

Hierarchical Anatomical Structure Segmentation Guided by Spatial Correlations (AnatSeg-Gspac): VISCERAL Anatomy3

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Abstract

Medical image analysis techniques require an initial localization and segmentation of the corresponding anatomical structures. As part of the VISCERAL Anatomy segmentation benchmarks, a hierarchical multi-atlas multi-structure segmentation approach guided by anatomical correlations is proposed (AnatSeg-Gspac). The method defines a global alignment of the images and refines locally the anatomical regions of interest for the smaller structures. In this paper, the method is evaluated in the VISCERAL Anatomy3 benchmark in twenty anatomical structures in both contrast-enhanced and non-enhanced computed tomography (CT) scans. AnatSeg-Gspac obtained the lowest average Hausdorff distance in 19 out of the 40 possible structure scores in the test set CT scans.

1 Introduction

Medical image analysis and computer-aided diagnosis initially require an accurate location and segmentation of the anatomical structures present. The time expensive task of manually annotating the current large amounts of medical image data daily produced restricts the implementation of further analysis by computer algorithms [Doi05]. Different approaches have been proposed to automatically detect multiple or single anatomical structures within the patient images [LSL⁺10, CRK⁺13]. The VISual Concept Extraction challenge in RAdioLogY project (VISCERAL¹) organizes public

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In: O. Goksel (ed.): Proceedings of the VISCERAL Anatomy Grand Challenge at the 2015 IEEE International Symposium on Biomedical Imaging (ISBI), New York, NY, Apr 16th, 2015 published at <http://ceur-ws.org>

¹<http://www.visceral.eu/>, as of 1 April 2015

benchmarks to test multiple segmentation approaches on the same available medical dataset for an objective evaluation of the algorithms [JdTGM⁺14]. The VISCERAL data set has been manually annotated by radiologists and includes real medical images obtained from clinical routine in hospitals. The benchmarks are set up in a cloud environment platform designed to host large amounts of medical data with equal computing instances for the participating research groups [LMMH13].

A hierarchic Anatomical structure Segmentation Guided by spatial correlations (AnatSeg-Gspac)[JdT⁺M13, JdTGM⁺14, JdT⁺M14b] has been previously proposed and tested in the first two VISCERAL Anatomy benchmarks. This approach requires no interaction from the user and generates a robust segmentation for multiple anatomical structures with short re-training phase for new scan parameters or additional structures [JdT⁺M14a]. The evaluation and results of AnatSeg-Gspac in the VISCERAL Anatomy3 benchmark are presented in the following sections.

2 Materials and Methods

2.1 Dataset

For the VISCERAL Anatomy3 benchmark 20 CT contrast-enhanced of the trunk (CTce) and 20 CT whole body unenhanced (CTwb) with their manual annotations (up to 20 anatomical structures), were provided to the participants for training. For the implementation of AnatSeg-Gspac in this benchmark a subset of volumes (7) with all or the majority of manual annotations were selected per modality as atlases. Further information on the VISCERAL data set can be found in [JdTGM⁺14].

