SlideSeg: A Python Module for the Creation of Annotated Image Repositories From Whole Slide Images

Brendan Crabb[a] and Niels Olson[b,c]

[a] SSC Pacific, 53560 Hull St, San Diego, CA 92152
[b] Naval Hospital Camp Pendleton, 200 Mercy Cir, Oceanside, CA 92055
[c] Naval Medical Center, 34800 Bob Wilson Dr., San Diego, CA 92134

INTRODUCTION

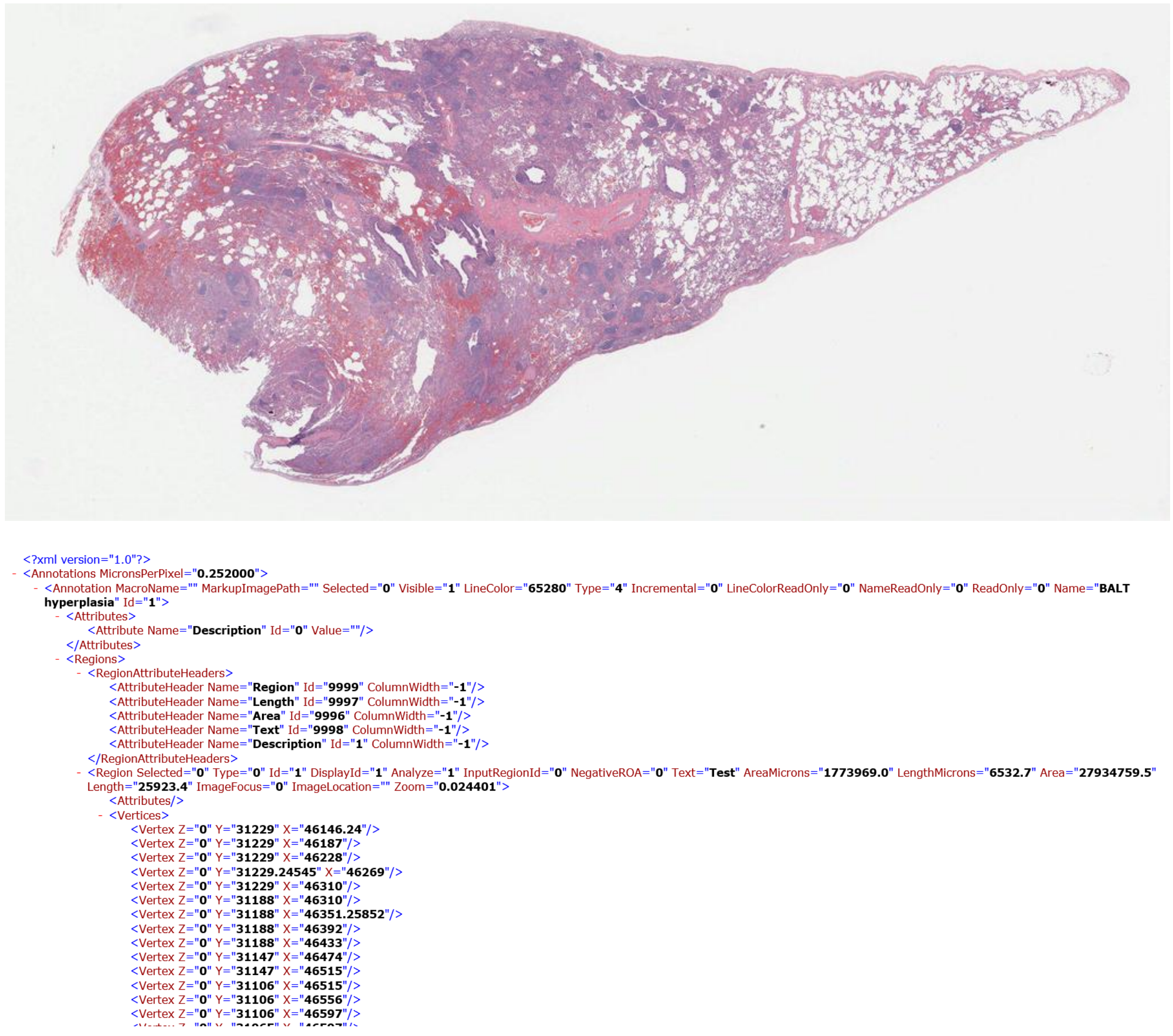
Convolutional neural networks have driven advances in computer vision tasks such as object recognition and whole-image classification; however, more recent approaches have focused on dense prediction tasks, such as semantic segmentation, in which each pixel is labeled with the class of its enclosing object.[1] To train deep learning networks for semantic segmentation, large datasets of accurately labeled ground truth data are required; however, in the area of digital pathology, whole slide images are often on the scale of 10+ gigapixels when digitized at 40X magnification, contain multiple magnification levels, and have unstandardized formats.[2,3] Due to these characteristics, traditional techniques for the production of training and validation data cannot be used, resulting in the limited availability of annotated datasets for deep learning in digital pathology. This research presents a Python module and method to rapidly produce accurately annotated image patches from whole slide images.

