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Understanding radiomics interconnections using network graphs

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INTRODUCTION

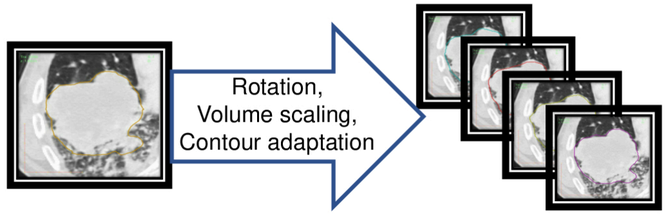
Radiomics allows high-throughput mining of quantitative imaging features from medical images to understand biological phenotypes and treatment responses. Image features are affected by variabilities in imaging systems and multiple observers delineating regions of interest. Classical statistical approaches, which are commonly used to quantify such variability in image features don't provide the means to visualize their interconnections. This presents challenges in identifying robust image features [1-3] as well as understanding their interconnections.

AIM

In this work we propose a graph-based method to (i) create robust mini-networks useful for modeling response and (ii) visualize existing radiomics signatures on a network to help in their interpretation.

METHOD

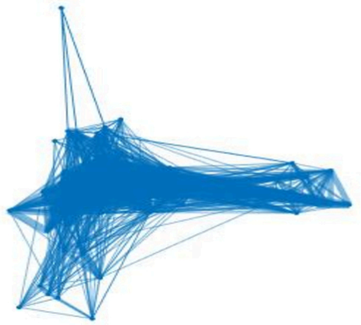
- Multiple feature-sets were generated by applying perturbation chains [4,5]. Perturbation chains have been shown to capture variability observed due to test-retest imaging.
- Network graph was derived by averaging partial correlation coefficients across feature sets.
- The sparsity of the network was controlled by thresholding partial correlations.



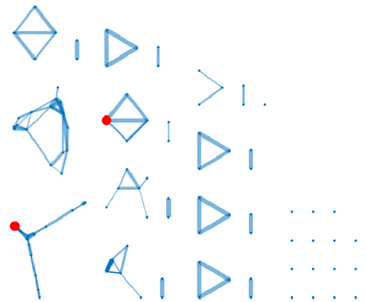
RESULTS

Understanding feature interconnections in an open source dataset

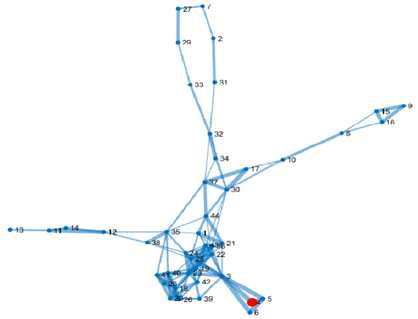
- CT scans of 420 patients from the TCIA dataset for lung cancer were used to create radiomics network graph.
- 50 feature sets were derived by perturbing original images and segmentations, using a CERR radiomics toolbox [5].
- A dense network was initially generated to obtain an idea of interconnections between features. The network was further split into its components to understand feature clusters.



Dense network resulting from perturbations of TCIA lung data, consisting of 420 scans. Partial correlation coefficients were used to build the network, considering correlations between features after removing their linear dependence on other features.



Various components of the network. A threshold of partial correlation was applied, cutting edges with weak correlations. Nodes in red indicate the features from Aerts et al [6] signature.



Details of one of the largest components in the network. Image features from published signatures can by displayed on the network.

CONCLUSIONS

- The visualization of features found significant in the published signatures helps understand their relationships with other features.
- The network graphs serve to identify robust and complimentary features for analysis.
- Further analysis is needed to investigate prognostic or predictive power of the robust radiomic features identified.
- This network approach can be coupled with mathematical or machine learning approaches to build predictive models.
- Network of radiomics features allow for exploring the relationship with genomic features using network analysis methods.

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