Computerized Lesion Segmentation on DCE-MRI using Active Contours and Spectral Embedding.

S. Agner¹, J. Xu¹, S. Karthigeyan¹, and A. Madabhushi¹

¹Biomedical Engineering, Rutgers University, Piscataway, New Jersey, United States

Introduction: Accurate lesion segmentation is an important component of determining quantitative features for lesions on MRI. In this study, we develop an automated lesion segmentation method for delineating lesions on dynamic contrast enhanced (DCE)-MRI. We present a new active contour model which uses spectral embedding (SE), a process that partitions images in order to maximize intercluster similarity and minimize intracluster similarity while preserving object adjacencies [1]. SE has been used previously for classification of high dimensional data [2], but this is the first known application of SE in the context of segmentation. SE transforms the images into a data representation that accentuates the gradients at the lesion borders which allows the active contour to accurately identify the lesion boundaries. This will allow better characterization of lesion morphology, which facilitates discrimination between lesions with subtle shape differences. We demonstrate on a cohort of 50 breast lesions imaged on DCE-MRI that automated segmentation using our spectral embedding based active contour (SEAC) model is more similar to the manual lesion segmentation performed by a radiologist who is a breast imaging specialist than the popular fuzzy c-means (FCM) method [3] combined with an active contour model.

Methods: DCE-MRIs of 50 breast lesions from 50 patients were collected under IRB approval. Sagittal T1-weighted, spoiled gradient echo sequences with fat suppression consisting of one series before contrast injection of Gd-DTPA (precontrast) and 3-8 series after contrast injection (postcontrast) were acquired at either 1.5 Tesla or 3 Tesla (Siemens Magnetom or Trio, respectively). Single slice dimensions were 384x384, 512x512, or 896x896 pixels with a slice thickness of 3 mm. Temporal resolution between postcontrast acquisitions was a minimum of 90 seconds. An attending radiologist selected the 2D slice that was most representative of the lesion, and the radiologist manually delineated the boundary of the lesion. SE is performed along the time dimension to reduce the dimensionality of the time domain from 4-9 (i.e., total number of time points) to 3. Each resulting dimension is then represented as one color channel of a hue/saturation/value (HSV) color space. A color active contour method is then evolved on the embedding color map. For the comparison FCM method [3], voxels in each image were clustered into 3 data classes. The 3 channel color map resulting from these 3 data classes was then used in conjunction with the same color active contour method used with SEAC.

Results: The resulting image boundary when the active contour model is applied to the embedding image is compared to the boundary derived from applying an active contour model driven by gradients of fuzzy c-means (FCM) clustering as described in Chen et al. [3]. Figure 1 shows the comparison between the manual segmentation performed by a radiologist and the two automated segmentation methods. The SEAC segmentations in Figure 1(c,f) are more comparable to the manual segmentations in Figure 1(a,d) than the FCM initialized active contour (FCM+AC) segmentations in Figure 1(b,e). In particular, Figure 1(f) shows that the SEAC model was able to capture the spicularity of the lesion whereas the FCM+AC segmentation in Figure 1(e) was not. Overlap measures including mean absolute difference (MAD) and Dice similarity coefficient (DSC) were calculated across all lesions for the two automated segmentation methods by comparing to the manual segmentation. The mean and variance of both MAD and DSC for FCM+AC and SEAC are shown in Table 1. Lower values of MAD and higher values of DSC indicate better performance.

Table 1: Evaluation of SEAC vs. FCM+AC		
Segmentation Method	MAD (μ±σ)	DSC (μ±σ)
FCM+AC	7.2 ± 7.4	0.58 ± 0.32
SEAC	3.2 ± 2.1	0.74 ± 0.013

Concluding Remarks: In this study, we presented a new active contour model (SEAC) involving use of spectral embedding for segmentation. SE transforms the high dimensional DCE-MRI time series data to a reduced dimensional space. This transformed space provides strong gradients needed for driving

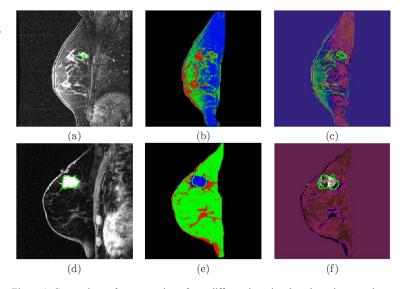


Figure 1. Comparison of segmentation of two different invasive ductal carcinomas via (a,d) manual delineation (b,e) FCM+AC, and (c,f) SEAC. Note that in (b) and (e) the FCM image does not provide a strong enough gradient at the lesion boundary for curve evolution to find the boundary between the lesion and the other breast tissue. However, SEAC (c,f) yields a lesion segmentation that is very close to the manual delineation of the tumor in (a,d).

an active contour model. On a cohort of 50 breast DCE-MRI studies, we showed that SEAC outperformed the commonly used FCM method [3]. While we demonstrate the use of SEAC with breast DCE-MRI data, SEAC could be easily applied to segmenting structures on other high dimensional, time-series imaging data as well.

References

- [1] J. Shi and J. Malik, "Normalized cuts and image segmentation," IEEE PAMI 22(8), pp. 888–905, 2000.
- [2] G. Lee, C. Rodriguez, and A. Madabhushi, "Investigating the efficacy on nonlinear dimensionality reduction schemes in classifying gene and protein expression studies," IEEE/ACM Transactions on Computational Biology and Bioinformatics 5, pp. 368–384, 2008.
- [3] W. Chen, M. L. Giger, U. Bick, and G. M. Newstead, "Automatic identification and classification of characteristic kinetic curves of breast lesions on dce-mri," Medical Physics 33(8), pp. 2878–2887, 2006.