

# Spot Nuclei. Speed Cures

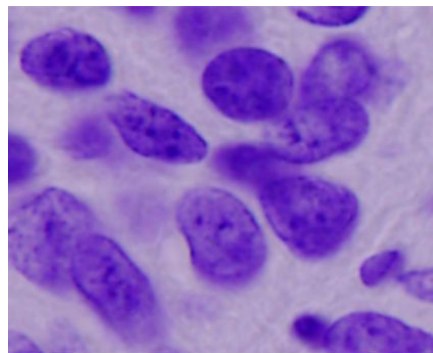
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# Outline

- Introduction
- Dataset
- Approaches
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  - CNN
  - Post-processing
- Results
- Future work

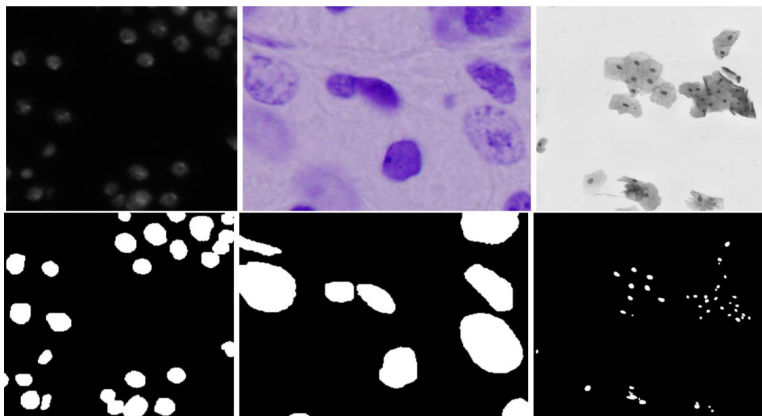
# Introduction

- Identifying the nuclei of cells is the starting point for most medical analyses
- It allows researchers to locate each individual cell and understand the underlying biological processes
- It costs considerable time and effort for human researchers to label the cells
- Our goal is to advance medical discovery by automating the identification of nuclei in diverse images

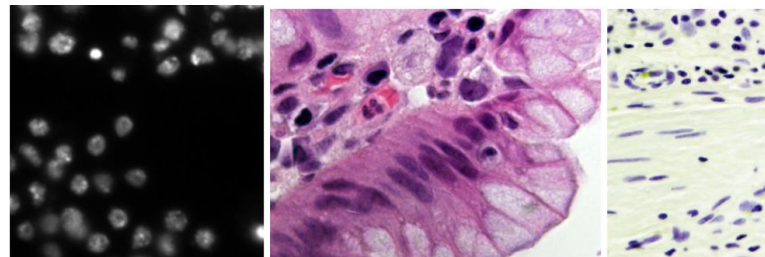


# Dataset

- Kaggle 2018 Data Science Bowl
- 670 training images with 29462 segmentation masks
- 65 testing images with no ground truth
- Each image has different size

