Deep Generative Model-based Quality Control for Cardiac MRI Segmentation

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Abstract. In recent years, convolutional neural networks have demonstrated promising performance in a variety of medical image segmentation tasks. However, when a trained segmentation model is deployed into the real clinical world, the model may not perform optimally. A major challenge is the potential poor-quality segmentations generated due to degraded image quality or domain shift issues. There is a timely need to develop an automated quality control method that can detect poor segmentations and feedback to clinicians. Here we propose a novel deep generative model-based framework for quality control of cardiac MRI segmentation. It first learns a manifold of good-quality image-segmentation pairs using a generative model. The quality of a given test segmentation is then assessed by evaluating the difference from its projection onto the good-quality manifold. In particular, the projection is refined through iterative search in the latent space. The proposed method achieves high prediction accuracy on two publicly available cardiac MRI datasets. Moreover, it shows better generalisation ability than traditional regression-based methods. Our approach provides a real-time and model-agnostic quality control for cardiac MRI segmentation, which has the potential to be integrated into clinical image analysis workflows.

Keywords: Cardiac segmentation · Quality control · Generative model.

1 Introduction

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Related work:
[6,7,8] [9,10]

Learning-based quality control:
[11] 42
85%
[12]
[13]
[14]

Registration-based quality control:
[15]
[9]
[16]

Contributions:

2 Methodology

2.1 Problem Formulation

Let F denote a segmentation function that maps an image I to a segmentation $\hat{S} = F(I)$. The segmentation $\hat{S}$ is evaluated by a quality function $q(S_{gt}, \hat{S})$ where S_{gt} is the ground truth segmentation and q is a scalar (e.g. Dice). Since S_{gt} is unknown at test time, we aim to learn a function Q such that $Q(\hat{S}; I) \approx q(S_{gt}, \hat{S})$.

2.2 Deep Generative Model-based Quality Control

Instead of learning Q directly from S_{gt}, we propose to learn it from a surrogate ground truth S_{sur} such that $q(S_{sur}, \hat{S}) \approx q(S_{gt}, \hat{S})$. This is achieved by projecting $(I, \hat{S})$ onto a good-quality manifold (Fig. 1).

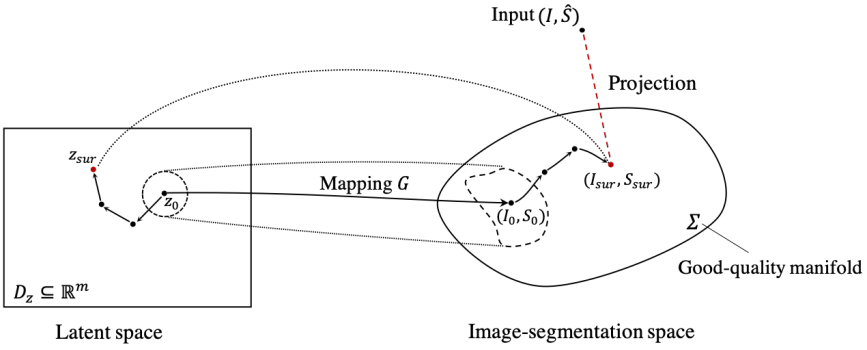

Fig. 1. Overview of the deep generative model-based quality control framework. The generative model G is trained to learn a mapping $G(z)$ from the low-dimensional latent space D_z to the good-quality manifold Σ. The input image-segmentation pair $(I, \hat{S})$ is projected to (S_{sur}, I_{sur}) on the manifold through iterative search, which is in turn used as surrogate ground truth for quality prediction. z_0 is the initial guess in the latent space and it converges to z_{sur}.

Good-quality manifold: We define a good-quality manifold as the set of all good-quality image-segmentation pairs. Let G be a generative model that learns a mapping from a latent space D_z to the joint image-segmentation space $X = (I, S) \in D_I \times D_S$. Here D_I and D_S are the image and segmentation spaces. Given a set of good-quality image-segmentation pairs (I, S_{gt}), we assume that G learns a manifold $\Sigma \subset D_I \times D_S$, called the *good-quality manifold*. The

G $D_z \subseteq \mathbb{R}^m$

$$G(z) : D_z \ni z \mapsto X = G(z) \in D_I \times D_S \tag{1}$$

z m. $G(z)$

Iterative search in the latent space:

$$z_{sur} = \arg\min_{z \in D_z} \mathcal{L}(G(z), (I, \hat{S})) \tag{2}$$

$\mathcal{L}$ $G(z)$ $I, \hat{S})$.

