Comparison of Different Approaches of Pattern Matching for MR Fingerprinting

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Purpose: A new method for multi-parametric quantitative measurement and tissue characterization has recently been proposed under the name of Magnetic Resonance Fingerprinting (MRF) [1]. A measurement is performed using a sequence of arbitrary RF pulses and repetition times, and the resulting signal is matched to a dictionary of pre-calculated signals for different tissue parameters. In [1], this template matching is performed by selecting the dictionary entry, which has the largest inner product with the measured signal. This method becomes inaccurate, if the parameter sampling of the dictionary is too sparse, since two very different dictionary entries may yield similar inner products with the test signal. This is particularly problematic for coarse B_0 sampling with bSSFP-based MRF sequences. However, it is not always feasible to sample a dictionary sufficiently densely, especially when multiple parameters are encoded. Therefore, we investigate alternative methods for MRF tissue classification in this study. We employ several different machine learning algorithms for classification of the measured data. These differ from the inner product approach in that they do not aim at finding an exact T_1, T_2, and B_0 match, but instead classify the signal by assigning it to clusters of T_1/T_2 combinations without exact prediction of B_0.

Methods: We studied the MRF classification problem on a gel phantom (Diagnostic Sonar, Eurospin II) containing 13 substances with different T_1/T_2 combinations, some of which are very similar (see Fig. 1a). The study was based on a random bSSFP-based MRF sequence [1] with n=250 steps (Fig. 1b). The pre-calculated dictionary contained signals for all 13 substances, with B_0 sampled in 2Hz steps in the range from 0 to 100Hz, which makes a total of 650 dictionary entries. This dictionary was used for both, template matching through dot products and training of five different machine learning algorithms. Classification accuracy was then probed by matching 1300 calculated test signals for all substances with fixed T_1 and T_2, but random (continuous) B_0 values within the range 0 to 100Hz. Prior to training and matching, the dictionary was compressed along the time axis using singular value decomposition (SVD). This dimensionality reduction increases the matching speed while keeping dictionary entries well distinguishable [3]. Some of the investigated classification algorithms even require a low-dimensional feature space. The following algorithms were used in this study: Support vector machines (SVMs) based on radial basis function (RBF) and polynomial kernels [2], a Decision Tree classifier, and k-Nearest Neighbors (k-NN) classifiers, all implemented using a single processor core for better comparison. An experiment has also been performed using the same gel samples. The measurement took about 20 minutes using the fingerprint sequence presented here with Cartesian sampling.

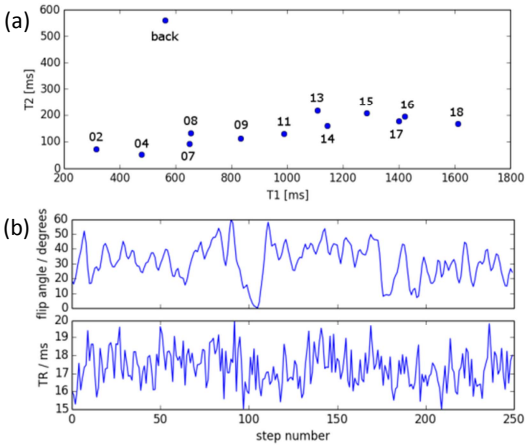

Fig. 1: (a) T1 and T2 parameters of the substance to be distinguished, (b) MRF sequence with 250 flip angles and TR values

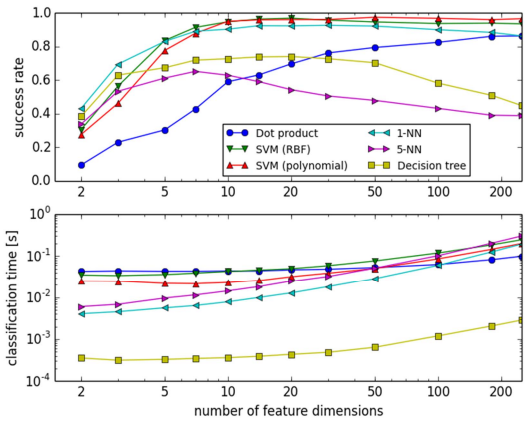

Fig. 2: Classification scores and times as functions of feature space dimensionality

Results and Discussion: The upper graph in Fig. 2 shows the success rate (ratio of correctly classified probe signals) as a function of feature space dimensionality for the different classification types. The SVM algorithm (scoring up to 97%) clearly outperformed the standard dot product map (scoring 86% at n=250) in accuracy. While dot product matching becomes worse for lower-dimensional feature space, the other algorithms require dimensionality reduction for best operation. Decision Tree and k-NN classifiers are most accurate for $n \approx 10$, with the 1-NN classifier achieving almost the same accuracy as the SVMs while being about an order of magnitude faster (lower graph in Fig. 2). The Decision Tree algorithm offers only moderate accuracy, but it is extremely fast. Therefore, it can be the algorithm of choice for very quick tissue classification. A visual example for differences in matching quality is shown in Fig. 3, where the phantom data is classified via dot product and SVM methods, the SVM yielding higher accuracy.

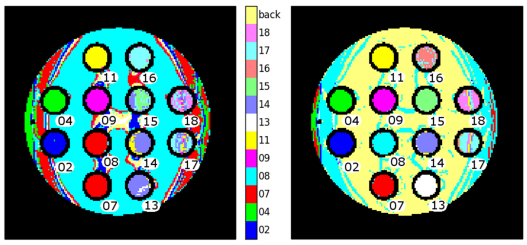

Fig. 3: Phantom measurement classified via dot product (left) and SVM (RBF) (right) for n=20

Conclusions: MRF classification of a large number of similar substances is difficult for dictionaries sparsely sampled in B_0. In this case, classification by machine learning algorithms can lead to higher match accuracy than simple comparison of dot products. Furthermore, the use of specific classification algorithms can reduce the computation time significantly. Dimensionality reduction prior to training the classifier is often required for more accurate results.

References: [1] Ma D et al., Nature 495, 187 (2013), [2] Chang C et al., http://140.112.30.28/~cjlin/papers/libsvm.pdf, [3] McGivney et al., Proc. Intl. Soc. Mag. Reson. Med. 22, 4287 (2014)