METHODS

SlideSeg was developed on Python 2.7 and is built on several open source libraries including NumPy, OpenCV, and OpenSlide. The SlideSeg module is built to ingest a folder of annotated whole slide images. An example whole slide image, along with it's associated annotations, can be seen in Fig. 2. The user can specify several parameters, including output patch size, quality, and format. Furthermore, the pixel values for each semantic label can be viewed and specified in the annotation key, which can be seen in Fig. 1.

```
Key: AIR DRIED                              Mask_Color: [255]
Key: ARTERIES                               Mask_Color: [254]
Key: BLOOD VESSEL                           Mask_Color: [253]
Key: CALCIFICATION                          Mask_Color: [252]
Key: CORPORA AMYLACEA                       Mask_Color: [251]
Key: CRYSTALLOID                            Mask_Color: [250]
Key: EPE                                    Mask_Color: [249]
Key: FAT                                    Mask_Color: [248]
Key: INFLAMMATION                           Mask_Color: [247]
Key: INK                                    Mask_Color: [246]
Key: LEIOMYOMA                              Mask_Color: [245]
Key: MARKING INK                            Mask_Color: [244]
Key: NERVE                                  Mask_Color: [243]
```

Fig. 1. The annotation key, which specifies the semantic labels for each annotation in the XML metadata file.



```
<?xml version="1.0"?>
- <Annotations MicronsPerPixel="0.252000">
  - <Annotation MacroName="" MarkupImagePath="" Selected="0" Visible="1" LineColor="65280" Type="4" Incremental="0" LineColorReadOnly="0" NameReadOnly="0" ReadOnly="0" Name="BALT
    hyperplasia" Id="1">
    - <Attributes>
        <Attribute Name="Description" Id="0" Value=""/>
      </Attributes>
    - <Regions>
      - <RegionAttributeHeaders>
          <AttributeHeader Name="Region" Id="9999" ColumnWidth="-1"/>
          <AttributeHeader Name="Length" Id="9997" ColumnWidth="-1"/>
          <AttributeHeader Name="Area" Id="9996" ColumnWidth="-1"/>
          <AttributeHeader Name="Text" Id="9998" ColumnWidth="-1"/>
          <AttributeHeader Name="Description" Id="1" ColumnWidth="-1"/>
        </RegionAttributeHeaders>
      - <Region Selected="0" Type="0" Id="1" DisplayId="1" Analyze="1" InputRegionId="0" NegativeROA="0" Text="Test" AreaMicrons="1773969.0" LengthMicrons="6532.7" Area="27934759.5"
        Length="25923.4" ImageFocus="0" ImageLocation="" Zoom="0.024401">
          <Attributes/>
        - <Vertices>
            <Vertex Z="0" Y="31229" X="46146.24"/>
            <Vertex Z="0" Y="31229" X="46187"/>
            <Vertex Z="0" Y="31229" X="46228"/>
            <Vertex Z="0" Y="31229.24545" X="46269"/>
            <Vertex Z="0" Y="31229" X="46310"/>
            <Vertex Z="0" Y="31188" X="46310"/>
            <Vertex Z="0" Y="31188" X="46351.25852"/>
            <Vertex Z="0" Y="31188" X="46392"/>
            <Vertex Z="0" Y="31188" X="46433"/>
            <Vertex Z="0" Y="31147" X="46474"/>
            <Vertex Z="0" Y="31147" X="46515"/>
            <Vertex Z="0" Y="31106" X="46515"/>
            <Vertex Z="0" Y="31106" X="46556"/>
            <Vertex Z="0" Y="31106" X="46597"/>
```

Fig. 2. A whole slide image (top) with a pathologist's annotations in an associated XML file (bottom).

Step 1: SlideSeg uses OpenCV and the annotation key to generate a multidimensional NumPy array of annotations contained in the XML metadata file.

