

SemAnatomy3D: Annotation of Patient-Specific Anatomy

Imon Banerjee¹, Giuseppe Patanè², Michela Spagnuolo²

^{1,2}CNR-IMATI, Genova, Italy

Abstract

In the digital age of medicine, patient-specific 3D anatomical reconstructions are becoming increasingly relevant in several applications, starting from bio-mechanical simulation, virtual surgery, implant design to computer-assisted diagnosis. While problems related to imaging and 3D reconstruction have been largely resolved by the advancement in technologies, tools for extracting, coding, sharing and retrieving the semantic content of the patient-specific 3D models are still far from being satisfactory. In this context, we propose SemAnatomy3D framework that aims to bridge the semantic gap between patient-specific 3D geometry and formalized domain knowledge for making the semantics more usable for the definition of patient-specific atlas of anatomy. The purpose of this paper is to describe primary components of the framework. We specialized our framework for the carpal region, but, in principle, it can support similar tasks for other anatomical districts.

1. Introduction

3D model of human anatomy can be distinguished between *canonical anatomy* represented by generic atlases that are designed from synthetic/canonical data, and *patient-specific anatomy* typically come as an output of reconstruction algorithms executed on the real patient data. While 3D canonical models are quite popular in medical teaching and training activities, 3D patient-specific models (3D-PSM) have still a quite limited use in clinical practice. However in the digital era, 3D-PSM are expected to be extremely useful not only for visualization but also for computer assisted diagnosis and therapy planning, bio-mechanical simulation, and prosthesis fitting. While there is an agreement on the importance of 3D-PSM, the integration between medical knowledge and 3D-PSM has not yet been fully realized. This gap creates a demand for tools to support the analysis of 3D-PSM for automatic extraction of relevant parameters, and to document the analysis in an integrated manner. We believe that semantic annotation of 3D-PSM can act as a key to bridge the gap between patient-specific geometry and their semantics.

Existing initiatives in medical research [RRSB08, MRS09] try to couple acquired 2D images with their semantic context (e.g. anatomical label, functionality, clinical findings etc.) through annotation. For example, iPad [RRSB08] extends the functionality of the image viewing platform OsiriX to add semantic tags from the RadLex ontology [Lan06] to 2D medical scans, and stores the annotation in the Annotation and Image Markup schema (AIM). How-

ever, the process is mostly manual and can only support the annotation of 2D DICOM images. A similar semantic annotation tool for medical images is RadSem which leverages the MEDICO ontology to cover various aspects of clinical procedures [MRS09].

In the bio-medical community, few initiatives aim to couple 3D anatomical models with their semantic formalizations [BCRS14]; in fact segmenting and annotating 3D models has higher complexity compare to 2D images. Since only local low-level features are not sufficient for 3D shape analysis, rather global high-level geometric and topological properties have to be evaluated [SF09]. BodyParts3D [MFT*09] platform integrates canonical 3D anatomical models with the formalization defined in Foundational Model of Anatomy ontology (FMA) [RMJ08] for training purposes and does not include patient-specific anatomical information to support clinical investigation. Primal picture [PRI] is a commercial platform that presents an initiative to link structured knowledge not only to the whole canonical 3D models but also to its Parts-of-Relevance (PoRs) mainly for educational purpose.

Going one step further, MyCorporisFabrira [PBJ*09] extends FMA with patient-specific 3D geometrical data and bio-mechanical parameters. The goal is to derive a patient-specific 3D representation from a formal description of anatomy to support the simulation of anatomical joint functions. Finally, 3DSlicer, a medical image visualization tool [PLSK06], attempts to annotate the 3D patient-specific or-

gans models segmented from images by a hierarchical structure of pre-defined anatomical labels.

In the available systems, however, there is no support to analyze and annotate a 3D-PSM and its PoRs with anatomical characterizations and parameters, properly formalized and reflecting specific domain knowledge. This is partly due to lack of methods for the automatic extraction of semantic content of the 3D-PSM. In past years, research in 3D shape modeling was highly focused on the geometric and structural aspects of the shape [ABM*06], when in fact the analysis of 3D-PSM needs methods and algorithms that concur to the formalization and computation of the properties useful to characterize the particular anatomy.

In this context, we developed computational methods and integrated the methods within a prototype system - SemAnatomy3D, in order to provide a rich set of tools for 3D shape analysis that supports semantic annotation of 3D-PSM with concepts derived from the ontology and with the quantitative attributes.

To summarize, our contribution is threefold. First, we present various components of SemAnatomy3D system for the creation of *self-explanatory* patient-specific 3D models (Sec. 2). Second, we propose a specialized set of feature descriptors to characterize the carpal district, in terms of functional regions and pathological markers (Sec. 2.3). Finally, we highlight possible usages of the semantic-based representation of patient anatomy in clinical applications (Sec. 3).

