Cognition Network Technology for a Fully Automated 3D Segmentation of Liver Tumors

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Abstract. The Definiens Cognition Network Technology is applied to detect automatically tumors in a human liver. On the basis of a test data set containing ten tumors we show first quantitative results which are compared to manual segmentations provided by medical experts.

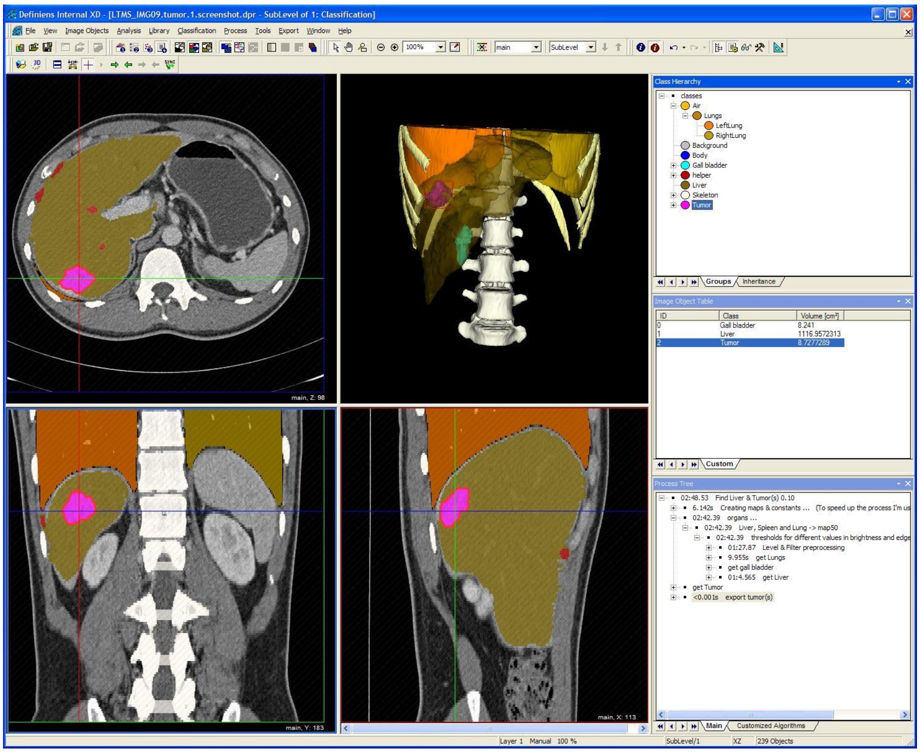
1 Introduction

Rationale The reliable detection of liver tumors in CT scans and the precise measurement of their shape is the basis for diagnosis, surgery planning and therapy control of liver cancer. Since manual measurement of 3D structures is extremely time consuming, cost intensive and subjective, automated methods are required in today's challenging clinical environment. Due to a large variability in appearance and shape of liver tumors, the automated reliable segmentation represents a nontrivial task.

State of the art The MICCAI 2007 Workshop *3D Segmentation in the Clinic: A Grand challenge* provided an excellent comparison of recent segmentation algorithms (see HEIMANN et al. [1]). These methods include level-set methods, shape and appearance models, atlas matching and rule-based systems [1].

Context-based approach In this paper, we follow the successful context-based approach of SCHMIDT et al. [2] where the liver was segmented in its anatomical context. Their results show that using contextual information increases the robustness and accuracy of the segmentation.

The suitable software framework for context-based image object processing is provided by the Definiens Cognition Network Technology (ATHELOGOU et al. [3]). This framework has been applied with great success to a variety of image analysis tasks based on data from very different kind of sensors ranging from satellites equipped with radar or optical sensors, over electron or optical microscopes to three-dimensional computer tomographs (see, e.g., example applications in [3] and SCHÖNMEYER et al. [4]).



