

Supplementary Materials: A whole slide image managing library based on fastai for deep learning in the context of histopathology: Two use-cases explained

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Dataset	gonadotroph	corticotroph
Patients	229	181
All WSI ¹	644	405
H&E WSI	229	202
ROIs	7,796	5,373
Tiles	206,517	63,893

¹ H&E and immunostained

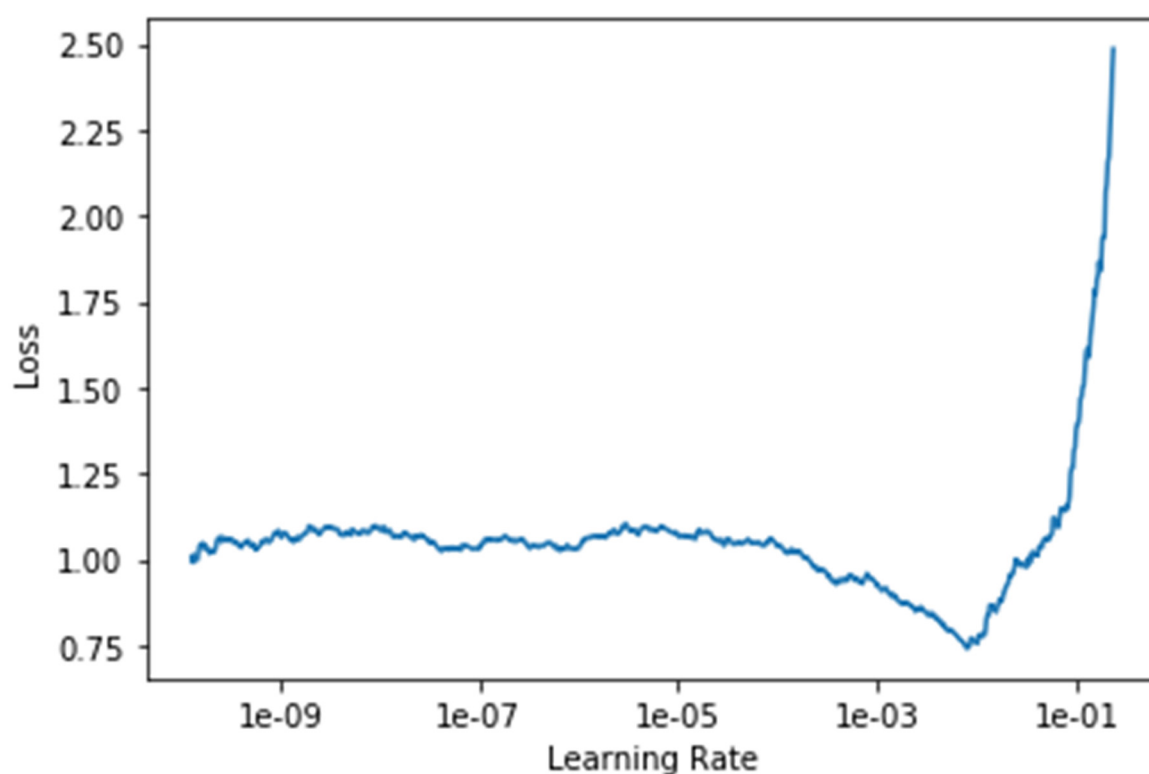
SUPPLEMENT S1 | Dataset First, we selected 410 patients and identified one case of pituitary adenoma per patient. Then we scanned H&E-stained slides with their positive immunostained slides respectively. After that, ROIs with matching hormone expression in the immunostained slides were extracted from the H&E slides manually. After that the ROIs were split into smaller 1024x1024 pixel tiles via a self-written algorithm.

Class distribution	cases	tiles
ACTH	44.7%	23.6%
silent ACTH	9.5%	9.7%
LH	49.0%	59.3%
FSH	44.1%	62.3%
LH or FSH	55.3%	76.4%

SUPPLEMENT S2 | Class distribution E.g. 23.6% means, that 23.6% of all tiles had the label ACTH. It was a multilabel classification problem. Only cases, where in the end tiles had been extracted from, were used for that calculation.

```
(0): AdaptiveConcatPool2d(
  (ap): AdaptiveAvgPool2d(output_size=1)
  (mp): AdaptiveMaxPool2d(output_size=1)
)
(1): Flatten()
(2): BatchNorm1d(4096, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
(3): Dropout(p=0.25, inplace=False)
(4): Linear(in_features=4096, out_features=512, bias=False)
(5): ReLU(inplace=True)
(6): BatchNorm1d(512, eps=1e-05, momentum=0.1, affine=True,
track_running_stats=True)
(7): Dropout(p=0.5, inplace=False)
(8): Linear(in_features=512, out_features=4/2, bias=False)
```

SUPPLEMENT S3 | Custom head (PyTorch). We used ResNext101/resnet50 as our final network architecture with weights pretrained on ImageNet. ImageNet has 1000 different classes. We only had 4/2. So, we had to change the head of the models, to only have 4/2 output probabilities. This is done conveniently by the fastai library. (4 outputs for the pituitary gland adenoma classifier and 2 outputs for the DNET-ganglioglioma classifier. The rest of the head was the same.)