As case-study, we have selected the Rheumatoid Arthritis (RA) focusing on carpal district. Carpal district is the anatomical assembly of 8 carpal bones, which constitutes one of the most complex joint of human body. RA, a chronic inflammatory disorder, affects the lining of inter-bone joints of carpal district, causing a painful swelling that can eventually result in bone erosion and joint deformity. The diagnostic analyses aims to monitor the individual bones and the district as a whole by analyzing anatomical landmarks and functional regions (ligament insertion, articulation facets, prominent features), quantify relevant parameters (area, volume of the bones and lesion, inter-bone distance), and aggregating the analysis result into clinical findings [ØPC*03]. Thus, the RA diagnostic procedure constitutes a valuable use case for us to verify the potential of SemAnatomy3D framework.

In this particular scenario, our goals are to: (i) identify the PoRs (articulation regions, prominent features, ligament origin & insertion sites) from the patient-specific carpal bones and annotate with semantic concepts; compute the descriptions doctors associate to the district; (ii) define novel characterization that could be informative for diagnosis in future. Another crucial aspect of our system is the structured storage of annotated 3D-PSM to support intelligent 3D indexing.

We use a training dataset of carpal district that contains 30 healthy and 18 pathological samples manually segmented

from T1 weighted MRI images. We also run some preliminary validation checks with the digital database of wrist bone anatomy [MCTL07] where the models are segmented from CT images.

2. Semantic annotation of carpal district

2.1. Knowledge formalization - Carpus Ontology

From the survey of bio-medical ontologies [BCRS14], we realized the fact that the reference bio-medical ontologies provide an extensive model of the whole human anatomy without defining quantitative attributes and relations among the concepts. To address our case study, a detailed conceptualization related to the carpal district is required together with the well-defined relations and attributes, and none of the popular reference ontologies actually satisfy these specific needs. We target to use a formalization that captures the minimal medical context, in order to support our targeted user-scenarios (Sec. 3.2). The considered medical context includes medical background knowledge on: i) patients, acquisition sessions, carpus anatomy, ii) quantitative properties/attributes of the concepts that can properly characterize the entities.

We defined an ad hoc *Carpus Ontology* to realize a anatomical conceptualization at the granularity required, and appropriate for its practical usage. More precisely, we extracted the FMA's anatomy formalization related only to the carpal bones and extended it with part-hood and articulation relations between facets and the properties of anatomical concepts (e.g. bone volume, bone surface area). For instance, FMA:Scaphoid concept is extended by defining `hasArticularFacet`, `hasligamentInsertion` and `hasPart` relations with the following concepts FMA:Articulation_facet_of_short_bone, Prominent_feature and Ligament_insertion_sites (Fig. 1). Further, we grouped all the bones of carpal region under a top class `Carpal_region` which helps us to define the properties and attributes not only on the individual bone but also for the entire carpal district, e.g., adjacency graph, joint width (Fig. 2).

The next step is to formalize relevant parameters/attributes of the anatomical concepts to model them according to the specific context. We identified a list of attributes/parameters that are currently used by the doctors or could provide relevant information in future for the rheumatoid arthritis diagnosis and treatment on carpal region (Table 1). Further, we extracted a subpart of MultiScaleHuman ontology [MSH] related to MSH:Patient and MSH:AcquisitionSession, and merged with our *Carpus Ontology* to complete the domain knowledge required to formalize the context.

