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1 Machine Learning cardiac-MRI features predict mortality in newly diagnosed 2 pulmonary arterial hypertension

3 Samer Alabed MD^{a,b,c}, Johanna Uthoff PhD^d, Shuo Zhou^d, Pankaj Garg PhD^a, Krit Dwivedi MD^{a,b},
4 Faisal Alandejani MD^a, Rebecca Gosling PhD^a, Lawrence Schobs^d, Martin Brook^a, Dave Capener^a,
5 Chris Johns PhD^{a,b}, Jim M Wild PhD^{a,c}, Alexander MK Rothman PhD^a, Rob J. van der Geest PhD^e,
6 Robin Condliffe MD^{a,f}, David G Kiely MD^{a,c,f}, Haiping Lu PhD^{c,d*}, Andrew J Swift PhD^{a,b,c*}

7 * contributed equally to the manuscript

8 ^aDepartment of Infection, Immunity and Cardiovascular Disease, University of Sheffield, Sheffield,
9 UK

10 ^bDepartment of Clinical Radiology, Sheffield Teaching Hospitals, Sheffield, UK

11 ^cINSIGNEO, Institute for in silico medicine, University of Sheffield, UK.

12 ^dDepartment of Computer Science, University of Sheffield, Sheffield, UK

13 ^eLeiden University Medical Center, Leiden, The Netherlands

14 ^fSheffield Pulmonary Vascular Disease Unit, Royal Hallamshire Hospital, Sheffield, UK

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22 **Data Availability**

23 The data underlying this article will be shared on reasonable request to the corresponding
24 author.

26 **Address for correspondence**

27 Dr Samer Alabed

28 Cardiac MRI Research Fellow

29 Department of Infection, Immunity and Cardiovascular Disease,

30 University of Sheffield, Glossop Road, Sheffield, S10 2JF, United Kingdom

31 Tel: 0114 243 4343

32 Email: s.alabed@nhs.net

33 Twitter: smrabd

1 Abstract

2 Background

3 Pulmonary arterial hypertension (PAH) is a rare but serious disease associated with high mortality if left
4 untreated. This study aims to assess the prognostic cardiac magnetic resonance (CMR) features in PAH
5 using machine learning.

6 Methods

7 723 consecutive treatment-naive PAH patients were identified from the ASPIRE registry; 516 were
8 included in the training and 207 in the validation cohort. A multilinear principal component analysis
9 (MPCA) based machine learning approach was used to extract mortality and survival features throughout
10 the cardiac cycle. The features were overlaid on the original imaging using thresholding and clustering of
11 high- and low-risk of mortality prediction values.

12 Results

13 The one-year mortality rate in the validation cohort was 10%. Univariable Cox regression analysis of the
14 combined short-axis and 4-chamber MPCA-based predictions was statistically significant (Hazard Ratios
15 2.1, 95% CI 1.3, 3.4, c-index = 0.70, $p = .002$). The MPCA features improved the one-year mortality
16 prediction of REVEAL from c-index = 0.71 to 0.76 ($p = < .001$). Abnormalities in the end-systolic
17 interventricular septum and end-diastolic left ventricle indicated the highest risk of mortality.
18

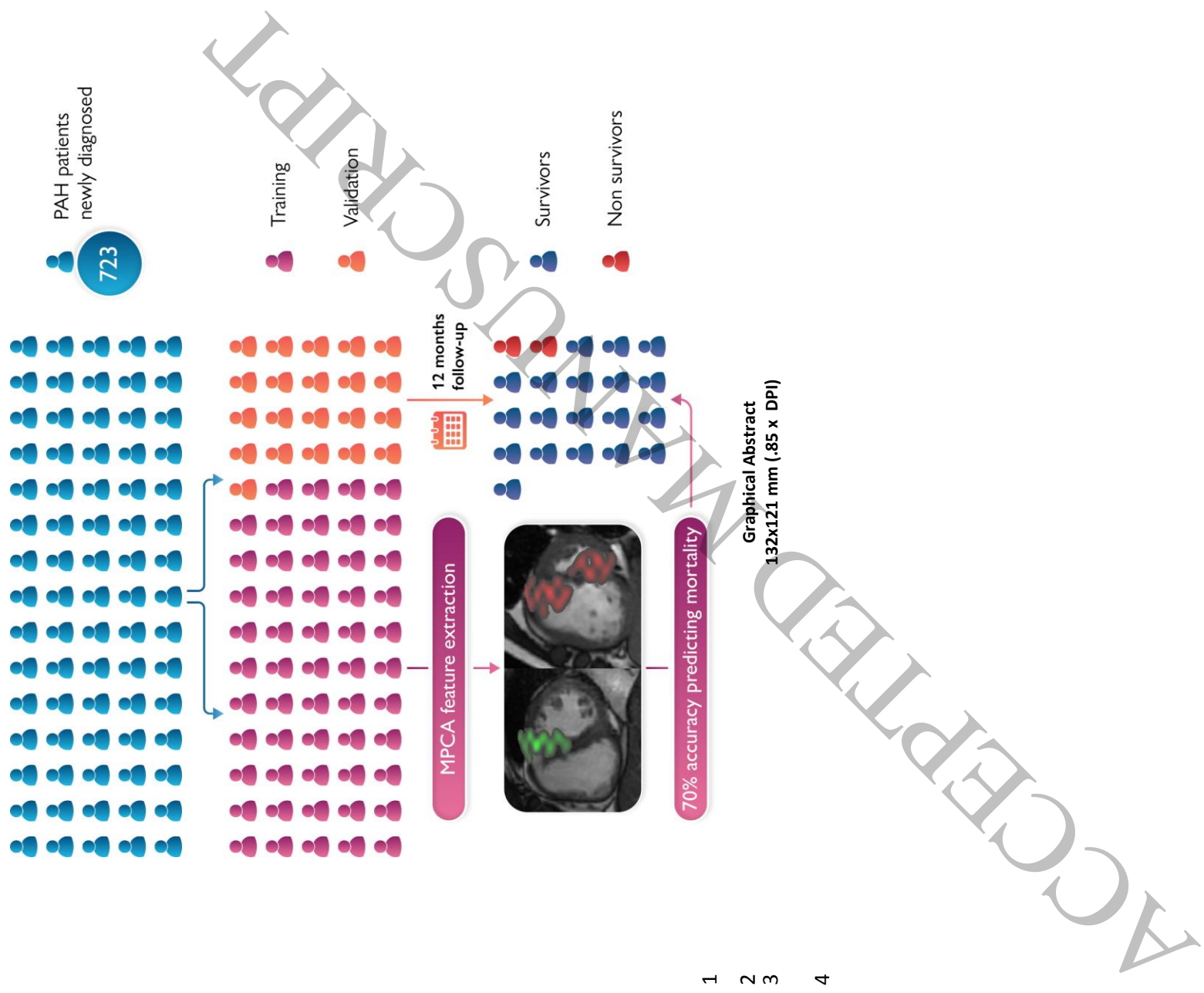
19 Conclusion

20 The MPCA-based machine learning is an explainable time-resolved approach that allows visualisation of
21 prognostic cardiac features throughout the cardiac cycle at population level, making this approach
22 transparent and clinically interpretable. In addition, the added prognostic value over the REVEAL risk
23 score and CMR volumetric measurements allows for a more accurate prediction of one-year mortality risk
24 in PAH.

