AI-Driven Malignancy Detection in Cardiac Tumors via T1-Weighted MRI Imaging

Meri Ferretti[1,2], Michele Pagliaccia[2], Andrea Baggiano[4,5], Gianluca Pontone[4,6], Francesco Angeli[7,8], Matteo Armillotta[7,8], Luca Bergamaschi[7,8], Luigi Lovato[9], Carmine Pizzi[7,8], Valentina D A Corino[1,2]

[1]Cardio Tech-Lab, Centro Cardiologico Monzino, Milan, Italy
[2]Department of Electronics, Information and Bioengineering, Politecnico di Milano, Milan, Italy
[3]Cardiology Department, San Giovanni Battista Hospital, Foligno, Italy
[4]Department of Clinical Sciences and Community Health, University of Milan, Italy
[5]Department of Perioperative cardiology and Cardiovascular Imaging, Centro Cardiologico Monzino, Milan, Italy
[6]Department of Biomedical, Surgical and Dentals Sciences, University of Milan, Italy
[7]Department of Medical and Surgical Sciences, Alma Mater Studiorum University of Bologna, Bologna, Italy
[8]Cardiovascular Division, Morgagni-Pierantoni University Hospital, Forlì, Italy
[9]Department of Pediatric and Adult Cardio-Thoracovascular, Oncohematologic and Emergencies Radiology Unit, IRCCS Azienda Ospedaliero-Universitaria di Bologna, Bologna, Italy

Abstract

We propose a novel tool to early differentiate primary from metastatic malignant cardiac masses (CMs). The approach relies exclusively on contrast-free T1-weighted cine magnetic resonance imaging (MRI), ensuring reproducibility and potential clinical integration.

We analyzed tumors from 36 patients, segmenting the lesion and then extracting volumetric radiomic features.

To identify the most informative features, we tested three feature selection pipelines all beginning with a correlation analysis followed by either Mann-Whitney significance testing, minimum Redundancy - Maximum Relevance, or Least Absolute Shrinkage and Selection Operator (LASSO) regression. The selected features were then fed to 5 different machine learning classifiers, with performance assessed through 10-fold cross-validation.

The best model resulted from the combination of correlation+LASSO for feature selection and Support Vector Machine for classification yielding a mean validation accuracy of 0.90 ± 0.15. After re-training the best model on the entire training set, it achieved 0.83 accuracy when tested on a cohort of 6 patients.

These findings support the potential of our AI-based tool to accurately classify primary versus metastatic cardiac tumors using standard MRI, without the need for contrast agents and specialized expertise.

1. Introduction

Cardiac masses (CMs) present significant diagnostic and therapeutic challenges due to their rarity and diverse nature, which includes benign and malignant tumors, as well as non-neoplastic lesions such as thrombi and cysts. Among malignant tumors, distinguishing primary cardiac neoplasms from metastatic involvement is crucial, as early differentiation, preferably before invasive procedures, has profound implications for treatment strategies and prognosis [1], [2]. While pathologic confirmation remains the gold standard, many tumors are not amenable to biopsy, emphasizing the vital role of accurate imaging.

Modern imaging, particularly cardiovascular magnetic resonance (CMR), is essential for the non-invasive evaluation of CMs. CMR provides multiplanar views and advanced tissue characterization, enabling the differentiation of lesions, with few studies demonstrating high diagnostic accuracy (79-98.4%) in CM assessment [3], [4]. However, imaging methods are subject to inter-operator variability, require substantial clinician expertise, and often rely on contrast agents.

