Standardized Evaluation of Current Ultrasound Bone Segmentation Algorithms on Multiple Datasets

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Abstract

Ultrasound (US) bone segmentation is an important component of US-guided orthopaedic procedures. While there are many published segmentation techniques, there is no direct way to compare their performance. We present a solution to this, by curating a multi-institutional set of US images and corresponding segmentations, and systematically evaluating six previously-published bone segmentation algorithms using consistent metric definitions. We find that learning-based segmentation methods outperform traditional algorithms that rely on hand-crafted image features, as measured by their Dice scores, RMS distance errors and segmentation success rates. However, there is no single best performing algorithm across the datasets, emphasizing the need for carefully evaluating techniques on large, heterogenous datasets. The datasets and evaluation framework described can be used to accelerate development of new segmentation algorithms.

1 Introduction

Ultrasound (US) is increasingly being used in orthopaedic procedures, as a radiation-free alternative to fluoroscopic (X-ray) imaging. In particular, identifying bone surfaces in US images is a core task in enabling several computer-assisted orthopaedic surgeries (CAOS) [8], whilst minimizing harmful radiation exposure [4]. However, interpreting US images remains a challenging task for physicians and algorithms alike, due to significant speckle and noise, limited field-of-view, and sensitivity to machine and patient characteristics.

Several algorithms for segmenting bone in US images have been proposed, in efforts to automate and improve the repeatability of clinical care [8, 2]. However, most of these algorithms are developed in isolated 'silos', and are therefore evaluated on datasets which are unique to each institution and using non-standardized definitions and implementations of evaluation metrics [8]. This makes it difficult to directly compare segmentation techniques with each other, and therefore evaluating the contribution of new techniques over previous ones.

In this paper we attempt to resolve these issues by making three contributions: 1) Curating a multi-institutional dataset of 20,810 unique US images containing labeled bone surfaces; 2) Defining and implementing a set of standardized evaluation metrics; 3) Performing a systematic evaluation of six previously-published bone segmentation algorithms on the curated datasets

using the proposed evaluation metrics. We believe these contributions will help standardize and democratize US bone imaging, and facilitate developing US bone segmentation techniques in the future.

2   Methods

We organized US bone imaging data from three institutions into datasets, and created automated evaluation environments for each of these. Six previously published automatic bone segmentation algorithms were benchmarked using this system. Example images and reference segmentations are presented in Figure 1A.

2.1   Datasets

The University of British Columbia (UBC) dataset consists of 16,995 2D US images collected from 10 healthy subjects at UBC, using a Telemed MicrUS system with a L12-5L40S-3 (Telemed, Italy). We split the dataset into a training set of 13,687 images from 8 subjects and a private test set of 3,308 images from 2 subjects.

The RWTH Aachen dataset consists of 2,550 slice images depicting 11 healthy subjects, imaged at RWTH Aachen University with a SonixTouch Q+ machine (Ultrasonix, USA). We split the dataset into a training set of 2,030 images from 9 subjects and a private test set of 520 images from 2 subjects.

The Rutgers University dataset consists of 1,265 2D US images collected from 14 healthy subjects at Rutgers University. Subjects were scanned with either a SonixTouch system or a Clarius convex C3 probe (Clarius Mobile Health Corporation, Canada). We split this dataset into a training set of 962 2D images from 11 subjects, and a private test of 303 2D images from 3 subjects.

2.2   Automated Evaluation

Each dataset was organized into its own evaluation task, in the style of typical medical image segmentation 'challenge'. When relevant, we followed the best practice guidelines proposed in [6], as our intention is to make this dataset and evaluation framework publicly available in the future. The private test set segmentation labels from each dataset were not used or available for training or guiding the development of segmentation algorithms.

Each evaluation was deployed as a Docker container, which included a program to process each segmentation prediction, as generated by each algorithm, against the reference segmentation using the evaluation metrics described below.

