Abstract—We present a novel method for the automatic classification and grading of liver fibrosis based on hepatic hemodynamic changes measured non-invasively from fMRI scans combined with hypercapnia and hyperoxia. The supervised learning method automatically creates a classification and grading model for liver fibrosis grade from training datasets. It constructs a statistical model of liver fibrosis by evaluating the signal intensity time-course and local variance in T2'-W fMRI scans acquired during the breathing of air, air-carbon dioxide, and carbogen with a hierarchical multi-class binary-based Support Vector Machine (SVM) classifier. Two experimental studies on 162 slices from 34 mice with the hierarchical multi-class binary-based SVM classifier yield a 96.9% separation accuracy between healthy and histological-based fibrosis graded subjects, and an overall accuracy of 75.3% for separation between healthy, fibrosis, and cirrhosis subjects. These results outperform existing image-based methods which can discriminate between healthy and mild grade fibrosis subjects.

Index Terms—abdominal, characterization, fibrosis, liver, machine learning, fMRI imaging, early detection.

I. INTRODUCTION

CHRONIC liver diseases are the 12th leading cause of death in the USA. Hepatic fibrosis occurs in response to almost all causes of chronic liver injury, and consists of an accumulation of fibrillar extracellular matrix. Although hepatic fibrosis was long thought to be an irreversible process, it is accumulation of fibrillar extracellular matrix. Although hepatic fibrosis occurs in response to almost all causes of chronic liver injury, and consists of an accumulation of fibrillar extracellular matrix. Although hepatic fibrosis was long thought to be an irreversible process, it is now clear that it is a dynamic process with significant potential for reversal.

The degree and rate of liver fibrosis progression are important prognostic factors in patients with chronic liver disease [1], [2]. The degree of fibrosis is currently assessed with a biopsy, an invasive procedure that carries a risk of serious complications with a procedure-related mortality rate of 1:10,000 [3]. Liver biopsy has additional limitations, including: 1) lack of functional assessment of the whole organ and disease development grading due to the local nature of the information; 2) biopsy sampling error [4], [5], [6]; 3) complications and patient discomfort [7], [8]; and 4) morbidity and ethical issues of repeated liver biopsies.

Existing non-invasive imaging methods for liver fibrosis grading are based on elastography [9], [10], texture analysis [11], perfusion [12], and diffusion [13], [14], [15]. For a detailed review of current liver fibrosis imaging methods, see [12], [16]. Elastography-based methods require modeling the mechanical properties of the liver parenchyma. Current models of the liver mechanical behavior are not patient-specific, and therefore have limited accuracy [9], [10], [17]. In addition, elastography-based imaging requires attaching specialized mechanical equipment to the patient that must also fit into the imaging device. Texture and perfusion-based methods require the intravenous injection of a contrast agent, which may induce renal toxicity and is a major cause of acute renal failure [18], [19]. The main limitations of these imaging methods include low spatial resolution in radionuclide studies, and lack of reproducibility in Doppler ultrasound and radiation exposure in CT. Diffusion weighted imaging (DWI) allows non-invasive measurement of the microscopic motion of water in tissue. Several studies have evaluated the use of DWI and apparent diffusion coefficient values for the diagnosis of hepatic fibrosis or cirrhosis [13], [14], [15], [20], [21]. DWI has been successfully applied to differentiate cirrhotic from healthy tissue. However, attempts to differentiate between earlier stages of fibrosis in humans showed a much lower diagnostic performance [16].

A key physiological observation is that changes in liver blood supply can serve as an indicator for the normal activity of the liver tissue. While the blood supply of the healthy liver enters predominantly from the portal vein, in patients with different stages of hepatic fibrosis, a higher proportion of the liver blood flow is derived from the hepatic artery [22], [23], [24]. Thus, monitoring hemodynamical changes can serve as the basis for detection and staging of hepatic fibrosis. In perfusion-based CT and MRI images, a good separation of the arterial from the portal phase requires a high temporal resolution, which comes at the cost of reduced spatial resolution. Current experience [16] shows that these methods can differentiate between healthy and high-grade fibrosis patients (f0 and f4-5 stages) [25]. However, they cannot differentiate the earlier stages (f1-3) [16] based on the Batts and Ludwig scoring system [26].