Radiomics offers a promising solution to these limitations by transforming medical images into high-dimensional datasets, providing an objective and quantitative approach to tissue analysis. This methodology has the potential to uncover detailed insights into tissue characteristics that has been recently applied in the cardiovascular field. Despite its promise, only one study has applied CMR radiomics to cardiac tumors, achieving 95%

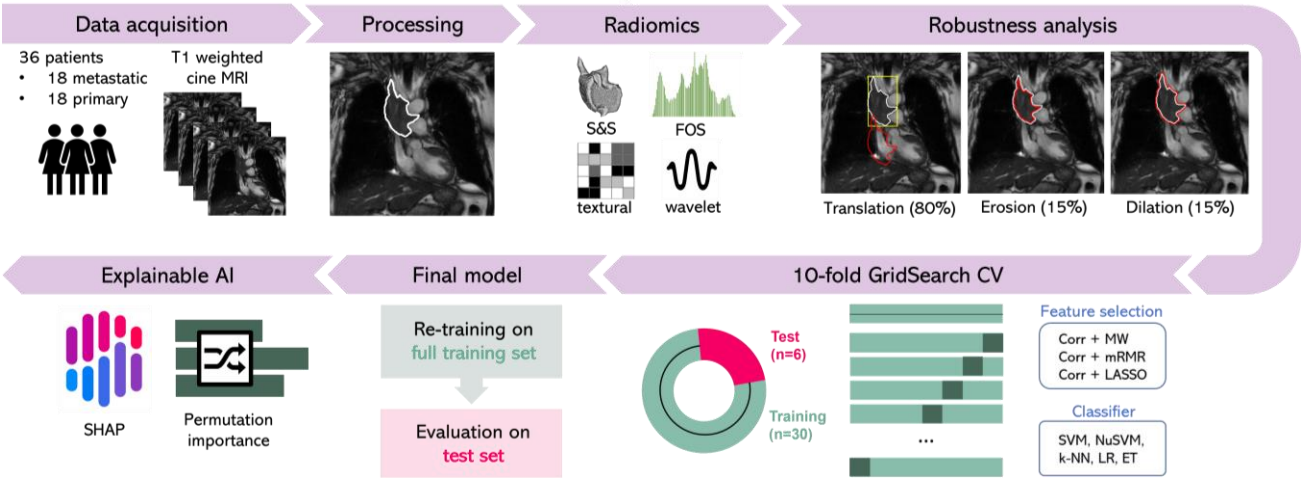

Figure 1. Schematic representation of the project workflow.

accuracy in differentiating thrombi from cardiac tumors (both benign and malignant), thus having a quite general diagnostic focus [5].

This study aims to develop a radiomics-based model utilizing contrast-free cine T1-weighted sequences to objectively differentiate primary from metastatic malignant cardiac tumors. By leveraging radiomic features, this approach seeks to improve the accuracy and consistency of CM characterization, providing a more reliable and reproducible tool to support clinical decision-making in managing these complex conditions.

2. Materials and Methods

2.1. Dataset

This retrospective study included 36 patients from the University Hospital Policlinico Sant'Orsola Malpighi (Bologna, Italy) who underwent CMR for suspected CMs. Definitive histological diagnoses were obtained from biopsy or surgical specimens. All cases were classified based on the World Health Organization's 2021 Classification of Tumors of the Heart and Pericardium [6]. The study was conducted according to the guidelines of the Declaration of Helsinki. The study protocol was approved by the local Ethics Committee (Registration No. 102/2017/Oss/AOUBo) and all the patients signed the informed consent.

Figure 1 shows an overview of the project workflow. In particular, radiomic analysis was performed on T1-weighted cine (CINE) volumes acquired in axial, frontal, long-axis, and short-axis orientations. Processing involved Gaussian noise removal, intensity inhomogeneity correction using the N4ITK filter, standardization, and resampling to achieve isotropic resolution. Specifically, the volumes were resampled to 1 mm in all three axes to match the average spatial resolution of the transverse plane. Then, lesion segmentation was manually conducted by a clinician using the "3D Slicer" software, with the entire CM segmented across all slices to generate a volume of interest (VOI).

