

# Visual Analytics for the Exploration of Multiparametric Cancer Imaging

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## ABSTRACT

Tumor tissue characterization is believed to play an important role in the effectiveness of cancer diagnosis and treatment. In order to gather and combine all the necessary tissue information, multimodal imaging is employed to derive a number of parameters indicative of tissue properties. Clinical researchers show specific interest in exploring and analyzing relationships between parameters and, especially, differences among distinct intra-tumor regions. However, due to data dimensionality and complexity, the current clinical workflow is time demanding and does not provide the necessary insight. We implemented a new application for the exploration of the relationships between parameters and intra-tumor heterogeneity. We employ a well-known dimensionality reduction technique [4] to map our high-dimensional space into a 2D information space that can be interactively explored with integrated information visualization techniques. As a proof of concept, 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 might have an impact on the diagnosis and treatment effectiveness. Tumor tissue characterization employs multiparametric imaging: several imaging modalities are combined to derive per voxel all the distinctive information on tissue properties. The exploration of these properties can provide further insight into the tumor mechanisms and enable a more targeted treatment. In current clinical practice, the exploration and analysis of this multi-dimensional parameter space, i.e. the 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 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 the visualization and exploration of time-varying 3D

medical imaging datasets [1, 2] or to the analysis of perfusion parameters [3]. We implemented a new application for the easy exploration and visual analysis of the multiparametric space of tumor characteristics that allows the comparative exploration of the properties of distinct regions within tumors. We expect that clinical users will gain further insight into tumor heterogeneity and 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) [4]. In the t-SNE map, datapoints plotted close to each other represent voxels of the anatomical images that have similar values in the multiparametric 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. Instead of showing the distribution on each plot in the scatterplot matrix, we simplify it by showing the correlation between parameters (Pearson's  $\rho$ ), using a divergent cool-to-warm colormap. Following a details-on-demand approach, the user can click 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, within one region of the tumor, or comparatively, across heterogeneous regions, linking their observations from the exploratory level

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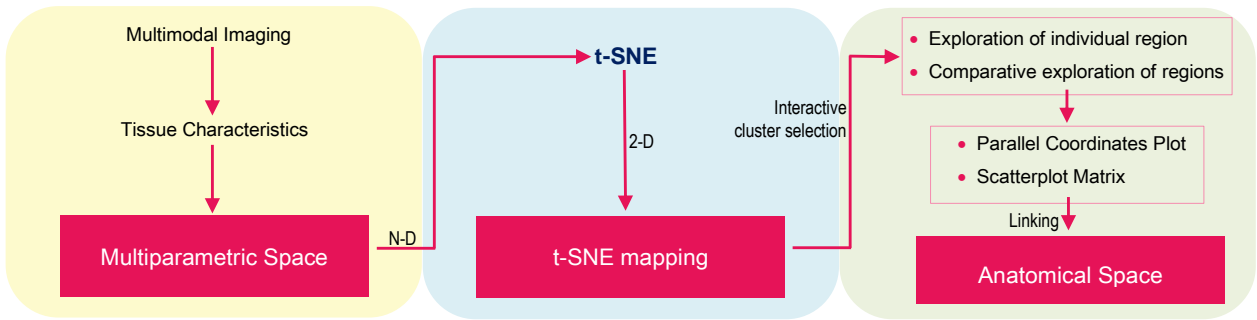


Figure 1: Workflow adopted for our application (yellow: acquisition/pre-processing, blue: t-SNE mapping, green: core of application).

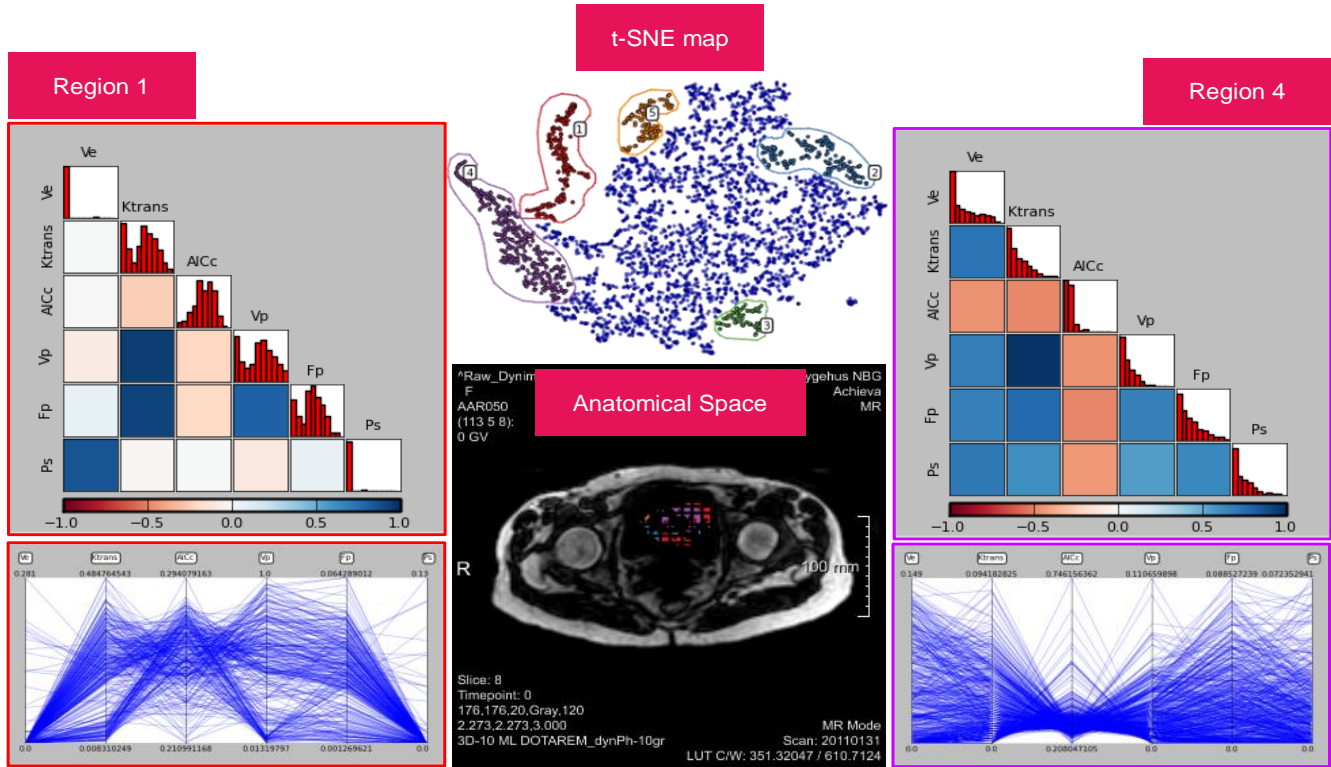


Figure 2: Usage scenario for the exploration and visual analysis of a cervical tumor patient. From the t-SNE map, a number of cluster regions are selected (here, five in total) and the user can individually or comparatively explore them, using their color-coded scatterplot matrices (to investigate eventual 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).

to the anatomical space and vice-versa. An informal discussion with prospective clinical users also confirmed the potential of the application. However, an extensive evaluation is required to validate our initial indications.

#### 4 CONCLUSION

In this poster, we introduce 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.

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