Recently, Abramovitch et al. [27], [28], [29] demonstrated the feasibility of functional MRI (fMRI) combined with hypercapnia and hyperoxia for monitoring changes in liver perfusion and hemodynamics without contrast agent administration. They established that this method enables imaging of the hemodynamic changes occurring under different pathologi-
eral states such as liver tumor progression[29], liver fibrosis [30], acute bleeding and during liver regeneration [27], [28]. Unlike contrast agent based methods, this method can detect steady state levels without compromising between the spatial and temporal resolutions. Since the hemodynamical changes in low-grade fibrosis can be subtle, relative, and spatially distributed, direct observation of these changes is sometimes difficult, unreliable, and time-consuming [31]. In Barash et al. [27] and in Freiman et al [31], only two parameters were extracted from the entire time-course scans based on the differences between the mean fMRI signal intensity values during the inhalation of each gas. However, basing the entire analysis on mean values may lead to erroneous conclusions, as it ignores the entire kinetics information and the variance of each scan. The hemodynamic fMRI technique has shown great promise on mice and is currently under evaluation for humans.

In this paper, we present a supervised learning method for the automatic creation of a classification and grading model for mice liver fibrosis from fMRI signal intensity time-courses [30]. Since fibrosis grades are hierarchical, our method uses the entire signal intensity time-course of each image as input to a multi-step classifier that discriminates them into Batts and Ludwig fibrosis grades. First, the classifier separates between maps of healthy and fibrotic livers (of all grades), and then between cirrhosis (f4-f5) and fibrosis grades using a binary Support Vector Machine (SVM). Since this method does not require a mechanical model and uses all the time-course information, it is potentially more accurate than existing methods and provides a quantitative evaluation of the entire liver. This may provide the radiologist an additional tool for better separation of the fibrosis level.

To evaluate our supervised learning method, we compared its performance to the main traditional multi-class classifiers: 1) One Against One Support Vector Machine (OAO-SVM) [32], [33]; 2) One Against All Support Vector Machine (OAA-SVM) [34], [35], [36]; 3) Multi-class Support Vector Machine (MSVM) [37], [38]; and 4) K-Nearest Neighbor (KNN) classifier [39]. All the computer generated classifiers were compared to the ground-truth classification method based on histological analysis performed by an expert pathologist. Experimental results on 162 images from 34 mice show that the fMRI based multi-class classification method can accurately differentiate between healthy and low grade fibrosis livers based on the imaging results at a level comparable to histology. This is highly encouraging since existing imaging-based methods can distinguish between healthy and mild grade fibrosis subjects [16]. These results suggest that the fMRI based approach may be useful for human datasets, with appropriate pre-processing steps such as respiratory motion corrections [40] and liver segmentation [41].

### II. Methods

Our method follows the supervised learning paradigm. First, we build an hierarchical multi-class classification model from a fMRI dataset of images from healthy and fibrotic subjects that were graded based on histological analysis. The model performance was evaluated by classifying and grading datasets of additional subjects with available grading based on histological analysis. We describe first the animal models that were used to induce fibrosis and their ground-truth grading based on histological analysis.

#### A. Fibrosis mice models

Human liver fibrosis could result from either toxic liver injury, genetic diseases or viral infections. Therefore, an accurate animal model that represents both phenotypes is required [42]. For our study, we define two experimental mice models of fibrosis, one for each phenotype.

The first model is chemically induced by intraperitoneal administration of carbon tetrachloride (CCl4) to (C57BL/6) mice [43] for different time periods (1–4 weeks). To allow assessment of fibrosis resolution, the CCl4 administration was stopped for two additional weeks. The second model is multidrug resistance protein 2 gene knockout (Mdr2−/−) mice at ages 6–16 weeks. The Mdr2−/− mice are deficient in the canalicular phospholipid flippase and spontaneously develop liver injury and chronic inflammation due to the absence of phospholipid from bile, which leads to the formation of periportal biliary fibrosis at their early age [44].

We use 34 mice for the two experimental models of liver fibrosis. Each mouse was scanned once and sacrificed immediately after. The fibrosis grade of each mouse was determined from liver specimens taken shortly after the MRI scan. Histological slides were stained with hematoxylin, eosin, and Masson’s trichrome for the identification of connective tissue. All histological slides were reviewed by an expert pathologist who was blind to the fMRI results. Table I shows the distribution of the fibrosis grades of the entire mice population.

