Visual Analytics for the Exploration of Multiparametric Cancer Imaging

Renata Georgia Raidou*
Eindhoven University of Technology

Marta Paes Moreira†
Eindhoven University of Technology

Wouter van Elmpt‡
MAASTRO Clinic
Eindhoven University of Technology

Marcel Breeuwer§
Philips Healthcare Best
Eindhoven University of Technology

Anna Vilanova¶
Delft University of Technology
Eindhoven University of Technology

Abstract

Tumor tissue characterization can play an important role in the diagnosis and design of effective treatment strategies. In order to gather and combine the necessary tissue information, multimodal imaging is used to derive a number of parameters indicative of tissue properties. The exploration and analysis of relationships between parameters and, especially, of differences among distinct intra-tumor regions is particularly interesting for clinical researchers to individualize tumor treatment. However, due to high data dimensionality and complexity, the current clinical workflow is time demanding and does not provide the necessary intra-tumor insight. We implemented a new application for the exploration of the relationships between parameters and heterogeneity within tumors. In our approach, we employ a well-known dimensionality reduction technique [5] to map the high-dimensional space of tissue properties into a 2D information space that can be interactively explored with integrated information visualization techniques. We conducted several usage scenarios with real-patient data, of which we present a case of advanced cervical cancer. First indications show that our application introduces new features and functionalities that are not available within the current clinical approach.

Index Terms: I.3.8 [Computer Graphics]: Applications—Applications; J.3 [Computer Applications]: Life and Medical Sciences—Life and Medical Sciences

1 Introduction

Tumors are heterogeneous tissues, enclosing multiple regions with distinct characteristics that are hypothesized to have an impact on treatment effectiveness. Tumor tissue characterization employs multiparametric imaging: several imaging modalities are combined to derive per voxel distinctive information on tissue properties. Investigating these properties can provide further insight into tumor mechanisms and enable a more targeted treatment. In current clinical practice, the exploration and analysis of this multi-dimensional parameter space of tissue characteristics is conducted using a simplistic slice-based technique. This approach, apart from being cumbersome and time demanding, also requires to manually inspect the data side-by-side and mentally reconstruct their relationships and patterns. To improve this procedure, simple scatterplots are sometimes used, but exploration and analysis at a voxel level is still not possible. Although an extensive literature review exists on Visual Analytics techniques employed in multiparametric medical imaging, those addressing tumor exploration are mainly restricted to visualization and exploration of time-varying 3D medical imaging datasets [1, 2] or to analysis of perfusion parameters [3, 4].

We present a new application, designed and implemented for the easy exploration and visual analysis of the multiparametric space of tumor characteristics to allow the comparative investigation of the properties of distinct regions within tumors. We expect that clinical researchers will gain further insight into tumor heterogeneity and will be able to perform an interactive tumor analysis, at both region and voxel level. The *contributions* of our work are the following:

(1) We implemented an integral visual framework to improve the current clinical workflow, by supporting the exploration and analysis of large multiparametric cancer imaging data.

(2) Our application supports the identification, exploration and analysis of anatomically significant intra-tumor regions with different characteristics - individually and comparatively.

(3) We integrate a dimensionality reduction technique and multiple interactive data views, to decrease the complexity of the exploration and to facilitate the analysis of the multiparametric space.

2 Methods

Figure 1 depicts the workflow adopted for our application. After data acquisition and pre-processing, we create a two-dimensional map from the high-dimensional multiparametric space, using a well-known non-linear dimensionality reduction technique, called t-Distributed Stochastic Neighbor Embedding (t-SNE) [5]. In the t-SNE map, datapoints plotted close to each other represent voxels of the anatomical images that have similar values in the multiparameteric space, i.e. similar tissue characteristics. When the user manually selects one or multiple clusters in the t-SNE mapping, the respective anatomical regions are highlighted in the medical data. Further exploration of the clusters requires the investigation of correlations, trends and outliers in the data, either for each individual cluster or comparatively for multiple clusters. For that, we employ a parallel coordinates plot and a color-coded reduced scatterplot matrix. With the former, the user can explore all the dimensions of each cluster in a single view, while the latter shows all pairwise data relationships and associations. We simplify the view of the scatterplot matrix: instead of showing the distribution on each single plot of the matrix, we initially show the correlation between parameters (Pearson's ρ), using a divergent cool-to-warm colormap. Following a details-on-demand approach, the user can click the individual plots, to zoom into the underlying distribution and inspect it.

