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Result analysis for Competition 1

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Executive Summary

The Anatomy Benchmark of the Visceral project has two tasks, segmentation of anatomical structures (lung, liver, kidney, ...) in non-annotated whole body MR- and CT- volumes (participants can choose which of the organs to segment), and identification of anatomical landmarks in this data. More details on the tasks of the Anatomy Benchmark are in Section 2.4.

The data sets used for the Benchmark have been acquired during daily clinical routine work. Whole body MRI and CT scans or examinations of the whole trunk are used. Furthermore, imaging of the abdomen in MRI and contrast-enhanced CT for oncological staging purposes is used. Four combinations are available (i) Abdomen/thorax contrast enhanced CT (ThAb/Ctce), (ii) Whole body CT (wb/CT), (iii) Whole body MR T1 (wb/MRT1), and (iv) Abdomen contrast-enhanced fat-saturated MR T1 (Ab/MRT1cefs). Annotated structures in the segmentations are left/right kidney, spleen, liver, left/right lung, urinary bladder, rectus abdominis muscle, 1st lumbar vertebra, pancreas, left/right psoas major muscle, gall bladder, sternum, L1, aorta, trachea, left/right adrenal gland, and thyroid gland. Annotated landmarks are left clavicle, right clavicle, left crista iliaca, right crista iliaca symphysis, left rochanter major, right trochanter major, left trochanter minor, right trochanter minor, aortic arch, trachea bifurcation, aorta bifurcation, C2, C3, C4, C5, C6, C7, Th1, Th2, Th3, Th4, Th5, Th6, Th7, Th8, Th9, Th10, Th11, Th12, L1, L2, L3, L4, L5, xyphoideus, aortic valve, left sternoclavicular, right sternoclavicular, VCI bifurcation, left tuberculum, right tuberculum, left renal, pelvis right renal, pelvis left bronchus, right bronchus, left eye, right eye, left ventricle, right ventricle, left ischiadicum, and right ischiadicum Coronaria. The whole training data set was available for the participants in the cloud storage of cloud virtual machines assigned to them, so that the participants do not need to download it. More information on the data set and its availability is in Section 2.1.

The Gold Corpus contains the image data together with manual annotations that have been performed and quality checked by trained and experienced radiologists. It is the reference annotation necessary to train and to evaluate the algorithms that automatically segment anatomical structures and localize anatomical landmarks. More information on the gold corpus is in Section 2.2 and a summary of the annotated volumes is provided in Table 1 and Table 2221.

The VISCERAL project uses and recommends NIFTI as an image format, because it has many advantages that are described in more detail in Section 2.3.

The Anatomy benchmark runs as a series of cycles. Two of them, Anatomy1 and Anatomy2 (with the latter including an ISBI challenge as an early teaser) have been completed. In the benchmarks already completed, there were 20 participants who provided segmentation outputs for 80 different cases (a case means a combination of a modality, a region and a configuration) and landmark outputs for 29 different cases. These were distributed as follows: 7 participants, 35 segmentation cases and 9 landmark cases in Anatomy1; 5 participants, 11 segmentation cases and 4 landmark cases in Anatomy 2 ISBI; and 8 participants, 34 segmentation cases and 16 landmark cases for the Anatomy 2 final submission. More information about participants and description of the submitted algorithms in each benchmark is in Section 3.

Four evaluation metrics have been used for the result analysis, namely the Dice coefficient (DICE), the interclass correlation (ICC), the adjusted Rand index (ADJRIND), and the Average distance (AVGDST). These metrics were selected from a metric pool of 20 evaluation metrics that were found as a result of a literature review on evaluation of medical volume segmentation. For evaluating the landmark localization, the Euclidean distance was used.

The results for each benchmark are presented in Section 4. The analysis of the segmentation task is structured as follows: For each participant, the four metrics, mentioned above, are provided as averages for each organ where different modalities and regions are provided in separated scores. The available combinations are ThAb/Ctce, wb/CT, wb/MRT1, and Ab/MRT1cefs. When participants

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provided submissions with different configurations (up to five configurations were permitted), the scores for each configuration were calculated and provided separately.

The identification task (landmark localization) was evaluated using the Euclidean distance. For each participant, the Euclidean distance was given as an average for each landmark and case (modality and region). The percentage contribution of the participant was calculated in each case – this is the ratio between the number of landmarks provided by the participant and the number of landmarks annotated in the ground truth for each case.

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List of Abbreviations

MR	Magnetic Resonance Imaging
CT	Computed Tomography
wb	Whole-body
Ab	Abdomen
Th	Thorax
ce	contrast-enhanced
fs	fat-saturated

1 Introduction

The Anatomy Benchmark of the VISCERAL project with its two tasks, organ identification and segmentation of bones, inner organs and other relevant structures, has a series of cycles. Anatomy1 and Anatomy2 (where the latter includes an ISBI challenge as an early teaser) have been completed. In this document, we briefly describe the tasks of this Benchmark and the large scale 3D radiology data sets used for the benchmarks. We give a short overview of each participating algorithm, and we present a result analysis for each benchmark.

2 Data and Tasks

2.1 Dataset

The data sets used for the Benchmark have been acquired during daily clinical routine work. Whole body MRI and CT scans or examinations of the whole trunk are used. Furthermore, imaging of the abdomen in MRI and contrast-enhanced CT for oncological staging purposes is used, since there is a higher resolution for segmentation especially of smaller inner organs, such as the adrenal glands. Four combinations are available (i) Abdomen/thorax contrast enhanced CT (ThAb/Ctce), (ii) Whole body CT (wb/CT), (iii) Whole body MR T1 (wb/MRT1), and (iv) Abdomen contrast-enhanced fat-saturated MR T1 (Ab/MRT1cefs).

Annotated structures found in the corpus:

- Segmentations: Left/right kidney, spleen, liver, left/right lung, urinary bladder, rectus abdominis muscle, 1st lumbar vertebra, pancreas, left/right psoas major muscle, gall bladder, sternum, L1, aorta, trachea, left/right adrenal gland, and thyroid gland.
- Landmarks: Left clavicle, right clavicle, left crista iliaca, right crista iliaca symphysis, left rochanter major, right trochanter major, left trochanter minor, right trochanter minor, aortic arch, trachea bifurcation, aorta bifurcation, C2, C3, C4, C5, C6, C7, Th1, Th2, Th3, Th4, Th5, Th6, Th7, Th8, Th9, Th10, Th11, Th12, L1, L2, L3, L4, L5, xyphoideus, aortic valve, left sternoclavicular, right sternoclavicular, VCI bifurcation, left tuberculum, right tuberculum, left renal, pelvis right renal, pelvis left bronchus, right bronchus, left eye, right eye, left ventricle, right ventricle, left ischiadicum, and right ischiadicum Coronaria.

More information on the dataset used can be found in Deliverable D2.3.1 Dataset for the first competition.

2.2 Gold Corpus

The Gold Corpus contains the image data together with manual annotations that have been performed and quality checked by trained and experienced radiologists. The Anatomy Benchmark focuses on whole-body (wb) labelling in 3D medical imaging data. The gold corpus is the reference annotation necessary to train and to evaluate the algorithms that automatically segment anatomical structures, and localize anatomical landmarks.

2.2.1 Training Gold Corpus

The training gold corpus comprises 28 fully annotated volumes in Anatomy1 (segmentations of organs/structures and landmarks). Although the MR annotations were only manually performed in one MR sequence (T1-weighted), the T2-weighted MR volumes from the same patients were also made available to the participants in the training set. In total 42 volumes were available to the participants during the Anatomy1 benchmark. For Anatomy2, 80 volumes were fully annotated, 120 volumes were in total distributed to the participants. The total volumes included the corresponding 40 MR T2-weighted volumes not annotated for each annotated MR T1-weighted volume. For the ISBI VISCERAL challenge that took place during the Anatomy2 Benchmark, a subset of the Anatomy2 training set was available to participants (60 annotated volumes, 90 volumes distributed in total). Once the ISBI Challenge concluded, the test set used for this challenge was added to the Anatomy 2 training set. Table 1 provides a summary of the volumes annotated for each of the benchmarks from the different modalities and regions.

Benchmark	Vol.	Wb/CT	ThAb/Ctce	Ab/MRT1ce	Wb/MRT1	Structures	Landmarks
Anatomy 1	42	7	7	7	7	491	42 volumes
Anatomy 2 ISBI	90	15	15	15	15	946	60 volumes
Anatomy 2 Main	120	20	20	20	20	1295	80 volumes

Table 1. Summary of the training corpus volumes annotated for each of the benchmarks

2.2.2 Test Gold Corpus

Overall 48 volumes were included in the gold corpus test set for Anatomy 1 (12 CT whole body data sets, 12 CT contrast-enhanced Thorax/Abdomen data sets, 12 MRT1 whole body, 12 MRT1 contrast-enhanced Abdomen). For the Anatomy 2 benchmark 40 volumes were considered in the gold corpus test set. This is summarised in Table 2221.

More detailed information on the gold corpus can be found in D 3.2.2 Evaluation Gold Corpus for competition 1.

Benchmark	Vol.	Wb/CT	ThAb/Ctce	Ab/MRT1ce	Wb/MRT1,	Structures	Landmarks
Anatomy 1	48	12	12	12	12	761	48 volumes
Anatomy 2 ISBI	20	5	5	5	5	305	20 volumes
Anatomy 2 Main	40	10	10	10	10	643	40 volumes

Table 2. Summary of the test corpus volumes annotated for each of the benchmarks

2.3 NIFTI Image Format

NIFTI is a good choice for challenges in computer science research for the reasons discussed in this section.

Clinical medical imaging is dominated by the Digital Imaging and Communications in Medicine (DICOM) file format (DICOM²). It is ubiquitous in hospital image management systems such as Picture Archiving and Communication Systems (PACS), and its standard has facilitated clinical

² Digital Imaging and Communications in Medicine: <http://dicom.nema.org/>

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integration and widespread deployment of medical informatics frameworks substantially. Notably the DICOM standard was developed in a time of significantly different information technology environment than we typically face today. One example is slower data transfer times that made the splitting of large amounts of data sensible.

In the VISCERAL project we revisited the choice between image format alternatives and decided for the Neuroimaging Informatics Technology Initiative (NIFTI) format. The NIFTI format was established by the NIFTI Data Format Working Group (NIFTI-DFWG) as part of an effort to enhance and disseminate neuroimaging informatics tools³. NIFTI-1 was adapted from the ANALYZE 7.5 format, and NIFTI-2 updated NIFTI-1 to 64 bits. One of the main differences to ANALYZE and DICOM is that the format stores volume, or volume + time information in a single file, together with information such as coordinate transformations that establish the link between voxel- and real space.

In VISCERAL we chose the NIFTI format for several reasons:

1. NIFTI files are easier to handle and to exchange, since one imaging volume is stored as a single self-contained file. Among other information, this file contains the imaging data, and coordinate transforms between scanner space, and voxel space.
2. In challenge and evaluation scenarios involving computer science focused groups data is typically managed by individuals, and not by central image management systems such as PACS in hospitals. Dealing with a single file instead of thousands of files facilitates file management considerably, since file naming allows for a straight-forward identification of files (in contrast to DICOM directory information)
3. Transferring and storing thousands of large files, instead of millions of small files is typically more efficient in file systems and can avoid delays.
4. Read- and write functionality for NIFTI files exists for most of the popular computing frameworks, such as for instance, MATLAB, Python, or R.
5. Preparing the writing of DICOM files for annotations can be complicated and it is considered easier for research groups to generate NIFTI.

The feedback by benchmark participants corroborated these points. We did not get a single complaint, and transfer of data was reported to be swift, and easy to manage.

2.4 Tasks

There are two tasks in which it was possible to participate in the Anatomy Benchmarks:

1. Segmentation of anatomical structures (lung, liver, kidney, ...) in non-annotated whole body MR- and CT- volumes (participants can choose which of the organs to segment), and
2. Identification of anatomical landmarks in this data.

Deliverable D4.1 provides more information on the tasks. The surprise organ task offered for Anatomy1 was discontinued for Anatomy2 due to little interest by participants in this task.

For the Anatomy2 Benchmark, an intermediate workshop was held at the ISBI 2014 Conference, for which participants could submit intermediate algorithms and discuss them at the workshop. The final submissions were then evaluated and discussed at the Medical Computer Vision Workshop at the MICCAI 2014 conference.

