A Rician-Gaussian Mixture Model for Segmenting Delayed Enhancement MRI Images

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Abstract

Delayed Enhancement (DE) MRI is an imaging modality for assessing myocardial viability and scars due to infarction. Infarcted areas are in DE-MRI contrasted using a gadolinium-based contrast agent that remains longer in fibrous tissue. The goal of this work is to segment the myocardium in the DE-MRI images into normal and damaged tissue. Previous approaches to this problem select an image intensity threshold manually or based on heuristic rules applied to the histogram of the image intensity values [1,2]. In this contribution, the well-known statistics of MRI data are utilized to find a threshold automatically via a Rician-Gaussian mixture model.

Rician-Gaussian EM-algorithm

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Given: Voxel intensity values $x_i, i = 1 \dots n$
Initialize: $\hat{\mu}, \hat{\sigma}_G^2, \widehat{m}, \hat{\sigma}_R^2, \widehat{w}_G, \widehat{w}_R$

Repeat E-step and M-step until convergence:
E-step:
    $p_R^{(i)} = \widehat{w}_R f_R(x_i; \widehat{m}, \hat{\sigma}_R^2)$ and $p_G^{(i)} = \widehat{w}_G f_G(x_i; \hat{\mu}, \hat{\sigma}_G^2)$
    $p_R^{(i)} \leftarrow p_R^{(i)} / \left(p_R^{(i)} + p_G^{(i)}\right)$ and $p_G^{(i)} \leftarrow p_G^{(i)} / \left(p_R^{(i)} + p_G^{(i)}\right)$

M-step:
    $\widehat{w}_R = \frac{1}{n} \sum_{i=1}^{n} p_R^{(i)}$ and $\widehat{w}_G = \frac{1}{n} \sum_{i=1}^{n} p_G^{(i)}$

    $\hat{\mu} = \frac{1}{n\widehat{\mathrm{w}}_{\mathrm{G}}} \sum_{i=1}^{n} p_G^{(i)} x_i$ and $\hat{\sigma}_G^2 = \frac{1}{n\widehat{\mathrm{w}}_{\mathrm{G}}} \sum_{i=1}^{n} p_G^{(i)} (x_i - \hat{\mu})^2$

    $M_R^2 = \frac{1}{n\widehat{\mathrm{w}}_{\mathrm{R}}} \sum_{i=1}^{n} p_R^{(i)} x_i^2$
    Fixed-point iteration (iterate until convergence):
    {
        $\widehat{m} \leftarrow \frac{1}{n\widehat{\mathrm{w}}_{\mathrm{R}}} \sum_{i=1}^{n} p_R^{(i)} x_i K\left(\frac{x_i \widehat{m}}{\hat{\sigma}_R^2}\right)$ where $K(z) = \frac{I_1(z)}{I_0(z)}$
        $\hat{\sigma}_R^2 = \frac{M_R^2 - \widehat{m}^2}{2}$
    }
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Method

It is known that the noise in magnitude MRI images follows a Rice-distribution. At high SNR, the Rice-distribution is well approximated by a Gaussian distribution. The probability density functions (pdf's) of the Rice and Gauss distributions are

$$f_R(x; m, \sigma_R^2) = \frac{x}{\sigma_R^2} e^{-\frac{x^2+m^2}{2\sigma_R^2}} I_0\left(\frac{xm}{\sigma_R^2}\right) \quad \text{and} \quad f_G(x; \mu, \sigma_G^2) = \frac{1}{\sqrt{2\pi\sigma_G^2}} e^{-\frac{(x-\mu)^2}{2\sigma_G^2}}$$

where m, σ_R^2, μ and σ_G^2 are parameters and $I_n(z)$ is a modified Bessel function of the first kind. Moreover, for *m* equal zero, the Rice-distribution becomes a Rayleigh distribution. In DE-MRI, normal myocardium has low intensity due to an inversion recovery RF pulse, whereas scar tissue has a slightly higher intensity due to the remaining contrast agent. Because the scar tissue has higher intensity, the voxel intensities can be approximately modeled by a Gaussian pdf. The normal myocardium has low intensity and consequently low SNR (m/σ_R^2 is small). These voxels must therefore be modeled with the full Rician distribution. Hence, the following mixture model is applied to model the histogram of the voxel intensities in the entire myocardium: $w_R f_R(x; m, \sigma_R^2) + w_G f_G(x; \mu, \sigma_G^2)$, where w_R and w_G are the relative proportions of normal and abnormal tissue respectively. The Expectation-Maximization (EM) framework is applied to estimate the parameters in this mixture model. Whereas well-known formulas exist for pure Gaussian mixture models, the Rice distribution is mathematically intractable and no closed form EM update rule exists. Instead, an efficient updating scheme based on a fixed-point iteration is presented in this contribution; see the table to the right. The EM-algorithm generally converges in a few steps. Recommended initial parameter settings are $\widehat{m} = 5, \widehat{w}_G = 0.2$ and $\widehat{w}_R = 0.8$, meaning 80% normal myocardium, 20% damaged tissue and a mean value above zero in normal tissue. The initial guesses of $\hat{\mu}, \hat{\sigma}_G^2$ and $\hat{\sigma}_R^2$ are deduced from the mean and variance of the histogram of the voxels in the myocardium. Once the mixture model has been fitted, a threshold for segmenting abnormal tissue is found at the intersection between the Rician and Gaussian distributions.

