Comparison of Model Initialization Methods for Liver Segmentation using Statistical Shape Models

Authors

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Purpose

Statistical shape models (SSM) are often employed in automatic segmentation algorithms in order to constrain the domain of plausible results. In a training phase, typical shapes are captured in form of a mean shape and typical modes of variation. At segmentation time, active contour algorithms depend on an appropriate initial placement of a model instance in the image to be segmented. To the best of authors knowledge, the segmentation quality of SSM-based algorithms with respect to the initialization method has received little attention in the literature, although the initialization is indispensable for a fully automatic segmentation. This contribution investigates the influence of different initialization methods for automatic 3D liver segmentation on CT and MR data.

Methods

Data: Two datasets with a total of 219 liver CT volumes from * [HOSPITAL ANONYMIZED FOR REVIEW] and a first set of 24 MR images (using a LAVA sequence for liver imaging) from ** [HOSPITAL ANONYMIZED FOR REVIEW] were used in this study. For every volume in these datasets, one high-precision reference liver segmentation was created semi-automatically by qualified medical staff for surgery planning using an established algorithm [1]. The datasets were divided into non-overlapping groups for training, method optimization, and final testing, respectively.

SSM-based segmentation algorithm: One SSM was built for each modality using 117 CT and 14 MR livers, respectively. Shape correspondences between the shapes were established using the MDL algorithm [2] with additional landmark distribution refinement step [3]. The examined SSM-based segmentation pipeline runs stepwise, where for each step the scale and the search mode can be specified: In active shape model (ASM) mode, every iteration starts with a model instance that is adapted to the image. In deformable model (DM) [4] mode, the shape model is used to guide an active contours method, which allows for more deformation. The appearance model is based on a Random Forests classifier trained using profiles sampled along node normals of meshes obtained from the correspondence establishment.

Initialization methods: In this work, we examine the following initialization methods:

1. **Mean_Alg**: Align the mean shape with a preliminary liver mask Mask_Alg (produced by one of the two algorithms described below) using the iterative closest point algorithm with a rigid body transformation mode
2. **Model_Alg:** Same as Mean_Alg, but additionally adapt the mean shape to the liver mask using the ASM search mode
3. **Deformed_Alg:** Same as Model_Alg, but the mean shape is additionally adapted using the DM search

The preliminary liver masks are produced either by a rough histogram-based algorithm (Mask_Rough) or by a 2D convolutional neural network (CNN) applied to axial slices (Mask_DL,Axial). The CNN employed used a simplified U-net architecture as in [5] but with only four resolution levels, resulting in a 2D receptive field of 105x105 voxels. The final segmentation mask was produced by choosing the largest connected component after thresholding the softmax output at 0.5. We did not perform any kind of data augmentation.

Evaluation: The SSM-based segmentation algorithm was run for 40 CT cases and 4 MR cases, respectively, and the results were compared against the corresponding reference masks. Various quality measures were computed, e.g., based on volumetric overlap and surface distances. In the following presentation, we focus on the Jaccard similarity coefficient and the average surface distance as two representative measures from these groups. In addition to the SSM segmentation results, we also report on the quality of the masks produced by the two algorithms described above.

Results

The plots of the Jaccard similarity coefficient and the average surface distance of SSM segmentation results for each investigated initialization modes are shown in Figure 1 and 2, respectively.

