ME-GAN: Learning Panoptic Electrocardio Representations for Multi-view ECG Synthesis Conditioned on Heart Diseases

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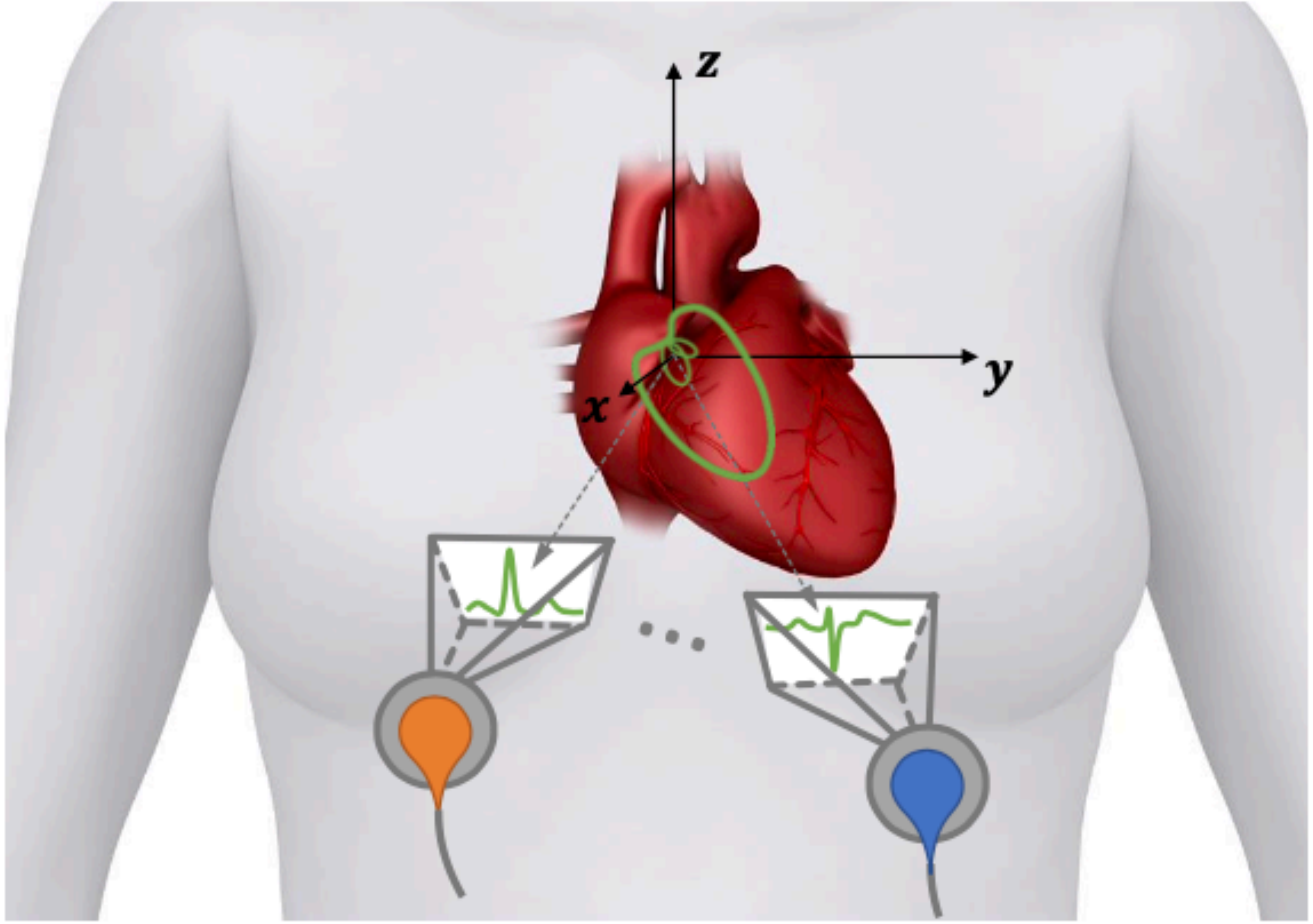
Background

- ECG is a widely used noninvasive diagnostic tool for heart diseases.
- Synthesizing ECG data is thus quiet helpful to **increasing training samples**, **privacy protection**, and **annotation burden reduction**

