MRL Medical Imaging & Reconstruction Lab

Single Stage Signet ring Cell Detection

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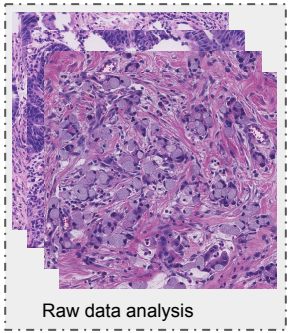
INTRODUCTION

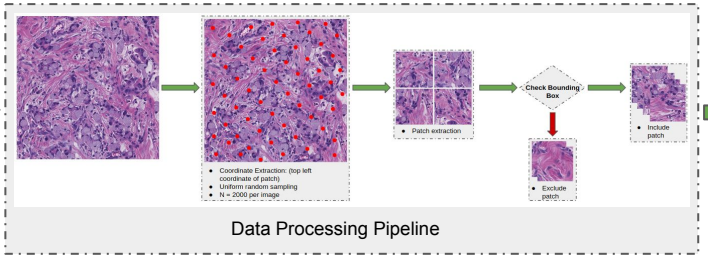
- ➔ Signet ring cell carcinoma (SRCC) is a type of rare and highly malignant adenocarcinoma
- ➔ Signet-ring cells are large vacuole cells that are predominantly found in carcinomas or gastric cancer
- ➔ Early-stage detection of gastric cancer helps in resection of these signet-ring cells and further treatment planning

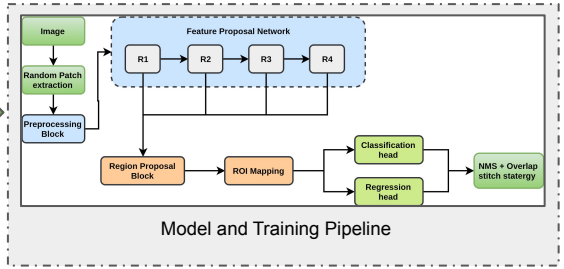
DATA

- ➔ Dataset which consists of 455 pathological images taken from 90 different patients
- ➔ The data consists of 378 negative and 77 positive samples extracted from 79 and 20 whole slide images (WSI) respectively
- ➔ All whole slide images were stained by hematoxylin and eosin, which were scanned at 40x

DATA FLOW PIPELINE



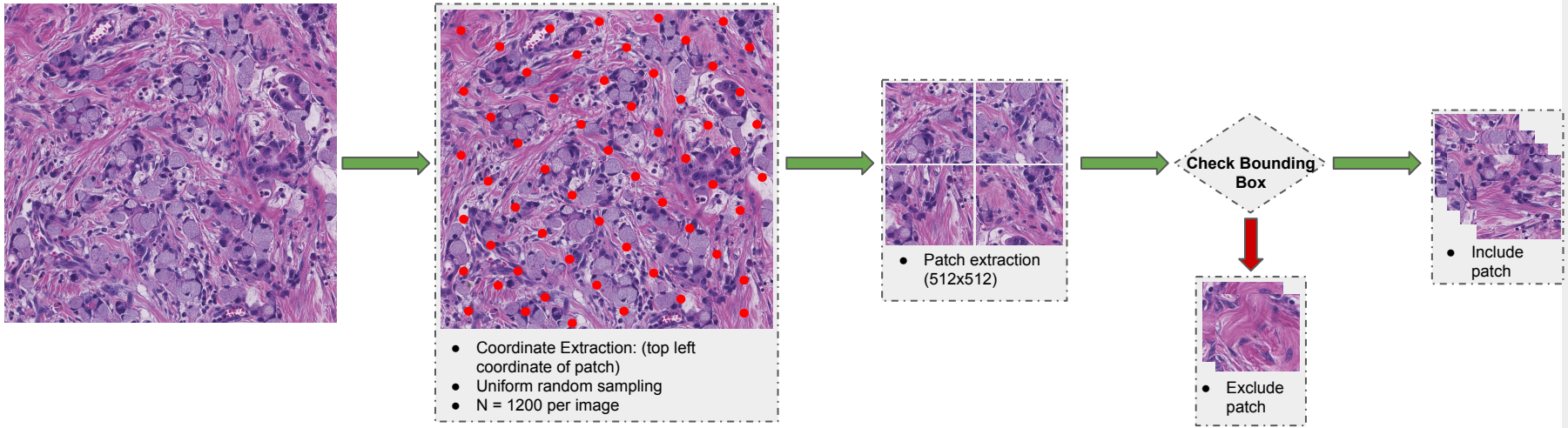




DATA STATS

- ➔ Number of training images: 62 positive 303 negative
- ➔ Number of validation images: 15 positive 75 negative
- ➔ Average signet cells per image = 135
- ➔ Average width of bounding box = 62
- ➔ Average height of bounding box = 62

