CONTEXTUAL AND VISUAL MODELING FOR DETECTION OF MILD TRAUMATIC BRAIN INJURY IN MRI

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ABSTRACT

Mild traumatic brain injury (mTBI) is difficult to detect as the current tools are qualitative, which can lead to poor diagnosis and treatment. The low contrast appearance of mTBI abnormalities on magnetic resonance (MR) images makes quantification problematic for image processing and analysis techniques. To overcome these difficulties, an algorithm is proposed that takes advantage of subject information and texture information from MR images. A contextual model is developed to simulate the progression of the disease using multiple inputs, such as the time post-injury and the location of injury. Textural features are used along with feature selection for a single MR modality. Results from a probabilistic support vector machine using textural features are fused with the contextual model to obtain a robust estimation of abnormal tissue. A novel rat temporal dataset demonstrates the ability of our approach to outperform other state of the art approaches.

Index Terms— Context, Low Contrast Images, Magnetic Resonance Images, Traumatic Brain Injury

1. INTRODUCTION

Mild traumatic brain injury (mTBI) is a silent epidemic in the United States [1]. mTBI includes sports injuries, blast related injuries to military personnel, injuries in automobile accidents and falls in the workplace. Much of the current public awareness of mTBI is due to increasing popular press reports and long term studies of athletes who exhibit numerous neurological deficits [1].

Evaluation of mTBI is generally qualitative using indications such as the loss of consciousness, loss of memory, alteration in mental status, focal neurological deficits, Glasgow coma scale and visual assessment of neuroimaging studies, if performed. When MRI or computed tomography (CT) is performed to assist in diagnosis qualitative assessments do not provide a measure of the amount and location of injured tissues. Quantitative analysis is essential for improved diagnosis and treatment. Current approaches for quantitative analysis of moderate and severe TBI have been semi-automated [2]. However, mTBI has subtle MR signatures that can result in failure of current automated approaches. Computational methods used in detecting abnormalities in brain tumors and multiple sclerosis have been considered for mTBI [3,4]. Most of the current computational approaches rely on image registration to bring all the data into a common space. Once the objects are in the registered space, a model of the normal brain is constructed. There are inter-subject variations within registered brains, leading to distributions to be made for a normal appearing brain model. Tissue level alterations in mTBI have low contrast and encompass small regions (Figure 1), so the lesion values (such as T2) may fall within the values of the normal tissue distributions. Previous methods have used texture to increase the discriminatory value of MR images [4]. The proposed approach adopts and extends this concept to improve detection of brain abnormalities following mTBI.

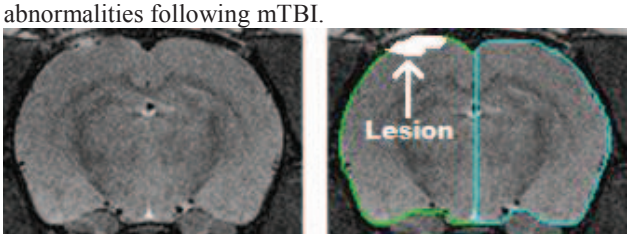

Figure 1: Sample T2 weighted MR images from the rodent model dataset. Left, original image; Right, manual detection. Lesion is the white highlighted region

To overcome the low contrast appearance of mTBI in MR images a contextual model is proposed. Context has been an active research area in image analysis [5]. Context is needed when traditional visual based methods for detection fail. Context is defined as, "any information that might be relevant to object detection, categorization and classification tasks, but not directly due to the physical appearance of the object, as perceived by the image acquisition system [5]." Various types of context can be used for object detection: local pixel, 2d scene gist, 3d geometric, semantic, photogrammetric, illumination, weather, geographic, temporal, and cultural [6]. The proposed contextual model utilizes semantic context to build a probability map for estimating the location of mTBI abnormalities.

The contributions of this paper are: 1) a contextual disease model based on Bayesian networks to estimate the spatial location of mTBI abnormalities. The contextual

model helps to overcome the low contrast nature of the abnormalities. 2) The contextual model is fused with a visual model that uses textural features to build a probabilistic support vector machine (PSVM). 3) A novel extensive temporal dataset of rats with mTBI is used. It consists of rat controlled cortical impact (CCI) mTBI with samples of the disease at multiple time points post-injury using T2 weighted MRI. The proposed method is compared to other state of the art methods on this dataset.