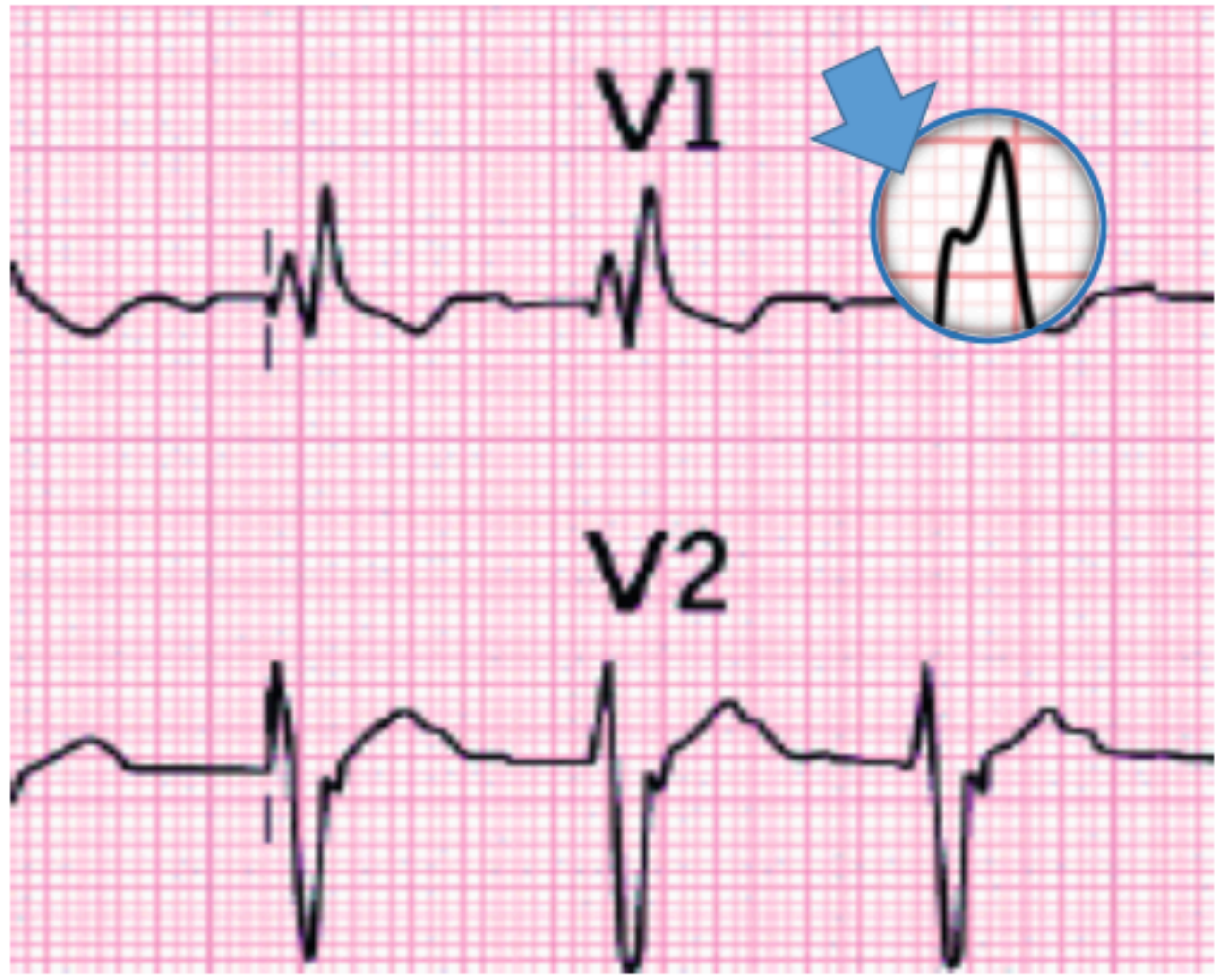
Issues

- How to ensure the multi-view ECG synthesis is trusty?
    - Different views were highly correlated because they represent the same heart beat signals from different viewpoints

