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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☒	☐	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	No software was used
Data analysis	Manual volumetric analysis of images (acquired from cardiac magnetic resonance imaging) was performed using the proprietary software cmr42 (Circle Cardiovascular Imaging, Calgary, Canada) Training and validation of deep learning and conventional parameter models was carried out using custom algorithms (available at: https://github.com/UK-Digital-Heart-Project/4Dsurvival) implemented with open-source Python language libraries Keras (v2.1.3 [http://keras.io]), Tensorflow-GPU (v1.4.0 [https://www.tensorflow.org/]), Optunity (v1.1.1 [https://github.com/claesenm/optunity]) and Lifelines (v0.14.6 [https://lifelines.readthedocs.io/en/latest/]).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Algorithms, motion models and statistical analysis are publicly available under a GNU General Public License. A training simulation is available as a Docker image with an interactive Jupyter notebook hosted on Binder. Personal data are not available due to privacy restrictions.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Our power calculations use classifier performance estimates obtained from preliminary data in 256 PH patients comparing the sensitivity for identifying high-risk patients using supervised learning of cardiac motion versus conventional risk factors [Dawes et al. (2017) Radiology; 283(2):381-390]. A bootstrap cross-validation of our feasibility data using nested multivariable models demonstrated an incremental benefit of ML using complex phenotypes in outcome prediction (ANOVA, Hazard Ratio: F=80.2, p<0.001; AUC: F=94.2, p<0.001).
Data exclusions	Criteria for inclusion were a documented diagnosis of Group 4 pulmonary hypertension (PH) investigated by right heart catheterization (RHC) and non-invasive imaging. Subjects with congenital heart disease were excluded.
Replication	Results have not been replicated in an external cohort. The current work represents the preliminary stage of a multicentre study that will involve external validation in a future study (for further details, see published prospective study design: Dawes TJW, Bello GA, O'Regan DP. Multicentre study of machine learning to predict survival in pulmonary hypertension. Open Science Framework (2018). DOI 10.17605/OSF.IO/BG6T9 [https://osf.io/qvx69/])
Randomization	No experimental groups were used in this study
Blinding	Blinding is not relevant to this study, as we did not utilize experimental groups.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☐	☒ MRI-based neuroimaging

Human research participants

Policy information about studies involving human research participants

Population characteristics	Age (years): Mean=62.9, SD=14.5 Body surface area (m2): Mean=1.92, SD=0.25 Male: n=169 (56%); Female: n=133 (34%) Race: Caucasian 71.2%, Asian 2.3%, Black 4.3%, Other 9.3%, Unknown 12.9%

WHO functional class: Class I 0%, Class II 15%, Class III 71%, Class IV 14%
Systolic BP (mmHg): Mean=131.5, SD=25.2
Diastolic BP (mmHg): Mean=75, SD=13
Heart rate (beats/min): Mean=69.8, SD=22.5
Mean right atrial pressure (mmHg): Mean=9.9, SD=5.8
Mean pulmonary artery pressure (mmHg): Mean=44.1, SD=12.6
Pulmonary vascular resistance (Wood units): Mean=8.9, SD=5.0
Cardiac output (l/min): Mean=4.3, SD=1.5
LV ejection fraction (%): Mean=61, SD=11.1
LV end diastolic volume index (ml/m): Mean=110, SD=37.4
LV end systolic volume index (ml/m): Mean=44, SD=22.9
RV ejection fraction (%): Mean=38, SD=13.7
RV end diastolic volume (ml/m): Mean=194, SD=62
RV end systolic volume (ml/m): Mean=125, SD=59.3

Recruitment

This study was part of a continuous prospective research program into the prognosis of patients with PH by using conventional clinical and imaging biomarkers. Our study used data (cross-sectional) collected from patients referred to the National Pulmonary Hypertension Service (at the Imperial College Healthcare NHS Trust) for routine diagnostic assessment and cardiac imaging.

Magnetic resonance imaging

Experimental design

Design type

Indicate task or resting state; event-related or block design.

Design specifications

Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.

Behavioral performance measures

State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).

Acquisition

Imaging type(s)

Structural imaging (Cardiac)

Field strength

1.5

Sequence & imaging parameters

A standard clinical protocol for cardiac MRI was followed according to published international guidelines (Kramer, JCMR 2013;15:91). Cardiac ventricular function was assessed using balanced-steady state free precession (b-SSFP) cine imaging acquired in conventional cardiac short- and long- axis planes typically with: repetition time msec/echo time msec, 3.2/1.6; voxel size, 1.5 x 1.5 x 8 mm; flip angle, 60°; sensitivity encoding factor (SENSE), 2.0; bandwidth, 962 Hz/pixel; temporal resolution 29 msec; slice thickness 10mm; field of view 400 x 400 mm, 30 time phases.

Area of acquisition

Protocolised, three-plane, low-resolution localizer images were used to define the ventricles as the region of interest, after which long- and short-axes planes were described using a line from the apex of the heart to centre of the left ventricular base. Margins of ~1cm in all planes were added to allow for variable breath-holding.

Diffusion MRI ☐ Used ☒ Not used

Preprocessing

Preprocessing software

Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).

Normalization

If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.

Normalization template

Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.

Noise and artifact removal

Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).

Volume censoring

Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.

Statistical modeling & inference

Model type and settings

Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).

Effect(s) tested

Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference
(See Eklund et al. 2016)

Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.

Correction

Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).

Models & analysis

n/a	Involved in the study
☒	☐ Functional and/or effective connectivity
☒	☐ Graph analysis
☐	☒ Multivariate modeling or predictive analysis

Multivariate modeling and predictive analysis

Feature extraction was carried out via an image processing pipeline consisting of segmentation, co-registration and mesh generation. The output of this pipeline was a set of high-resolution, three-dimensional surface mesh representations of the heart's right ventricle (RV) at various phases of the cardiac cycle (total of 20 phases). These were used to derive point-wise displacement values representing the distance traveled by each mesh vertex (corresponding to an anatomical location on the RV) from frame to frame. These displacement values were fed as independent variables into a predictive neural network model. The neural network architecture used in this study was a 'supervised autoencoder', which combines dimension reduction with survival prediction via a Cox Proportional Hazards model. Training and validation metrics included the hazard ratio and Harrell's concordance index.