25 **Keywords:** Machine learning, Artificial Intelligence, Cardiac MRI, prognosis, mortality, Pulmonary
26 hypertension

27 Abbreviations and Acronyms

4Ch	four-chamber
CMR	cardiac magnetic resonance
MPCA	multilinear principal component analysis
mPAP	mean pulmonary artery pressure
PAH	pulmonary arterial hypertension
PVR	pulmonary vascular resistance
RHC	right heart catheter
RV	right ventricular
SA	short axis
SVM	support vector machines



1 Introduction

2 Cardiac magnetic resonance (CMR) is a powerful prognostic tool owing to its ability to assess cardio-
3 physiological parameters such as the volume and function of the cardiac chambers, tissue characterisation
4 and anatomical structure. Machine learning methods harnessing CMR's prognostic abilities remain rare
5 and mainly focus on segmenting cardiac chambers to automate CMR measurements ¹. The process of
6 automating CMR measurements has matured over recent years, proving to be accurate and comparable to
7 results obtained from manual segmentation ²⁻⁴. However, there is a wealth of data available in CMR
8 studies other than those based on volumetric measurements. A recent machine learning model based on the
9 motion of segmented right ventricle predicted mortality in a mixed cohort of pulmonary hypertension
10 patients ⁵. This study linked impaired basal longitudinal shortening and transverse contraction at the
11 interventricular septum and free wall with an increased risk of mortality ⁵. Another recent machine learning
12 model based on CMR disease features extracted by multilinear principal component analysis (MPCA) has
13 been used to predict the presence or absence of pulmonary arterial hypertension (PAH) ⁶ without the need
14 for segmentation.

15 The MPCA-based model is interpretable because MPCA is a linear and transparent feature extraction
16 method, thus a particularly promising machine learning approach for CMR imaging. Each CMR image
17 sequence is a three-dimensional array (e.g. 512x512pixels x6mm slice thickness x20images throughout the
18 cardiac cycle), with each element being a voxel capturing different tissue characteristics, anatomical
19 location and temporal variation in the cardiac cycle. Such a multidimensional array can be naturally
20 represented as a mathematical object called a tensor. MPCA extracts features directly from such multi-
21 dimensional tensor representation which preserves the multidimensional structure of the original CMR data
22 more accurately than reshaping it into one dimensional, vector representation⁷. The extracted MPCA
23 features can then be weighted in classification or regression models to optimise the prediction of the
24 desired outcome.

25 PAH is a rare but serious disease that is associated with high mortality if left untreated ⁸. This study aims
26 to assess the prognostic accuracy of the above MPCA-based model to predict one-year mortality in PAH.
27 Therefore, evaluating prognosis is key to identifying high-risk patients and optimising their management
28 strategies as recommended by the European Society of Cardiology guidelines ^{9,10}. Multiple clinical
29 parameters are routinely obtained to evaluate PAH disease progression, including pulmonary
30 haemodynamics from right heart catheterization (RHC), functional data from exercise tolerance and
31 pulmonary function tests, biochemistry including N-terminal pro-B-type natriuretic peptide (NT-proBNP)
32 and imaging including echocardiogram and CMR. The REVEAL score is a composite clinical risk score
33 for mortality that combines these clinical parameters to predict one-year mortality ¹¹. In addition, CMR
34 measurements such as right ventricular volumes and function have been shown to predict mortality in PAH
35 ¹². Thus, the availability of detailed patient phenotyping and prediction scores allows setting a clinical
36 benchmark for the performance of machine learning prognostic models in PAH. This study assesses the
37 additive value of the MPCA-based model to predict mortality compared to established prognostic
38 parameters such as the REVEAL risk score and CMR measurements.

1 Methods

2 The TRIPOD checklist for reporting prediction model development and validation was followed ¹³ and is
3 available in the supplemental material.

4 Study Population

5 All consecutive treatment-naïve patients with PAH referred for a baseline CMR between 2008 and 2019
6 were identified from the ASPIRE registry ¹⁴. Eligibility criteria included; i) a baseline CMR study
7 performed within 14 days of a PAH diagnosis, confirmed by right heart catheterisation (RHC), and before
8 the commencement of PAH treatment. ii) minimum 12 months follow-up or death within 12 months post
9 CMR study. The study population was divided into two cohorts; i) a training cohort whose CMR images
10 were used to develop and optimise the prognostic algorithm and ii) a validation cohort that was left out of
11 training and used to validate the performance of the prognostic model. The cohort was split 70:30 into the
12 model development and model validation cohort.

13 Ethical approval was obtained from the local ethics committee and written consent was waived for this
14 retrospective study (ref c06/Q2308/8).

15 MR Imaging Protocol

16 CMR was performed with a 1.5 Tesla GE HDx (GE Healthcare, Milwaukee, USA) system using an eight-
17 channel cardiac coil. Four-chamber (4Ch) and short-axis (SA) cine images were acquired using a cardiac
18 gated multislice balanced steady-state free precession sequence (20 frames per cardiac cycle, slice
19 thickness 10mm, 0mm inter-slice gap, field of view 480mm, acquisition matrix 256x200, flip angle 60°,
20 BW 125 KHz/pixel, TR/TE 3.7/1.6ms). A stack of images in the short-axis plane were acquired fully
21 covering both ventricles from base to apex. End-systole was considered to be the smallest cavity area. End-
22 diastole was defined as the first cine phase of the R-wave triggered acquisition or largest volume. Patients
23 were in the supine position with a surface coil and with retrospective ECG gating.

24 Volumetric and ventricular function analysis was performed by contouring the ventricular endocardial
25 borders at end-diastole and end-systole on the SA images using MASS software (MASS, 2020; Leiden
26 University Medical Center, Leiden, the Netherlands). Papillary muscles and trabecula were included in the
27 blood volume.

28 Image Preprocessing

29 Mid-chamber SA and 4Ch cine images were used in this study. Images were processed following methods
30 in a previous study ¹⁵. In brief, images were preprocessed by standardising CMR voxel units between
31 subjects, registering to each other using three anatomical landmarks, masking surrounding tissues, and
32 downscaling image size (Figure 1).

33 CMR voxel units were standardised between subjects by z-scores. Rigid image registration was used based
34 on three predefined fixed anatomic landmarks. The landmarks were manually placed on SA (superior
35 insertion point; right ventricular free wall inflexion; mid-left ventricular lateral wall) and 4Ch (left
36 ventricle apex; lateral mitral annulus; lateral tricuspid annulus). CMR images were landmarked by a single
37 reader (SA) with independent visual quality assurance checks (SA; JU). In order to focus on spatially
38 relevant features, an ellipsoidal mask was fitted around the heart. Downsampling was performed to four
39 image sizes (32x32, 64x64, 128x128, 256x256).