2. TECHNICAL APPROACH

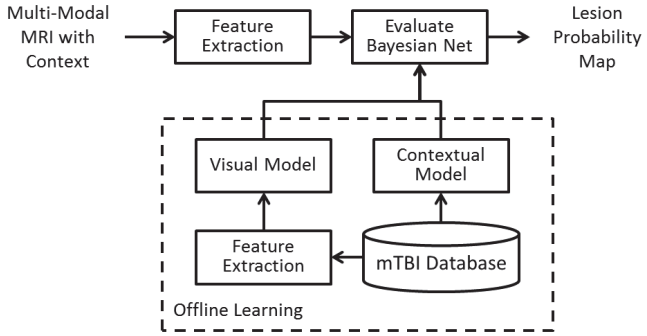

Figure 2: System flow diagram.

The general flow of the proposed system for detecting brain mTBI abnormalities is shown in Figure 2. A database of manually extracted mTBI volumes, and their contexts, provides previous experiences of correctly classified abnormalities. This data is used to train both the visual and contextual models. The visual model utilizes the volume information by constructing a PSVM with 3D textural features computed from each volume. While the contextual model utilizes a Bayesian network based on the known contextual information from all the samples. The visual model captures visual cues from the texture space, and the contextual model captures location and temporal information about the mTBI abnormalities. When an MR volume enters the system it undergoes texture feature extraction followed by evaluation in the Bayesian network. Along with the MRI volume, contextual information may also be passed to the system. The contextual information can be an exact (e.g. 1day since injury) or a ranged value (eg. 3-5days since injury). Evaluation of the Bayesian network with a sample estimates abnormality at every voxel.

2.1. Contextual Modeling

Horsfield et al. [7] have used Contextual models based solely on the location information by using the average location of all the binary masks representing the positive detections in a known database. Unlike this work, in this paper a more detailed model of the disease is incorporated into our Bayesian network (Figure 3) that allows for multiple semantic contextual inputs. The contextual inputs in the proposed system are: time since injury, central location of injury, and anatomical constraints. Each node in the network is a random variable. The output is a probability map calculated using eq. (1) at every voxel. Having a known distribution for each node reduces the number of training samples needed to sufficiently represent the distribution. Parameters of each distribution are learned from known examples in the database.

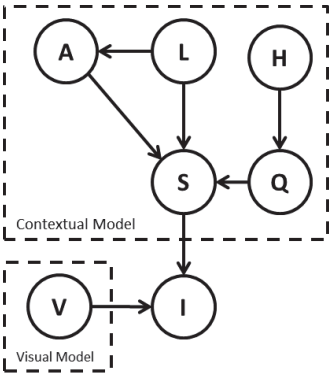

Figure 3: Graphical representation of the Bayesian network, showing the dependencies of each distribution. A – anatomical constraints, L – focal location of injury, H – time since the hit event, Q – quantity of injury with time, S – spread of injury, V – visual, I – injury.

$$P(I|S,V) = \sum_{\forall i|P(L_i)>0,\, \forall j|P(H_j)>0} P(L_i)P(H_j)P(S_{ij})P(V) \quad (1)$$

2.1.1 Time

Time is a powerful semantic input as mTBI will evolve over time. It is modeled as an exponential distribution see eq. (2), which describes the time since the mTBI event occurred. Normally, subjects are seen soon after the mTBI event, which is captured in equation (2). λ is a parameter learned from the data to control the rate of decay.

$$P(H) = \lambda e^{-\lambda t} \quad (2)$$

$\boldsymbol{Q}$ is the probability of the volume of injury over time. This distribution is modeled using a log-normal distribution (3). This distribution follows the natural progression of the disease where there is a temporal peak in abnormalities that tapers over time. Two parameters need to be learned in this distribution μ and σ.

$$P(Q|H) = \frac{1}{H\sqrt{2\pi\sigma^2}} e^{-\frac{(\ln(H)-\mu)^2}{\sqrt{2\sigma^2}}} \quad (3)$$

2.1.2 Anatomical Constraints

When considering the progression of mTBI there are certain anatomical barriers that restrict the disease. There are two natural boundaries that TBI is not likely to progress beyond: a) The midline, which is a physical separation to the left and right hemispheres of the brain, and b) the corpus callosum due to the mild nature of the injury.

2.1.3 Location and Spread

An estimated location of the focal point of the mTBI is one of the possible contextual inputs. To represent this input as a

distribution two variables are considered, the distance from the midline along the perimeter and the z axis location. These are modeled using a Gaussian distribution since it is known that many TBIs occur to the front of the head.