2.2. Radiomic feature extraction

Radiomic features were extracted using PyRadiomics version 3.0.1 and grouped into three categories: shape/size features (capturing geometric aspects of the VOI), first-order statistics (reflecting the distribution of gray values), and textural features (describing spatial gray value patterns). The latter two categories were computed from both the original CINE volumes and eight Discrete Wavelet Transform (DWT)-derived volumes, resulting in a total of 851 features per VOI.

Then, features' robustness was assessed. Briefly, to simulate segmentation variability, VOIs were subjected to slight erosion or dilation (15% of the CM area) with the hypothesis that features should be similar for small variations. A maximal translation (up to 80% of the bounding box) was used to incorporate surrounding healthy tissue, with the hypothesis that features characterizing the VOI should be different between CM and healthy myocardium. Features were retained based on their Interclass Correlation Coefficient (ICC), excluding those with ICC ≤ 0.75 under minimal changes or ICC ≥ 0.50 under maximal translations.

2.3. Model development

The dataset was divided into a training set of 30 volumes and a test set of 6 volumes using stratified sampling. Feature selection was performed on the training set using stable radiomic features extracted from CM VOIs,employing a 10-fold cross-validation (CV) approach.

During CV, the training set was split into 10 folds, with 9 folds used for training and 1 for validation in each iteration. Three distinct feature selection methods were applied during the training phase and subsequently used to transform the validation set. In all of them a correlation filtering step was first applied, discarding the feature in highly correlated pairs (correlation above 90%) that had a weaker correlation with the target.
The three selection methods were:

- the Mann-Whitney U test (MW test) comparing the two groups (primary and metastatic CM) to retain features significantly different between the two groups (p-value < 0.05);
- the minimum Redundancy Maximum Relevance (mRMR) to select the 10 features that were most relevant to the target while least redundant;
- the Least Absolute Shrinkage and Selection Operator (LASSO) regression (with alpha regularization parameter set to 0.1), leveraging regularization to identify features with the strongest predictive contributions.

Five different models have been tested through the 10-fold CV approach, specifically the following algorithms have been considered: Support Vector Machine (SVM) and its softer version NuSVM, k Nearest Neighbors (k-NN), Logistic Regression (LR) and ExtraTrees (ET).

To assess model explainability, permutation importance was employed to evaluate the impact of each of the selected feature on model performance as well as SHapley Additive exPlanations (SHAP) to quantify the contribution of individual features to predictions.

3. Results

Table 1 summarizes the results on the CV from testing various combinations of feature selection strategies and classifiers. The best-performing pipeline, selected for its highest mean accuracy on the validation set, involved correlation filtering followed by LASSO regression for feature selection and the SVM model for classification.

Table 1. Cross-validation results. MW: Mann-Whitney, mRMR: minimum Redundancy Maximum Relevance, LASSO: Least Absolute Shrinkage and Selection Operator, SVM: Support Vector Machine, NuSVM: Nu Support Vector Machine, k-NN: k-Neighbor Network, LR: Logistic Regression, ET: ExtraTrees.

		Feature selection strategy		
Model		Correlation + MW test	Correlation + mRMR	Correlation + LASSO
SVM				
	train	0.94 ± 0.03	0.88 ± 0.03	0.91 ± 0.03
	val	0.87 ± 0.21	0.77 ± 0.15	0.90 ± 0.15
NuSVM				
	train	0.89 ± 0.04	0.84 ± 0.02	0.92 ± 0.03
	val	0.80 ± 0.22	0.77 ± 0.15	0.83 ± 0.17
k-NN				
	train	0.83 ± 0.04	0.72 ± 0.08	0.92 ± 0.02
	val	0.83 ± 0.22	0.73 ± 0.13	0.80 ± 0.16
LR				
	train	0.87 ± 0.25	0.90 ± 0.04	0.88 ± 0.04
	val	0.83 ± 0.17	0.80 ± 0.22	0.83 ± 0.17
ET				
	train	0.98 ± 0.02	0.94 ± 0.02	0.96 ± 0.00
	val	0.80 ± 0.16	0.83 ± 0.17	0.77 ± 0.17

The model utilized a radial basis function kernel, ideal for non-linear decision boundaries, and employed a regularization parameter set to 1. This combination achieved a mean validation accuracy of 0.90 across the 10 validation folds.