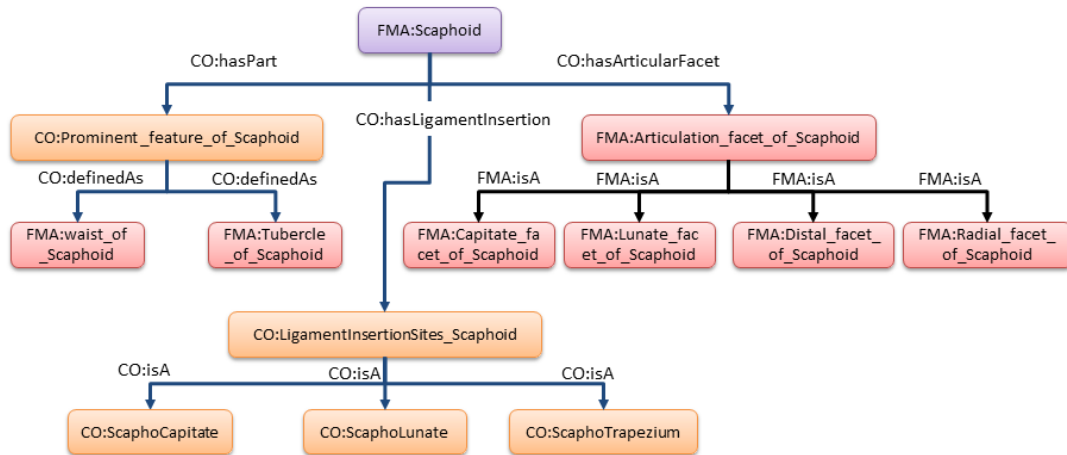


Figure 1: Conceptualization of Scaphoid bone in Carpus ontology

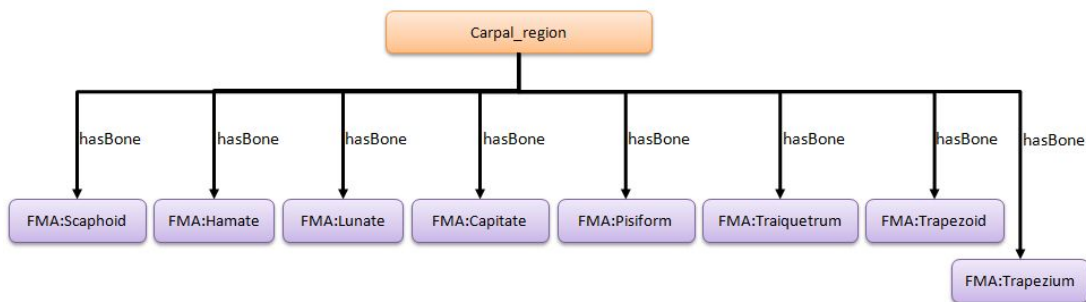


Figure 2: Conceptualization of Carpal region in Carpus ontology

Table 1: List of quantitative attributes in Carpus ontology

Concepts	Attributes & representation
Carpal_region	Shadow Map (scalar map)
	Inter-bone articulation graph (weighted graph)
	Adjacency Map (scalar map)
	Joint width (scalar)
short bone	Bone volume (scalar)
	Bone surface area (scalar)
	Erosion score (scalar)
	Erosion map (scalar map)
	Mean curvature (scalar map)
zone of short bone	Gaussian curvature (scalar map)
	Surface area (scalar)
	Mean curvature (scalar map)

2.2. Descriptive annotation

The descriptive annotation of 3D-PSM aims to describe the semantics of the models and its PoRs by means of the concepts/terms defined in the domain ontologies (Fig. 3). To this end, SemAnatomy3D includes functionalities to associate descriptive information to 3D subparts either via interactive or via controlled mode. Interactive mode is more flexible, but manual, while controlled mode is automatic yet has less adaptability. Both modalities are equally important: the manual annotation mechanism maybe used to associate even completely free-text annotations to 3D parts, and may be also used to fine-tune the controlled annotations, if needed.

Manual annotation - flexible: The annotator can define and select any type of PoRs (surface patch, edges, vertices) within a 3D surface from the interactive tool palette, where interaction tools such as smart-cut, draw, paint and delete strokes, picking of points, are offered. In this process, there are methods to assist the annotation: for instance, the user can simply drag the mouse and select the articulation facets and the prominent features of scaphoid over a patient-

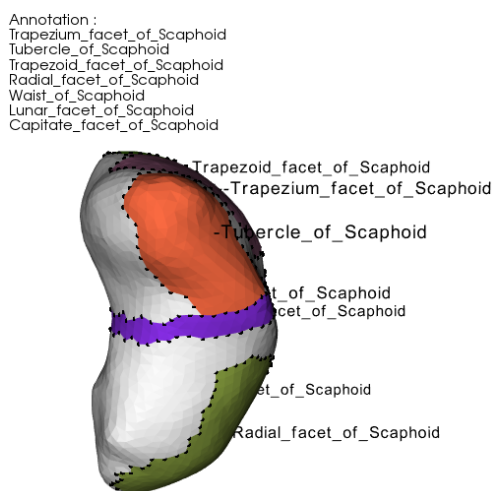


Figure 3: Descriptive annotation of Scaphoid bone

specific model by using the smart-cut tool. The system automatically computes the entire cut in the 3D surface including the region that is not visible from the viewpoint, and the selected portion of the model is colored accordingly. Further, the system allows fine-tuning of the PoRs boundary by using simple interaction tools, such as paint and delete strokes. After having identified the PoR, the user can annotate it with the conceptual tags selected from the *Carpus Ontology* in our case study.

Automatic annotation - controlled: As an alternative approach, we have developed an automatic template-based method that associates automatically conceptual tags of the Carpal bone Ontology to parts of 3D-PSM. In this process, a 3D template model for each carpal bone is used, which is generated according to the methodology presented in [BLP⁺15]. The templates, built from a statistical analysis of real patient data, can be considered as the average healthy shape of the sample population which captures the healthy shape variability and preserves important anatomical landmark features. Given the template, the basic idea is to transfer the annotation of the template automatically onto the 3D-PSM, by co-registering the annotated 3D template with the 3D-PSM, and transferring to the latter the positions of anatomical landmarks.

Algorithm 1 summarizes the steps of the automatic annotation process in SemAnatomy3D. To this end, we apply a non-rigid variation of the Iterative Closest Point algorithm initialized with coarse alignment using centroid to find the matching between template and target model. This automatic method only supports annotation with the controlled terms from *Carpus ontology* that have been pre-associated with the parametric 3D template model.

