Supplementary Materials

Patient Inclusion Criteria

Patients with hypertrophic cardiomyopathy who had an unexplained left ventricular (LV) wall thickness of ≥ 15 mm with a positive family history or positive genetic markers. Cardiac amyloidosis was diagnosed using either endomyocardial biopsy or extracardiac biopsy with typical cardiac imaging features. The diagnosis was confirmed by genetic testing in all patients with Fabry disease. Dilated cardiomyopathy was defined as systolic dysfunction with dilation (LV volume ≥ 2 standard deviation reference value), with no significant coronary artery disease. Healthy volunteers did not have a history of cardiovascular disease, cardiovascular risk factors (smoking, diabetes, hypertension, or arrhythmia), or abnormal electrocardiograms.

Deep Learning Models for Myocardial Segmentation on Native and Post-T1 Maps

Dataset

Cardiac magnetic resonance (CMR) studies consisting of native and post-T1 series, acquired from July 2017 to July 2020, were retrospectively collected. CMR data were acquired using a Siemens 3.0 Tesla Prisma fit MRI system. Before the development of the convolutional neural network (CNN) model, data that could be used for testing (from November 2018 to December 2019) were excluded from the training and internal validation set of deep learning. After data selection, the patient information was removed, but the MR image acquisition parameters were preserved.

The native and post-contrast T1 series consisted of a stack of three short-axis images including basal, mid, and apical slices. A total of 5-(3)-3 MOLLI sequences were used for native T1 map acquisition and 4-(1)-3-(1)-2 MOLLI sequences were used for post-T1 mapping. All series were acquired with the following typical MR parameters except for some outliers: images were acquired at the end-diastolic cardiac phase with the breath-hold technique, 8 mm of slice thickness, 10 mm of inter-slice gap, around 360 mm² of the field of view, and approximately 1.5 mm² of in-plane resolution. The entire T1 map was calculated using the system provided by the MR manufacturer.

The native T1 map included 678 patients and the post-T1 map included 580 patients. Each dataset was randomly divided into two groups. The native T1 dataset was divided into a 94:6 ratio for training (594 cases, 1782 images) and internal validation (42 cases, 126 images) groups. The post-contrast T1 dataset was divided into a 93:7 ratio for training (498 cases, 1494 images) and internal validation (41 cases, 123 images) groups.

Manual Segmentation

The manual definition was used as the ground truth to train the CNN model and evaluate automatic segmentation. Manual annotation was performed using a commercial software (CVI42, Circle Cardiovascular Imaging Inc.). Three experienced researchers manually drew the LV endocardial and epicardial contours in the fixed cardiac phase. The contour of the endocardium included papillary muscles and trabeculations. After the initial annotation, two cardiac radiologists reviewed all contours and re-drew the inaccurate ones.

After manual segmentation, a parsing procedure was applied to utilize the annotation as the ground truth for training and evaluation. The output of the software was an index of contours in xml format. The x- and y-coordinates were converted to points in a 2D matrix. The outside of the endocardial contour and inside of the epicardial contour were then filled with 1. The final format of the annotation was a 2D mask image, in which the myocardium was labeled 1.

Pre-Processing

All datasets imported in DICOM format were subjected to a series of image-processing steps. To minimize the variation in size, resolution, and signal intensity, image processing steps included restoration of the resolution, cropping of the center region, and intensity normalization. First, if images were interpolated to double the size in the reconstruction process, they
were resized to the original matrix size, and based on the center of the image, the 128 × 128 region was cropped as the region of interest. After cropping, signal intensity was normalized from 0 to 1. The labeled images underwent the same pre-processing and consisted of the myocardium as 1 and background as 0.

**Training the U-Net**

U-Net [1], a well-established CNN network, was used to segment tasks on T1 maps. Figure 2 shows the network architecture used for the myocardium segmentation model. Each 2D U-Net model was trained to predict the LV myocardium using the respective data. The performance and generalization of the model were improved by applying data augmentation, including rotation, flipping, and shifting, to the training dataset. The models were constructed using the Keras deep learning library in TensorFlow (https://www.tensorflow.org/). The training and internal validation processes were implemented on an Ubuntu 18.04 system with Intel(R) Xeon Silver 4116 CPU @ 2.10 GHz and an Nvidia RTX 3090 GPU (24GB memory). The Adam optimizer with a learning rate = 1.0E–04, β1 = 0.9, β2 = 0.999, and batch size = 32 was used to compile the models. For the activation function, a rectified linear unit (ReLU) was used in the convolution layer, except for the last layer (softmax layer, simple binary thresholding). A Dice loss function was employed to train the models. The network was trained for 150 epochs, and it required 4–6 hours with a single GPU.

**Post-Processing**

After training, the models infer the probability map of each pixel to belong to the myocardium region. The 2D predictions were rescaled to their original size and resolution. After the rescaling procedure, multiple disconnected components may be present in the prediction image. In this case, the largest component was considered to be the myocardium region and was stored in the images. The other isolated pixels were considered to be noise and were removed.