3 Results

As a proof of concept, we conducted several usage scenarios with real-patient data, i.e. lung, prostate and cervix, to test the capabilities of the implementation. In this poster, we demonstrate our implementation on advanced cervical tumor patient data (Figure 2).

First results show that the implemented framework introduces new exploratory features and functionalities that are not possible within the current approach. The user can explore and analyze multiple views on the provided data, such as *correlation plots* between the parameters and *parallel coordinates plots* - either *individually*,

*e-mail: r.raidou@tue.nl
†e-mail:marta.paes.moreira@gmail.com
‡e-mail:wouter.vanelmpt@maastro.nl
§e-mail:marcel.breeuwer@philips.com
¶e-mail:a.vilanova@tudelft.nl

IEEE Symposium on Visual Analytics Science and Technology 2014
November 9-14, Paris, France
978-1-4799-6227-3/14/$31.00 ©2014 IEEE

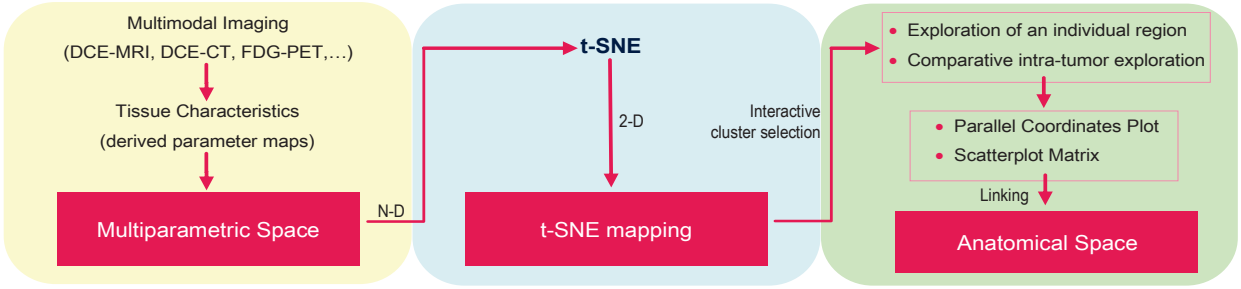

Figure 1: Workflow adopted for our application (yellow: acquisition/pre-processing, blue: t-SNE mapping, green: core of application).