Algorithm 1 Automatic annotation of the PoRs

```

1: procedure PARAMETRIC METHOD
2:   Input:  $M \leftarrow$  Target 3D-PSM
3:    $T \leftarrow$  "Template" model
4:   Output: Sub-parts of  $M$  annotated with labels.
5:    $R \leftarrow$  Coarse_alignment( $T, M$ )  $\triangleright$  using centroid
      matching.
6:    $K \leftarrow$  Nonrigid_ICP( $R, M$ )  $\triangleright$  to refine the alignment
      locally.
7:    $KDTree \leftarrow$  BuildKDTree( $M$ )
8:    $Subparts_M \leftarrow$  Propagate_annotation( $T, M, KDTree$ )
       $\triangleright$  by nearest neighbour search method.
9:   Filtering_regions( $Subparts_M$ )  $\triangleright$  to generate
      continuous regions.
10: note: Adjustment of the subparts and modification of the
      annotation can be done interactively.

```

2.3. Quantitative annotation

Quantitative annotation tries to associate numeric values that reflect the characterization of individual anatomy at the various levels, e.g., anatomical, functional, pathological. Thanks to the 3D representation of the anatomy, it is possible to compute a wide range of parameters, that describes the shapes and their structure.

In the current implementation of SemAnatomy3D, we included three types of computational method to address the measurement of quantitative metadata (Table 1):

Quantitative measurements: We developed a set of tools by implementing popular geometric and shape analysis algorithms [BFGS14], and integrated within the system to automatically measure the quantitative attributes (Table 1) that can be computed directly from the 3D-PSM, e.g., Bone volume, Bone surface area, Mean & Gaussian curvature. To support reliable outcome of these characterization methods, we also incorporate a few popular 3D mesh repairing algorithms within our platform, e.g., filling holes, removing self-intersecting triangles etc.

(Dis)similarity measurements: Measuring dissimilarity is not trivial. We adopt two possible ways of computing the dissimilarity:

1. deviation of the target 3D-PSM from the normality defined by the template shape which is useful to indicate a pathological situation;
2. monitoring of differences among the bone models of same patient acquired in two different time-stamps, therefore supporting the follow-up analysis;

The *Erosion score* is computed as the difference in Bone volume of the target shape in compare to the healthy template. This score gives a global characterization of pathological data, although it does not give an idea of the exact location of erosion. Through a rigid co-registration method [Rus10], we compute the vertex-wise dissimilarity

between the template and the patient-specific 3D model. It aims to compute the Erosion map (Table 1) of the targeted data by measuring the vertex-wise distance from the co-registered model. This investigation not only classifies the pathological data but can recognize specific area of anomalies for fine grain analysis, as well.

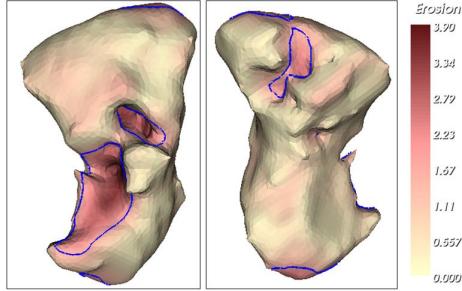


Figure 4: Erosion map - measure the distance from healthy template

The initial result of Erosion map computation on scaphoid bone is shown in Fig. 4, where a healthy template is used to define the *normality*.

Characterization of the district: Understanding the implicit knowledge carried by the 3D models of carpal bones requires the recognition of the most representative features in the context of our case study. Carpal district is one of the more complex joints in the human body since it is a collection of multiple bones and joints. All of these bones participate in complex articulations that allow variable mobility of the wrist. To study the district with its true complexity, we target a *feature-based* modeling to correlate the 3D characterization with the functional information related to the articulation and adjacency.

In the last decades, a lot of techniques have been developed for the analysis of 3D shapes. However, characterization of a set of 3D shapes that portray crucial aspects of patient-specific anatomy of a particular district is quite peculiar. While there have been studies that attempted to study the anatomical shape, they mostly took a 2D perspective based on scan images [PKKH93]. However, the projection of anatomical structure in 2D can cause gaps due to occlusion.

We propose three feature descriptors to automatically characterize the functional regions (articulation and adjacency) of the carpal district from the 3D-PSM.

Shadow Map represents the shadow of one adjacent bone on the other which can be correlated with the articulation facets. Algorithm 2 summarizes the steps to compute the Shadow Map from the carpal bones based on the articulation matrix $R[8][8]$, where the dimension refers to the number of bones in carpus. The articulation matrix is defined by the

formalization of *Carpus Ontology* (Sec. 2.1) as $R[i][j] = 1$ when *Bone* $[i]$ and *Bone* $[j]$ are articulatesWith each other, and $R[i][j] = 0$ otherwise. For instance, according to formalization of Fig. 5 $R[Hamate][Capitate] = 1$ and $R[Capitate][Hamate] = 1$, as Capitate and Hamate articulatesWith each other.