1 MPCA Pipeline

2 The prognostic prediction was achieved by training support vector machines (SVMs) on MPCA features
3 extracted from CMR studies ^{6,7}. The methodology followed the MPCA-based pipeline in previous studies
4 ^{6,15}. This pipeline was trained through 10 rounds of 10-fold cross-validation on the development cohort
5 (n=516). For each fold during training, MPCA features were extracted and ranked for prognostic capability
6 using Fisher's Discriminant Analysis in the following way. Extracted features were ranked and selected
7 using a step-wise feature inclusion method. This was performed using a random tuning-set (n ~50) of
8 cases. The feature set with the highest tuning-set performance was used to train an SVM and tested on the
9 left-out fold. The feature set with the highest fold-performance was used to train the final development
10 SVM. This MPCA-based machine learning model was then applied to the completely left out validation
11 cohort (n=207). On a standard computer, the time it takes to process each image and perform inference is
12 much less than 0.1 second. A Jupyter notebook tutorial of the open-source pipeline code is available at:
13 https://colab.research.google.com/github/pykale/pykale/blob/main/examples/cmri_mPCA/tutorial.ipynb

14 Visualisation of Tensor Features

15 Trained features were visualised by utilising MPCA reconstruction to obtain spatially relevant feature
16 maps. To visually inspect the impact of specific regions on high- and low-risk of mortality prediction, a
17 two-step procedure of thresholding and clustering was implemented. Voxels containing high absolute
18 values (high positive = high-risk, high negative = low-risk) of MPCA features were thresholded.
19 Morphological dilation-erosion using a spherical structural element (r=2) was performed and clusters of
20 visually significant size were overlaid on individual patients' original CMR scans.

21 Clinical and Mortality Data

22 Clinical data including intermittent shuttle walking test (ISWT), pulmonary function test, and serum level
23 of NT-proBNP were collected before treatment was commenced. Demographic data, WHO functional
24 status, PAH subgroup diagnosis, and outcome were collected from the electronic medical system.
25 Mortality data were collected from the electronic records of the National Health Service (NHS) Personal
26 Demographics Service. The NHS automatically updates the mortality records once a death is registered in
27 the United Kingdom. All patients were followed up as part of the national service specification for patients
28 with pulmonary hypertension for a minimum of 12 months. No patients were lost to follow-up.

29 Statistical Analysis

30 Continuous variables are presented as proportions, means \pm standard deviations, or median and
31 interquartile range for data not following a normal distribution. The sample size for developing the
32 prediction model was calculated using a one-year mortality prevalence of 10% and 7 predictor parameters
33 and required 420 patients to develop the mortality prediction model ¹⁶. The REVEAL score was calculated
34 from composite clinical parameters ¹¹ and modified to include the incremental shuttle walk test instead of
35 the 6-minute walking test ^{17,18}. The CMR volumetric measurements were indexed for body surface area
36 and corrected for age and sex by calculating the percentage predicted values as per published reference
37 data ^{19,20}. The outcome of the MPCA-based pipeline was calculated as the SA and 4Ch probabilities based
38 on the SVM prediction. A combined probability was calculated by further training a dual-scan SVM from
39 the selected features of both individual models - SA and 4Ch. All variables were standardised by

1 subtracting the mean for each variable and dividing it by its standard deviation (SD) to allow for more
2 meaningful comparisons.
3 A univariable Cox proportional hazards regression was performed to estimate the one-year mortality
4 prediction of the REVEAL score, CMR measurements and the MPCA probabilities. For the multivariable
5 analysis, we planned to include the CMR measurements that were identified in previous prognostic studies,
6 namely right ventricular ejection fraction (RVEF), right ventricular end-systolic volume index (RVESVi),
7 right ventricular end-diastolic volume index (RVEDVi), left ventricular end-diastolic volume index
8 (LVEDVi), left ventricular stroke volume index (LVSVi) and pulmonary artery relative area change (PA
9 RAC)^{12,21}. Due to the high correlation between RVESVi and RVEDVi ($r=0.89$) we only included RVESVi
10 as the stronger predictor in the multivariable analysis. The proportional hazards assumption was confirmed
11 using scaled Schoenfeld residuals. The c-index was used to measure the relative goodness of fit between
12 the different regression models. The c-index indicates the rate of correct predictions of survival the model
13 makes. We also computed the Akaike information criterion (AIC) for each model. The AIC estimates the
14 rate of incorrect prediction and compares the quality of different models relative to each other while
15 penalising the models with more variables. While a higher c-index indicates a better model fit, a lower AIC
16 value indicates fewer prediction errors²².
17 In addition, the likelihood ratio test was performed to assess if there is a statistically significant difference
18 between the different models and to determine the additive predictive value of the MPCA probabilities.
19 The models compared were the univariable REVEAL score, the REVEAL score combined with prognostic
20 CMR measurements and finally a multiple variable model including the REVEAL score, CMR
21 measurement and the MPCA probabilities. Kaplan-Meier curves were analysed to demonstrate the
22 prognostic value of MPCA predictions dividing patients based on the median MPCA value as the
23 threshold. The high and low mortality risk groups were compared using the log-rank (Mantel-Cox) test.
24 The receiver-operating characteristic curve (ROC) and the area under the curve (AUC) were used to
25 estimate the prognostic accuracy of the different MPCA features.

26 Results

27 Study Population Characteristics

28 A total of 737 consecutive incident patients with PAH were identified. Incomplete scans because of
29 claustrophobia or patient intolerance were excluded, leaving 723 scans for the analysis. The training cohort
30 included 516 and the validation cohort 207 subjects (Figure 2).

31 The baseline characteristics of both cohorts are presented in Table 1. In summary, the study population
32 were 74% females aged 59 ± 16 years and included PAH secondary to connective tissue disease CTD
33 (46%), idiopathic PAH (IPAH) (27%), congenital heart disease (CHD) (16%), secondary to portal
34 hypertension (7%) and other PAH subtypes (4%).

35 Mortality Prediction

36 Survival analysis

37 The one-year mortality rate in the validation cohort was 10% with an overall mortality rate over the total
38 follow-up period of 29%. Kaplan-Meier survival analysis demonstrated a significant difference in survival
39 in patients with high and low mortality risk in the validation cohort (Log-rank test <0.001) (Figure 3). The

1 ROC curve for each model is shown in Figure 4. The AUC was 0.73 for the SA model, 0.64 for 4Ch and
2 0.70 for the combined MPCA-based features to predict one-year mortality in the validation cohort.
3 Univariable Cox regression analysis confirmed a strong prognostic utility of the SA and combined SA and
4 4Ch MPCA-based predictions (Table 2). However, the 4Ch features alone were not significant predictors
5 of mortality. The univariable Cox regression hazard ratios for the demographics, RHC and CMR
6 measurements, functional tests and clinical parameters are shown in Table 2. The REVEAL score and, PA
7 RAC and age and sex-adjusted RVESVi were significant predictors of one-year mortality.