SUPPLEMENT S4 | Learning rate finder pituitary adenoma classifier. Ideally, a learning rate at the steepest part of the curve with a descending slope should be picked. Left: For training the head a maximum learning rate of 10^{-3} was picked. Right: For training the body maximum differential learning rates between 10^{-9} and 10^{-6} were picked.

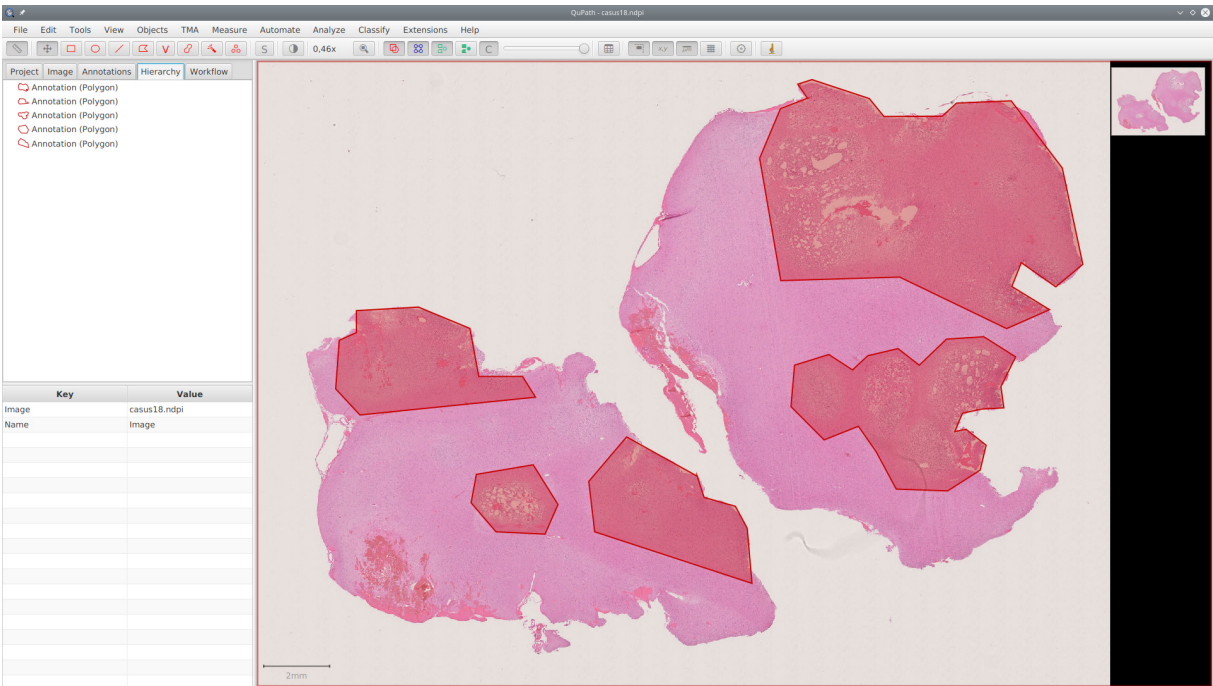
Networks	ACTH	Silent ACTH	LH	FSH
ResNet50	0.91/0.83	0.85/0.74	0.84/0.84	0.84/0.87
ResNet101	0.90/0.85	0.83/0.76	0.82/0.85	0.83/0.85
ResNet152	0.89/0.84	0.84/0.75	0.86/0.82	0.85/0.86
DenseNet121	0.87/0.82	0.83/0.71	0.81/0.80	0.82/0.83
Xception	0.85/0.87	0.95/0.81	0.85/0.90	0.75/0.81
Inceptionv4	0.93/0.90	0.96/0.81	0.93/0.94	0.78/0.84
se_ResNext101_32x4d	0.96/0.87	0.93/0.81	0.95/0.94	0.89/0.87
ResNext101_32x8d	0.93/0.96	0.96/0.96	0.91/0.90	0.87/0.90

SUPPLEMENT S5 | Evaluated Networks. We specified a validation and a test set. Then we trained this spectrum of network architectures and tried to optimize the accuracy on a case basis for the validation set. The final trained models were then evaluated on the test set. This table shows validation/test accuracy for the four classes. Our final choice fell on ResNext101, which was then trained and evaluated using 5-fold cross validation (see Supplement 6).

