Probabilistic Tissue Characterization for Ultrasound Images

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Abstract

This document describes the derivation of the mixture models commonly used in the literature to describe the probabilistic nature of speckle: The Gaussian Mixture Model, the Rayleigh Mixture Model, the Gamma Mixture Model and the Generalized Gamma Mixture Model. New algorithms were implemented using the Insight Toolkit ITK www.itk.org for tissue characterization by means of a mixture model. The source code is composed of a set of reusable ITK filters and classes. In addition to an overview of our implementation, we provide the source code, input data, parameters and output data that the authors used for validating the different probabilistic tissue characterization variants described in this paper. This adheres to the fundamental principle that scientific publications must facilitate reproducibility of the reported results.

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Contents

1 Introduction

The analysis of backscattered echo from tissues has gained an increasing attention during the last decades in ultrasound imaging. The main reason is that the parameters of the statistical models lead to identify the features of tissues and provide important descriptors for classification.

Several statistical models have been proposed over the last years. Probably the most well known is the Rayleigh model, which is a one-parameter distribution which describes the so-called fully formed (or developed) speckle. This probabilistic distribution describes the behavior of a speckle when a high number of effective scatterers are present in the resolution cell. However, real images show a deviation from this model, this non-Rayleigh behavior can be due to a small number of scatterers in the resolution cell or when there are some dominant components in the cell. The most commonly accepted distributions that try to model non-Rayleigh distributions are the Rice (fully resolved speckle), K (partially formed speckle), and Homodyned K (partially resolved speckle).

Although those models are based on physical assumptions of the backscattering process, some other distributions have proven to provide a good performance on real images. This is the case of Gamma [15, 13, 18] and Nakagami [11] distributions. The first is proposed as a two-parameter distribution that describes the result of interpolated/filtered fully formed speckle [18] and also has shown good results in empirical tests among other distributions [15, 13]. The Nakagami distribution proposed by Shankar for the case US characterization [11] is also a two-parameter distribution which generalizes the Rayleigh distribution. This distribution was adopted from the models proposed to describe the statistics of the returned echo radar.

In ultrasound imaging, the presence of different scatteres within the resolution cell is common. This effect causes a mixed echolucid response that must be characterized by different distributions. In these cases, a mixture model becomes an opportune strategy to statistically describe the backscattered echo. The use of mixture models has been increasingly extended in the literature for multiple applications such as filtering [16, 14], registration [4, 6], segmentation [10, 1, 3, 2, 8].

In this document we describe the derivation of the mixture models commonly used in the literature to describe the probabilistic nature of speckle: The Gaussian Mixture Model, the Rayleigh Mixture Model, the Gamma Mixture Model and the Generalized Gamma Mixture Model. Note that the Nakagami Mixture Model can be directly estimated from the Gamma mixture model [7].

1.1 Mixture Model

The mixture model can describe the contribution of different statistic distributions in the speckle image and, thus, provides a probabilistic information of the nature of each tissue. The mixture model can be calcu-

lated by means of the expectation maximization (EM) algorithm [12], which maximizes the log-likelihood function for hidden discrete random variables, $\boldsymbol{Z} = \{Z_i\}$. Formally speaking, let $\boldsymbol{X} = \{x_i\}, 1 \leq i \leq N$ be an identically distributed and independent set of samples (pixel intensities) and x_i belongs to the distributions class j when $Z_i = j$. The mixture model considers that these samples result from the contributions of J distributions:

$$p(x_i|\boldsymbol{\Theta}) = \sum_{j=1}^{J} \pi_j f_X(x_i|\Theta_j) \tag{1}$$

where $\boldsymbol{\Theta}$ is a vector of parameters of the mixture model (π_j, Θ_j) and Θ_j are the parameters of the distribution function (Gaussian, Rayleigh, Gamma or Generalized Gamma), $\sum_{j=1}^{J} \pi_j = 1$ and f_X is the probability density function (PDF) of the marginalized random variable. The Expectation-Maximization algorithm is applied in the following way:

1. An initial estimation of the hidden variables is obtained by any clustering methodology, such the k-means [9]. For each cluster, j, the parameter $\hat{\pi}_j^{(0)}$ is calculated as follows:

$$\hat{\pi}_j^{(0)} = \frac{n_j}{N} \tag{2}$$

   where n_j corresponds to the number of samples in the cluster and N is the total number of samples. The j parameters, $\Theta_j^{(0)}$, are calculated from samples according to its PDF as we will explain later in this section.