8 Additive prognostic value

9 Several multivariable prognostic models were compared in Table 3 to compare the predictive value of the
10 REVEAL score alone, REVEAL score combined with CMR measurements or MPCA features and finally
11 REVEAL score combined with CMR measurements and MPCA features. The prognostic models were
12 compared using the c-index and AIC test for goodness of fit and the log-rank test to assess the statistical
13 significance of the difference between the models. The univariable REVEAL model allows the assessment
14 of the one-year risk of mortality based on available composite clinical data alone. Adding the MPCA-based
15 predictions allows evaluating the added incremental value in predicting death compared to REVEAL and
16 segmentation based CMR parameters.

17 The REVEAL score alone had a c-index of 0.71 and AIC of 203. Adding CMR measurements improved
18 the model statistically significantly, to 0.78 and AIC of 205 (log-rank test $p = 0.003$). The model including
19 MPCA prediction, REVEAL score and CMR measurements, showed the strongest prognostic utility (c-
20 index 0.83 and AIC 193, log-rank test $p < 0.001$). The MPCA model alone had similar accuracy to the
21 REVEAL score with a c-index of 0.71 and AIC of 204.

22 Temporal prognostic dynamics

23 The MPCA-based features were assessed throughout the cardiac cycle and grouped according to the
24 anatomical region into the right ventricle (RV), left ventricle (LV) and septum. For visualisation purposes,
25 we manually segmented the averaged SA and 4Ch slice to group the MPCA features into anatomical
26 regions. The features were divided into low and high-risk features based on the median MPCA feature
27 values used in the Kaplan-Meier analysis (Figure 4). On the SA views, abnormal interventricular septum
28 during systole and particularly at end-systole and the LV chamber during diastole and particularly at end-
29 diastole indicated a higher risk of mortality. On 4Ch views, the features with the highest impact on
30 predicting mortality were at the RV at early systole. A normal LV and interventricular septum in diastole
31 on SA and 4Ch imaging were the strongest predictors of survival, whereas the RV was a poor indicator of
32 survival (Figure 5).

33 Discussion

34 This study assessed the prognostic utility of an MPCA-based machine learning model in CMR in patients
35 with treatment naïve pulmonary arterial hypertension. This is the first study to localise prognostic PAH
36 features with an explainable AI approach dynamically over the cardiac cycle. In addition, we have shown
37 the incremental prognostic value of the MPCA model compared to known prognostic markers such as the
38 REVEAL score and CMR volumetric measurements.

1 The advantage of using MPCA is its interpretability. The ability to directly relate prognostic features
2 identified in the machine learning process helps understand and explain the machine learning model's
3 findings. Diagnostic and prognostic models based on deep learning methods have been criticised for
4 creating a "black-box" situation where the predictions are often difficult to comprehend and retrace²³.
5 Visualising the MPCA features throughout the cardiac cycle allowed discerning the most significant
6 discriminatory predictors of death on CMR in PAH. The known prognostic features identified in
7 pulmonary hypertension of diastolic interventricular septal flattening²⁴, reduced LV size and increased RV
8 size²⁵ can all be visually assessed on SA images. The most significant features identified in non-survivors
9 on SA imaging were located at the septum at end-systole and LV at end-diastole. Changes in the
10 interventricular septum at end-systole are the result of RV pressure overload. The altered pressure gradient
11 between the LV and RV results in flattening of the septum giving a characteristic D-shaped LV and
12 eventually results in impaired LV diastolic function and reduced LV filling^{26,27}. Survivors showed the
13 opposite with features in the septum at end-diastole and LV at end-systole. We found fewer overall
14 features on SA images at the RV. However, on 4Ch imaging the most significant features were identified
15 in RV systole. Whereas the septal and LV features were less important on 4Ch imaging. The 4Ch view
16 allows assessing the longitudinal RV contractility which for example can be inferred on echocardiogram
17 by assessing the tricuspid annular plane systolic excursion (TAPSE). RV longitudinal contraction is known
18 to be the larger component of RV contraction and a key prognostic indicator²⁸⁻³⁰ which explains its
19 prognostic importance in PAH.

20 The MPCA-based model was developed and validated on CMR imaging performed at diagnosis and in
21 treatment-naïve PAH patients. Disease severity assessed at baseline assessment is important for planning
22 an optimal treatment strategy. Almost all published prognostic CMR studies in PAH are based on disease
23 prevalent PAH patients in later stages of the disease process¹². A meta-analysis of 22 studies and almost
24 2000 patients with PAH showed that RVEF, RVESVi, RVEDVi, LVEDVi and LVSVi were significant
25 predictors of mortality¹². RVEF, RVEDVi, LVEDVi and LVSVi did not predict mortality in our baseline
26 PAH cohort. The MPCA pipeline can therefore elicit cardiac changes before they affect RV function and
27 size and adds prognostic value at baseline evaluation. In addition, comparing the MPCA to the REVEAL
28 score allowed us to evaluate the incremental value benchmarked against a clinically validated baseline
29 prognostic tool. The MPCA-based predictions significantly improved the one-year mortality prediction of
30 the REVEAL score. The prognostic model accuracy (c-index) using REVEAL improved from 71% to 83%
31 (log-rank test $p < 0.001$) when it was combined with CMR data including MPCA predictions and CMR
32 measurements. However, even without REVEAL data, mortality can still be accurately predicted based on
33 MPCA features alone with an accuracy (c-index) of 70%.

34 The application of stepwise cardiac features extraction using CMR has further potential that can be
35 evaluated in future developments. Comparing prognostic features at follow-up with baseline features might
36 provide a better understanding of disease progression on CMR and might offer a standardised disease
37 monitoring tool. In addition, technical improvements would allow to fully automate the prognostic model,
38 which currently requires manual image registration. Deep learning automated landmarking for image
39 registration would reduce the manual processing of CMR images and reduce the time and cost associated
40 with it^{31,32}.

1 **Limitations**

2 This was an exploratory retrospective single centre study on patients with PAH. Findings will need to be
3 confirmed in a prospective trial with an external validation cohort. In addition, applying the model to other
4 diseases and MRI systems would further validate its generalisability.

