

Achieving high quality image rendering requires interpreting each intensity value according to a given tissue. In consequence, a correct representation of information through semantic annotations should ensure: i) minimal error tissue classification due to reasoning and inference, and ii) an accurate visual representation. Figure 1 shows the main components of ANISE: an annotator, a rule-based system, and a visualization module. The Annotator extends an image original annotations with terms that encode the properties of the classified tissues. The rule-based system relies on inference tasks to process

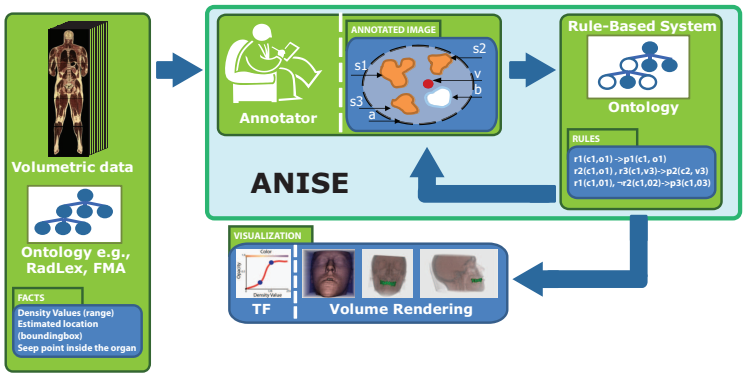

Fig. 1. The ANISE architecture.

original annotations and derive facts that will be used to annotate an image. Annotations regarding to visualization methods and anatomic parts are inferred using Ontology relations (e.g., Subclass) for specific classes (e.g., the Anatomical Set). Finally, the Visualization module executes visualization algorithms on the annotated volumetric data.

Annotator: annotates an image with information about: i) resource authoring, type and identification; ii) acquisition modality; iii) acquisition characteristics like patient orientation in the image; iv) structural and anatomic elements presented and identified in the image; v) regions and points of particular interest; and vi) rendering information. ANISE relies on the following ontologies to extend original image annotations:

- ***Foundational Model of Anatomy*:** FMA allows to describe membership and spatial relationships among voxels in the volume to infer new facts. Furthermore, there are terms in this ontology that can be used for annotating non-anatomical elements, e.g., bounding boxes around particular anatomical organs or some particular points of interest.
- ***RadLex*:** RadLex is an ontology defined for radiologist; it is composed of terms required to annotate medical images. ANISE relies on RadLex terms to describe characteristic from the image itself such as modality, and other acquisition related characteristics that may alter the interpretation and visualization of an image, e.g., orientation.

Rule-Based System: annotations are used during the inference process to derive new annotations. First, it analyses the image acquisition characteristics and correlates body structures of particular interest in order to normalize information for further processing. A bounding box method is used to model anatomic information [3]. Then, combining this information with tissue pre-classification, the inference process is expressed in Probabilistic Soft Logic (PSL) [1]; this process determines the likelihood for a given tissue to be included in a particular region. Closely located tissues with similar intensity values are usually treated as the same values; thus, spatial and anatomic information is used to discriminate by annotating specific points; segmentation based on

voxels neighborhood represent these tissues considering the associated semantic annotations. Ontology classification reasoning tasks are performed with Jena[8]. **Visualization Module:** derived annotations are used by rendering algorithms to visualize the classified tissues. Partial piece-wise transfer functions are used to select appropriate color and opacity values and rendering them. Default transfer functions are only applied on non-annotated voxels and regions.

3 Applying an ANISE Workflow- A Use Case

We illustrate the ANISE workflow in three different datasets (Table 1), to visualize the FMA term *dentition* from a CT-Head volume data.

Volume Data	Dimensions (voxels)	Voxel size (mm)	File size (MB)
skewed_head.dat	184x256x170	1x1x1	16.0
visible_head.dat	512x512x245	1x1x1	128.0
ct_head.dat	256x256x113	1x1x2	14.8

Table 1. Datasets used for illustrating the utility of using semantic annotations on Medical Images. These datasets are available in [10], [11] and [4] respectively.

Figure 2(a),(d),(g) illustrate the rendering of the images applying a simple TF that maps density values to visualize the tissues that have the same density that dentition; these tissues are colored in *green*. Although data were properly pre-classified, it is not possible to discriminate only dentition by just considering the corresponding densities, i.e., some other tissue were painted, and it was not possible further tuning the TF. In this case the density value range for identifying the dentition overlaps with density value range of other tissues like bone for example. Nevertheless, if semantic annotations are used in conjunction with knowledge encoded in the FMA and RadLex ontologies, ANISE can determine that only the teeth should be colored different than the rest (*green* in our example); this is done by selecting appropriate set of points, applying **Normalization** rules, and considering the **Image Modality** taxonomy. Thus, a better classification for different tissues can be done in an automatic way.

