

# 3D contour based local manual correction of liver segmentations in CT scans

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## Purpose

Liver segmentation is a challenging image processing task because of the wide variety of shapes and surrounding structures and the influence of contrast agents. Thus automatic liver segmentation algorithms cannot produce acceptable results in all cases. In contrast semi-automatic or pure manual segmentations are time-consuming.

However most parts of an automatically computed segmentation are usually correct and only some regions are erroneous. Therefore one solution to the segmentation problem is a fully automatic segmentation followed by a local manual correction of erroneous parts. For clinical acceptance the manual correction has to be both intuitive and fast which implies that modifications would ideally be three-dimensional.

## Methods

Our method for local three-dimensional manual correction of liver segmentations is based on our manual correction algorithm for segmentations of lung nodules, liver metastases and lymph nodes in CT scans<sup>1</sup> that is briefly described in the following paragraph.

User interaction is done in an intuitive manner. The user simply draws a partial two-dimensional contour  $C^u$  defining the actual border of the object in one slice (see Fig. 1(a)). The algorithm works on contours generated from the initial segmentation mask and consists of two main steps: a *live-wire extrapolation* of the user contour followed by a *morphological postprocessing*.

In the *live-wire extrapolation* the user drawn contour  $C^u$  is automatically moved to adjacent slices to simulate the user interaction in those slices (see Fig. 1(b)). This is done recursively by moving equidistant *seed points* on  $C^u$  to the adjacent slice using a *2D block matching algorithm*. This algorithm locates the most similar position of a seed point based on the median of squared differences of the intensity values in a given block and a given search area. The seed points are then connected by a *live-wire algorithm*. For preferring paths similar to the user drawn contour a feature called *preferred gradient magnitude* is used. Finally some part of the initial contour is replaced by the extrapolated user contour.

The *morphological postprocessing* is applied to the mask that has been generated from the contours computed by the live-wire extrapolation (see Fig. 1(c)). It removes artifacts resulting from outliers of the extrapolation step. Furthermore it ensures that the segmentation mask is coherent. This is done in three steps: a morphological opening, a connected component analysis and a morphological closing. After the connected component analysis only the component that is closest to a given reference point is kept.

The algorithm can be applied because the liver is a compact and coherent structure. But in contrast to lesions the liver is more difficult to handle because of its shape and the variability of surrounding structures. Thus some modifications to the algorithm have been necessary.

First the liver is much larger than a lesion which reduces the performance of the algorithm significantly. This is solved by cutting out a ROI that completely contains the liver including some offset and then downsampling this ROI to one fourth in the x- and y-direction. In z-direction the dimension is set such that one voxel covers at least 2mm. This way the liver ROI has a similar size as a lesion ROI used in the original algorithm. The segmentation error introduced by downsampling needs to be further investigated. But for a large object like the liver and depending on the application it should be negligible compared to the error of fully automated or manual segmentations. Moreover noise is suppressed by downsampling making the live-wire extrapolation more robust. Additionally the performance has been improved by utilizing multi-core processor capabilities. Both the live-wire cost computation and the conversion from contours to a mask has been parallelized. This way a speedup of 5 to 20% is achieved using 2 threads on a dual-core CPU.

Secondly the liver is not located at the center of the ROI. Hence the center cannot be used as reference point for the algorithm. Instead we use the center of gravity of the segmentation in the slice the user interacted with.

The third difference to lesions is the higher variety of structures surrounding the segmented object. Therefore the algorithm's parameters have been adapted to generate better results in our test cases. The distance between the seed points is set to 13mm. Both the preferred gradient magnitude feature and the gradient direction feature are weighted by 0.5. The Laplacian zero-crossing feature is not used. The block matching has been extended to adjacent slices as well using a 5x5x3 reference block and an 11x11x3 search area. It has shown that this allows locating the seed points more robustly. To handle the different shape of the liver in contrast to a lesion an additional termination condition for the extrapolation has been added. If the distance of the start or the end point of the user contour in the current slice to the initial contour in that slice is above a threshold the extrapolation stops. A threshold of 20mm has worked well in most cases.

## Results

The modified algorithm has been evaluated by four radiologists and one technical expert on 51 automatically computed liver segmentations where 24 segmentations have been rated as insufficient (--, -) and 27 as acceptable (0). Using our algorithm 21 insufficient segmentations (88%) could be improved to acceptable or better (+, ++) and 21 acceptable ones (78%) to good (+) or excellent (++).

One correction step takes about 1 to 5 seconds. The whole correction time was rated as acceptable.

## Conclusion

We have shown that our algorithm for 3D local manual correction of tumor segmentations can effectively be used for correcting liver segmentations as well. It is independent of the algorithm used for the initial segmentation, operates locally and allows an intuitive, interactive and fast correction.

In comparison to lesion segmentations, correcting liver segmentations is a more challenging task due to wider biological variability in both healthy and pathological livers. Hence some minor modifications to the original algorithm have been necessary. However a fixed parameter set cannot cover all situations adequately and more sophisticated on-the-fly training strategies or more robust features are required.

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## References

[1] Heckel, F, Moltz, J. H., Bornemann, L, Dicken, V., Bauknecht, H.-C., Fabel, M., Hittinger, M., Kießling, A., Meier, S., Püsken, M. and Peitgen, H.-O., "3D contour based local manual correction of tumor segmentations in CT scans", Proceedings of SPIE Medical Imaging, 2009

