

Analysis on the use of Multi-Sequence MRI Series for Segmentation of Abdominal Organs

M A SELVER¹, E SELVİ², E KAVUR², O DİCLE³

¹Dokuz Eylül University, Department of Electrical and Electronics Engineering, Tınaztepe Campus, 35160, Buca, İzmir, TURKEY

²Dokuz Eylül University, Institute of Natural and Applied Sciences, Tınaztepe Campus, 35160, Buca, İzmir, TURKEY

³Dokuz Eylül University, Faculty of Medicine, Department of Radiology, Tınaztepe Campus, Balçova, İzmir, TURKEY

E-mail: alper.selver@deu.edu.tr, esref.selvi@gmail.com, oguz.dicle@deu.edu.tr

Abstract. Segmentation of abdominal organs from MRI data sets is a challenging task due to various limitations and artefacts. During the routine clinical practice, radiologists use multiple MR sequences in order to analyze different anatomical properties. These sequences have different characteristics in terms of acquisition parameters (such as contrast mechanisms and pulse sequence designs) and image properties (such as pixel spacing, slice thicknesses and dynamic range). For a complete understanding of the data, computational techniques should combine the information coming from these various MRI sequences. These sequences are not acquired in parallel but in a sequential manner (one after another). Therefore, patient movements and respiratory motions change the position and shape of the abdominal organs. In this study, the amount of these effects is measured using three different symmetric surface distance metrics performed to three dimensional data acquired from various MRI sequences. The results are compared to intra and inter observer differences and discussions on using multiple MRI sequences for segmentation and the necessities for registration are presented.

1. Introduction

Magnetic Resonance Imaging (MRI) can provide very detailed and contemporary mappings of a patient through the use of different sequences. Therefore, MRI has become a unique tool in radiology for diagnostic imaging. The abdominal organs can be analyzed more precisely using these various sequences. Once an abdominal organ is segmented in each sequence, the results can be fused to extract the information of interest instead of using a single data. Moreover, segmentation of abdominal organs is a very challenging field of application due to the overlapping intensity ranges of the organs, variations in human anatomy and pathology. Therefore, these different MRI sequences can also be used to improve the segmentation accuracy. Since it is necessary to analyze and visualize abdominal organs (i.e. liver, right/left kidneys, spleen, pancreas, gall bladder) for several medical procedures, the analysis of these sequences are necessary in order to test their usability for data fusion.

Multiple MR sequences, which are acquired during the routine clinical practice, are being used by radiologists to help diagnosis. These sequences are sequentially acquired and therefore affected by two kinds of differences: i) differences in acquisition parameters such as contrast mechanisms and pulse



sequence designs, ii) differences in image characteristics such as pixel spacing, slice thicknesses and dynamic range. To be able to use the information coming from these various MRI sequences in computational techniques such as segmentation and fusion, patient movements and respiratory motions should be at acceptable levels. For instance, these levels should preferably be lower than inter- and intra-observer variations on manual organ border delineation. In this study, the amount of these effects is measured using three different symmetric surface distance metrics that are performed to evaluate three dimensional data acquired from various MRI sequences. The results are compared to intra- and inter- observer differences reported in the literature and discussions on using multiple MRI sequences for segmentation and the necessities for registration are presented.

2. Datasets

The analyses are performed on MRI DICOM series, which are collected from the PACS of Dokuz Eylül University Radiology Department. The data sets were acquired using a 1.5 Tesla Philips MRI system, which produces 12 bit images having 256 x 256 pixels. Four different MRI sequences (i.e. T1-DUAL (in-phase and out-phase), T2-SPIR, THRIVE, SSH) are used to test the proposed method.

The sequences are used to scan the same part of the body but each sequence is obtained from a different combination of radiofrequency pulses and gradients. Since, the name of the sequences depends on the vendor, the above mentioned sequence acronyms are explained below [1, 2].

