

# Camelyon17 challenge

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## Model

In the CAMELYON17 challenge the objective is to make a patient level prediction based on information from several whole slide images. Our proposed method has two stages. First the tumor segmentation for each slide is computed using a deep convolutional neural network. Secondly, geometrical properties from these segmentation maps are extracted and used as features for a classification model predicting the slide level metastasis grading. Patient level gradings are finally inferred according to the rules.

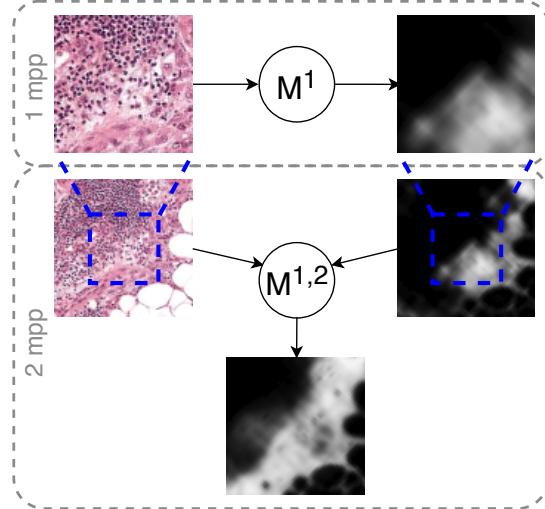
We propose an ensemble approach: we combine several segmentation models learned on different pixel resolutions in a directed acyclic graph (DAG) structure as described in (1) (figure 1). The segmentation model being a pixel wise classification model (as to compare with a patch wise classification model), its output and input are in the same domain, this allows to combine different models together by concatenating the output of one (or several) model to the input of another.

Since we can learn a model on any slide level resolution, this architecture allows integrate the information available from these different levels. It also has the benefits of ensemble learning, we can learn the individual model with different strategies or hyper-parameters inducing different modeling expressiveness that can be integrated in their combination. Another advantage of such approach is that the resources spent to train the models are cumulative. The classical non ensemble approach would spend resources to learn different models in order to choose the best hypothesis among different architectures or hyper parameter sets, and then choose the best candidate and disregard the others. This is resource wise expensive because discarded models only contribute in the choice of the best candidate. In our ensemble approach the models are combined and they contribute by providing statistical information about the joint distribution between pixels and annotation data to another model.

Our approach uses a composition of three Deeplab(2) models trained on three different resolutions: 0.5, 1 and 2 micrometer per pixels (mpp). The model is trained to segment 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

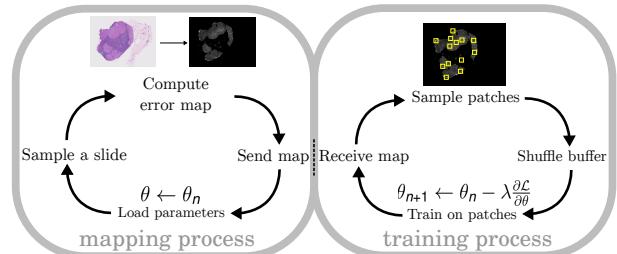
**Dataset.** We used all the annotated slides from camelyon16 and camelyon17 for training.



**Fig. 1.** An illustration of our model compounding principle. A first model  $M^1$  is trained on 1 mpp. A second model  $M^{1,2}$  is trained on 2 mpp by taking the output of  $M^1$  as an extra channel. This principle can be extended to compose any number of model in a directed acyclic graph structure.

**Augmentation.** We augmented the data using rotation, color jittering and elastic deformation as shown in figure ???. This was made on the fly during training, on a separate GPU, and allowed to train the model on a virtually infinite source of data variation.

**Quasi Online Hard Example Mining.** The training pipeline is illustrated on Figure 2. It has two processes running synchronously and in parallel. This allows to perform *quasi online hard example mining* on two levels. First, on the WSI level, the most difficult slides are sampled more frequently. Secondly, within a slide, the model is trained from patches extracted from the most difficult regions.