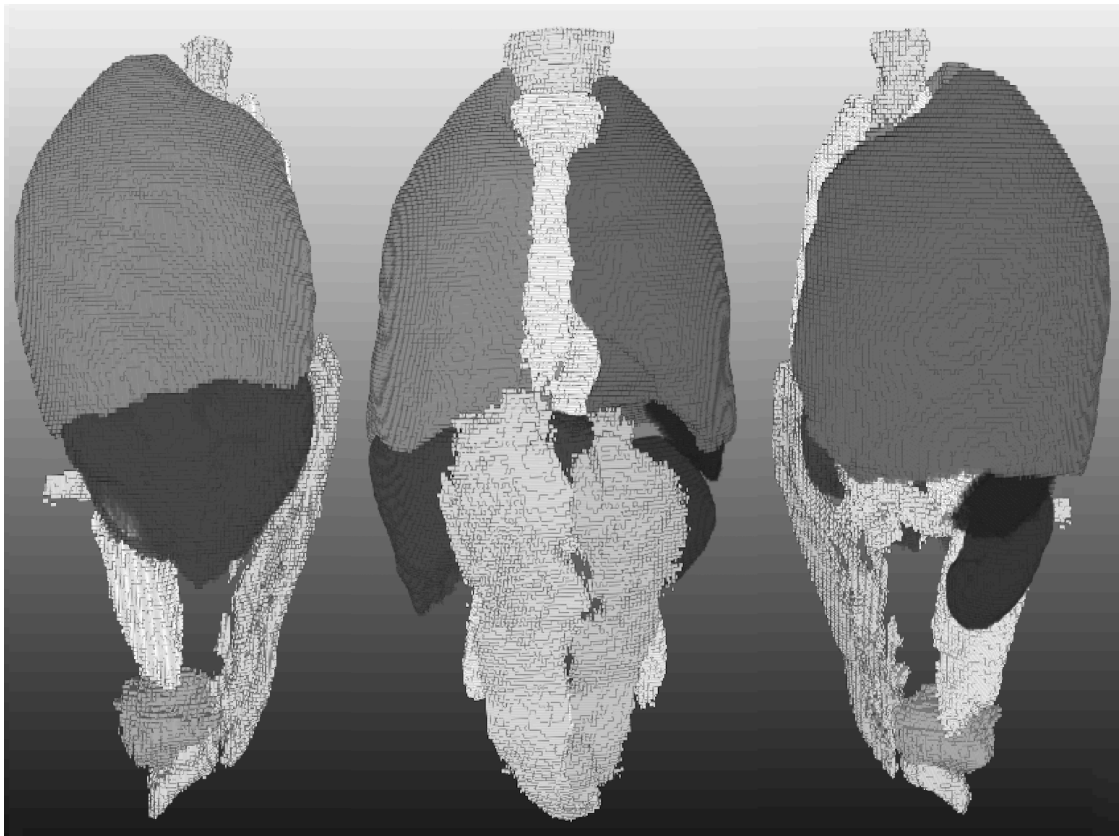


Figure 1: 3D rendering sample output using AnatSeg-Gspac.

2.2 AnatSeg-Gspac

The proposed method performs a hierarchic multi-atlas multi-structure segmentation defining anatomical regions of interest in their spatial domain. The bigger and high contrast anatomical structures are used as reference for smaller structures with low contrast, which are consequently harder to segment. The registration pipeline has been optimized to reduce the amount of registrations needed for the smaller structures obtaining also a robust localization. In Figure 1, a sample segmentation output for one unused training volume including all the anatomical structures evaluated in the VISCERAL benchmarks is shown. Further information on the AnatSeg-Gspac method can be found in the previously referenced papers.

3 Evaluation

For the Anatomy3 benchmark the test set included 10 CTce volumes and 10 CTwb scans. Twenty different evaluation metrics are provided to the participants about their algorithm performance for each anatomical structure. The evaluation phase is performed in the Azure cloud by the organizers with no intervention from the participants.

Table 1: Average Hausdorff distance results in trunk CTce test set of the VISCERAL Anatomy3 benchmark (Anatomy3 Leaderboard, <http://www.visceral.eu/Leaderboard/>, as of 1 April 2015). Competitive scores were obtained for kidneys and lungs compared to other organ-specific methods.

Average Hausdorff Distance																					
CTce	left kidney	right kidney	spleen	liver	left lung	right lung	urinary bladder	muscle body of left rectus abdominis	muscle body of right rectus abdominis	lumbar Vertebra 1	thyroid	pancreas	left psoas major muscle	right psoas major muscle	gallbladder	sternum	aorta	trachea	left adrenal gland	right adrenal gland	
	29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324	
Dicente et al.					0.050	0.052															
Jia et al.	0.171	0.131	0.385	0.203	0.069	0.078															
JiménezdelToro et al.	0.172	0.243	2.005	0.514	0.071	0.065	1.879	6.068	6.600	4.504	3.337	3.804	0.742	0.757	3.603	0.899	1.094	0.223	3.115	2.660	
Wang et al.	0.137	0.072	0.573	0.174	0.076	0.070	0.485						0.934	0.734							

Table 2: Average Hausdorff distance results in CT whole body (CTwb) test set of the VISCERAL Anatomy3 benchmark (Anatomy3 Leaderboard, <http://www.visceral.eu/Leaderboard/>, as of 1 April 2015). The method AnatSeg-Gspac generates robust segmentations for the big structures like the lungs (best benchmark scores highlighted). Moreover, it also shows overall better results particularly for small structures like thyroid, gallbladder and both adrenal glands.