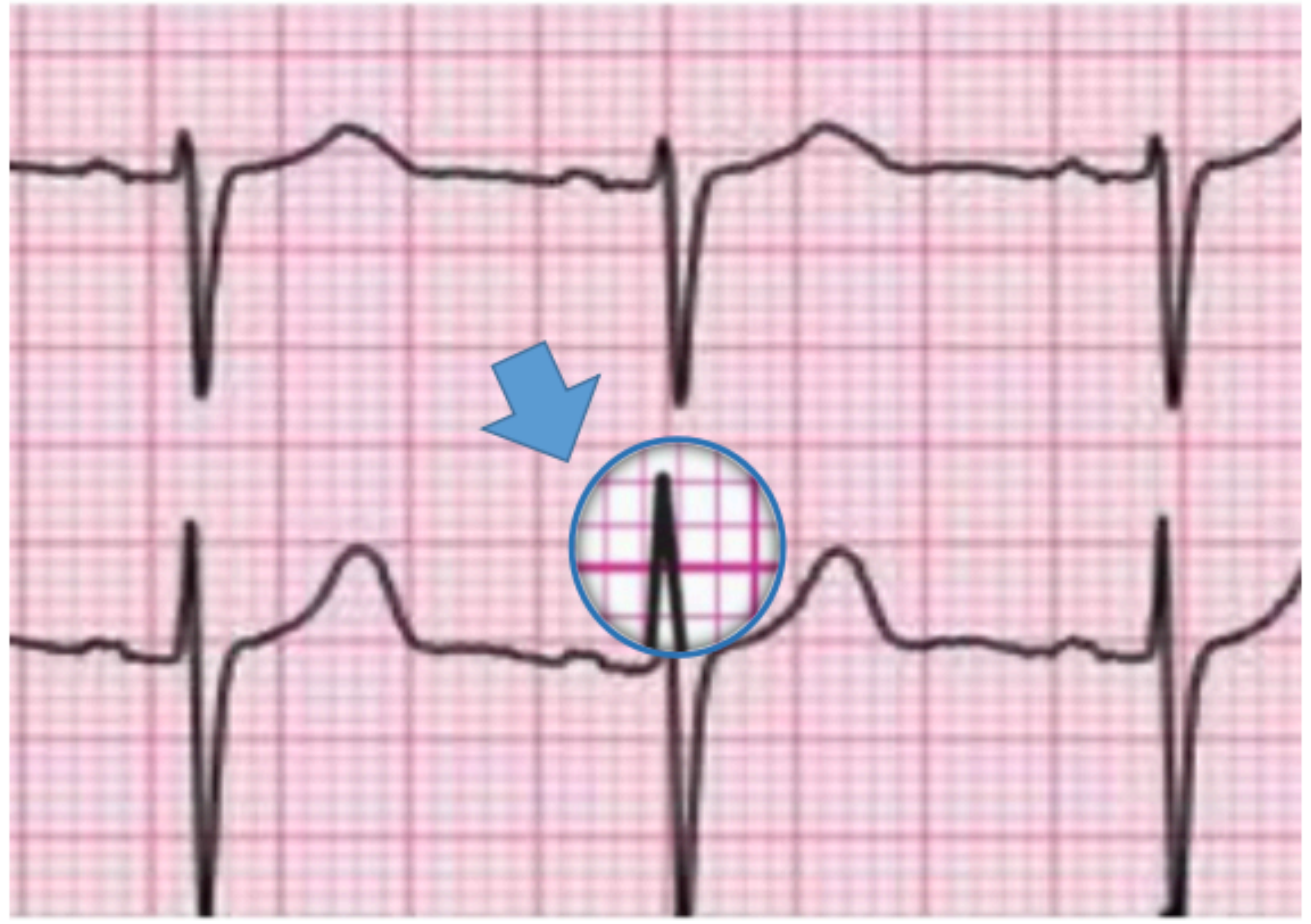


Issues

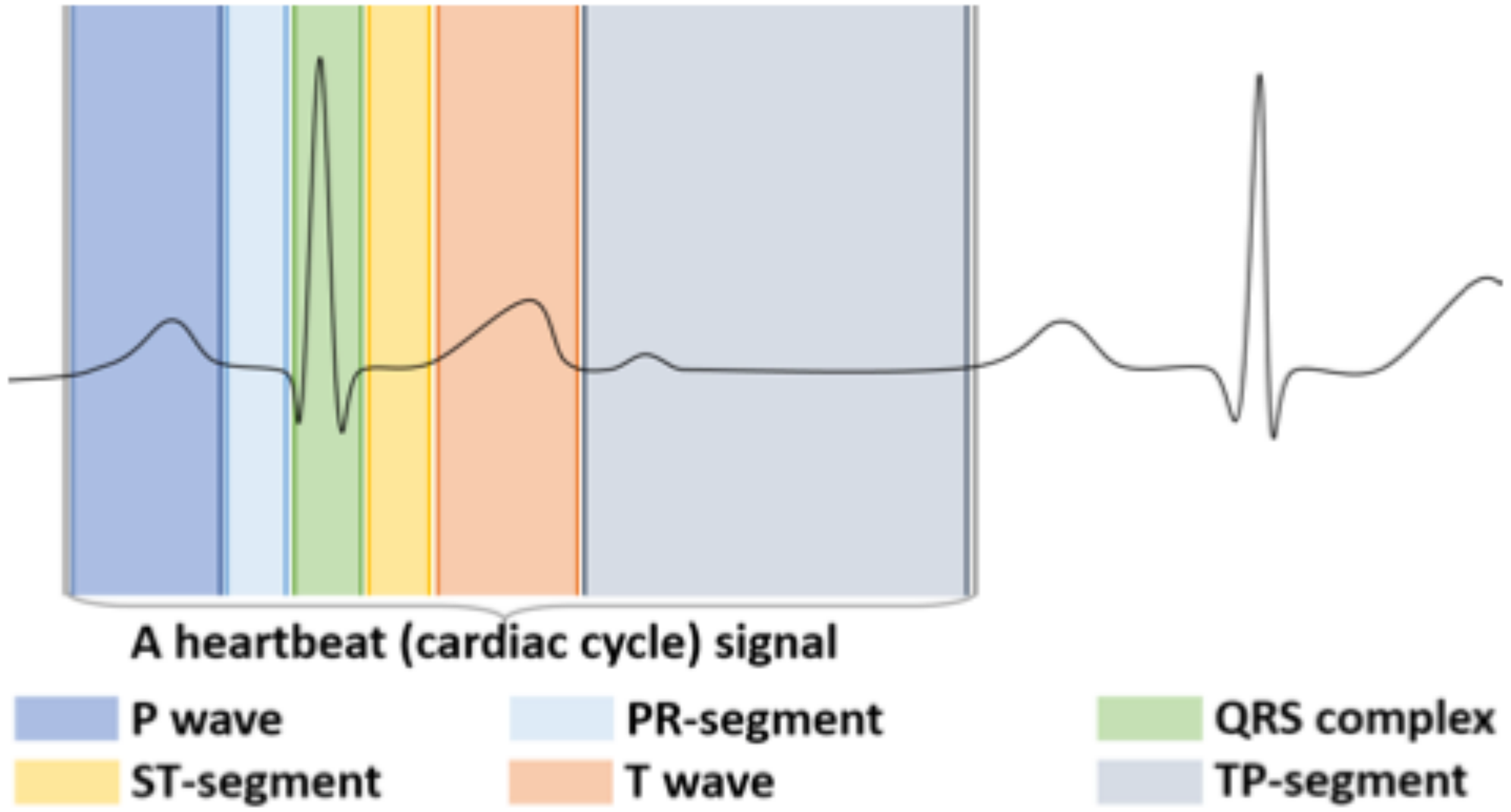
- How to synthesize ECG conditioned on heart diseases?
  - ECG manifestations of some heart diseases are often localized in specific waveforms and were shown as some fine-grained waveform deformations.



Abnormal waveform with LBBB.

