

ECGI Without Geometry: a Deep Learning Based Estimation of Heart Surface Potentials

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Abstract

We developed a deep learning framework to estimate heart surface potentials solely from body surface potentials and a torso geometry, hence omitting information about the heart geometry. The framework is based on image-to-image translation and introduces three components: transformation of 3D torso and heart geometries into corresponding standard 2D representations, and development of a customized deep learning model based on Pix2Pix network. Using 11 healthy subjects and 29 idiopathic ventricular fibrillation (IVF) patients, the framework achieved an average mean absolute error (MAE) for the heart surface potential maps (HSPMs) of 0.012 ± 0.011 , and an average similarity index measure (SSIM) of 0.984 ± 0.026 . For the concatenated electrograms (EGMs), the average MAE was 0.004 ± 0.004 , and the average Pearson correlation coefficient (PCC) 0.643 ± 0.352 . The absolute mean of the time differences between estimated and reference activation and recovery times was 6.048 ± 5.188 ms, and 18.768 ± 17.299 ms, respectively. These results demonstrate performance comparable to standard ECGI without the need for CT/MRI, indicating potential clinical applications for this framework.

1. Introduction

Electrocardiographic Imaging (ECGI) is a noninvasive technique to visualise the heart's electrical activity, enhancing diagnostic accuracy and providing therapeutic guidance [1]. ECGI requires a patient-specific torso-heart geometry which is obtained from CT or MRI, which limits the application of ECGI in clinical settings. The aim of this study is to develop a framework, based on image-to-image translation, that can provide reconstructions, i.e. estimating ventricular HSPMs from measured BSPMs, without the need of CT/MRI to estimate the heart geometry, which would enable fast screening and follow-up. The model uses 2D torso representations as input, and provides

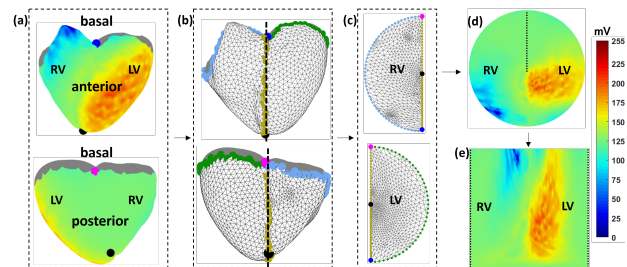


Figure 1. The process of generating standardized 2D heart representations. Light blue (green) points: boundary vertices of the right (left) ventricle. (a) select three reference points: blue (magenta) point on the interventricular septum at the anterior (posterior) base, black point at the apical side; (b) align the interventricular septum (yellow points) vertical to the XY-plane, passing through the origin; (c) turn the right and left ventricle into a unit semicircle separately using TEM; (d) integrate the right and left ventricle to form a full bullseye; (e) unfold the bullseye plot into a square plot by coordinate transformation.

2D heart representations as output, standardized across patients. It is a novel modification of the Pix2Pix network [2], a sequential conditional generative adversarial network (ScGAN). The 2D torso and heart representations are provided to the network as rectangular images, simplifying the image processing task. The ScGAN leverages BSPMs from adjacent snapshots, using them as an input sequence to account for the temporal structure of the signals. We validated our approach using clinical human data from both healthy subjects and patients affected by IVF [3].

2. Methods

Using 2D representations can reduce computational complexity compared to 3D surfaces and leverage well-established deep learning techniques for 2D images. Figure 1 depicts the four steps for obtaining a standardized 2D heart representation from the 3D geometry exported

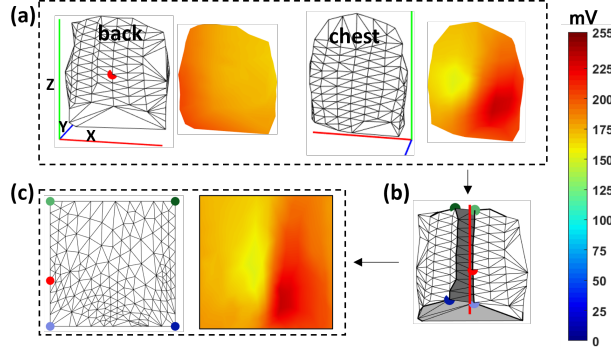


Figure 2. The process of generating standardized 2D torso representation. Red point: opening electrode in the middle of the posterior part of the torso. Red line: corresponding opening line. Gray faces: faces that need to be disconnected. (a) selection of opening electrode and transformation to achieve a standardized orientation of the 3D torso; (b) disconnection through the opening line; (c) turning of the 3D torso geometry into a square plot using TEM.