- **Image Modality:** supports a generic tissue classification process which is independent on the image modality. The RadLex term used for *Tomography* is `RID28840`[9] and the term `RID10311` (imaging modality) can be reached by using the SubClass relationship. Further, whenever the image is an MRI the term `RID10312` from the same taxonomy is used to annotate the image, i.e., terms `RID28840` and `RID10312` share an ancestor `RID10311`. Tissues' density ranges are represented as facts and used during the inference process in conjunction with these annotations to pre-classify the image voxels.
- **Volume format:** ANISE current version receives images in raw format, i.e., data correspond to a sequence of intensity values. This information is recovered from the attribute `format` from DCMI[10] metadata.

[8] http://jena.apache.org/
[9] http://purl.bioontology.org/ontology/RID/RID28840
[10] http://dublincore.org/documents/dcmi-terms/

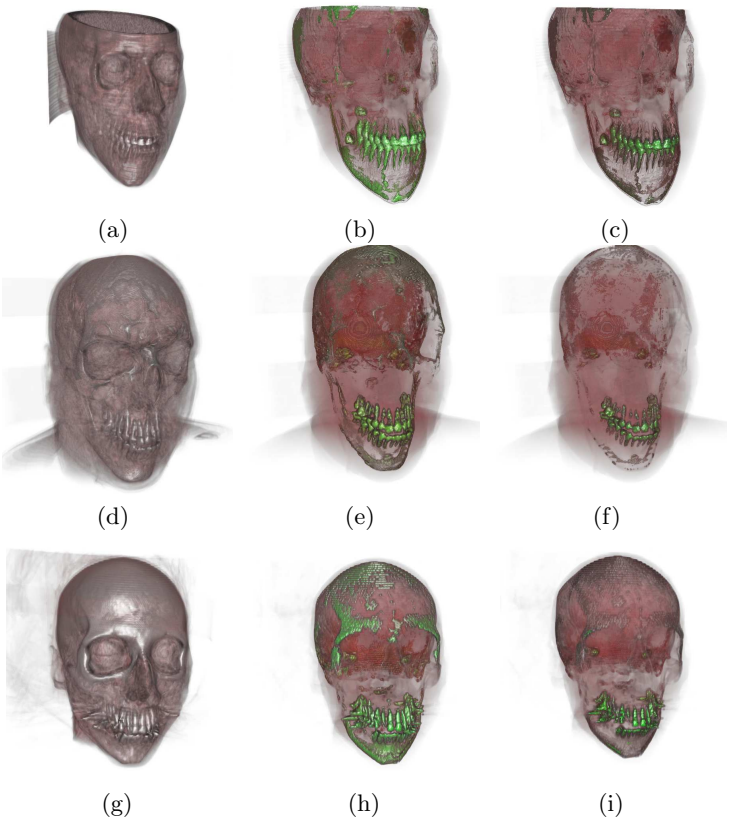

Fig. 2. Results of running the proposed approach with three different datasets: (a) skewed_head.dat, (d) visible_head.dat and (g) ct_head.dat. Images (b), (e), (h) results from rendering without annotation and using a simple TF. Images (c), (f), (i) results from rendering with the application of rule (1) and a semantically enhanced TF.

- **Normalization** rules: are used to transform volumes into a uniform scale considering orientation, voxel size, and modality. Default values are assumed if they are not given. In our use case, we used the term *voxel geometry* `RID2903` from RadLex and its ancestors in the *subClass* branch, i.e., *non-isotropic voxels*, *near-isotropic voxels*, *isotropic voxels*.
- **Dimension:** we used the term *location* (`RID39038`) from RadLex to represent header size, and dimensions in x, y and z of the volume.
- **Tissue:** *dentition* from FMA is the most relevant term in our use case.

We chose *dentition* because it is characterized as the tissue with the higher density value, and the challenge consists on separating the dentition tissue from tissues around it. PSL rules are used to compute the degrees of membership of a voxel to the tissue of interest (*dentition*); it is mainly based on the density value range. The rules that comprise the rule-based system are as follows; they specify

TFs that better visualize the tissue of interest:

$$tissue(X,Y,Z,I) \wedge inside(X,Y,Z,R) \wedge inOrgan(X,Y,Z,I) \rightarrow opacity(X,Y,Z). \quad (1)$$

where, truth values of $opacity(X,Y,Z)$ are determined by the sum of truth values of the following predicates:

- $tissue(X,Y,Z,I)$ describes truth values of the voxel X,Y,Z with intensity I that belong to the objective tissue. This value is defined by:

$$baseVoxel(X,Y,Z,I) \wedge tissueMap(D,I) \rightarrow tissue(X,Y,Z,I). \quad (2)$$

  where, *baseVoxel(X,Y,Z,I)* is a fact; *tissueMap(D,I)* is a PSL predicate that assigns to an objective tissue D (e.g., *dentition*) the probability of the voxel *X,Y,Z* belongs to the density value range. Initially a density value range is specified, and as far as the inference over the annotations are generated, a new density value range is produced and then, a more precise TF is defined.
- *inside(X,Y,Z,R)* describes truth values of the voxel X,Y,Z belonging to a region R. Applying the inference process, a bounding box that best fits the area of the tissue of interest is derived from an initial location.
- *inOrgan(X,Y,Z,I)* describes truth values of the voxel X,Y,Z belonging to the same organ with intensity I. This value is defined by the rule:

$$baseVoxel(X,Y,Z,I) \wedge seed(X,Y,Z) \rightarrow inOrgan(X,Y,Z,I). \quad (3)$$

  Given a seed point (*seed(X,Y,Z)*), known to be part of the tissue of interest and analyzing its neighborhood, the area around this seed point is augmented. A point will be part of the tissue if its density value is inside the density value range of the tissue, and close to the tissue area.