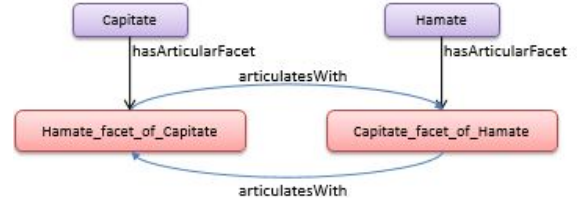


Figure 5: Articulation relation in Carpus ontology

Algorithm 2 Shadow map computation

```

1: procedure SHADOW MAP COMPUTATION OF CARPUS
2:   Input: Bones $[8] \leftarrow 8$  carpal bone surface models
3:   R $[8][8] \leftarrow$  Articulation Matrix
4:   Output: ShadowMap $[8][NoOfVertices] \leftarrow$ 
      scalar value map defined each surface model.
5:   for  $\langle i = 1 \text{ to } 8 \rangle$  do
6:     for  $\langle j = 1 \text{ to } 8 \rangle$  do
7:       if  $(i \neq j \text{ and } R[i][j] = 1)$  then
8:         Shadow $[i] \leftarrow$ 
          COMPUTESHADOW(Bone $[i]$ , Bone $[j]$ )  $\triangleright$  calling the
          function
9:         DrawContour(Shadow $[i]$ )  $\triangleright$  Contour drawn based
          on the pre-defined range
10:  procedure COMPUTESHADOW(Model $_1$ , Model $_2$ )
11:    KDTree  $\leftarrow$  BuildKDTree(Model $_2$ )
12:    for each vertex $_k$  of Model $_1$  do
13:      CloseP  $\leftarrow$  FindClosestPoint(vertex $_k$ , KDTree)
14:      SquareDis  $\leftarrow$  EuclideanDistance(vertex $_k$ , CloseP)
15:      if SquareDis  $<$  Shadow $[i][k]$  then
16:        Shadow $[Model_1][k] \leftarrow$  SquareDis
    
```

We present a preliminary result of the Shadow map computation by Algorithm 2 in Fig. 6, where the surfaces are colored according to the *ShadowMap* value and the contours are drawn based on a pre-defined scalar value range.

Inter-bone articulation graph represents the articulation relation between carpal bones defined in the *Carpus ontology* (Fig. 5), in such a way that if Capitate bone has relation articulatesWith Hamate there is an edge connecting the centroid of the capitate and hamate surface models. The edge weight represented in mm, signifies the minimum distance between the bone surfaces. This operator helps to

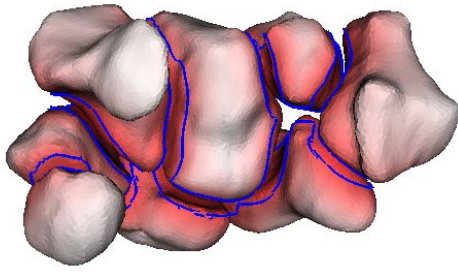


Figure 6: Computation of “Shadow Map” of carpal region

quantify the inter-bone distance that is useful to define carpal stability. A result of our implementation is shown in Fig. 7.

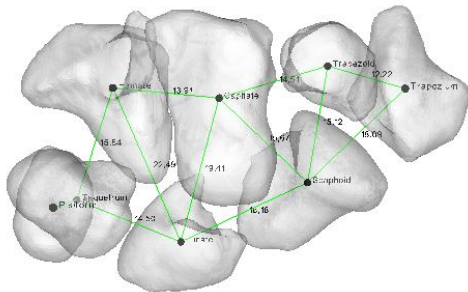


Figure 7: Computation of “Inter-bone articulation graph” of carpal region

Adjacency Map signifies a joint distance map computed by utilizing the inter-bone articulation graph. The idea behind this is to compute the minimum geodesic distance map where the sources are the intersection points of inter-bone articulation graph. Formally, the *AdjacencyValue* of the i th vertex can be computed as: $AdjacencyValue_i = \min[d(v_i, s_1), d(v_i, s_2), \dots, d(v_i, s_n)]$, where v_i is the i th vertex, s_j is the j th source, and $d(v, s)$ is the geodesic distance between the vertex v and source s . If a bone articulates with three other bones, as in the case of Hamate, then $n = 3$. The *Adjacency Map* can help to characterize 3D structures of each bone as well as spatial relations in complex joints like *Carpus*.

In Fig. 8, the green points represents the intersecting points and the dark color signifies the regions with minimum geodesic distance. This can be used as a tool to explore hidden structures and subtle kinematics of carpal joints in vivo.