- classes
  - Air
    - Lungs
      - LeftLung
      - RightLung
  - Background
  - Body
  - Gall bladder
  - helper
  - Liver
  - Skeleton
  - Tumor

ID	Class	Volume [cm³]
0	Gall bladder	8.241
1	Liver	1116.9572313
2	Tumor	8.7277289

```
02:48.53   Find Liver & Tumor(s) 0.10
   6.142s   Creating maps & constants ...   (To speed up the process I'm us
   02:42.39   organs ...
      02:42.39   Liver, Spleen and Lung -> map50
         02:42.39   thresholds for different values in brightness and edge
            01:27.87   Level & Filter preprocessing
            9.955s   get Lungs
            get gall bladder
            01:4.565   get Liver
   get Tumor
   <0.001s   export tumor(s)
```

Fig. 1. Screenshot of the Definiens Developer XD 1.0 software depicting the segmentation result for the test data set LTS_IMG09. In the 3D visualization, the detected liver tumor is colored pink while the liver is transparent and brown. Also, the lower parts of the lungs (orange and light brown), the gall bladder (green) and the skeleton are shown. The figure also depicts the associated sagittal, coronal, and transversal view. On the right-hand side the Class Hierarchy, the Image Object Table, and the CNL script are shown. For simplicity, only one feature (volume) of a few selected objects (gall bladder, liver, and tumor) is presented in the Image Object Table.

In the following, we describe the application of the Cognition Network Technology on a fully automated segmentation of liver tumors. The results are evaluated on a data set containing ten tumor samples based on the performance metrics volume overlap error, volume difference, average, RMS and maximal surface distance.

2 Preliminaries

2.1 Cognition Network Technology

The Cognition Network Technology [3] is implemented in the software platforms Definiens Enterprise Image Intelligence and Definiens XD[1]. Both platforms feature an environment where scripts written in the Cognition Network Language can be developed and executed. This environment allows the user to load image data, and generate, execute and edit graphically the analysis script. Results can be visualized (see Fig. 1), and properties and overall statistics of the resulting image objects (segments) can be exported as raster image masks. The interactive mode allows a rapid script development with a steep learning and progress curve. The execution environment uses a workspace concept in which the user may process many images offline and – if needed – in parallel on a computer cluster.

Definiens XD is a newly developed platform that is specifically designed for multi-dimensional image data. In particular, it facilitates a wide range of multidimensional image analysis applications such as Medical Imaging and Pre-Clinical Small Animal Imaging.

2.2 Cognition Network Language

The Cognition Network Language [3] is an object-based procedural computer language which is specifically designed to enable the automated analysis of complex, context-dependent image analysis tasks. It consists of four basic data structures: Processes, Domains, Image Objects and Image Object Classes. The language was designed to provide an easy to learn but very powerful approach to specify a complex image analysis task which consists of an iterative execution of less complex tasks. Each language element representing the dynamic of the analysis is called Process. There are Processes to manage Image Objects, object features, Classes, and variables, file IO, image filters, segmentation, object linkage and classification operations, and control structures such as conditional execution commands and loops. The Processes are organized in a process tree hierarchy.

The Process execution engine recursively executes a root process and then subsequently all its child Processes in a depth-first order. By selecting and parameterizing the Processes the particular processing algorithms are specified for a given programming step, whereas through the definition of a Domain the system is guided to the data structure that is going to be processed. The Processes define *what* and the Domains *where* processing takes place. The most important Domains are Pixel Level Domains for filtering and initial segmentation operations, Image Object Domain for Processes which operate on Image Objects (segments) with specific classification and properties, and Image Object Relation Domain which allows the navigation in the image object network. Navigation

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is in particular useful to process the neighbors or sub-objects of a given Image Object in the current Process with the algorithms in its sub-Processes.