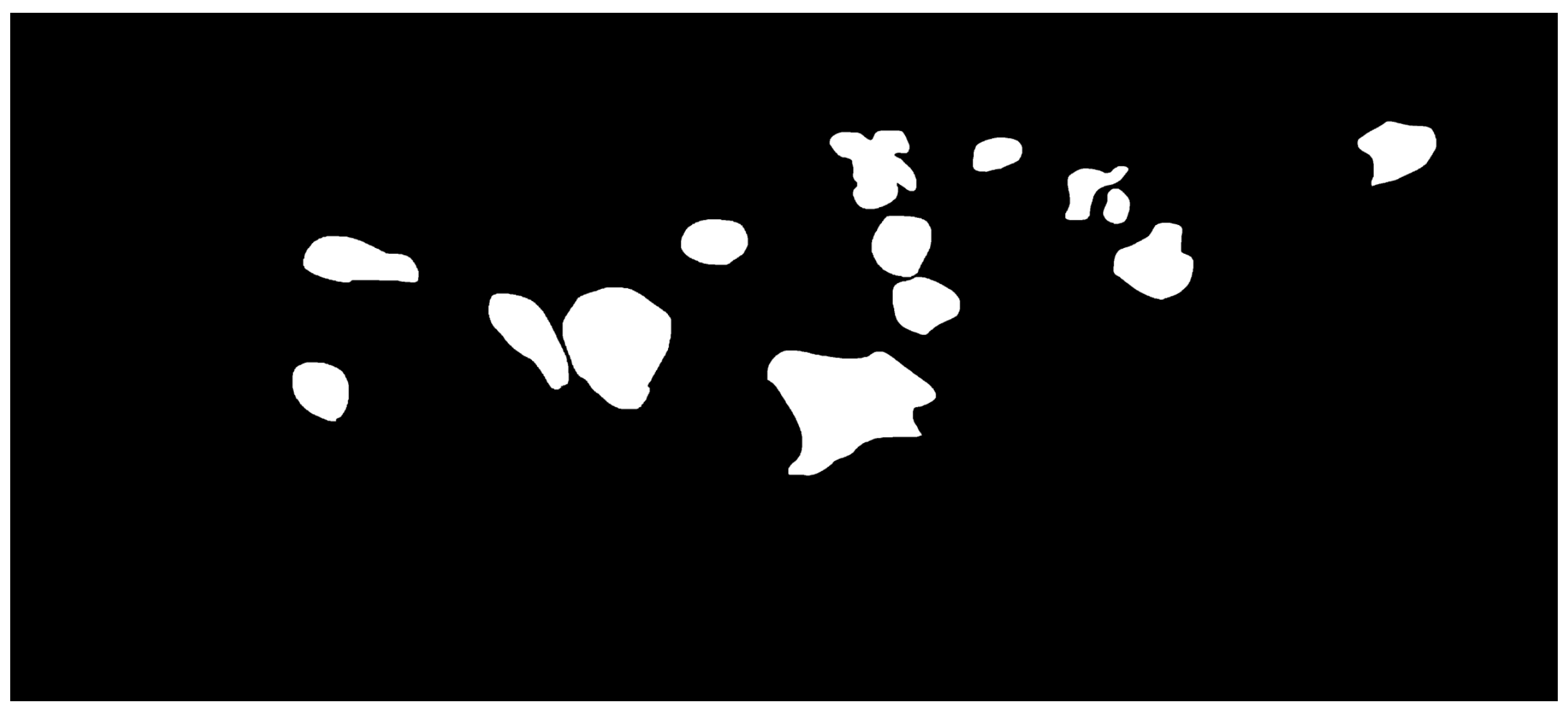


Fig. 3. The intermediate annotation mask generated by SlideSeg for each whole slide image.

Step 2: Image patches and annotation masks are generated and saved according to the user's specified parameters.