³ Neuroimaging Informatics Technology Initiative: <http://nifti.nimh.nih.gov/>

3 Participants and Algorithms

3.1 Anatomy1

The information that participants have provided about their techniques is below (linked to the result tables in Section 4.3 by the abbreviations in square brackets):

[SJ]

Title: A New Rule-Based Approach For Body Multi-Organ Automatic Segmentation in CT Scans

Authors: Assaf B. Spanier and Leo Joskowicz, School of Eng. and Computer Science, The Hebrew Univ. of Jerusalem, Israel University

Abstract: We describe a new generic method for the automatic rule-based segmentation of multiple organs from 3D CT scans in the VISCERAL challenge. The rules determine the order in which the organs are isolated and detected from simple to difficult. Following the isolation of the body, the breathing system organs are segmented: the trachea and the left and right lungs. Next, the organs with high blood content are segmented: the spleen, liver and the left and right kidneys. The segmentation of each organ itself is then performed in three steps: 1) definition of the Organ Binary Inclusive Region Of Interest (BI-ROI) from the target organ intensity values; 2) identification of the organ's Largest Axial Cross Section Slice (LACSS), the slice where the organ has the largest axial area, and; 3) organ segmentation by 3D region growing to adjacent slices from the BI-ROI and the LACSS while preserving smoothness and curvature constraints between two adjacent slices. The key advantages of our method are that it uses the organs segmentations, known locations, and anatomical context to guide the automated the segmentation process and that the organ segmentation itself follows a generic three-step process. Our experimental results on the 7 CT training dataset of VISCERAL Challenge Anatomy1 Benchmark yield a Dice volume overlap similarity of 96.4 for the left lung, 96.6 for the right lung, 79.1 for the trachea, 89.2 for the spleen, 92.8 for the left kidney, 92.0 for the liver, 90.0 for the right kidney. For the 11 CT scans test datasets, the Dice scores are 84.8 for the left lung, 97.5 for the right lung, 78.5 for the trachea, 69.0 for the spleen, 63.1 for the left kidney, 74.7 for the liver, 63.1 for the right kidney. Our method was ranked first in the segmentation of the lung among 6 methods participated in the challenge.

[HJ]

Title: Automatic Liver Segmentation using Multiple Prior Knowledge Models and Free-Form Deformation

Authors: Cheng Huang and Fucang Jia, Research Lab. for Medical Imaging and Digital Surgery, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences.

Abstract: An automatic and robust coarse-to-fine liver image segmentation method is proposed. The workflow can be divided into four steps: liver localization, shape model fitting, appearance profile fitting and free-form deformation. For liver localization, an atlas image based rigid registration with correlation coefficient histogram metric is used to detect liver region of interest (ROI), an AdaBoost classifier is trained via multiple low level image features including intensity, gradient and context features, then liver probability map is generated. For generation of prior models, shape correspondence is established by deformation registration of manual segmented liver image to the atlas image, then Statismo toolkit is used to build the shape and appearance model, both intensity and gradient profile information inside, outside and at the true liver boundary are sampled and KNN classifier is used to construct appearance model. For model fitting, registration of the distance map image of AdaBoost classified liver mask and the point sets of the mean shape model is used, the mesh vertexes of

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deformed shape are moved to liver boundary location more accurately with major shape variation constraints. For free-form deformation, simplex mesh deformable model with gradient and intensity KNN classifier as external force is used to conquer local specific variation of liver shape. Fifty manually segmented datasets, fourteen VISCERAL challenge CT and CTce training datasets are used to train prior models.

[JM]

Title: Multi-atlas based segmentation

Authors: Oscar Alfonso Jiménez del Toro, Henning Müller, University of Applied Sciences Western Switzerland (HES-SO) and University and University Hospitals of Geneva, Switzerland

Abstract: Multi-atlas based segmentation is an approach that requires little or no interaction from the user. It has been evaluated with high accuracy and consistent reproducibility in different anatomical structures. In this method, multiple atlases identify the location of one or more structures in the patient volume. The label volumes of the atlases are transformed taking the coordinate transformation obtained from image registration of each atlas to the target volume. A stochastic gradient descent optimisation is performed for the desired metric during the process. 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 individual affine registrations using a local binary mask 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 method is repeated for the non-rigid registration. 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. Also the creation of regions-of-interest with the local masks speeds up the image registrations and improves the output estimations. The labels from the different atlases are fused using a per-voxel majority voting threshold in a single label volume that provides a final estimate location of the structures in the target volume. The images are downsampled in all but the final step to increase even more the speed of the algorithm. The method was tested with contrast-enhanced computed tomography images and 10 different anatomical structures: liver, spleen, kidneys, lungs, urinary bladder, trachea, lumbar vertebra and gallbladder. It can be then applied to any modality and any anatomical structure using a relatively small training set.

[GG]

Title: Segmentation and Landmark Localization Based on Multiple Atlases

Authors: Tobias Gass and Orcun Goksel, Computer Vision Lab, ETH Zurich, Switzerland

Abstract: In this work, we present multi-atlas based techniques for both segmentation and landmark detection.

We focus on modality and anatomy independent techniques to be applied in a wide range of image modalities, in contrast to methods customized to a specific anatomy or modality.

For segmentation, we use label propagation from several atlases to a target image via a Markov random field (MRF) based registration method, followed by label fusion by majority voting weighted by local cross-correlations. The registrations are computed on the full images as provided by the challenge, thus requiring only one registration per image pair independent of the number of segmentation labels. The multi-atlas segmentation fusion is also performed on all labels simultaneously, assigning the anatomical label with the highest weighted vote to each voxel. Local correlations are computed efficiently using a technique based on convolutions with Gaussian kernels. This is very generic method, also demonstrated by being the only submission applied to all anatomical

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structures in all modalities. It has comparable results to more specific segmentation algorithms in the VISCERAL challenge.

For landmark localization, we use a consensus-based fusion of location estimates from several atlases identified by a customized template-matching approach. Here, each atlas votes for candidate landmark locations, which are found by matching a fixed region of interest around the atlas landmark to a sliding window in a fixed region of the test image. For this matching, cross-correlation is employed which can be computed very efficiently in the frequency domain for such sliding windows. The top-ranked candidate locations of all atlases are combined using the median operator. Similar to the segmentation approach presented above, our landmark detection algorithm is applied to all images of all modalities in the VISCERAL challenge, yielding satisfactory results.

[DMB]

Title: Classification Forests for Landmark Detection

Authors: Mohammad A. Dabbah, Sean Murphy, Erin Beveridge, Daniel Wyeth, Ian Poole, Toshiba Medical Visualization Systems, Ltd.

Abstract: We use a voxel-level trained solution based on classification forests. Datasets are rotated to be aligned in DICOM Patient Coordinates, then downsampled to an isotropic resolution of 4mm per voxel with Gaussian smoothing to avoid aliasing effects. Features are simple densities in Hounsfield units at chosen random offsets to each voxel.

Each classification tree is trained using 40 datasets randomly selected from the 369 available. Additionally, random samples are taken for a background class throughout the volume. A number of background samples is taken equal to the total number of landmark samples in each dataset. At each node of the decision tree, 2,500 randomly selected features are searched for greatest information gain, the threshold being selected by an efficient incremental algorithm. Each leaf node stores the proportion by class of weighted training samples reaching that node. A classification forest of 80 trees is trained each with different randomly selected datasets.

At detection time, each downscaled voxel is passed down each tree in the forest, the resulting normalized likelihoods being averaged across each tree in the forest. For each landmark, the voxel with the greatest normalized likelihood for that landmark is selected as the potential detection point. Brent interpolation (ie fitting a quadratic) is used to deliver a sub-voxel result.

An issue often overlooked or unreported in other published work is how to deal with voxels for which some features cannot be measured either at training time or detection time, because the randomly selected offset references a voxel outside the dataset or in padding. Padding occurs in CT datasets outside the cylindrical acquisition region of the volume, and possibly elsewhere. The problem will very likely occur for voxels close to the edge of the volume, within the 52mm maximum feature offset. Our approach is to treat these unmeasurable values as missing features} in the manner described by Quinlan. In brief, when applying a decision rule at a node which involves a missing (unmeasurable) feature, that voxel is sent both ways down the tree, with modified weights. Quinlan discusses various ways of determining these weights, and we have experimented with these, settling on simply assigning the sample 50/50 to each branch, in both training and detection. Like Quinlan we also found it beneficial during training to scale the information gain for a candidate feature by the proportion of samples for which the feature was measurable (ie not missing).

[W]

Title: Automatic multi-organ segmentation using fast model based level set method and hierarchical shape priors

Authors: Chunliang Wang and Örjan Smedby, Center for Medical Image Science and Visualization (CMIV), Linköping University, and Department of Radiology and Department of Medical and Health Sciences, Linköping University, Linköping, Sweden.

Abstract: An automatic multi-organ segmentation pipeline is presented. The segmentation starts with stripping the body of skin and subcutaneous fat using threshold-based level-set methods. After registering the image to be processed against a standard subject picked from the training datasets, a series of model-based level set segmentation operations is carried out guided by hierarchical shape priors. The hierarchical shape priors are organized according to the anatomical hierarchy of the human body, starting with ventral cavity, and then divided into thoracic cavity and abdominopelvic cavity. The third level contains the individual organs such as lungs, liver and kidneys. Statistical shape models of structures and organs are created by registering the binary segmentation masks of individual organs against the picked standard subject. The position of a lower-level structure relative to an upper-level structure is computed by registering the statistical mean shape against a trust zone created by thresholding the probability atlas of that anatomical structure in the upper-level structure's space. The segmentation is performed in a top-down fashion, where major structures are segmented first, and their location information is then passed down to the lower level to initialize the segmentation, while boundary information from higher-level structures also constrains the segmentation of the lower-level structures. A threshold-based speed function is used to drive the level set segmentation while the thresholds are iteratively updated based on statistical analysis of preliminary segmentation results. The proposed method was combined with a novel coherent propagating level-set method, which is capable to detect local convergence and skip calculation in those parts, thereby significantly reducing computation time. In our preliminary experiments, the proposed method yielded a Dice coefficient around 90% for most major thoracic and abdominal organs in both contrast-enhanced CT and non-enhanced datasets, while the average running time for segmenting 10 organs was about 10 minutes.

[K]

Title: 3D Multiobject Segmentation via Clustering and Graph Cut Using Shortest-Path Constraints for Spatial Relations and Atlas-Based Shape Priors

Authors: Razmig Kechichian, Michel Desvignes (Gipsa-lab, Grenoble INP; France), Sébastien Valette (Creatis, INSA de Lyon; France)

Abstract: Our automatic multiple organ segmentation method is based on a multi-label Graph Cut optimization approach which uses prior information of organ spatial relationships and shape. The former is derived from shortest-path pairwise constraints defined on a graph model of structure adjacency relations and the latter is represented by probabilistic organ atlases learned from a training dataset. The pairwise prior in particular is a piecewise-constant model incurring multiple levels of penalization capturing the spatial configuration of structures in multiobject segmentation. Organ atlases are mapped to the image via a hierarchical image registration method based on SURF keypoints and are additionally used to derive image intensity statistics automatically. Prior models and intensity statistics are then introduced in a joint centroidal Voronoi image clustering and Graph Cut multiobject segmentation framework. The clustering approach we take to simplify images prior to segmentation strikes a good balance between boundary adaptivity and cluster compactness criteria furthermore allowing to control the trade-off. Compared to a direct application of segmentation on voxels, the clustering step improves the overall runtime and memory footprint of the segmentation process up to an order of magnitude virtually without compromising the quality of the result. An initial implementation has allowed to evaluate the method on the contrast-enhanced CT subset of the VISCERAL dataset.

3.2 Anatomy2

The information that participants have provided about their techniques is below (linked to the result tables in Sections 4.4.1 and 4.4.2 by the abbreviations in square brackets). More details on the approaches for the ISBI challenge are available online⁴. The full details for some of the final submissions will appear in the Springer proceedings of the MICCAI Medical Computer Vision Workshop.

3.2.1 ISBI Challenge

[SJ]

Assaf B. Spanier and Leo Joskowicz

School of Engineering and Computer Science, The Hebrew University of Jerusalem, Israel

Rule-Based Ventral Cavity Multi-Organ Automatic Segmentation in CT Scans

[JM]

Oscar Alfonso Jiménez del Toro and Henning Müller

University of Applied Sciences Western Switzerland, Switzerland

Hierarchical Multi-structure Segmentation Guided by Anatomical Correlations

[WS]

Chunliang Wang* and Örjan Smedby~

*Center for Medical Imaging Science and Visualization(CMIV) and ~Dept of Medical and Health Sciences (IMH), Linköping University, Sweden

Automatic multi-organ segmentation using fast model based level set method and hierarchical shape priors

[GGS]

Orcun Goksel, Tobias Gass, and Gabor Szekely

Computer Vision Lab, ETH Zurich, Switzerland

Segmentation and Landmark Localization Based on Multiple Atlases

[HLJ]

Cheng Huang, Xuhui Li, and Fucang Jia

Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences, China

Automatic Liver Segmentation using Multiple Prior Knowledge Models and Free-Form Deformation

⁴ <http://ceur-ws.org/Vol-1194/>

3.2.2 Final Submission

[SJ]

Title: Rule-Based Ventral Cavity Multi-Organ Automatic Segmentation in CT Scans

Authors: Assaf B. Spanier, Leo Joskowicz, School of Eng. and Computer Science, The Hebrew Univ. of Jerusalem, Israel University

Abstract: We describe a new method for the automatic segmentation of multiple organs of the ventral cavity in CT scans. The method is based on a set of rules that determine the order in which the organs are isolated and segmented, from the simplest one to the most difficult one. First, the air-containing organs are segmented: the trachea and the lungs. Then, the organs with high blood content: the spleen, the kidneys and the liver, are segmented. Each organ is individually segmented with a generic four-step procedure that consists of: 1) ROI Identification; 2) Thresholding; 3) 2D-seed identification; 4) Slice region growing with clustering classification algorithms. Our method is unique in that it uses the same generic segmentation approach for all organs and in that it relies on the segmentation difficulty of organs to guide the segmentation process. Experimental results on 20 CT scans of the VISCERAL Anatomy2 Challenge training datasets yield a Dice volume overlap similarity score of 79.5 for the trachea, 97.4 and 97.6 for the left and right lungs, 89.2 for the spleen, 92.8 and 89.2, respectively, for the left and right kidney, and 83.5 for the liver. For the 10 CT scans test datasets, the Dice scores are 85.1, 97.0, 96.8, 82.2, 82.9 and 87.0, respectively. Our method achieved an overall DICE volume overlap similarity score of 88.5. For the segmentation of air containing organs (i.e. lungs and trachea) in CTce we ranked first among other methods that participated in the challenge.

