

Unsupervised Liver Tumor Segmentation with Pseudo Anomaly Synthesis

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Motivation

Q1: Should pseudo-anomalies approximate the queries in test phase?

- There is no clear definition of what constitutes an anomaly, there shouldn't be any bound or limit on pseudo anomaly.
- advocate generating a diversity of anomalies to We facilitate a model to learn the comprehensive normal spectrum, instead of matching known abnormal patterns.

Q2: How should the segmentation model be trained on the synthesis data?

• A covariate shift is likely to exist between the synthesized and real anomalies, according to Fig 1(C). Good-fit models on the pseudo-anomalies may fail to detect real anomalies.



• The model optimization on anomaly synthesis for pseudosupervised segmentation should stop early to preserve the model's generalizability on queries.

Method

We adopted the DREAM[1] architecture and incorporated three key elements: random-shape anomaly generation, two-phase learning mechanism, and UNet reconstruction network.

Random-shape Anomaly Generation

Algorithm 1 Random-shape Pseudo Anomaly Generation

Input: Image, Threshold

Output: AnomalyMask, Label

 $NoiseImage \leftarrow gaussianNoise(Image_height, Image_width)$ $BlurImage \leftarrow gaussianBlur(NoiseImage, kernal_size)$ $StretchImage \leftarrow rescaleIntesity(BlurImage, (0, 255))$ $AnomalyMask \leftarrow binarize(StretchImage, Threshold)$ $AnomalyMask \leftarrow Morph_open_close(AnomalyMask, kernel_ellipse)$ if sum(AnomalyMask) > 0 then $Label \leftarrow 1$ else $Label \leftarrow 0$ end if



Fig. 1. (A) Systematic diagram of the proposed unsupervised liver tumor segmentation scheme. During training, synthetic abnormalities are fed to a restoration net followed by a segmentation net. The two models are trained in two phases to avoid model overfitting on synthesis. (B) Proposed synthesis pipeline based on Gaussian noise stretching. (C) Liver image embedding by 2-D TSNE.



Evaluation performance of the segmentation network Fig. 2. reveals a tendency to overfit shortly after a short period of training.

The pseudo anomaly synthesis is shown in Fig. 1(B) and formulated as:

 $I_{s} = (1 - M_{s}) \odot (I + C) + M_{s} \odot I,$ $|C| \in (minRange, maxRange)$

where I_s represents synthesized anomalies, \odot is the elementwise multiplication, and C is randomly drawn from a Gaussian distribution within a defined range

Two-stage Training Strategy

Due to the covariate shift of the synthesized anomalies, we high perturbations in evaluation performance, observed therefore, we propose to train the networks in two steps: As Depicted in Fig. 2(A), the reconstruction network is trained to restore anomalous regions, while the segmentation network estimates an accurate segmentation map for the anomaly.

Results



Fig. 3. Qualitative results of tumor segmentation on real liver tumor data. I_{in} : Input, M_{sea} : segmentation mask, and M_{at} : Ground-Truth.

• The reconstruction model is first trained with L_1 loss:

 $L_{rec}(I_s - \tilde{I}_s) = |I_s - \tilde{I}_s|$

After freezing the well-trained generative module, Focal Loss [2] is adopted to slightly train the segmentation model to avoid bias introduced by the covariance shift, :

$$L_{seg}(M_s - \widetilde{M}_s) = -\frac{1}{N} \sum_{i=1}^{N} \sum_{j=1}^{C} \alpha_j (1 - \widetilde{m}_{s,ij})^{\gamma} \log(\widetilde{m}_{s,ij})$$

where \tilde{I}_{s} is the reconstruction image, \tilde{M}_{s} is the estimated anomaly mask, $\tilde{m}_{s,ij}$ denotes the predicted probability of class j at pixel *i*, and α_i is the weight for class *j*.

Table 1. Ablation study of two-phase training (TP), pseudo anomaly (PA), and reconstructive network. The baseline is DRAEM model [1]. +TP+PA+UNetDice 14.75 <u>+</u> 14.28 21.31 ± 12.54 Base 30.17 ± 5.50 line 40.06 ± 6.85 53.03 ± 1.78