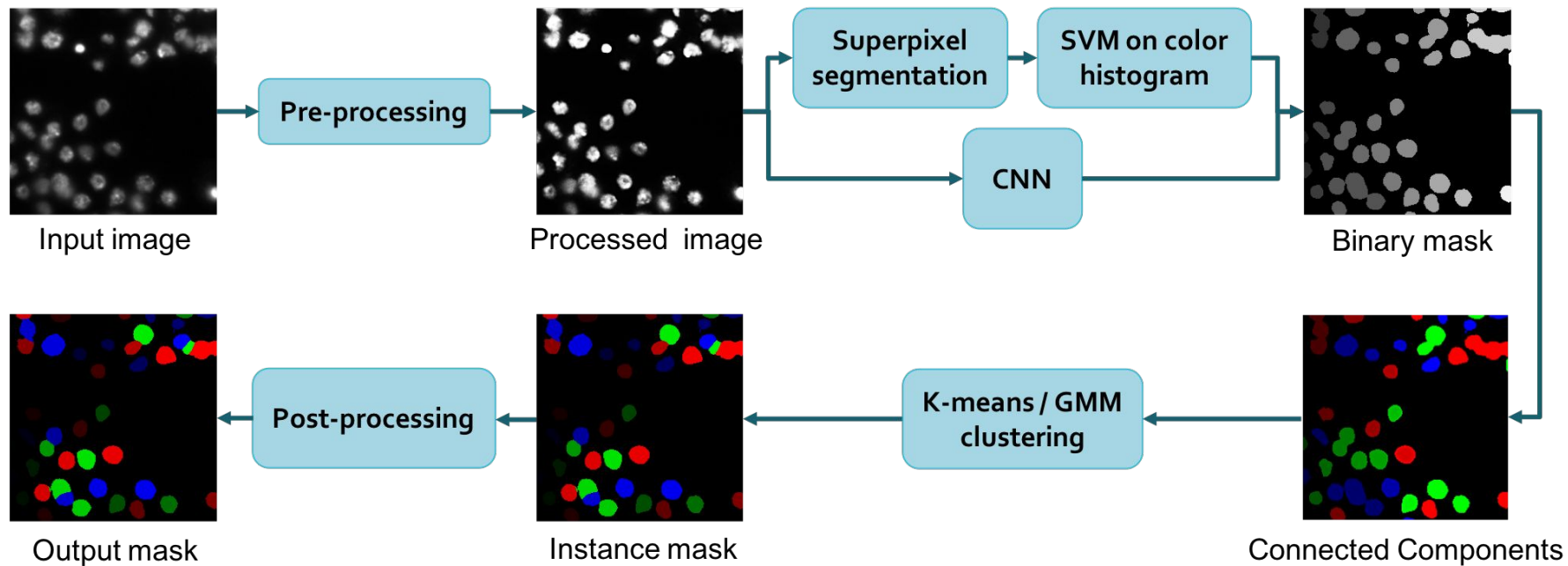


Example training images



Example testing images

# Framework overview

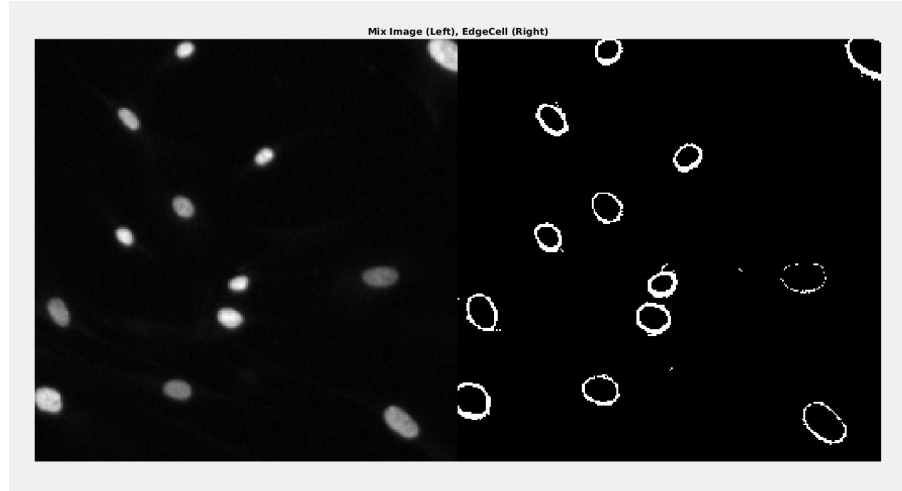


# Approaches -- Pre-processing

- Several types of input images, such as RGB, grayscale and HSV are experimented
- Pre-classify the source of the image into sub-classes
- Histogram equalization
- Different input sizes (128 - 512)