<table>
<thead>
<tr>
<th>GRADE</th>
<th># MICE</th>
<th># SLICES</th>
<th>MODEL</th>
</tr>
</thead>
<tbody>
<tr>
<td>f0</td>
<td>6</td>
<td>28</td>
<td>healthy</td>
</tr>
<tr>
<td>f1</td>
<td>2</td>
<td>9</td>
<td>CCl4 injected</td>
</tr>
<tr>
<td>f2</td>
<td>3</td>
<td>12</td>
<td>CCl4 injected</td>
</tr>
<tr>
<td>f3</td>
<td>2</td>
<td>10</td>
<td>Mdr2−/− mice</td>
</tr>
<tr>
<td>f4</td>
<td>4</td>
<td>20</td>
<td>CCl4 injected</td>
</tr>
<tr>
<td>f5</td>
<td>1</td>
<td>5</td>
<td>CCl4 injected</td>
</tr>
<tr>
<td>f6</td>
<td>7</td>
<td>35</td>
<td>Mdr2−/− mice</td>
</tr>
<tr>
<td>f7</td>
<td>2</td>
<td>9</td>
<td>Mdr2−/− mice</td>
</tr>
<tr>
<td>TOTAL</td>
<td>34</td>
<td>162</td>
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</tr>
</tbody>
</table>

**TABLE I:** Fibrosis grades distribution for the mice population.
Fig. 1: Data for three representative mice with different fibrosis grades: (a)-(c) Anatomical T1-weighted images (the liver contour is red; the white bar is 1 cm long), and their corresponding; (d)-(i) fMRI-based hemodynamic maps [27]; (j)-(l) local variance maps, and; (m)-(o) histological specimens stained with Masson’s trichrome stain (the connective tissue is blue).

Hemodynamics were evaluated from T2*-weighted gradient echo images (repetition time = 147 ms; echo time = 10 ms; flip angle = 30°; field of view = 3 cm; 256×128 pixels; in-plane resolution = 117 μm; spectral width of 25,000 Hz; two averages; 37 secs/image) acquired during breathing of air, air-CO₂ (95% air and 5% CO₂), and carbogen (95% oxygen and 5% CO₂) [27]. Eight repeats were acquired at each gas mixture. Zero filling of k-space data was applied to obtain 256×256 pixels matrices. Maps of the percentage change in the intensity of the MRI signal induced by hypercapnia (ΔSCO₂) and by hyperoxia (ΔSO₂) were computed (5 slices per liver) as described in [27], [28]. A few slices that showed breathing-motion artifacts were excluded from the study. We performed B-spline based non-rigid registration [45] and concluded that there was no need to co-register the images (e.g., that the deep anesthesia and table immobilization guarantee that there is no motion).

C. Classification scheme

Fig. 3 shows the classification scheme steps. First the data is normalized to overcome the inter-subject variability of the gradient echo signal. Next, feature vectors are computed from the raw data. Then, the data from subjects with available observer-based classification is used to construct a classification model. Finally, the classification model is used to classify new subjects. We describe each step in detail next.
1) Data normalization: The input dataset consists of a set of fMRI-based signal-intensity time-courses representing hepatic response under hypercapnic and hyperoxic challenges for each pixel of the liver. Normalization of the hemodynamic response vectors is necessary due to the high variability of the gradient echo signal from different subjects and at different time points. Since the goal is to learn from changes in the signal intensity of the fMRI images during the different gas inhalations, we use the room-air breathing part of the time-courses to normalize the fMRI signal-intensity values of the entire vector.

The normalization proceeds as follows: First, the liver contours are interactively segmented on the corresponding T1-weighted images with the Analyze-7.0 software (BIR Mayo Clinic, Rochester, Minnesota) and the remaining structures are eliminated from the fMRI images. Next, the first time point of each inhaled gas is removed to ensure the stability of the fMRI signal during the inhalations. Then, the hemodynamic response vectors are normalized to be correlated to a mean value of 1 during room-air breathing:

\[
\tilde{S}(\vec{x}) = \frac{I(\vec{x})}{\mu_{\text{air}}},
\]

where \(\vec{x}\) is the pixel coordinates and \(\mu_{\text{air}}\) is the trimmed mean intensity value during room-air breathing. The 10% trimmed mean, achieved by removing the 10% bounds in each side, was used to reduce MRI noise and discard pixels from large blood vessels. Finally, the median liver hemodynamic response vector is computed for each fMRI slice.