SPIR is the abbreviation for “Spectral Pre-saturation Inversion Recovery” and it is being used as a hybrid imaging sequence. The SPIR sequence uses T2-weighted contrast mechanism for imaging. It relies on selective suppression of fat protons [3]. The pre-saturation pulse is applied separately to each slice selection gradient. This sequence requires sensitive adjustment of calibration and a very homogenous magnetic field. The above mentioned features of SPIR makes it a preferred sequence to study liver, because the liver parenchyma can be analyzed very well with suppression of the fat content inside the parenchyma. Especially, mass lesions belong to parenchyma are more visible in this sequence. Because of being T2-weighted, it is possible to navigate the vessels within liver since they appear hyper-intense. The liver border appearance gets visually clearer, because of the suppression of the fat tissue around the liver. The adjacent abdominal organs and tissues such as gall bladder, duodenum contents, pancreas and right kidney become more separable from liver with their high-valued signal. One more important contribution of the SPIR sequence is its low sensitivity to motion. This feature provides minimization of the artifacts that adversely affects image quality in liver studies.

T1-DUAL (in-phase and out-phase) is a fat suppression sequence, which uses the difference in T1 times of fat and water protons. The signal is acquired twice: first when water and fat protons are in phase and second, when they are out of phase (while exciting protons are returning to their first position). For 1.5 Tesla devices the in-phase time, which water and fat protons are in same direction is 4,6 millisecond and the out-phase time, which fat and water protons are opposite directions, is 2,3 milliseconds. By determining TE (Time of Echo) value with this information, fat suppression is accomplished by subtracting corresponding frequencies of fat and water signals. This sequence is very useful to understand the fat content in lesions. Since T1-DUAL is a T1-weighted sequence, it is very effective to identify blood and tissues that are rich in protein. This sequence also helps determining the level of liver lubrication. In out-phase images, the border of the organs appear to be black, due to the sudden change in the amount of fat and water at the organ boundaries that cancels the acquired signal. This property of T1-DUAL is sometimes used for border delineation algorithms [4].

SSH refers to single shot imaging and it is a very useful sequence for the abdominal analysis, which are affected by the motion caused due to vessels, intestinal gas and diaphragm. By using this sequence, steady liquids can be studied very well, which allows analysis of biliary tracts.

THRIVE is a fast imaging sequence that is obtained by scanning the liver consecutive in a short time with thin slices to get respond of a known lesion to a contrast agent. THRIVE provides observation of the signal increase originating from the contrast agent instead of image quality.