Algorithm 1

Require: A trained generator $G : D_z \ni z \mapsto G(z) = (I, S) \in \Sigma$
Input: Image-segmentation pair $(I, \hat{S})$
Output: Quality prediction $Q(\hat{S}; I)$
Initialization $z = z_0 \in D_z$
while L not converge **do**
  $L = \mathcal{L}(G(z), (I, \hat{S}))$
  $grad = \nabla_z L$ # calculate gradient through back-propagation
  $z = z - \alpha \cdot grad$ # gradient descent with learning rate α
end while
$S_{sur} = G(z_{sur})$
$Q(\hat{S}; I) = q(S_{sur}, \hat{S})$ # perform quality control q (e.g. Dice)

2.3 Generative Model using VAE

E_φ D_ϕ, φ ϕ [17] $I, S)$ E_φ $\mathcal{N}(\mu_z, \sigma_z^2)$ μ_z σ_z^2

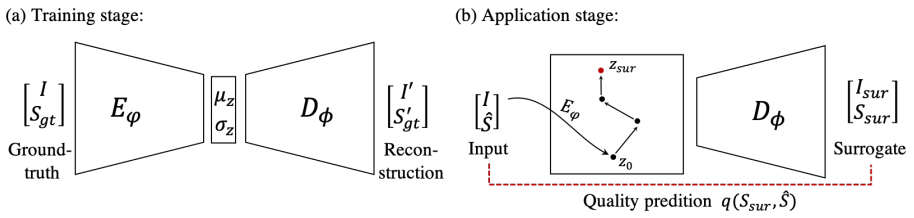

Fig. 2. Framework implementation using the variational autoencoder (VAE). In the training stage, the ground-truth image-segmentation pairs are used. In the application stage, the VAE decoder is used as the generator for iterative search of the surrogate segmentation on the good-quality manifold. Initial guess z_0 is from the encoder.

D_ϕ.

[18]

$$\mathcal{L}_{VAE} = \mathcal{L}_{recon} + \beta \cdot D_{KL}(\mathcal{N}(\mu_z, \sigma_z^2)||\mathcal{N}(0, \mathbf{I})) \quad (3)$$

$$\mathcal{L}_{recon} = BCE(S_{GT}, S'_{GT}) + MSE(I, I') \quad (4)$$

β m

D_ϕ

E_φ.

S_{sur}

$q(S_{sur}, \hat{S})$,

3 Experiments

3.1 Datasets

UK Biobank dataset:

1,500 (800 , 200 , 500).

1.8 1.8 68

2 10 12

ACDC dataset: 100 [illegible]

3.2 Experimental Design

[illegible]

VAE implementation and training: [illegible] *ReLU* [illegible] *Sigmoid* [illegible] m [illegible] β [illegible] 0.01 [illegible] 0.0001 [illegible] 16. [illegible] 100 [illegible] 96 [illegible] 96 [illegible] [illegible] [illegible]

4 Results and Discussion

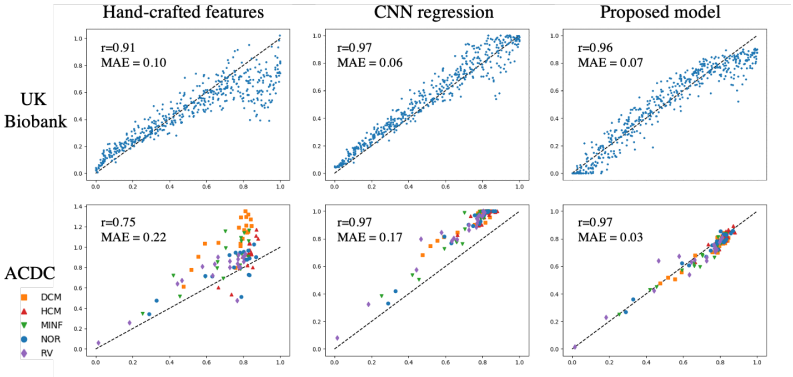

Fig. 3. Comparison of the performance of different quality control methods. The x-axis is the real Dice of each subject and the y-axis is the predicted Dice by each method. The dashed line is the $y = x$, plotted for reference. Top row: UK Biobank data ($n = 500$). Bottom row: ACDC data ($n = 100$), with five subgroups plotted in different colors.