After determining the best pipeline and top-performing classifier, the model was re-trained using the entire training set and tested on the external test set. Seven radiomic features were identified as the most crucial by reapplying the complete best pipeline for feature selection (i.e., correlation and LASSO regression) on the full training set,

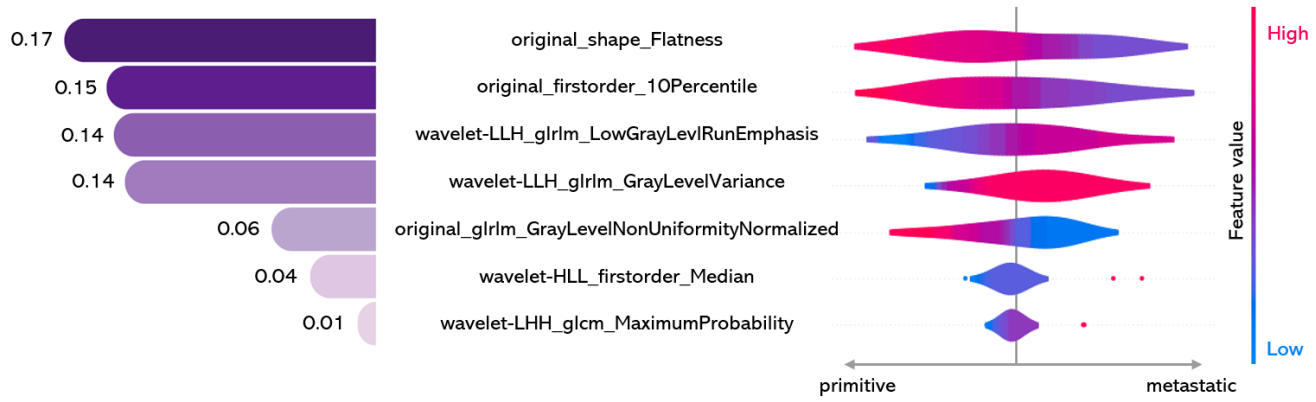

Figure 2. Permutation feature importance coefficients (on the left) and SHapley Additive exPlanations (SHAP) distributions (on the right) illustrating the contribution of each the seven selected features to the model's prediction. Features are displayed in order of importance from top to bottom.

with 3 features derived from the original VOI and 4 from the wavelet-transformed version. Figure 2 highlights the importance of these seven selected features in predicting malignancy both through permutation technique (on the left) and SHAP technique (on the right). The re-trained model achieved an accuracy of 93% on the full training set and 83% on the test set, misclassifying just one sample, resulting in one false positive and no false negatives.

4. Discussion

In this study we developed a radiomics-based model using contrast-free cine T1-weighted sequences to discriminate primary from metastatic malignant tumors.
The optimal machine learning pipeline included correlation filtering discarding the feature in highly correlated pairs (correlation > 90%), LASSO regression for feature selection and an SVM classifier. This configuration achieved a mean validation accuracy of 0.90 across 10-fold CV, demonstrating robust handling of non-linear relationships. The model's performance remained strong when retrained on the complete training set, achieving 93% accuracy on the training data and 83% on the external test set. Through feature selection, we identified seven radiomic features predictive of malignancy. The most significant feature was "original_shape_Flatness": SHAP analysis revealed that higher VOI flatness values corresponded to a lower probability of the tumor being metastatic. The second most important feature was "original_firstOrder_10Percentile": SHAP analysis indicated that higher values of this feature correlate with a lower probability of metastasis, suggesting that darker regions may be characteristic of metastatic tumors. Conversely, the third most important feature, "wavelet-LLH_glrlm_lowGrayLevelRunEmphasis":
SHAP analysis showed that tumors exhibiting more pronounced, longer stretches of low-intensity regions in the wavelet-transformed image have a higher likelihood of being metastatic.