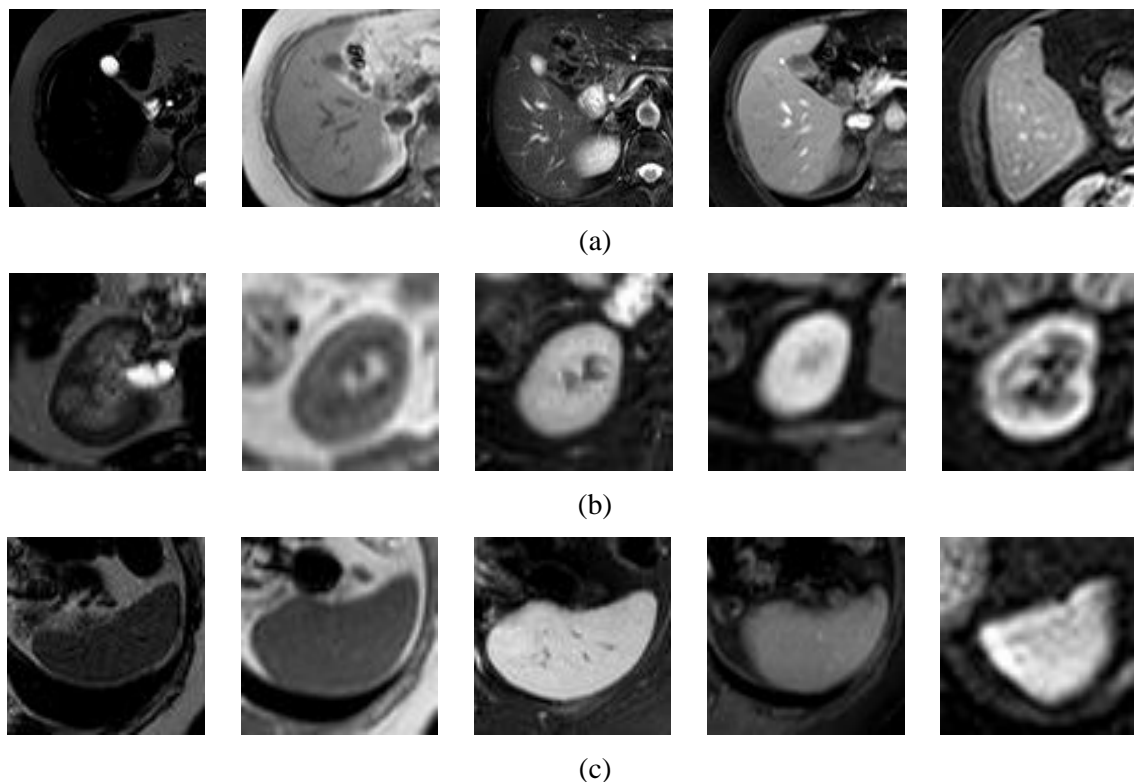


Figure 1. Images acquired from different MRI sequences used in this study. (a) liver, (b) right kidney, (c) spleen (From left to right: SSH, T1-DUAL, T2-SPIR, WATS, THRIVE)

In this study, MR images obtained from 21 patients are used. The details about the characteristics of these data sets are given in Table 1. Four different sequences are acquired for each patient except one, who has 3 different sequences. While T2-SPIR, SSH and T1-DUAL sequences are common for each 21 patient, 20 patient has either THRIVE (7) or T1-WATS (13) sequences. For T2-SPIR, which is common for all 21 patients, slice thickness value changes between 7.7 mm and 9 mm and has an average value equal to 8.6 mm. Moreover, the x-y spacing in this sequence changes between 1.63 mm and 1.89 mm with an average of 1.53 mm. The number of slices for T2-SPIR sequence is 26 as minimum, 36 as maximum and 30 as average. On the other hand T1-DUAL sequences include two different series mentioned above. Each series has same x-y spacing, slice thickness and number of slices. For T1-DUAL sequences, slice thickness has a value between 5.5 mm and 9 mm with an average of 7.84 mm. The x-y spacing value in this sequence is between 1.44 mm and 1.89 mm and the average value is 1.61 mm. While the average number of slices is 32.8, minimum number is 26 and maximum number is 50. SSH sequence has slice thickness between 5.5 mm and 9 mm with an average of 7.84 mm. For SSH, sequences x-y spacing changes between 1,34mm and 1,82mm and has an average as 56mm. While average number of slices is 32.2, it is 50 at most and 25 at least. T1-WATS sequence, which is acquired for 13 patients, has slice thickness value between 5.5 mm and 9 mm like T1-DUAL and SSH sequences with an average of 7.9 mm. While x-y spacing in T1-WATS sequences changes between 1.36 mm and 1.67 mm, the average value of x-y spacing is 1.43mm. Finally, THRIVE sequences, which only have 7 data sets, has differences from the other sequences. The slice thickness is smaller and does not change between patients for THRIVE. All THRIVE series have 2.5 mm slice thickness. Since the slice thickness is smaller, THRIVE sequence has more number of slices in one series. Number of slices is 110 at most and 80 at least. Average number of slices is 92.9. For THRIVE, x-y spacing changes between 1.56 mm and 1.97 mm with an average 1.67 mm.

Slice thickness is one of the priority factors for the volume segmentation. Although it seems like that small slice thickness is better for volume segmentation, it is shown that small slice thickness is not always better [5].

Table 1. The list of the data sets and the MR sequences used in this study.