Average Hausdorff Distance																					
CTwb	left kidney	right kidney	spleen	liver	left lung	right lung	urinary bladder	muscle body of left rectus abdominis	muscle body of right rectus abdominis	lumbar Vertebra 1	thyroid	pancreas	left psoas major muscle	right psoas major muscle	gallbladder	sternum	aorta	trachea	left adrenal gland	right adrenal gland	
	29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324	
Dicente et al.					0.050	0.046															
Jia et al.			0.360	0.239	0.101	0.094															
JiménezdelToro et al.	1.209	1.307	1.974	0.780	0.043	0.038	1.457	3.550	4.032	1.953	1.466	5.521	0.595	0.775	5.938	0.938	1.193	0.103	2.672	3.445	
Kahl et al.	0.147	0.229	0.534	0.299	0.045	0.043	1.057	1.614	1.922	2.424	2.163	4.478	0.443	0.550	9.617	0.542	0.798	0.083	3.298	7.046	
Wang et al.	0.758	2.751	0.248	0.191	0.356	0.096	2.155						0.705	0.812							

The proposed method obtained the lowest average Hausdorff distance of the Anatomy3 benchmark in 12/20 structures in CTce (Table 1) and 7/20 structures in CTwb (Table 2). The DICE coefficient scores are also presented for all the methods submitted in the benchmark (Table 3 and Table 4).

Table 3: DICE coefficient results in the test set trunk CT contrast-enhanced (CTce) of the VISCERAL Anatomy3 benchmark (Anatomy3 Leaderboard, <http://www.visceral.eu/Leaderboard/>, as of 1 April 2015). The proposed AnatSeg-Gspac (Jiménez del Toro et al. in light grey) was the only submitted method that segmented all available anatomical structures in both CT modalities (enhanced and unenhanced).

DICE Coefficient																					
CTce	left kidney	right kidney	spleen	liver	left lung	right lung	urinary bladder	muscle body of left rectus abdominis	muscle body of right rectus abdominis	lumbar Vertebra 1	thyroid	pancreas	left psoas major muscle	right psoas major muscle	gallbladder	sternum	aorta	trachea	left adrenal gland	right adrenal gland	
	29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324	
Dicente et al.	0.974 0.973																				
Jia et al.	0.910	0.922	0.869	0.933	0.966	0.966															
JiménezdelToro et al.	0.910	0.889	0.730	0.887	0.959	0.963	0.679	0.474	0.453	0.523	0.410	0.423	0.794	0.799	0.484	0.721	0.762	0.855	0.331	0.342	
Wang et al.	0.945	0.959	0.909	0.949	0.972	0.971	0.856	0.830 0.845													

Table 4: DICE coefficient results in the test set unenhanced CT of the whole body (CTwb) of the VISCERAL Anatomy3 benchmark (Anatomy3 Leaderboard, <http://www.visceral.eu/Leaderboard/>, as of 1 April 2015). Highlighted are the best DICE overlap scores obtained in the benchmark by AnatSeg-Gspac in 7 clinically relevant anatomical structures: left and right lungs, thyroid, pancreas, gallbladder, left and right adrenal gland.

DICE Coefficient																					
CTwb	left kidney	right kidney	spleen	liver	left lung	right lung	urinary bladder	muscle body of left rectus abdominis	muscle body of right rectus abdominis	lumbar Vertebra 1	thyroid	pancreas	left psoas major muscle	right psoas major muscle	gallbladder	sternum	aorta	trachea	left adrenal gland	right adrenal gland	
	29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324	
Dicente et al.	0.972 0.974																				
Jia et al.	0.874 0.923 0.952 0.957																				
JiménezdelToro et al.	0.784	0.790	0.703	0.866	0.972	0.975	0.698	0.551	0.519	0.718	0.549	0.408	0.806	0.787	0.276	0.761	0.753	0.920	0.373	0.355	
Kahl et al.	0.934	0.915	0.870	0.921	0.972	0.975	0.763	0.746	0.679	0.775	0.424	0.383	0.861	0.847	0.190	0.847	0.830	0.931	0.282	0.220	
Wang et al.	0.896	0.796	0.910	0.936	0.961	0.970	0.713	0.828 0.817													

4 Discussion and Conclusions

The proposed method showed robustness in the segmentation of multiple structures from two different imaging modalities using a small training set. Both the distance and overlap scores in this and the previous Anatomy benchmarks show AnatSeg-Gspac outperforms other algorithms in some of the smaller anatomical structures (e.g. both adrenal glands, gallbladder). It can also obtain the best overlap for bigger and high contrasted structures like the lungs.

A limitation of the method is the computation cost, mainly for the B-spline non-rigid registrations. Although the number of registrations and the size of registered regions are reduced using anatomical correlations, the execution time is around 13 hours for a complete CT volume. A faster

code implementation and better selection of the relevant atlases may reduce the number of needed registrations and thus the execution time of the method.

The method can be extended to the other imaging modalities and include more anatomical structures with short re-training phases. This is particularly important for its application with new or different scanners contained in large not annotated data sets. Further clinical image analyses, that may require the location of additional structures, might also benefit from this feature or include the output locations of the method as an initialization step.

5 Acknowledgments

This work was supported by the EU/FP7 through VISCERAL (318068).

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