REALISTIC HETEROGENEOUS TISSUE MODEL FOR EVALUATING BACKGROUND SUPPRESSION TECHNIQUES IN ENDOVASCULAR MAGNETIC RESONANCE

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1 INTRODUCTION

Endovascular therapy is used to treat vascular diseases like atherosclerosis. In endovascular therapy using magnetic resonance (MR), an image is typically acquired from a thick-slice of tissue that potentially includes a thin endovascular catheter. Conventional imaging methods generally provide low contrast between the catheter and the background tissue (Fig.1a). To improve catheter conspicuity, background tissue suppression methods are used. For example, we have recently proposed a novel tissue suppression method using Hadamard radio frequency pulses (Fig.1b) [1].

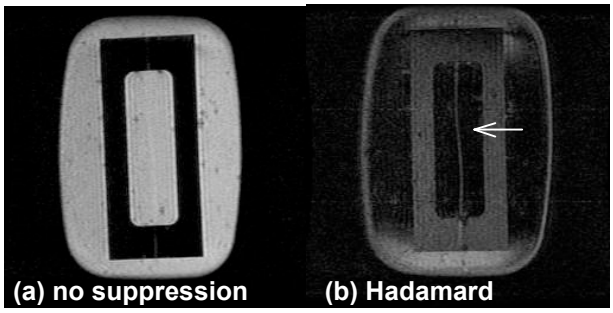

Figure 1. 4-French catheter (diameter D_c = 1.35 mm) in a uniform yogurt phantom (a) without suppression, and (b) with background suppression (HD method) [1].

Homogeneous phantoms (Fig.1) or simulated *homogeneous* backgrounds are useful for evaluating performance of different suppression techniques; however, in practice, tissue texture is heterogeneous. For better evaluation of suppression techniques, a heterogeneous tissue model that mimics representative tissue is necessary. In this paper, we propose a parametric *stochastic heterogeneous* model whose characteristics like variance, frequency and smoothness of pixel intensities can be varied to resemble real tissue. In this work, we have selected brain parenchyma as our real (or control) tissue and have developed parametric *stochastic heterogeneous* models that mimic its texture. The model, however, could be extended to mimic any other real tissue.

Our approach generates varied modeled tissues for a range of parameters. These tissues and real tissue are first quantified using texture analysis (TA). Then, we statistically assess the modeled tissues with the actual tissue to identify those textures that are most similar to control tissue.

Texture analysis is commonly used to provide quantitative measure of image texture based on statistical or syntactic features of the tissue. TA has been successfully used in a variety of areas, including separating cirrhotic liver patients from healthy subjects [2]. TA has also been used to quantitatively compare performance of MR scanners [3]. TA approaches can be based on statistical features; utilizing information based on the histogram, the run-length matrix and the co-occurrence matrices. Another approach for TA is syntactic feature evaluation that relies on placement rules governing pixel intensities in the given data. In this paper, we have used statistical TA to quantitatively determine textural features in modeled and actual tissues.

The objectives of this paper are three fold: (1) to develop a parametric stochastic heterogeneous tissue model, (2) to obtain statistical TA features from the modeled tissues for a range of parameters, and (3) to suggest model tissue parameters which generate tissues that are most representative of (or similar to) brain parenchyma. Further, we have evaluated two suppression methods namely, the Hadamard (HD) and more widely used projection dephaser (PD) [4] methods on these model textures, and compared the resulting background intensity with a simulated homogeneous background and representative background tissues.

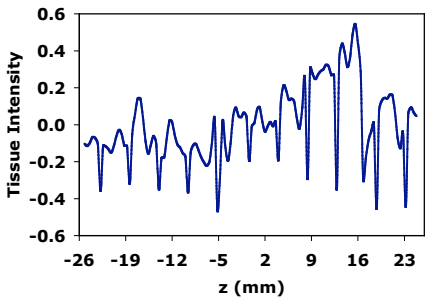

Figure 2. Sample slice profile in brain, mostly from white matter: The mean signal had been set to zero. Standard deviation was σ_b= 0.2.

2 METHODS

2.1 Brain parenchyma (Control tissue)

3D MR images of brain parenchyma were collected on a 3 T scanner (Signa; General Electric Medical Systems, Waukesha, WI) using a fast T1-weighted spoiled gradient-echo (SPGR) sequence with 4 signal averages (NEX), a matrix size of 256 × 128 × 256, a FOV of 240 mm × 240 mm, and a slab thickness of 102 mm. A high *z*-resolution (0.4 mm) was acquired to obtain sufficient samples were obtained from brain parenchyma in the anterior-posterior direction. To avoid edge effects, only the middle 126 slices (or 50.4 mm) were used. Twenty-five profiles were obtained randomly from regions of mainly white matter, as this would be the tissue excited in many endovascular applications in the head (Fig. 2 shows one such profile). The mean and standard deviation of the signal intensities along the profile were measured. The standard deviation was also measured from a region with no signal (*i.e.,* in air surrounding the head) and used to estimate image noise.