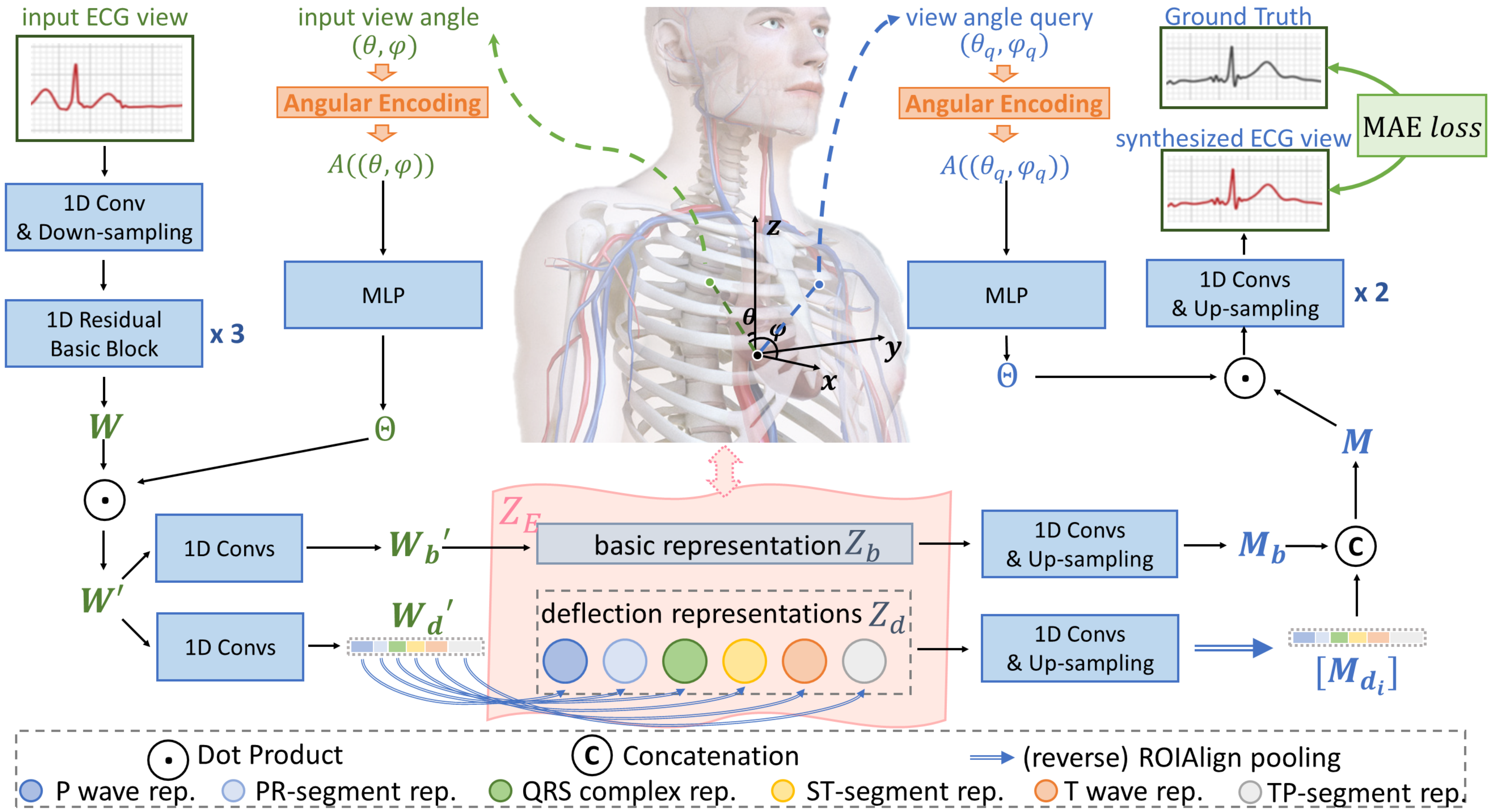


Normal waveform at R peak.



