Differentiating Tumor cells from healthy cells using CNNs

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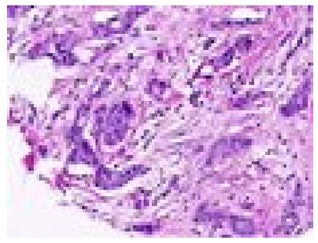
Motivation and Introduction

- Develop deep-learning models that can assist pathologists in examining cancerous tissue biopsies.
- Allow doctors to more easily gauge the progress of diseases.
- Previous work has included feature-based approaches.
- Our models will instead work on the raw pixels.

Data

- 168 H&E stained histological images of breast cancer TMAs.
- Each image has a corresponding labeled image.
- Green = healthy cells, red = tumor cells, black = background/unclassified



Sample biopsy

Corresponding labeled image

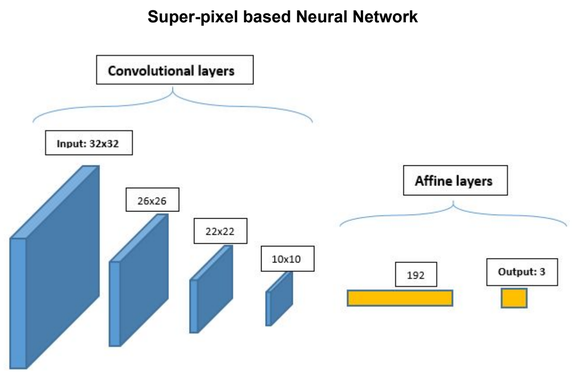
Approach

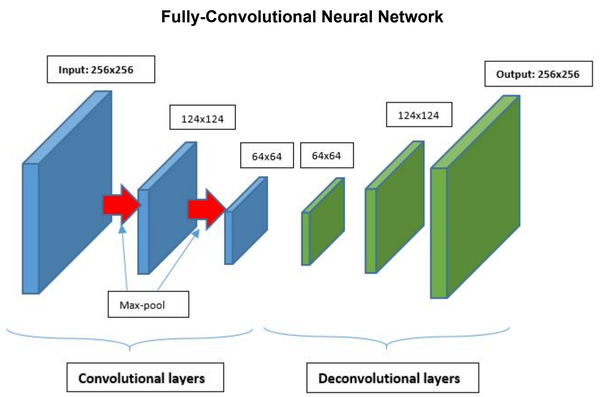
Our approach can be broadly divided into the following;

1. Super-pixel based approach:
   a. Divide each image into small crops of size 32*32 and 16*16.
   b. Assign a label ϵ {0, 1, 2} to each of these superpixels based on the color of the majority of the constituent pixels, where 0, 1, 2 correspond to Red, Green and Black respectively.
   c. Train different CNN models consisting of conv, pool and FC layers.

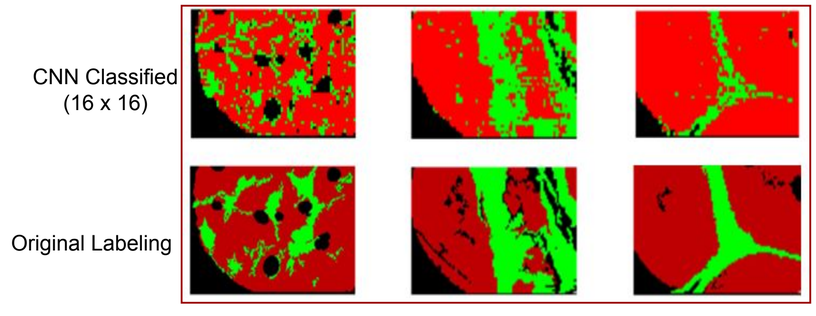
2. Per-pixel approach (Using Fully Convolutional Networks):
   a. Divide each image into crops of spatial size 256*256, to reduce the number of parameters in the network.
   b. Create pixel wise label masks for these images.
   c. Train FCNs consisting of conv, pool and deconv layers. Batchnorm after each conv/deconv

Models

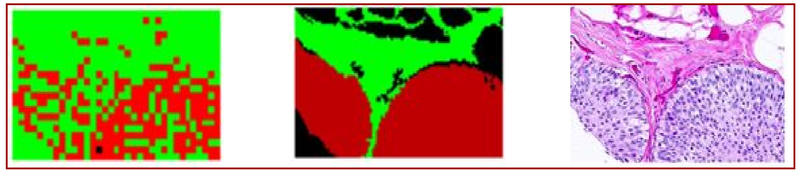




Results and Discussion



Misclassified sample



	Fully Convolutional	Super Pixel based NN 16x16	Super Pixel based NN 32x32
Training	68.2%	67.3 %	87.2%
Validation	65.2%	76.7 %	65.4%
Test	66%	71 %	61.2%

Challenges:

1. 32x32 conv net may have overfitted.
2. Background/Black pixels still not classified correctly.
3. Non-symmetric FCN architecture.

Future Work

- Try using a deeper architecture for our FCN
- Use state of the art models e.g. AlexNet
- Network visualization

References

1. Beck, Andrew H., et al. "Systematic analysis of breast cancer morphology uncovers stromal features associated with survival." *Science translational medicine* 3.108 (2011): 108ra113-108ra113.
2. Long, Jonathan, Evan Shelhamer, and Trevor Darrell. "Fully convolutional networks for semantic segmentation." *Proceedings of the IEEE Conference on Computer Vision and Pattern Recognition*. 2015.
3. Noh, Hyeonwoo, Seunghoon Hong, and Bohyung Han. "Learning deconvolution network for semantic segmentation." *Proceedings of the IEEE International Conference on Computer Vision*. 2015.