Deep Learning Framework for Breast Cancer Detection on BreCaHad Histopathology Dataset

ABSTRACT

Background: Cancer is a global health burden which leads to increased morbidity and mortality across countries worldwide. Among many of the cancer types, breast cancers make up the highest proportion of cancers which lead to premature death among women of reproductive age group. It is the most prevalent cancer among women followed by lung cancers. Diagnosing cancer in its early stages is of utmost importance owing to the fact that it significantly reduces morbidity and mortality and improve prognosis. Staging and grading of tumors are done to predict clinical outcome of cancers. Histopathology is the process where slices of tissue are examined under microscope to visualise the tissue architecture. It is an important process in diagnosing and deciding further management. Histopathological procedures are done by pathologists by using stained specimens of glass slides and observing through microscopes. Deep learning architecture is inspired by hierarchial organization of human biological neural system. This paper is first in a series of papers which is intended to provide insight into possibility of Deep learning for classifying biopsy images for cancer diagnosis.

Objectives: To analyze cancer statistics in India, Implement Deep Learning in classifying biopsy images for cancer diagnosis, Application of Deep Learning in cancer prognosis and diagnosis

Materials and Methods: The scientific novelty of the research is by using trained Deep Learning models on the BreCaHAD dataset for histopathological analysis. The theory of deep learning neural networks and mathematical statistics methods are used. In this research, BreCaHAD (breast cancer histopathological annotation and diagnosis dataset) has been used which contains a total of 162 breast cancer histopathology images of 1360 × 1024 pixel at 40X resolution stored in uncompressed (.TIFF) image format. For sample acquisition, biopsy slides from breast tissue were stained with **Hematoxylin and eosin** (H&E) and then examined under brightfield illumination. Input image with annotations, red bounding boxes represent malignant cells. Redundant pixels were eliminated by using compression techniques. Then began the implementation of the deep net by processing the images in the dataset with the help of the python and pytorch.

Results: We obtained a classification accuracy of 99.02% of tumors for a Faster - RCNN on the test data but Faster- RCNN also produced many false positive bounding boxes.

Conclusions: Faster RCNN is able to detect 99.02% of the tumors but it also produces many false positive bounding boxes besides true positives. Thresholding can reduce the effects of false positives but introduces its own bias. It is possible to apply different methods to get rid of false positive bounding boxes while preserving true positive boxes. For an example, graph network can be used to remove negative bounding boxes, use of post-processing methods like score-level fusion of two CNNs etc

Keywords: Deep Learning, Faster-RCNN, Breast Cancer, Histopathological Analysis, Biopsy images, BreCaHAD.

INTRODUCTION

Cancer is a global health burden which leads to high morbidity and mortality world wide. In low and middle income countries cancer is a major health problem due to insufficient facilities in health care system(1). GLOBOCAN 2018 database which is compiled and disseminated by International Agency for Research on Cancer (IARC) includes data of worldwide incidence and mortality from 36 cancers. (2). Each year more than 2 million women are diagnosed with either breast cancer or cervical cancer. Yearly 1.7 million women are diagnosed with breast cancers which makes it the most common cancer among women (3, 4). According to Indian population census data, mortality rates are alarmingly high which makes up the second most common cause of mortality resulting more than 0.3 million deaths per year. It has shown increasing trends of cancer patients during past decades. Incidence of cancer tends to continuously increase upto 2009(5). In 2016 all cancers have accounted for 5% of the total disability adjusted life years and 8.3% of total deaths in India. From 1990 to 2016 crude cancer disability adjusted life year rate has increased.(6) In India, oral cancers are found to be more prevalent among men (7) while among women breast cancer was the most common cause of cancer related deaths with an estimation of 27.7% (1,62,468) of all new cases and 23.45% (87,090) of cancer related deaths in 2018. According to Indian population registry death due to cancer surpasses 8 lakhs reported cases by 2020(5, 8). Even If we consider worldwide distribution, breast cancers are the most prevalent cancer type found among women. In India in 2016 around 1.5 lakh new cases with breast cancers have been registered.(7)

Prognosis depends on the stage of tumor where when presented extensively outcome is poor compared to tumors which are localized. Staging of tumor determines anatomically how extended disease is, and it is based on TNM system.For early detection of cancerous and precancerous lesions; Breast cancer screening (BCS) by mammography and clinical breast examination (CBE) are done. But it has been shown that results from BCS and diagnostic tools can lead to misinterpretations resulting in false positives, false negatives. So that artificial intelligence is under development which is a multidisciplinary effort where technology experts, biomedical researchers and physicians get together and reduce the chance of misinterpretation of data.(9) When pathological investigations are done, histological and prognostic parameters are required. In established clinical and pathological investigations, degree of axillary lymph node involvement, tumour size and histological grade are the three prognostic parameters required. Lymph node status is among the key factors which determine the spread and overall survival of breast cancer. It is incorporated in both TNM staging and Nottingham grading system.(10, 11) Tissue slices are stained with different stains in order to visualize clearly from microscope. After staining procedure pathologist gather qualitative data through examining under microscope. Examination under microscope consumes considerable amount of time and it is not efficient enough to diagnose cancer more accurately due to lack of quantitative data.(12)

