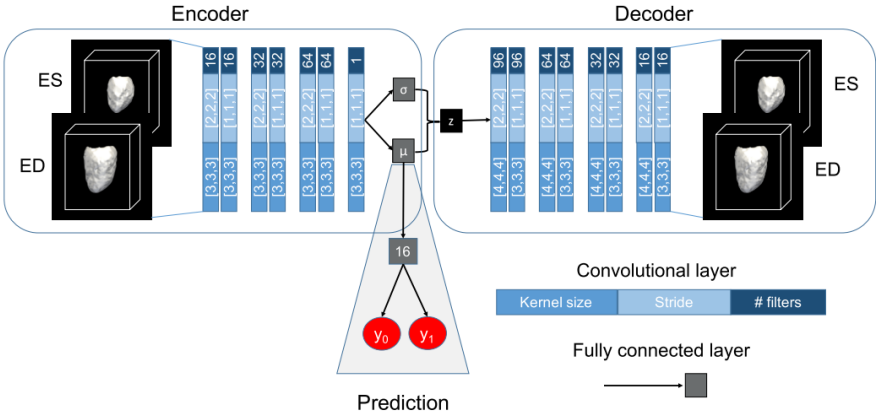

Fig. 1. Generative model architecture. Registered LV segmentations at ED and ES phases are mapped to a low-dimensional latent space. Each latent dimension is forced to be normally distributed with mean $\boldsymbol{\mu}$ and standard deviation $\boldsymbol{\sigma}$. A decoder network is then used to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

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

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

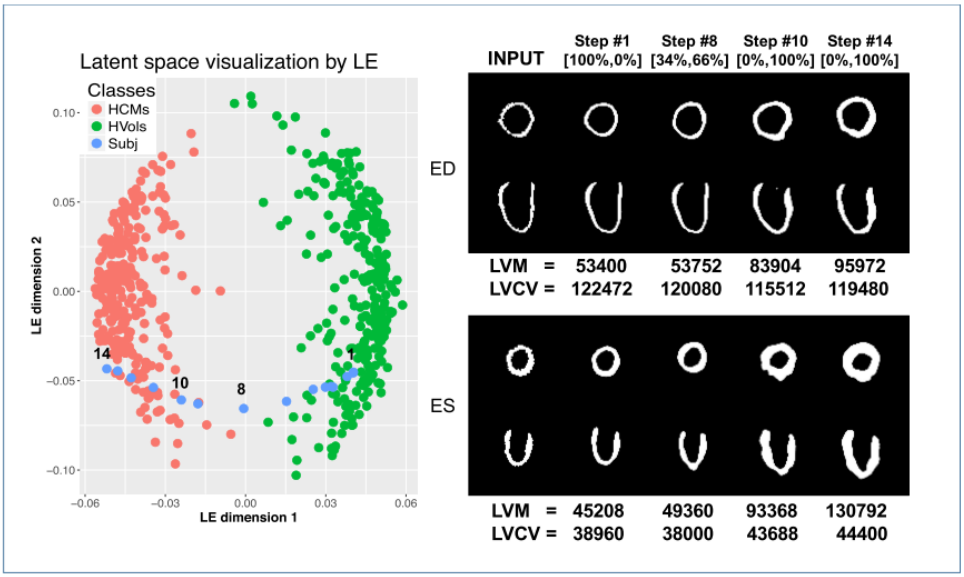

Fig. 2. On the left, Laplacian Eigenmaps (LE) bi-dimensional representation of the latent $\boldsymbol{\mu}$ of each subject in the training set (red and green dots) and of the $\boldsymbol{\mu}_t$ obtained through latent space navigation (light blue dots) for a random healthy shape. This latter is displayed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