AMONuSeg: A Histological Dataset for African Multi-Organ Nuclei Semantic Segmentation

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Introduction

Nuclei semantic segmentation is critical for advancing machine learning and deep learning in **digital pathology**. However, most current models are trained on high-quality data obtained using expensive equipment like whole slide scanners, which are not accessible to pathologists in developing countries. These professionals often work with low-resource data captured using low-precision microscopes, smartphones, or digital cameras, presenting unique challenges. This work introduces **the first fully annotated African multi-organ dataset for histopathology nuclei segmentation (AMONUSEG),** acquired with a low-precision microscope. We also evaluate state-of-the-art segmentation models, including **spectral feature extraction encoder [1]** and **vision transformer-based (ViT) models [2],** and **stain normalization techniques [3]** for color normalization of Hematoxylin and Eosin (H&E) stained histopathology slides.

Contribution

The main contributions of this study are:

- Introducing the first fully annotated, publicly available African Multi-Organ dataset for nuclei semantic segmentation (AMONuSeg).
- Analyzing the impact of stain color normalization techniques on the segmentation performance.
- Assessing the impact of State-of-the-art SOTA segmentation models on nuclei histopathology segmentation
- Proposing a modified merged FD-NET segmentation model.

Methodology

1 The AMONuSeg Dataset

AMONuSeg Dataset Description:

- **48 H&E histological images** with a size of **1280x960** and **250x** Magnification Factor.
- **4 body parts**: Breast, Skin, Cervical and Inguinal.
- **19,036** annotated nuclei.
- Collected using digital microscopic camera (MA 500 AmScope Matlab ®, USA) .

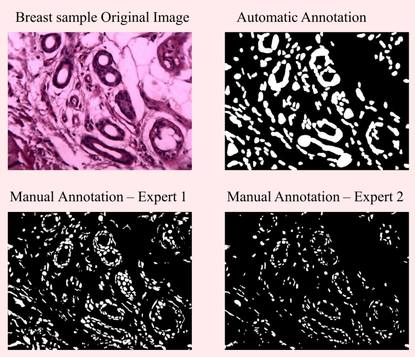

Figure 1: The difference between automatic annotations generated using the Fiji ImageJ and the manual annotations validated by expert 1 & 2.

Annotation Process:

Two trained annotators performed manual annotation following the steps bellow:

1. Unsupervised automatic nuclei segmentation masks are generated using Fiji ImageJ software to provide rough preliminary annotations for tissue slides.
2. Manual annotation was performed using LabelStudio tool.
3. Intra Observation to validate the annotations by the two trained annotators.
4. Validation of the annotations by three experts' anatomists and pathologists.
5. In case of disagreements, provide two masks for the annotated image.

2 FD-NET Empirical Design

FD-Net Two Branches:

- **Spatial encoder** branch that processes spatial features and consists of convolutional blocks.
- **Spectral branch** that processes spectral features and consists of fast Fourier convolutional blocks [1].

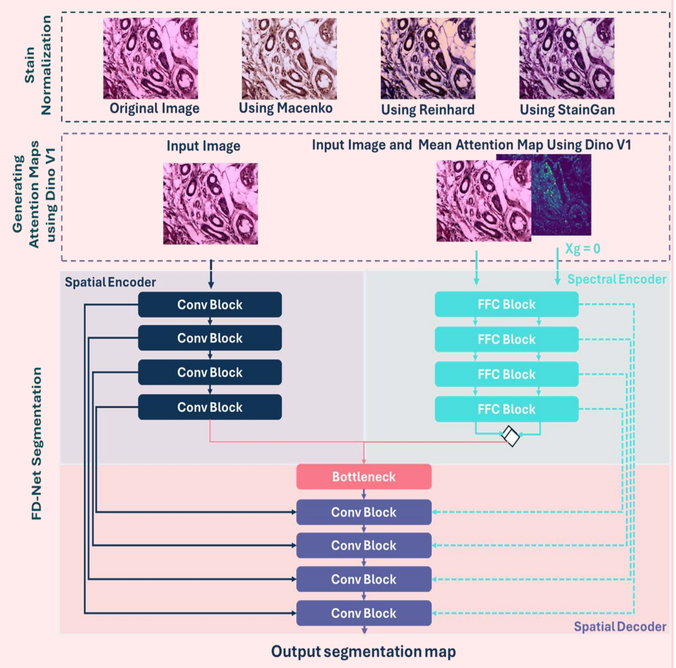

Figure 2: The Empirical design of the FD-Net Model

The Input Images:

For the spatial encoder branch: The input image can be either the original image or a stain-normalized preprocessed image using Macenko, Reinhard, or StainGAN methods.

For the spectral encoder branch: The input image and the generated mean attention map using Dino v1 [2] are fed to the spectral branch.

Main Results

Table 1: The average Dice score of the evaluated segmentation models on the Original and pre-processed AMONuSeg dataset .

Model	Original Dataset	Preprocessing		
		Macenko	Reinhard	StainGan
U-Net [4]	0.823	0.794	**0.825**	0.826
SegNet [5]	0.809	0.755	0.799	0.809
Ynet [1]	**0.830**	0.794	**0.825**	0.826
DAINet [2]	0.824	0.793	0.822	0.828
TransNuseg [6]	0.815	0.791	0.814	0.813
FD-Net	0.828	**0.796**	0.822	**0.830**

The best performance achieved a higher average Dice score of **0.830** using both Y-Net with the original AMONuSeg and FD-Net with the StainGAN pre-processed dataset..

Conclusion

In conclusion, our findings suggest that despite employing stain normalization techniques, spectral feature extraction encoder, and ViT-based models, the segmentation of nuclei was not be improved due to the different levels of granularity and the small size of nuclei in H&E-stained histopathology images.

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