An Image Object represents a group of pixels or a group of Image Objects. An Image Object comprises methods to calculate its properties such as shape, position, mean spectral values or texture. Since Image Objects may be linked to other Image Objects using specific Processes, relational properties such as Relative Surface Contact Area or Relative Brightness can be easily computed and used in the processing. Image Objects are either generated by basic segmentation (e.g., multi-resolution segmentation [5]) or by grouping existing Image Objects on a higher Image Object level. The Cognition Network Language provides operations to re-segment or to re-classify Image Objects with specific, eventually context-dependent properties. Each Image Object may be assigned to a specific class by execution of a Class Assignment Process if certain conditions are fulfilled.

Image Object Classes describe the kind of objects to be searched for in a given image. The Classes may be grouped in a Class hierarchy to enable the addressing of Process operations on groups of Classes. Each Class carries a name, a visualization color and optionally a logical expression of Fuzzy membership functions. The membership functions are piecewise linear functions which describe the contribution of each specified Image Object property (e.g., area, brightness, distance to another image object with given classification) to the overall class membership.

3 Materials and methods

3.1 Image data

The liver tumor data set used in the analysis was provided by the organizers of the MICCAI 2008 workshop *3D Segmentation in the Clinic*[2]. It contains ten annotated tumors from four patients (training set) and ten tumors from six patients (test set; no annotations). The voxel spacing varies between 0.6 and 0.9 mm, the inter-slice distance varies from 1.0 to 1.5 mm. There is no overlap between neighboring slices. The resolution of all volumes is 512-by-512 voxels in-plane.

3.2 Evaluation Measures and Scoring System

For each image from the testing data set, a reference segmentation was provided by the organizers of the MICCAI 2008 workshop. Based on this reference, five evaluation measures are defined: (1) volumetric overlap, (2) relative absolute volume difference, (3) average symmetric absolute surface distance, (4) symmetric RMS surface distance, and (5) maximum symmetric absolute surface distance. For more detailed information see the homepage[3] of the MICCAI 2008 workshop and Gerig et al. [6].

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[2] See `http://grand-challenge2008.bigr.nl`

[3] See `http://lts08.bigr.nl/about.php`

3.3 Liver tumor segmentation algorithm

The segmentation algorithm was developed in the Cognition Network Language (CNL; see Section 2.2) with Definiens Developer XD. Since Definiens Developer XD offers built-in features for multi-dimensional data, the CNL script by Schmidt et al. [2] was completely re-written and simplified.

The algorithm contains the following two parts: liver segmentation and liver tumor segmentation.

Part 1: Liver segmentation

1. In the initial step, the 3D data set is segmented using heuristic threshold values for the intensity. Thus, the body is separated from the background.
2. Within the body, the Image Objects are refined based on their volume and their intensity, which gives an approximation of the lungs, the fat tissue, the muscle layer, the organs, and the skeleton.
3. Based on these body parts, a new layer of 3D edge information is calculated, which in turn provides a reference for further refining the body parts.
4. After this pre-processing step, the left and right lung are given as Image Objects with maximal volume on the left and right side of the body, respectively.
5. Beside the right lung, the gall bladder is segmented.
6. The skeleton is segmented in order to give further constraints for the liver.
7. Finally, the liver is given as the Image Object with maximal volume which is located below the right lung and delimited by the gall bladder and the skeleton (in particular the ribs).

Part 2: Liver tumor segmentation

1. The mean intensity value and the standard deviation of the liver is calculated, which gives two threshold values for partitioning the liver into segments with high, medium, and low intensity. The segments with high or low intensity provide the tumor candidates.
2. The tumor candidates are smoothed using on a ‘shrink & grow’ strategy.
3. The tumor candidates are filtered by using a threshold for the volume.
4. The ‘normal’ liver parts (i.e., liver segments with medium intensity) that are enclosed by tumor candidates are merged with the latter.
5. The tumor candidates are smoothed by shrinking with a given surface tension.
6. The volume criterion is used again to remove candidates which are too small.
7. Further refinement is performed by growing the tumor candidates.
8. The tumor candidates are filtered by the criteria roundness and relative border to the liver.
9. Finally, the tumor candidates are smoothed by additional shrinking and growing with a given surface tension.

