

Fig. 1. Generative model architecture. Registered LV segmentations at ED and ES phases are mapped to a low-dimensional latent space. Each latent dimension is forced to be normally distributed with mean μ and standard deviation σ . A decoder network is then used to reconstruct the input segmentation from a low-dimensional vector \boldsymbol{z} sampled from the learned latent distribution (training) or the μ vector (testing). The $\pmb{\mu}$ latent representation is used as input of a MLP to predict disease status.

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$$\mathcal{L} = \mathcal{L}_{rec} + \alpha \mathcal{L}_{KL} + \beta \mathcal{L}_{MLP}.$$

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$$\mu_{i,t} = \mu_{i,t-1} + \lambda \frac{\partial y_1}{\partial \mu_{i,t-1}}, \quad \forall i = 1, \dots d$$
 (1)

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Step #1 Step #8 Step #10 Step #14 [100%,0%] [34%,66%] [0%,100%] [0%,100%] INPUT Latent space visualization by LE Classes HCMsHVols ED 53400 LVM = 53752 83904 95972 LVCV = 122472 120080 115512 119480 ES -0.10 0.06 LVM = 45208 49360 93368 130792 LVCV = 38960 38000 43688 44400

Fig. 2. On the left, Laplacian Eigenmaps (LE) bi-dimensional representation of the latent μ of each subject in the training set (red and green dots) and of the μ_t obtained through latent space navigation (light blue dots) for a random healthy shape. This latter is displayed on the right, together with the decoded segmentations corresponding to the sampled μ_t reported on the left at 4 exemplary iterations. The probabilities of class HVOls and HCM, and the computed LVM and LVCV are also shown.

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10/5/2018		Learning Interpretable Anatomical Features Through Deep Generative Models: Application to Cardiac Remodeling
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