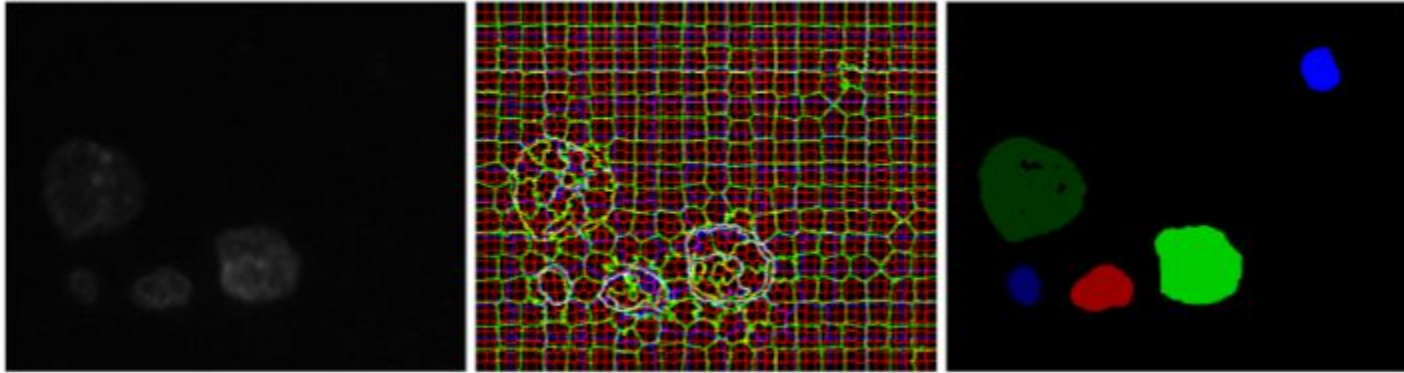
# Approaches -- Physical Method

- Treat the whole image itself as a distribution of light. Employ the intensity and gradient as features to capture cells.



Original Image in Grayscale (Left) ; Features to Capture Cells (Right)

# Approaches -- Computer Vision Method

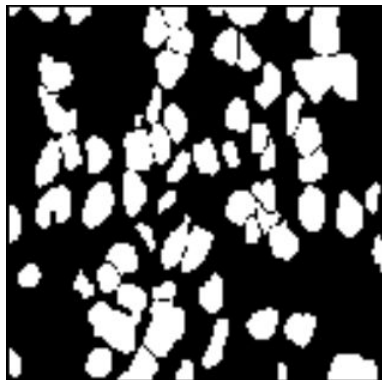


Qualitative result of superpixel segmentation with SVM classification and GMM clustering. The input image, superpixel segmentation at multiple scale, and the predicted mask are shown from left to right.

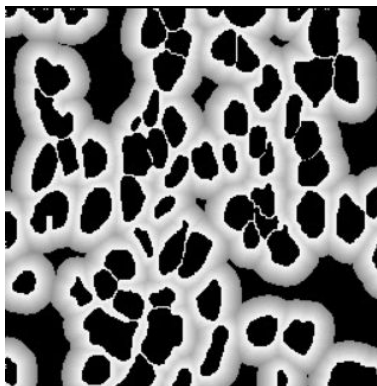


# Approaches -- CNN

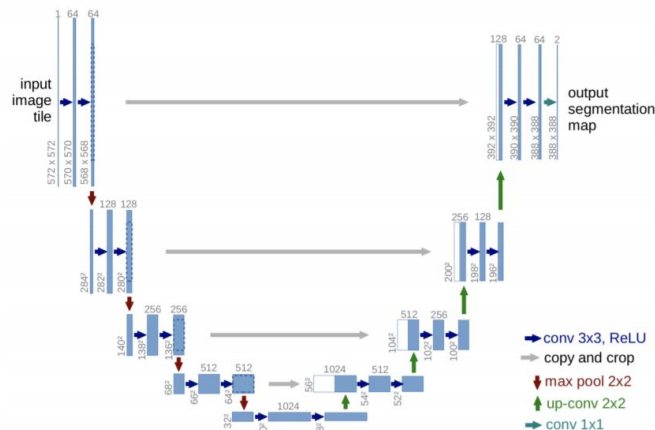
- UNet is designed for biomedical image segmentation, where the precision of mask boundary is critical
- Prediction error at the boundaries are heavily penalized
- We found that changing the input size and post processing works better