MRI Sequence	# of images	Slice Thickness			x- / y- spacing			Number of Slices		
		Min	Max	Average	Min	Max	Average	Min	Max	Average
T2-SPIR	21	7,7	9	8,6	1,36	1,89	1,53	26	36	30
T1-DUAL	21	5,5	9	7,84	1,44	1,89	1,61	26	50	32,8
THRIVE	7	2,5	2,5	2,5	1,56	1,97	1,67	80	110	92,9
T1-WATS	13	5,5	9	7,9	1,36	1,67	1,43	26	40	30,6
SSH	21	5,5	9	8,1	1,34	1,82	1,56	25	50	32,2

3. Method

As mentioned in the earlier sections, the aim is to evaluate the similarity (i.e. position and shape) of the same organ in different sequences of the same patient so that the effects of patient movement and respiratory motions can be analyzed. The comparison of the data sets acquired for the same patient using different sequences is performed using Symmetric Surface Distance (SSD) metrics, which are designed to compare two objects in three dimensions [6]. SSD is based on the distance between surface voxels of two volumes, which correspond to the segmented (V_S) and the reference (V_R) data. Surface voxels can be defined as the voxels having at least one non-object voxel within their 18-neighbourhood. SSD is obtained by calculating the Euclidean distance for each surface voxel of V_R to the closest surface voxel of V_S .

$$d(v_r, S(V_S)) = \min_{\substack{v_r \in S(V_R) \\ \forall q \in S(V_S)}} (\|v_r - q\|) \quad (4.1)$$

Here, $s(V_S)$ is the set of surface voxels of V_S and $s(V_R)$ is the set of surface voxels of V_R .

There are three different SSD measures, each of which aim to evaluate a different characteristic of the difference between the segmented and the reference objects.

The first metric is the Average Symmetric Surface Distance (ASSD), which is calculated by averaging the SSD values of each voxel and determined as follows:

$$ASSD(V_R, V_S) = \frac{1}{|S(V_S)| + |S(V_R)|} \left(\sum_{v_r \in S(V_R)} d(v_r, S(V_S)) + \sum_{v_s \in S(V_S)} d(v_s, S(V_R)) \right) (mm) \quad (4.2)$$

For perfect segmentation, ASSD is equal to 0. ASSD metric is not affected much by local errors even if they are big. Therefore, it provides information on the similarity of two objects in general.

The second metric is the Root Mean Square SSD (RMSSD), which is calculated similar to ASSD but with an important difference. The square of the distances between surface voxels are calculated. This difference results with exaggeration of the large distances, while smaller errors do not change much. RMSSD can be calculated using:

$$RMSSD(V_R, V_S) = \sqrt{\frac{1}{|S(V_S)| + |S(V_R)|} \left(\sum_{v_r \in S(V_R)} d^2(v_r, S(V_S)) + \sum_{v_s \in S(V_S)} d^2(v_s, S(V_R)) \right)} (mm) \quad (4.3)$$

Similar to ASSD, RMSSD should be 0 for the perfect segmentation. The RMSSD also provide a general information about the error rate, but it is also gives a better opinion about the distribution of the distance error when it is compared with ASSD.

The third metric extracted using SSD is the Maximum Symmetric Surface Distance (MSSD), which is calculated as:

$$MSSD(V_R, V_S) = \max \left\{ \max_{v_r \in S(V_R)} \{d(v_r, S(V_S))\}, \max_{v_s \in S(V_S)} \{d(v_s, S(V_R))\} \right\} (mm) \quad (4.4)$$

MSSD is equal to zero for the perfect segmentation, but the information provided by MSSD is significantly different than ASSD and MSSD. By calculating the maximum values of the error, it provides the important information about error margin. This information is critically important for the operations, in which the worst case scenario is of particular interest. A good example is surgical planning using the segmented objects.

To determine correlation of different sequences, the voxel dimensions should be converted in millimeters because of the differences x-y spacing and slice thickness.