[LHJ]

Title: Automatic Liver Segmentation using Statistical Prior Models and Free-form Deformation

Authors: Xuhui Li, Cheng Huang, Fucang Jia, Zongmin Li, Chihua Fang, Yingfang Fan. Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences, China University of Petroleum and Southern Medical University, China

Abstract: An automatic and robust coarse-to-fine liver image segmentation method is proposed. Multiple prior knowledge models are built to implement liver localization and segmentation: voxel-based AdaBoost classifier is trained to localize liver position robustly, shape and appearance models are constructed to fit liver these models to original CT volume. Free-form deformation is incorporated to improve the models' ability of refining liver boundary. The method was submitted to VISCERAL big data challenge, and had been tested on IBSI 2014 challenge datasets and the result demonstrates that the proposed method is accurate and efficient.

[WS]

Title: Automatic Multi-Organ Segmentation Using Fast Model Based Level Set Method and Hierarchical Shape Priors

Authors: Chunliang Wang and Örjan Smedby, Center for Medical Image Science and Visualization (CMIV), Linköping University, and Department of Radiology and Department of Medical and Health Sciences, Linköping University, Linköping, Sweden

Abstract: An automatic multi-organ segmentation pipeline is presented. The segmentation starts with stripping the body of skin and subcutaneous fat using threshold-based level-set methods. After registering the image to be processed against a standard subject picked from the training datasets, a series of model-based level set segmentation operations is carried out guided by hierarchical shape priors. The hierarchical shape priors are organized according to the anatomical hierarchy of the human body, starting with ventral cavity, and then divided into thoracic cavity and abdominopelvic cavity.

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The third level contains the individual organs such as lungs, liver and kidneys. Statistical shape models of structures and organs are created by registering the binary segmentation masks of individual organs against the picked standard subject. The position of a lower-level structure relative to an upper-level structure is computed by registering the statistical mean shape against a trust zone created by thresholding the probability atlas of that anatomical structure in the upper-level structure's space. The segmentation is performed in a top-down fashion, where major structures are segmented first, and their location information is then passed down to the lower level to initialize the segmentation, while boundary information from higher-level structures also constrains the segmentation of the lower-level structures. A threshold-based speed function is used to drive the level set segmentation while the thresholds are iteratively updated based on statistical analysis of preliminary segmentation results. The proposed method was combined with a novel coherent propagating level-set method, which is capable to detect local convergence and skip calculation in those parts, thereby significantly reducing computation time.

[H]

Title: Automatic segmentation of abdominal organs in a framework based on Active Appearance Models

Author: Graham Vincent and Richard Haworth, Imorphics Ltd., Manchester, UK

Abstract: We present a single fully automatic model based framework for segmenting the aorta, kidneys, liver, lungs and the psoas major muscles in thoracic contrast enhanced and wide field of view CT images. These anatomies were chosen as a representative subset of the structures in the full VISCERAL database, in order to contribute to the VISCERAL Anatomy2 benchmark. The models were built from approximately 35 manually segmented examples provided by the VISCERAL organisers. The segmentation framework is generic and has been successfully used for segmentation in CT and/or MR for bone and soft tissue in the hands, knee, hip and ankle, spine, for prostate and for sub-cortical structures in the brain.

The framework is based on Active Appearance Models (AAM). High quality correspondences for the AAM are generated using a Minimum Description Length group-wise image registration method. A hierarchical multi-start optimisation scheme is used to robustly match the AAMs to new images which fits low density low resolution models followed by increasingly detailed and high resolution models. The model result helps define a region of uncertainty in a narrow halo around the model boundary. The voxels in this region are assigned a probability of belonging to the structure using a non-linear regression function, trained using a PAC-learning method. Finally, the probability image can be turned into a binary image by thresholding at $p=0.5$ for comparison with binary golden data.

The results on the VISCERAL data are very good across all anatomies. In DICE overlap scores, the method ranked top for the aorta, left and right psoas major muscles and left kidney for both wide beam and thoracic images, and the right lung for contrast enhanced images.

Note: This was the only method to produce fuzzy segmentations, with grey levels indicating the probability of membership of the organ. For this reason, two sets of results were produced. "-f" contains the metrics calculated directly on the fuzzy images; "-b" contains the metrics calculated on binary images produced from the fuzzy images with a threshold at 0.5.

[KDV]

Title: Automatic 3D Multiorgan Segmentation via Clustering and Graph Cut Using Spatial Relations and Hierarchically-Registered Atlases

Authors: Razmig Kechichian, Michel Desvignes (Gipsa-lab, Grenoble INP; France), Sébastien Valette, Michael Sdika (Creatis, INSA de Lyon; France)

Abstract: We propose a generic method for automatic multiple-organ segmentation based on a multilabel Graph Cut optimization approach which uses location likelihood of organs and prior information of spatial relationships between them. The latter is derived from shortest-path constraints defined on the adjacency graph of structures and the former is defined by probabilistic atlases learned from a training dataset. Organ atlases are mapped to the image by a fast (2+1)D hierarchical registration method based on SURF keypoints. Registered atlases are furthermore used to derive organ intensity likelihoods. Prior and likelihood models are then introduced in a joint centroidal Voronoi image clustering and Graph Cut multiobject segmentation framework. Qualitative and quantitative evaluation has been performed on contrast-enhanced CT images from the Visceral Benchmark dataset.

[GGS]

Title: Multi-Atlas Segmentation and Landmark Localization in Images with Large Field of View

Authors: Tobias Gass, Gabor Szekely, Orcun Goksel, ETH Zürich, Switzerland

Abstract: In this work, we present multi-atlas based techniques for both segmentation and landmark detection in images with large field-of-view (FOV). Such images can provide important insight in the anatomical structure of the human body, but are challenging to deal with since the localization search space for landmarks and organs, in addition to the raw amount of data, is large. In many studies, segmentation and localization techniques are developed specifically for an individual target anatomy or image modality. This can leave a substantial amount of the potential of large FOV images untapped, as the co-localization and shape variability of organs are neglected. We thus focus on modality and anatomy independent techniques to be applied to a wide range of input images. For segmentation, we propagate the multi-organ label maps from several atlases to a target image via a large FOV Markov random field (MRF) based non-rigid registration method. The propagated labels are then fused in the target domain using similarity-weighted majority voting. For landmark localization, we use a consensus based fusion of location estimates from several atlases identified by a template-matching approach. We present our results in the IEEE ISBI 2014 VISCERAL challenge as well as VISCERAL Anatomy1 and Anatomy2 benchmarks.

[JM]

Title: Hierarchic Multi-atlas Based Segmentation for Anatomical Structures: Evaluation in the VISCERAL Anatomy Benchmarks

Authors: Oscar Jimenez del Toro, Henning Müller, University of Applied Sciences Western Switzerland

Abstract: Computer-based medical image analysis is often initialized with the localization of anatomical structures in clinical scans. Many methods have been proposed for segmenting single and multiple anatomical structures. However, it is uncommon to compare different approaches with the same test set, namely a publicly available one. The comparison of these methods objectively denotes the advantages and limitations for each method. A hierarchic multi-atlas based segmentation approach was proposed for the segmentation of multiple anatomical structures in computed tomography scans. The method relies on an anatomical hierarchy that exploits the inherent spatial and anatomical variability of medical images using image registration techniques. It was submitted and tested in the VISCERAL project Anatomy benchmarks. In this paper, the results are analyzed and compared to the results of the other segmentation methods submitted in the benchmark. Various anatomical structures in both unenhanced and contrast-enhanced CT scans resulted in the highest overlap with the proposed method compared to the other evaluated approaches. Although the method was trained with a small training set it generated accurate output segmentations for liver, lungs and other anatomical structures.

[M]

Title: 3D Landmark detection with Histograms of Oriented Gradients

Authors: Dominic Mai, Olaf Ronneberger, University of Freiburg, Germany

Abstract: We present an approach to landmark detection in volumetric images based on the popular Histograms of Oriented Gradients Descriptor (HOG) and linear support vector machines. We rigidly align the positive training examples and compute 3D HOG descriptors with 20 orientation bins for the patch surrounding the landmark location. As negative examples we randomly sample patches from the 3D volume that do not contain the sought landmark. We train a linear support vector machine on the kernel matrix of our training set to cope with the high dimensionality of the data. At test time we use a sliding window approach that we compute efficiently as a convolution in Fourier space.

4 Result Analysis

4.1 Evaluation Metrics

Four evaluation metrics are used for the result analysis, namely the Dice coefficient (DICE), the interclass correlation (ICC), the adjusted Rand index (ADJRIND), and the Average distance (AVGDST). These metrics were selected from a metric pool of 20 evaluation metrics that were found as a result of a literature review on evaluation of medical volume segmentation. The four metrics were selected from the pool, so that they belong to different categories, namely one overlap metric (DICE), one metric with chance adjustment (ADJRIND), one probabilistic metric (ICC), and one distance based metric (AVGDST). For evaluating the landmark localization, the Euclidean distance was used. For more information on the evaluation see Deliverable D4.1.

In the next sections the evaluation results for each participant are presented for each of the four metrics. For each case (modality, region, configuration, and organ), the average score was calculated from all submitted segmentations for that case.

4.2 Result structure

The results for each benchmark are presented below. The analysis of the segmentation task is structured as follows: For each participant, the four metrics, mentioned above, are provided as averages for each organ where different modalities and regions are provided in separated scores. The available combinations are ThAb/CTce, wb/CT, wb/MRT1, and Ab/MRT1cefs. When participants have provided submissions with different configurations, the scores for each configuration were calculated and provided separately

The identification task (Landmark localization) was evaluated using the Euclidean distance. For each participant, the Euclidean distance was given as an average for each landmark and case (modality and region). The percentage contribution of the participant was calculated in each case, that is the ratio between the number of landmarks provided by the participant and the number of landmarks annotated in the ground truth for each case.

In the next sections, the results, as described above, are provided for each benchmark in tabular form.

4.3 Anatomy1

4.3.1 Segmentation

Participant	Modality	Region	configuration	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	gallblader	sternum	aorta	trachea	left adrenal gland	right adrenal gland	Average	image count	count of empty images			
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324						
Measure			DICE coefficient																										
[SJ]	Ctce	ThAb	1	0.631	0.663	0.690	0.747	0.848	0.975																	0.763	69	1	
[HJ]	Ctce	ThAb	1				0.886																			0.886	12		
[HJ]	Ctce	ThAb	2				0.886																			0.886	12		
[HJ]	Ctce	ThAb	3				0.884																			0.884	12		
[HJ]	Ctce	ThAb	4				0.887																			0.887	12		
[HJ]	Ctce	ThAb	5				0.891																			0.891	12		
[HJ]	CT	wb	1				0.892																			0.892	15		
[HJ]	CT	wb	2				0.877																			0.877	15		
[HJ]	CT	wb	3				0.889																			0.889	15		
[HJ]	CT	wb	4				0.892																			0.892	15		
[HJ]	CT	wb	5				0.888																			0.888	15		
[W]	CT	wb	1	0.820	0.802	0.868	0.910	0.961	0.963	0.732						0.764	0.771		0.683							0.827	140		



