

## Research Article

# GCP-Net: A Gating Context-Aware Pooling Network for Cervical Cell Nuclei Segmentation

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DVM[hW \$\* < gSk \$" \$\$-DVM[eW \$# 8VWdgSk \$" \$\$-3UWmfW \$\$? SdLZ \$" \$\$-BgT[eZW + 3bd^\$" \$\$

Academic Editor: Jinan Fiaidhi

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Accurate segmentation of cervical nuclei is an essential step in the early diagnosis of cervical cancer. Still, there are few studies on the segmentation of clustered nuclei in clusters of cells. Because of the complexities of high cell overlap, blurred nuclei boundaries, and clustered cells, the accurate segmentation of clustered nuclei remains a pressing challenge. In this paper, we purposefully propose a GCP-Net deep learning network to handle the challenging cervical cluster cell images. The proposed U-Net-based GCP-Net consists of a pretrained ResNet-34 model as encoder, a Gating Context-aware Pooling (GCP) module, and a modified decoder. The GCP module is the primary building block of the network to improve the quality of feature learning. It allows the GCP-Net to refine details of feature maps leveraging multiscale context gating and Global Context Attention for the spatial and texture dependencies. The decoder block including Global Context Attention- (GCA-) Residual Block helps build long-range dependencies and global context interaction in the decoder to refine the predicted masks. We conducted extensive comparative experiments with seven existing models on our ClusteredCell dataset and three typical medical image datasets, respectively. The experimental results showed that the GCP-Net obtained promising results on three evaluation metrics AJI, Dice, and PQ, demonstrating the superiorities and generalizability of our GCP-Net for automatic medical image segmentation in comparison with some SOAT baselines.

## 1. Introduction

Cervical cancer is the fourth most common cancer among women worldwide [1]. According to data from the Global Cancer Observatory (GCO) in 2018, there were an estimated 570,000 new cases and 311,000 deaths due to cervical cancer [2]. According to the latest data from GCO, it estimates that there will be 604,127 new cases of cervical cancer in 2020. Therefore, early detection of cervical lesions is of great significance in reducing cervical cancer mortality. Cervical routine Pap smear or liquid-based cytology (LBC) [3] is the most popular screening method for preventing and early detection of cervical cancer. It has been widely used and has dramatically reduced its incidence and deaths [4]. However, most countries' existing leading smear screening technology still

uses manual reading, which is very troublesome and prone to human error [5]. Therefore, in the past few decades, much research has been devoted to creating a computer-aided reading system based on automatic image analysis [6]. This system automatically selects potential abnormal cells in a given cervical cytology specimen, and finally, the cytopathologist completes the classification. This task includes three steps: cell (cytoplasm and nucleus) segmentation, feature extraction/selection, and cell classification. Precise cell nucleus segmentation is a prerequisite and indispensable part of the computer-assisted analysis of cervical cells and diagnostic decisions.

Some previous conventional methods [7–10] focused on segmenting overlapping nuclei, but they generally used some indirect processing methods. In addition, some ways [11, 12]



























