

Camelyon17 challenge

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Model. Our approach uses three Deeplab(1) models trained on three different resolutions: 0.5, 1 and 2 micrometer per pixels (mpp). They are combined in a graph structure as described in (2). The model is trained to predict cancerous areas at pixel resolution. The segmentation is then used to predict the slide's largest tumor type (Normal, ITC, Micro or Macro) using a random forest on hand-crafted features. Finally, the pN-stage for each patient is computed according to the rules.

Training the segmentation model. We used all the annotated slides from camelyon16 and camelyon17 for training. We used an otsu threshold to identify tissue areas and remove the background. We extracted 512×512 shaped patches from those tissue region. They were augmented using rotation, color jittering and elastic deformation. After each epoch, we performed an hard example mining procedure to focus the training on the most difficult patches. The training was done on 50 epochs.

pN-Stage prediction. We extracted the cancer probability maps using the segmentation model at a resolution of 8mpp. For each slide we extracted the diameter, area, mean value and max value of the largest tumor after applying a dilation filter on the probability map with a size of 250 micrometers followed with an erosion of the same size, at the threshold of 0.5. These 4 features were used as the input of a random forest classifier trained to predict the largest tumor type per slide. The pN-stage was then inferred using the rules.

Bibliography

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