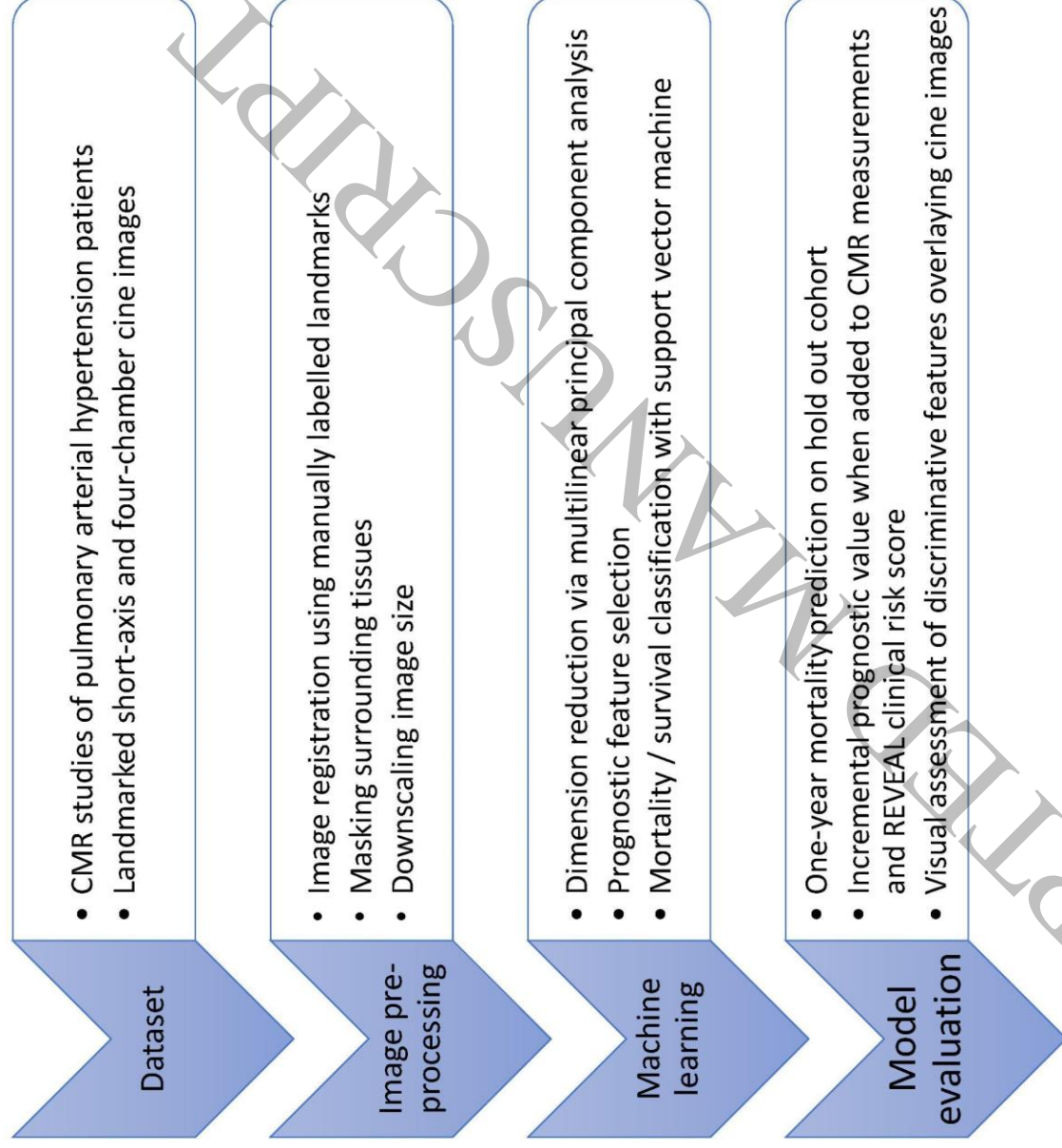
5 The MPCA method was applied on cine images of the mid-chamber slice throughout the cardiac cycle.
6 Stack imaging of the whole heart can currently not be included in the MPCA model training. However,
7 because of the strong prognostic signal from the SA and 4Ch cine images we envisage that future
8 developments including 3D data of the heart will further improve prognosis prediction.

9 **Conclusion**

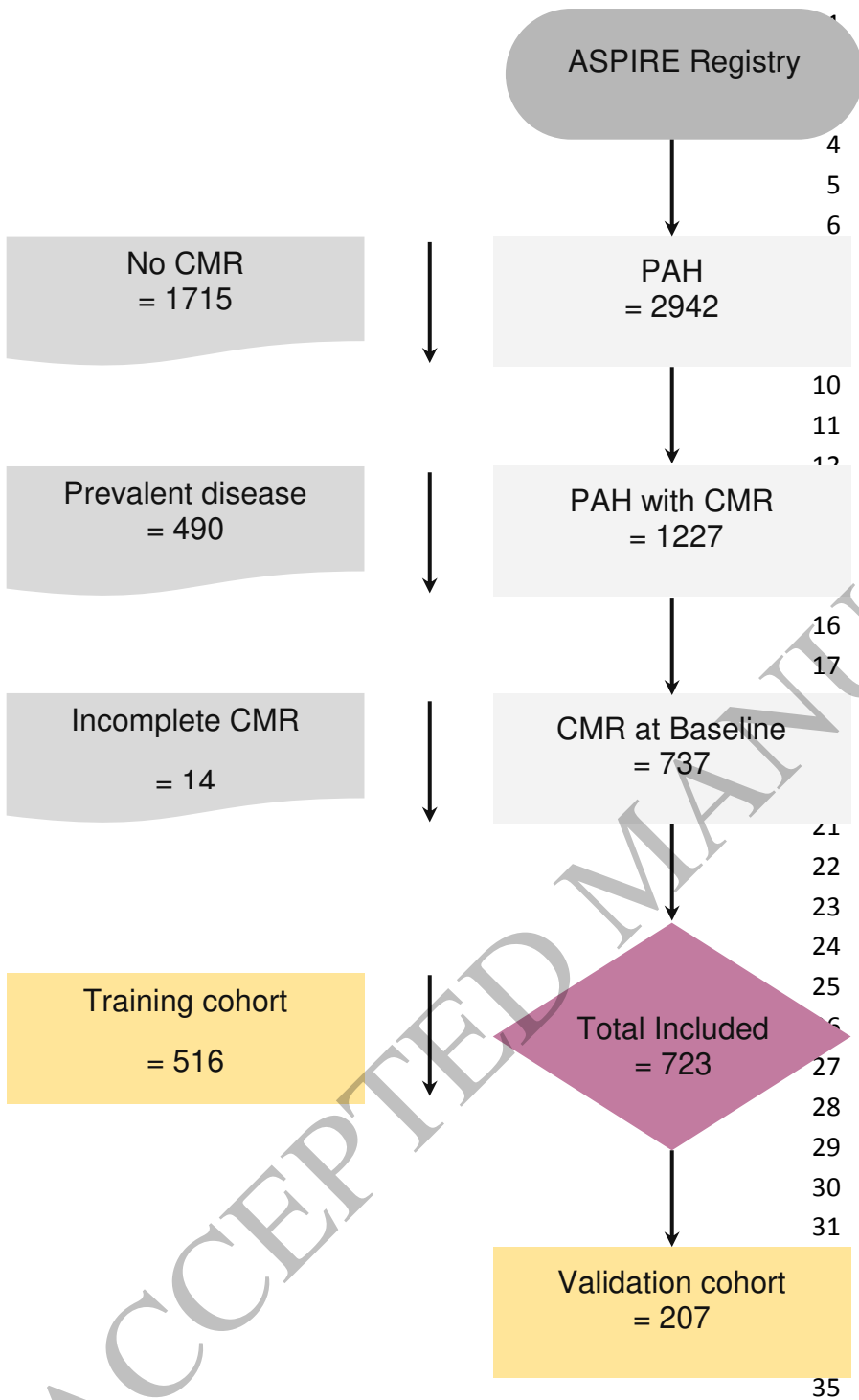
10 Patient outcome prediction in pulmonary arterial hypertension can be enhanced by adding MPCA-based
11 machine learning to CMR volumetric data and clinical risk scores. The MPCA analysis gives a population
12 insight into the prognostic cardiac features in pulmonary arterial hypertension in an explainable and
13 visualisable approach.