Fig. 1 shows the anatomical T1-weighted MRI images of three representative subjects with fibrosis levels f0, f2 and f4 (a-c) along with their corresponding fMRI-based hemodynamic response maps (d-i) [27], local variance measured as explained in Sec. II-C2 (j-l), and their corresponding histological specimens (m-o). Fig. 2 shows the average normalized time-course hemodynamic response vectors of the five fibrosis grades, along with their standard deviations.

2) Feature vector extraction: The feature vector for the classification consists of the median signal-intensity time-course representing the hepatic response under hypercapnia and hyperoxia for each region of interest (ROI) that covers the liver in the slice:

\[
g_1 = \text{median } \tilde{S}(\vec{x},t)
\]

where \(t \in \{0, \ldots, T\}\) and \(T\) is the number of time points in the normalized hemodynamic response vector.

Since the median is computed over the pixel-wise hemodynamic response vectors, it does not reflect the spatial homogeneity of the hemodynamic response. To include this information, we also computed a local variance measure which represents the pixel’s neighborhood hepatic response.

The lower the fibrosis grade, the higher the expected local variance of the liver fMRI maps: as the vasculature of healthy parts of the liver respond to hypercapnia and hyperoxia while the fibrotic tissue hardly responds to the inhalation challenges.

The local variance is computed as follows: First, the local variance \(v_t(\vec{x})\) in the neighborhood of each pixel \(\vec{x}\) is computed from the hemodynamic response vectors data \(\Delta S(\vec{x})\) for each time point \(t\) independently. Next, the variance map \(v(\vec{x})\) is computed as the average variance over the time points:

\[
v(\vec{x}) = \frac{1}{N} \sum_{t=1}^{N} v_t(\vec{x})
\]

Finally, the average variance is calculated for the liver ROI:

\[
g_2 = \frac{1}{M} \sum_{\vec{x} \in \text{ROI}} v(\vec{x})
\]

where \(M\) is the number of pixels in the liver ROI that were included.

Fig. 1(j-l) shows the local variance maps of three representative subjects with different fibrosis levels. Note that the lower the fibrosis grade is, the higher is the local variance of the liver fMRI maps. Fig. 4 shows the box-plots of the distributions of the average local variances calculated from the hemodynamic maps for all the fibrosis grades.

The final feature vector \(g\) is the concatenation of \(g_1\) and \(g_2\): \(g = [g_1, g_2]\). The length of \(g_1\) is the number of time points in the normalized hemodynamic response vector - 20 in our study; \(g_2\) is the single scalar number that represents the variance feature. Consequently, the overall length of \(g\) is 21.

3) Hierarchical multi-class classification: Given a dataset of hemodynamic response vectors - one for each slice, and five slices per mouse - the goal is to classify each vector to the accurate fibrosis grade as either: healthy- no fibrosis f0, portal fibrosis f1, periporal fibrosis f2, septal fibrosis f3 or cirrhosis f4-5. The classification results are verified by comparing them to the actual fibrosis degree of the same mouse as determined from the corresponding histological specimens as evaluated by an expert pathologist.

Since the fibrosis severity is naturally graded, we designed a hierarchical multi-step classification method based on a sequence of binary SVM as follows. In the first step, we separate between healthy f0 and fibrotic livers f1-5. Next, we separate the fibrotic livers into low grade fibrosis f1-3 and cirrhosis f4-5.
For both binary SVM classifiers, we use a Gaussian Radial Basis Function (GRBF) kernel defined as:

\[
k(\tilde{x}_i, \tilde{x}_j) = \exp\left(-\frac{||\tilde{x}_i - \tilde{x}_j||^2}{2\sigma^2}\right)
\]

(5)

D. Evaluation methodology

The performance of our hierarchical classifier was evaluated compared to the ground-truth histology-based fibrosis grading done by an expert pathologist. For this purpose, we use the Leave-One-Out (LOO) cross-validation methodology, in which at each time one mouse is the test data and all other mice are used for training [47]. We also compared it to the performance of four main traditional multi-class classifiers: 1) One Against One (OAO-SVM) [32], [33]; 2) One Against All (OAA-SVM) [35], [36]; 3) single optimization Multi class SVM (MSVM) [37], [38], and: 4) KNN classifier [39].