Ground truth



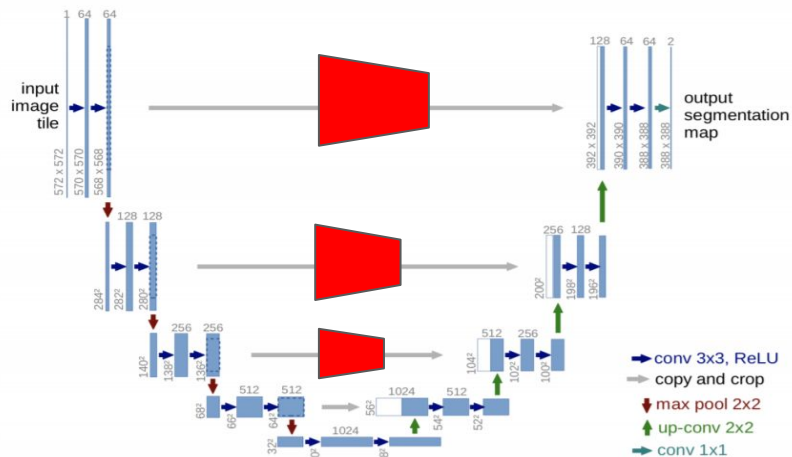
Weighted penalty



UNet architecture

# Approaches -- CNN

- Modified UNet architecture
- Instead of concatenating the upsampled feature map with original feature map, an extra 'high way' path is provided
- The pooling layer is also replaced by convolution layer with larger stride
- This improves the accuracy by 6%