	Overlap Error		Volume Diff.		Ave. Dist.		RMS Dist.		Max. Dist.		Total
Tumor	[%]	Score	[%]	Score	[mm]	Score	[mm]	Score	[mm]	Score	Score
IMG05_L1	63.73	51	55.56	42	6.24	0	9.03	0	26.92	33	25
IMG05_L2	56.22	57	42.96	55	2.31	42	2.89	60	7.27	82	59
IMG05_L3	36.25	72	3.11	97	1.52	62	2.09	71	6.80	83	77
IMG06_L1	83.03	36	418.01	0	7.31	0	9.15	0	25.46	36	14
IMG06_L2	62.75	52	102.39	0	2.43	39	3.45	52	9.18	77	44
IMG07_L1	44.54	66	42.15	56	6.11	0	8.64	0	30.02	25	29
IMG07_L2	66.04	49	63.18	34	3.18	20	3.88	46	11.61	71	44
IMG08_L1	61.70	52	61.31	36	7.76	0	9.41	0	28.52	29	23
IMG09_L1	35.52	73	0.74	99	1.27	68	1.92	73	11.52	71	77
IMG10_L1	19.74	85	10.81	89	1.02	74	1.39	81	5.55	86	83
Average	52.95	59	80.02	51	3.91	31	5.19	38	16.28	59	48

Table 1. Results of the comparison metrics and scores for all ten test cases.

4 Results and discussion

The above algorithm was applied to the training set and the test set. Figure 1 shows an example of the segmentation results with the corresponding CNL script, Class hierarchy, and Image Object features.

Table 1 shows an evaluation of all segmentation results for the test set using the measures and scores described in Section 3.2.

The computer run times varied from 3 min for a data set with 145 slices to 10 min for a data set with 304 slices on a computer with a dual core processor (2.4 GHz, 3.5 GB RAM).

A visual inspection of the segmentation results in combination with the scores from Table 1 indicates that our tumor segmentation algorithm tends toward finding a superset of the reference segmentations without a smooth surface. This result is a consequence of our conservative approach where the goal is to find a guaranteed enclosure for each tumor. Additional smoothing with certain restrictions may improve this method.

Furthermore, the differentiation of tumors from blood vessels is not satisfactory yet (see Figure 2). Since tumors can be both brighter and darker than the surrounding liver, small parts of blood vessels close to a tumor were misinterpreted as belonging to the latter.[4]

5 Conclusion and future work

In this paper we presented an algorithm for the segmentation of liver tumor in 3D data that uses contextual information and is based on the Cognition Network

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[4] These artifacts do not occur anymore in the current version of the tumor segmentation algorithm.

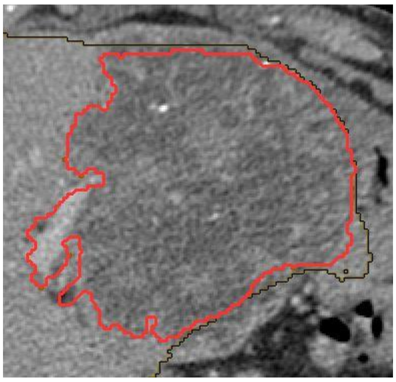

Fig. 2. Segmentation artifact for the data set LTS_IMG07. A part of a blood vessel is misclassified as a bright part of a dark tumor.

Technology. Although the current version is not suitable yet for clinical use, the results show that it is a promising step in the development of a computer-aided diagnosis system.