2.2.1   Evaluation Metrics

We implemented three evaluation metrics. The first was the Dice score (equivalent to F1 score), defined as the overlap between the dilated predicted and reference segmentations. The reference R and predicted P segmentations were dilated by a 1 mm disk structuring element, and the Dice score was calculated as $Dice = \frac{2|R \cap P|}{|R| + |P|}$. Here $|R|$ represents the count of all bone surface pixels in the reference segmentation.
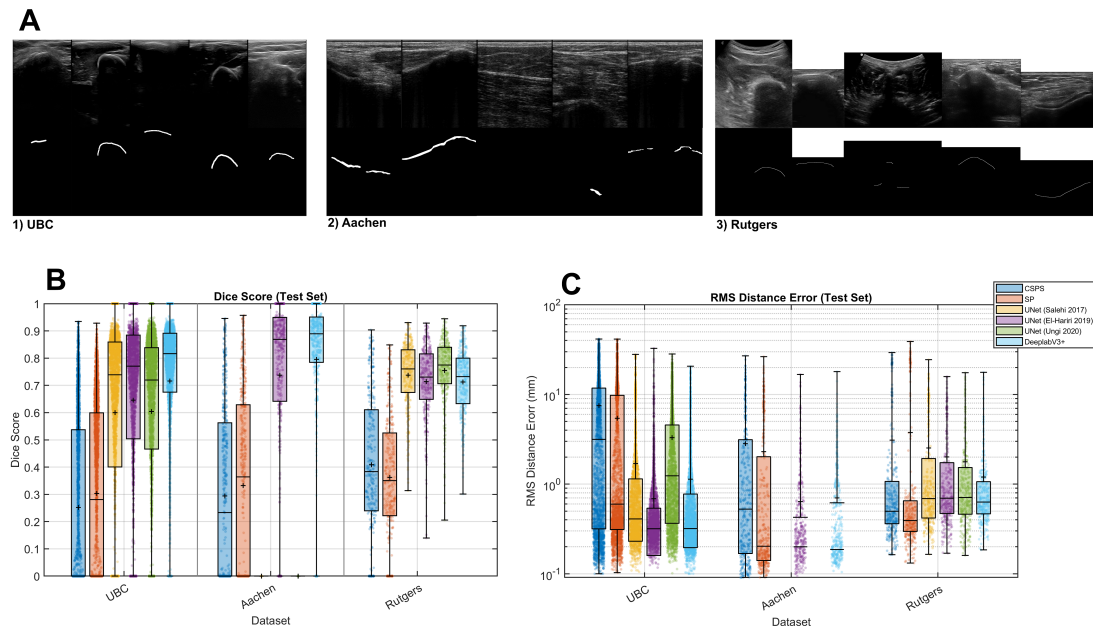
Figure 1: **A:** Examples of ultrasound images and corresponding reference segmentations from the three datasets. **B:** Dice score and **C:** Root-mean-squared (RMS) distance error box plots of each segmentation algorithm on each dataset. Central horizontal line represents the median and black cross represents the mean of each algorithm.

We also calculated the root-mean-squared (RMS) Euclidean distance error from the predicted segmentation to the reference segmentation after the segmentations had been skeletonized. Finally, we reported the success rate, where a successful segmentation is defined as where the predicted and reference bone surface share at least one scan-line in the US image.

2.3   Bone Segmentation Algorithms

We evaluated a total of six bone segmentation algorithms, two 'classical' non-learning methods and four learning methods based on deep convolutional neural networks (CNNs). The non-learning methods were Confidence-weighted Structured Phase Symmetry (CSPS) [9], and Shadow Peak (SP) [7]. The learning algorithms included three U-Net bone segmentation methods: U-Net (Salehi 2017) [10], U-Net (El-Hariri 2019) [1], U-Net (Ungi 2020) [11], and a DeepLabV3+ based model [3]. Further details of each method can be found in the original cited publications.

2.4   Statistical Analyses

We used a Friedman test to compare segmentation algorithms within each dataset evaluation, as it is a non-parametric, repeated measures analysis. This was followed by multiple post-hoc Wilcoxon signed-rank tests with Bonferroni's correction to find statistically significant differences ($p < 0.05$) between each algorithm.

