DEEP LEARNING BASED CANCER METASTASES DETECTION

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TASKS

- **Training and Evaluation**
  - 110 tumor slides
  - 160 normal slides
  - 130 evaluation slides

- **1st Task**
  - Whole slide level prediction
  - *Binary classification problem*

- **2nd Task**
  - Find metastasis location
  - *Segmentation problem*
SEVERAL ESSENTIAL COMPONENTS

• Network architecture

• Training set construction

• Computing environment

• Post-processing for classification and segmentation
We compared several networks

- **GoogLeNet (Szegedy et al. ILSCV 2014):** 98.4%
- **VGG16 (Simonyan and Zisserman):** 97.9%
- **FaceNet (Wang et al. 2015):** 96.8%
- **AlexNet (Krizhevsky et al. NIPS 2012):** 92.1%

Details of GoogLeNet

- 27 layers in total
- ~6 million parameters
- three loss layers
- Christian Szegedy et al. Going Deeper with Convolutions
TRAINING SET CONSTRUCTION

• Preprocessing
  • Tissue region segmentation (Otsu’s method of foreground segmentation)
  • Remove 82% of WSI region on average
TRAINING SET CONSTRUCTION

• Step 1:
  • Randomly extract patches (256 x 256) on the tissue region
    • Tumor slide: 1K positive and 1K negative from each slide
    • Normal slide: 1K negative from each slide
    • ~290K training patches

• Step 2:
  • Make predictions and construct heatmaps
  • Extract additional ~60K training patches from false positive regions
  • 290K + 60K = 350K training patches in total
**PATCH EXTRACTION AT 40X**

- We evaluate performance with patch extraction at several magnifications
  - Experimental results indicate that 40x is the best

Example patches of size 256 x 256 with 40x, 20x and 10x magnification

Normal Slide, ID: 001
DATA AUGMENTATION

• Randomly crop a 224 x 224 sub-region and flip patches horizontally

or
• Deep model is trained from scratch using mini-batch SGD

Environment
• GPU:
  • 2 x NVidia Tesla K80 graphics cards
• CPU:
  • Intel ® Xeon® CPU E5-2620 v3 @ 2.40GHz
  • #cores=12
• Hard Disk:
  • 4T SSD
• Memory:
  • 64 GB RAM
TUMOR PROBABILITY
HEATMAP GENERATION

Visualization

Heatmap
POST-PROCESSING FOR SLIDE-BASED TUMOR CLASSIFICATION

• Extracting higher level features from tumor heatmaps
  • the percentage of tumor region over the whole tissue region
  • the area ratio between tumor region and the minimum surrounding convex region
  • the average prediction values
  • the longest axis of the tumor region
  • ……

28-dim feature vector
Random Forest Classifier (#tree = 50)

Tumor
Normal
Top 5 important features, computed using the “regionprops” function in skimage. $t$ is the threshold value

- **Feature 10**: given $t=0.5$, the longest axis in the largest tumor region
- **Feature 09**: given $t=0.5$, ratio of pixels in the region to pixels in the total bounding box (“extent”)
- **Feature 08**: eccentricity of the ellipse that has the same second–moments as the region. (“eccentricity”)
- **Feature 04**: ratio of tumor region when $t=0.9$ to the tissue region
- **Feature 05**: given $t = 0.5$, the area of largest tumor region
POST-PROCESSING FOR LESION-BASED TUMOR REGION SEGMENTATION

• Train a sensitive model (D-1) for estimation of tumor location (threshold = 0.9)

• Train a more specific model (D-2) for tumor probability estimation
  • ~30K extra training patches extracted from normal area adjacent to tumor region
LESION-BASED TUMOR REGION SEGMENTATION

- Generate the locations using H-1

- Use central point as the tumor position

- Largest region, label = 74

- (x, y) positions
LESION-BASED TUMOR REGION SEGMENTATION

- Generate the prediction value using H-1 and H-2

(x, y) positions Based on H-1

Region mask

H-1

sum of heatmap over the mask

v1

v=(v1+v2)/2

H-2

v2
CONCLUSIONS

• We developed a deep learning based framework for metastatic cancer detection in lymph nodes
  
  • **Architecture**: Based on GoogLeNet
  
  • **Training**: Additional training patches from false positive and tumor adjacent regions
  
  • **Post-processing**:
    
    • Random forest classifier on heatmap-based features for classification task
    
    • Integration of a more sensitive (for tumor location) and more specific (for tumor probability) model for segmentation task