2. A Bayesian inference step is performed to calculate the posterior probability, $\gamma_{i,j}$, in the *Expectation step* as:

$$\gamma_{i,j} = p(Z_i = j|x_i, \boldsymbol{\Theta}^{(n-1)}) = \frac{\pi_j^{(n-1)} f_X(x_i|\Theta_j^{(n-1)})}{p(x_i|\boldsymbol{\Theta}^{(n-1)})} \tag{3}$$

3. The parameters for the mixture ($\Theta_j^{(n)}$ and $\hat{\pi}_j^{(n)}$) are estimated in the *Maximization step*.

4. Until an acceptable tolerance is reached, $||\boldsymbol{\Theta}^{(n)} - \boldsymbol{\Theta}^{(n-1)}||^2 < \varepsilon$, an iterative estimation of the parameters is performed repeating step 2 and 3.

Note that the mixture model formulation provides the probability of belonging to each class, for instance blood or tissue. The probability of belonging to the j-th class for sample x_i is obtained by means of the Bayes' theorem as:

$$\Upsilon_j(x_i) = P\{Z_i = j|x_i\} = \frac{f_X(x_i|\Theta_j)\pi_j}{p(x_i|\boldsymbol{\Theta})} \tag{4}$$

In what follows, $\boldsymbol{\Upsilon} = \{\Upsilon_j\}_{j=1\ldots J}$ will denote the set of probabilistic characterizations for all tissue classes.

Gaussian Mixture Model

The tissues response can be described by means of the Gaussian mixture model. This mixture model can describe the contribution of different Gaussian distributions in the speckle image as it was described in Eq. 1, where Θ_j are the parameters of the Gaussian distribution function and f_X is the PDF of the marginalized Gaussian random variable with the following parametrization:

$$f_X(x|\{\overbrace{\mu_j,\sigma_j}^{\Theta_j}\}) = \frac{1}{\sqrt{2\pi\sigma_j^2}}\exp\left(\frac{-(x_i-\mu_j)^2}{\sigma_j^2}\right) \tag{5}$$

where $j \in \{1,\cdots,J\}$. According to this distribution, the Expectation-Maximization algorithm is applied as it was described in Section 1.1 where the steps 1 and 3 are:

1. The initial parameters of Eq. 5 are obtained by computing the mean and variance of each cluster, X_j, as follows:
$$\mu_j^{(0)} = \frac{1}{n_j}\sum_{i=1}^{n_j} x_i, \qquad \sigma^{2(0)} = \frac{1}{N_j-1}\sum_{i=1}^{n_j}(x_i-\mu_j^{(0)})^2 \tag{6}$$
where $x_i \in X_j$ and $n_j = |X_j|$.

3. The parameters for the mixture of Gaussian distributions ($\hat{\mu}_j$ and $\hat{\sigma}_j$) are estimated in the *Maximization step* for each distribution as follows:
$$\mu_j^{(n)} = \frac{\sum_{i=1}^{N}\gamma_{i,j}\,x_i}{\sum_{i=1}^{N}\gamma_{ij}}, \qquad \sigma^{2(n)} = \frac{\sum_{i=1}^{N_j}\gamma_{i,j}\,(x_i-\mu_j^{(n)})^2}{\sum_{i=1}^{N}\gamma_{ij}} \tag{7}$$
$$\hat{\pi}_j^{(n)} = \frac{1}{N}\sum_{i=1}^{N}\gamma_{i,j} \tag{8}$$

Rayleigh Mixture Model

The tissue response can be described by means of the Rayleigh mixture model. This mixture model can model the contribution of different Rayleigh distributions in the speckle image as it was described in Eq. 1, where Θ_j are the parameters of the Rayleigh distribution function and f_X is the PDF of the marginalized Rayleigh random variable with the following parametrization:

$$f_X(x|\{\overbrace{\sigma_j}^{\Theta_j}\}) = \frac{x}{\sigma_j^2}\exp\left(\frac{-x^2}{2\sigma_j^2}\right), \quad x \geq 0 \text{ and } \sigma_j > 0 \tag{9}$$

where $j \in \{1,\cdots,J\}$. According to this distribution, the Expectation-Maximization algorithm is applied as it was described in Section 1.1 where the steps 1 and 3 are:

1. The initial parameters of Eq. 9 are obtained by computing the mean of each cluster (μ_j) as follows:
$$\hat{\sigma}_j^{(0)} = \mu_j\sqrt{\frac{2}{\pi}} \tag{10}$$
where $\mu_j = \sigma_j\sqrt{\pi/2}$ according to the parametrization used.