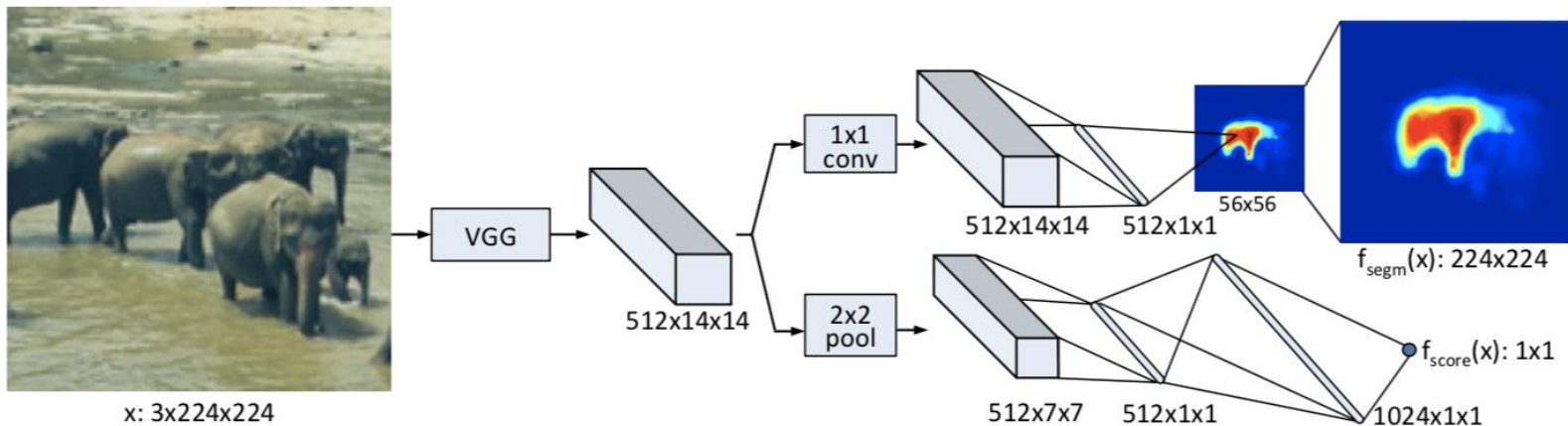


Convolution layers

# Approaches -- CNN (DeepMask/SharpMask)

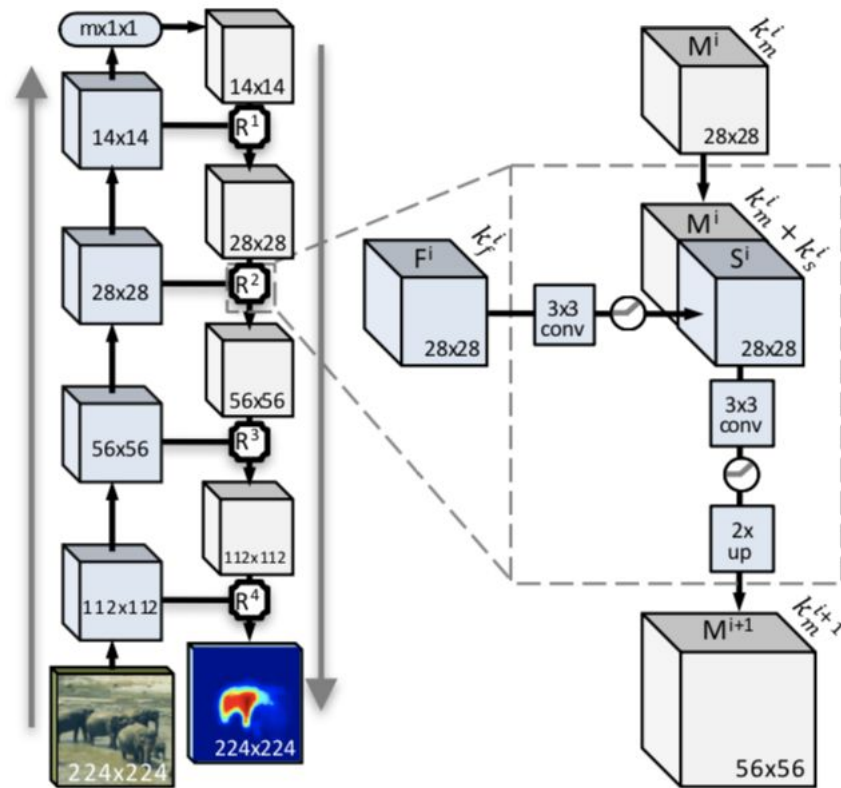
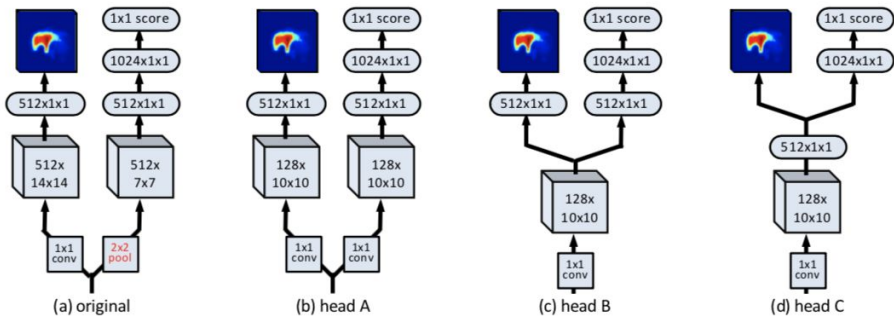
- DeepMask

- Introduced by FAIR (Facebook AI Research)
- Two outputs (Score, Mask)



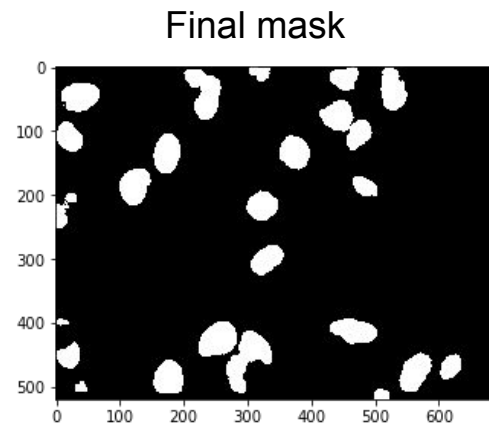
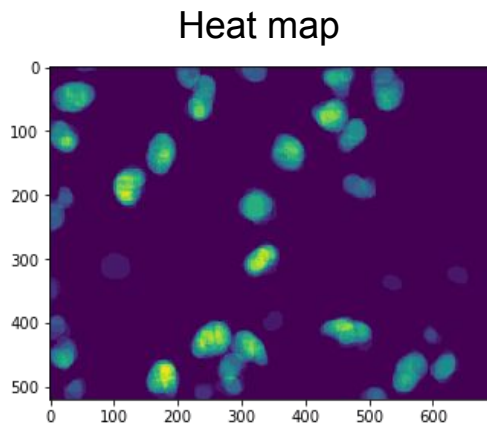
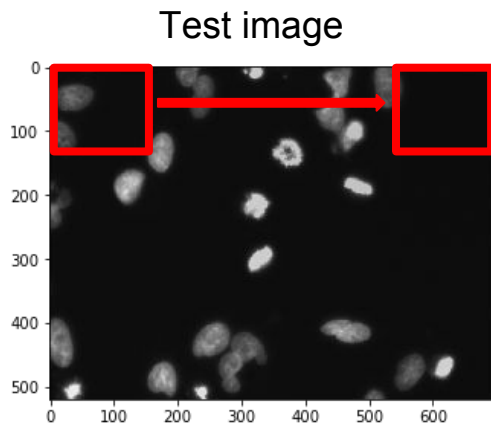
# Approaches -- CNN (DeepMask/SharpMask)