from CT data, including both ventricles, for training of the model. First, three reference vertices are chosen to define the reference plane of the interventricular septum (Fig. 1a), which is then aligned vertically to the XY-plane with the center of gravity of the three reference points landing at the origin (Fig. 1b). Third, focusing on the right ventricle, the boundary vertices (Fig. 1b) are directly mapped onto the 2D plane, making the vertices closely attached to the interventricular septum evenly distributed along the Y-axis, with the apical point at the origin. The remaining boundary vertices are evenly distributed on the circumference of a unit semicircle (Fig. 1c). Then, by using Tutte Embedding Method (TEM) [4], the inner vertices are assigned to the interior of the semicircle, such that face overlap is avoided. The same step is applied to the left ventricle to achieve a unit semicircle. Both ventricles are then transformed into a bullseye plot (Fig. 1d). Finally, after rotating the bullseye plot counterclockwise by 90° , the Cartesian coordinates are converted to polar coordinates (Fig. 1e).

Figure 2 depicts the steps for obtaining a standardized 2D torso representation from a 3D geometry. The 3D torso geometry extracted from the CT data is initially positioned upright. Following the unfolding process outlined in our prior research [5], we first select an opening electrode in the middle of the posterior part of the torso (Fig. 2a). After moving the torso’s center of gravity to the origin and rotating it to align the chest with the XZ-plane, the lower abdominal connection is disconnected due to its lack of anatomical significance (Fig. 2b). The upper connection (through shoulders and neck) between the chest and back is also disconnected to avoid overlapping in the 2D representation. Subsequently, the 3D torso geometry is directly

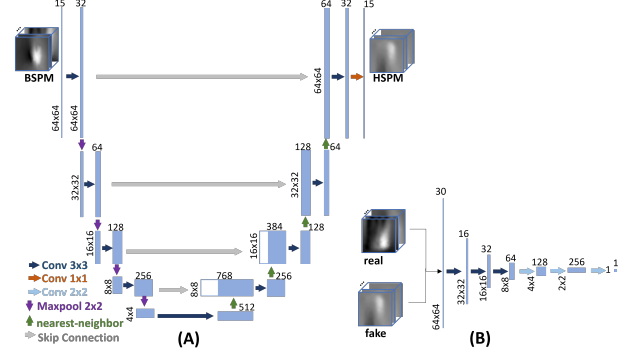


Figure 3. ScGAN. (A) generator. (B) discriminator

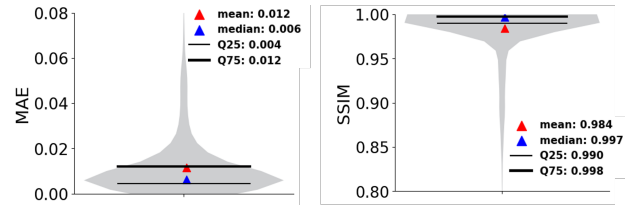


Figure 4. The violin plot of MAE and SSIM values between predicted HSPMs from ScGAN and reconstructed HSPMs from ECGI.

mapped into a square plot using TEM. After disconnecting the faces across the “opening line”, the very top and bottom vertices along both sides of this line are designated as the four corner points of the square plot (Fig. 2b). Regarding the boundary vertices, they are assigned to the four sides of the square plot in a counterclockwise direction starting from the bottom left corner (Fig. 2c). To minimize distortion, the 3D torso geometry information is utilized to determine the 2D coordinate values of the boundary vertices.

In this study, we used the Pix2Pix network [2] with a U-shaped architecture as generator. However, since the U-Net architecture was originally designed for medical image segmentation [2], we tailored it to better suit our BSPM-to-HSPM task (Figure 3; network architecture employed in this study). We also designed a novel loss function by incorporating cosine similarity, image entropy, and a regularization term into the generator.

Zeroth order Tikhonov reconstructions of the epicardial potentials at each time instant were used for training the model and as ground truth for testing [6]. After generating 2D heart and torso representations, the potential values of the grid points are interpolated using 3D thin plate spline (TPS) [7]. This interpolation produces 2D images suitable for use in the network. Both HSPs and BSPs should be normalized to the range $[0, 1]$ for deep learning models. The resulting potential values at these grid points within the chosen time window form the input and output cubes.