3. The parameters for the mixture of Rayleigh distributions ($\hat{\sigma}_j$ and $\hat{\pi}_j$) are estimated in the *Maximization step* for each distribution as follow:

$$\hat{\pi}_j^{(n)} = \frac{1}{N}\sum_{i=1}^{N}\gamma_{i,j}, \qquad \hat{\sigma}_j^{(n)} = \sqrt{\frac{1}{2}\frac{\sum_{i=1}^{N}\gamma_{i,j}x_i^2}{\sum_i^N \gamma_{i,j}}} \tag{11}$$

Gamma Mixture Model

In this case, the tissues response can be described by means of the Gamma mixture model proposed by [19]. This mixture model can describe the contribution of different Gamma distributions in the speckle image as it was described in Eq. 1, where Θ_j are the parameters of the Gamma distribution function and f_X is the PDF of the marginalized Gamma random variable with the following parametrization:

$$f_X(x|\{\overbrace{\alpha_j,\beta_j}^{\Theta_j}\}) = \frac{x^{\alpha_j-1}}{\beta_j^{\alpha_j}\Gamma(\alpha_j)}x^{\alpha_j-1}\exp\left(-\frac{x}{\beta_j}\right), \quad x \geq 0 \text{ and } \alpha_j,\beta_j > 0 \tag{12}$$

where $j \in \{1,\cdots,J\}$, α_j and β_j are the shape and scale parameters respectively. According to this distribution, the Expectation-Maximization algorithm is applied as it was described in Section 1.1 where the steps 1 and 3 are [19]:

1. The initial parameters of Eq. 12 are obtained by computing the mean and variance of each cluster (σ_j^2 and μ_j) as follows:

$$\hat{\beta}_j^{(0)} = \frac{\sigma_j^2}{\mu_j}, \qquad \hat{\alpha}_j^{(0)} = \frac{\mu_j}{\hat{\beta}_j^{(0)}} \tag{13}$$

   where $\sigma_j^2 = \alpha_j\beta_j^2$ and $\mu_j = \alpha\beta$ according to the parametrization used.

3. The parameters for the mixture of Gamma distributions ($\hat{\alpha}_j, \hat{\beta}_j$ and $\hat{\pi}_j$) are estimated in the *Maximization step* for each distribution as follow:

$$\hat{\alpha}_j^{(n)} \leftarrow \log(\hat{\alpha}_j) - \psi(\hat{\alpha}_j) = \log\left(\frac{\sum_{i=1}^{N}\gamma_{i,j}x_i}{\sum_{i=1}^{N}\gamma_{i,j}}\right) - \frac{\sum_{i=1}^{N}\gamma_{i,j}\log(x_i)}{\sum_{i=1}^{N}\gamma_{i,j}} \tag{14}$$

$$\hat{\pi}_j^{(n)} = \frac{1}{N}\sum_{i=1}^{N}\gamma_{i,j}, \qquad \hat{\beta}_j^{(n)} = \frac{1}{\hat{\alpha}_j^{(n)}}\frac{\sum_{i=1}^{N}\gamma_{i,j}x_i}{\sum_i^N\gamma_{i,j}} \tag{15}$$

   where ψ is the digamma function.

Generalized Gamma Mixture Model

Similarly to the previous probabilistic tissue characterization, the different response of tissues can be described by means of the GG mixture model proposed by [17]. This mixture model can describe the contribution of different GG distributions in the speckle image as it was described in Eq. 1, where in this case Θ_j are the parameters of the GG distribution function and f_X is the PDF of the marginalized GG random variable with the following parametrization:

$$f_X(x|\{\overbrace{a_j,\nu_j,p_j}^{\Theta_j}\}) = \frac{p_j x^{(p_j\nu_j-1)}}{a_j^{p_j\nu_j}\Gamma(\nu_j)} e^{-(x/a_j)^p}, \quad x \geq 0 \text{ and } a_j,\nu_j,p_j > 0 \tag{16}$$

where $j \in \{1,\cdots,J\}$, a_j is a scale parameter, ν_j and p_j are shape parameters. In this way, the Expectation-Maximization algorithm is applied as it was described in Section 1.1 where the steps 1 and 3 are [17]:

1. The initial parameters of Eq. 16 are obtained for each cluster, X_j, by estimating:

$$\hat{p}_j^{(0)} = \arg\max_{\hat{p}_j} \left\{ \sum_{i=1}^{n_j} \log f_X\left(x_i|\hat{a}_j(\hat{p}_j),\hat{\nu}_j(\hat{p}_j),\hat{p}_j\right) \right\} \tag{17}$$

   where $x_i \in X_j$ and $n_j = |X_j|$. The parameters $\hat{a}_j(\hat{p}_j)$ and $\hat{\nu}_j(\hat{p}_j)$ in Eq. 17 are estimated from the Gamma$(X_j^{\hat{p}_j},\alpha,\beta)$ distribution where $\hat{a}_j(\hat{p}_j) = \beta^{-1/\hat{p}_j}$ and $\hat{\nu}_j(\hat{p}_j) = \alpha$. In particular, $\hat{a}_j^{(0)} = \hat{a}_j(\hat{p}_j^{(0)})$ and $\hat{\nu}_j^{(0)} = \hat{\nu}_j(\hat{p}_j^{(0)})$.

