

# MULTI ATLAS–BASED SEGMENTATION WITH DATA DRIVEN REFINEMENT

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## ABSTRACT

Anatomical structure segmentation is the basis for further image analysis processes. Although there are many available segmentation methods there is still the need to improve the accuracy and speed of them to be used in a clinical environment. The VISCERAL project organizes a benchmark to compare approaches for organ segmentation in big data. A fully–automatic segmentation method using the VISCERAL data set is proposed in this paper. It incorporates both the local contrast of the image using an intensity feature as well as atlas probabilistic information to compute the definite labelling of the structure of interest. The usefulness of the new intensity feature is evaluated using contrast–enhanced CT images of the trunk. An overall average increase is computed in the overlap of the segmentations with an improvement of up to 33% for several anatomical structures when compared to only using an atlas based segmentation method. Qualitative results are also shown for MR images supporting the inclusion of this contrast feature in atlas–based segmentation methods for several modalities.

**Index Terms**— Multi–organ segmentation, atlas–based segmentation.

## 1. INTRODUCTION

There are many clinical situations that benefit from organ segmentation as the basis for further image analysis [1, 2]. In addition, the increasingly available imaging data will require automatic image processing to reduce the radiologists’ workload. A more efficient image interpretation [3], and segmentation can help to facilitate navigation in image sets. The Visual Concept Extraction Challenge in Radiology (VISCERAL) [4] Benchmark<sup>1</sup> focuses on whole body labelling in 3D medical imaging data. The goal is to compare approaches for multiple anatomical structure segmentation in various imaging modalities. All data are stored in a cloud infrastructure to share large amounts of imaging data between the participants and evaluate their algorithms on a common training and testing dataset.

<sup>1</sup>VISCERAL benchmark: <http://www.visceral.eu>, 2012. [Online; accessed 20-March-2014].

Some of the current approaches to multi–structure segmentation like regression forests [5] are fully probabilistic and have been incorporated into medical image analysis, recently. Atlas based segmentation is also an approach that has a straightforward implementation and has shown robustness in the segmentation of different anatomical structures [6, 7]. However, some of these segmentation methods have not been implemented successfully in more than a single imaging modality besides computed tomography (CT). Another remaining challenge is that their segmentation accuracies and implementation speed still need to be improved for real clinical usage.

A new method for multi–organ segmentation is proposed in this paper to include both local and global information in the label estimation. The method is presented in the Material and Methods section. An evaluation of the method using contrast–enhanced CT scans of the trunk is presented in the experimental setup and results sections. An analysis of the results showing the advantages of using this method as well as suggestions for further improvement are discussed in the Discussion and Conclusion.

## 2. MATERIAL AND METHODS

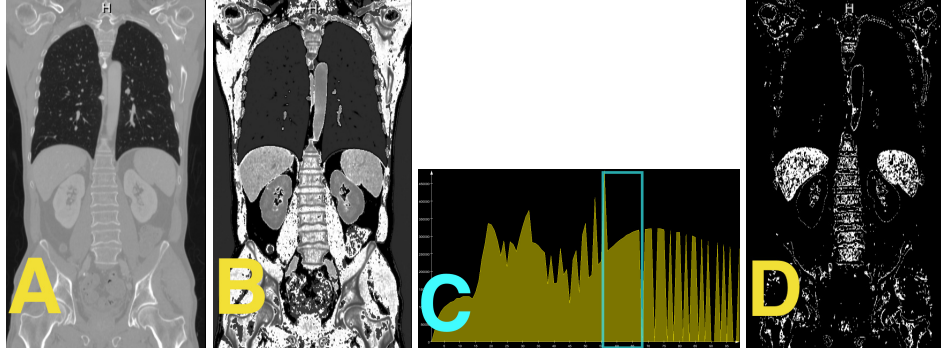
The method proposed in this paper consists of three steps: Image pre–processing for intensity based structure estimation, atlas registration and label refinement. A description of each step is explained in the following section.