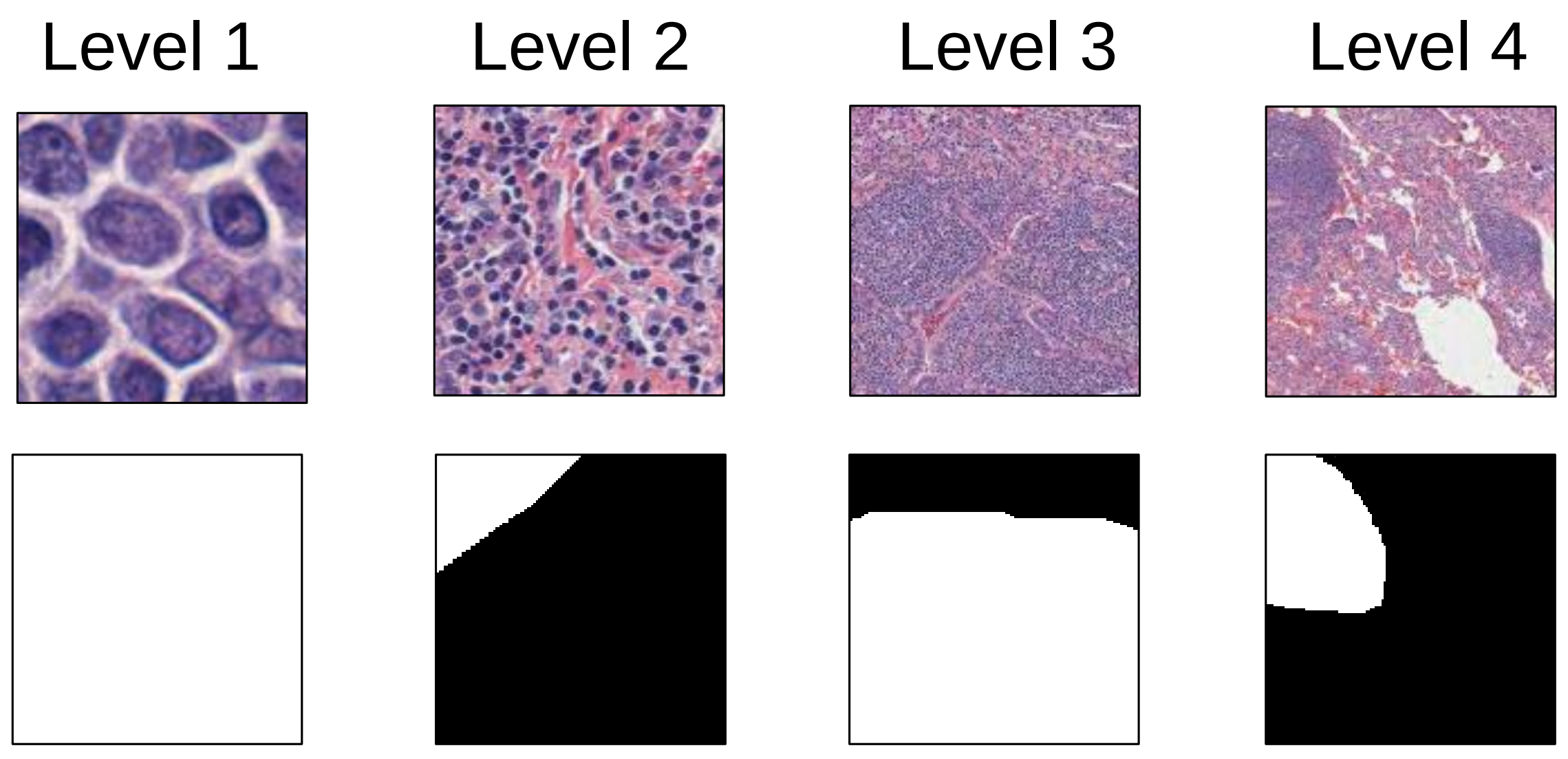


Fig. 4. Example image patches (250 x 250 pixels) and associated masks produced by SlideSeg for each magnification level in the whole slide image.

RESULTS

SlideSeg successfully produces image patches with semantic labeling from annotated whole slide images, as shown in Fig. 4. For an example image with annotated regions of lung malignancies, 28,000 image patches containing annotations, along with their associated image masks, were generated and saved in approximately twenty five minutes. These patches can be used to train a deep neural network for pixel-wise classification tasks, as shown in Fig. 5.

