

# Detecting Cancer Metastases on Gigapixel Pathology Images

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Literature review

## 1. Introduction

In (Liu et al. 2017), the authors proposed a framework to automatically detect and localise local (lymph node) metastatic lesions in gigapixel pathology images, basing their models on the detection framework proposed in (Wang et al. 2016), and the convolutional neural network (CNN) architecture “Inception” (V3) presented in (Szegedy et al. 2015). Moreover, a custom sampling strategy along with different data augmentation techniques were employed to address the imbalanced nature of the used dataset (Camelyon16).

## 2. Methods

### 2.1. Training set sampling

The authors trained their models with 270 pathology slides (images) from the Camelyon16 dataset. Each slide represents H&E-stained (Hematoxylin and Eosin) human lymph node tissue scanned at a magnification of 40X. Given the size of the whole slide images (WSI), each slide was divided into smaller patches.

The number of patches per slide ranged from 10,000 to 400,000 (median 90,000), and tumour slides contained only 20 to 150,000 tumour patches (median 2,000). In order to avoid bias towards slides containing more patches (normal or tumour), the following sampling strategy was adopted: after selecting “normal” or “tumour” with equal probability, a slide containing that class of patches was selected uniformly at random, and then patches were sampled from that slide. Likewise, to mitigate the imbalance between tumour patches and normal ones, different data augmentations were applied on the tumour patches, such as rotations and image flips.

### 2.2. Training

The training was done in two phases: the patch-based classification phase and the heatmap-based inference stage (Wang et al. 2016).

During the patch-based classification phase, the Inception V3 architecture is used, with input patches of size  $299 \times 299$  pixels. For each input patch, the label of the centre  $128 \times 128$  region is considered for prediction. A patch is labelled as tumour if at least one pixel in the centre region is labelled as such. Here, the influence of the number of Inception V3 parameters was investigated, and a multi-scale approach where the models were trained with down-sampled patches of 20X and 10X magnifications was also explored.

Next, inference was performed across the slide in a sliding window with a stride of 128 to match the centre region’s size, thus generating a probability heatmap. The maximum value in the heatmap was reported as the slide-level tumour prediction.

During training, the following approaches were tested but did not yield improvements in the models’ performance:

- Multi-scale detection approach (at 20X and 10X magnifications)
- Pre-training the model on ImageNet image recognition
- Colour normalisation

### 3. Tests and results

The authors used the Camelyon16 dataset to train and test their model, with 270 pixel-level-annotated slides for training and validation (159 normal and 110 tumour) and 130 slides for testing. Background patches, representing biological tissues other than those of interest (such as adipocytes), were removed to reduce computation. Additionally, NHO-1, a 110-slide dataset, was digitised and labelled in order to be used as an independent evaluation set.

Two metrics were used to evaluate the models: area under the ROC curve (AUC), and FROC which is a metric used to evaluate tumour detection and localisation.

Regarding the slide-level classification, which is obtained by taking the maximum probability value of a slide's corresponding heatmap, the models achieved AUCs greater than 97%. For tumour-level classification, the models achieved FROCs ranging from 85.5% to 88.5%.

On the NHO-1 independent dataset, the models achieved an AUC of 97.6%.

### 4. References

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