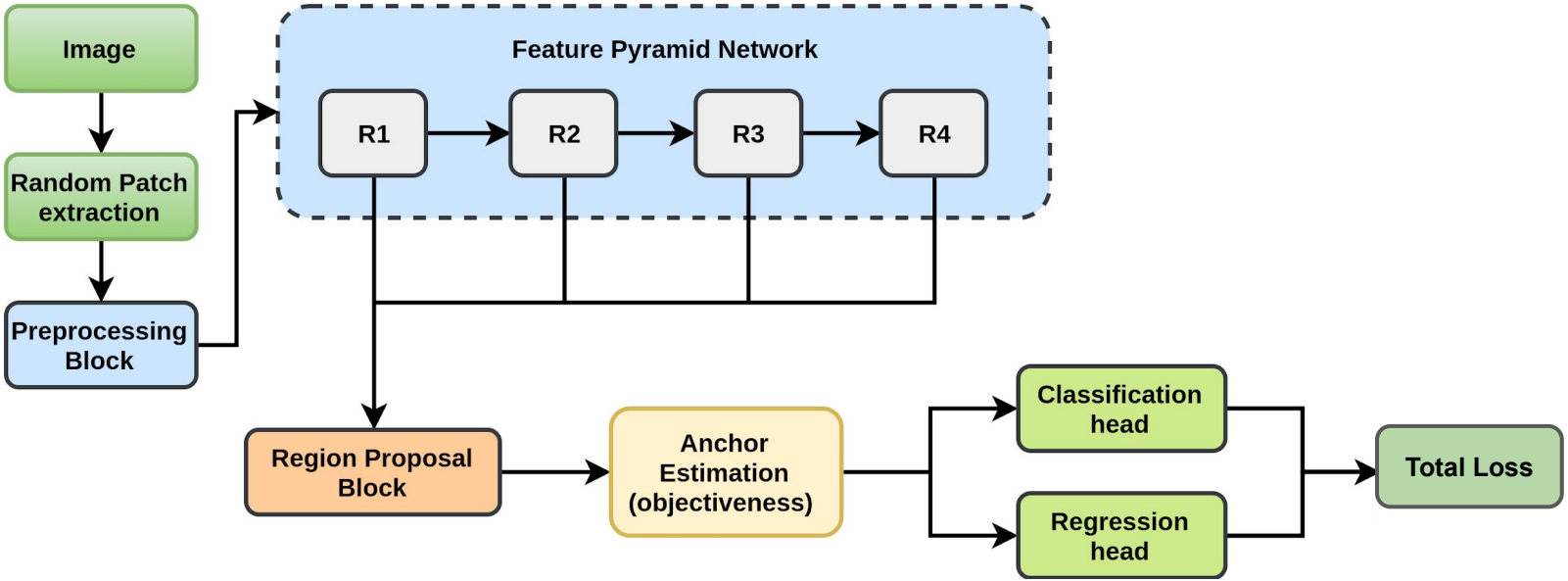
DATA PREPARATION



➔ Patches are extracted using Uniform random sampling to generate training samples, and retained only those which has at least one ground truth bounding box