Results

Two DE-MRI data sets, acquired using a 3T and a 1.5T scanner respectively, are used for demonstrating the result of the Rician-Gaussian mixture model. The data sets consist of 11 and 8 short-axis images of the heart respectively. The voxel size is 1.3x1.3x10 mm. As a pre-processing step, a rigid registration was applied to align the image slices and the myocardia were manually outlined by drawing epicardial and endocardial contours. The EM-algorithm presented in the table above was then applied to the voxel values in the outlined myocardia to find the parameters of the Rician and Gaussian distributions:

Dataset 1: $\widehat{m} = 8.1$ $\hat{\sigma}_R^2 = 20$ $\hat{\mu} = 27.9$ $\hat{\sigma}_G^2 = 102$ $\widehat{w}_R = 0.81$ $\widehat{w}_G = 0.19$
Dataset 2: $\widehat{m} = 8.4$ $\hat{\sigma}_R^2 = 9.3$ $\hat{\mu} = 46.8$ $\hat{\sigma}_G^2 = 479$ $\widehat{w}_R = 0.56$ $\widehat{w}_G = 0.44$

The corresponding pdf's and mixture models are shown in Fig. 1. It is clear that a Gaussian pdf cannot approximate the Rician pdf in Data set 1 and that a Rayleigh pdf cannot replace the Rician pdf in Data set 2. Hence, the full Rician distribution must be used to model normal myocardium. A second observation is that there is a partial volume effect owing to the large voxel size, which is seen as an excess of voxels between the Rician and Gaussian pdf's (arrows). This effect broadens the fitted curves. However, overall, the mixture model fits well. Next, thresholds were found as described above and applied to the DE-MRI images. One representative short-axis slice for each data set is shown in Fig. 1. No further spatial processing was applied, e.g., smoothing or removal of small regions. A larger study, in which a variant of the described methodology is applied, is presented elsewhere [3].

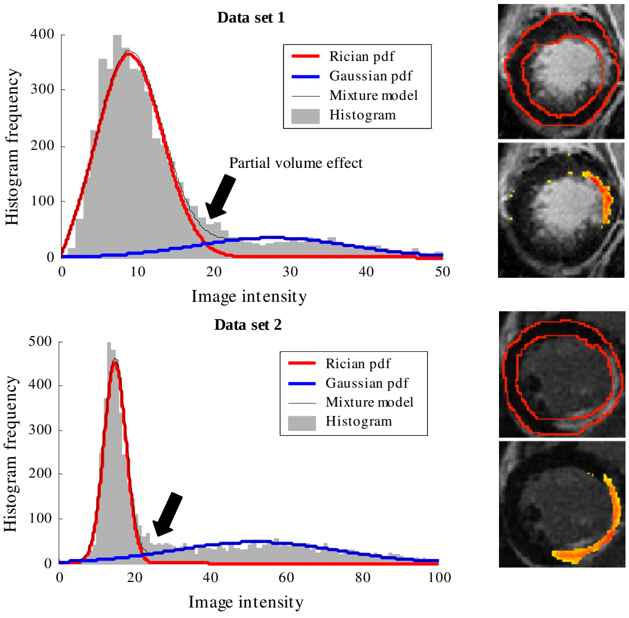

Figure 1. Left: Mixture model fits and voxel intensity histograms for two example data sets. Thresholds are found at the intersections between the Rician and Gaussian pdf's. **Right:** One slice from each data set with the manually delineated myocardium outlined in red and with the segmentation of abnormal tissue obtained by applying the threshold given by the mixture model.

Conclusion

A Rician-Gaussian mixture model for finding thresholds for Delayed-Enhancement MRI images has been presented. A main contribution is an EM-algorithm adapted to estimate the parameters in this mixture model. Future work is to account for partial volume effects, for example by incorporating spatial context via a Markov Random Field.

References

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