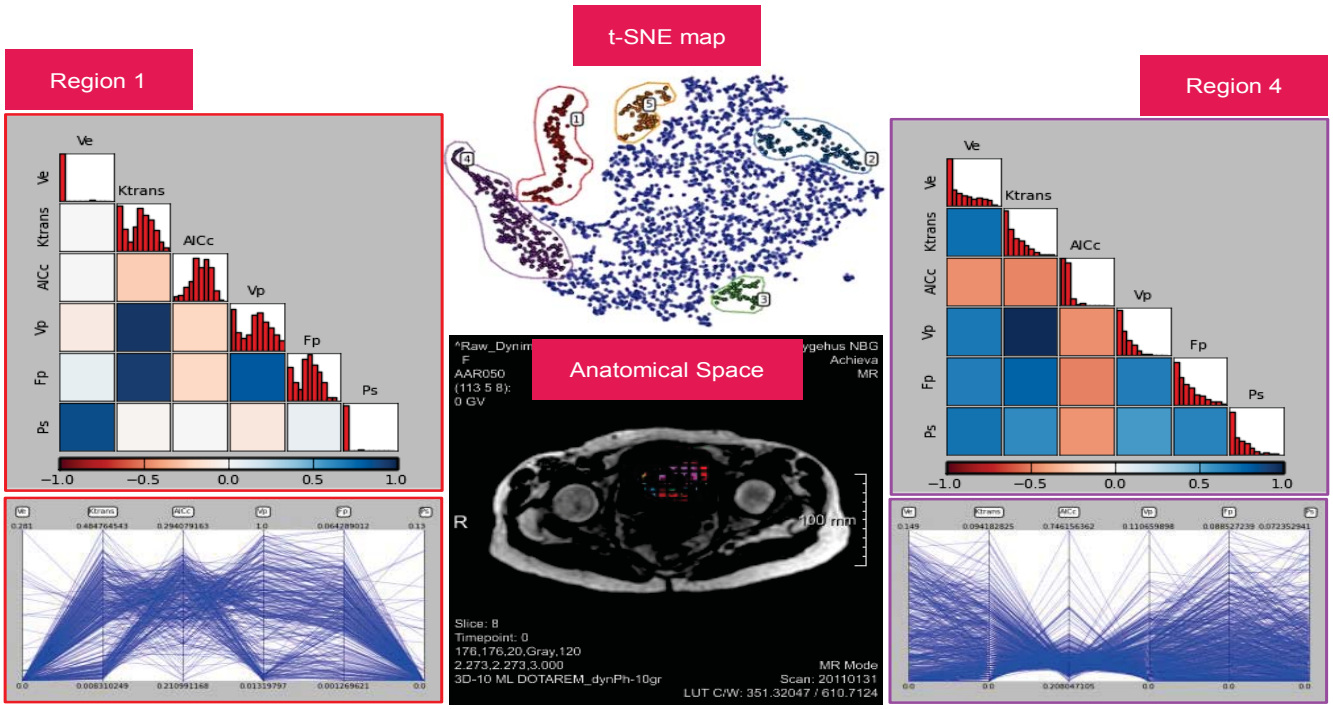

Figure 2: Usage scenario for the exploration and visual analysis of a cervical tumor patient (*data courtesy of J. Kallehauge, Oncology Department of Aarhus University*). From the t-SNE map, a number of cluster regions are selected (here, five in total) and the user can individually or comparatively explore them, using their color-coded scatterplot matrices (to investigate eventual correlations in the data) or their parallel coordinates plot (to explore the inter-parameter relations). Here, we compare two dissimilar regions of the tumor (red: periphery of the tumor; magenta: intermediate tumor area).

within one region of the tumor, or *comparatively*, across heterogeneous regions, linking their observations from the exploratory level to the *anatomical space* and vice-versa. A discussion with prospective clinical users also confirmed the potential of the application. However, an extensive evaluation is required to validate these initial observations.

4 Conclusion

We introduced a new application for the exploration and analysis of large multiparametric cancer imaging data. The integration of t-SNE in our approach allows the identification of anatomically significant intra-tumor regions with distinct tissue characteristics that can be individually and comparatively analyzed, to gain further insight into tumor heterogeneity, at both tumor and voxel level. Although further evaluation of the tool is required, first indications show the potential of the application to facilitate and improve the current analysis workflow. A clinically significant direction for future work includes the extension of the application to allow meaningful follow-up or inter-patient analysis, but also the identification of specific parameters of the heterogeneous tumor regions that are more influential in diagnosis or treatment.

References

[1] E. Coto, S. Grimm, S. Bruckner, E. Gröller, A. Kanitsar, and O. Rodriguez. Mammoexplorer: an advanced CAD application for breast DCE-MRI. 2005.

[2] Z. Fang, T. Möller, G. Hamarneh, and A. Celler. Visualization and exploration of time-varying medical image data sets. In *Proceedings of Graphics Interface 2007*, GI '07, pages 281–288, New York, NY, USA, 2007. ACM.

[3] S. Glaßer, S. Schäfer, S. Oeltze, U. Preim, K. D. Tönnies, and B. Preim. A visual analytics approach to diagnosis of breast DCE-MRI data. *Computers & Graphics*, 34(5):602–611, 2010.

[4] B. Preim, S. Oeltze, M. Mlejnek, E. Gröller, A. Hennemuth, and S. Behrens. Survey of the visual exploration and analysis of perfusion data. *IEEE Transactions on Visualization and Computer Graphics*, 15(2):205–220, 2009.

[5] L. Van der Maaten and G. Hinton. Visualizing high-dimensional data using t-SNE. *Journal of Machine Learning Research*, 9(2579-2605):85, 2008.