➔ This increases the number of training samples significantly

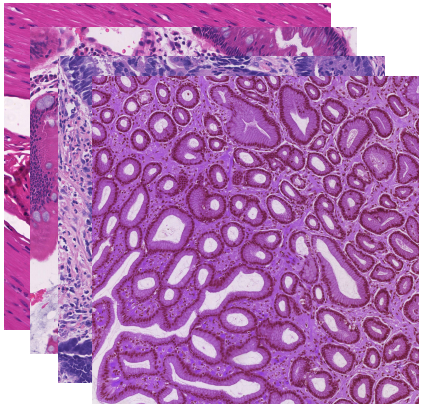
MASK R-CNN NETWORK



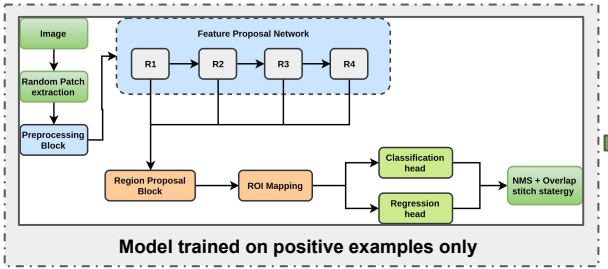
NETWORK & TRAINING DETAILS

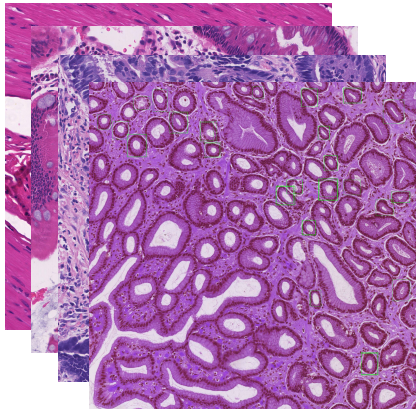
- ResNet 101 was used as a backbone feature extractor
- Anchor sizes - 32, 64, and 128, Anchor stride - 16, Anchor aspect ratios - 0.5, 1.0 and 2.0
- Adam optimizer, Base LR - 0.0025, Weight decay - 0.0001
- Training loss = Objectness loss (Anchor) + Classifier loss + Anchor box regression loss + Final bounding box regression
- BCE Loss for objectness and classifier, L2 loss for bounding box regression
- Batch size = 6, with 3 positive and 3 negative samples

HARD NEGATIVE MINING



Negative training images



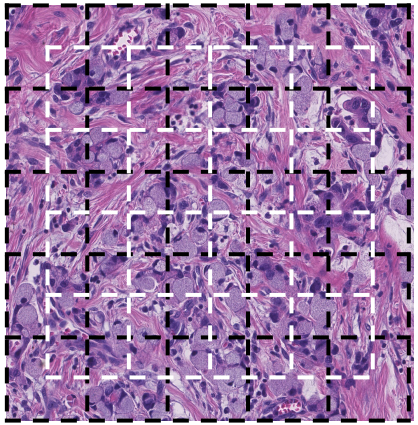


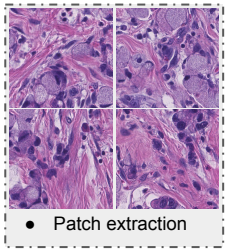
False positive boxes generated

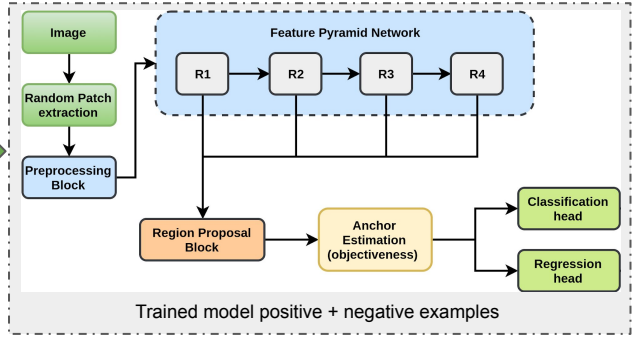
Extracted patches and bounding boxes are stored in database with the background class

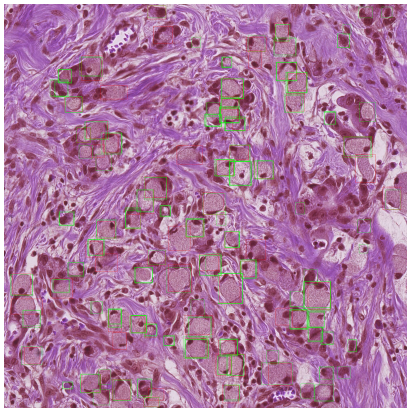
Patch sampling

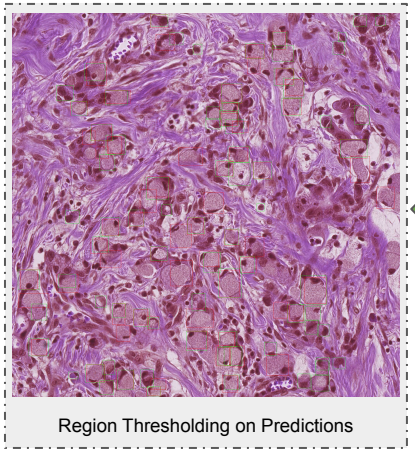
INFERENCE PIPELINE











➔ Patchwise inference is done on images using a sliding window of size 512x512 with stride 256

➔ Multiple bounding boxes generated due to overlapping strides are removed using Region thresholding

INFERENCE STATISTICS

- ➔ Time taken = 20 sec/tissue
- ➔ Patch size = 512x512
- ➔ Stride = 256
- ➔ Batch size = 6
- ➔ Hardware = NVIDIA GeForce GTX TITAN X
- ➔ Region Threshold = 30 px

RESULTS AND CONCLUSION

- ➔ Validation Recall = 0.61
- ➔ Validation FP on normal tissue = 0.0

- ➔ Testing Recall = 0.47
- ➔ Testing FP on normal tissue = 0.03

- ➔ Patch-based training and inference pipeline
- ➔ Faster Inference, trained and tested with 512 x 512
- ➔ Proposed overlapping strategy reduces false positives and removes edge effects induced while working with patches

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