On the other hand, assessing all these measures helps us to understand specific conditions. For example, for a good segmentation but a local error can be detected by looking these metrics. In this condition MSSD should be high while ASSD is low. If MSSD is close to ASSD, then it can be sign that is because of a shift on one volume in this condition.

4. Simulations and Results

Table 2 and Table 3 present the calculated SSD values for each organ among the selected MRI sequences presented in Table 1.

Table 2. SSD results for liver and spleen (mm)

ASSD					MSSD				
liver	SSH	T1DUAL	T2SPIR	THRIVE	liver	SSH	T1DUAL	T2SPIR	THRIVE
SSH	0	6,4±2,8	6,3±2,9	7,4±5,5	SSH	0	30,9±9,6	30,9±9	32±10,4
T1DUAL	6,4±2,8	0	5,17±1,81	5,24±6,23	T1DUAL	30,9±9,6	0	24,6±8,1	22,4±9,1
T2SPIR	6,3±2,9	5,17±1,81	0	7,37±5,62	T2SPIR	30,9±9	24,6±8,1	0	28,6±10,9
THRIVE	7,4±5,5	5,24±6,23	7,37±5,62	0	THRIVE	32±10,4	22,4±9,1	28,6±10,9	0

RMSSD					RMSSD				
liver	SSH	T1DUAL	T2SPIR	THRIVE	spleen	SSH	T1DUAL	T2SPIR	THRIVE
SSH	0	8,4±3,4	8,1±3,4	9,34±6,2	SSH	0	8,9±10,1	7,1±11	10±11,6
T1DUAL	8,4±3,4	0	6,64	6,55±6,76	T1DUAL	8,9±10,1	0	9,2±12,1	11,3±12,8
T2SPIR	8,1±3,4	8,1±3,46	0	9,1±6,2	T2SPIR	7,1±11	9,2±12,1	0	5,9±6,1
THRIVE	9,4±6,2	6,55±6,76	9,1±6,2	0	THRIVE	10±11,6	11,3±12,8	5,9±6,1	0

ASSD					MSSD				
spleen	SSH	T1DUAL	T2SPIR	THRIVE	spleen	SSH	T1DUAL	T2SPIR	THRIVE
SSH	0	6,1±6,7	5,4±8,4	7,6±9	SSH	0	27,4±2,8	24,9±31	29,6±31,3
T1DUAL	6,1±6,7	0	7,5±9,3	8,9±10	T1DUAL	27,4±2,8	0	32,7±34	34±34,4
T2SPIR	5,4±8,4	7,5±9,3	0	4,8±5,1	T2SPIR	24,9±31	32,7±34	0	17,5±11,5
THRIVE	7,6±9	8,9±10	4,8±5,1	0	THRIVE	29,6±31,3	34±34,4	17,5±11,5	0

Table 3. SSD results for right and left kidneys (mm)

Right kidney	ASSD				Right kidney	MSSD			
	SSH	T1DUAL	T2SPIR	THRIVE		SSH	T1DUAL	T2SPIR	THRIVE
SSH	0	2±1,8	1,9±0,4	5,6±4,5	SSH	0	7,5±0,5	9,5±1,7	17,4±9,28
T1DUAL	2±1,8	0	2,7±0,7	5,2±3,9	T1DUAL	7,5±0,5	0	11,67±2,9	15,4±7,4
T2SPIR	1,9±0,4	2,7±0,7	0	6,7±5,6	T2SPIR	9,5±1,7	11,67±2,9	0	19,2±13,4
THRIVE	5,6±4,5	5,2±3,9	6,7±5,6	0	THRIVE	17,4±9,28	15,4±7,4	19,2±13,4	0