Beside the possible improvements mentioned in the previous section, future work includes the following two items:

1. **Complete anatomical model.** In the current analysis, a complete anatomical model is not included yet. In particular, contextual information provided by the organs heart, spleen, and stomach will improve the quality and the robustness of the segmentation algorithm.
2. **Tumor feature.** Experiments indicate that the quotient

   $$\tau(x) := \frac{\text{Volume}(x)}{\text{Surface}(x)}$$

   where x is an Image Object and Volume(x) and Surface(x) are the volume and the approximated surface of x, respectively, seems to be a suitable feature for discriminating tumor objects from other Image Objects (see Figure 3), which will be further investigated.

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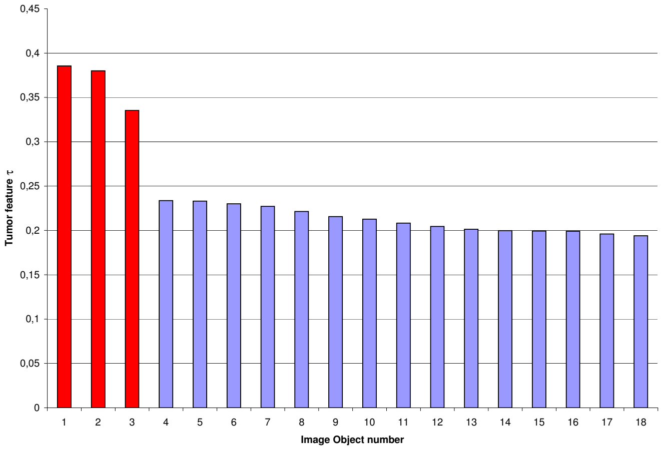

Fig. 3. Tumor feature values for the data set LTS_IMG05. The segmentation algorithm was applied on the the data set LTS_IMG05 and returned a partition of the liver containing 18 Image Objects. The graph shows their tumor feature values (sorted). Image Objects 1–3 (red) were marked by the organizers as liver tumors.

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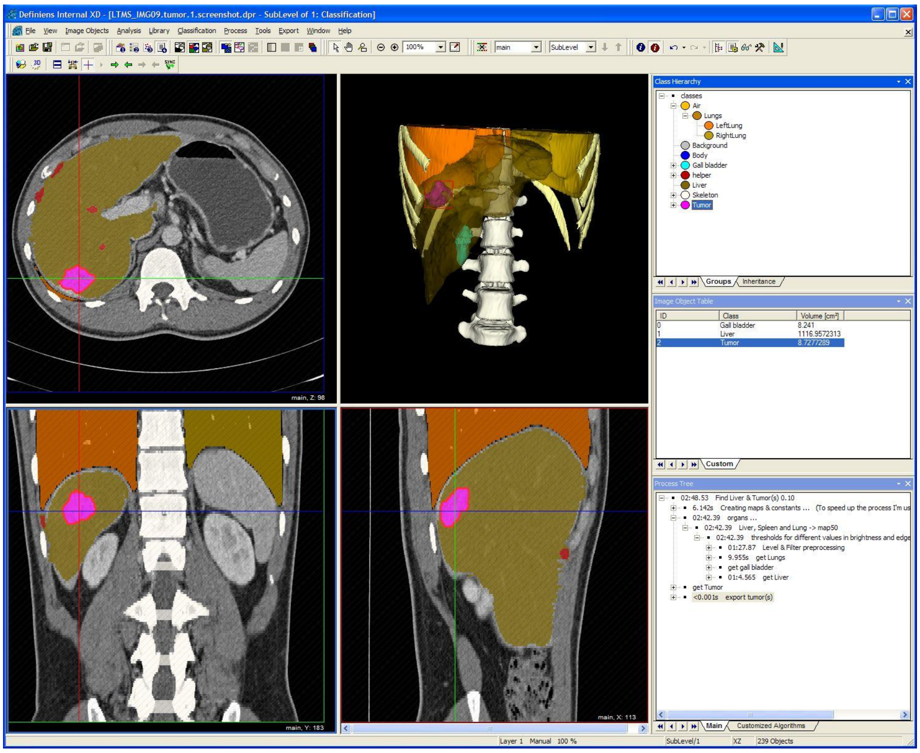

