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| Predicting Gleason Score in Prostate Cancer Using Explainable Machine Learning Radiomics and Quantitative Diffusion MRI  **Georgios S. Ioannidis**1#\*,, **Katerina Nikiforaki**1, **Michalis Goumenakis**2 and **Kostas Marias**1,3  1 Computational BioMedicine Laboratory (CBML), Foundation for Research and Technology—Hellas (FORTH), 70013 Heraklion, Greece  2 Department of Radiology, Medical School, University of Crete, 71003 Heraklion, Greece  3 Department of Electrical & Computer Engineering, Hellenic Mediterranean University, 71410 Heraklion, Greece  # Presenting author: Georgios S. Ioannidis , email: geo3721@ics.forth.gr  \* Corresponding author: Georgios S. Ioannidis , email: geo3721@ics.forth.gr |

abstract

Prostate cancer (PCa) is one of the most frequently diagnosed cancers in men, with an average age of diagnosis at 66 years. A critical challenge in managing PCa is the need for precise early-stage characterization to differentiate between patients with indolent disease and those at high risk for aggressive forms. According to the World Health Organization guidelines, the Gleason score is central to prostate cancer management. Lower-grade cancers generally grow more slowly and are less likely to metastasize, whereas higher-grade cancers often require more aggressive treatment, such as prostatectomy. A Gleason score of 7 represents an intermediate-grade cancer, making clinical management particularly challenging and subjective, leading to potential over-treatment or under-treatment, both of which can result in adverse outcomes [1].

To address this issue, a retrospective study involving 102 histopathologically confirmed PCa patients was conducted using explainable machine learning (ML) radiomics models derived from quantitative diffusion MRI modeling. These models aimed to automatically classify Gleason scores (GS) into two groups: GS < 7 and GS ≥ 7. The ML models leveraged parametric mapping that included metrics related to tissue heterogeneity, micro-perfusion, and diffusivity, using a variety of classifiers to predict Gleason score. The model's explainability was evaluated through Shapley Additive Explanations (SHAP) [2], a method that elucidates the contribution of individual features in the prediction process.

The results demonstrated robust predictive performance, with the combined model achieving a mean accuracy of 78.8% and an area under the curve (AUC) of 83.3%. The integration of tissue heterogeneity and blood micro-perfusion was found to be particularly significant for predicting PCa aggressiveness, providing key insights for improving the stratification and treatment of patients based on their Gleason score.

**REFERENCES**

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