2.2 Stochastic heterogeneous background model

In order to simulate tissue texture, we assumed that real tissue was comprised of a number of spatially discrete tissue subtypes. Changes in tissue texture (*i.e*., the extent of each tissue subtype) were assumed to be Poisson-distributed; hence the distance (or subtype extent) between changes is exponentially-distributed, with a mean extent of λ. Intuitively, decreasing λ has the effect of increasing the number of tissue sub-types and thus the frequency of signal variations in the model. The intensity of each tissue sub-type was assumed to be normally distributed with zero mean and a variance of σ_b^2. A moving average (MA) filter (of length N_f) was then applied to smooth the transitions between tissue subtypes. Finally, to account for system noise, a zero-mean, normally distributed signal (variance σ_n^2) was added.

Forty-eight modeled profiles were constructed for each combination of λ, σ_b, and N_f. The selected λ's were {1/10, 1/50, 1/100, 1/126}, σ_b's were {0.1, 0.2, 0.3}, and N_f's were {1, 2, 3, 4}. The system noise was held constant at σ_n = 0.03. Subroutines to generate modeled profiles were implemented in commercial simulation software (Matlab; Mathworks, Natick, MA). Modeled profiles for each parameter combination were generated 450 times.

2.3 Feature extraction

Features for each of the forty-eight modeled textures and the control tissue (*i.e.*, actual tissue) were obtained as follows: profiles from the modeled and control tissues were normalized to have the same mean. Statistical features based on gray-tone spatial dependence (GSD) matrix [5], run-length matrix (RM) [6] were then calculated for each profile.

The GSD matrix, denoted by *p(i,j)*, contains texture information specified as the relative probability *p*, by which two neighbouring pixels, separated by distance *d* occur in the data - one with a gray value *i* and the other with a gray value *j*. The GSD matrix was calculated for *d* = 1. The RM, denoted by *RM(i,j)*, quantifies texture by determining the relative frequencies with which neighboring pixels of run-length *j* have the gray level *i*. A "run" is a set of consecutive pixels with the same gray level value. The run-length is the number of pixels in the run.

The nine features examined in this study are outlined, along with the definitions for the three features that exhibited highest *F*-statistic, as explained in data analysis section.

2.3.1 *GSD matrix based features*

Entropy is defined as

$$H = -\sum_{i}^{N_g}\sum_{j}^{N_g} p(i,j)log(p(i,j))$$

where *i* and *j* are indexes into the gray-tone spatial dependence probability matrix *p*, and N_g is the maximum number of gray levels [5]. *Entropy* measures the complexity or randomness between adjacent pixel pairs in the slice profile. For example, the entropy of models with large λ will normally have lower entropy.

Correlation (ρ) [5] which gives a measure of linear dependencies in the slice profile was computed. In addition, the *angular second moment* (*ASM*) or measure of homogeneity and *sum of squares (SS)* [5] or measure of variance of GSD matrix were computed.

2.3.2 *Run-length matrix based features*

Short run emphasis (*SRE*) inverse moment is defined as:

$$SRE = \sum_{i=1}^{N_g}\sum_{j=1}^{N_r} \frac{RM(i,j)}{j^2} R$$

where N_r is the number of run-lengths [6] and *R* is:

$$R = \sum_{i=1}^{N_g}\sum_{j=1}^{N_r} RM(i,j)$$

In SRE, runs with smaller run-lengths are given higher weighting. Generally models with small λ and N_f will have higher SRE.

Run percentage (Φ) is defined as:

$$\Phi = \frac{R}{\sum_{i=1}^{N_g}\sum_{j=1}^{N_r} j.RM(i,j)}$$

and measures the fraction of matrix in run-lengths. The value of Φ will be higher for more heterogeneous profiles.

Run-length non-uniformity (*RLN*), which is a measure of periodicity in the profile, was computed. Models constructed with small λ will generally be more periodic and, thus, have a higher *RLN*. In addition to the above, *long run emphasis* (*LRE*), *inverse moment* and *gray-level non-uniformity* (*GLN*) were computed [6]. In computing *LRE*, higher weighting is given to longer run-length gray-levels and the *GLN* is a measure of gray-level non-uniformity.