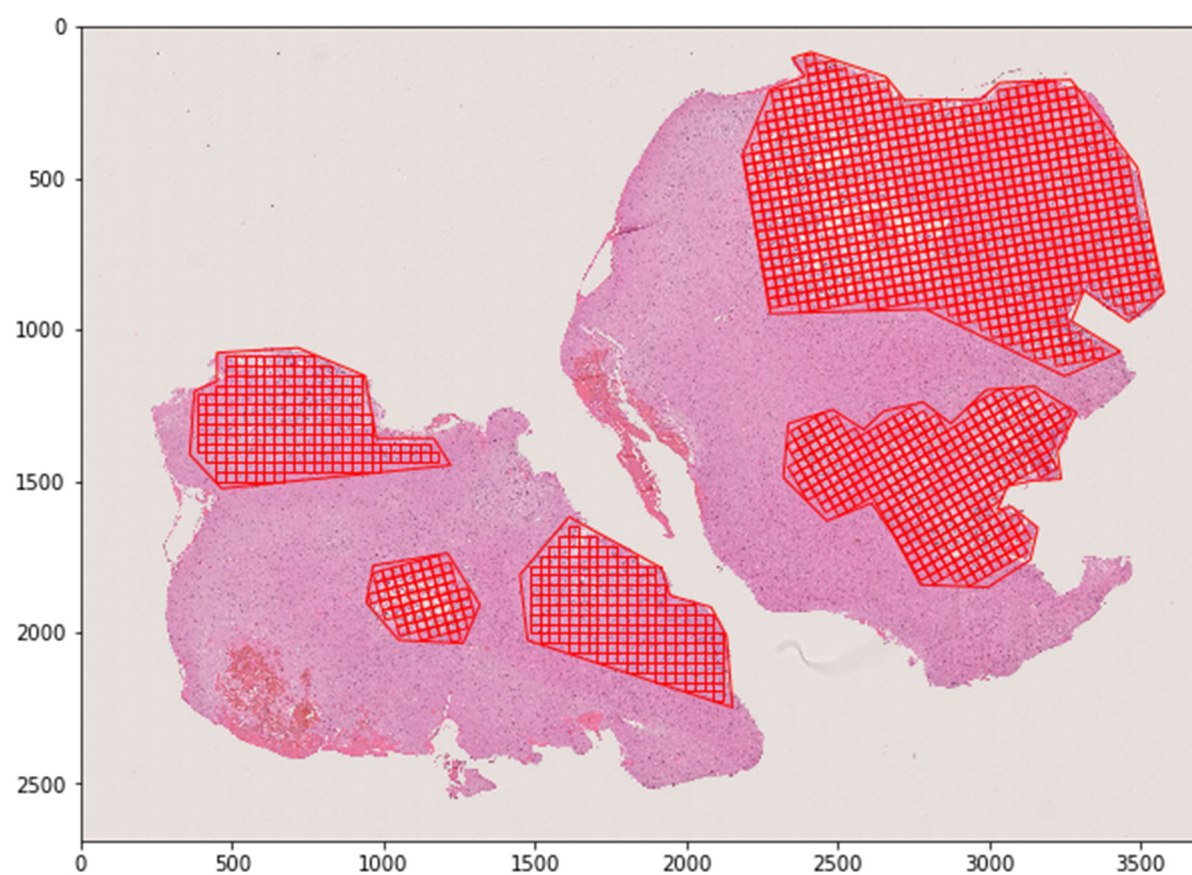
	ACTH	Silent ACTH	LH	FSH	LH or FSH
Validation set 1	0.94	0.97	0.98	0.95	0.98

Validation set 2	0.99	0.90	0.95	0.93	0.98
Validation set 3	0.97	0.89	1.00	0.94	1.00
Validation set 4	0.94	0.98	0.98	0.94	1.00
Validation set 5	0.99	0.98	0.97	0.89	0.99

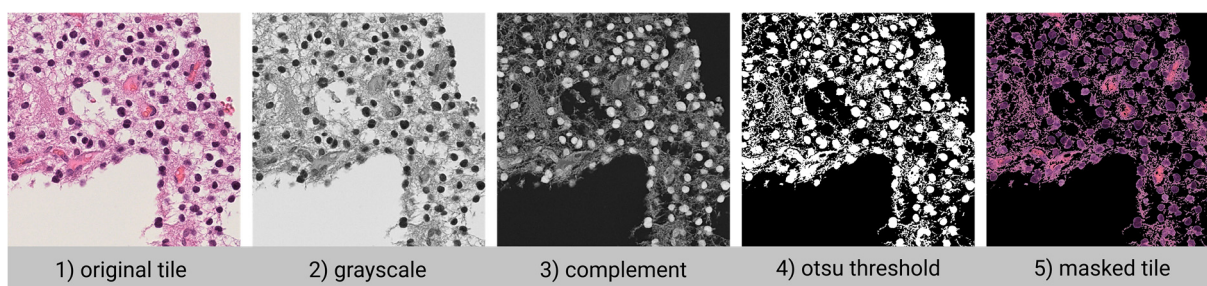
SUPPLEMENT S6 | AUCs of the ROC-curves for the five validation sets of 5-fold cross-validation. *We trained and evaluated ResNext101 using 5-fold cross validation. We let each model predict its validation set respectively and calculated the labels on a case basis to finally compute AUCs for each class.*