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1 Graphs

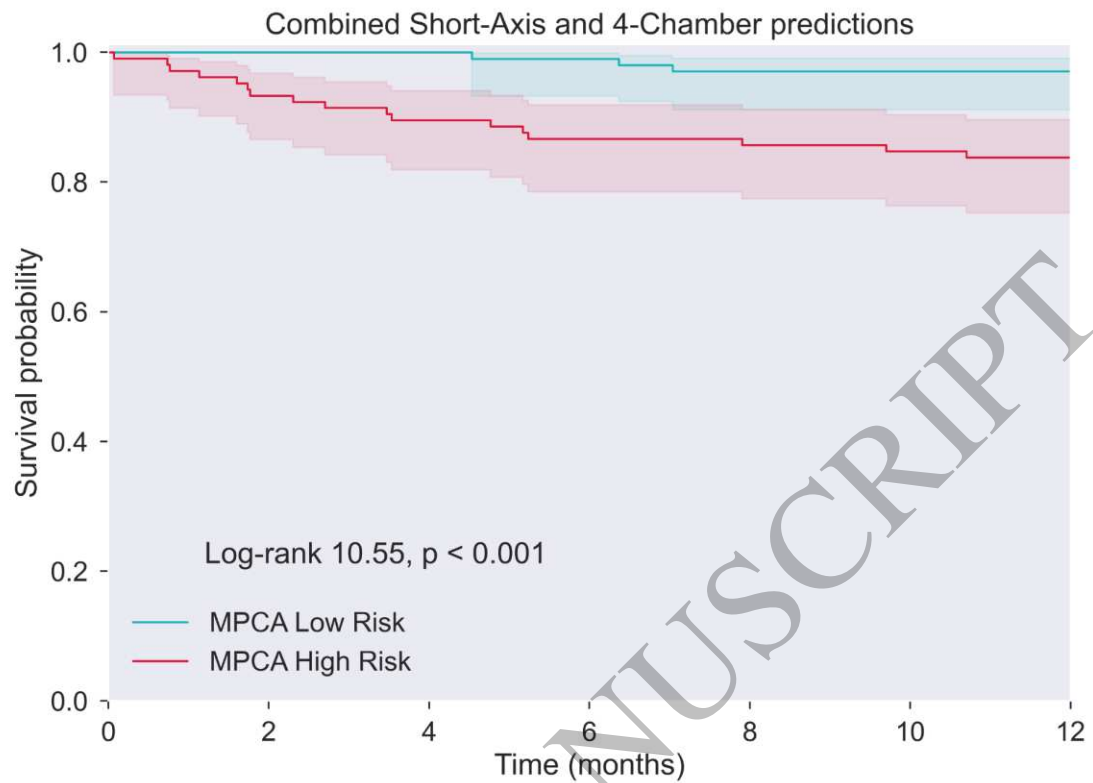


2
3 Figure 1: Model pipeline flow chart.



36 Figure 2: Study participants flow chart.

37

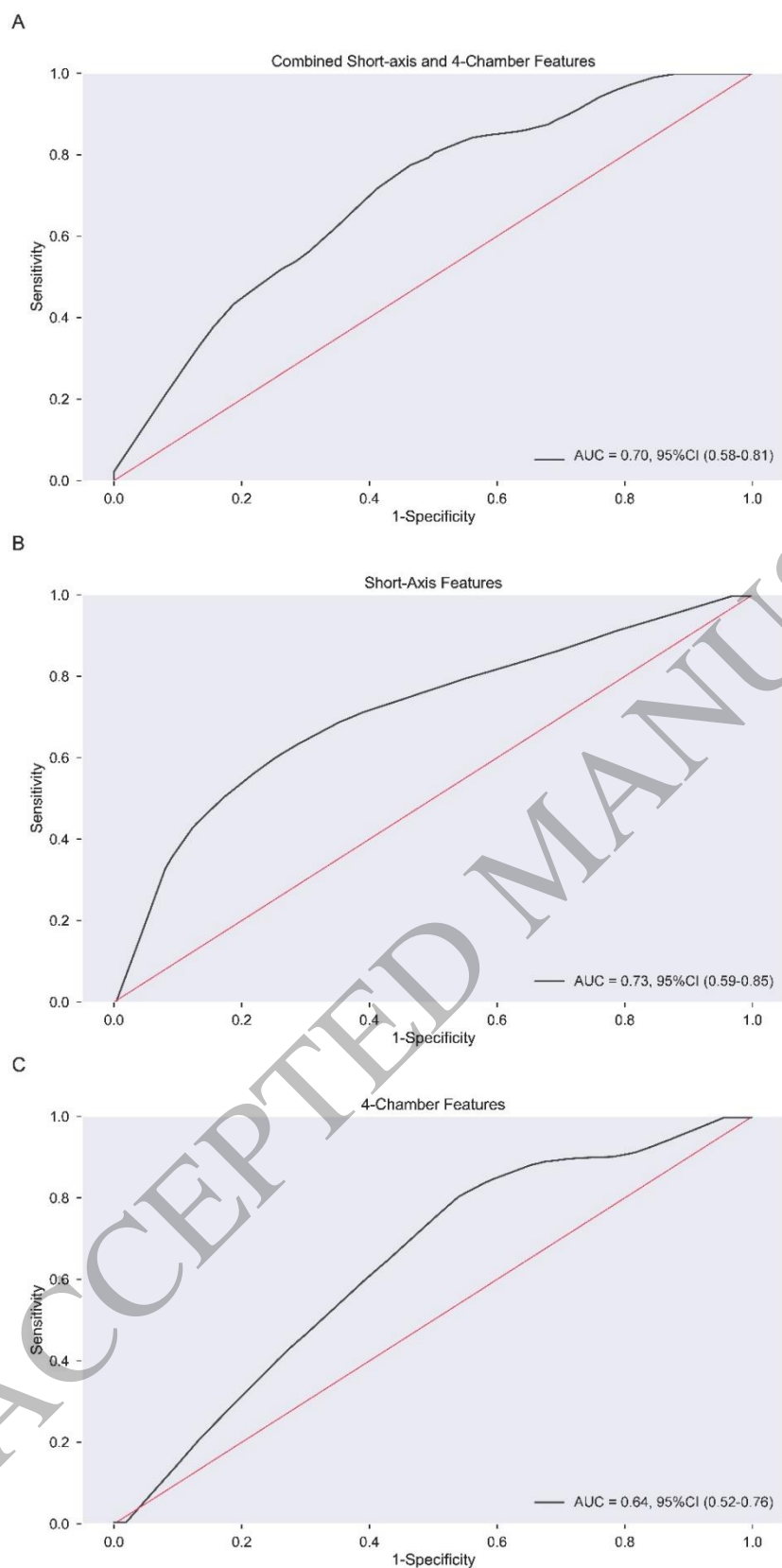


MPCA High Risk							
At risk	105	98	94	91	90	89	88
Censored	0	0	0	0	0	0	0
Events	0	7	11	14	15	16	17
MPCA Low Risk							
At risk	102	102	102	101	99	99	99
Censored	0	0	0	0	0	0	0
Events	0	0	0	1	3	3	3

