UNIVERSITÄT AUGSBURG
Universitätsbibliothek

OPEN ACCESS
OPUS AUGSBURG

A multi-method radiomics pipeline for survival analysis: robust feature identification in computed tomography data [Abstract]

Alexia Rizoudis, Charlotte Lind, Jakob Voran, Hannes Ulrich, Frank Kramer, Dominik Müller

Angaben zur Veröffentlichung / Publication details:

Rizoudis, Alexia, Charlotte Lind, Jakob Voran, Hannes Ulrich, Frank Kramer, and Dominik Müller. 2026. "A multi-method radiomics pipeline for survival analysis: robust feature identification in computed tomography data [Abstract]." *Biomedical Engineering / Biomedizinische Technik* 71 (s1). https://doi.org/10.1515/bmt-2026-1001.

Nutzungsbedingungen / Terms of use:

CC BY 4.0

Dieses Dokument wird unter folgenden Bedingungen zur Verfügung gestellt: / This document is made available under these conditions:
CC-BY 4.0: Creative Commons: Namensnennung
Weitere Informationen finden Sie unter: / For more information see:
https://creativecommons.org/licenses/by/4.0/deed.de

A Multi-Method Radiomics Pipeline for Survival Analysis: Robust Feature Identification in Computed Tomography Data

Alexia Rizoudis, IT-Infrastructure for Translational Medical Research, University of Augsburg, Germany, Alexia.Rizoudis@uni-a.de
Charlotte Lind, University Hospital Schleswig-Holstein, Department of Internal Medicine III, Kiel, Germany, Charlotte.Lind2@uksh.de
Jakob Voran, University Hospital Schleswig-Holstein, Department of Internal Medicine III, Kiel, Germany, JakobChristoph.Voran@uksh.de
Hannes Ulrich, University Hospital Schleswig-Holstein, Institute for Medical Informatics and Statistics, Kiel, Germany, Hannes.Ulrich@uksh.de
Frank Kramer, IT-Infrastructure for Translational Medical Research, University of Augsburg, Germany, Frank.Kramer@informatik.uni-augsburg.de
Dominik Müller, IT-Infrastructure for Translational Medical Research, University of Augsburg, Germany, Dominik.Mueller@informatik.uni-augsburg.de

Introduction

Although imaging data contain high-dimensional information potentially relevant to outcomes, their use in survival analysis is limited by manual interpretation and the lack of systematic feature extraction. Radiomics derived from computed tomography (CT) imaging offers promising biomarkers. This study presents a CT radiomics pipeline for partially automated survival analysis and evaluates its robustness across complementary analytical methods.

Methods

The proposed pipeline integrates partially automated CT processing, feature extraction, statistical analysis, and machine learning. CT scans were automatically processed from the hospital PACS using the Body and Organ Analysis framework (University Hospital Essen), integrating TotalSegmentator and body composition analysis to extract radiomic features from organs, bones, muscles, and fat tissue. A multi-step analysis workflow was applied: (1) association analysis using Pearson correlation with Benjamini-Hochberg correction, (2) univariate Cox regression and Kaplan-Meier log-rank tests, and (3) XGBoost with SHAP-based feature importance. Results were compared to identify consistently relevant features.

Results

The proposed approach was evaluated in 972 TAVI patients who underwent pre-procedural CT imaging (mean age 81.7 years, 50% female, 1-year survival 88.8%, 3-year survival 52.3%) as a clinical use case. It identified clinically plausible features associated with survival, including established risk markers (e.g., age, STS score, cardiac biomarkers) alongside imaging-derived features. Notably, several of these established markers were consistently identified across all analytical approaches, indicating robust associations independent of the applied method. The XGBoost model showed predictive capability for survival group classification (short ≤12m, intermediate 12-36m, long >36m), with class-dependent performance (F1-score: long 0.81, intermediate 0.22, short 0.39).

Conclusion

This study demonstrates the usefulness of our multi-method radiomics pipeline for survival analysis in clinical imaging data. Consistent findings across approaches highlight the robustness of identified features and support their potential relevance for clinical research. Future work will extend the pipeline to additional applications and develop end-to-end solutions for practical use.

Open Access. © 2026 The Author(s), published by De Gruyter. This work is licensed under the Creative Commons Attribution 4.0 International License.