ML–ResNet: A novel network to detect and locate myocardial infarction using 12 leads ECG

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Objective:-

The paper presents a novel method to detect and locate MI combining a multi-lead residual neural network (ML-ResNet) structure with three residual blocks and feature fusion via 12 leads ECG records.

Table 1
Summary of PTB dataset samples in the paper.

Class	No. of subjects	No. of records	No. of 12-lead records
HC	52	80	6945
MI	113	312	17,212
AMI	17	47	2287
ASMI	27	77	4312
ALMI	16	43	2575
IMI	30	89	4452
ILMI	23	56	3586
Total	165	392	24,157

HC: healthy control, MI: myocardial infarction, AMI: anterior myocardial infarction, ASMI: anteroseptal myocardial infarction recordings, ALMI: anterolateral myocardial infarction recordings, IMI: inferior myocardial infarction recordings, ILMI: inferolateral myocardial infarction recordings.

This paper used PTB database. There are 17,212 MI recordings and 6945 HC recordings.

Preprocessing:-

The pre-processing steps include denoising, down-sampling, QRS detection and data augmentation.

- Wavelet denoising method is presented to eliminate different noise in the first step. Then, the denoised signal is down sampled to 200 Hz.
- Further, the Pan-Tompkins algorithm is employed to detect the QRS wave and perform beat segmentation.
- 800 sample points are chosen along with 99 points before QRS detection point and 700 points after QRS detection point.

Neural network architecture:-

- The proposed ML-ResNet network is employed to detect MI and localize MI, which has 13 layers including one lead feature branch.
- In detail, the single feature branch consists of 3 residual blocks with three convolutional layers per block.

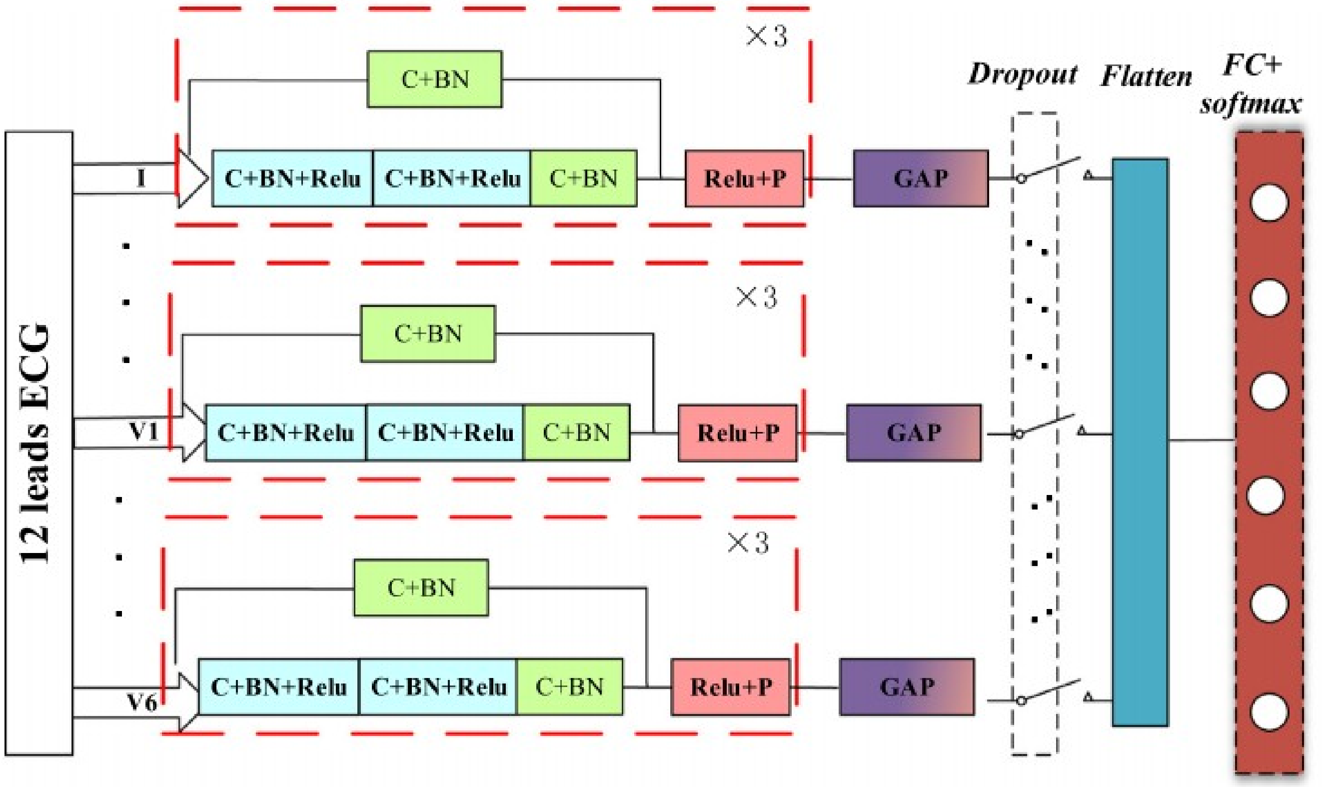

Fig. 2. The architecture of the proposed ML-ResNet.