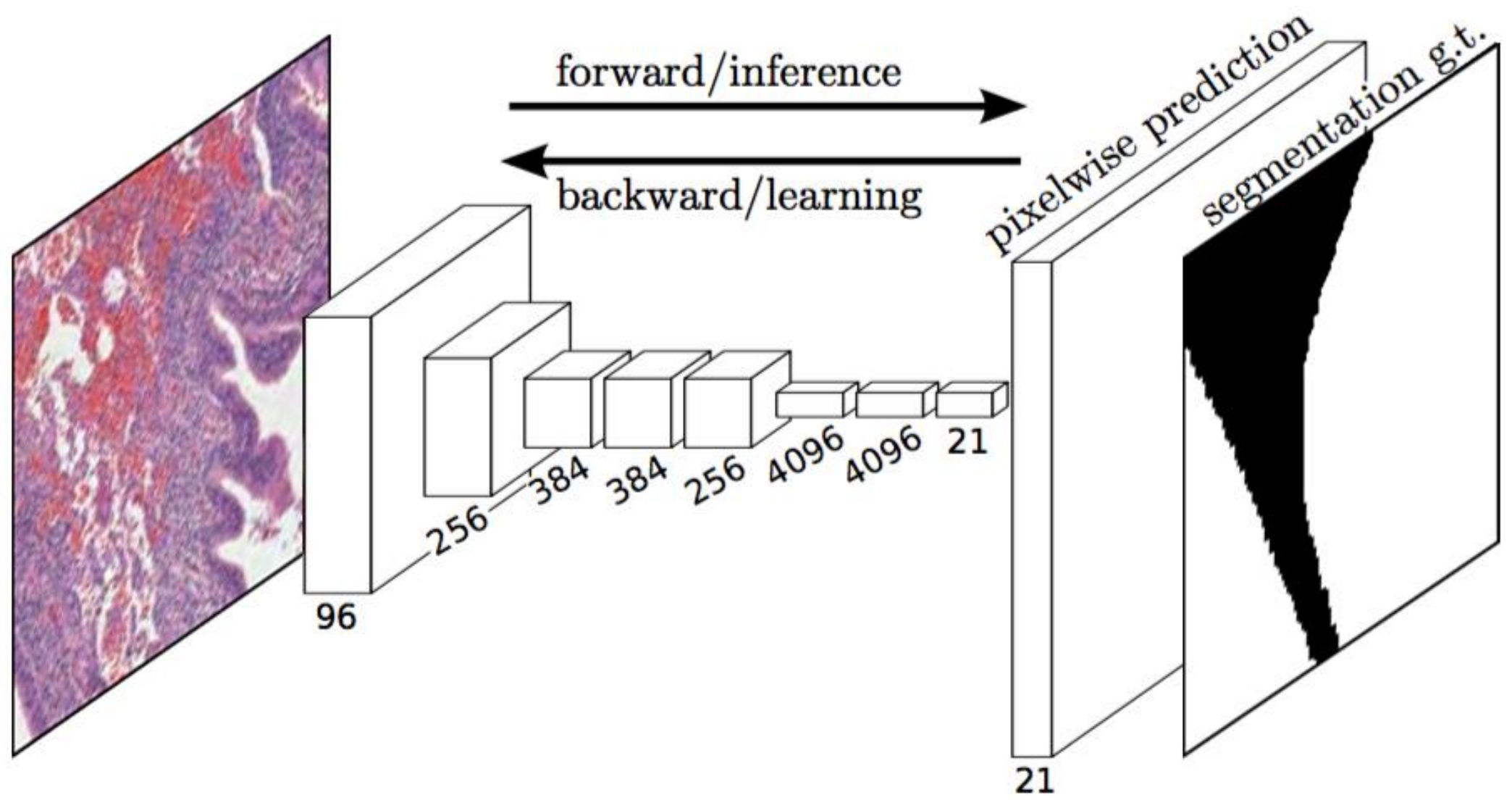


Fig. 5. Using the image patches and masks from SlideSeg to train a deep neural network.

DISCUSSION

This publicly available module overcomes the challenges of whole slide images, such as file size and format variability, and produces 'ground truth' image repositories from whole slide images for deep learning applications in digital pathology. This much needed functionality will allow research labs and clinics to use semantic segmentation, and other dense prediction methods, to detect and diagnose malignancies in whole slide images. Currently, the quality of the annotation masks produced by SlideSeg are limited by the quality of the original delineation of cancer regions by a pathologist using whole slide viewing software. Future work will focus on enabling SlideSeg to utilize GPU capabilities and parallel processing.

REFERENCES

1. Long, J., Shelhamer, E., and Darrell, T., "Fully convolutional networks for semantic segmentation," CVPR (2015).
2. Ghaznavi, F., et. al., "Digital imaging in pathology: whole-slide imaging and beyond," Annual Review of Pathology: Mechanisms of Disease 8, 331-59 (2013).
3. Farahani, N., et. al., "Whole slide imaging in pathology: advantages, limitations, and emerging perspectives," Pathology and Laboratory Med. Int. 7, 23-33 (2015).

The complete SlideSeg project can be found at https://github.com/btcrabb/SlideSeg