(c) An ECG view

Related Work

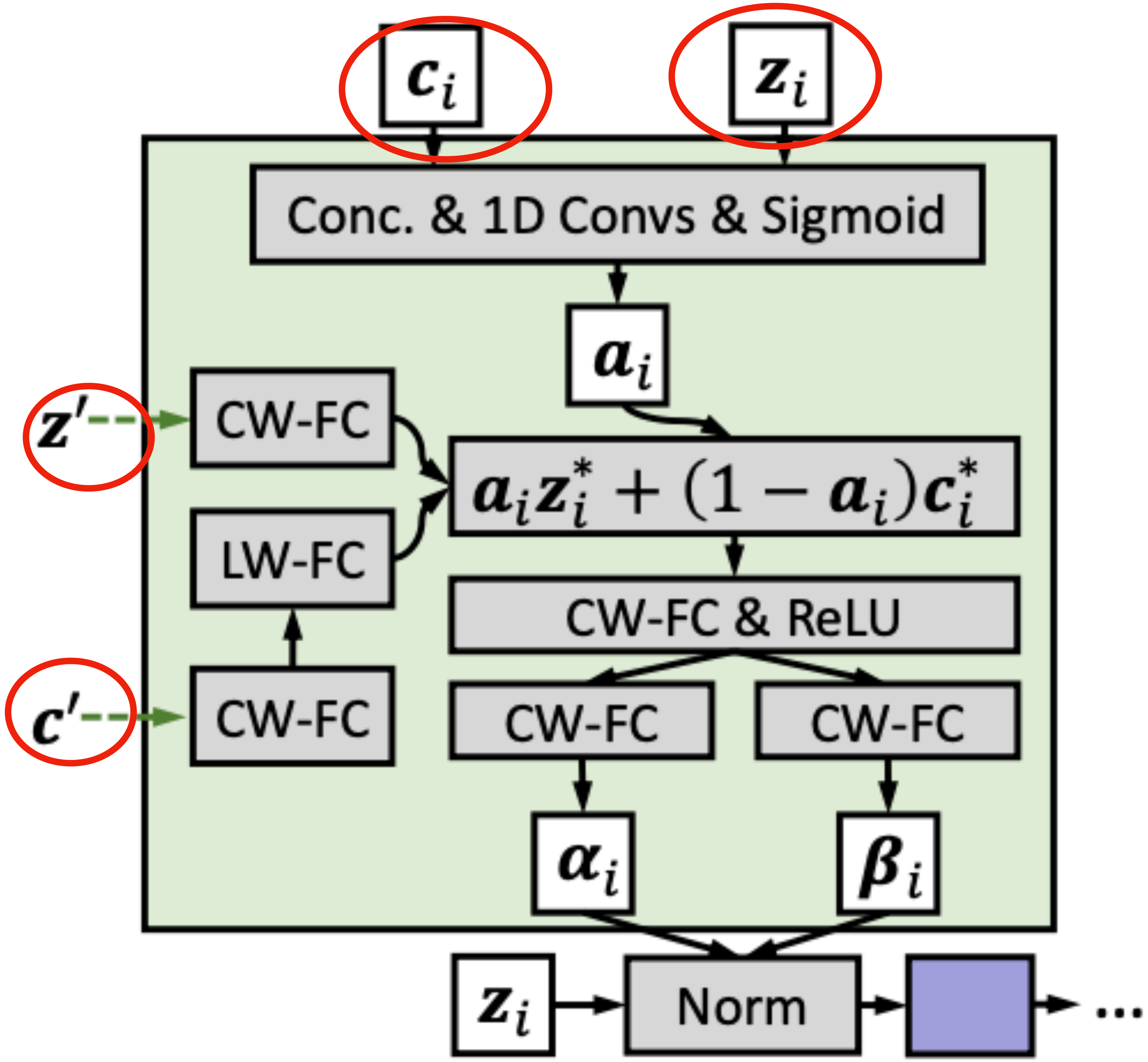


Chen, J., Zheng, X., et al. Electrocardio panorama: Synthesizing new ECG views with self-supervision. In *IJCAI*, 2021.