### 2.1. Image pre–processing

The images are pre–processed using a normalization step that preserves the intensity contrast between structures but significantly reduces the search space for selecting meaningful intensity thresholds within the images. The image  $A$  is normalized using Equation 1:

$$A_{norm} = \frac{k}{A} - 1, \quad (1)$$

where  $k$  is the difference between maximum and minimum intensity. After applying this pre–processing step to the images, the more relevant intensity ranges for the structures of interest are found in the histogram regions closer to zero. The



**Fig. 1:** Image pre-processing. Image A is the original image. Image B is the output from the pre-processing proposed in the Methods section. C is a windowed view of the pre-processed image histogram in the first 100 intensities. The rest of the histogram repeats the isolated peaks pattern shown in the far left region of C. Binary mask D is obtained when the image is thresholded in the blue rectangle area overlaid on C. This automatically computed binary mask is used as a first estimation for the location of the liver and spleen. It is then combined with the output labels obtained from the atlas registrations to have a better segmentation of the structures of interest.

normalization is useful because it maximizes the contrast between intensities that are equivalent in the original and inverse versions of the image. The histogram of the output image is easier to analyse with more peaks and nadirs in the intensities closely related to the structures of interest. A visual analysis of the histograms shows similar regions of interest in different images and different modalities that can be used as preset parameters for threshold selection. A large range of the intensities in the histogram can be automatically discarded because it is composed of isolated peaks at different intensity levels in the regions more distant to zero intensity. This is due to the effect of the preprocessing step proposed in this paper (See Fig. 1).

## 2.2. Atlas registration

An atlas in the context of this paper includes both a medical image and a binary label image with the manually annotated structure of interest. The target or query image is used as fixed image and registered to the moving atlas. The coordinate transformation obtained is applied to the label image to have an estimation for the location of the atlas labelled structure in the target image. The images are registered using the implementation of the elastix software [8]. An adaptive stochastic gradient descent optimizer is computed in a multi-resolution approach. For the purpose of measuring solely the impact of the pre-processing step proposed in this paper, a single global affine registration is performed in the experiments. The segmentation output could be improved adding a non-rigid registration step, but this is out of the scope of this paper.

## 2.3. Label refinement

For each of the organs to be segmented, a binary mask is obtained selecting an intensity threshold using the intensity histogram from the pre-processed image. For this work, a visual inspection of the histogram in three CT scans was necessary to select the thresholds for the four organs evaluated. The thresholds were then applied to all the scans without further inspection to create the binary masks that incorporate this intensity feature ( $S_{int}$ ). With the atlas registration label output ( $S_{atlas}$ ), a new binary mask annotation of the structure is created with the intersection of the two masks mentioned:

$$S_{int} \cap S_{atlas}$$

This mask incorporates both data driven information from the target image and a probabilistic estimation from the atlas registration output.

## 2.4. Experimental setup

Ten contrast-enhanced CT (ceCT) scans of the trunk were used to test the method. The images were acquired primarily in patients with malignant lymphoma. All volumes have a field of view from the corpus mandibulae to the pelvis and are enhanced by a iodine-containing contrast agent that improves tissue contrasts for detecting pathological lymph nodes. Image resolution is  $0.793 \times 0.793 \times 3$  mm. Four organs were manually segmented from each scan by a radiologist. The right and left lungs, liver and spleen manual annotations were used as ground truth to evaluate the proposed method. A leave-one-out cross validation approach using 9 ceCT images as atlases and the remaining scan as target image was used. To measure the overlap between the output labels from the proposed method and the ground truth, the Jaccard coefficient is calculated. This measure is a spatial overlap metric

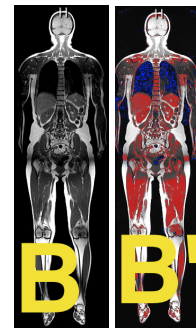
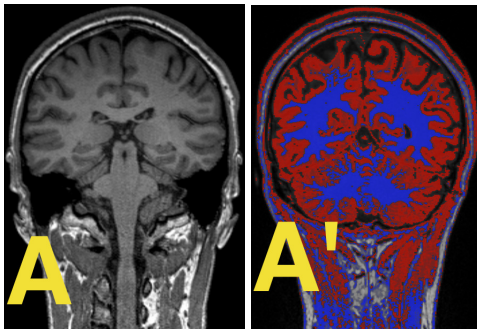
where a coefficient of 1 means a perfect overlap and 0 means no overlap.

For the liver and spleen the same intensity region of interest is used to create the binary mask ( $S_{int}$ ). This region includes the intensities from the highest peak in the normalized image histogram to the first empty intensity space in the histogram after this peak. For the lungs all values in the negative intensities are selected as positives for the mask.