2.4. SemAnatomy3D knowledge base

Another issue is to manage the annotation in a knowledge base such that it stores the annotation of varying dimensional

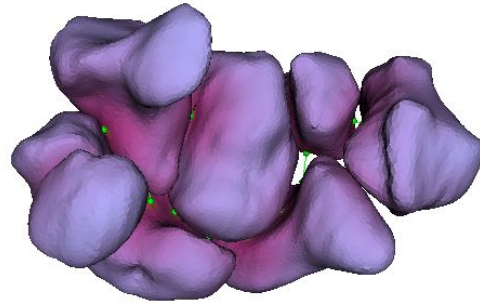


Figure 8: Computation of “Adjacency Map” of carpal region

3D subparts (surface patch, line, vertices) in a structured way. More specific requirements are: (i) subparts should be in a stored standard format to be easily shared and re-used; (ii) single 3D model can have multiple annotations; (iii) no need to replicate the whole 3D model, a reference to the original model is sufficient for the subpart annotation;

We aim to constitute the knowledge base based on two main ingredients: (i) annotation data-model to manage 3D annotation, and (ii) standard file format to identify the annotated 3D sub-parts.

2.4.1. SemAnatomy3D data model

SemAnatomy3D data model facilitates interoperability, querying, reasoning and discovery of 3D-PSM as a whole and its subparts. A number of semantic annotation data models [KKPS02], [HCSVdS10] have been proposed which aim to support interoperability on the Web. Unfortunately, none of these common models provides sufficient detailed specifications for annotating 3D-PSM and their varying dimensional subparts.

The OA data model [SCVdS13] developed by W3C Open Annotation Community Group, specifies an extensible data model to support interoperable annotations for enabling discovery and sharing of annotations without using a particular set of protocols. We extended the OA model to fulfill the main requirements of SemAnatomy3D framework: (i) store the annotation of varying-dimensional 3D fragment; (ii) support whole and part-based annotation with descriptive and quantitative attributes; We present our proposed schema in Fig. 9.

Addition to Open annotation model (OA) new concepts in Sem3D annotation data model are defined as:

- `sem3D:3DFragmentSelector` is specified as a `rdfSubClassOf` the `oa:Selector` element to model different representations of the 3D PoRs (surface patch, edge, vertex).

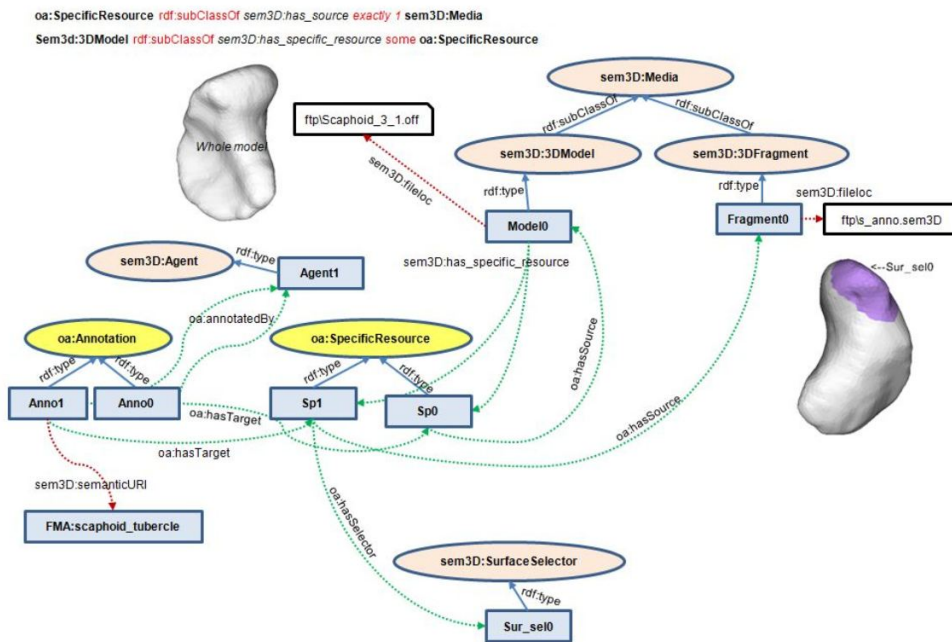


Figure 9: SemAnatomy3D extension of OA data model

- `sem3D:Media` stores various types of data format, e.g., 3D triangulated models, 3D fragments (.sem3D), 2D images, textDocument, which can either have their own annotation (*source of annotation*) or can be considered as annotation of another data (*body of annotation*).
- `sem3D:Quantitativevalue` stores single numeric value parameter or scalar value map computed from the `sem3D:Media`. It can be considered as a form of annotation. It has two `rdf:DataProperties`: (i) `sem3D:paramtype` - describes the type of quantitative parameters, e.g., volume, area, curvature map; (ii) `sem3D:paramvalue` - stores the numeric value of the parameter.
- **Restrictions** - We put the following restrictions on `oa:SpecificResource` and `sem3d:3DModel`:
`oa:SpecificResource rdf:subClassOf sem3D:has_source exactly 1 sem3D:Media`
 that means `oa:SpecificResource` should have exactly one data file.
`sem3d:3DModel rdf:subClassOf sem3D:has_specific_resource some oa:SpecificResource`
 that means `sem3d:3DModel` can have some (one or multiple) specific resource, i.e. subparts.