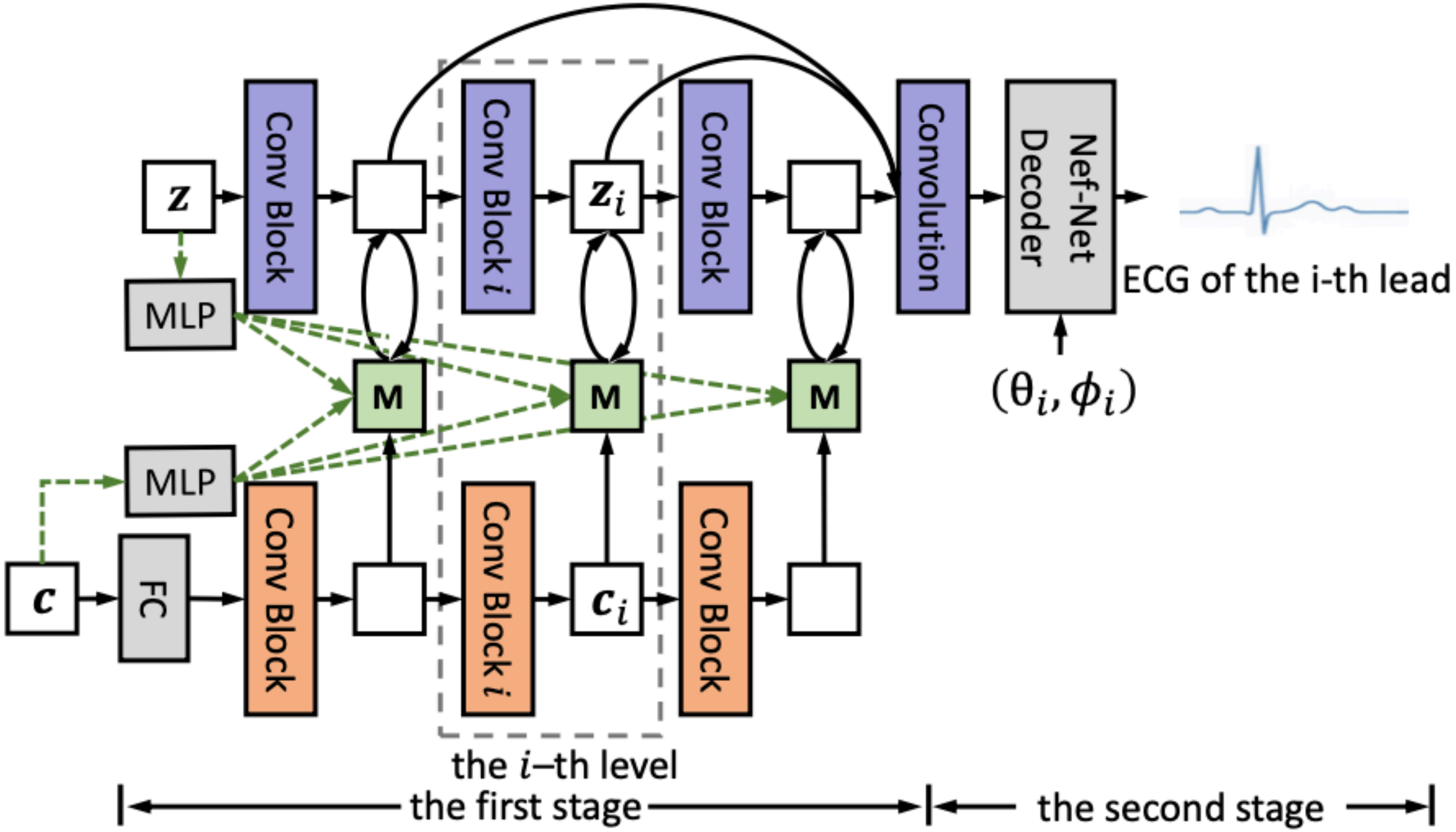
Method

- **Mixup Normalization Layer**
    - Synthesize fine-grained waveformed conditioned on heart diseases