D4.3 Result analysis for Competition 1

[W]	Ctce	ThAb	1	0.790	0.861	0.868	0.889	0.964	0.968	0.805						0.773	0.803		0.681							0.840	120	
[W]	CT	wb	2	0.819	0.798	0.891	0.913	0.965	0.965	0.782						0.774	0.771		0.663							0.834	109	1
[W]	Ctce	ThAb	2	0.793	0.872	0.873	0.893	0.964	0.968	0.796						0.792	0.806		0.713							0.847	120	
[W]	CT	wb	3	0.818	0.839	0.882	0.914	0.964	0.965	0.747						0.770	0.769		0.655							0.832	110	
[W]	Ctce	ThAb	3	0.804	0.867	0.871	0.892	0.964	0.968	0.799						0.786	0.807		0.699							0.846	120	
[W]	CT	wb	4	0.812	0.806	0.882	0.914	0.941	0.942	0.752						0.768	0.767		0.677							0.826	110	
[W]	Ctce	ThAb	4	0.782	0.862	0.848	0.898	0.965	0.969	0.794						0.788	0.811		0.688							0.840	120	
[W]	CT	wb	5	0.799	0.777	0.885	0.909	0.961	0.964	0.732						0.773	0.750		0.653							0.820	110	
[W]	Ctce	ThAb	5	0.789	0.871	0.862	0.887	0.963	0.967	0.781						0.783	0.802		0.658							0.836	120	
[JM]	Ctce	ThAb	1	0.872	0.887	0.528	0.856	0.953	0.962	0.668			0.504						0.566				0.816			0.761	120	
[JM]	Ctce	ThAb	2	0.909	0.909	0.715	0.900	0.955	0.965	0.700			0.522						0.549				0.836			0.796	120	
[JM]	Ctce	ThAb	3	0.921	0.913	0.827	0.917	0.955	0.964	0.696			0.310						0.361				0.832			0.770	120	
[JM]	Ctce	ThAb	4	0.918	0.902	0.852	0.918	0.953	0.962	0.652			0.264						0.151				0.816			0.739	111	9
[JM]	Ctce	ThAb	5	0.866	0.855	0.849	0.906	0.947	0.957	0.545			0.002						0.072				0.739			0.674	99	12
[K]	Ctce	ThAb	1	0.739	0.624	0.768	0.806	0.853	0.892	0.705	0.051	0.067	0.417		0.118	0.691	0.609	0.281	0.228	0.495	0.696					0.532	170	56
[K]	Ctce	ThAb	2	0.731	0.632	0.768	0.803	0.848	0.891	0.714	0.073	0.080	0.431		0.124	0.706	0.629	0.251	0.323	0.472	0.346	0.000	0.000			0.519	189	39
[K]	Ctce	ThAb	3	0.721	0.628	0.767	0.801	0.847	0.891	0.718	0.112	0.118	0.440	0.004	0.149	0.674	0.631	0.267	0.429	0.465	0.427	0.000	0.007			0.479	194	34
[K]	Ctce	ThAb	4	0.713	0.624	0.766	0.800	0.845	0.891	0.717	0.130	0.171	0.447	0.004	0.155	0.661	0.633	0.238	0.454	0.455	0.365	0.000	0.004			0.478	200	28
[K]	Ctce	ThAb	5	0.747	0.626	0.765	0.806	0.856	0.892	0.682	0.043	0.053	0.404		0.000	0.678	0.593	0.221	0.187	0.505	0.612					0.542	158	70
[GG]	Ctce	ThAb	2	0.903	0.877	0.802	0.899	0.961	0.968	0.676			0.604	0.252	0.465	0.811		0.334	0.595	0.785	0.847	0.204	0.164			0.656	191	34
[GG]	MRT1	wb	2	0.730	0.733	0.668	0.822	0.533	0.900	0.656			0.396	0.367		0.801		0.023	0.358	0.744	0.736	0.109	0.215			0.549	168	4
[GG]	CT	wb	2	0.805	0.754	0.688	0.830	0.952	0.960	0.640			0.350	0.469	0.438	0.772	0.787	0.102	0.648	0.723	0.822	0.165	0.138			0.614	222	29



D4.3 Result analysis for Competition 1

[GG]	MRT1cefs	Ab	2	0.782	0.787	0.689	0.847	0.650	0.664	0.280				0.060		0.356	0.644		0.035		0.616		0.000	0.107	0.501	76	10
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Participant	Modality	Region	configuration	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	gallblader	sternum	aorta	trachea	left adrenal gland	right adrenal gland	Average	image count	count of empty images		
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324					
Measure				Adjusted Rand Index																								
[SJ]	Ctce	ThAb	1	0.630	0.663	0.690	0.741	0.834	0.972																	0.759	69	1
[HJ]	Ctce	ThAb	1				0.881																			0.881	12	
[HJ]	Ctce	ThAb	2				0.880																			0.880	12	
[HJ]	Ctce	ThAb	3				0.878																			0.878	12	
[HJ]	Ctce	ThAb	4				0.881																			0.881	12	
[HJ]	Ctce	ThAb	5				0.886																			0.886	12	
[HJ]	CT	wb	1				0.890																			0.890	15	
[HJ]	CT	wb	2				0.875																			0.875	15	
[HJ]	CT	wb	3				0.887																			0.887	15	
[HJ]	CT	wb	4				0.890																			0.890	15	
[HJ]	CT	wb	5				0.886																			0.886	15	
[W]	CT	wb	1	0.819	0.802	0.868	0.908	0.960	0.962	0.732						0.764	0.771		0.683							0.827	140	



D4.3 Result analysis for Competition 1

[W]	Ctce	ThAb	1	0.789	0.860	0.867	0.884	0.960	0.965	0.803						0.772	0.802		0.680							0.838	120		
[JM]	Ctce	ThAb	1	0.871	0.887	0.524	0.848	0.949	0.958	0.665			0.503					0.566			0.816						0.759	120	
[JM]	Ctce	ThAb	2	0.909	0.909	0.713	0.894	0.952	0.961	0.698			0.522					0.549			0.836						0.794	120	
[JM]	Ctce	ThAb	3	0.921	0.913	0.826	0.912	0.952	0.961	0.695			0.310					0.361			0.832						0.768	120	
[JM]	Ctce	ThAb	4	0.917	0.901	0.851	0.914	0.949	0.958	0.650			0.264					0.151			0.816						0.737	111	9
[JM]	Ctce	ThAb	5	0.866	0.854	0.848	0.901	0.943	0.952	0.544			0.002					0.072			0.739						0.672	99	12
[K]	Ctce	ThAb	1	0.738	0.623	0.767	0.796	0.841	0.881	0.704	0.050	0.066	0.417		0.118	0.690	0.608	0.281	0.228	0.493	0.696						0.529	170	56
[K]	Ctce	ThAb	2	0.729	0.630	0.767	0.793	0.836	0.880	0.713	0.072	0.079	0.431		0.124	0.704	0.627	0.251	0.322	0.469	0.346	0.000	0.000				0.516	189	39
[K]	Ctce	ThAb	3	0.720	0.627	0.766	0.791	0.834	0.880	0.717	0.111	0.117	0.440	0.004	0.149	0.673	0.629	0.267	0.429	0.462	0.427	0.000	0.007				0.476	194	34
[K]	Ctce	ThAb	4	0.712	0.623	0.764	0.789	0.832	0.880	0.715	0.129	0.170	0.447	0.004	0.155	0.659	0.631	0.237	0.453	0.452	0.365	0.000	0.004				0.475	200	28
[K]	Ctce	ThAb	5	0.746	0.625	0.763	0.796	0.844	0.882	0.680	0.043	0.052	0.404		0.000	0.676	0.591	0.221	0.187	0.502	0.611						0.539	158	70
[GG]	Ctce	ThAb	2	0.903	0.876	0.801	0.894	0.958	0.964	0.674			0.604	0.251	0.464	0.810		0.334	0.595	0.784	0.847	0.204	0.164				0.655	191	34
[GG]	MRT1	wb	2	0.729	0.732	0.667	0.818	0.523	0.897	0.656			0.396	0.367		0.801		0.023	0.358	0.743	0.736	0.109	0.215				0.548	168	4
[GG]	CT	wb	2	0.805	0.754	0.688	0.828	0.951	0.959	0.640			0.350	0.469	0.438	0.771	0.787	0.102	0.648	0.722	0.822	0.165	0.138				0.613	222	29
[GG]	MRT1cefs	Ab	2	0.780	0.785	0.686	0.831	0.639	0.651	0.277			0.060		0.355	0.641		0.035		0.614		0.000	0.107				0.497	76	10



D4.3 Result analysis for Competition 1

Participant	Modality	Region	configuration	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	Average	image count	count of empty images		
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324					
Measure				Interclass Correlation																								
[SJ]	Ctce	ThAb	1	0.631	0.663	0.690	0.747	0.848	0.975																	0.763	69	1
[HJ]	Ctce	ThAb	1				0.886																			0.886	12	
[HJ]	Ctce	ThAb	2				0.886																			0.886	12	
[HJ]	Ctce	ThAb	3				0.884																			0.884	12	
[HJ]	Ctce	ThAb	4				0.887																			0.887	12	
[HJ]	Ctce	ThAb	5				0.891																			0.891	12	
[HJ]	CT	wb	1				0.892																			0.892	15	
[HJ]	CT	wb	2				0.877																			0.877	15	
[HJ]	CT	wb	3				0.889																			0.889	15	
[HJ]	CT	wb	4				0.892																			0.892	15	
[HJ]	CT	wb	5				0.888																			0.888	15	
[W]	CT	wb	1	0.820	0.802	0.868	0.910	0.961	0.963	0.732						0.764	0.771		0.683							0.827	140	
[W]	Ctce	ThAb	1	0.790	0.860	0.868	0.889	0.964	0.968	0.805						0.773	0.803		0.681							0.840	120	
[JM]	Ctce	ThAb	1	0.872	0.887	0.528	0.856	0.953	0.962	0.668			0.504						0.566			0.816				0.761	120	
[JM]	Ctce	ThAb	2	0.909	0.909	0.715	0.900	0.955	0.965	0.700			0.522						0.549			0.836				0.796	120	
[JM]	Ctce	ThAb	3	0.921	0.913	0.827	0.917	0.955	0.964	0.696			0.310						0.361			0.832				0.770	120	
[JM]	Ctce	ThAb	4	0.918	0.902	0.852	0.918	0.953	0.962	0.652			0.264						0.151			0.816				0.739	111	9

4.3.2 Landmark Localization

Participant	Modality	Region	configuration	aorta_bifurcation	aortic_arch	clavicle_left	clavicle_right	crista_iliaca_left	crista_iliaca_right	symphysis	trachea_bifurcation	trochanter_major_left	trochanter_major_right	trochanter_minor_left	trochanter_minor_right	average
Measure				Euclidean distance												
[DMB]	CT	wb	1	17.41	22.64	82.48	85.13	11.19	7.80	7.13	3.90	7.44	7.03	9.88	8.88	22.58
[DMB]	CT	wb	2	16.34	22.64	83.07	85.69	11.19	7.80	56.50	3.90	9.51	8.78	16.60	16.49	28.21
[DMB]	CT	wb	3	17.41	22.64			11.19	7.80	7.13	3.90	9.49	8.77	9.88	8.88	10.71
[DMB]	CT	wb	4	17.41	12.87	46.49	45.62	11.19	7.80	7.13	3.90	9.49	8.77	9.88	8.88	15.79
[DMB]	CT	wb	5	17.41	9.70	18.50	20.65	11.19	7.80	7.13	3.90	9.49	8.77	9.88	8.88	11.11
[GG]	CT	wb	1	39.15	16.05	8.21	9.36	10.75	10.51	9.90	4.51	5.08	5.06	6.83	5.41	10.90
[GG]	CT	wb	2	33.65	26.05	27.16	13.23	9.50	9.35	9.38	11.41	4.74	4.17	6.32	6.02	13.42
[GG]	MRT1cefs	Ab	1	48.65				85.34	57.75	52.25		66.69	78.88	98.11	39.63	65.91
[GG]	MRT1cefs	Ab	2	52.24				74.60	55.92	63.24		78.54	77.79	103.97	47.86	69.27

Volume	10000079	10000080	10000081	10000082	10000085	10000086	10000087	10000088	10000089	10000090	10000092	10000094	10000095
total landmarks	12	12	12	12	12	12	12	12	12	12	12	12	12



D4.3 Result analysis for Competition 1

				Measure	percentage contribution											
[DMB]	CT	wb	1	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
[DMB]	CT	wb	2	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
[DMB]	CT	wb	3	83%	83%	83%	83%	83%	83%	83%	83%	83%	83%	83%	83%	83%
[DMB]	CT	wb	4	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
[DMB]	CT	wb	5	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
[GG]	CT	wb	1	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
[GG]	CT	wb	2	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
[GG]	MRT1cefs	Ab	1	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%
[GG]	MRT1cefs	Ab	2	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%

Volume	10000096	10000099	10000336	10000337	10000339	10000340	10000342	10000343	10000346	10000419	10000427	10000428
total landmarks	12	12	12	12	12	12	12	12	12	12	12	12

				Measure	percentage contribution											
[DMB]	CT	wb	1	100%	100%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	
[DMB]	CT	wb	2	100%	100%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	
[DMB]	CT	wb	3	83%	83%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	
[DMB]	CT	wb	4	100%	100%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	
[DMB]	CT	wb	5	100%	100%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	
[GG]	CT	wb	1	100%	100%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	
[GG]	CT	wb	2	100%	100%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	
[GG]	MRT1cefs	Ab	1	0%	0%	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%	
[GG]	MRT1cefs	Ab	2	0%	0%	100%	100%	100%	100%	100%	100%	100%	100%	100%		

