Page2：

Automatic cell segmentation is an essential step in the pipeline of computer-aided diagnosis (CAD), such as the detection and grading of breast cancer. In this paper, we propose an Attention Enforced Network (AENet), which is built on spatial attention module and channel attention module, to integrate local features with global dependencies and weight effective channels adaptively. Besides, we introduce a feature fusion branch to bridge high-level and low-level features. Finally, the marker controlled watershed algorithm is applied to post-process the predicted segmentation maps for reducing the fragmented regions. In the test stage, we present an individual color normalization method to deal with the stain variation problem. We evaluate this model on the MoNuSeg dataset. The quantitative comparisons against several prior methods demonstrate the priority of our approach.

Page3：

The proposed network utilizes VGG16 as the backbone to extract features. We take the image I as the input of VGG16. The output is a set of feature maps f_1 and a feature vector v_1. After the feature maps f_1 is fed into spatial attention module, decoder module and channel attention module successively, the low-level features f_{low} extracted from the input image I and the high-level features f_{high} obtained from VGG16 will be combined to get more location and global information. In addition, marker controlled watershed algorithm is applied to post-process the predicted semantic segmentation maps aimed at reducing the fragmented regions.

The spatial attention module is employed to obtain non-local information, which can fuse local features and global dependencies adaptively. The channel attention module is applied to weight useful feature maps adaptively.

Page4：

We evaluate our method on MoNuSeg. It is initially used in [2], composed of 30 images, each with size 1000*1000. These images are taken from seven organs: 6 of breast, 6 of liver, 6 of kidney, 6 of prostate, 2 of bladder, 2 of colon and 2 of stomach, with annotations of 21623 individual nuclei.

We split the dataset into training set, same organ test set (ST) and different organ test set (DT).

Page5：

To make our method more convincing, we compare the proposed network against general segmentation frameworks: Fcn, Unet, FPN, PSPNet and SegNet.

As represented in the tables, our method achieves better results than others. PSPNet and SegNet performs poorly on ST, and FPN beats them by a fairly large margin. But for DT, SegNet perfroms well. Notably, Unet outperforms FPN by an increase of 1.8% and 2.9% for ST and DT with respet to the score of dice, respectively. Compared to Unet, the performance of Fcn for ST is qualitatively similar.

However, for DT, Fcn achieves an improvement of 2.9% for F1-score. Moreover, for both ST and DT, our method can achieve the highest scores of accuracy, F1-score, dice and mIoU, compared to other methods. It is worth mentioning that our method outperforms Fcn by 2.8% and 2.9% on ST and DT with respect to accuracy respectively.

Page6：

In this paper, we present a deep convolutional network (AENet) for cell segmentation in multi-tissue pathology images. The proposed network employs two attention modules and a feature fusion

branch. Marker controlled watershed algorithm follows to post-process the predicted segmentation maps, which can reduce the noise obviously. In addition, we report the effect of individual color normalization and multi-scale inference. The result shows that our approach outperforms other prior methods and demonstrates the ability of our model to generalize well on the images from unseen tissues.