3. The parameters for the mixture of Generalized Gamma distributions, $\hat{a}_j,\hat{p}_j,\hat{\nu}_j$ and $\hat{\pi}_j$, are estimated in the *Maximization step* for each distribution as follow:

$$\hat{p}_j^{(n)} = \arg\max_{\hat{p}_j} \left\{ \sum_{i=1}^{N} \gamma_{i,j} \log f_X\left(x_i|\frac{\sum_{i=1}^N \gamma_{i,j} x_i^{\hat{p}_j}}{\hat{\nu}_j(\hat{p}_j)\sum_{i=1}^N \gamma_{i,j}},\hat{\nu}_j(\hat{p}_j),\hat{p}_j\right) \right\} \tag{18}$$

$$\hat{\nu}_j^{(n)} \leftarrow \log(\hat{\nu}_j) - \psi(\hat{\nu}_j) = \log\left(\frac{\sum_{i=1}^N \gamma_{i,j} x_i^{\hat{p}_j^{(n)}}}{\sum_{i=1}^N \gamma_{i,j}}\right) - \frac{\sum_{i=1}^N \gamma_{i,j} \log(x_i^{\hat{p}_j^{(n)}})}{\sum_{i=1}^N \gamma_{i,j}} \tag{19}$$

$$\hat{a}_j^{(n)} = \left(\frac{\sum_{i=1}^N \gamma_{i,j} x_i^{\hat{p}_j^{(n)}}}{\hat{\nu}_j^{(n)}\sum_{i=1}^N \gamma_{i,j}}\right)^{1/\hat{p}_j^{(n)}}, \qquad \hat{\pi}_j^{(n)} = \frac{1}{N}\sum_{i=1}^{N} \gamma_{i,j} \tag{20}$$

   where ψ is the digamma function and $\hat{\nu}_j(\hat{p}_j)$ is estimated as Eq. 19 for a particular $\hat{p}_j$.

2 Brief note on the Implementation

The main contribution of this work is to extend the Gaussian mixture model to three new mixture models commonly used for characterizing the tissue in ultrasound images, Rayleigh, Gamma and Generalized Gamma. In particular, the tissue characterization is done by means of two filters and the mixture model. As shown in section 1.1, several blocks can be distinguished for the EM strategy used to calculate the mixture model. In particular, one can see three necessary parts, a density function (`itk::Statistics::MixtureModelMembershipFunctionBase`), an initialization (`itk::Statistics::MixtureModelInitHelper`), and a component where the maximization step is done (`itk::Statistics::MixtureModelComponentBase`). The EM strategy is implemented in the `itk::Statistics::ExpectationMaximizationMixtureModelEstimator` class (Fig. 1) and corresponds to the step between 2 and 4 according to the EM strategy described in section 1.1. Figure 1 shows the classes and relations between all the components of the EM strategy where the following classes correspond to the ITK implementation:

- itk::Statistics::ExpectationMaximizationMixtureModelEstimator
- itk::Statistics::WeightedCovarianceSampleFilter
- itk::Statistics::WeightedMeanSampleFilter

