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Corresponding author(s): Brandon K. Fornwalt

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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 our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the 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
☐	☒	A statement on 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 statistical parameters 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

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Dcm4chee (JAVA DICOM command line toolkit, version 2.0.29) scheduled the moves to the Clinical Trial Processor, which stored the DICOM as files. Images in Philips iSite were retrieved using AcuoMed Batch Processing (version 6.0) to schedule the moves, and a Research PACS (DCM4CHEE v2.17) to receive the images.
Data analysis	We used pydicom v1.02 to read the binary data from the (200D, 3CF4) DICOM element. For data processing we used python v3.6, tensorflow v1.14, pandas v1.0.1, and statmodels v0.11.

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 and reviewers. 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

The main data supporting the results in this study are available within the paper and its Supplementary Information. All requests for raw and analysed data will be reviewed by the Legal Department of Geisinger Clinic to verify whether the request is subject to any intellectual property or confidentiality constraints. Requests for patient-related data not included in the paper will not be considered. Any data that can be shared will be released via a Material Transfer Agreement for non-commercial research purposes.

Field-specific reporting

Please select the one below that is 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/documents/nr-reporting-summary-flat.pdf

Life sciences study design

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

Sample size	We needed at least 600 patients (300 alive, 300 deceased), as indicated by a Pearson Chi-square test-sample-size calculation, to estimate and compare prognostic accuracy between the model and a cardiologist's predictions. We assumed a 10% difference in accuracy between machine and cardiologist (80% vs 70%), 80% power, a significance level of 5%, and an approximate 40% discordance. This was calculated using Power Analysis Software (PASS v15).
Data exclusions	Pre-established criteria for exclusion of data were: 1. Exclude echocardiography studies acquired before February 2011, without raw video data available, 2. Exclude videos from the echocardiography study that did not contain view label information, 3. Exclude patients without enough follow up, as we can not define the survival status. Additional criteria were imposed to remove rare echocardiography views (less than 5,000 samples).
Replication	We contained all our software dependencies in a Docker container. All code is version-controlled and experiments can be reproduced on hardware with NVIDIA V100 GPUs. Data used in this study was stored and backed up for future experimental reproducibility.
Randomization	The dataset was randomly divided in training and testing folds for cross-validation. The 600 studies for the survey set consisted of 300 randomly drawn samples from each group (survives or dies within a year of the echocardiography study).
Blinding	The cardiologists were blinded from actual patient-survival data, from each other's and from the model's performance, until the final release of the results.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

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	The sample in our study represents a patient population in a clinical setting. The average patient ages for the cross-validation survey and the two heart-failure datasets were 66 (+/– 16; s.d.), 68 (+/–16, s.d.), and 73 (+/–14, s.d.), respectively. The proportion of studies from male patients was 51%, 56%, and 56% respectively. Supplementary Table 1 provides a detailed description.
Recruitment	We collected samples from a clinical database. Potential sources of bias are the large prevalence of Caucasians (>95%) in our geographical area and the availability of raw echocardiography videos as inclusion criteria.
Ethics oversight	This retrospective study was approved by Geisinger's institutional Review Board and was performed with a waiver of consent.

Note that full information on the approval of the study protocol must also be provided in the manuscript.