ID	Class	Volume [cm³]
0	Gall bladder	8.241
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```
02:48.53   Find Liver & Tumor(s) 0.10
    6.142s   Creating maps & constants ...   (To speed up the process I'm us
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Fig. 1. Screenshot of the Definiens Developer XD 1.0 software depicting the segmentation result for the test data set LTS_IMG09. In the 3D visualization, the detected liver tumor is colored pink while the liver is transparent and brown. Also, the lower parts of the lungs (orange and light brown), the gall bladder (green) and the skeleton are shown. The figure also depicts the associated sagittal, coronal, and transversal view. On the right-hand side the Class Hierarchy, the Image Object Table, and the CNL script are shown. For simplicity, only one feature (volume) of a few selected objects (gall bladder, liver, and tumor) is presented in the Image Object Table.

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3.2 Evaluation Measures and Scoring System

For each image from the testing data set, a reference segmentation was provided by the organizers of the MICCAI 2008 workshop. Based on this reference, five evaluation measures are defined: (1) volumetric overlap, (2) relative absolute volume difference, (3) average symmetric absolute surface distance, (4) symmetric RMS surface distance, and (5) maximum symmetric absolute surface distance. For more detailed information see the homepage[3] of the MICCAI 2008 workshop and GERIG et al. [6].

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The segmentation algorithm was developed in the Cognition Network Language (CNL; see Section 2.2) with Definiens Developer XD. Since Definiens Developer XD offers built-in features for multi-dimensional data, the CNL script by SCHMIDT et al. [2] was completely re-written and simplified.

The algorithm contains the following two parts: liver segmentation and liver tumor segmentation.

Part 1: Liver segmentation In the initial step, the 3D data set is segmented using heuristic threshold values for the intensity. Thus, the body is separated from the background. Within the body, the Image Objects are refined based on their volume and their intensity, which gives an approximation of the lungs, the fat tissue, the muscle layer, the organs, and the skeleton. Based on these body parts, a new layer of 3D edge information is calculated, which in turn provides a reference for further refining the body parts.

After this pre-processing step, the left and right lung are given as Image Objects with maximal volume on the left and right side of the body, respectively. Beside the right lung, the gall bladder is segmented. Finally, the liver is given as the Image Object with maximal volume which is located below the right lung and delimited by the gall bladder.

Part 2: Liver tumor segmentation The mean intensity value and the standard deviation of the liver is calculated, which gives two threshold values for partitioning the liver into segments with high, medium, and low intensity. These segments are refined using on a ‘shrink & grow’ strategy based on surface tension. Finally, the liver tumors are derived from the segments with high and low intensity.

4 Results and discussion

The above algorithm was applied to the training set and the test set. Figure 1 shows an example of the segmentation results with the corresponding CNL script, Class hierarchy, and Image Object features.

Table 1 shows an evaluation of all segmentation results for the test set using the measures and scores described in Section 3.2.

The computer run times varied from 3 min for a data set with 145 slices to 10 min for a data set with 304 slices on a computer with a dual core processor (2.4 GHz, 3.5 GB RAM).

A visual inspection of the segmentation results in combination with the scores from Table 1 indicates that our tumor segmentation algorithm tends toward finding a superset of the reference segmentations without a smooth surface.

Furthermore, the differentiation of tumors from blood vessels is not satisfactory yet (see Figure 2). Artifacts of this kind were introduced as a consequence of the observation that a tumor can be both brighter and darker than the surrounding liver.

