Hierarchical multi–structure segmentation guided by anatomical correlations

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Abstract

Many medical image analysis techniques require an initial localization and segmentation of anatomical structures. As part of the VISCERAL benchmarks on Anatomy segmentation, a hierarchical multi–atlas multi–structure segmentation approach guided by anatomical correlations is proposed. The method begins with a global alignment of the volumes and refines the alignenment of the structures locally. The alignment of the bigger structures is used as reference for the smaller and harder to segment structures. The method is evaluated in the ISBI VISCERAL testset on ten anatomical structures in both contrast–enhanced and non–enhanced computed tomography scans. The proposed method obtained the highest DICE overlap score for some structures like kidneys and gallbladder. Similar segmentation accuracies compared to the highest results of the other methods proposed in the challenge are obtained for most of the other structures segmented with the method.

1 Introduction

Anatomical structure segmentation in medical imaging is a fundamental step for further image analysis and computer–aided diagnosis[Doi05]. With the ongoing increase in medical image data, it is necessary to develop fast and automatic algorithms that can process a large quantity of images with high accuracy and sufficient speed for clinical daily use. Although many different methods have already been proposed[LSL10, CRK13], it is uncommon to test multiple approaches on the same available dataset. The Visual Concept Extraction Challenge in Radiology (VISCERAL[1])

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[1] http://www.visceral.eu, as of 27 April 2014

benchmarks have been organized with the objective to evaluate the available state-of-the-art segmenting approaches in a large public dataset. Twenty different anatomical structures in four different imaging modalities, enhanced and non–enhanced magetic resonance (MR) and computed tomography volumes, are included in both the training and testing sets provided to the participants. The benchmarks are handled in a novel cloud environment, that allows to distribute large quantities of volumes and implement their algorithms in similar computing power conditions in the cloud [LMM13].

Multi–atlas based segmentation is an approach that requires little or no interaction from the user. It has been evaluated showing high accuracy and consistent reproducibility in different anatomical structures[LSL10, RBM04]. In this method, an atlas includes a patient volume and a label volume, created by manual annotation, that identifies the location of one or more structures in the patient volume. The target is the query volume where the location of the structures is unknown. Using image registration, the spatial relationship between the target and atlas volume is estimated. The label volumes are transformed taking the coordinate transformation obtained from the registration. Afterwards the labels are fused resulting in a single label volume that provides an estimate location of the label in the target volume. When multiple atlases are used, the local errors of the registration will be removed by a per–voxel classification.

The proposed method was tested in computed tomography scans with ten different anatomical structures. The method can be extended and applied to the other modalities and any of the anatomical structures in the VISCERAL dataset.

2 Method

All volumes are resampled to obtain isotropic 1mm voxels. Afterwards they are down–sampled half their size in all three dimensions to speed up the registrations and resampled to their original size for the label fusion.

2.1 Image registration

The atlas patient volume, considered as moving volume $V_A(x)$, is registered to the fixed query volume $V_Q(x)$ using the image registration implementation of Elastix software[2][KSM10]. The registration is evaluated in every iterative optimization by a cost function C of the parameterized coordinate transformation T_μ from the moving atlas volume V_A to the query volume V_Q. The adaptive stochastic gradient descent optimizer proposed in [KPS09] is applied. A coordinate transformation is obtained by minimizing the value of C with respect to the transformation:

$$\hat{\mu} \quad = \quad \underset{\mu}{arg\ min}\ C(T_\mu; V_Q, V_A), \tag{1}$$

the subscript μ indicates that the transform has been parameterized with a vector μ that contains the transformation parameters. Normalized Cross–Correlation (NCC) is selected as the similarity metric for cost function C.

2.2 Hierarchical anatomical structure alignment

The anatomy can differ considerably from patient to patient, particularly the spatial relations between the different structures in the same patient volume [JiM13]. Since multiple structures are segmentation targets in the VISCERAL benchmark, a hierarchical selection of the registrations improves the segmentations of all the structures. A global affine registration is followed by

[2]Elastix: http://elastix.isi.uu.nl, 2014.[Online; accesed 27–April–2014].

individual affine registrations using local binary masks to enforce the spatial correlation of each anatomical structure separately. These masks are obtained from the morphological dilation of the output labels of the different atlases registered in the previous step. The registrations of the bigger structures are used as a starting point for the closely related smaller structures, which are harder to segment. Most of the registrations of the initial bigger structures (liver, lungs, urinary bladder) will be reused in the method which makes it faster than segmenting each structure individually from the start. The method is repeated for the non-rigid registrations of all the target structures. Also the creation of regions-of-interest with the local masks speeds up the image registrations and improves the output estimations.