- SharpMask
- Inherited from DeepMask
- Use Resnet instead of VGG
- Additional refinement module
- Experiment different head options



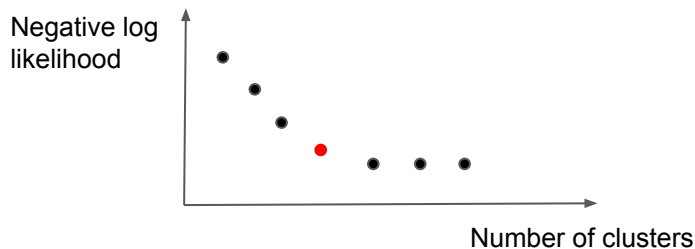
# Approaches -- CNN (DeepMask/SharpMask)

- Inference stage
- Sliding window
- Masks with high scores → Heat map



# Approaches -- Post-processing

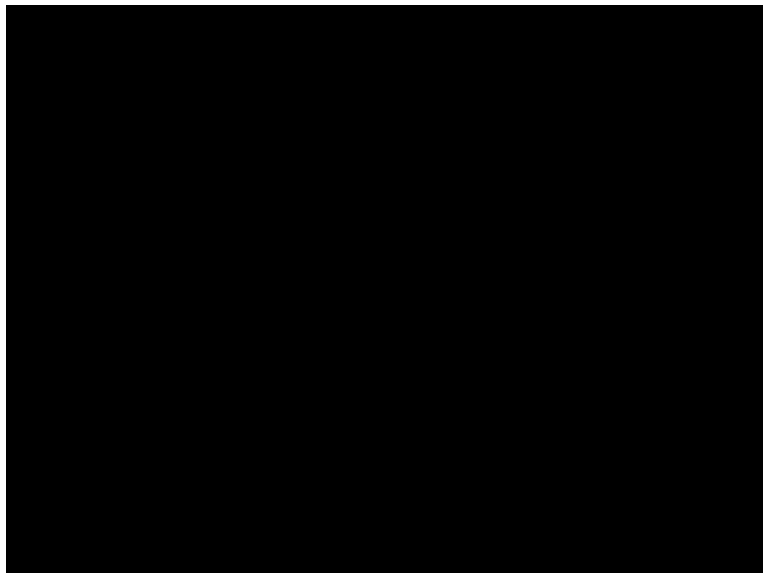
- Fill the holes in each connected components
- Gaussian Mixture Model (GMM) clustering
  - The number of clusters is determined by **log likelihood thresholding** and the “**elbow method**”



- Remove the instances with irregular size and shape
- Ensemble method
  - Collect result from several models
  - Every pixel is voted and the majority rule is applied

# Current Results

- Top 12% in current Kaggle leaderboard



Approaches	mAP
FCN	0.315
U-Net	0.340
U-Net + GMM	<b>0.392</b>
U-Net + K-means	0.307
Superspixel + SVM	0.237
Physical model + Bayesian	0.234
DeepMask/SharpMask	0.170
Model ensemble	0.392
Model ensemble + GMM	<b>0.413</b>

# Future work

- Implement architecture that includes both detection and segmentation, such as mask RCNN
- Figure out how a cell nucleus is defined, and then modify the formulation(s) to improve the models