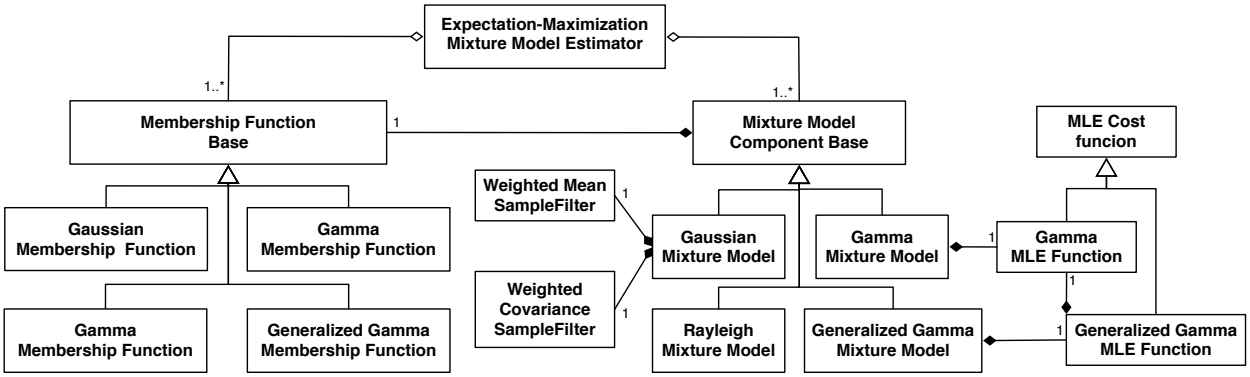

Figure 1: Class Diagram for Mixture Model.

Minor changes were added to the following classes to unified the parameter setting for all the membership functions:

- itk::Statistics::MixtureModelMembershipFunctionBase
- itk::Statistics::itkMixtureModelComponentBase
- itk::Statistics::GaussianMembershipFunction
- itk::Statistics::GaussianMixtureModelComponent

Since the Gamma and Generalized Gamma mixture model have no close form, the EM strategy is performed by doing an optimization step of a cost function which corresponds to the Eq. 14 for the Gamma mixture model and Eq. 18 and Eq. 19 for the Generalized Gamma mixture model. Additionally, the proposed initialization described in section 1.1 is implemented by the itk::Statistics::MixtureModelInitHelper filter (Fig. 2).

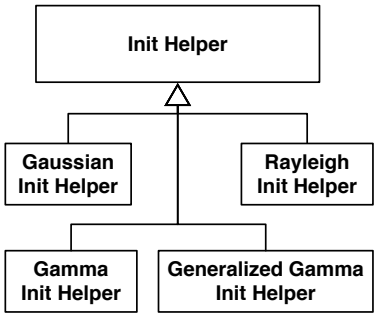

Figure 2: Illustration of the hierarchy for the initialization.

The probabilistic tissue characterization (Eq. 4) is implemented in the itk::Statistics::LikelihoodMapImageFilter class. If we take into account two classes for the

mixture model (blood and tissue), the probabilistic characterizations of the tissue will belong to the distribution class j with the highest mean. However, this criteria can be modified in the `SortValue()` defined in each concrete class of `itk::Statistics::MixtureModelComponentBase`. This method can be useful, for example, if we are using three classes for the mixture model. In this case, we could modified the sort criteria to use the middle mean instead of the highest, or the lowest if we want to characterize the blood instead of the tissue. Finally, the complete procedure to initialize, estimate the mixture model parameters and create the probabilistic tissue characterization is encapsulated in `itk::Statistics::TissueCharacterizationFilter` and the relation between classes is depicted in Figure 3.

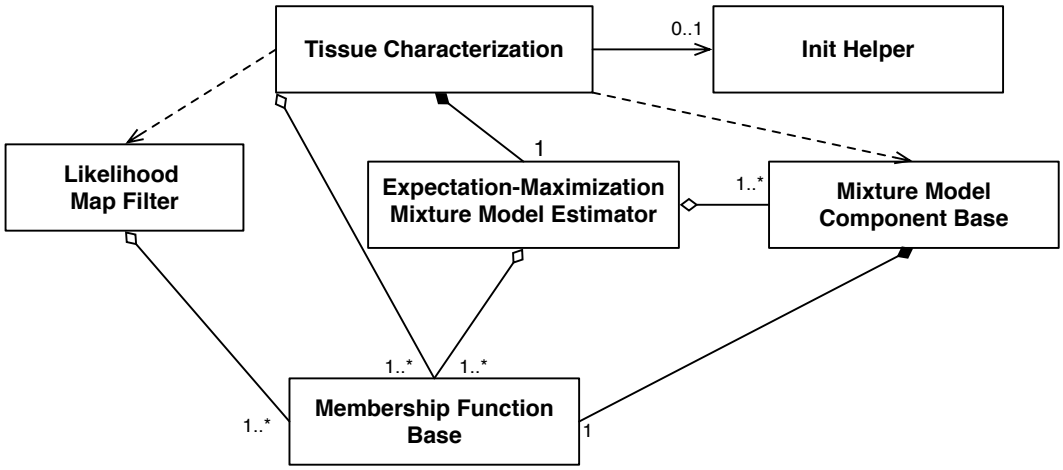

Figure 3: Tissue characterization class diagram.