2.4 Data Analysis

For each of the nine proposed features, one-way analysis of variance (ANOVA) and Dunnett's test were performed (SPSS; SPSS Inc, Chicago, IL) between the forty-eight modeled tissues and the control tissue. The ANOVA *F*-statistic was recorded for each feature. For each feature with statistically significant changes (found by ANOVA, $p < 0.05$), Dunnett's test was used to find statistical significance between each of the forty-eight modeled tissues and the control tissue. Only modeled tissues that had non-significant features (found by Dunnett's test, $p > 0.05$) were considered for further assessment. Features with a large *F*-statistic and the smallest number of modeled-control tissue pairs with $p > 0.05$ (via Dunnett's test) formed the set of most discriminating features (MDFs).

Simulations using both HD and PD background suppression methods were conducted to demonstrate the application of stochastic heterogeneous modeling using the tissue models identified by the MDFs as being similar to brain parenchyma. The background signal, S_b, was obtained for both HD and PD methods as follows: for the HD stochastic method, the heterogeneous slice profiles were multiplied by a Hadamard slice-excitation profile [1]; For the PD method, modeled slice profiles were multiplied by a rectangular slice-excitation profile and a phase twist of 2π rad was applied across each profile. S_b was determined by summing individual intensities along each profile.

3 RESULTS

The profiles in brain parenchyma had an average signal standard deviation of 20% and an average noise standard deviation of 3% relative to the mean signal. As shown in Figs 3a and 3b, decreasing λ increased the frequency of tissue changes. Decreasing N_f also increases the frequency of modeled signal variations. The effect of increasing σ_b or σ_n was to increase the overall variance in the model tissues. The parameters (λ, σ_b, and N_f) were found to be inter-related in how they affected the texture of the modeled tissues. As shown in Figs 3c and 3d, modeled tissues constructed with different parameters had similar textures.

The nine previously described texture features were computed for each modeled tissue, as well as for the control tissue profiles. Table 1 lists the ANOVA *F*-statistic and the number of non-significant modeled textures for each feature. A large *F*-statistic signifies large between-tissue variance, and a small number of modeled textures with non-significant *p*-value suggests that a feature is capable of differentiating modeled tissues that are most similar from those that are dissimilar to the control tissue. Each of the MDFs identified several modeled tissues as being similar to control tissue. Entropy (*H*), correlation (ρ), *SRE*, *RLN* and run percentage (Φ) were identified as MDFs.

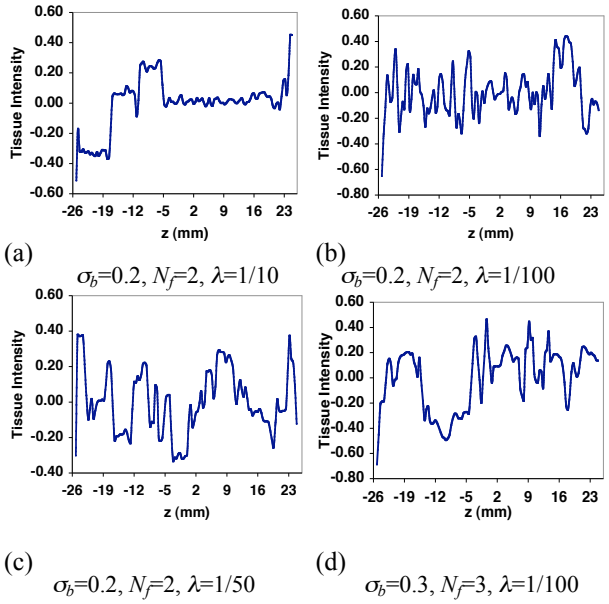

Figure 3. Tissue intensity for models when (a,b) λ is changed from 1/10 to 1/100; (c,d) σ_b is changed from 0.2 to 0.3, N_f is changed from 2 to 3 and λ is changed from 1/50 to 1/100.

Of the forty-eight modeled tissues, those that had non-significant *p*-values for three (good models), four (better models) and five (best models) of the most discriminating features are listed in Table 2. The model $\{\sigma_b, N_f, \lambda\} = \{0.3, 4, 1/126\}$ was selected by all five MDFs, suggesting this to be the most similar to control tissue. The $\{0.2, 2, 100\}$ and $\{0.2, 2, 1/126\}$ models were selected by four of five MDFs.

Background signal S_b, was calculated for the most tissue-like models (Table 2), for a homogeneous tissue model and for the control tissue. The S_b obtained from modeled tissue was smaller than S_b of control tissue; however, higher than S_b of homogeneous tissue model.

Table 1. List of features evaluated in this study. Features with a large F-statistic and low number of non-significant features formed the set of most discriminating feature (MDFs; highlighted).