To classify the entire liver of a mouse specimen, we determine the liver grade according to the grade of the majority of its axial MRI slices, each classified separately. For the evaluation, we obtained histology-based gradings for each liver.

Receiver Operating Characteristics (ROC) curves [48], [49] were computed using the distance to the hyperplane as the probabilistic classification result. The best thresholds for the binary classifiers were selected based on their ROC analysis. The classifiers performance was evaluated with classification confusion matrices and their derived performance measures, including, accuracy, precision and recall [50].

III. RESULTS

A. Hierarchical multi-class classifier evaluation

We first evaluated the performance of our hierarchical classifier. For each SVM model, we experimentally set an optimal \(\sigma\) for its kernel. The KNN classifier was evaluated for \(K = 5\) with the Euclidean distance function. All the parameters were optimized experimentally. The variance feature computed on a local neighborhood of diameter=5 pixels around each pixel. For this part of the study, 100 slices obtained from 22 (Mdr2−/−) mice and equivalent control (FVB/NJ) mice were included. The fibrosis grade of the 100 slices that were included was distributed as follows: 28 slices of control mice were graded as no-fibrosis \(f_0\), 40 slices were graded as periportal fibrosis \(f_2\), and 32 slice were graded as septal fibrosis \(f_3\).

Table II shows the confusion matrices [50] of all five classifiers. The sensitivity of our hierarchical SVM model was computed for each class against the others separately. The MSVM and KNN classifiers discriminate with 98% accuracy between non-fibrotic and fibrotic subjects, while the OAA-SVM and OAO-SVM classifiers had a discrimination accuracy of 99%. Both are lower than the accuracy of our hierarchical classifier (100%).

For mice specimens with \(f_2\) and \(f_3\) fibrosis grades, the OAA-SVM and OAO-SVM classifiers performed slightly better than the KNN and MSVM classifiers. The overall accuracy of the OAA-SVM and OAO-SVM was 73%, which was better than the KNN classifier accuracy of 71%. Our hierarchical SVM model performed better than all other classifiers, and yielded an overall accuracy of 76%.

B. Classification results

To evaluate our fMRI-based hierarchical SVM classification method, we conducted a second study using mice from both liver fibrosis models. In this study, we assessed 164 MRI slices from 34 mice. For each MRI slice, the exact fibrosis grade was determined beforehand by an expert pathologist based on the histological specimens.

In the first step, we separated between healthy and fibrotic slices of any grade with binary SVM classification [51]. The kernel \(\sigma\) parameter in Eq. 5 was set to 10 after binary search for the optimal value with the LOO method. Fig 1 shows representative examples of subjects with fibrosis grades \(f_0-f_4\) with their corresponding histological specimens. Fig. 2 shows the average normalized median time-course fMRI signal over the entire mice population grouped by their ground-truth fibrosis grades. Fig. 4 shows box-plots of the variance feature distribution for the entire mice population grouped by their fibrosis grades. Note that the variance feature separates well between healthy and fibrotic subjects. The classifier accuracy for this step was 96.9% with 88.1% precision [50] and 100% recall [50].

In the second step, all the slices that were classified as fibrotic were further separated into fibrosis \(f_1-3\) and cirrhosis \(f_4-5\). The classifier accuracy for this step was 72.5% with 77.8% precision and 69% recall. A more specific separation between fibrosis grades \(f_2\) and \(f_3\) was found to be problematic in this dataset because of the natural overlap between these grades.

Table II: Confusion matrices [50] for the OAO-SVM, OAA-SVM, MSVM, KNN and Hierarchical SVM-based classifiers. The rows indicate the true class and the columns indicate the hypothesized class. The last column indicates the sensitivity.

![Table II](image)

Fig. 5 shows the ROC curves [48], [49] of the two steps of the hierarchical SVM-based model. Table III shows the confusion matrices obtained from the hierarchical SVM-based classifier for both steps. The sensitivity of our model was
TABLE III: Confusion matrices for: (a) the separation between healthy \( f_0 \) and fibrotic \( f_{1-5} \) subjects using the hierarchical SVM-based model. The rows show the ground-truth class from histology; the columns show the hypothesized class from the classifier; (b) the slices classified as fibrosis specimens that were further separated into low grade fibrosis \( f_{1-3} \) and cirrhosis \( f_{4-5} \) with the hierarchical SVM-based model – the rows and columns are as in (a).