The function that unifies these concepts is a spread function (4). This sigmoid is the Gompertz function and is used to model tumors and population growth. Each asymptote is approached at different rates, which can be controlled by parameter selection (Figure 4). The rate of change is not only determined by parameters (***m***,***n***), ***Q*** also affects the shape of the function. When ***Q*** is small, the function has a sharp transition between the asymptotes and a gradual slope when ***Q*** is large. This represents the location being well known when there is supposed to be less injury and more uncertainty when there is supposed to be more injury. ***m*** determines the shift in the sigmoid and ***n*** controls the shape of the slope.

$$P(S|L,A,Q) = Ae^{\frac{-m}{Q}e^{\frac{n}{Q}d}} \quad (4)$$

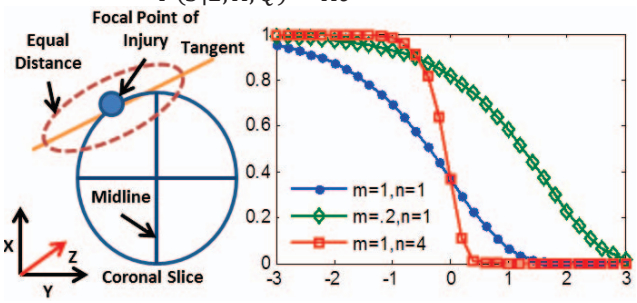

Figure 4: Left: Diagram explaining the weighted distance function. Right: Effects of the parameters in eq. (4).

d (5) is a distance metric, weighted by ***Σ***, from the central point of contact in the xyz space. ***Σ*** accounts for the rotation of the weighted distance function. The distance function is weighted such that the major axis of change is along the same axis as the xy (coronal) tangent at the central point of contact. **x** is a point in the 3D space. σ_x and σ_y are parameters that set the weight of the distance along the major and minor axis respectively. The injury spreads along the perimeter of the brain more than into the center of the brain. This is due to the anatomy of the brain. ***g*** is the weight of the distance in the z axis. The tangent ***θ*** at the central point of contact is calculated using Fourier descriptor of the perimeter with the upper twenty percent of the spectrum set to zero to give a smooth surface. Each parameter in the contextual model is estimated using non-linear least squares. The resulting volume from this equation is a probability map.

$$d = \sqrt{(x-L)^T \Sigma (x-L)} \quad (5)$$

$$\Sigma = \begin{bmatrix} a & b & 0 \\ b & c & 0 \\ 0 & 0 & g \end{bmatrix} \quad (6)$$

$$a = \frac{\cos^2\theta}{2\sigma_x^2} + \frac{\sin^2\theta}{2\sigma_y^2} \quad (7)$$

$$b = \frac{\sin 2\theta}{4\sigma_x^2} + \frac{\sin 2\theta}{4\sigma_y^2} \quad (8)$$

$$c = \frac{\sin^2\theta}{2\sigma_x^2} + \frac{\cos^2\theta}{2\sigma_y^2} \quad (9)$$

2.2. Visual Modeling

Chang et al. [8] proposes a method for PSVM, which allows for SVM with maximum a posteri probability (MAP) estimation. This assigns a probabilistic output for each sample, so it can be fused with the results from the contextual model.

The features that are used in PSVM ultimately determine the discriminatory ability of the model. T2 MRI can visualize edema (increased water content) and increased extravascular blood. While both of these can be visualized in the MRI the values on the image are only locally increased at the injury site and are subtle (Figure 1). To increase the discriminatory ability of the MRI texture features are extracted. The extracted texture features include: local entropy, range, mean, variance, skewness, kurtosis, and xyz gradients. Feature selection is then carried out by choosing the features with the largest Bhattacharyya distance between the normal and abnormal distributions. PSVM is trained using the radial basis function kernel due to the low dimensionality of the space which gives a nonlinear boundary in the feature space. The visual model is multiplied with the contextual model since they are independent for a final probability estimate of the injury abnormality due to mTBI as shown in eq. (1).

