Methods: The study involved 89 computed tomography (CT) scans, including a control group of clinical routine cases and 13 balanced study groups representing various structural abnormalities (spine and chest wall deformities (SCWD), hypertrophic cardiomyopathies (HCM), aortic, mitral and tricuspid valve replacements, left ventricular assist devices (LVAD), newborns (under age 1), preschool children (age 1 to 4), elementary school children (age 5 to 9), secondary school children (age 10 to 16), adults with transposition of the great arteries, with situs inversus and with Fontan circulation. Imaging was retrospectively chosen from multiple CT scanners (years 2012 to 2024), utilising soft-tissue kernel and intravenous contrast agents. Automated segmentation of six mediastinal structures (left and right atrium, left and right ventricle, aorta, pulmonary artery) was followed by manual corrections. Statistical analysis with the dice coefficient, surface dice, jaccard index and volume similarity index ensued to assess structural distinctiveness dependent on pathology or age.
Results: The model performed well (dice=0.9) on the clinical routine collective.
It did not perform significantly ($p>0.05$) inferior on patients with SCWDs (dice=0.87), HCMs (dice=0.88), with aortic (dice=0.87), mitral (dice=0.88) and tricuspid valve replacements (dice=0.88) and with LVADs (dice=0.87), except for the left atrium (surface dice=0.20) and the left ventricle (dice=0.69).
In newborns the tool was not able to reliably detect the cardiac chambers and the great vessels (dice=0.23). The precision increased with age. Only the great arteries were segmented significantly inferior in secondary school children (total dice=0.88, aorta surface dice=0.51, pulmonary surface dice=0.37).
In adults with congenital heart disease the algorithm performed inferior than on the clinical routine collective with a dice of 0.46 in patients with transposition of the great arteries, 0.38 in patients with a situs inversus and 0.53 in patients with Fontan circulation.
Conclusion: The algorithm provides dependable automatic segmentation of the heart chambers and great arteries in clinical routine patients, in patients with SCWDs, HCMs and in replaced heart valves. In patients with a LVAD only the segmentation of the right heart and the great arteries is robust. Patients aged 0 to 9 need manual segmentation. Adolescents between 10 and 16 years of age had good automatic results of the heart chambers, but the great arteries were limited. In adults with congenital heart disease the algorithm does not perform adequately.

Results

Blue marked values are significantly inferior compared to the control group

	Aorta Dice	Aorta Surface Dice	Atrium Left Dice	Atrium Left Surface Dice	Atrium Right Dice	Atrium Right Surface Dice	Ventricle Left Dice	Ventricle Left Surface Dice	Ventricle Right Dice	Ventricle Right Surface Dice	Pulmonary Artery Dice	Pulmonary Artery Surface Dice	Dice Total	Surface Dice Total
Control group	0,9680	0,7859	0,9055	0,4325	0,8599	0,2988	0,8967	0,4276	0,8846	0,3850	0,9213	0,5617	0,9060	0,4819
Chest wall deformities	0,9578	0,7167	0,8703	0,3135	0,8027	0,2377	0,8651	0,3154	0,8355	0,2749	0,8871	0,4634	0,8698	0,3869
Aortic valve replacement	0,9611	0,7104	0,8855	0,3424	0,8231	0,2219	0,8582	0,2849	0,8102	0,2192	0,8771	0,4638	0,8692	0,3738
Mitral valve replacement	0,9547	0,6834	0,8546	0,2571	0,8540	0,2393	0,8936	0,3535	0,8516	0,2826	0,8922	0,5092	0,8835	0,3875
Tricuspid valve replacement	0,9526	0,6709	0,9012	0,3038	0,8447	0,2450	0,8103	0,1909	0,8743	0,3158	0,8926	0,4265	0,8793	0,3588
Left ventricular assist device	0,9627	0,7183	0,8325	0,1950	0,9189	0,3629	0,6905	0,0926	0,9155	0,4170	0,8933	0,4290	0,8689	0,3691
Age 0	0,0657	0,0138	0,3383	0,0836	0,1842	0,0417	0,4735	0,0848	0,2661	0,0389	0,0434	0,0146	0,2285	0,0462
Age 1-4	0,5861	0,2059	0,8202	0,2176	0,8169	0,1878	0,8553	0,2299	0,8313	0,2156	0,7183	0,2348	0,7718	0,2153
Age 5-9	0,8023	0,3322	0,8249	0,2354	0,7941	0,1917	0,8362	0,1914	0,8321	0,2289	0,6645	0,2223	0,7924	0,2337
Age 10-16	0,9096	0,5139	0,8590	0,2994	0,8637	0,2846	0,9142	0,3866	0,9121	0,3955	0,8255	0,3742	0,8807	0,3757
Transposition of great arteries	0,8421	0,6133	0,5235	0,1422	0,2132	0,0357	0,2723	0,1086	0,1945	0,0389	0,7058	0,2484	0,4886	0,1979
Situs inversus	0,7962	0,4629	0,5797	0,1351	0,0034	0,0016	0,0000	0,0000	0,4947	0,1144	0,4279	0,1274	0,3836	0,1387
Fontan circulation	0,7876	0,5580	0,8007	0,1998	0,1254	0,0248	0,6026	0,1184	0,3411	0,0610	0,5339	0,2069	0,5319	0,1948