	Overlap Error		Volume Diff.		Ave. Dist.		RMS Dist.		Max. Dist.		Total
Tumor	[%]	Score	[%]	Score	[mm]	Score	[mm]	Score	[mm]	Score	Score
IMG05_L1	63.73	51	55.56	42	6.24	0	9.03	0	26.92	33	25
IMG05_L2	56.22	57	42.96	55	2.31	42	2.89	60	7.27	82	59
IMG05_L3	36.25	72	3.11	97	1.52	62	2.09	71	6.80	83	77
IMG06_L1	83.03	36	418.01	0	7.31	0	9.15	0	25.46	36	14
IMG06_L2	62.75	52	102.39	0	2.43	39	3.45	52	9.18	77	44
IMG07_L1	44.54	66	42.15	56	6.11	0	8.64	0	30.02	25	29
IMG07_L2	66.04	49	63.18	34	3.18	20	3.88	46	11.61	71	44
IMG08_L1	61.70	52	61.31	36	7.76	0	9.41	0	28.52	29	23
IMG09_L1	35.52	73	0.74	99	1.27	68	1.92	73	11.52	71	77
IMG10_L1	19.74	85	10.81	89	1.02	74	1.39	81	5.55	86	83
Average	52.95	59	80.02	51	3.91	31	5.19	38	16.28	59	48

Table 1. Results of the comparison metrics and scores for all ten test cases.

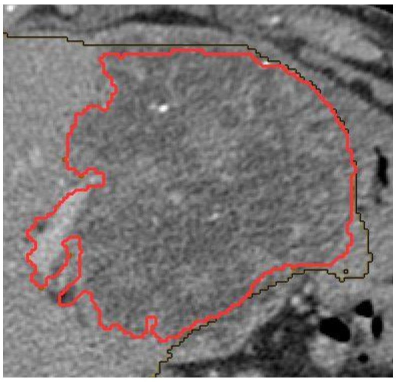

Fig. 2. Segmentation artifact for the data set LTS_IMG07.

5 Conclusion and future work

In this paper we presented an algorithm for the segmentation of liver tumor in 3D data that uses contextual information and is based on the Cognition Network Technology. Although the current version is not suitable yet for clinical use, the results show that it is a promising step in the development of a computer-aided diagnosis system.

Beside the possible improvements mentioned in the previous section, future work includes the following two items:

1. **Complete anatomical model.** In the current analysis, a complete anatomical model is not included yet. In particular, contextual information provided by the organs heart, spleen, and stomach will improve the quality and the robustness of the segmentation algorithm.

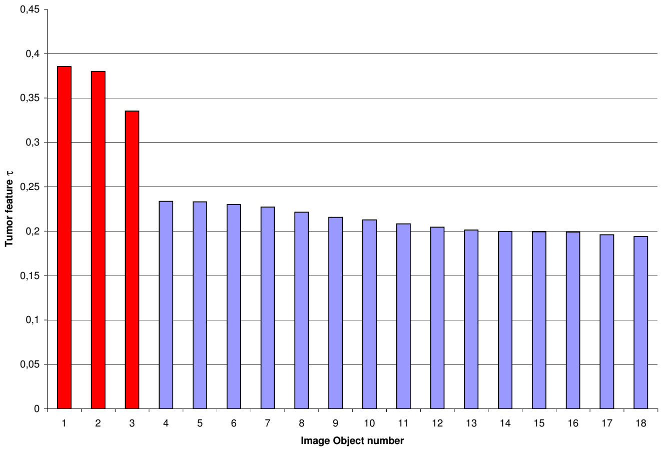

Fig. 3. Tumor feature values for the data set LTS_IMG05. The segmentation algorithm was applied on the the data set LTS_IMG05 and returned a partition of the liver containing 18 Image Objects. The graph shows their tumor feature values (sorted). Image Objects 1–3 (red) were marked by the organizers as liver tumors.

2. **Tumor feature.** Experiments indicate that the quotient

$$\tau(x) := \frac{\mathrm{Volume}(x)}{\mathrm{Surface}(x)}$$

where x is an Image Object and Volume(x) and Surface(x) are the volume and the approximated surface of x, respectively, seems to be a suitable feature for discriminating tumor objects from other Image Objects (see Figure 3), which will be further investigated.

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