- Here, single lead feature branch network for every lead is used, which consists of residual blocks, including convolutional layer (C), batch normalization layer (BN), rectified linear unit layer (Relu), and pooling layer (P).

Table 2
Architecture of three residual blocks of the model.

Type	Kernel/Pool size	Number of kernel
input	–	–
Convolutional 1D	17×1	2/4/8
BN+Relu	–	–
Convolutional 1D	11×1	2/4/8
BN+Relu	–	–
Convolutional 1D	5 × 1	2/4/8
BN	–	–
Expand input (C)	1 × 1	2/4/8
Skip connection	–	–
Pooling	5	–

Table 3
Detailed information of ML-ResNet.

Layers	Type	Number of kernel	Output shape
0	Input	–	800 × 1
1–4	Residual block	2	160 × 2
5–8	Residual block	4	32 × 4
9–12	Residual block	8	6 × 8
–	GAP	–	1 × 8
–	Dropout	–	1 × 8
–	Flatten		12 × 8
13	Fully-connected		2 or 6

- Every residual block network includes 3 convolutional layers (Conv1D), whose layer are followed by batch normalization layer (BN) and a Relu operation, and in the end an average pooling layer.
- An additional convolutional layer (Conv1D) with a 1 × 1 filter and batch normalization layer (BN) are developed to increase the dimension to be used for addition in the residual block.
- As each residual block is designed to learn fused ECG features at multiple spatial resolution, the filter shape with N filters is M × 1 in the convolutional layer.
- In first residual block, we use 2 kernels (filters), in second block, 4 kernels and in final block, we use 8 kernels.
- Meanwhile, zero padding is used in the blocks to ensure input and output vector are of same length. After this we perform pooling operation with size 5.
- After this, GAP and dropout with a probability of 0.5 is also applied to extract core features and promote generalization ability.

- Thus, we will get 12 leads feature (of dimension 16x1) from each single lead feature branch network.
- We will get a matrix with dimensionality is 16 × 12. We use Flatten layer to reshape it to 192 × 1.
- After tflattening, the data is fed to the fully connected softmax layer with 2 output classes or 6 classes for MI detection and MI location, respectively.

Results:-

The performance of MI detection along with MI location is analyzed based upon 5-fold cross validation. The results are as follows.

(1) For intra patient scheme:-

Table 5
Confusion matrix and performance for MI detection across 5-fold cross validation based on intra-patient scheme.

		Predicted		Acc(%)	Se(%)	Sp(%)	PPV (%)	F1(%)
		MI	HC					
Original	MI	17,208	4	99.92	99.98	99.77	99.91	99.94
	HC	16	6929					

Table 7
Confusion matrix and performance for MI location across 5-fold cross validation based on intra-patient scheme.

	Predicted						Acc(%)	Se(%)	Sp(%)	PPV(%)	F1(%)
	AMI	ASMI	ALMI	IMI	ILMI	HC					
AMI	2262	17	3	0	0	0	99.72	99.12	99.78	99.87	99.49
ASMI	2	4323	8	1	2	0	99.72	99.70	99.72	99.27	99.48
ALMI	1	14	2560	0	1	0	99.72	99.38	99.76	99.57	99.48
IMI	0	1	0	4441	12	1	99.72	99.69	99.73	99.89	99.79
ILMI	0	0	0	4	3578	0	99.72	99.89	99.69	99.56	99.72
HC	0	0	0	0	1	6926	99.72	99.99	99.61	99.99	99.99
AVE	/	/	/	/	/	/	99.72	99.63	99.72	99.69	99.67

(2) For Inter-patient scheme:-

Table 8
Confusion matrix for MI detection based on inter-patient scheme.

		Predicted MI	Predicted HC	Acc(%)	Se(%)	Sp(%)	PPV(%)	F1(%)
Original	MI	6157	334	95.49	94.85	97.37	99.07	96.92
	HC	58	2147					

Table 9
Confusion matrix for MI location based on inter-patient scheme.

	Predicted						Acc(%)	Se(%)	Sp(%)	PPV(%)	F1(%)
	AMI	ASMI	ALMI	IMI	ILMI	HC					
AMI	251	93	23	0	5	401	55.74	32.47	58.01	54.45	40.68
ASMI	57	1295	29	166	124	153	55.74	71.00	51.688	70.92	70.96
ALMI	90	357	235	37	180	52	55.74	24.71	59.55	78.60	37.60
IMI	0	78	12	607	480	495	55.74	36.30	60.36	48.44	41.50
ILMI	63	2	0	414	284	508	55.74	22.35	61.46	26.47	24.23
HC	0	1	0	29	0	2175	55.74	98.64	41.17	57.48	72.63
AVE	/	/	/	/	/	/	55.74	47.58	55.37	56.06	47.94

Conclusions:-

- The proposed method for MI detection and localization has achieved superior results for inter-patient scheme.
- However, the performance based on MI localization for the inter-patient scheme is not up to the mark. The improvement depends significantly on the mass data and the novel model which reflects spatial location information of different leads subtly.