$$\widetilde{z} = \alpha \odot \frac{z_i - u}{\sigma} + \beta_i$$

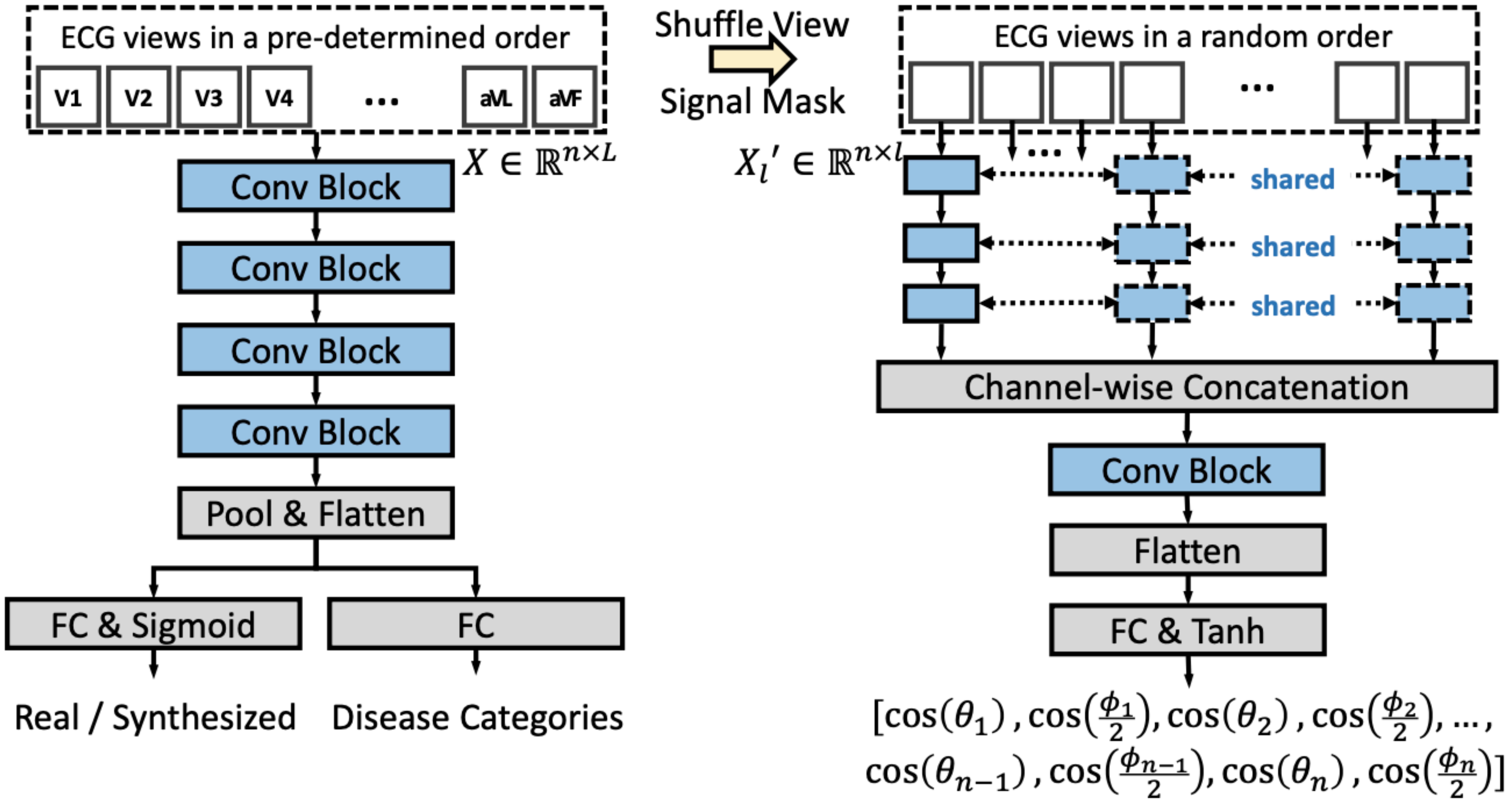


Generator



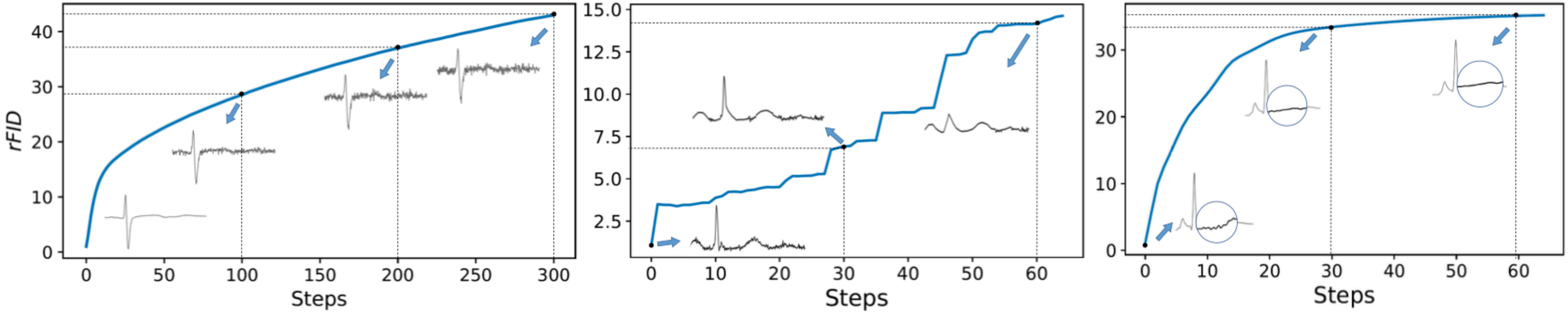
(a) Generator of ME-GAN

Discriminator



(a) Major Discriminator **(b) View Discriminator**

rFID



(a) *rFID* changes with continuously added noises. **(b) *rFID* changes with ECG signals replaced by line segments.** **(c) *rFID* changes with ECG signal blurring.**

Figure 5. **Illustrating *rFID* changes during a process in which noise is continually added onto ECG signals.** The "V2" view of an ECG signal is presented for visually showing the signal quality.

Result

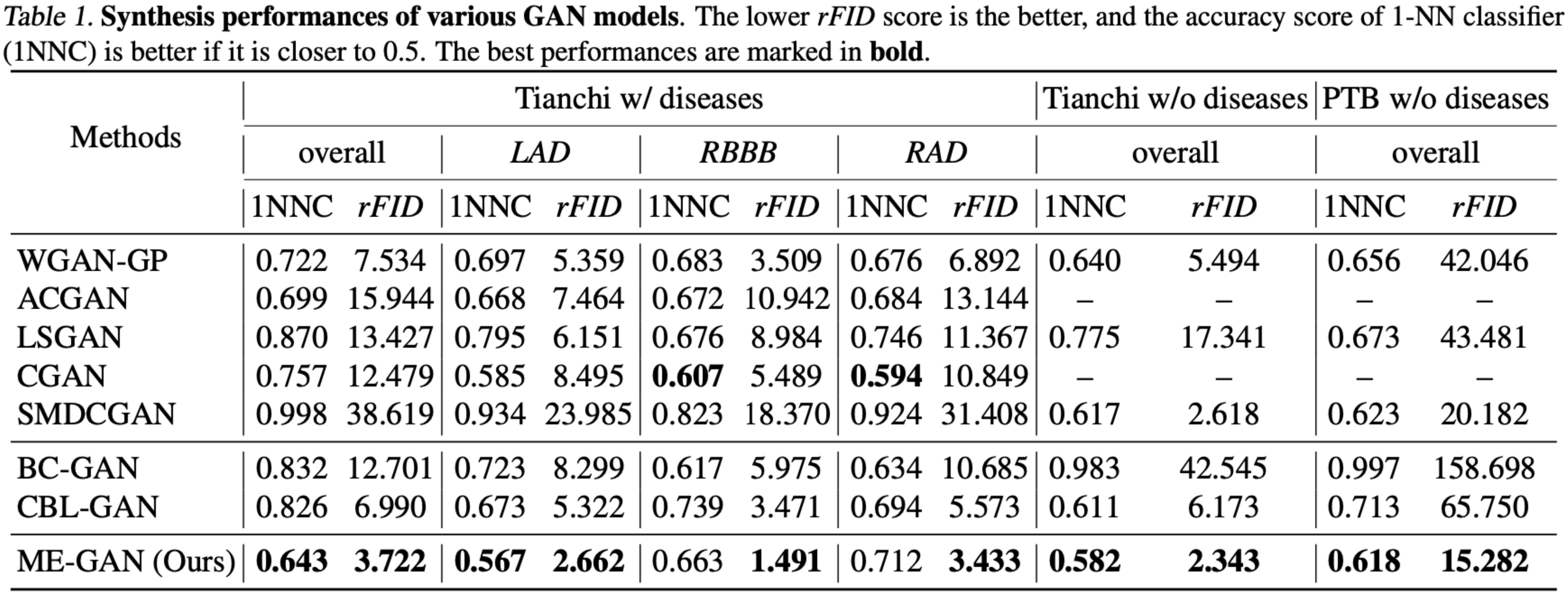


Table 1. **Synthesis performances of various GAN models**. The lower *rFID* score is the better, and the accuracy score of 1-NN classifier (1NNC) is better if it is closer to 0.5. The best performances are marked in **bold**.