Table 1. Quality control performance of three models on two cardiac datasets. The Pearson correlation coefficient r and the mean absolute error (MAE) between predicted and true Dice metrics are reported. MAE is reported as mean (standard deviation). For ACDC dataset, the performance on five subgroups [4] are aslo reported.

Dataset	Hand-crafted features [11]		CNN regression [12]		Proposed model	
	r	MAE	r	MAE	r	MAE
UK Biobank	0.909	0.100(0.100)	**0.973**	**0.061(0.049)**	0.958	0.067(0.052)
ACDC	0.728	0.182(0.130)	0.968	0.165(0.044)	**0.969**	**0.033(0.028)**
DCM	0.802	0.353(0.123)	0.956	0.186(0.034)	**0.964**	**0.036(0.020)**
HCM	0.838	0.131(0.075)	0.836	0.155(0.027)	**0.896**	**0.023(0.015)**
MINF	0.815	0.184(0.123)	0.969	0.156(0.051)	**0.976**	**0.033(0.029)**
NOR	0.775	0.114(0.065)	0.985	0.158(0.040)	**0.985**	**0.026(0.017)**
RV	0.877	0.129(0.073)	0.974	0.169(0.053)	**0.960**	**0.045(0.042)**

prior to

5 Conclusion

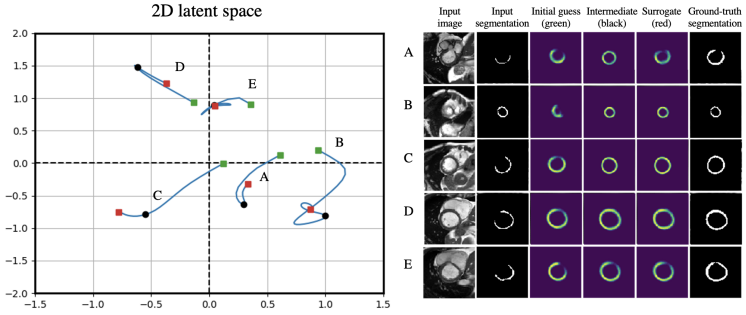

Fig. 4. Visualisation of searching path in a two-dimensional latent space. Left: searching paths for five exemplar samples (green point: initial guess from the VAE encoder; black point: intermediate state during iterative search; red point: convergence point for surrogate segmentation). Right: the input image and segmentation, reconstructed segmentations along the searching path and the ground-truth segmentation.

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Appendix

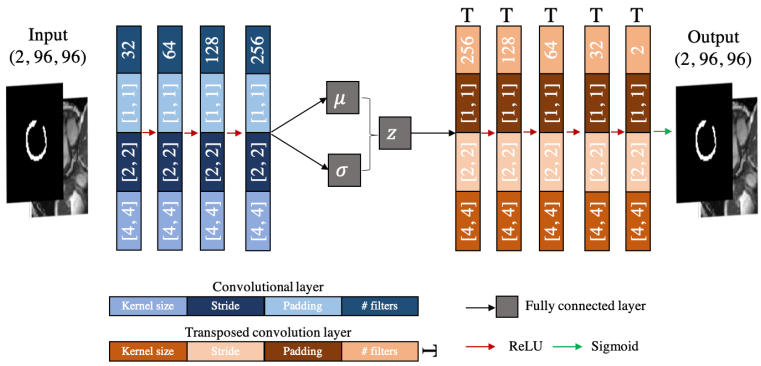

Fig. A1. Network architecture of the VAE.

Table A1. Ablation study of the latent space dimension m and the hyperparameter *beta*. The mean absolute error (MAE) between predicted and true Dice metrics on UKBB validation set are reported. m=8 and $\beta = 0.01$ were selected as the optimal parameters according to the results.

m	β			
	0	1E-3	1E-2	1E-1
2	0.095	0.094	0.105	0.502
4	0.086	0.092	0.114	0.416
8	0.088	0.072	**0.068**	0.229
16	0.147	0.141	0.095	0.091