3. EXPERIMENTAL RESULTS

3.1 Dataset

Sprague Dawley rats were used as an animal model of mTBI using controlled cortical impact (CCI). A total of 51 mTBI brain volumes ranging 1-60 days after injury are used. MRI data were acquired using a Bruker Advance 4.7T for T2 weighted images (T2WI; TR/TE/FA=3453 ms/20 ms/20°, 25x1 mm slices) with a 256^2 matrix and 3cm field of view. ROIs were manually segmented using Cheshire image processing software (Hayden Image/Processing Group, Waltham, MA) and included the right and left hemispheres and injured tissue volumes that were defined as abnormal (hyper/hypo-intense) signal intensities within the cortex with the remaining tissues designated as normal appearing brain matter.

3.2 Experimental Results

To give a sense of where errors are coming from and how the regions are correctly detected the receiver operator characteristic (ROC) curve is given. ROC illustrates the tradeoff between the true positive rate (TPR) and the false positive rate (FPR) The Dice coefficient eq. (12) measures set agreement, which is the intersection of the known object and the detected object divided by the size of the known and

detected objects. Dice gives a better idea of the intersection between the detected object and the actual object since it does not include true negatives in the calculation. In eq. (12) the notations are: true positive (TP), False Positive (FP), False Negative (FN).

$$Dice = \frac{2TP}{(TP + FP) + (TP + FN)} \quad (12)$$

Testing was carried out using leave one out validation. Three cases of context were tested: all contexts known, focal position unknown, and focal position and time unknown. Figure 5 shows the receiver operator characteristic (ROC) curve for each context case demonstrating that with increasing context the performance increases.

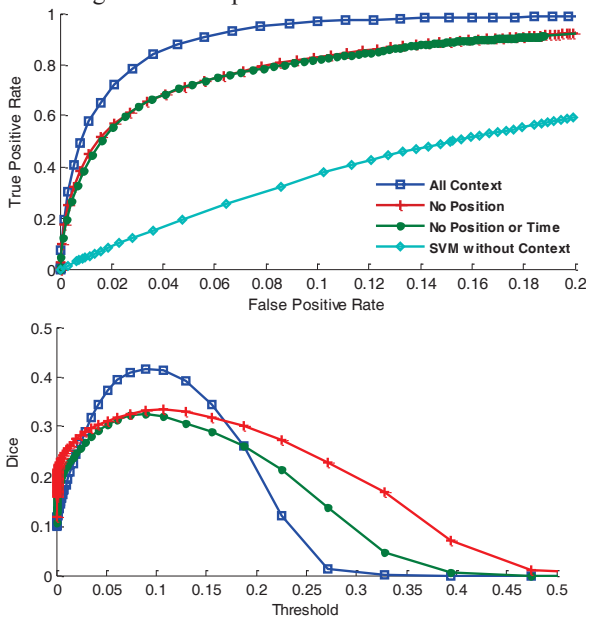

Figure 5: Top: ROC plot on varying contextual inputs. The threshold on the probability map is varied. Bottom: Dice versus threshold curves.

Figure 6: Example outputs from the thresholded probability maps of the proposed approach. The thresholds are from the highest point of the Dice curves. Left: All contexts, Middle: No Position, Right: No Context. Green: TP, Teal: TN, Red: FP, Brown: FN. (note: should be viewed in color.)

Table 1 shows the performance comparison (mean and standard deviation) of the proposed approach against two state-of-the-art approaches. Sun et al. [9] is a data driven approach that uses asymmetry to detect brain abnormalities. Anbeek et al. [3] is a model approach that puts the known database into a registered space and uses KNN including xyz as a feature to determine lesions.

	TPR	FPR	Dice
Symmetry [9]	0.03±.09	0.003±.007	0.02±.04
KNN [3]	0.09±.02	0.002±.001	0.15±.02
SVM Alone	0.38±.16	0.102±.08	0.09±.07
All Context Known	**0.91±.17**	**0.06±.008**	**0.42±.15**
Position Unknown	0.83±.25	0.10±.011	0.34±.2
Context Unknown	0.81±.23	0.10±.02	0.32±.12

Table 1: Comparison with state of the art approaches. All values are the mean results with leave one out validation. The threshold is at the highest average Dice value.

4. CONCLUSIONS

This paper proposes a system for detecting mTBI from T2 weighted MR images. The model is a fusion of a visual model that utilizes texture features to enhance low contrast detection and a semantic contextual model that estimates the location of the injury. The method utilizes contextual knowledge that may be known when a subject is being evaluated. Analysis of an mTBI dataset by our model outperformed other state of the art approaches. The proposed approach performs better than the other approaches even under varying contextual inputs. This model can be expanded to include repeated mTBI events.

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