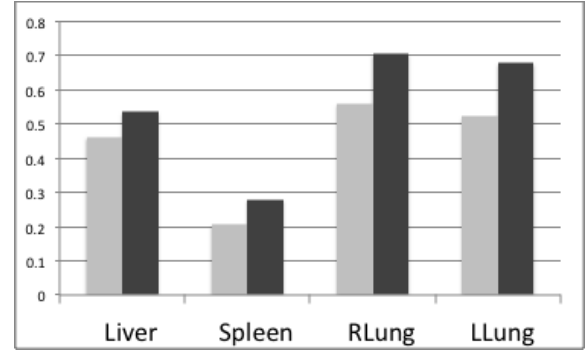
Morphological dilation with a small sized 3D kernel is used to maximize the mask space location obtained from the thresholded pre-processed image. Both the training and test images are then evaluated for the overlap of the structures. The output labels of the atlas-based registration are compared with the output labels obtained with the method described that also incorporates the intensity features obtained from the thresholded pre-processed image.

### 3. RESULTS

The results expressed in both Fig. 3 and Fig. 4 are the output after a single global affine registration of the scans for the atlases labels and our proposed method. Our method showed an increase in the mean Jaccard coefficient for all of the tested structures (liver, spleen and lungs). The most significant improvement is seen in the spleen with a 34.9% increase, followed by the lungs with a 25.9% and 29.7% increase respectively, and finally a 15.4% higher mean Jaccard in the liver Fig.3. The best overlap score for the complete set of atlases is also increased in all of the tested structures as can be seen in Fig. 4.



**Fig. 2:** Qualitative results in magnetic resonance imaging (MRI). The intensity-based label evaluated for contrast-enhanced CT in this paper is applied in the head (i.e. A, A') and the whole body (i.e. B, B') T1 MR scans. For the head scan A a threshold of intensity value 3 is shown in blue and intensity value 5 in red in A'. The blue label strongly correlates with white matter segmentation and the red label gives a good estimation of the grey matter. For the whole body scan B two regions were selected in the first 100 values of the output histogram in a similar approach to what is proposed in the paper for contrast-enhanced CT. The red label in B' obtains an initial segmentation of structures such as liver, kidneys and the spleen that can be coupled with the atlas registration labels of each structure for a more accurate location in the image. The blue label is associated with the lungs. Although the intensity range in MR scans can vary, the intensity regions of interest remain constant for the selection of intensity thresholds using the pre-processing step of the method

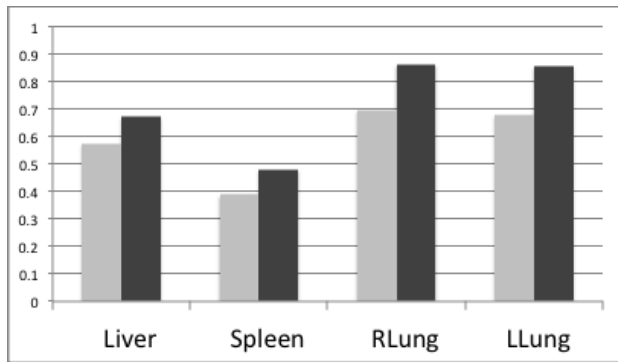


**Fig. 3:** Mean average Jaccard coefficients. Segmentation results after a global affine registration (light gray bars in Fig. 3) vs. segmentation adding the proposed intensity features in the method (dark gray bars in Fig. 3) for liver, spleen, right lung (RLung) and left lung (LLung). There is an overall increase in the overlap after including the label estimation step to the affine registration output for all the tested organs.

### 4. DISCUSSIONS AND CONCLUSIONS

This method introduces a new image intensity feature that is based on the inherent image contrast of medical structures in different modalities. It reduces the search space considerably to define similar intensities that represent the anatomical structures in the images. The method showed an improvement in the overlap of the segmentations when compared to just using the output labels from atlas registration. Although, the results are evaluated after a single affine registration, better results could be obtained with a following non-rigid registration and more complex label fusion methods in a multi-atlas

based segmentation method, which is known to produce better results than single atlas segmentation [7].