<table>
<thead>
<tr>
<th></th>
<th>Predicted</th>
<th></th>
<th>Predicted</th>
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<tbody>
<tr>
<td>( f_0 )</td>
<td>( f_0 )</td>
<td>( f_{1-3} )</td>
<td>( f_{4-5} )</td>
</tr>
<tr>
<td>( f_{1-5} )</td>
<td>37</td>
<td>0</td>
<td>14</td>
</tr>
<tr>
<td>( f_{1-3} )</td>
<td>5</td>
<td>120</td>
<td></td>
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</tbody>
</table>

computed for each class against the others separately. The model separated between healthy and fibrosis subjects with 96.9% accuracy, and between fibrosis and cirrhosis with 72.5% accuracy.

The overall separation accuracy between cirrhosis, fibrosis, and healthy mice was 82.3%. Note that this outperforms the reported 76% separation accuracy between adjacent grades with biopsy, which is considered the gold standard for fibrosis grading [4], [5], [6]. Note also that our classifier had a perfect score of 100% in separating between healthy \( f_0 \) and diseased specimens, including \( f_1 \).

IV. DISCUSSION

Our experimental studies indicate that, based on the Leave-One-Out cross-validation method, our model has a nearly 100% accuracy for the discrimination of non-fibrotic and low grade fibrosis specimens using only the hypercapnia response maps. An accuracy of 72.5% for the separation of slices from fibrotic and cirrhotic mice was achieved. In addition, the classification of each subject into cirrhosis, fibrosis, or healthy based on the majority of its slices has an even higher accuracy of 82.3%. A good differentiation between healthy and low grade fibrosis subjects can be achieved with the hypercapnia response map alone using only one fMRI slice from the entire liver, thus simplifying and significantly decreasing the cost of the MRI scanning, without compromising accuracy.

Our results suggest that our fMRI-based classification method can accurately differentiate between healthy and low grade fibrosis subjects based on the imaging information alone, with an accuracy level comparable to that of the histological-based grading.

Evaluating the degree of liver fibrosis is important for both diagnosis and treatment. While liver biopsy has been the gold standard for fibrosis grading for a long time, recent studies report excessive rates of sampling error – between 25% and 40% – resulting in poor reproducibility. Thus, alternative non-invasive techniques for liver fibrosis grading are currently under research.

Existing imaging techniques currently enable only the evaluation of progressive stages of liver disease. Hepatic fibrosis results in reduced functionality and obliteration of hepatic vasculature. The liver hemodynamic status, therefore, includes changes involving arterializations of the liver and development of a hyperdynamic circulatory state.

Our results indicate that by using fMRI imaging combined with hierarchical multi-class SVM-based model, it is possible to identify hemodynamical changes that occur early during the liver fibrotic process. Our method proved to be sensitive enough to detect changes occurring as a result of mild fibrosis in animal models. The change in the livers of these mice occur both by attenuation of \( \Delta S \) responsiveness and homogeneity of the liver parenchyma reactivity. These changes reflect the structural and functional alterations in the liver vasculature [29], [27].

Liver fMRI in humans can be limited by a breathing-related motion artifact which is very critical for achieving significant \( \Delta S \) maps. The Echo-planar MR imaging technique is used for brain fMRI in humans; however, it still suffers from lower...
imaging resolution.

V. CONCLUSION

We have presented a new method for liver fibrosis grading based on a model constructed from the fMRI hemodynamic response to hypercapnic and hyperoxic challenges and a hierarchical multi-class SVM classifier. Our method enables the automatic non-invasive grading of liver fibrosis.

We are currently refining the fMRI protocol to adapt it for human liver hemodynamics assessment. For this purpose, we are developing an automatic liver contour segmentation algorithm [41], and a method to co-register datasets to compensate for respiratory motions [40]. Once the liver regions are identified and co-registered, the algorithm described in this paper may be used for liver fibrosis grading in humans.

In the future, our method may be used for non-invasive classification and progression monitoring of liver fibrosis patients as an alternative to more invasive approaches, such as biopsy and contrast-enhanced imaging. In particular, the successful differentiation between healthy regenerative livers and low grade fibrosis slices may play a key role in non-invasive surveillance of the liver recovery process.

REFERENCES