Right kidney	RMSSD				Left kidney	ASSD			
	SSH	T1DUAL	T2SPIR	THRIVE		SSH	T1DUAL	T2SPIR	THRIVE
SSH	0	2,6±0,2	2,6±0,6	7±5,3	SSH	0	2,4±1	2,1±1	3,4±3,4
T1DUAL	2,6±0,2	0	3,6±1,2	6,2±4,5	T1DUAL	2,4±1	0	2,5±0,8	3,1±3,6
T2SPIR	2,6±0,6	3,6±1,2	0	8,4±6,7	T2SPIR	2,1±1	2,5±0,8	0	3,8±3,5
THRIVE	7±5,3	6,2±4,5	8,4±6,7	0	THRIVE	3,4±3,4	3,1±3,6	3,8±3,5	0

Left kidney	MSSD				Left kidney	RMSSD			
	SSH	T1DUAL	T2SPIR	THRIVE		SSH	T1DUAL	T2SPIR	THRIVE
SSH	0	12,8±4,2	10,7±2,2	14,15±6,5	SSH	0	3,12±1,3	2,7±1	4,4±3,9
T1DUAL	12,8±4,2	0	12,3±3,1	13,4±8,2	T1DUAL	3,12±1,3	0	3,32±0,9	4±4,2
T2SPIR	10,7±2,2	12,3±3,1	0	13,2±6,6	T2SPIR	2,7±1	3,32±0,9	0	4,6±4,1
THRIVE	14,15±6,5	13,4±8,2	13,2±6,6	0	THRIVE	4,4±3,9	4±4,2	4,6±4,1	0

As seen on table 1 and table 2, SSD values between different sequences are different from each other. Liver is the biggest organ in the abdominal region and therefore, correlation between livers from different sequences can give us a strong opinion about the correlation of the abdominal region. ASSD values between different sequences are close to each other and they vary between 5.2 mm and 7.4 mm. MSSD values between different sequences are also close to each other like ASSD values. MSSD has values between 22.4 mm and 32 mm. As mentioned before, RMSSD values are in the same order as ASSD with a slight difference that exaggerates the bigger values. The RMSS values are between 8.4 mm and 9.2 mm.

Spleen is the second biggest organ in the abdomen. Although it is smaller than the liver, SSD values of the spleen are close to the SSD values of the liver. The SSD values of the spleen also have a wide range varying between from 4.8 mm to 8.9 mm. The MSSD values for the spleen have a wide range and they change from 17.4 mm to 34.4 mm. The RMSSD values for the spleen in different MRI sequences change between 7.1 mm and 11.3 mm. Moreover, the standard deviations of the all values are much greater than the values of the liver.

When the results for the right kidney are analyzed, it can be seen that the ASSD values between SSH, T1DUAL and T2SPIR are very small, which lie between 1.9 mm and 2.7 mm. On the other hand, THRIVE has greater ASSD values with the other sequences as 5.2 mm to 6.7 mm. The results of the MSSD is not very different from ASSD results. The MSSD values for sequences except THRIVE have small values that are from 7.5 mm to 11.6 mm. However, the MSSD values between the THRIVE and the other sequences are greater than the other ones as they change from 15.4 mm to 19.2 mm.

ASSD, MSSD and RMSSD values of the left kidney are close to the values of the right kidney. The ASSD values are between 2.1 mm and 3.8 mm, the MSSD values are between 10.7 mm and 14.1 mm. Finally, the RMSSD values lie between 2.7 mm and 4.7 mm.

Conclusion

The values of the liver are found close enough for all of the sequences compared to intra- and inter-observer manual delineation differences. Therefore, it can be concluded that liver can be segmented in different sequences and then these results can be combined in order to obtain more accurate results. On the other hand, spleen has more ASSD, MSSD and RMSSD values with greater standard deviation compared to its size. This decreases the reliability of the design of such a combination system for the spleen. Thus, it would be hard to combine the segmentation results of the spleen collected from different MRI sequences. The kidneys have ASSD, MSSD and RMSSD that are close enough compared to their size and they can be used for generating such combinations.

In conclusion, the SSD values of the liver and kidneys are close enough to each other in order to use for combining multi-Sequence MRI series for segmentation.

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