2.4.2. .sem3D: 3D sub-part identifier

We developed a simple file format .sem3D with three main goals: (i) support a faster way of reading, writing and render-

ing of 3D subpart annotation; (ii) to be as simple as it can, so that it can be customized for various applications; (iii) avoid storing redundant information in a standard manner.

We came up with an index-based method of storing varying topological dimensional 3D fragments in a .sem3D file as follows,

1. *Surface fragment in .sem3D* - We store only the index of the cells (triangle) belonging to the fragment.
2. *Line fragment in .sem3D* - We store index of the points belonging to the line fragment. We maintain adjacency of the points in the form of - xy, yz, zk, \dots
3. *Point fragment in .sem3D* - We only store the index of the points.

With this approach, a .sem3D file which stores a surface fragment containing 717 cells and 379 points will be of size less than 1KB.

To describe the whole idea we present a snapshot of the SemAnatomy3D knowledgebase in Fig. 9, which is related to saving of a 3D-PSM of the scaphoid bone and its 3D surface fragment annotated as `FMA:scaphoid_tubercle`. Each instance of `oa:Annotation` is linked to the instance of `oa:specific_resource` and each `oa:specific_resource` instance `oa:has_source` exactly 1 `sem3D:Media` instance. The `sem3D:Media` instance describes the data by storing the actual file location of annotation source. If a `oa:specific_resource` instance corresponds to a PoR (sub-part) annotation then it will

be linked with a specific `sem3D:FragmentSelector` instance and `sem3D:3DFragment`, e.g., `FMA:scaphoid_tubercle` is linked with an instance `sem3D:SurfaceSelector` and an instance of `sem3D:3DFragment`. The instance of `sem3D:3DFragment` has a `.sem3D` file location which stores the reference of the annotated geometry.

3. Semantic-driven analysis

In this section, we investigate how the semantic annotation and the SemAnatomy3D knowledge base can be utilized in order to enhance the re-use, sharing and interoperability of patient-specific 3D models. For this setting, we discuss SemAnatomy3D query engine and how it attempts to support our clinical user scenarios.

3.1. SemAnatomy3D query engine

The coding of medical knowledge in the form of structured metadata is a crucial ingredient for the development of effective search engine that takes into account not only the geometry of 3D models but their semantics, or meaning. Coupling of part-based annotation and knowledge formalization could foster the development of totally new approaches to part-based shape retrieval in medicine. For example, the engine could be able to answer queries of the type “search a Scaphoid bone model having erosion score as the current data and detected as Osteoarthritis stage II”, or even refer directly to the PoRs, “find `RAD:scaphoid_tubercle` with 2.5 average erosion”, obtaining as results proper subparts of 3D-PSM.

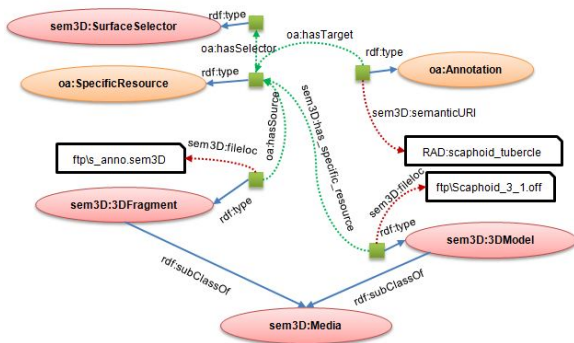


Figure 10: SPARQL query: example 1

In our query engine implementation, the system retrieves the 3D shapes based on the SPARQL query to the SemAnatomy3D knowledge base. SPARQL queries use graph pattern matching techniques to evaluate answers. To address our requirements, two complimentary retrieval services have

been implemented: (i) retrieval of 3D models where the subparts have particular semantics, i.e., they have been annotated with a specific conceptual tag or comprise of a specific attribute value; (ii) retrieve all the annotations which have been attached to a specific 3D models.

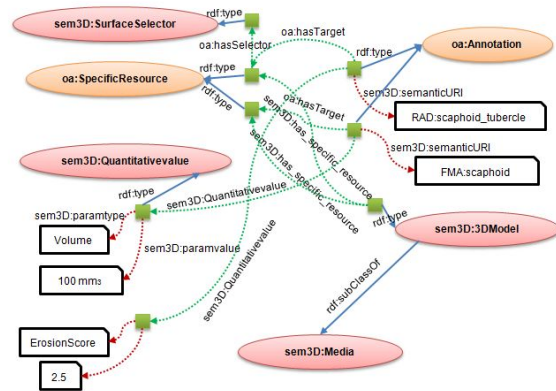


Figure 11: SPARQL query: example 2

In Fig. 10, we present a simple SPARQL query to retrieve all the 3D models where a subpart has been annotated with the conceptual tag `RAD:scaphoid_tubercle`. As a result, the query retrieves the file location of the original 3D model as well as the `.sem3D` file location which identifies the annotated geometry of the subpart, which then can be combined together in SemAnatomy3D graphical interface for rendering. In Fig. 11, the SPARQL query retrieves all *descriptive* and *quantitative* metadata that have been associated with a particular instance of `sem3D:3DModel` or with its subparts.