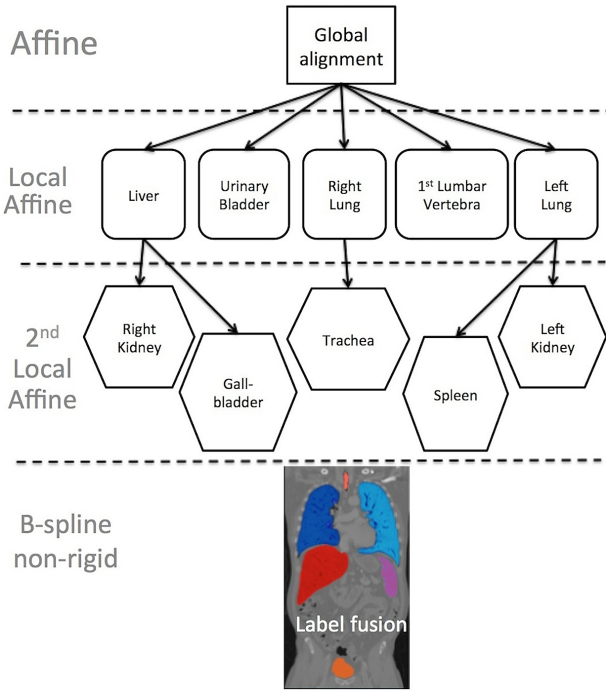

Figure 1: Method Pipeline.

2.3 Non-rigid registration

After each anatomical structure has it's own independent ROI mask, the volumes are registered again but using a non–rigid B–spline transformation model. This non–rigid registration allows local deformations obtaining a higher spatial similarity between the volumes. The B–spline registration was also performed in a multi–resolution approach with an adaptive stochastic gradient descent optimizer. This final registration step has a higher computational cost than the affine registration. The transformed labels are updated using the coordinate transformation parameters from the B–spline registration. The new transformed label volumes for each structure constitute the individual votes that will be used for the label fusion step.

2.4 Label fusion

A different label volume is obtained for every atlas registered to the target volume. In order to combine the information obtained from the multiple atlases registered, the output labels are fused in a single label for the target volume. Defining a majority voting threshold is a commonly used label fusion method. An optimal threshold is found for each of the different structures on a per–voxel basis with this approach. Majority voting has also the advantage of providing more than one output segmentation varying the threshold parameter with no additional computations required.

3 Experimental Setup

Ten CT volumes were used to evaluate the performance of the algorithm for the International Symposium on Biomedical Imaging (ISBI) 2014 VISCERAL challenge. Five of them are contrast–enhanced (ceCT) with a field–of–view from below the skull base to the pelvis. The other five are non–enhanced whole body CT scans(wbCT). For the ten CT volumes, ten structures were included in the proposed segmentation method: liver, 2 kidneys, 2 lungs, urinary bladder, spleen, trachea, first lumbar vertebra and gallbladder.

An initial global affine registration is followed by individual affine registrations of the independent structures using local masks as described in the method. The liver, both lungs, $1st$ lumbar vertebra and urinary bladder were segmented with individual affine and non–rigid registrations. The gallbladder and right kidney have the affine alignment of the volume after the liver registrations as a starting point. The left lung affine alignment is used for the spleen and the left kidney. The right lung affine alignment is refined for the trachea segmentation. All structures are refined with non–rigid b–spline registration for the final estimation.

According to the results of the VISCERAL Benchmark 1, an individual majority vote threshold was selected in each structure for the label fusion.

4 Results

The method obtained a total average DICE of 0.789 for ten structures in ceCT and 0.694 for the same ten structures in wbCT (Table 1). All the overlap scores were higher in ceCT and in close relation to the results from the other participants in the challenge for the same anatomical structures. The method obtained the best DICE score of the ISBI Visceral challenge for the left kidney, right kidney and the gallbladder in ceCT. For wbCT the method had the best DICE in the 1st lumbar vertebra, gallbladder and trachea.

Table 1: Average Segmentation Accuracy

Structure	Reference structure	DICE CTwb	DICE ceCT
Liver	none	0.823	0.908
Right lung	none	0.967	0.963
Left lung	none	0.969	0.952
Urinary bladder	none	0.616	0.68
1st Lumbar vertebra	none	0.44	0.472
Right kidney	liver	0.649	0.905
Gallbladder	liver	0.271	0.4
trachea	right lung	0.855	0.83
Spleen	left lung	0.677	0.859
Left kidney	left lung	0.678	0.923

5 Conclusion

The proposed method showed robustness in the segmentation of multiple structures from two different modalities of the challenge using a relatively small dataset. The overlap accuracies are consistent for most of the evaluated anatomical structures and obtained some of the best structure overlap of the challenge when compared to the other proposed methods in the same testset.

Due to the flexibility of the method for adding more structures, for future work the method will be extended to include all of the anatomical structures in the VISCERAL dataset. An evaluation of the method for the other modalities (MR and contrast–enhanced MR) is also foreseen for the VISCERAL benchmark 2 Anatomy with a much bigger testset.

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