3 Software Requirements

You need the following software installed:

- Insight Toolkit 4.x available in http://www.itk.org/ITK/resources/software.html
- CMake 3.2 available in http://http://www.cmake.org/download/
- Boost C++ Library 1.58 available in http://www.boost.org/users/download/

4 User's Guide

From a user's point of view, the most important file of our submission is the example application provided in `src/MixtureModel.cxx`. The goal of this example is to provide a command-line tool to perform a tissue characterization for all the mixture models described in this paper. This tool works in 3D and can trivially be extended to other dimensions. Three images are provided to be used as example (Fig. 4). The first image was acquired using a comercial ultrasound system, Philips iE33 xMatrix (Philips Healthcare, Best, Netherlands), with a transthoracic transducer X5-1 matrix-array (TTE.mhd). The second image was acquired using a similar comercial ultrasound system, Philips iE33 xMatrix, with a transesophageal transducer X7-2t matrix-array (TEE.mhd). Finally, the third image correspond to a synthetic image (Normal_000.mhd) described

in [5]. The user can choose the input image, the maximum number of iterations, the subsampling ratio, a threshold value used to improve the mixture model approach and the number of classes. The image IO operations use standard ITK filters meaning that all file formats supported by ITK can be used. This command-line tool is used within several unit tests triggered by CMake (ctest). For example, the command line to launch the example is:

```
$  ./MixtureModel ../Data/Normal_000.mhd 700 100 10 2
```