3.2. User scenarios

In this section, we describe the foreseen medical usages of the SemAnatomy3D knowledge base (Sec. 2.4) by employing the query engine (Sec. 3.1).

Bio-mechanical simulation: Normal carpal mechanics rely on the interplay between the arrangement of carpal ligaments and carpal bone morphology. Studying carpal kinematics is very difficult compared to other anatomical joints due to the complex bony and ligamentous structure of the wrist and the intricate and intimate interactions of the different components. Locating anatomical landmarks positions automatically on the 3D model of patient-specific carpal bones has a huge potential in the study of kinematic descriptions.

SemAnatomy3D framework allows to retrieve the `.sem3D` files corresponding to the patient-specific geometry of the particular ligament origin and insertion

positions. A sample query will be: “retrieve *Scapholunate_ligament_origin* site in model X and *Scapholunate_ligament_insertion* sites in model Y”. The execution of such a query is supported by the formalization (cf. Sec. 2.1), capturing the origin and insertion sites of each ligament. Thus, the SPARQL query similar to the one described in Fig. 10, will retrieve the subpart of 3D model X annotated as *Scapholunate_ligament_origin* and the subpart of model Y annotated as *Scapholunate_ligament_insertion*.

Moreover, if the patient-specific parameter corresponding to that position is not available, then the system automatically annotates model X and Y via the template-based method (Sec. 2.2).

Comparative analysis: Part-based annotations are important also to support comparative analysis of clinical cases. Indeed, descriptions attached to PoRs can be used as actual signatures. Signatures are abstract descriptions of the content of the original resource and allow comparisons and similarity assessment; in the medical domain they are helpful to provide a second opinion for clinical diagnosis.

Thanks to the detailed descriptive and quantitative annotation of 3D-PSMs, SemAnatomy3D query engine can support retrieval based on abstract descriptions of the content, such as “Find all records of clinical cases where the inter-bone distance between *FMA:Scaphoid* and *FMA:Lunate* is more than 2mm, and the average erosion value of *FMA:Scaphoid_facets_of_Lunate* is larger than 2.5?”. Answering the query is quite trivial because of the conceptualization which models the domain, and the semantic annotations that link the conceptualization with the data.

Evaluation of patient follow-up: Concerning the follow-up, SemAnatomy3D offers the functionality to evaluate the *distance to normality*. It can be used as a tool to evaluate quantitatively the differences between two different stages of pathology evolution in the same patient.

SemAnatomy3D query engine can retrieve all the carpal district data of a patient with different time-stamp. To this end, the quantitative evaluation can be to either measure the volume difference between the carpal bone models or to compute the erosion map by co-registration. In Fig. 12, we present our preliminary results where the Erosion Map of model with t_2 timestamp has been computed by registering the model with t_1 timestamp, and the red color represent the regions where erosion escalated compared to the baseline model.

Discussion on this aspect triggered further suggestions to set up a library of tools to quantify automatically the evolution of other significant parameters relevant for the follow-up (e.g., the “Shadow Map”, “Inter-bone articulation graph”).

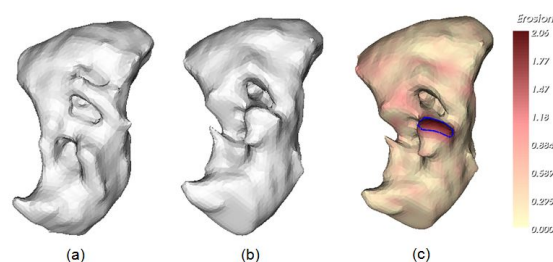


Figure 12: Follow up evaluation of Scaphoid: (a) model with t_1 timestamp; (b) model with t_2 timestamp; (c) Erosion Map

4. Conclusions

In this study, we have discussed SemAnatomy3D framework for creating expressive 3D-PSMs, through the process of 3D annotation, which associates semantics with the whole 3D model and to its Parts-of-Relevance. As a main contribution, we proposed a specialized set of feature descriptors to characterize the carpal district in terms of functional regions. We also discussed the potentiality of the SemAnatomy3D framework to support the clinical scenarios. We are now in the clinical validation phase, where we consult various medical professionals (surgeon, anatomist, radiologists) to assess our framework and its ability to support the clinical practice. As a first important feedback, we mention that the implementation of the SemAnatomy3D platform per se was perceived as novel and very useful by the experts.

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