4.4 Anatomy2

4.4.1 ISBI Challenge

4.4.1.1 Segmentation

Participant	Modality	Region	configuration	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	gallblader	sternum	aorta	trachea	left adrenal gland	right adrenal gland	Average	image count	count of empty images				
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324							
Measure				DICE coefficient																										
[SJ]	Ctce	ThAb	1	0.902		0.934		0.970	0.979																0.856			0.928	25	
[HLJ]	Ctce	ThAb	1				0.922																				0.922	5		
[HLJ]	CT	wb	1				0.911																				0.911	5		
[WS]	CT	wb	1	0.729	0.777	0.887	0.904	0.971	0.972	0.806						0.722	0.764		0.712								0.824	50		
[WS]	Ctce	ThAb	1	0.896	0.890	0.842	0.887	0.956	0.942	0.738						0.737	0.752		0.590								0.823	50		
[JM]	CT	wb	1	0.678	0.649	0.677	0.823	0.969	0.967	0.616			0.440					0.271			0.855						0.694	50		
[JM]	Ctce	ThAb	1	0.923	0.905	0.859	0.908	0.952	0.963	0.680			0.472					0.400			0.830						0.789	50		
[GGS]	Ctce	ThAb	1	0.885	0.827	0.803	0.882	0.960	0.966	0.657			0.548	0.315	0.442	0.797		0.212	0.612	0.787	0.839	0.099	0.019			0.627	76	16		
[GGS]	MRT1	wb	1	0.548	0.589	0.646	0.817	0.486	0.909	0.577			0.623	0.488		0.765		0.044	0.359	0.783	0.747	0.144	0.268			0.550	63	7		
[GGS]	CT	wb	1	0.756	0.679	0.684	0.798	0.955	0.965	0.636			0.333	0.439	0.466	0.773	0.780	0.078	0.630	0.724	0.837	0.282	0.133			0.608	89	11		
[GGS]	MRT1cefs	Ab	1	0.888	0.732	0.785	0.861			0.334			0.084		0.356	0.654		0.000								0.587	38	5		

D4.3 Result analysis for Competition 1

Participant	Modality	Region	configuration	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	Average	image count	count of empty images				
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324							
Measure				Adjusted Rand Index																										
[SJ]	Ctce	ThAb	1	0.901		0.933		0.967	0.977																0.856			0.927	25	
[HLJ]	Ctce	ThAb	1				0.918																					0.918	5	
[HLJ]	CT	wb	1				0.909																					0.909	5	
[WS]	CT	wb	1	0.728	0.776	0.886	0.901	0.970	0.971	0.806						0.721	0.764		0.711									0.824	50	
[WS]	Ctce	ThAb	1	0.896	0.889	0.840	0.882	0.952	0.936	0.736						0.736	0.751		0.589									0.821	50	
[JM]	CT	wb	1	0.677	0.648	0.676	0.820	0.968	0.966	0.616			0.439					0.271							0.855			0.694	50	
[JM]	Ctce	ThAb	1	0.922	0.904	0.858	0.903	0.948	0.959	0.678			0.471					0.400						0.830			0.787	50		
[GGS]	Ctce	ThAb	1	0.885	0.826	0.802	0.876	0.956	0.962	0.655			0.548	0.315	0.442	0.796		0.212	0.612	0.786	0.839	0.099	0.019				0.625	76	16	
[GGS]	MRT1	wb	1	0.547	0.588	0.645	0.812	0.474	0.907	0.576			0.623	0.488		0.765		0.044	0.359	0.782	0.747	0.144	0.268				0.548	63	7	
[GGS]	CT	wb	1	0.756	0.679	0.684	0.794	0.954	0.964	0.635			0.333	0.439	0.466	0.773	0.780	0.078	0.630	0.723	0.837	0.282	0.133				0.608	89	11	
[GGS]	MRT1cefs	Ab	1	0.886	0.730	0.781	0.847						0.084		0.355	0.651		0.000										0.583	38	5



D4.3 Result analysis for Competition 1

Participant	Modality	Region	configuration	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	Average	image count	count of empty images				
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324							
Measure				Interclass Correlation																										
[SJ]	Ctce	ThAb	1	0.902		0.934		0.970	0.979																0.856			0.928	25	
[HLJ]	Ctce	ThAb	1				0.922																					0.922	5	
[HLJ]	CT	wb	1				0.911																					0.911	5	
[WS]	CT	wb	1	0.729	0.777	0.887	0.904	0.971	0.972	0.806						0.722	0.764		0.712									0.824	50	
[WS]	Ctce	ThAb	1	0.896	0.890	0.842	0.887	0.956	0.942	0.738						0.737	0.752		0.590									0.823	50	
[JM]	CT	wb	1	0.678	0.649	0.677	0.823	0.969	0.967	0.616			0.440						0.271						0.855			0.694	50	
[JM]	Ctce	ThAb	1	0.923	0.905	0.859	0.908	0.952	0.963	0.680			0.472						0.400						0.830			0.789	50	
[GGS]	Ctce	ThAb	1	0.885	0.827	0.803	0.882	0.960	0.966	0.657			0.548	0.315	0.442	0.797			0.212	0.612	0.787	0.839	0.099	0.019			0.627	76	16	
[GGS]	MRT1	wb	1	0.548	0.589	0.646	0.817	0.486	0.909	0.577			0.623	0.488		0.765			0.044	0.359	0.783	0.747	0.144	0.268			0.550	63	7	
[GGS]	CT	wb	1	0.756	0.679	0.684	0.798	0.955	0.965	0.636			0.333	0.439	0.466	0.773	0.780		0.078	0.630	0.724	0.837	0.282	0.133			0.608	89	11	
[GGS]	MRT1cefs	Ab	1	0.888	0.732	0.785	0.861			0.334			0.084		0.356	0.654			0.000								0.587	38	5	

D4.3 Result analysis for Competition 1

Participant	Modality	Region	configuration	29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324	Average	image count	count of empty images					
				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								
Measure				Average distance																											
[SJ]	Ctce	ThAb	1	0.23		0.14		0.08	0.04																	0.30			0.16	25	
[HLJ]	Ctce	ThAb	1				0.29																						0.29	5	
[HLJ]	CT	wb	1				0.31																						0.31	5	
[WS]	CT	wb	1	3.63	1.21	0.45	0.46	0.07	0.06	0.78						1.77	1.15			1.24									1.08	50	
[WS]	Ctce	ThAb	1	0.27	0.28	0.87	0.65	0.15	0.20	1.59						1.75	1.58			4.14									1.15	50	
[JM]	CT	wb	1	3.057	3.308	2.636	1.764	0.050	0.056	2.082			4.179							25.021					0.297				4.245	50	
[JM]	Ctce	ThAb	1	0.152	0.365	0.596	0.373	0.107	0.067	1.689			4.219							4.341					0.582				1.249	50	
[GGS]	Ctce	ThAb	1	0.39	1.48	1.08	0.73	0.38	0.92	1.93			2.46	5.54	6.83	0.80			13.50	1.13	0.78	0.71	9.63	15.07				3.73	76	16	
[GGS]	MRT1	wb	1	21.23	16.73	0.83	0.90	159.4	0.28	1.44			1.21	1.01		0.94			8.18	5.44	0.45	0.53	12.09	3.64				14.64	63	7	
[GGS]	CT	wb	1	1.42	3.66	2.15	1.60	0.88	0.10	2.32			6.99	3.57	3.36	1.33	1.33		14.55	1.33	1.02	0.87	6.01	6.62				3.28	89	11	
[GGS]	MRT1cefs	Ab	1	0.34	3.76	0.82	0.83			5.91			9.14		5.91	1.63			11.54										4.43	38	5

D4.3 Result analysis for Competition 1

4.4.1.2 Landmark Localization

Single Participant Results: [GGS]

Modality	Region	configuration		aorta_bifurcation	aortic_arch	clavicle_left	clavicle_right	crista_iliaca_left	crista_iliaca_right	symphysis	trachea_bifurcation	trochanter_major_left	trochanter_major_right	trochanter_minor_left	trochanter_minor_right	Average, count
Measure			Euclidean distance													
CT	wb	1	count	0	0	0	0	0	0	0	0	0	0	0	0	
CT	wb	1	count	5	5	5	5	5	5	5	5	5	5	5	5	60
CT	wb	1	min	4,34	2,66	6,31	2,74	1,42	2,39	2,45	2,35	26,74	30,17	4,50	2,51	
CT	wb	1	max	35,77	37,58	10,45	12,25	12,41	13,03	19,60	7,98	42,17	44,18	6,64	6,85	
CT	wb	1	median	17,06	14,86	9,79	3,83	9,55	5,81	6,02	3,38	34,14	32,45	4,90	3,49	
CT	wb	1	average	19,05	17,68	9,27	5,69	7,70	6,12	8,01	3,99	34,37	36,18	5,16	4,06	13,11
Ctce	ThAb	1	count	0	0	3	3	0	0	0	0	0	0	0	0	6
Ctce	ThAb	1	count	5	5	2	2	5	5	5	5	5	5	5	5	54
Ctce	ThAb	1	min	2,82	8,52	13,23	11,37	3,98	1,34	11,72	0,85	35,07	35,24	5,25	5,95	
Ctce	ThAb	1	max	86,02	29,10	19,30	53,33	24,58	24,66	18,63	6,74	44,05	42,13	18,09	18,41	
Ctce	ThAb	1	median	8,48	14,29	16,26	32,35	12,30	8,82	16,89	2,73	36,75	37,99	11,58	14,06	
Ctce	ThAb	1	average	36,22	16,18	16,26	32,35	13,93	10,38	15,59	3,35	37,84	38,31	11,22	12,64	20,36
MRT1	wb	1	count	0	0	0	0	0	0	1	0	0	0	0	0	1
MRT1	wb	1	count	5	5	5	5	5	5	4	5	5	5	5	5	59
MRT1	wb	1	min	51,27	10,81	4,45	5,72	5,35	8,15	8,25	3,83	5,45	13,04	3,83	11,70	
MRT1	wb	1	max	394,28	90,60	28,14	47,84	69,38	35,41	433,29	273,23	108,92	96,37	64,80	253,76	

D4.3 Result analysis for Competition 1

MRT1	wb	1	median	238,71	38,13	12,70	26,49	12,98	16,10	24,13	7,19	9,45	37,52	7,93	16,13	
MRT1	wb	1	average	252,49	43,67	13,05	23,31	23,29	19,21	122,45	61,20	29,57	44,40	18,51	62,40	59,46
MRT1cefs	Ab	1	count	0	5	5	5	0	0	0	5	0	0	1	1	22
MRT1cefs	Ab	1	count	5	0	0	0	5	5	5	0	5	5	4	4	38
MRT1cefs	Ab	1	min	53,93				30,31	20,68	24,22		6,83	3,78	3,04	8,12	
MRT1cefs	Ab	1	max	74,06				221,66	111,07	78,16		97,29	147,37	75,68	50,30	
MRT1cefs	Ab	1	median	57,11				67,91	43,65	46,39		8,54	51,80	17,72	40,48	
MRT1cefs	Ab	1	average	61,28				88,92	57,65	50,86		30,49	59,81	28,54	34,84	51,55

4.4.2 Final Submission

4.4.2.1 Segmentation

Participant	Modality	Region	configuration	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	gallblader	sternum	aorta	trachea	left adrenal gland	right adrenal gland	Average	image count	count of empty images					
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324								
Measure				DICE coefficient																											
[SJ]	CTce	ThAb	1	0,829	0,870	0,822		0,970	0,968																	0,851			0,885	60	10
[LHJ]	CTce	ThAb	1				0,937																					0,937	10		
[LHJ]	CT	wb	1				0,831																					0,831	10		
[WS]	CT	wb	1	0,760	0,623	0,908	0,929	0,958	0,960	0,713						0,833	0,823		0,625									0,813	79		
[WS]	CTce	ThAb	1	0,927	0,923	0,862	0,927	0,966	0,965	0,863						0,811	0,839		0,762									0,885	100		
[WS]	CT	wb	2	0,873	0,871	0,914	0,934	0,959	0,962	0,697						0,813	0,770		0,660									0,845	79		