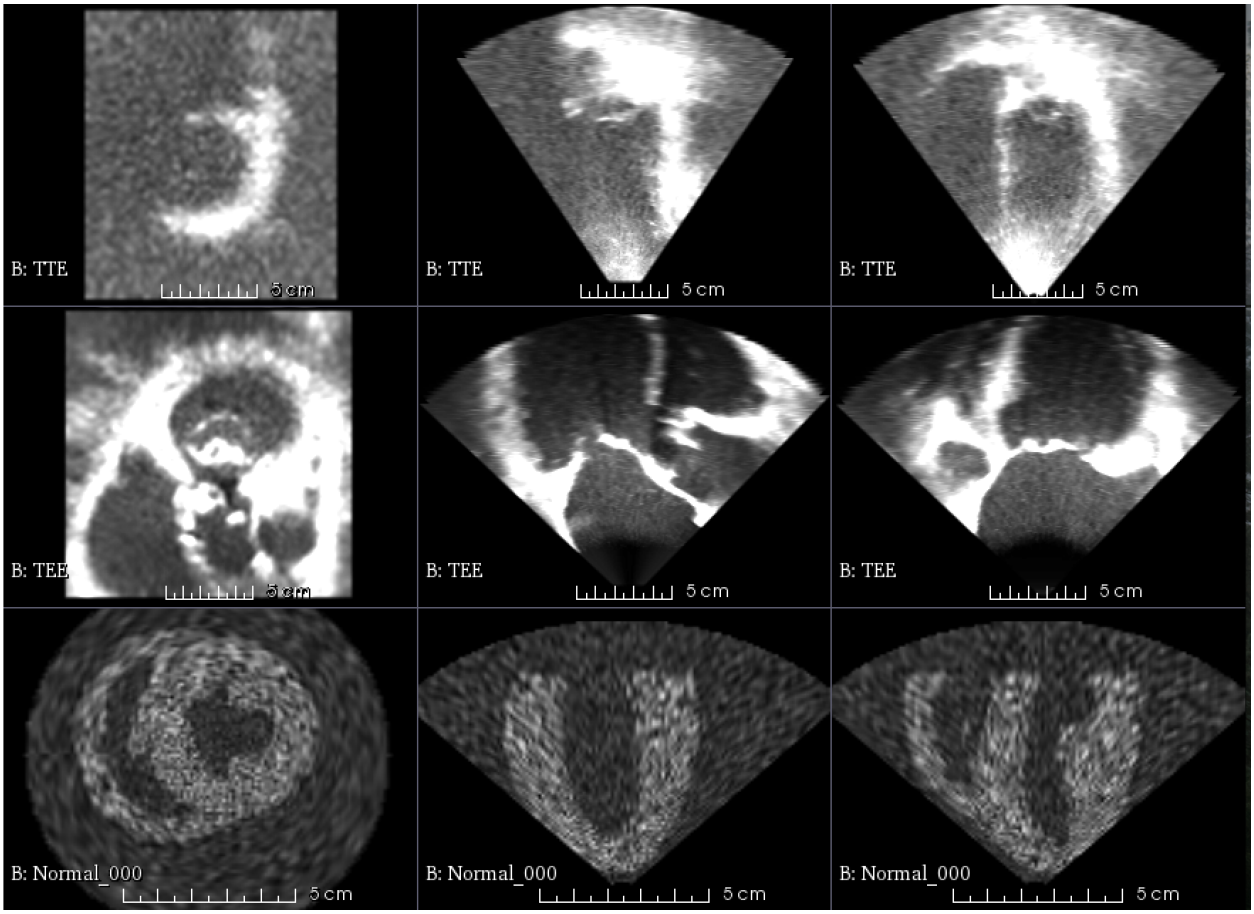

Figure 4: Dataset provided. (TTE) Transthoracic echocardiography. (TEE) Transesophageal echocardiography. (Normal_000) Synthetic image.

5 Results

In this section, we describe the probabilistic tissue characterization for the mixture model studied for the dataset provided. However, a detailed analysis about the performance of mixture models in ultrasound tissue classification can be found in [16, 17, 19]. Figures 5, 6 and 7 show the probabilistic tissue characterization for the mixture model taking into account two classes, one for the blood and the other one for the tissue. Aditionally, the processing time and memory of the tissue characterization for the mixture models studied for the dataset images provided are shown in Table 1. Since the parameter estimates for the Gamma and Generalized Gamma mixture model involve an optimization step of a cost function (`MLEFunction`), the processing time depends on particular settings and image, i.e. the number of iterations, the threshold and

	TTE (TTE.mhd)		TEE (TEE.mhd)		Synthetic (Normal_000.mhd)	
	Time (s)	Memory (kB)	Time (s)	Memory (kB)	Time (s)	Memory (kB)
Gamma Tissue Characterization	0.922776	73156	3.08795	115992	0.148964	15108
Gaussian Tissue Characterization	1.68256	1644	3.34721	1584	0.412031	644
Generalized Gamma Tissue Characterization	8.86709	2852	48.1509	2860	1.94123	708
Rayleigh Tissue Characterization	0.637129	155616	0.481413	247656	0.0925519	39640

Table 1: Processing time and memory of the tissue characterization for the mixture models studied for the transthoracic echocardiography (TTE), transesophageal echocardiography (TEE) and synthetic image provided.

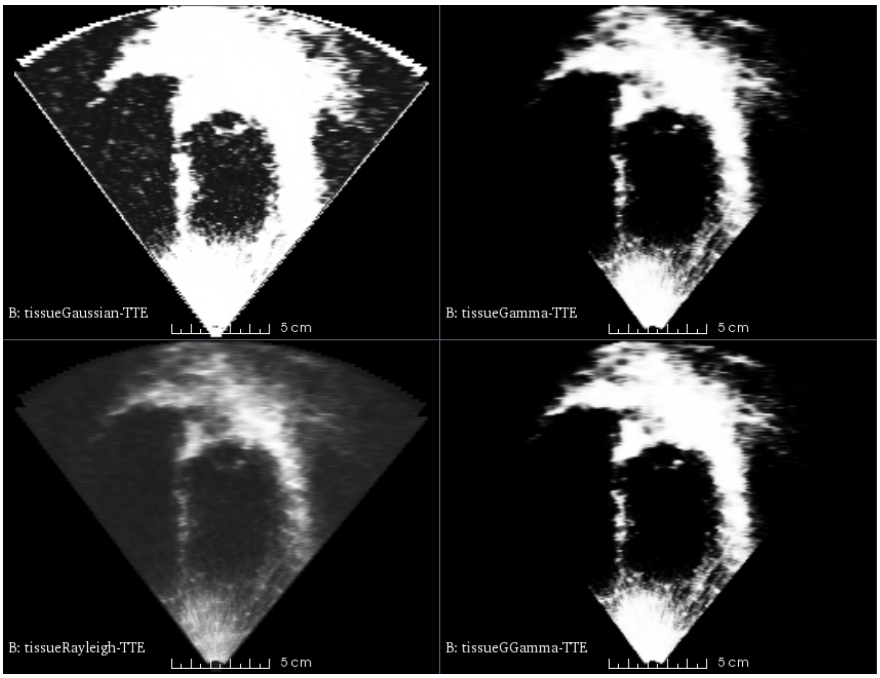

Figure 5: Tissue characterization for the Gaussian, Rayleigh, Gamma and Generalized Gamma Mixture models for the transthoracic echocardiography (TTE).

the quality of the image.

6 Conclusion

We have proposed several ITK implementations of mixture models (Rayleigh, Gamma and Generalized Gamma), and several filters used for initialization of the expectation maximization strategy and for tissue characterization. To the best of our knowledge, this is the first open-source implementation of these mixture models and filters within the Insight Toolkit. The design of our implementation tries to follow the design of ITK and thus provides templated N-dimensional filters. The code should be easily integrated to ITK and provide reusable blocks.

