Radiomics and Habitat Analysis on Spatial-Temporal Manifolds via Fokker-Plank Dynamics

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Motivation

- The analysis of metabolic response of patients undergoing definitive radiotherapy for oropharyngeal cancer is a crucial but challenging task, especially due to the discontinuous, sparse nature of the dataset.
- To address this issue, we model the images as potential functions and apply non-linear time-evolution operations described by the Fokker-Plank equation.
- Using cluster analysis, radiomics and habitat features were extracted to characterize clinically useful imaging phenotypes and disease morphology.
- We propose a new radiomics paradigm for sparse, time series imaging data, where radiomic and habitat features are extracted from a spatial-temporal manifold modeling the time evolution between two images.

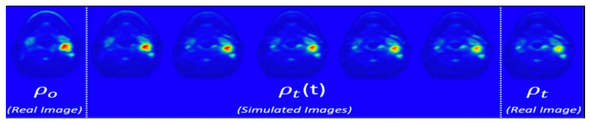


Figure 1. Illustration of Fokker-Plank dynamics on PET images.

Methods

- To simulate the time-frames between ρ_0 $(t = 0)$ and ρ_t $(t = 2\,weeks)$, the position and momentum of each pixel in ρ_0 were propagated according to the Fokker-Plank equation:

$$\partial_t \rho = \Delta\rho + \nabla \cdot (\rho \nabla \phi) = \nabla \cdot \left(\pi \nabla \left(\frac{\rho}{\pi}\right)\right)$$

- For 57 patients, the time evolution was modeled using two PET/CT images, pre- and intra-treatment (2 weeks/20 Gy), as boundary conditions.
- Using the produced spatial-temporal manifold, a k-means clustering analysis was applied to extract temporal radiomic features.
- Spatial features were combined with extracted temporal features to allow for volumetric analysis of disease habitats.

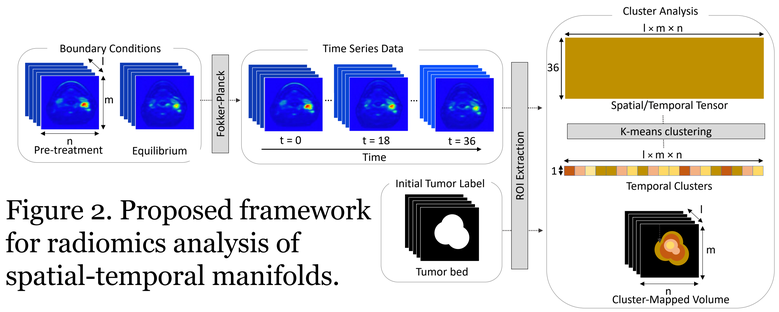


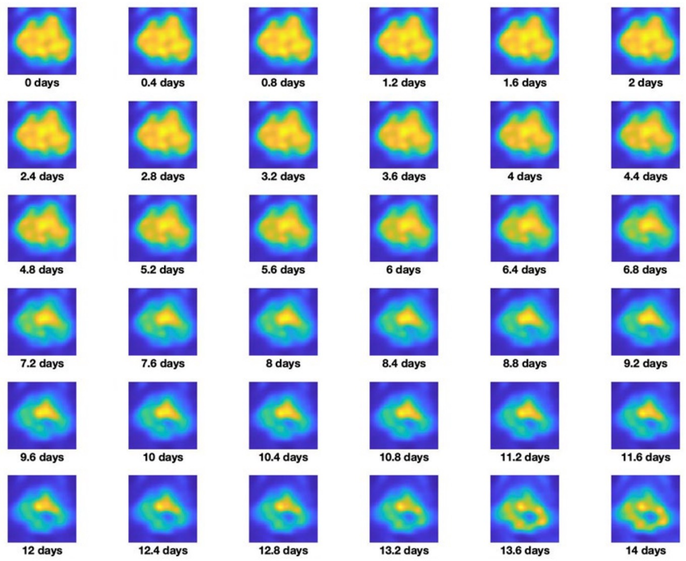
Figure 2. Proposed framework for radiomics analysis of spatial-temporal manifolds.

Results

Volumetric analysis of temporal manifolds as a tool for visualizing disease progression

- Temporal evolution throughout the 2 weeks of radiation treatment was calculated using the boundary and utilized for volumetric analysis of tumor progression. The evolution indicate a reduction in FDG uptake. The experimental application confirmed that our technique can reconstruct radiomic characteristics and capture complex morphological and textural changes given sparse input data.
- The reconstructed volume from the spatial-temporal manifolds can be further utilized as a tool for assessing tumor prognosis.

(a)



(b)

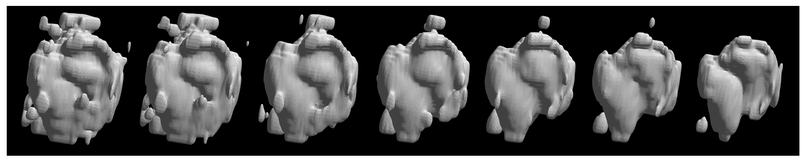


Figure 3. Simulation of temporal manifolds and spatial analysis of the data. (a) Temporal evolution for a single axial slice across the two-week period (b) Volumetric visualization of the simulated evolution data show tumor shrinkage in response to radiation therapy over time.

Results, cont'd

Cluster analysis identify patterns in disease habitat

- Four different clusters were identified when k-means clustering analysis was applied on the simulated evolution data. The pipeline is capable of capturing temporal changes in morphological features as the outermost cluster characterizes a shrinkage in tumor volume.

(a) **(b)**

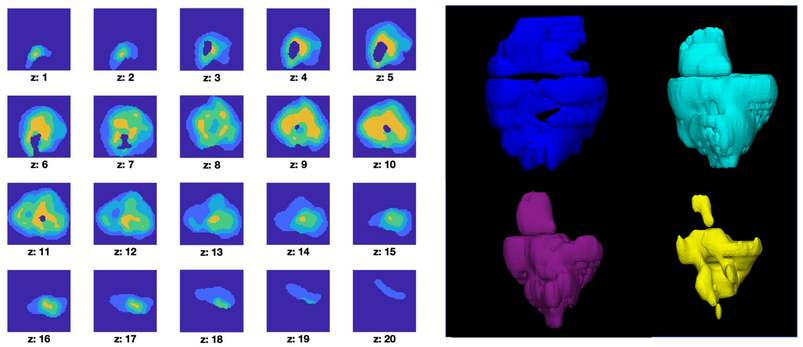


Figure 4. (a) Clustering analysis of time series data capturing textural features. (b) Volumetric analysis of each clusters (clockwise starting top left: cluster 1, 2, 3, 4) where the outermost cluster corresponds to cluster 1 and the rest ordered with regards to total cluster volume.

Figure 5. Scan here to see a dynamic demonstration of our technology

Conclusion

- We demonstrated that radiomics and habitat analysis of temporal manifolds can be utilized to characterize early metabolic response of patients undergoing definitive radiation therapy to treat oropharyngeal cancer (OPC).
- Further analysis of the extracted habitat and textural features can be performed to investigate tissue microenvironments as well as radiogenomic interactions.

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