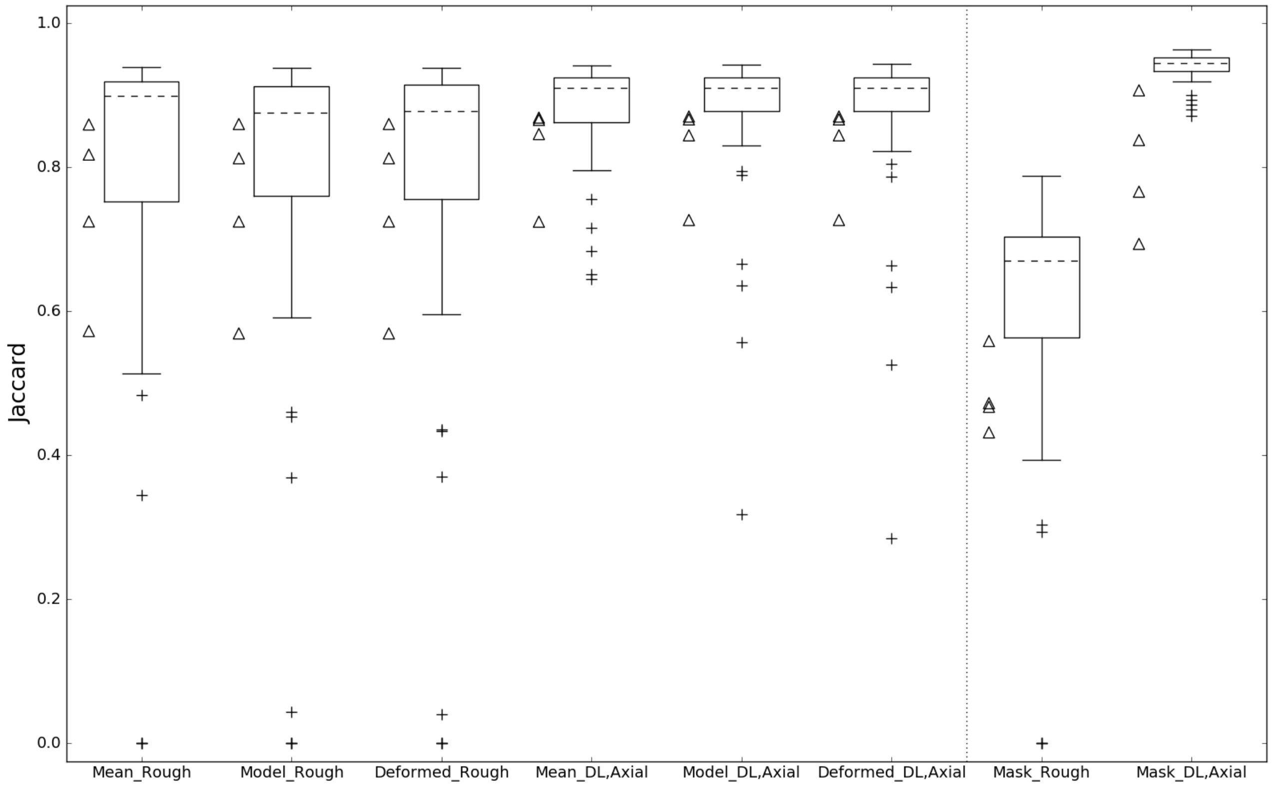

Figure 1: Jaccard similarity coefficient of SSM segmentation results per initialization method. The box plots summarize the results for the CT dataset, and the triangles to their left depict the results for the smaller MR dataset.

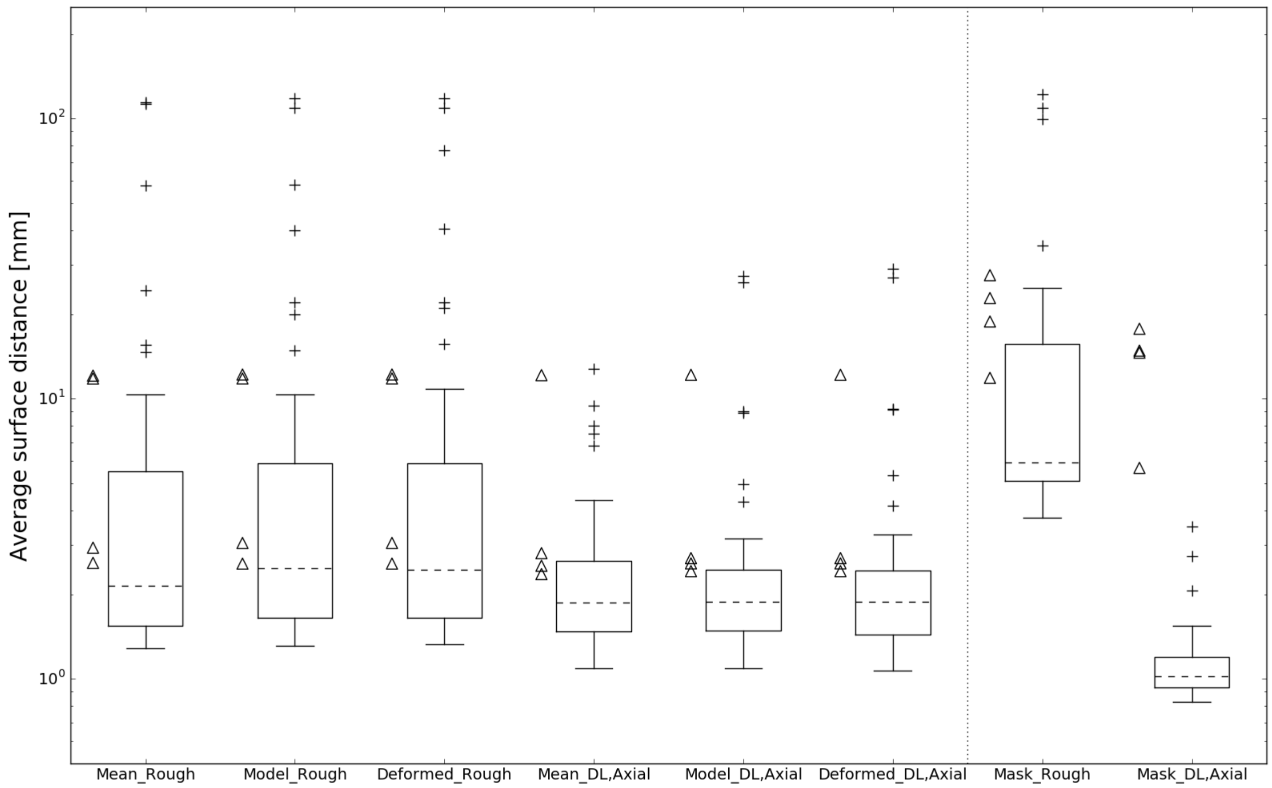

Figure 2: Average surface distance of SSM segmentation results per initialization method. As in Fig. 1, the box plots and triangles show the CT and MR datasets, respectively.

Conclusion

In this work different model initialization modes for a SSM-based segmentation pipeline were compared. Each investigated initialization modes was based on a preliminary liver mask, for which two algorithms were investigated. In the following, we will focus on the results obtained for the CT dataset, as the size of the test set from the MR dataset was too small to reason statistically. In case of CT dataset, the

Mask_DL,Axial algorithm delivered masks (mean. Jaccard index 0.94) of a significantly better quality (all tests were made using the Wilcoxon signed-rank test at a 0.05 significance level) than the Mask_Rough (mean Jaccard index 0.58). We observed a significant improvement of results when using an input liver mask of a better quality. The different initialization modes (Mean, Model, Deformed) for the same input liver mask produced results of no significant difference. When looking on a case-by-case basis, however, we observed that the adaptation to masks with leakages may impair final results. An interesting observation is that the Deformed_DL,Axial was not able to improve or even maintain the quality of the Mask_DL,Axial masks. A possible reason for this is the fact, that the mask adaptation performed in the Deformed mode is not capable of fitting the mask accurately, if the mask's shape deviates strongly from the shapes seen by the SSM.

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