# Spectral Clustering of Time-Intensity Signals: Application to Dynamic Contrast-Enhanced MR Images Segmentation

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***Abstract – In this paper, we propose to apply a spectral clustering approach to analyse dynamic contrast-enhance magnetic resonance (DCE-MR) time-intensity signals. This graph theory-based method allows for grouping of signals after space transformation. Grouped signals are then used to segment their related voxels. The number of clusters is automatically selected by maximizing the normalized modularity criterion. We have performed experiments with simulated data generated via pharmacokinetic modelling in order to demonstrate the feasibility and applicability of this kind of unsupervised approach.***

***Index terms - Contrast agents, Image Processing, Magnetic Resonance Imaging***

## I- INTRODUCTION

Perfusion or Dynamic contrast enhanced magnetic resonance (DCE-MR) imaging becomes a reference tool to study precocious cancers. It involves rapid and repeated acquisition of T1W images before, during and after bolus injection of a contrast agent.
The quantitative analysis is based on a pharmacokinetic model. By applying this model to the DCE-MRI data, it is possible to obtain physiologic parameters [1].
Data analysis techniques were recently investigated and showed promising results in analysing these data without any prior knowledge about parametric models. In this context, the aim is to group the voxels into homogeneous patterns sharing the same properties. Each voxel is represented by a time-intensity curve obtained by converting each frame of the sequential images into a 1D row signal vector. The curves have similar shapes whereas their evolutions as well as their magnitudes are tissue dependent.
In this paper, we investigate the use of a graph-based approach, spectral clustering, to analyze DCE-MRI time-intensity signals. Unlike classical K-means and mixture models, graph-based methods are non-parametric and do not require *a priori* assumptions on the size, shape or distribution of clusters [2]. The clustering finds an embedding space in which the projected data signals are linearly separable and then groups them by a classical K-means algorithm.

## II- METHODS

Figure 1 shows the pipeline of the method. Starting from the images, the radiologist selects a region of interest (ROI) to be analysed then the time-intensity curves $\{x_1, \dots, x_i, \dots, x_n\}$ are formed by converting each voxel of each frame of the sequential images into a 1D row, denoted by $x_i = (x_{i1}, \dots, x_{it}, \dots, x_{im})^T$, where n is the total number of voxels and m represents the number of scans (i.e. number of acquisitions).

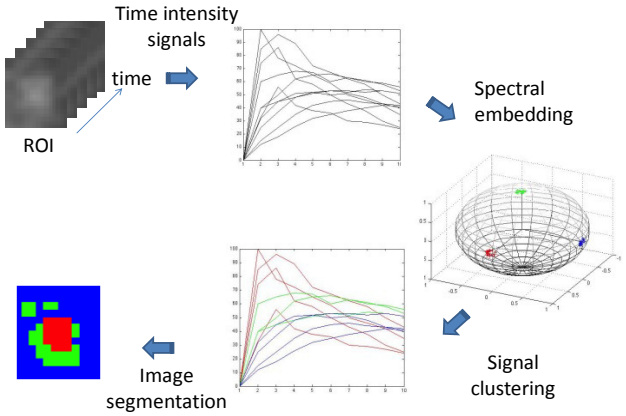


Figure 1: The DCE–MRI analysis method. Arrows indicate the processing steps.

Globally, the idea is to perform a classification of the curves and to group them according to their shapes. However, this step is difficult directly in the original space. Thus, the first step consists in the spectral transformation, which allows to the projected data to be easily separable. After, this transformation, a clustering using the K-Means algorithm is done and lastly a labelling is made to the clusters. A final step consists in a return back to the images space to group the voxels into homogeneous clusters.
More formally, the spectral clustering algorithms typically consist of the following three basic steps:

***Pre-processing***

- Construct the graph and the similarity matrix to represent the dataset

***Spectral embedding***

- Form the associated Laplacian matrix

- Compute eigenvalues and eigenvectors of the Laplacian matrix
- Map each point to a lower-dimensional representation based on one or more eigenvectors

***Clustering***

- Assign points to two or more classes, based on the new representation

## III- EXPERIMENTS ANS RESULTS

Since exact ground truths are not available for real DCE-MR image data, the algorithm performance is evaluated with simulated data. The simulation is generated using validated pharmacokinetic models [4] without any assumption regarding the data distribution. A large set of synthetic DCE-MRI time series is constructed. Generated data contain some features of real situations.

The curves are based on Chen *et al*. work [5] with more additional behaviours possibilities. These 1D simulations are combined with a 3D model of prostate: ProstateAtlas [6] to obtain 4D data set. The data are immersed in an environment with iliac and obturator arteries.