3   Results

Table 1: Mean (and standard deviations) of Dice score, RMS distance error, and success rate for each algorithm and dataset evaluation. Bold values indicate best performers per dataset, tested statistically.

	UBC	RWTH Aachen	Rutgers
CSPS	0.25 (0.30) 7.50 mm (9.50 mm) 56%	0.29 (0.31) 2.83 mm (4.74 mm) 65%	0.41 (0.26) 3.10 mm (6.54 mm) 92%
SP	0.30 (0.31) 5.43 mm (7.94 mm) 59%	0.33 (0.33) 2.31 mm (4.18 mm) 61%	0.36 (0.23) 3.76 mm (8.43 mm) 86%
U-Net (Salehi 2017)	0.60 (0.35) 1.69 mm (3.53 mm) 78%	-	0.74 (0.12) 2.53 mm (3.92 mm) 100%
U-Net (El-Hariri 2019)	0.65 (0.35) **0.69 mm (1.76 mm)** 81%	0.74 (0.32) **0.64 mm (1.66 mm)** 87%	0.71 (0.13) **2.01 mm (2.88 mm)** 100%
U-Net (Ungi 2020)	0.60 (0.32) 3.30 mm (4.44 mm) 83%	-	**0.75 (0.12)** **1.77 mm (2.81 mm)** 100%
DeeplabV3+	**0.72 (0.29)** 1.14 mm (2.46) **89%**	**0.80 (0.28)** **0.70 mm (1.55 mm)** **91%**	0.71 (0.12) **1.20 mm (2.01 mm)** 100%

The performance of each algorithm on the datasets is summarized in Table 1, and box plots illustrating the Dice score and RMS distance errors are presented in Figure 1.

The DeeplabV3+ algorithm achieved the highest success rate across all three evaluations (range 89% - 100%), and all four learning algorithms achieved a 100% success rate on the Rutgers dataset (Table 1). DeeplabV3+ also achieved the highest mean Dice scores of 0.72 and 0.80 on the UBC and RWTH Aachen evaluations respectively, compared to the other methods ($p < 0.05$). The U-Net (El-Hariri 2019) algorithm achieved the lowest RMS distance errors on the UBC evaluation (mean: 0.69 mm, stdev: 1.76 mm; $p < 0.05$), and along with DeeplabV3+ achieved the lowest RMS distance error on the Aachen dataset (means: 0.64 mm and 0.70 mm, stdevs: 1.66 mm and 1.55 mm respectively). The U-Net (El-Hariri 2019), U-Net (Ungi 2020), and DeeplabV3+ algorithms achieved the lowest, statistically equivalent, RMS distance errors

on the Rutgers dataset. The learning methods outperformed the non-learning methods across all metrics over the three evaluations.

4 Discussion And Conclusion

We curated three US bone segmentation image datasets, on which we benchmarked six bone segmentation algorithms. Our results demonstrated that learning-based methods are the best performing over all datasets. However, there was no single algorithm that performed best across all datasets and metrics (Table 1). Furthermore, the performance of the same algorithms across the datasets varied significantly, emphasizing the need to validate algorithms on large, heterogeneous sets of data [6]. The results also indicated that differences in hyperparameters, such as learning rate and loss function, can lead to significant performance differences even when the network architecture is similar or identical, as demonstrated by the three U-Net based methods.

Our future work aims to benchmark these algorithms across additional institutional datasets. Furthermore, we plan to define new evaluation metrics specifically suited to bone surfaces, as Dice overlap and RMS distance error provide two different measurements of performance which are not always in agreement [5].

To the best of our knowledge, this work is the first to provide a framework for systematically comparing bone segmentation algorithms to each other across multiple datasets in a consistent manner [8]. We plan to release the datasets and evaluation frameworks publicly in order to facilitate the development of new bone segmentation algorithms and to accelerate US-guided CAOS.

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