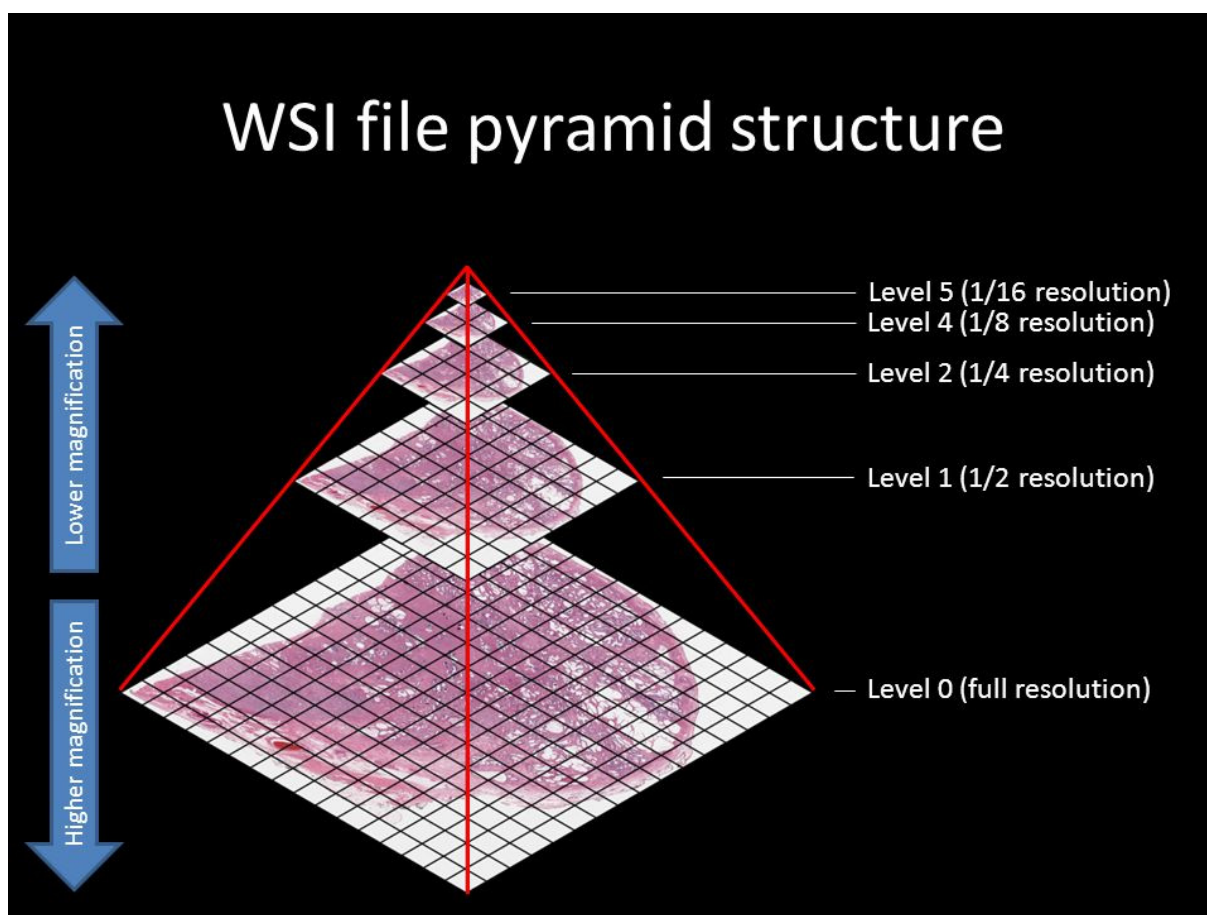
SUPPLEMENT S7 | QuPath Defining regions of interest in QuPath



SUPPLEMENT S8 | ROIs with overlaid grids Over each ROI a grid with all possible tile locations is drawn.



SUPPLEMENT S9 | Tissue filtering Separate tissue from background.



SUPPLEMENT S10 | WSI file pyramid structure