**Model Evaluation**

The performance of the trained models was evaluated by calculating the Dice similarity coefficient (DSC) between the ground truth and segmentation results. The definition of DSC is as follows: given two sets, \( X \) and \( Y \), \( DSC = \frac{2|X \cap Y|}{|X| + |Y|} \). Using the internal validation dataset, the results were generated using model inference and postprocessing. The DSC of every image was calculated using the results and ground truth. The mean DSC of the native T1 model was 0.87 and post-contrast T1 was 0.78.

**Automatic Analysis and Reporting**

The measured myocardial T1 values were expressed as 16 American Heart Association segments in the form of a bull’s eye map. Three reference points (the center of mass of the LV endocardial contour and two right ventricular insertion points) were used to generate a bull’s eye map.

**REFERENCE**

1. Ronneberger O, Fischer P, Brox T. U-Net: convolutional networks for biomedical image segmentation. Proceedings of the Medical Image Computing and Computer-Assisted Intervention – MICCAI 2015; 2015 Oct 5-9; Munich, Germany: Springer International Publishing; 2015; p. 234-241
## Supplementary Table 1. Interobserver Agreement of the Automated and Manually Measured Native T1 and ECV Fraction in the Three Groups

| Measurement                  | Native T1                      | ECV                      |
|------------------------------|--------------------------------|--------------------------|
|                              | Left Ventricular Hypertrophy   | Dilated Cardiomyopathy   | Healthy Volunteers | Left Ventricular Hypertrophy | Dilated Cardiomyopathy | Healthy Volunteers |
| Automatic–reader 1           | 1.00 (0.99–1.00)               | 0.93 (0.86–0.97)         | 0.83 (-0.03–0.96)  | 0.99 (0.98–0.99)             | 0.97 (0.94–0.98)       | 0.80 (0.27–0.93)   |
| Automatic–reader 2           | 1.00 (1.00–1.00)               | 0.93 (0.84–0.97)         | 0.96 (0.92–0.98)   | 0.99 (0.97–0.99)             | 0.93 (0.82–0.97)       | 0.86 (0.71–0.93)   |
| Automatic–reader 3           | 1.00 (0.99–1.00)               | 0.90 (0.73–0.96)         | 0.84 (0.01–0.96)   | 0.99 (0.98–0.99)             | 0.96 (0.89–0.98)       | 0.78 (0.31–0.92)   |
| Automatic–reader 4           | 1.00 (0.99–1.00)               | 0.94 (0.87–0.97)         | 0.95 (0.90–0.98)   | 0.99 (0.98–0.99)             | 0.96 (0.91–0.98)       | 0.89 (0.78–0.95)   |
| Automatic–average of four readers | 1.00 (1.00–1.00)      | 0.94 (0.88–0.97)         | 0.97 (0.93–0.98)   | 0.99 (0.98–0.99)             | 0.96 (0.92–0.98)       | 0.89 (0.77–0.95)   |
| Reader 1–reader 2            | 1.00 (0.99–1.00)               | 0.94 (0.28–0.99)         | 0.80 (-0.05–0.95)  | 1.00 (0.98–1.00)             | 0.96 (0.43–0.99)       | 0.80 (-0.05–0.95)  |
| Reader 1–reader 3            | 1.00 (0.96–1.00)               | 0.90 (0.16–0.97)         | 0.61 (-0.04–0.89)  | 1.00 (0.99–1.00)             | 0.97 (0.55–0.99)       | 0.66 (-0.03–0.91)  |
| Reader 1–reader 4            | 1.00 (0.97–1.00)               | 0.96 (0.63–0.99)         | 0.86 (-0.03–0.97)  | 1.00 (0.99–1.00)             | 0.98 (0.91–0.99)       | 0.91 (0.21–0.98)   |
| Reader 2–reader 3            | 1.00 (1.00–1.00)               | 0.99 (0.96–0.99)         | 0.91 (0.00–0.98)   | 1.00 (1.00–1.00)             | 0.98 (0.96–0.99)       | 0.95 (0.18–0.99)   |
| Reader 2–reader 4            | 1.00 (1.00–1.00)               | 0.99 (0.97–1.00)         | 0.98 (0.93–0.99)   | 1.00 (1.00–1.00)             | 0.99 (0.79–1.00)       | 0.93 (0.33–0.98)   |
| Reader 3–reader 4            | 1.00 (1.00–1.00)               | 0.98 (0.83–0.99)         | 0.86 (-0.03–0.97)  | 1.00 (1.00–1.00)             | 0.98 (0.96–0.99)       | 0.83 (-0.04–0.96)  |
| Among four readers           | 1.00 (0.99–1.00)               | 0.96 (0.86–0.98)         | 0.82 (0.34–0.94)   | 1.00 (1.00–1.00)             | 0.98 (0.94–0.99)       | 0.83 (0.37–0.94)   |

Data are intraclass correlation coefficient (95% confidence interval). ECV = extracellular volume.
Supplementary Fig. 1. Segmentation performance of a deep learning algorithm. The DSC for the native T1 map and the post-T1 map are 0.86 ± 0.05 and 0.74 ± 0.17, respectively. In the post-T1 map, the CA group shows the lowest DSC (0.40 ± 0.24). CA = cardiac amyloidosis, DCM = dilated cardiomyopathy, DSC = Dice similarity coefficient, FD = Fabry disease, HCM = hypertrophic cardiomyopathy, HV = healthy volunteer.