D4.3 Result analysis for Competition 1

[WS]	CTce	ThAb	2	0,924	0,921	0,874	0,930	0,966	0,966	0,866						0,817	0,845		0,761					0,887	100
[WS]	CT	wb	3	0,867	0,867	0,912	0,931	0,959	0,961	0,713						0,833	0,823		0,646					0,851	79
[WS]	CTce	ThAb	3	0,927	0,922	0,870	0,929	0,966	0,966	0,866						0,816	0,844		0,773					0,888	100
[WS]	CT	wb	4	0,820	0,870	0,913	0,930	0,960	0,962	0,708						0,827	0,828		0,650					0,847	79
[WS]	CTce	ThAb	4	0,930	0,929	0,872	0,930	0,967	0,966	0,870						0,820	0,847		0,753					0,888	100
[WS]	CT	wb	5	0,870	0,904	0,912	0,931	0,958	0,960	0,713						0,827	0,818		0,654					0,855	79
[WS]	CTce	ThAb	5	0,904	0,917	0,867	0,927	0,965	0,965	0,859						0,810	0,842		0,755					0,881	100
[H]-b	CTce	ThAb	1	0,943	0,927		0,942	0,969	0,974							0,864	0,874		0,838					0,916	80
[H]-b	CT	wb	1	0,925	0,866		0,934	0,970	0,970							0,858	0,848		0,823					0,899	63
[H]-f	CTce	ThAb	1	0,912	0,885		0,912	0,956	0,964							0,808	0,806		0,760					0,875	80
[H]-f	CT	wb	1	0,906	0,838		0,907	0,959	0,960							0,808	0,786		0,769					0,866	63
[KDV]	CTce	ThAb	1	0,855	0,805	0,812	0,925	0,955	0,953	0,774	0,111	0,211	0,486	0,037	0,544	0,775	0,693		0,573	0,535	0,592	0,000	0,000	0,626	151
[KDV]	CTce	ThAb	2	0,849	0,795	0,839	0,933	0,957	0,953	0,772	0,013	0,006	0,485	0,031		0,792	0,711		0,274	0,490	0,624			0,595	138
[KDV]	CTce	ThAb	3	0,856	0,805	0,803	0,921	0,955	0,953	0,764	0,124	0,242	0,474	0,039	0,503	0,716	0,672		0,585	0,571	0,356	0,000	0,000	0,608	157
[KDV]	CTce	ThAb	4	0,845	0,803	0,799	0,916	0,954	0,952	0,755	0,124	0,246	0,462	0,037	0,351	0,696	0,658		0,634	0,570	0,239	0,000	0,000	0,591	162
[KDV]	CTce	ThAb	5	0,841	0,802	0,788	0,908	0,952	0,950	0,732	0,134	0,257	0,465	0,035	0,262	0,656	0,634	0,143	0,618	0,578	0,089	0,000	0,000	0,547	170
[GGS]	CTce	ThAb	2	0,913	0,914	0,781	0,908	0,961	0,965	0,683			0,624	0,184	0,460	0,813		0,381	0,635	0,785	0,847	0,250	0,213	0,666	165
[GGS]	MRT1	wb	2	0,808	0,812	0,684	0,827	0,567	0,903	0,709			0,415	0,306	0,196	0,820		0,000	0,006	0,750	0,731	0,151	0,077	0,548	116
[GGS]	CT	wb	2	0,778	0,748	0,671	0,831	0,952	0,960	0,666			0,412	0,450	0,415	0,777	0,747	0,191	0,633	0,741	0,840	0,067	0,186	0,615	133
[GGS]	MRT1cefs	Ab	2	0,845	0,880	0,659	0,834	0,528	0,725	0,205			0,077		0,372	0,640		0,043		0,525		0,048	0,020	0,457	99
[JM]	CT	wb	1	0,784	0,787	0,697	0,860	0,971	0,973	0,685	0,551	0,498	0,718	0,549	0,408	0,806	0,787	0,276	0,742	0,748	0,888	0,353	0,355	0,672	189
[JM]	CTce	ThAb	1	0,904	0,889	0,717	0,882	0,958	0,962	0,674	0,444	0,453	0,523	0,410	0,406	0,781	0,799	0,484	0,714	0,742	0,845	0,331	0,341	0,663	195



D4.3 Result analysis for Competition 1

[JM]	CT	wb	2	0,746	0,790	0,703	0,866	0,972	0,974	0,698	0,408	0,224	0,543	0,382	0,305	0,784	0,776	0,090	0,746	0,740	0,899	0,164	0,137	0,597	189
[JM]	CTce	ThAb	2	0,851	0,862	0,671	0,860	0,949	0,955	0,646	0,382	0,160	0,455	0,345	0,423	0,718	0,761	0,351	0,680	0,660	0,822	0,231	0,258	0,602	195
[JM]	CT	wb	3	0,784	0,785	0,645	0,860	0,971	0,975	0,685	0,507	0,385	0,623	0,480	0,373	0,806	0,787	0,264	0,760	0,753	0,911	0,345	0,305	0,650	189
[JM]	CTce	ThAb	3	0,886	0,883	0,730	0,887	0,959	0,963	0,679	0,474	0,363	0,506	0,372	0,410	0,755	0,791	0,469	0,721	0,762	0,855	0,302	0,342	0,655	195
[JM]	CT	wb	4	0,781	0,744	0,693	0,846	0,966	0,973	0,641	0,547	0,485	0,703	0,534	0,397	0,803	0,777	0,211	0,761	0,748	0,919	0,373	0,315	0,661	189
[JM]	CTce	ThAb	4	0,910	0,884	0,721	0,882	0,959	0,962	0,665	0,408	0,452	0,430	0,311	0,330	0,794	0,785	0,477	0,693	0,758	0,849	0,316	0,341	0,646	195
[JM]	CT	wb	5	0,682	0,649	0,581	0,821	0,941	0,962	0,586	0,516	0,519	0,668	0,542	0,355	0,765	0,738	0,102	0,737	0,716	0,920	0,306	0,224	0,616	189
[JM]	CTce	ThAb	5	0,906	0,835	0,690	0,866	0,957	0,960	0,629	0,170	0,411	0,275	0,208	0,169	0,786	0,742	0,349	0,616	0,741	0,838	0,256	0,297	0,585	195

Participant	Modality	Region	configuration	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	Average	image count	count of empty images	
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324				
			Measure	Adjusted Rand Index																							
[SJ]	CTce	ThAb	1	0,828	0,870	0,821		0,967	0,966												0,851			0,884	60	10	
[LHJ]	CTce	ThAb	1				0,934																	0,934	10		
[LHJ]	CT	wb	1				0,830																	0,830	10		
[WS]	CT	wb	1	0,760	0,622	0,908	0,927	0,957	0,959	0,712						0,833	0,823		0,625					0,813	79		
[WS]	CTce	ThAb	1	0,926	0,923	0,861	0,923	0,963	0,962	0,862						0,810	0,839		0,762					0,883	100		
[WS]	CT	wb	2	0,873	0,870	0,913	0,933	0,957	0,961	0,696						0,812	0,769		0,660					0,845	79		
[WS]	CTce	ThAb	2	0,924	0,921	0,873	0,926	0,964	0,963	0,865						0,816	0,845		0,760					0,886	100		



D4.3 Result analysis for Competition 1

[WS]	CT	wb	3	0,867	0,867	0,912	0,930	0,958	0,960	0,713						0,833	0,823		0,645							0,851	79
[WS]	CTce	ThAb	3	0,927	0,922	0,869	0,925	0,964	0,963	0,865						0,815	0,843		0,773							0,887	100
[WS]	CT	wb	4	0,820	0,870	0,913	0,929	0,959	0,961	0,707						0,827	0,827		0,650							0,846	79
[WS]	CTce	ThAb	4	0,930	0,928	0,871	0,926	0,965	0,963	0,870						0,819	0,847		0,752							0,887	100
[WS]	CT	wb	5	0,869	0,904	0,912	0,929	0,957	0,959	0,713						0,827	0,818		0,654							0,854	79
[WS]	CTce	ThAb	5	0,904	0,916	0,866	0,923	0,963	0,962	0,858						0,809	0,841		0,754							0,880	100
[H]-b	CTce	ThAb	1	0,942	0,926		0,939	0,966	0,971							0,864	0,874		0,837							0,915	80
[H]-b	CT	wb	1	0,925	0,866		0,933	0,969	0,969							0,858	0,847		0,822							0,899	63
[H]-f	CTce	ThAb	1	0,912	0,885		0,907	0,953	0,960							0,807	0,805		0,759							0,873	80
[H]-f	CT	wb	1	0,906	0,837		0,905	0,958	0,959							0,808	0,786		0,769							0,866	63
[KDV]	CTce	ThAb	1	0,854	0,804	0,811	0,921	0,952	0,949	0,773	0,109	0,209	0,486	0,037	0,544	0,774	0,692		0,572	0,533	0,591	0,000	0,000			0,624	151
[KDV]	CTce	ThAb	2	0,848	0,794	0,838	0,929	0,954	0,949	0,771	0,011	0,005	0,485	0,031		0,791	0,710		0,274	0,488	0,624					0,594	138
[KDV]	CTce	ThAb	3	0,855	0,804	0,801	0,917	0,952	0,949	0,762	0,123	0,241	0,473	0,039	0,502	0,715	0,671		0,585	0,570	0,356	0,000	0,000			0,607	157
[KDV]	CTce	ThAb	4	0,845	0,803	0,797	0,911	0,951	0,948	0,754	0,122	0,244	0,462	0,037	0,351	0,695	0,656		0,634	0,568	0,238	0,000	0,000			0,589	162
[KDV]	CTce	ThAb	5	0,840	0,801	0,787	0,903	0,949	0,946	0,731	0,132	0,255	0,465	0,035	0,261	0,654	0,632	0,143	0,617	0,575	0,089	0,000	0,000			0,545	170
[GGS]	CTce	ThAb	2	0,912	0,914	0,780	0,903	0,958	0,962	0,681			0,624	0,184	0,459	0,812		0,381	0,635	0,784	0,847	0,250	0,213			0,665	165
[GGS]	MRT1	wb	2	0,808	0,812	0,683	0,823	0,558	0,901	0,709			0,415	0,306	0,196	0,820		0,000	0,006	0,750	0,731	0,151	0,077			0,547	116
[GGS]	CT	wb	2	0,778	0,748	0,670	0,829	0,951	0,958	0,665			0,412	0,450	0,415	0,777	0,747	0,191	0,633	0,741	0,840	0,067	0,186			0,614	133
[GGS]	MRT1cefs	Ab	2	0,843	0,879	0,655	0,818	0,515	0,713	0,203			0,077		0,370	0,638		0,042		0,524		0,048	0,020			0,453	99
[JM]	CT	wb	1	0,784	0,787	0,696	0,858	0,970	0,972	0,685	0,551	0,497	0,718	0,548	0,408	0,805	0,787	0,276	0,742	0,747	0,888	0,353	0,355			0,671	189
[JM]	CTce	ThAb	1	0,903	0,889	0,716	0,877	0,954	0,958	0,672	0,442	0,451	0,523	0,410	0,406	0,780	0,798	0,484	0,714	0,741	0,845	0,331	0,340			0,662	195
[JM]	CT	wb	2	0,746	0,790	0,703	0,863	0,971	0,974	0,698	0,407	0,222	0,543	0,382	0,305	0,784	0,776	0,090	0,746	0,740	0,899	0,164	0,137			0,597	189
[JM]	CTce	ThAb	2	0,850	0,861	0,669	0,854	0,945	0,951	0,644	0,379	0,155	0,454	0,344	0,423	0,717	0,759	0,351	0,679	0,659	0,822	0,231	0,258			0,600	195
[JM]	CT	wb	3	0,784	0,784	0,645	0,858	0,970	0,974	0,685	0,506	0,384	0,622	0,480	0,372	0,805	0,787	0,264	0,760	0,753	0,911	0,345	0,305			0,650	189
[JM]	CTce	ThAb	3	0,885	0,882	0,728	0,881	0,956	0,959	0,677	0,472	0,359	0,505	0,372	0,409	0,753	0,790	0,469	0,721	0,761	0,855	0,302	0,342			0,654	195



D4.3 Result analysis for Competition 1

[JM]	CT	wb	4	0,781	0,744	0,692	0,844	0,966	0,972	0,641	0,546	0,484	0,703	0,533	0,397	0,803	0,777	0,211	0,761	0,747	0,919	0,373	0,315	0,660	189
[JM]	CTce	ThAb	4	0,910	0,883	0,719	0,876	0,956	0,958	0,663	0,407	0,450	0,430	0,311	0,329	0,793	0,784	0,477	0,693	0,757	0,848	0,316	0,340	0,645	195
[JM]	CT	wb	5	0,682	0,649	0,581	0,818	0,940	0,961	0,585	0,515	0,518	0,667	0,542	0,355	0,765	0,737	0,102	0,737	0,715	0,920	0,306	0,224	0,616	189
[JM]	CTce	ThAb	5	0,905	0,834	0,688	0,859	0,954	0,956	0,627	0,165	0,410	0,273	0,208	0,168	0,785	0,741	0,348	0,615	0,740	0,838	0,256	0,297	0,583	195

Participant	Modality	Region	configuration	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	gallblader	sternum	aorta	trachea	left adrenal gland	right adrenal gland	Average	image count	count of empty images				
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324							
Measure				Interclass Correlation																										
[SJ]	CTce	ThAb	1	0,829	0,870	0,822		0,970	0,968																0,851			0,885	60	10
[LHJ]	CTce	ThAb	1				0,937																					0,937	10	
[LHJ]	CT	wb	1				0,831																					0,831	10	
[WS]	CT	wb	1	0,760	0,623	0,908	0,929	0,958	0,960	0,713						0,833	0,823		0,625									0,813	79	
[WS]	CTce	ThAb	1	0,927	0,923	0,862	0,927	0,966	0,965	0,863						0,811	0,839		0,762									0,885	100	
[WS]	CT	wb	2	0,873	0,871	0,914	0,934	0,959	0,962	0,697						0,813	0,770		0,660									0,845	79	
[WS]	CTce	ThAb	2	0,924	0,921	0,874	0,930	0,966	0,966	0,866						0,817	0,845		0,761									0,887	100	
[WS]	CT	wb	3	0,867	0,867	0,912	0,931	0,959	0,961	0,713						0,833	0,823		0,646									0,851	79	



