University of Central Missouri

Department of Computer Science

CS-5720: Neural Network Deep Learning

GenSelfDiff-HIS: Generative Self-Supervision Using Diffusion for Histopathological Image Segmentation

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Summary Report

Histopathological photograph segmentation is a crucial but hard work-intensive undertaking requiring expert pathologists. Even as supervised deep ultra-modern techniques were hired, they require big-scale annotated datasets, which are modern-day unavailable. Self-supervised cutting-edge (SSL) is an alternative paradigm that uses state-of-the-art unannotated facts to pre-educate fashions that may later be nice-tuned for precise obligations. but, SSL techniques for histopathological image segmentation remain underexplored.

Structure

The repository is organized into several directories and scripts, each serving a specific purpose in the workflow:

pre_process: Contains scripts for data preprocessing, including handling public datasets like MoNuSeg and GlaS. Users are expected to place these datasets into appropriate folders within this directory for preprocessing.

GenSelfDiff: Houses the main implementation of the generative self-supervision using diffusion models. This includes subdirectories for pre-training, downstream training, and testing.

- pretrain: Scripts related to the self-supervised pre-training phase using diffusion models.

- downstream_train: Contains scripts for fine-tuning the pre-trained models on the segmentation task.

- test: Includes scripts for evaluating the performance of the trained segmentation models.

HE_diff_general.py: A script that appears to be related to handling Hematoxylin and Eosin (HE) stained images, which are commonly used in histopathology.

image_generation.py and image_generation_general.py: Scripts likely responsible for generating images, possibly as part of the diffusion process.

sample_images.py and sample_images_general.py: Scripts for sampling images, which may be used for visualization or evaluation purposes.

utils_general.py: Contains utility functions that support various tasks across the repository.

This paper proposes a novel SSL method the use of generative diffusion fashions for histopathological photo segmentation, called "GenSelfDiff-HIS". The method leverages the potential cutting-edge diffusion models to carry out picture-to-photo translation obligations similar to segmentation.

Methodology

The proposed methodology consists of two main stages:

1. **Self-Supervised Pre-Training Using Diffusion Models:** The model is trained to perform a diffusion-based image-to-image translation task on unannotated histopathological images. This pretext task enables the model to learn meaningful representations without the need for labeled data. The diffusion process involves adding noise to an image and then learning to recover the original image, effectively teaching the model to understand the underlying structures within the images.

1. **Downstream Segmentation Task:** The pre-trained model is fine-tuned using a small set of annotated images to perform the specific task of histopathological image segmentation. A multi-loss function combining Structural Similarity (SS) loss and Focal Loss (FL) is employed to address challenges such as preserving structural information and handling class imbalance.

A "UNet-based generative diffusion process" is used because the SSL pretext mission educates the version in an unmanaged manner. The pre-skilled UNet is excellent-tuned with "segmentation loss capabilities" for downstream tasks. A "new Head and Neck (HN) cancer dataset" with Hematoxylin and Eosin (H&E) stained pictures and segmentation annotations is introduced. The proposed technique is proven on "3 datasets": HN most cancers, GlaS, and MoNuSeg.

Training and Evaluation

To train and evaluate the models, the repository provides specific scripts:

- **Pre-training:** The script GenSelfDiff/pretrain/SS_diff.py is used for the self-supervised pre-training phase. Users need to specify the path to the directory containing the unlabeled images in the script GenSelfDiff/pretrain/utils.py.

  CUDA_VISIBLE_DEVICES=0,1,2,3 python3 ./GenSelfDiff/pretrain/SS_diff.py

- **Downstream Training for Segmentation:** After pre-training, the model is fine-tuned on the segmentation task using the script GenSelfDiff/downstream_train/Diff_Seg.py. Paths to the images, labels, and pre-trained model should be specified within this script.

  CUDA_VISIBLE_DEVICES=0,1,2,3 python3 ./GenSelfDiff/$downstream_train/Diff_Seg.py$

- **Evaluation:** The performance of the trained segmentation model can be evaluated using the script GenSelfDiff/test/test_script.py. Users need to specify the paths to the images, labels, and the trained model within this script.

  python3 ./GenSelfDiff/test/test_script.py

Datasets

The methodology was validated on two publicly available datasets, MoNuSeg and GlaS, as well as a newly proposed head and neck (HN) cancer dataset containing Hematoxylin and

Eosin (H&E) stained images with annotations. The public datasets can be downloaded and placed into the appropriate folders within the pre_process directory for data preprocessing. The HN dataset will be made available for research purposes in the future.

A singular generative SSL approach the usage of denoising diffusion probabilistic models (DDPMs) for histopathological photograph segmentation. Quality-tuning modern-day the pre-trained UNet for segmentation of the usage of a multi-loss feature combining structural similarity and focal loss. Creation of modern day a new HN most cancers dataset containing annotated and unannotated histopathological pix. Assessment on more than one dataset showing advanced segmentation performance over conventional SSL pretext obligations and fully supervised fashions.

Conclusion

The proposed method outperforms other SSL techniques, including contrastive and predictive SSL, throughout more than one assessment metric. It achieves better segmentation accuracy than absolutely supervised strategies like UNet and interest UNet. The framework is more effective than DDPM-based supervised segmentation procedures. The go-dataset experiments show desirable generalizability.

GenSelfDiff-HIS provides a powerful SSL framework for histopathological segmentation through the use of generative diffusion models. The method reduces dependency on annotated information whilst reaching segmentation overall performance. The brand new HN cancer dataset in addition enriches research in histopathological image analysis.

The code references several baseline methods for comparison, including CS-CO, Wolleb et al., Baranchuk et al., CIMD, MedSegDiff, and FCT. Additionally, the implementation of the Attention-based U-Net architecture has been adopted from the Diffusion repository.