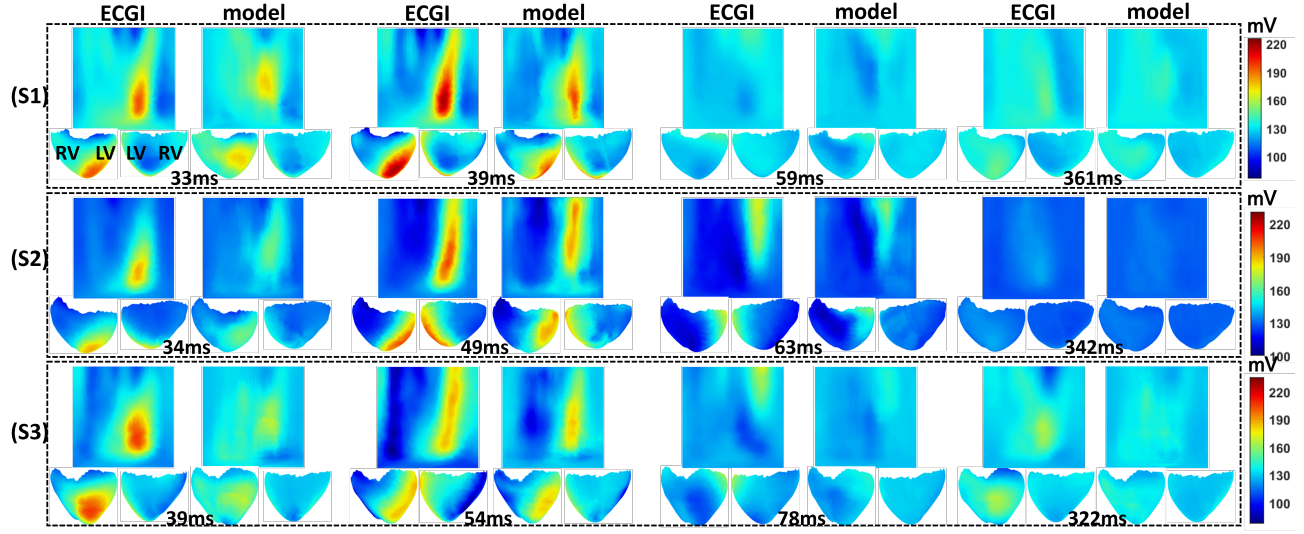


Figure 5. The 2D and 3D HSPMs from three subjects: (S1) and (S2) representing IVF patients and (S3) representing a healthy subject. Four distinct time snapshots are shown for each individual. The first three snapshots capture moments around the initiation, middle, and ending of the QRS complex, respectively, while the final snapshot corresponds to a moment around the middle of the T wave.

3. Experiments

The dataset includes 40 subjects: 11 healthy subjects (8 females, 3 males) and 29 patients diagnosed with (IVF) (11 females, 18 males). Each subject has one sinus beat, trimmed from the QRS onset to the end of the T-wave, totaling 32,000 distinct time points. The data set was divided randomly into a training set of 30 subjects (8 healthy subjects and 22 IVF patients). The test set consists of the remaining 10 subjects (3 healthy subjects and 7 IVF patients).

Performance of HSPM estimation by the ScGAN was evaluated against standard ECGI reconstruction using MAE and SSIM [8]. For accuracy within a single heartbeat, EGMs at each grid point were derived by concatenating potential values over time and quantified using MAE and PCC. Additionally, the AT at each gridpoint is computed using the spatial-temporal approach [9] over the entire time span. The RT for each gridpoint indicates the moment with maximum gradient during the T wave. Both AT and RT isochrones were smoothed with a median spatial filter of 30 mm [3]. Accuracy was assessed by comparing absolute time differences between model’s outputs and ECGI reconstructions.

4. Results

Fig. 4 displays the violin plot of both MAE, and SSIM between the predicted and reconstructed HSPMs on the test set. The mean value of MAE is $0.012 \pm$

0.011 , suggesting that differences in pixel intensity between deep learning estimated and ECGI reconstructed maps are small. The mean value of SSIM is 0.984 ± 0.026 , suggesting that estimated and ECGI reconstructed HSPM share similar structural and texture characteristics.