D4.3 Result analysis for Competition 1

[WS]	CTce	ThAb	3	0,927	0,922	0,870	0,929	0,966	0,966	0,866						0,816	0,844		0,773						0,888	100
[WS]	CT	wb	4	0,820	0,870	0,913	0,930	0,960	0,962	0,708						0,827	0,828		0,650						0,847	79
[WS]	CTce	ThAb	4	0,930	0,929	0,872	0,930	0,967	0,966	0,870						0,820	0,847		0,753						0,888	100
[WS]	CT	wb	5	0,870	0,904	0,912	0,931	0,958	0,960	0,713						0,827	0,818		0,654						0,855	79
[WS]	CTce	ThAb	5	0,904	0,917	0,867	0,927	0,965	0,965	0,859						0,810	0,842		0,755						0,881	100
[H]-b	CTce	ThAb	1	0,943	0,927		0,942	0,969	0,974							0,864	0,874		0,838						0,916	80
[H]-b	CT	wb	1	0,925	0,866		0,934	0,970	0,970							0,858	0,848		0,823						0,899	63
[H]-f	CTce	ThAb	1	0,951	0,938		0,950	0,975	0,979							0,886	0,888		0,859						0,928	80
[H]-f	CT	wb	1	0,940	0,885		0,945	0,976	0,975							0,880	0,866		0,849						0,915	63
[KDV]	CTce	ThAb	1	0,855	0,805	0,812	0,925	0,955	0,953	0,774	0,111	0,211	0,486	0,037	0,544	0,775	0,693		0,573	0,535	0,592	0,000	0,000		0,626	151
[KDV]	CTce	ThAb	2	0,849	0,795	0,839	0,933	0,957	0,953	0,772	0,013	0,006	0,485	0,031		0,792	0,711		0,274	0,490	0,624				0,595	138
[KDV]	CTce	ThAb	3	0,856	0,805	0,803	0,921	0,955	0,953	0,764	0,124	0,242	0,474	0,039	0,503	0,716	0,672		0,585	0,571	0,356	0,000	0,000		0,608	157
[KDV]	CTce	ThAb	4	0,845	0,803	0,799	0,916	0,954	0,952	0,755	0,124	0,246	0,462	0,037	0,351	0,696	0,658		0,634	0,570	0,239	0,000	0,000		0,591	162
[KDV]	CTce	ThAb	5	0,841	0,802	0,788	0,908	0,952	0,950	0,732	0,134	0,257	0,465	0,035	0,262	0,656	0,634	0,143	0,618	0,578	0,089	0,000	0,000		0,547	170
[GGS]	CTce	ThAb	2	0,913	0,914	0,781	0,908	0,961	0,965	0,683			0,624	0,184	0,460	0,813		0,381	0,635	0,785	0,847	0,250	0,213		0,666	165
[GGS]	MRT1	wb	2	0,808	0,812	0,684	0,827	0,567	0,903	0,709			0,415	0,306	0,196	0,820		0,000	0,006	0,750	0,731	0,151	0,077		0,548	116
[GGS]	CT	wb	2	0,778	0,748	0,671	0,831	0,952	0,960	0,666			0,412	0,450	0,415	0,777	0,747	0,191	0,633	0,741	0,840	0,067	0,186		0,615	133
[GGS]	MRT1cefs	Ab	2	0,845	0,880	0,659	0,834	0,528	0,725	0,205			0,077		0,372	0,640		0,043		0,525		0,048	0,020		0,457	99
[JM]	CT	wb	1	0,784	0,787	0,697	0,860	0,971	0,973	0,685	0,551	0,498	0,718	0,549	0,408	0,806	0,787	0,276	0,742	0,748	0,888	0,353	0,355		0,672	189
[JM]	CTce	ThAb	1	0,904	0,889	0,717	0,882	0,957	0,962	0,674	0,443	0,453	0,523	0,410	0,406	0,781	0,799	0,484	0,714	0,742	0,845	0,331	0,341		0,663	195
[JM]	CT	wb	2	0,746	0,790	0,703	0,866	0,972	0,974	0,698	0,408	0,224	0,543	0,382	0,305	0,784	0,776	0,090	0,746	0,740	0,899	0,164	0,137		0,597	189
[JM]	CTce	ThAb	2	0,851	0,862	0,671	0,860	0,949	0,955	0,646	0,382	0,160	0,455	0,345	0,423	0,718	0,761	0,351	0,680	0,660	0,822	0,231	0,258		0,602	195
[JM]	CT	wb	3	0,784	0,785	0,645	0,860	0,971	0,975	0,685	0,507	0,385	0,623	0,480	0,373	0,806	0,787	0,264	0,760	0,753	0,911	0,345	0,305		0,650	189
[JM]	CTce	ThAb	3	0,886	0,883	0,730	0,887	0,959	0,963	0,679	0,474	0,363	0,506	0,372	0,410	0,755	0,791	0,469	0,721	0,762	0,855	0,302	0,342		0,655	195



D4.3 Result analysis for Competition 1

[JM]	CT	wb	4	0,781	0,744	0,693	0,846	0,966	0,973	0,641	0,547	0,485	0,703	0,534	0,397	0,803	0,777	0,211	0,761	0,748	0,919	0,373	0,315	0,661	189
[JM]	CTce	ThAb	4	0,910	0,884	0,721	0,882	0,959	0,962	0,665	0,408	0,452	0,430	0,311	0,330	0,794	0,785	0,477	0,693	0,758	0,849	0,316	0,341	0,646	195
[JM]	CT	wb	5	0,682	0,649	0,581	0,821	0,941	0,962	0,586	0,516	0,519	0,668	0,542	0,355	0,765	0,738	0,102	0,737	0,716	0,920	0,306	0,224	0,616	189
[JM]	CTce	ThAb	5	0,906	0,835	0,690	0,866	0,957	0,960	0,629	0,170	0,411	0,275	0,208	0,169	0,786	0,742	0,349	0,616	0,741	0,838	0,256	0,297	0,585	195

Participant	Modality	Region	configuration	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	gallblader	sternum	aorta	trachea	left adrenal gland	right adrenal gland	Average	image count	count of empty images				
				29663	29662	86	58	1326	1302	237	40358	40357	29193	7578	170	32249	32248	187	2473	480	1247	30325	30324							
Measure				Average distance																										
[SJ]	CTce	ThAb	1	0,65	0,28	5,96		0,05	0,06												0,34				1,22	60	10			
[LHJ]	CTce	ThAb	1				0,17																		0,17	10				
[LHJ]	CT	wb	1				21,33																		21,33	10				
[WS]	CT	wb	1	1,74	5,21	0,20	0,22	0,15	0,11	1,79						0,52	0,69		2,14						1,28	79				
[WS]	CTce	ThAb	1	0,13	0,14	0,80	0,25	0,09	0,08	0,38						1,02	0,65		0,99						0,45	100				
[WS]	CT	wb	2	0,89	1,14	0,20	0,21	0,20	0,11	2,03						0,97	1,32		1,83						0,89	79				
[WS]	CTce	ThAb	2	0,13	0,14	0,68	0,23	0,09	0,08	0,38						1,00	0,64		1,12						0,45	100				
[WS]	CT	wb	3	0,98	1,10	0,20	0,22	0,15	0,11	1,80						0,55	0,70		1,96						0,77	79				



D4.3 Result analysis for Competition 1

[WS]	CTce	ThAb	3	0,13	0,14	0,72	0,23	0,09	0,08	0,37						1,00	0,63		0,94						0,43	100
[WS]	CT	wb	4	1,92	1,11	0,18	0,23	0,14	0,11	1,74						0,71	0,65		1,87						0,87	79
[WS]	CTce	ThAb	4	0,13	0,13	0,77	0,25	0,09	0,08	0,35						0,96	0,61		1,16						0,45	100
[WS]	CT	wb	5	0,86	0,27	0,20	0,23	0,16	0,11	1,89						0,60	0,81		1,78						0,69	79
[WS]	CTce	ThAb	5	0,27	0,15	0,72	0,24	0,09	0,08	0,40						1,07	0,64		1,09						0,48	100
[H]-b	CTce	ThAb	1	0,12	0,20		0,23	0,34	0,05							0,78	0,54								0,40	80
[H]-b	CT	wb	1	0,15	0,59		0,20	0,07	0,06							0,41	0,53								0,36	63
[H]-f	CTce	ThAb	1	0,12	0,20		0,23	0,34	0,05							0,78	0,54								0,40	80
[H]-f	CT	wb	1	0,15	0,59		0,20	0,07	0,06							0,41	0,53								0,36	63
[KDV]	CTce	ThAb	1	0,92	1,81	1,87	0,49	0,30	0,30	1,08	20,08	13,76	9,74	15,01	9,87	1,27	2,87		14,73	14,74	25,00	236,46	269,77	33,69	151	
[KDV]	CTce	ThAb	2	1,13	2,15	1,29	0,34	0,20	0,30	1,22	21,45	23,27	10,59	15,31		1,22	2,70		63,44	19,05	18,56			11,39	138	
[KDV]	CTce	ThAb	3	0,89	1,79	2,00	0,57	0,21	0,31	1,16	22,50	19,90	8,71	13,77	5,81	2,12	3,09		10,76	10,74	93,98	151,96	247,28	31,45	157	
[KDV]	CTce	ThAb	4	0,99	1,88	2,05	0,67	0,22	0,31	1,24	25,05	23,36	8,56	13,33	11,45	2,34	3,30		6,59	8,24	118,19	149,41	135,97	27,01	162	
[KDV]	CTce	ThAb	5	1,12	1,99	2,34	0,84	0,58	0,58	5,89	24,43	30,25	8,01	26,31	12,33	2,86	3,54	21,82	11,49	5,43	138,9	60,14	124,99	24,19	170	
[GGS]	CTce	ThAb	2	0,34	0,20	1,53	0,65	0,12	0,07	1,51			3,23	5,85	3,47	0,62		6,31	1,26	1,01	0,38	3,90	3,03	1,97	165	
[GGS]	MRT1	wb	2	0,73	0,91	1,02	0,85	95,7	0,36	0,98			2,80	2,40	81,06	0,52		220,10	238,28	0,56	1,28	61,70	37,64	43,93	116	
[GGS]	CT	wb	2	1,67	2,26	2,87	1,29	0,15	0,11	1,64			5,37	2,40	5,36	0,90	1,22	11,99	1,45	0,89	1,89	5,88	6,54	2,99	133	
[GGS]	MRT1cefs	Ab	2	1,27	0,44	1,75	1,65	2,92	1,30	9,85			9,28		5,93	1,55		13,17		4,65		13,66	7,61	5,36	99	
[JM]	CT	wb	1	1,21	1,35	1,94	0,87	0,05	0,04	1,55	3,55	3,93	1,95	1,47	5,52	0,60	0,78	5,94	1,09	1,14	0,17	2,97	3,45	1,98	189	
[JM]	CTce	ThAb	1	0,20	0,24	2,18	0,56	0,08	0,07	1,89	5,98	6,60	4,50	3,34	4,15	0,79	0,76	3,60	0,97	1,19	0,26	3,11	2,57	2,15	195	
[JM]	CT	wb	2	1,63	1,31	1,97	0,78	0,04	0,04	1,46	5,06	8,37	2,85	2,84	6,74	0,72	0,87	17,95	0,98	1,35	0,13	7,66	7,61	3,52	189	
[JM]	CTce	ThAb	2	0,58	0,37	2,58	0,77	0,12	0,09	2,07	8,93	21,14	5,12	4,32	3,80	1,15	0,92	4,42	1,22	1,87	0,36	3,98	4,39	3,41	195	
[JM]	CT	wb	3	1,21	1,21	2,35	0,87	0,05	0,04	1,55	3,97	5,09	2,46	1,97	5,79	0,60	0,78	6,16	0,95	1,19	0,11	2,92	3,67	2,15	189	
[JM]	CTce	ThAb	3	0,29	0,27	2,00	0,51	0,07	0,06	1,88	6,07	10,18	4,38	3,30	4,17	0,93	0,75	3,66	0,90	1,09	0,22	3,35	2,66	2,34	195	
[JM]	CT	wb	4	1,00	1,37	2,20	1,04	0,06	0,04	1,86	3,57	4,04	2,01	1,62	5,80	0,58	0,78	6,94	0,94	1,14	0,10	2,67	3,96	2,09	189	
[JM]	CTce	ThAb	4	0,17	0,26	1,99	0,53	0,07	0,07	2,09	6,77	6,73	4,72	3,71	5,38	0,74	0,83	3,82	1,02	1,12	0,24	3,18	2,57	2,30	195	
[JM]	CT	wb	5	1,40	1,70	3,02	1,35	0,23	0,07	2,24	3,60	4,03	2,46	1,50	6,31	0,72	0,97	8,53	1,10	1,40	0,10	2,87	4,38	2,40	189	