Methods	Tianchi w/ diseases								Tianchi w/o diseases		PTB w/o diseases	
	overall		*LAD*		*RBBB*		*RAD*		overall		overall	
	1NNC	*rFID*	1NNC	*rFID*	1NNC	*rFID*	1NNC	*rFID*	1NNC	*rFID*	1NNC	*rFID*
WGAN-GP	0.722	7.534	0.697	5.359	0.683	3.509	0.676	6.892	0.640	5.494	0.656	42.046
ACGAN	0.699	15.944	0.668	7.464	0.672	10.942	0.684	13.144	–	–	–	–
LSGAN	0.870	13.427	0.795	6.151	0.676	8.984	0.746	11.367	0.775	17.341	0.673	43.481
CGAN	0.757	12.479	0.585	8.495	**0.607**	5.489	**0.594**	10.849	–	–	–	–
SMDCGAN	0.998	38.619	0.934	23.985	0.823	18.370	0.924	31.408	0.617	2.618	0.623	20.182
BC-GAN	0.832	12.701	0.723	8.299	0.617	5.975	0.634	10.685	0.983	42.545	0.997	158.698
CBL-GAN	0.826	6.990	0.673	5.322	0.739	3.471	0.694	5.573	0.611	6.173	0.713	65.750
ME-GAN (Ours)	**0.643**	**3.722**	**0.567**	**2.662**	0.663	**1.491**	0.712	**3.433**	**0.582**	**2.343**	**0.618**	**15.282**

Result

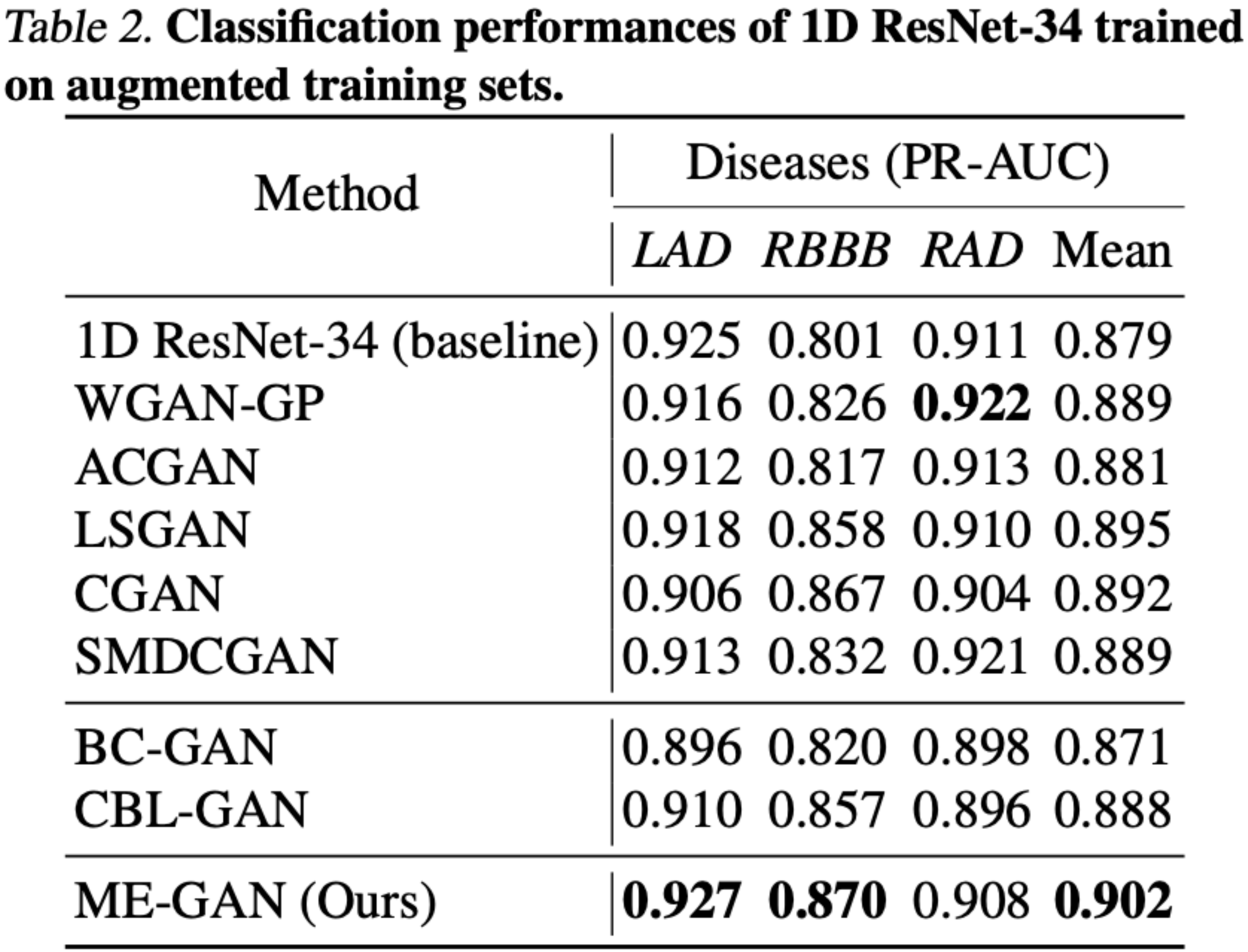


Table 2. **Classification performances of 1D ResNet-34 trained on augmented training sets.**

Method	Diseases (PR-AUC)			
	LAD	*RBBB*	*RAD*	Mean
1D ResNet-34 (baseline)	0.925	0.801	0.911	0.879
WGAN-GP	0.916	0.826	**0.922**	0.889
ACGAN	0.912	0.817	0.913	0.881
LSGAN	0.918	0.858	0.910	0.895
CGAN	0.906	0.867	0.904	0.892
SMDCGAN	0.913	0.832	0.921	0.889
BC-GAN	0.896	0.820	0.898	0.871
CBL-GAN	0.910	0.857	0.896	0.888
ME-GAN (Ours)	**0.927**	**0.870**	0.908	**0.902**

Thank you for listening