1

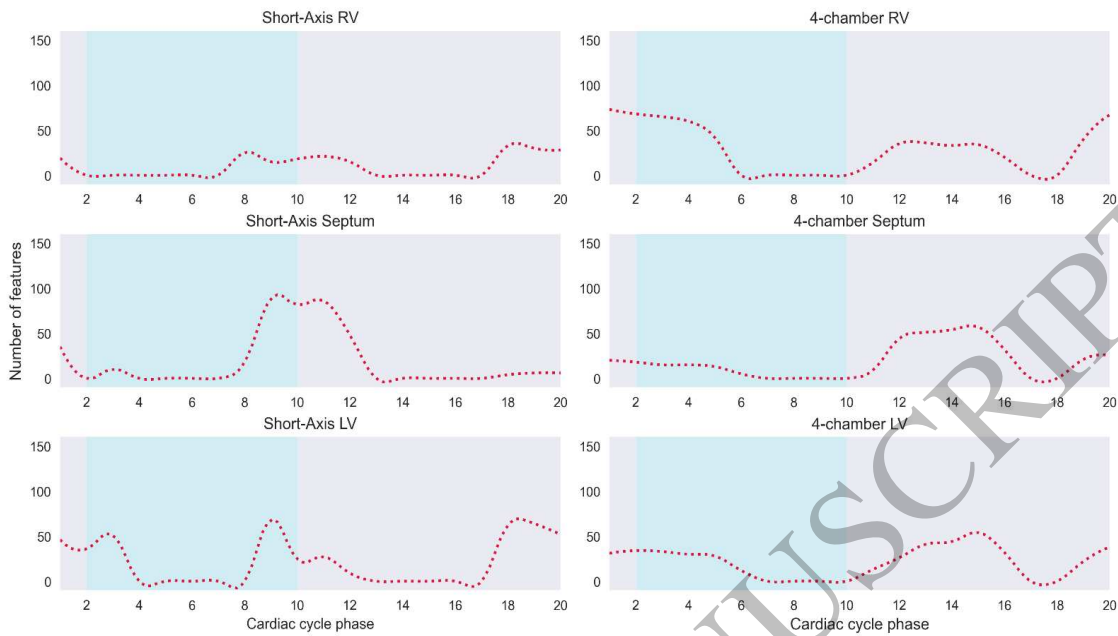
2 Figure 3: Kaplan-Meier curve.

3 The Kaplan-Meier curve shows the survival of high and low risk patients based on the combined short-axis
 4 and 4-chamber model predictions. The risk threshold was determined based on the median value of the
 5 MPCA predictions. The Kaplan Meier analysis shows a significant difference in survival between the high
 6 and low risk of mortality patient groups (log-rank $p < 0.001$).

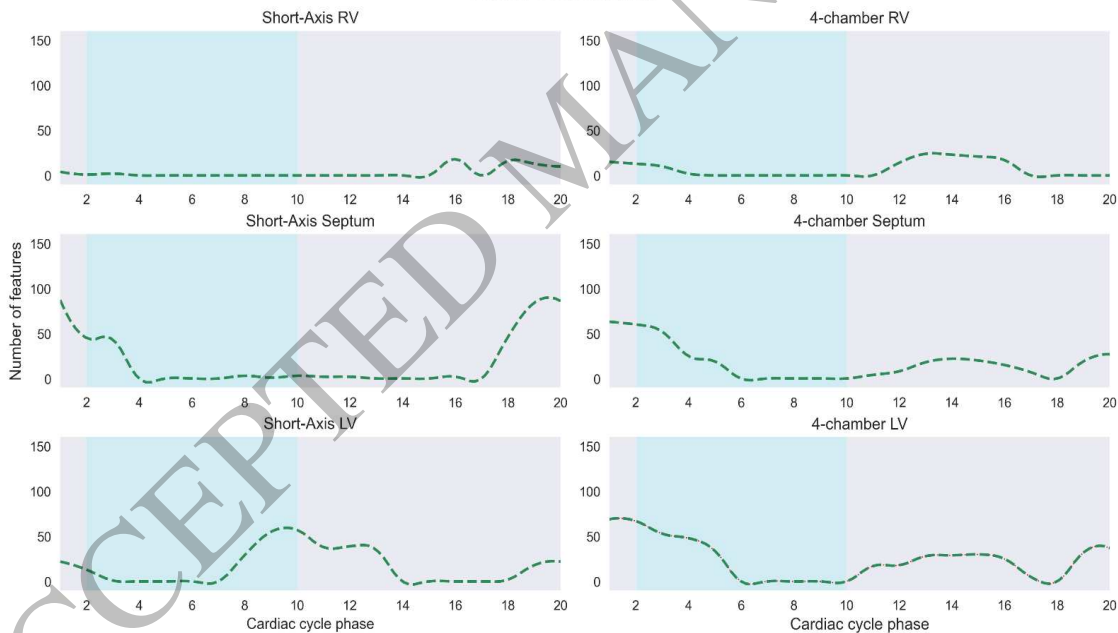


1
2 Figure 4: Receiver operating characteristic curves for one-year mortality prediction.
3 The prognostic accuracy of the different machine learning models were compared (A: combined model, B:
4 short-axis model and C: 4-chamber model). The highest area under the curve was achieved with the short-
5 axis model (AUC = 0.73).

Features of Mortality



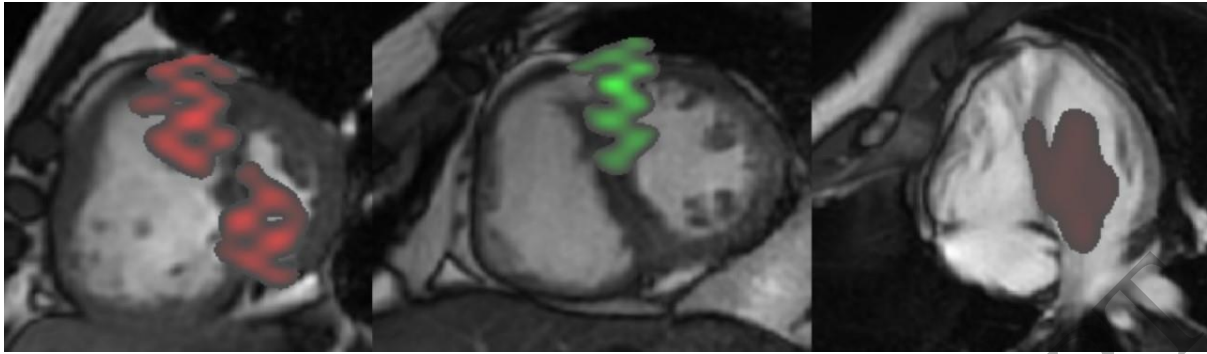
Features of Survival



Legend
 Number of mortality features
 --- Number of survival features
 Systolic phase
 Diastolic phase

39 Figure 5: Time-resolved prognostic cardiac features.

40 Features of poor prognosis and also protective features were examined throughout the cardiac cycle on the
 41 short-axis and 4-chamber views. The most significant cardiac features were the end-systolic and early
 42 diastolic septum on both the short-axis and 4-chamber views. The RV during systole and LV during
 43 diastole also were predictive of one-year mortality. In contrast, the most important features of survival
 44 were the end-diastolic septum on short-axis and 4-chamber views and the LV at systole.