D4.3 Result analysis for Competition 1

[JM]	CTce	ThAb	5	0,17	0,55	2,28	0,70	0,08	0,07	2,72	20,16	7,72	7,25	5,02	10,45	0,83	1,07	5,78	1,50	1,22	0,27	3,65	2,69	3,71	195
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4.4.2.2 Landmark Localization

Participant	Modality	Region	configuration	aorta_bifurcation	aortic_arch	aorticvalve	bronchus_left	bronchus_right	C2	C3	C4	C5	C6	C7	clavicle_left	clavicle_right	coronaria
				Measure Euclidean distance													
[M]	CT	wb	1	79,44	8,55	7,73	2,81	3,34	9,21	12,41	8,36	11,04	11,94	15,77	5,09	11,27	10,34
[M]	Ctce	ThAb	1	5,83	10,98	6,48	6,12	3,87						16,70	5,53	8,25	8,16
[M]	MRT1	wb	1	429,13	10,78	117,64	850,85	116,19	14,11	11,21	15,15	15,32	11,74	14,63	12,53	19,07	
[M]	MRT1cefs	Ab	1	17,06													
[M]	CT	wb	2	79,44	8,55	7,73	2,81	3,34	9,21	12,41	8,36	11,04	11,94	15,77	5,09	11,27	10,34
[M]	Ctce	ThAb	2	19,28	10,98	6,48	6,12	3,87					17,97	16,70	6,00	112,75	8,16
[M]	MRT1	wb	2	429,13	10,78	117,64	850,85	116,19	14,11	11,21	15,15	15,32	11,74	14,63	12,53	19,07	
[M]	MRT1cefs	Ab	2	43,95													
[GGS]	CT	wb	1	47,38	14,67	54,25	6,98	16,85	36,43	17,82	21,29	11,33	7,63	9,56	5,86	11,09	20,33
[GGS]	CTce	ThAb	1														
[GGS]	MRT1	wb	1	91,83	37,12	200,68	74,45	95,08	16,54	127,65	282,72	127,35	125,01	351,08	9,81	17,56	
[GGS]	MRT1cefs	Ab	1	63,99		192,35											

D4.3 Result analysis for Competition 1

[GGS]	CT	wb	2	35,48	26,87	59,54	18,85	38,17	287,49	302,63	317,14	332,48	347,64	363,65	25,83	14,47	489,67
[GGS]	CTce	ThAb	2														
[GGS]	MRT1	wb	2	127,26	136,16	189,02	125,52	138,81	96,47	257,13	304,72	229,45	225,79	328,86	13,45	36,47	
[GGS]	MRT1cefs	Ab	2	56,47		216,46											

Participant	Modality	Region	configuration	crista_iliaca_left	crista_iliaca_right	eye_left	eye_right	ischiadicum_left	ischiadicum_right	L1	L2	L3	L4	L5	renalpelvis_left	renalpelvis_right	sternoclavicular_left
Measure				Euclidean distance													
[M]	CT	wb	1	13,27	11,31	3,31	2,82	3,31	3,89	24,30	120,40	23,75	15,48	11,92	56,18	85,01	3,36
[M]	CTce	ThAb	1	13,77	14,84			14,18	13,70	14,62	6,16	16,40	16,17	18,20	6,77	20,55	3,34
[M]	MRT1	wb	1	63,94	13,44	12,01	1,99	11,24	9,52	20,28	9,03	28,07	23,02	11,94	51,95	50,99	204,31
[M]	MRT1cefs	Ab	1	64,85	38,16			47,75	35,59	20,57	13,38	11,75	20,01	29,68	22,30	45,96	
[M]	CT	wb	2	13,27	11,31	3,31	2,82	3,31	3,89	24,30	120,40	23,75	15,48	11,92	56,18	85,01	3,36
[M]	CTce	ThAb	2	13,77	14,84			14,18	13,70	14,62	6,16	16,40	16,17	18,20	6,77	20,55	3,34
[M]	MRT1	wb	2	63,94	13,44	12,01	1,99	11,24	9,52	20,28	9,03	28,07	27,99	32,56	51,95	50,99	204,31
[M]	MRT1cefs	Ab	2	86,28	41,73			35,89	37,69	16,38	11,85	13,68	50,67	99,38	22,30	43,96	
[GGS]	CT	wb	1	10,63	12,44	96,25	88,24	10,00	10,08	37,39	22,13	28,47	22,14	23,20	58,57	79,58	11,51
[GGS]	CTce	ThAb	1														
[GGS]	MRT1	wb	1	59,92	19,28	279,49	282,47	46,87	40,57	40,67	55,68	95,44	89,66	35,43	48,75	53,31	118,18
[GGS]	MRT1cefs	Ab	1	69,59	37,35			63,36	70,15	49,98	43,27	62,16	56,83	57,32	76,30	45,46	
[GGS]	CT	wb	2	11,23	10,72	81,68	75,66	19,03	16,72	33,90	21,34	30,92	28,29	24,47	60,98	71,83	20,87

D4.3 Result analysis for Competition 1

[GGS]	CTce	ThAb	2														
[GGS]	MRT1	wb	2	123,02	64,24	193,16	192,99	80,45	82,15	98,95	85,85	143,08	124,96	64,53	64,76	106,75	149,29
[GGS]	MRT1cefs	Ab	2	68,54	44,10			60,01	77,91	49,57	55,60	70,31	57,68	45,07	72,45	56,77	

Participant	Modality	Region	configuration	sternoclavicular_right	symphysis	Th1	Th2	Th3	Th4	Th5	Th6	Th7	Th8	Th9	Th10	Th11	Th12
				Measure Euclidean distance													
[M]	CT	wb	1	2,52	7,23	14,15	14,62	11,76	9,51	39,36	4,82	7,04	12,35	12,44	12,58	26,55	20,75
[M]	CTce	ThAb	1	3,77	4,41	11,10	9,86	7,07	9,17	13,21	15,77	17,27	11,85	19,19	25,32	22,96	26,60
[M]	MRT1	wb	1	122,02	13,19	12,81	60,55	13,84	14,10	75,80	9,80	55,59	13,35	20,19	67,44	15,57	18,93
[M]	MRT1cefs	Ab	1		60,77											18,85	9,17
[M]	CT	wb	2	2,52	7,23	14,15	14,62	11,76	9,51	39,36	4,82	7,04	12,35	12,44	12,58	26,55	20,75
[M]	CTce	ThAb	2	3,77	4,41	11,10	9,86	7,07	9,17	13,21	15,77	17,27	11,85	19,19	25,32	22,96	26,60
[M]	MRT1	wb	2	122,02	80,90	12,81	60,55	13,84	98,87	82,53	9,80	55,59	13,35	20,19	67,44	15,57	18,93
[M]	MRT1cefs	Ab	2		53,87								309,45	163,17	36,62	20,36	8,04
[GGS]	CT	wb	1	4,89	10,73	14,04	19,86	12,29	24,66	21,08	33,18	38,44	55,84	62,10	70,65	38,77	32,68
[GGS]	CTce	ThAb	1														
[GGS]	MRT1	wb	1	143,15	237,55	216,69	36,27	46,46	81,69	184,68	137,01	145,01	196,76	152,79	188,43	140,11	51,38
[GGS]	MRT1cefs	Ab	1		48,19						178,79	156,32	187,26	168,70	84,32	89,30	71,10

D4.3 Result analysis for Competition 1

[GGS]	CT	wb	2	12,15	11,44	15,20	21,96	18,07	31,90	42,12	48,49	51,64	59,64	55,86	66,80	46,44	41,86
[GGS]	CTce	ThAb	2														
[GGS]	MRT1	wb	2	178,47	191,88	252,39	179,22	137,58	185,91	165,64	166,52	155,77	184,15	139,07	195,83	163,43	117,66
[GGS]	MRT1cefs	Ab	2		59,76						186,75	164,59	192,11	180,75	88,95	85,63	61,47

Participant	Modality	Region	configuration	trachea_bifurcation	trochanter_major_left	trochanter_major_right	trochanter_minor_left	trochanter_minor_right	tuberculum_left	tuberculum_right	vci_bifurcation	ventricle_left	ventricle_right	xiphoides			
Measure				Euclidean distance													
[M]	CT	wb	1	2,60	4,58	6,19	4,97	4,49	120,91	7,69	10,19	4,72	5,28	122,47			
[M]	CTce	ThAb	1	4,94	6,27	3,70	2,82	2,67	12,68	83,16	14,14			14,32			
[M]	MRT1	wb	1	9,94	38,84	97,45	7,47	9,13	53,16	20,11	239,12	803,14	1076,85	154,09			
[M]	MRT1cefs	Ab	1		89,97	71,75	162,23	41,91			19,99			39,69			
[M]	CT	wb	2	2,60	4,58	6,19	4,97	4,49	120,91	7,69	10,19	4,72	5,28	122,47			
[M]	CTce	ThAb	2	4,94	6,27	3,70	39,47	70,06	81,20	83,16	14,14			14,32			
[M]	MRT1	wb	2	10,47	38,84	97,45	7,47	9,13	53,16	20,11	239,12	803,14	1076,85	154,09			
[M]	MRT1cefs	Ab	2		85,97	71,75	131,36	65,47			118,12			39,69			
[GGS]	CT	wb	1	4,68	5,22	5,05	9,29	6,57	8,45	11,59	16,14	6,32	7,14	28,76			
[GGS]	CTce	ThAb	1														
[GGS]	MRT1	wb	1	17,00	37,06	64,89	55,54	157,91	17,50	17,60	88,35	129,68	116,43	228,08			



D4.3 Result analysis for Competition 1

[GGS]	MRT1cefs	Ab	1		136,15	68,21	128,36	30,60			84,05			210,03			
[GGS]	CT	wb	2	12,14	4,44	4,77	8,53	7,37	27,21	16,02	22,82	15,41	12,70	40,14			
[GGS]	CTce	ThAb	2														
[GGS]	MRT1	wb	2	110,16	71,51	103,12	91,23	166,14	129,53	127,55	103,08	150,13	167,94	217,86			
[GGS]	MRT1cefs	Ab	2		127,11	82,24	125,94	52,36			80,31			223,80			

Volume				10000086	10000087	10000088	10000089	10000090	10000092	10000094	10000095	10000096	10000099
total landmarks				53	53	53	53	52	53	53	53	53	53
Measure				percentage contribution									

[M]	CT	wb	1	100%	100%	100%	100%	100%	100%	100%			100%
[M]	CT	wb	2	100%	100%	100%	100%	100%	100%	100%			100%
[GGS]	CT	wb	1	100%	100%	100%	100%	100%	100%	100%			100%
[GGS]	CT	wb	2	100%	100%	100%	100%	100%	100%	100%			100%

Volume				10000307	10000308	10000309	10000310	10000311	10000342	10000343	10000419	10000427	10000428
total landmarks				24	18	16	22	19	21	16	20	18	19
Measure				percentage contribution									

[M]	MRT1cefs	Ab	1		61%	56%	50%	32%	100%	44%	30%		
[M]	MRT1cefs	Ab	2		100%	100%	95%	100%	100%	100%	100%		
[GGS]	MRT1cefs	Ab	1	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%
[GGS]	MRT1cefs	Ab	2	100%	100%	100%	100%	100%	100%	100%	100%	100%	100%

D4.3 Result analysis for Competition 1

Volume				10000137	10000138	10000140	10000141	10000142	10000143	10000145	10000147	10000148	10000149
total landmarks				41	43	43	42	40	41	39	39	44	37
Measure				percentage contribution									
[M]	CTce	ThAb	1	95%	95%	95%	95%	100%	98%	97%	100%	95%	100%
[M]	CTce	ThAb	2	100%	100%	100%	98%	100%	100%	100%	103%	100%	100%
[GGS]	CTce	ThAb	1										
[GGS]	CTce	ThAb	2										

Volume				10000095	10000096	10000559	10000560	10000573	10000574	10000575	10000577	10000592
total landmarks				49	46	49	49	45	49	47	49	48
Measure				percentage contribution								
[M]	MRT1	wb	1	100%	100%	98%	98%	93%	98%	100%	100%	96%
[M]	MRT1	wb	2	100%	100%	100%	100%	100%	100%	100%	100%	100%
[GGS]	MRT1	wb	1	100%	100%	98%	98%	93%	98%	100%	100%	96%
[GGS]	MRT1	wb	2	100%	100%	100%	100%	100%	100%	100%	100%	100%

5 Conclusion

We provided an analysis of the segmentations submitted by the participants for the two cycles (Anatomy1 and Anatomy2) of the Benchmark 1 (segmentation and identification) of the VISCERAL project. The results are provided using four metrics, namely the Dice coefficient, the adjusted Rand index, the interclass correlation, and the average distance. Further deeper analysis of the benchmarks and their results, based on a deeper study of the results including the knowledge concluded from this study, will be provided in a separate deliverable, namely Deliverable D 4.5, Result meta-analysis.