Feature	*F*-statistic (ANOVA)	Number of non-significant models (Dunnet's test)
SRE	2192	7
RLN	1144	8
Run percentage, Φ	1707	8
Correlation, ρ	1123	8
Entropy, *H*	2957	11
SS	975	13
LRE	607	20
ASM	1076	26
GLN	328	34

Table 2. List of modeled textures that had a majority of the six MDFs. Calculated background signal (S_b) for control and homogenous-modeled tissues are also shown.

Modeled parameters			Supported MDFs	S_b, arb. units mean ± std dev	
σ_b	N_f	λ		HD	PD
Control Tissue			N/A	6.9 ± 5.0	15.7 ± 3.5
Homogenous Tissue Model			N/A	0.5 ± 1.9	9.74 ± 1.4
0.3	4	1/126	SRE,Φ, RLN, ρ, *H*	2.1 ± 1.6	10.9 ± 2.2
0.2	2	1/100	SRE, Φ, ρ, *H*	1.6 ± 1.3	10.2 ± 1.8
0.2	2	1/126	SRE, Φ, ρ, *H*	1.4 ± 1.0	10.0 ± 1.6
0.1	1	1/126	SRE, Φ, *H*	0.7 ± 0.5	9.8 ± 0.8
0.2	3	1/126	SRE, Φ, *H*	1.4 ± 1.1	10.4 ± 1.5
0.3	1	1/50	SRE, Φ, *H*	3.9 ± 3.1	11.3 ± 4.1

4 DISCUSSION AND CONCLUSION

We have proposed and evaluated a parametric stochastic *heterogeneous* tissue model to mimic some of the textural properties of actual tissue. A statistical approach for TA was performed to quantify the features of modeled and actual tissue profiles. We used ANOVA followed by Dunnett's test to determine modeled tissues that are most similar to selected brain parenchyma. Six of the forty-eight modeled tissues were found to be the most similar to control tissue. All of these modeled tissues were chosen based on features with very high *F*-statistic. A large *F*-statistic indicates the ability of a particular feature to differentiate similar from dissimilar modeled tissues versus the control tissue. Although, previous studies [7] have indicated that RM-based features are less effective for image texture analysis, we obtained statistical significance from RM based features (*i.e.*, *SRE*, *RLN* and Φ).

The key texture characteristics in tissue are the extent and intensity of each constituent tissue subtype. We have modeled these variations with four parameters: σ_b, σ_n, λ and N_f. The parameters σ_b and σ_n were used to change the standard deviation of pixel intensities in a tissue subtype, λ was used to vary the extent of tissue subtype in a stochastic manner and N_f was used to smooth the edges between tissue sub-types. We assumed that the intensity of the tissue subtypes was normally-distributed - based on the measured distribution in control tissue. Our assumption that the extent of the tissue subtypes was exponentially-distributed is analogous to common practice in communication systems where the time between two events is modeled as an exponential random variable.

To ensure determination of a valid tissue model, the range of model parameters had to be carefully selected. Modeled textures were constructed for σ_b both smaller and larger than the observed variance in the control tissue (Fig 2). The range of λ was selected to include both lower and higher frequencies than found in the control tissue. Investigation of all models, showed that because of the inter-relationship existing between parameters, models within certain ranges of parameter had similar textures.

The GSD matrix and RM-based features have been used to classify 2D image textures [2,3,7]. We have used these features to compare 1D-modeled tissues with the control tissue. For 2D image texture analysis, the GSD-matrix and RM-based features are defined at angles of 0°, 45°, 90° and 135° [5,6]. With 1D slice profiles, each pixel has, at most, two neighbours. Hence, the GSD matrix and RM based features were computed in one direction only. Each of the features used in this study characterizes structures such as periodicity, linearity, complexity or frequency variations of pixel intensities in the slice profile. Other features based on the co-occurrence matrix might provide additional information on modeled texture [5] and perhaps allow for better texture characterization. In our method, data were considered from MDFs only. Combining all features with appropriate weights is an alternative approach.

The best six heterogeneous tissue models were successfully applied to assess the performance of HD and PD background suppression techniques in endovascular MR. The average S_b obtained from the six modeled textures was intermediate to that obtained from homogeneous tissue model and control tissue for HD and PD methods (Table 2). This demonstrates the suitability of these tissue models to generate textures that more accurately mimic tissue.

We have shown that the *stochastic heterogeneous* tissue models can mimic actual tissue and have tested the applicability of this model in assessing background suppression methods. Our model can be extended to include more complex models where portions of the modeled profile have different parameters. Such would be the situation when the excited slab includes multiple different tissues.

5 REFERENCES

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