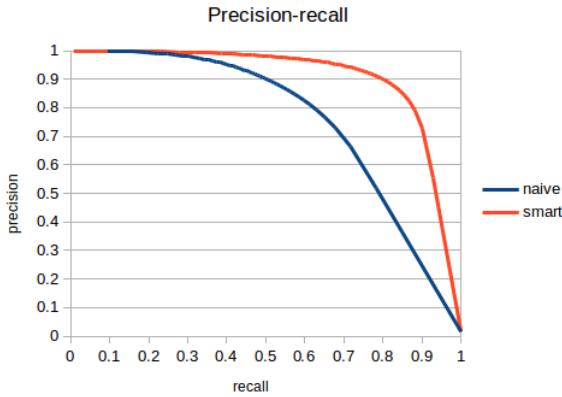


**Fig. 2. Dynamic sampling cycle.** A training process samples patches using an error map that indicates the regions where the model makes the most mistakes. Error maps are computed and provided by a mapping process. Both processes work synchronously and in parallel.

**Slide sampling.** The *mapping process* (Figure 2) chooses the next slide to sample patches from. This is done using a slide level sampling distribution that gives more probability on

slides that contains *greater errors*. This can be designed according to several optimizations strategies. Among them, we used probability distribution that emphasize the optimization of the recall, such that slides on which the model misses many cancer regions are prioritized. Similarly, we used distribution that optimize the slide level grading classification, slides whose segmentation induces wrong grading classification are sampled more often. As a third strategy we used distribution that optimized informedness score of slides. These different strategies allowed to learn models with wider expressivity. This is a desirable property in the context of model ensembling where we want reduced redundancy between models.

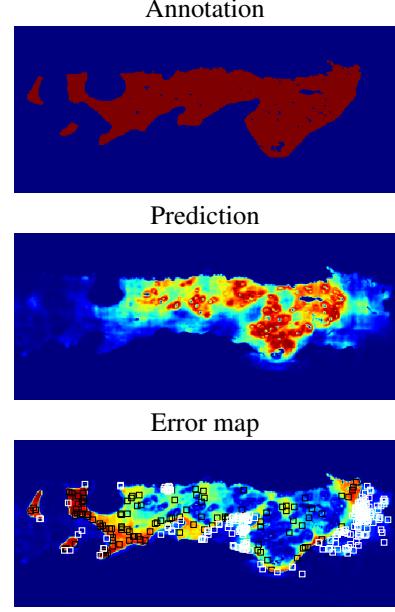
**Patches sampling.** The networks are trained on image patches dynamically sampled from WSIs. It was shown (3, 4) that the patch sampling strategy during training has a great impact on the final performance of the model. The patches of dimension  $512 \times 512$  were sampled from WSIs using a pixel-level probability density function inferred from the error of the model on the pixel-level classification. The figure 4 shows an example of an error region where patches are sampled more often on areas with higher error. This allowed to speed-up the training, because the computational resources were optimized and not used to train on uninformative or trivial regions. This also allowed to improve the accuracy of the model as shown in the figure 3.



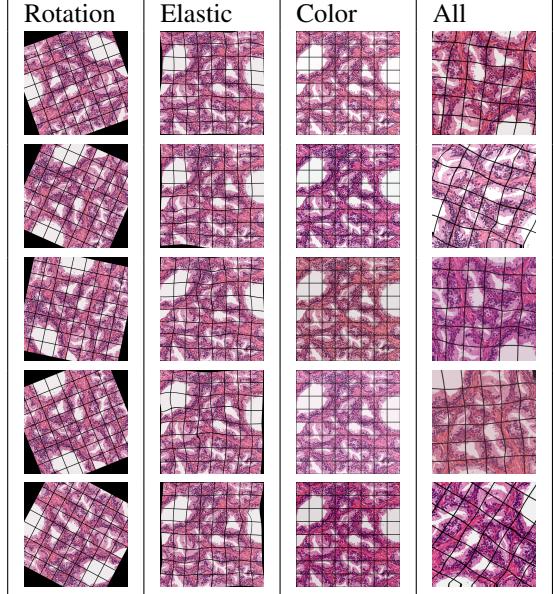
**Fig. 3.** Pixel-wise performances of two segmentation models trained with (*smart*) or without (*naive*) quasi online hard example mining on the Camelyon16 dataset. This shows that training using hard example mining significantly improves the performance of the model.

## 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.



**Fig. 4.** An example of a corresponding annotation mask, prediction heat map and error map. The error map is overlaid with examples of randomly sampled patches for benign (white) and tumor (black) areas. The patches are more likely to be sampled from high error regions.



**Table 1.** Augmentations applied on a patch. An overlaid grid illustrates the deformations.

## Bibliography

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