Fig. 5 shows the estimated HSPMs from the proposed model and those from the corresponding ECGI reconstruction for two IVF patients and one healthy subject, at different time instants of a heartbeat. Results show a high level of similarity in the patterns of electrical signals across various time instants, although the proposed model occasionally shows slightly lower contrast compared to the ECGI reconstructions.

Fig. 6A shows the violin plot of both MAE and PCC values between the estimated and reconstructed EGMs from the test set. It can be noticed that the MAE values remain low, with the mean value equal to 0.004 ± 0.004 . Additionally, PCC values show an average value of 0.643 ± 0.352 , with the majority of values consistently exceeding 0. This suggests that estimated and ECGI reconstructed EGM signals show similar amplitude and shape.

Fig. 6B provides several examples of EGM signals for the three individuals of Figure 5. The comparison reveals a good level of resemblance between the estimated EGM signals and those obtained through ECGI, showing overall consistency in both temporal dynamics and amplitude variations. Model estimates show sometimes small fluctuations in the QRS complex, and T-wave amplitudes generally lower compared to the ECGI reconstructions. Occasionally, completely opposite wave directions are dis-

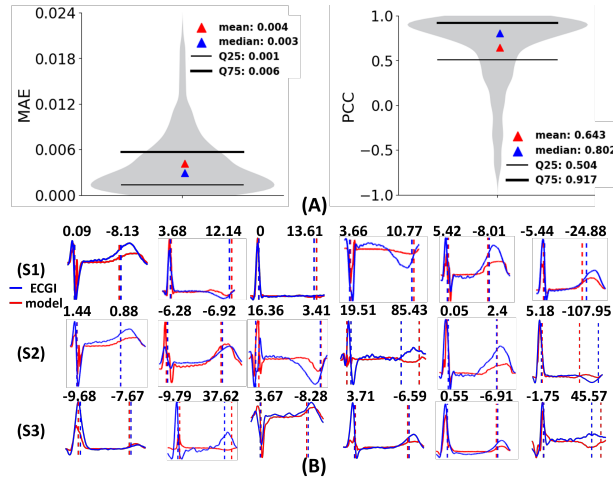


Figure 6. The comparison of concatenated EGMs derived from HSPMs based on the model prediction and ECGI reconstruction. (A) The violin plot of MAE and PCC between the EGMs. (B) Visualization of EGMs from the same three individuals as in Figure 5 (S1 and S2: IVF patients, S3: healthy subject). Numbers above the EGMs represent the time differences (ms) of AT and RT between model estimations and ECGI reconstructions.

played in T wave, and this generally can be observed near the boundaries of the 2D HSPMs. Fig. 6B also illustrates model performance in estimating AT and RT. Time differences of RTs are generally larger than those of ATs. This is in line with the results in Figure 7, where the violin plots depict the absolute time differences for both AT and RT computed from model estimations and ECGI reconstructions. The mean value of the absolute time differences is 6.048 ± 5.188 ms for AT, and 18.768 ± 17.299 ms for RT. Notably, the mean value in RT is much bigger than AT and a more substantial dispersion can be observed, indicating a lower accuracy and larger variability in RT time differences.

5. Conclusion

In this study, we proposed a deep learning pipeline for noninvasively estimating heart surface potentials without the need of geometric information about the heart. The approach consists of three key components: the 2D torso and heart representations, and a deep learning model. This approach eliminates the need for CT scan or MRI typical of standard ECGI techniques, while maintaining similar accuracy to standard ECGI. The intended use of this approach is to make ECGI fast and accessible in clinics, particularly for first screening and follow-up. This novel approach could also facilitate longer recordings, enabling more frequent and diverse studies of HSPs.

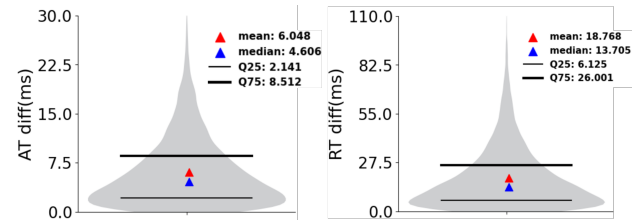


Figure 7. The violin plots of the absolute time differences of both AT and RT computed from predicted and reconstructed electrograms.

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