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A SCOPING REVIEW OF RADIOMIC TECHNIQUES USED TO INVESTIGATE CARDIOVASCULAR DISEASE

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Purpose: Cardiovascular disease affects the carotid arteries, coronary arteries, aorta and the peripheral arteries. Radiomics involves the extraction of quantitative data from imaging features that are imperceptible to the eye. There is a paucity of evidence summarising the expanding literature on radiomic analysis in cardiovascular disease.
Methods: MEDLINE and Embase databases were searched for eligible studies evaluating radiomic techniques in living human subjects derived from computed tomography (CT) or positron emission tomography CT (PET-CT) imaging investigating atherosclerotic disease. Data on study population, imaging characteristics and radiomics methodology were extracted.
Results: 29 studies consisting of 5,753 patients (3,752 males) were identified. 78.7% of patients were from coronary artery studies. Eight studies performed CT carotid angiography, 18 employed CT coronary angiography, and two studied PET-CT. Manual segmentation was most frequently undertaken. Processing techniques included voxel discretisation, voxel resampling and filtration. Various shape, first-order, second order and higher-order radiomic features were extracted. Logistic regression was most commonly used for machine learning.
Conclusion: Most published evidence was feasibility/proof of concept work. There was significant heterogeneity in image acquisition, segmentation techniques, processing and analysis between studies. There is a need for implementation of standardised imaging acquisition protocols, adherence to published reporting guidelines and economic evaluation.

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RISK IDENTIFICATION AND RELAPSE PREDICTION IN LUNG ADENOCARCINOMA (LUAD)

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Purpose: This study aims to utilise machine learning to predict the risk of cancer relapse in lung adenocarcinoma (LUAD) patients. By analysing clinical and genomic data, the research seeks to identify key factors influencing recurrence, thereby enhancing early detection and informing treatment strategies to improve patient outcomes.
Methods: The study employed a dataset consisting of clinical and genomic information from LUAD patients. Key features included tumour mutation burden (TMB), pathologic stage and mutation counts. The dataset was preprocessed through normalisation and encoding of categorical variables. A linear support vector machine (SVM) was used to construct the predictive model, with the data split into training (70–80%) and testing (20–30%) sets. Model performance was assessed using metrics such as accuracy, precision, recall, F1 score and ROC AUC score, alongside confusion matrix analysis to evaluate classification performance.
Results: The linear SVM model achieved an accuracy of 83%, with a precision of 80% for the recurrence class, indicating reliable prediction capability. However, the model exhibited a low recall rate of 17%, highlighting challenges in identifying true positive recurrence cases. The ROC AUC score of 80% demonstrated good discriminatory power. Feature importance analysis identified nonsynonymous TMB and pathologic stage as critical predictors of relapse risk, whereas higher mutation counts and early-stage diagnosis correlated with reduced relapse risk.
Conclusion: The study successfully identified significant predictors of recurrence in LUAD patients, offering insights into factors that could guide clinical decision-making. While the model demonstrates potential in risk stratification and personalised treatment planning, its low recall underscores the need for further refinement. Enhancements could include incorporating additional features, alternative modelling techniques and larger datasets to improve prediction accuracy. The findings advocate for comprehensive genomic analyses and ongoing surveillance in managing LUAD, particularly in high-risk individuals, to better anticipate and mitigate relapse.