Six cases were generated by varying the number of lesions and their positions on the images (Table 1). A seventh case was considered, it represents healthy tissue.

Figure 2 depicts some results for cases 1, 2, 4 and 7.

| Cases | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|---|---|---|---|---|---|---|---|
| **Canc nbr** | 3 | 2 | 1 | 3 | 3 | 1 | 0 |
| **Canc det.** | 3 | 2 | 1 | 3 | 3 | 1 | 0 |
| **Sens** | 1.00 | 0.97 | 1.00 | 0.96 | 0.97 | 1.00 | - |
| **Spe** | 0.99 | 1.00 | 0.86 | 1.00 | 1.00 | 1.00 | 0.84 |
| **Pre.** | 0.99 | 0.99 | 0.61 | 0.99 | 0.99 | 1.00 | 0.50 |
| **F-meas.** | 0.99 | 0.98 | 0.76 | 0.98 | 0.98 | 1.00 | - |
| **Dice** | 1.00 | 0.99 | 0.38 | 0.98 | 0.99 | 1.00 | |

Table 1: Quantitative results for the application of spectral clustering to analyze 7 cases of simulated data of DCE MR imaging. Cases 1 to 6 contain cancer zones while case 7 corresponds to healthy tissue.

From Table 1, it appears that the method presents good performances on the synthetic data: sensitivity (0.96 – 1.00), and specificity (0.86 – 1.00). Dice's coefficient confirms this finding.

## IV- DISCUSSION – CONCLUSION

We have presented an original analysis method for DCE-MR signals by grouping voxels presenting the same behaviours. The method is based on spectral clustering algorithm. The data are represented in a graph where each vertex is associated with a data sample and the weighted edges encode the relationship between the underlying data. Indeed, spectral clustering can handle complex and unknown cluster shapes where the commonly used methods such as K-means and mixture models may fail. More precisely, the top eigenvectors of the graph Laplacian can unfold the data structure to form meaningful clusters. Normalized modularity criterion was used to automatically select the optimal number of clusters.

After the conclusive preliminary results obtained on simulated images, a complete evaluation using clinical data including DCEMR images with associated anatomo-pathological analysis is in progress.

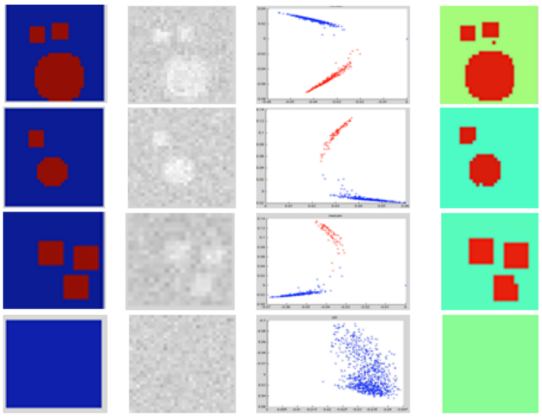

Figure 2: Results for cases 1, 2, 4 and 7 respectively. From left to right: ground truth, synthetic images of the ROI, display of the data plots in the spectral space and segmented image by spectral clustering.

## REFERENCES

[1] G.J. Parker GJ, J. Suckling, S.F. Tanner, A.R. Padhani, P.B. Revell, J.E. Husband, M.O. Leach, "Probing tumor microvascularity by measurement, analysis and display of contrast agent uptake kinetics", Volume 7, Issue 3, pages 564–574, 1997.

[2] H. Jia, S. Ding, X. Xu, R. Nie, "The latest research progress on spectral clustering. Neural Computing and Applications", DOI 10.1007/s00521-013-1439-2.

[3] J. Shi and J. Malik, "Normalized cuts and image segmentation". IEEE Trans. on Pattern Analysis and Machine Intelligence, 22, pp. 888-905, 2000.

[4] P.S. Tofts, "Modeling tracer kinetics in dynamic Gd-DTPA MR imaging", J. magn. Reson . Imag, pp. 91-101, 1997.

[5] L. Chen, L.P. Choyke, T.H. Chan, C.Y. Chi, G. Wang, Y. Wang Y, "Tissue_specific compartmental analysis for dynamic contrast-enhanced MR imaging", IEEE Trans. Med. Imaging 30[12], pp. 2042-2058, 2011.

[6] N. Betrouni, A. Iancu, P. Puech, S. Mordon, N. Makni, "ProstAtlas: A digital morphologic atlas of the prostate", European Journal of Radiology, 81, pp. 1969-1975, 2012.