**Fig. 4:** Highest average results for individual atlases. All the tested structures had a higher overlap score with the organ intensity based estimation from the method (dark gray bars in Fig. 4) vs. using only the registered atlas output label (light gray bars in Fig. 4).

The binary intensity masks from the pre-processed images do incorporate voxels from other structures in the image. However, the intersection with the atlas registration labels is able to primarily select those contained within the structure of interest. The overall overlap was equal or higher for the four structures evaluated supporting the robustness of the method particularly for the structures with a high contrast in the image. The cases where the intensity feature did not improve the overlap when combined to an atlas label had similar results to only using the atlas label. This feature of the method is a strong predictor that even in the worst cases means that the method will not significantly affect the original segmentation.

Qualitative results for MR images in Fig. 2 show promising results to evaluate the method in different imaging modalities. It is useful particularly for MR scans where noise removal is critical for an accurate segmentation. In conclusion, a new, simple and fast method using both local contrast information and atlas-based segmentation is proposed. The proposed image pre-treatment significantly reduces the search space for the intensities of the desired structures. It also decreases the amount of noise involved in the selection of intensity parameters from the structure. It improves the overall Jaccard coefficient for the majority of the atlases and can be used as a reference for guiding following registrations.

A more in-depth evaluation of the automatically selected threshold parameters is currently being evaluated and is expected to improve the threshold selection for the different structures and imaging modalities. A bigger testing dataset is foreseen with full implementation of the method using multi-atlas based segmentation. Such a data set will include scans from multiple modalities like CT and MR. This evaluation will also lead to a more extensive comparison of the proposed approach with other state-of-the-art methods.

## 5. ACKNOWLEDGMENTS

This work was supported by the EU/FP7 through VISCERAL (318068) and Khresmoi (257528).

## 6. REFERENCES

- [1] Akinobu Shimizu, Tatsuya Kimoto, Hidefumi Kobatake, Shigeru Nawano, and Kenji Shinozaki, "Automated pancreas segmentation from three-dimensional contrast-enhanced computed tomography," *International Journal of Computer Assisted Radiology and Surgery*, vol. 5, no. 1, pp. 85–98, 2010.
- [2] Yefeng Zheng, Adrian Barbu, Bogdan Georgescu, Michael Scheuering, and Dorin Comaniciu, "Four-chamber heart modeling and automatic segmentation for 3-D cardiac CT volumes using marginal space learning and steerable features," *IEEE Transactions on Medical Imaging*, vol. 27, no. 11, pp. 1668–1681, Nov 2008.
- [3] K Doi, "Current status and future potential of computer-aided diagnosis in medical imaging," *British Journal of Radiology*, vol. 78, pp. 3–19, 2005.
- [4] Georg Langs, Henning Müller, Bjoern H. Menze, and Allan Hanbury, "Visceral: Towards large data in medical imaging — challenges and directions," in *Medical Content-based Retrieval for Clinical Decision Support*, Oct. 2012, MCBR–CDS 2012.
- [5] Antonio Criminisi, Duncan Robertson, Ender Konukoglu, Jamie Shotton, Sayan Pathak, Steve White, and Khan Siddiqui, "Regression forests for efficient anatomy detection and localization in computed tomography scans," *Medical Image Analysis*, vol. 17, no. 8, pp. 1293–1303, 2013.
- [6] Marius George Linguraru, Jesse K. Sandberg, Zhixi Li, Furhawn Shah, and Ronald M. Summers, "Automated segmentation and quantification of liver and spleen from CT images using normalized probabilistic atlases and enhancement estimation," *Medical Physics*, vol. 37, no. 2, pp. 771–783, 2010.
- [7] Eva M. van Rikxoort, Ivana Isgum, Yulia Arzhaeva, Marius Staring, Stefan Klein, Max A. Viergever, Josien P.W. Pluim, and Bram van Ginneken, "Adaptive local multi-atlas segmentation: Application to the heart and the caudate nucleus," *Medical Image Analysis*, vol. 14, no. 1, pp. 39 – 49, 2010.
- [8] Stefan Klein, Marius Staring, Keelin Murphy, Max A. Viergever, and Josien P.W. Pluim, "Elastix: a toolbox for intensity-based medical image registration," *IEEE Transactions on medical imaging*, vol. 29, no. 1, pp. 196–205, 2010.