Finally, some facts that need to be defined for each dataset are the following:

- **Density value range:** a density value range can be specified initially; however, it can be adapted according to results inferred from the rules.
- **Seed point:** this is a fix value, received from the user describing a voxel known to be part of the tissue of interest.
- **Bounding box:** the rule-based system identifies from an input bounding box, one that better fits the tissue of interest.

4 Discussion

ANISE just considers the most likely localization of a given tissue. First, an initial and basic TF is defined for a normalized model. Then, this model is used for further inferences. Thus, rules are applied independently to the acquisition method by selecting when a density value for a given point in the space falls inside an appropriate interval. As previously stated, simple density classification is not enough to properly determinate matching between voxels of a same

tissue or anatomical organ. Additional inference processes need to be conducted; they depend on the annotations. In this example, the region of interest that describes the tissue to be analyzed is presented. A first approach consists of selecting the most likely location of a region of interest, i.e., a bounding box covering the organ of interest. Also, PSL predicates are considered as a possible better approximation of this region with non-zero probability. This is done by considering the neighborhood around the region of interest and knowing that *dentition*, for example, should not be located around eyes or upper areas of the head; voxels belonging to *dentition* should be closer around an area, and distance between dentition voxels should not be longer than certain threshold. Another inference process to adjust the probability for points is performed by considering knowledge derived from ontology relationships, i.e., the classification of the term *dentition* in the Anatomical Set branch. Considering the subClass transitive property (see Figure 3), a seed point is annotated to identify a set element. Then, the voxel neighborhood detection algorithm is performed using PSL predicates. Finally combining all inferred facts and probabilities for given points, likelihood of points that represent a particular tissue are estimated; Figure 4 illustrates the whole process. Further, appropriate TFs for each region are defined and performed. This is done just using the same TF (Fig. 2(b),(e),(h)) but performing a reasoning task that allows to detect the voxels that semantically do not correspond to the tooth tissue and that should not be included in the final volume rendering (see Fig. 2(c),(f),(i)).

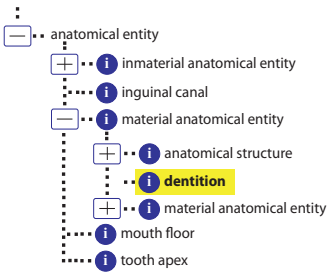

Fig. 3. Scheme from FMA ontology, identifying the Class and SubClass for dentition.

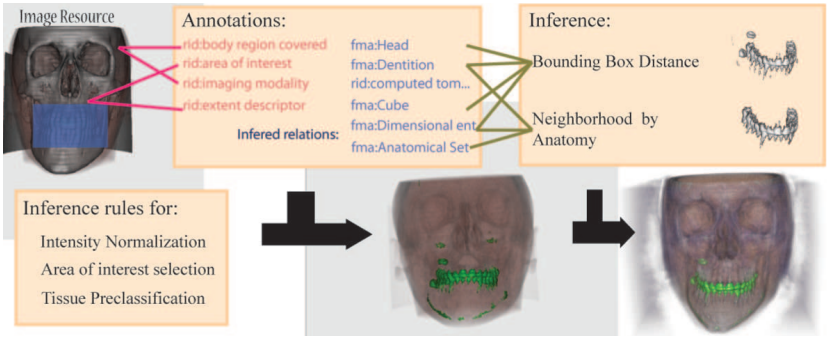

Fig. 4. The ANISE Workflow

5 Conclusions and Future Work

We present ANISE, a framework that exploits knowledge encoded by annotations of 3D medical images, and enhances the rendering process of the images. Quality of ANISE renderings have been studied in different images, and we have observed that they can accurately locate tissues that comprised a medical image. Annotations allow identifying or validating patterns on images, accurate image retrieval, and applying the visualization process on regions of interest. Methods to filter relevant information have been developed at high abstraction level, allowing extension of the inference process to perform particular algorithms, i.e., voxel neighborhood predicates could be improved to allow different methods. In the future, we plan to enhance the rule-based system to normalize a wider range of conditions, and include different image modalities (e.g., MR, and PET) as well as tissues (e.g., blood vessels). Furthermore, we will extend tissue identification algorithms and rules to: *i*) detect and annotate anomalies, and *ii*) identify special conditions on tissues inside the region of interest. Development of visualization algorithms to consider not only TF definitions but also different interpretations of semantic annotations of particular tissues of interest and its corresponding representation on rendered image is also part of our future work.

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