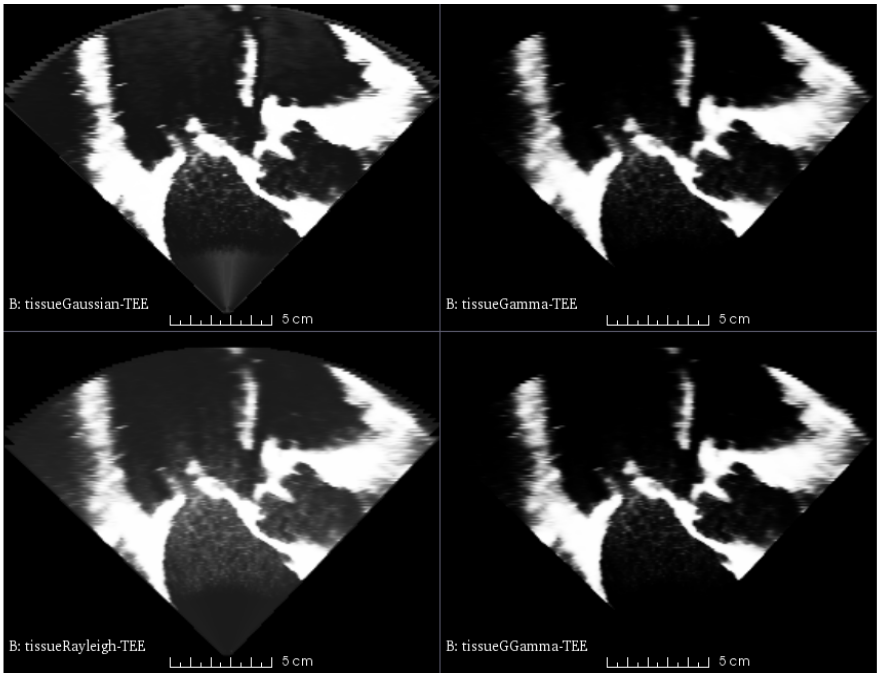

Figure 6: Tissue characterization for the Gaussian, Rayleigh, Gamma and Generalized Gamma Mixture models for the transesophageal echocardiography (TEE).

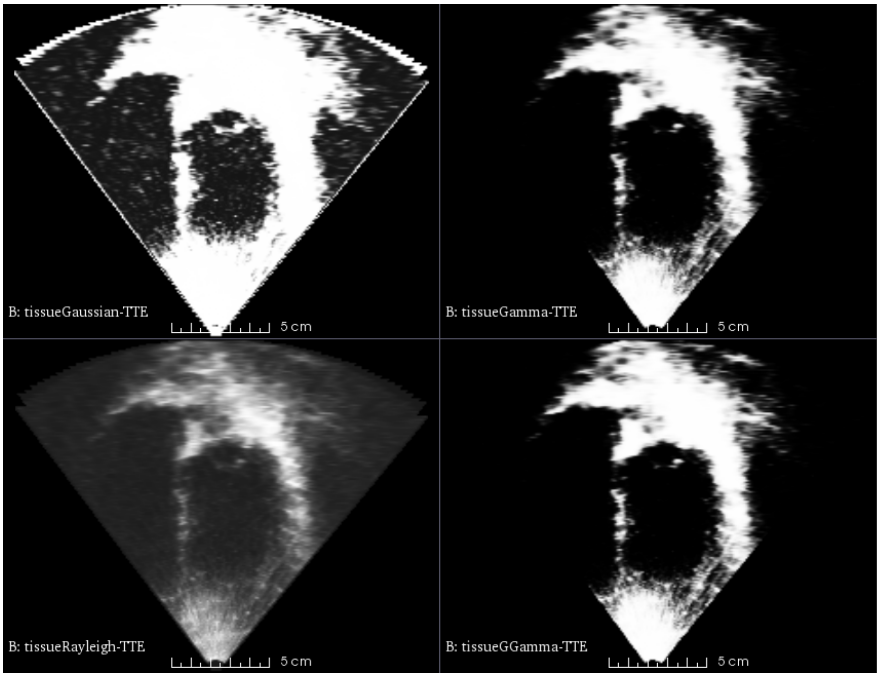

Figure 7: Tissue characterization for the Gaussian, Rayleigh, Gamma and Generalized Gamma Mixture models for the synthetic Normal_000 image.

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