Detection of Tumors in Dynamic Magnetic Resonance Images using Principal Component Analysis

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Introduction

The aim of this project was to develop a non-operator dependent method for detecting tumor tissue and necrotic tumor tissue in mice. This was pursued by using and combining two different methods. In the first method we identified different characteristic time curves, extracted using PCA, from a dynamic MRI (dMRI) dataset and correlated these with the images for classification. In the second method PCA was performed directly on the time series data.

Data

Eight mice bearing tumors implanted at the hind legs were split into two groups. One group (the last four mice) was treated with Hydralazine which limits blood flow to the tumor by dilating non-tumor vessels (steal effect), while the control group (the first four mice) was injected with saline.

Three cross-sectional slices through every mouse were imaged using dynamic MRI. After acquisition of 10 images, a gadolinium based contrast agent was injected into the tail vein of the mouse and the last 90 images were acquired. An example of dataset is shown in Figure 1.

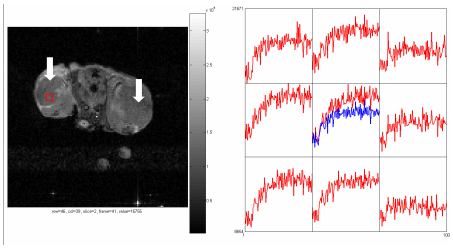


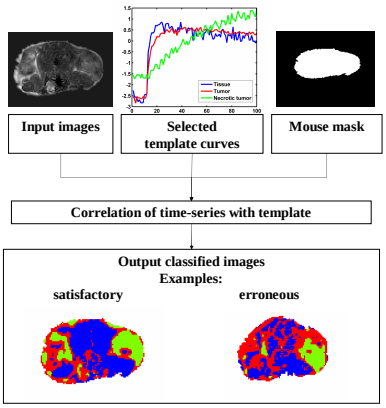
Figure 1 – Left: mouse cross-section (tumor indicated by arrows). Right: time-series for 3x3 pixels in the red box, the blue plot is a mean curve.

Methods

Due to the injected substances and to the physiological tissue properties, the change in image intensity over time is different for viable tumor tissue, necrotic tumor tissue and normal tissue. This information can potentially be used to classify the image into three different tissue classes. For this purpose, two methods were developed and combined.

a) First Method

As first step, in order to remove the background, the mice were segmented using a global threshold value to produce a mouse mask. Regions of interest were manually selected for the three tissue classes and PCA was used to extract a template of typical time curves (shown below).



The cross-correlation between the templates and the time series of images were then calculated and each pixel was assigned the class that showed the largest correlation. New templates were afterwards calculated using PCA on the pixels of each class and the cross correlation was again computed. This was repeated in an iterative manner until the number of misclassified pixels was minimized.

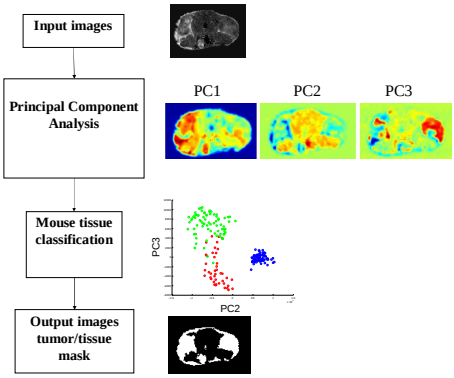
Typical results are shown above for two different mice: due to the similar template curves for tissue and viable tumor, pixels belonging to these two classes are sometimes misclassified (right hand example).

b) Second Method

In order to improve the results provided by the first method, an alternative method was developed.

Again PCA was used but in an unsupervised manner. For all pixels in the segmented mouse the time series were subjected to PCA and the three largest components extracted.

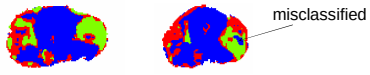
In the plot below, the tissue class (blue) is well separated from the two tumor classes (green and red).



The results were therefore used to produce a binary mask, discriminating between normal tissue and tumor tissue.

c) Combined Method

In order to improve the results provided by the first method, the binary tissue/tumor mask from the second method was used to update the pixels wrongly classified in the first method. The classification of the remaining pixels was performed as before by using the template curves correlation. The results were in general good. As seen below the output given by the combined method seems to be more probable. However, the method has still some limitations, since misclassified pixels were identified in the regions not covered by the tumor/tissue mask.



Conclusion

A new method for detecting tumors in mice has been developed, using and combining two different implementations of PCA. Three classes (tissue, viable tumor and necrotic tumor) were identified for eight mice. In general the achieved results are satisfying, showing anyway still some misclassifications. More work is needed to improve the robustness and accuracy of the method.