To the best of our knowledge, this is the first study using radiomics for discriminating primary from metastatic malignant tumors. The only other study using radiomics for CMs focused mainly on distinguishing thrombi from general cardiac tumors [5], while our model offers a more detailed approach to malignancy assessment. By using contrast-free cine T1-weighted sequences, which are part of standard cardiac MRI protocols, the model ensures broad clinical applicability and also speeds up the exam time. Additionally, since no contrast agents are needed, it is particularly beneficial for patients with contraindications to gadolinium-based contrast agents, ensuring that vulnerable populations can still benefit from CM characterization. The ability to non-invasively distinguish between primary and metastatic malignant tumors can support the oncological diagnostic process. If the method suggests a metastatic origin rather than a primary cardiac tumor, it can guide the clinician in identifying the primary tumor responsible for the metastasis and help determine the most accessible site for biopsy.

5. Conclusion

This study shows the possibility of utilizing a radiomics-based approach for distinguishing primitive from metastatic malignant cardiac tumors using contrast-free cine T1-weighted sequences. The radiomic model eliminates inter-operator variability, providing objective, reproducible results. Future work will focus on expanding the dataset for improved validation as well as exploring complementary imaging sequences to enhance the model's diagnostic capabilities and robustness.

Acknowledgments

M.F. is supported by the Italian Ministry of Health, PSC Salute, Traiettoria 2 - "Health, diagnostica avanzata, medical devices e mini invasività" Linea di azione 2.1 "Creazione di una rete nazionale per le malattie ad alto impatto", project T2-AN-29, RADIOAMICA, CUP B47G22000220008.

References

[1] M Gatti *et al.*, «Cardiovascular Magnetic Resonance of Cardiac Tumors and Masses», *World J. Cardiol.*, vol. 13, fasc. 11, pp. 628–649, nov. 2021, doi: 10.4330/wjc.v13.i11.628.

[2] F Angeli *et al.*, «Multimodality Imaging in the Diagnostic Work-Up of Patients With Cardiac Masses: JACC: CardioOncology State-of-the-Art Review», *JACC CardioOncology*, vol. 6, fasc. 6, pp. 847–862, dic. 2024, doi: 10.1016/j.jaccao.2024.09.006.

[3] P Pazos-López *et al.*, «Value of CMR for the Differential Diagnosis of Cardiac Masses», *JACC Cardiovasc. Imaging*, vol. 7, fasc. 9, pp. 896–905, set. 2014, doi: 10.1016/j.jcmg.2014.05.009.

[4] P Paolisso *et al.*, «Cardiac Magnetic Resonance to Predict Cardiac Mass Malignancy: The CMR Mass Score», *Circ. Cardiovasc. Imaging*, vol. 17, fasc. 3, mar. 2024, doi: 10.1161/circimaging.123.016115.

[5] J Son *et al.*, «Radiomics Feature Analysis Using Native T1 Mapping for Discriminating Between Cardiac Tumors and Thrombi», *Acad. Radiol.*, vol. 29, pp. S1–S8, apr. 2022, doi: 10.1016/j.acra.2020.12.009.

[6] J J Maleszewski *et al.*, «The 2021 WHO Classification of Tumors of the Heart», *J. Thorac. Oncol.*, vol. 17, fasc. 4, pp. 510–518, apr. 2022, doi: 10.1016/j.jtho.2021.10.021.

Address for correspondence:
Meri Ferretti
Department of Electronics, Information and Bioengineering, Politecnico di Milano, Via Ponzio, 34, 20133 Milan, Italy
meri.ferretti@polimi.it