1
2 Figure 6: Visualisation of prognostic mortality and survival features learnt from the training data.
3 The features were overlaid on three example short-axis / 4-chamber images from three different patients
4 with PAH to interpret the corresponding anatomical regions. Left: Septum and LV features of high risk of
5 mortality at end-systole. Middle image: Features of survival visualised at the septum at end-diastole. Right:
6 4-chamber view showing high-risk features in the septum and LV in diastole.
7

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1 Tables

2 Table 1: Baseline characteristics

	Training N = 516	Validation N = 207	p
Age (years)	62 (22)	62 (24)	.667
Sex (female)	376 (72%)	166 (80%)	.040
BSA (m²)	1.82 ± 0.2	1.83 ± 0.2	.933
Diagnosis			
CHD	71 (13%)	34 (16%)	
CTD	242 (46%)	96 (46%)	
IPAH	137 (26%)	55 (26%)	
Portal hypertension	35 (6%)	17 (8%)	
other PAH	31 (6%)	5 (2%)	
WHO functional class			.331
I	2 (0%)	0 (0%)	
II	37 (7%)	11 (5%)	
III	409 (79%)	170 (82%)	
IV	58 (11%)	26 (12%)	
RHC parameters			
mPAP (mmHg)	46 (22)	48 (18)	.164
PVR (dyns.s.cm ⁻⁵)	608 (556)	822 (791)	<.001
PAWP (mmHg)	11 (5)	10 (4)	<.001
RA mean (mmHg)	9 (8)	9 (8)	.548
CO (L/min)	5 (2)	4 (2)	<.001
SvO ₂ (%)	66 (13)	66 (14)	0.632
CMR parameters			
RVEF (%)	37 ± 13	36 ± 11	.539
RVESVi (ml/m ²)	74 ± 35	76 ± 31	.122
RVEDVi (ml/m ²)	113 ± 41	115 ± 39	.163
RVEDMi (g/m ²)	27 ± 8	28 ± 8	.016
LVEF (%)	53 ± 10	53 ± 9	.966
LVESVi (ml/m ²)	31 ± 11	31 ± 16	.212
LVEDVi (ml/m ²)	67 ± 19	64 ± 21	.079
LVSVi (ml/m ²)	36 ± 12	34 ± 9	.130
VMI (ratio)	0.58 ± 0.2	0.62 ± 0.2	.010

3 Data presented as mean ± standard deviation or median (range).
 4 BSA, body surface area; CHD, congenital heart disease; CO, cardiac output; CTD, connective tissue
 5 disease; CTEPH, chronic thromboembolic pulmonary hypertension; EDVi, end-diastolic volume index;
 6 ESVi, end-systolic volume index; IPAH, idiopathic pulmonary arterial hypertension; LV, left ventricle;
 7 mPAP, mean pulmonary artery pressure; PAH, pulmonary arterial hypertension; PAWP, pulmonary
 8 arterial wedge pressure; PH, pulmonary hypertension; PVR, pulmonary vascular resistance; RA, right
 9 atrium; RHC, right heart catheterization; RV, right ventricle; RVEF, right ventricle ejection fraction;
 10 RVEDMi, right ventricular end-diastolic mass index; SV, stroke volume; SvO₂ = mixed venous oxygen
 11 saturation; VMI, ventricular mass index; WHO, World Health Organisation

1 Table 2: Univariable Cox proportional hazard regression ratios for one-year mortality.

	<i>HR</i>	<i>95% CI</i>	<i>p</i>
Age (years)	1.039	1.005, 1.075	.026
Sex	1.036	0.346, 3.098	.950
WHO class	2.033	0.781, 5.292	.146
REVEAL	1.339	1.109, 1.618	.002
RHC parameters			
<i>mPAP (mmHg)</i>	0.982	0.947, 1.017	.311
<i>PVR (dyns.s.cm⁻⁵)</i>	1.000	0.999, 1.001	.616
<i>PAWP (mmHg)</i>	1.012	0.866, 1.183	.879
<i>RA mean (mmHg)</i>	1.081	1.020, 1.146	.008
<i>CO (L/min)</i>	0.842	0.599, 1.185	.324
<i>SvO₂ (%)</i>	0.969	0.929, 1.009	.127
CMR parameters			
<i>RVEF (% pred)</i>	0.762	0.445, 1.306	.324
<i>RVESVi (% pred)</i>	1.699	1.099, 2.628	.017
<i>RVEDVi (% pred)</i>	1.443	0.972, 2.141	.069
<i>RVEDMi (% pred)</i>	1.113	0.781, 1.587	.554
<i>LVEF (% pred)</i>	1.275	0.790, 2.060	.320
<i>LVESVi (% pred)</i>	1.036	0.652, 1.646	.881
<i>LVEDVi (% pred)</i>	0.918	0.559, 1.509	.736
<i>LVSVi (% pred)</i>	0.933	0.592, 1.471	.767
<i>VMI (ratio)</i>	0.962	0.530, 1.748	.899
<i>PA RAC (%)</i>	0.911	0.838, 0.991	.031
<i>Septal angle systole</i>	0.999	0.972, 1.027	.941
<i>Septal angle diastole</i>	0.987	0.935, 1.042	.636
MPCA-based features			
<i>SA features</i>	2.401	1.459, 3.951	.001
<i>4-chamber features</i>	1.472	0.978, 2.216	.064
<i>Combined features</i>	1.97	1.282, 3.028	.002

2 CMR parameters are corrected for age and sex (%pred). For abbreviations see Table 1.

	<i>C index</i>	<i>95% CI</i>	<i>AIC</i>	<i>p</i> <i>Log-rank test</i>
CMR measurements*	0.70	0.60-0.80	211	
MPCA**	0.70	0.59-0.81	204	
REVEAL score	0.71	0.61-0.81	203	
REVEAL + MPCA	0.76	0.67-0.85	197	.003
REVEAL+ CMR measurements	0.78	0.70-0.86	205	.003
REVEAL + CMR measurements + MPCA	0.83	0.76-0.90	193	<.001

1 Table 3: C-index and Akaike information criterion (AIC) for the univariable and multiple variable Cox
2 regression analysis for the REVEAL score, CMR measurements and the MPCA machine learning
3 model. A higher c-index indicates a better model fit and a lower AIC indicates a relative lower
4 prediction error. The log-rank test indicates that the combination of MPCA, CMR measurements and
5 REVEAL is statistically significantly more predictive than REVEAL score alone (c-index 0.83 vs 0.72,
6 $p < 0.001$).

7 * CMR measurements included age and sex corrected right ventricular ejection fraction, right
8 ventricular end-systolic volume index, left ventricular end-diastolic volume index, left ventricular
9 stroke volume index and pulmonary artery relative area change.

10 ** MPCA combined short-axis and four-chamber features

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