Implementing digital pathology in cancer diagnosis

The way histopathology is practiced can be significantly changed with digital pathology by increasing efficacy and diagnostic accuracy. Overtime with advancement of technology digital computer aided analytical techniques for histopathological data has increased rapidly. Also, by facilitating Artificial intelligence-based computer assisted diagnostics. There are multiple factors that work against adoption of digital pathology where limited evidence on how reliable is being the major cause. Literature in this area of interest is still sparse.(13) Researchers have

proposed many digital image analysis techniques for this purpose but cancer analysis had been carried out in insufficient dataset due to lack of public dataset which comprise huge number of images(7). There have been many technological advances in information technology, with availability of training data it has promoted application of powerful mathematical algorithms in Artificial Intelligence. AI is understanding of machines to communicate, reason and work independently in somewhat similar manner to a human being. There are many AI programs which are used in medical field to diagnose, treat and development of drugs. Now researchers have considered on using AI in cancer diagnosis. If AI is able to utilize efficiently it will be a step forward in diagnosing cancer in its early stage and deliver available treatment methods efficiently. At present, the major barrier for application of AI in cancer diagnosis is that there is no established gold standard of AI for cancer diagnosis. Trials that have been carried out are mostly observational studies which utilized very small data sets which makes it difficult to decide on how efficient AI is for diagnosis of cancer.(14) Use of AI has improved radiologists accuracy in differentiating between benign and malignant lesions which were detected in breast MRI(15, 16)

(i) Deep learning

Machine learning is an artificial functioning that consists of networks capable of learning from raw data which is unstructured and disorganized. It is a self- adaptive algorithm which gets better analysis with experience. Deep learning is a subset of machine learning used in object detection, speech recognition, language translation and decision making. It works exactly like how human brain processes data, learning from unstructured and unlabeled data without supervision. Deep neural learning or deep neural network also refers to deep learning. To carry out the process of machine learning, deep learning makes use of a hierarchical level of artificial neural networks. Hierarchical function enables to process data with a nonlinear approach while traditional programs build analysis in a linear way. These artificial neural networks resemble human brain where nodes are connected together like a web(17). Neural network architecture is used to implement Deep learning. Here in deep learning, "deep" refers to number of layers in the network, when there are more layers; Network gets deeper. A deep neural network incorporates several non- linear processing layers. Input layer, several hidden layers and output layer; all of these are interconnected via nodes. Each hidden layer uses output of previous layer as input (13). Deep learning has produced a set of image analysis techniques that automatically extract relevant features and then transforming the field of computer vision. Convolutional Neural Networks (CNNs) automatically learn feature representations for images by using a data-driven approach. CNN is currently used to analyze medical images.(12, 18, 19)

There are many types of Neural Networks in deep learning , following are some of the major types. Each of these networks are used for specific datasets, mainly on image, speech, video, text etc(20).

1. Multilayer Neural Network
2. Convolutional Neural Networks (CNN)
3. Recurrent Neural Network (RNN)
4. Long Short-Term Memory Networks (LSTMs)
5. Recursive Neural Network
6. Temporal Convolutional Machines (TCMs)
7. Stacked Autoencoders
8. Extreme Learning Machine (ELM)
9. Recursive Deep Learning
10. Generative Deep Learning

(ii) Convolutional Neural Network

Convolutional Neural Network is a deep learning approach for image processing. Deep learning concept was first brough in as hierarchical learning. Architecture of Deep learning uses data processing in several layers of neurons non-linear modules which works in such a way that each layer highlights different characteristics and provides it to next layer for processing. Deep learning is a branch of machine learning which is inspired by as its name suggests ability of human brain to analyse unstructured patterns. Their success rate is high. Because they are well trained in representations in a hierarchical manner. There are single layered and multi layered networks, where in multi-layer networks there is an ability of learning things which single layer networks are incapable of. Moreover, without any previous knowledge they are able to extract and reorganize different features. Data input to these deep learning algorithms must be in proper format and some network parameters should be appropriate to problem. Predesigned networks such as AlexNet, MobileNet, Inception, and many more can also be used. (20, 21)

Convolution networks comprise convolutional layers, pooling layers and a final component which is used in classification of detection. By sliding filter along input image, we compute convolution which results in feature map by eliminating pixels with low values, pooling decreases features in feature maps. RPN is a fully convolutional network which is used to extract proposal regions resulting in in putting an image and as output we get a series of bounding box proposals, as also as the score of each proposal.

2) Materials and Methods

2.1) General Study Details:

In this study, Faster R-CNN was used for classifying biopsy images of breast tumours into benign and malignant.

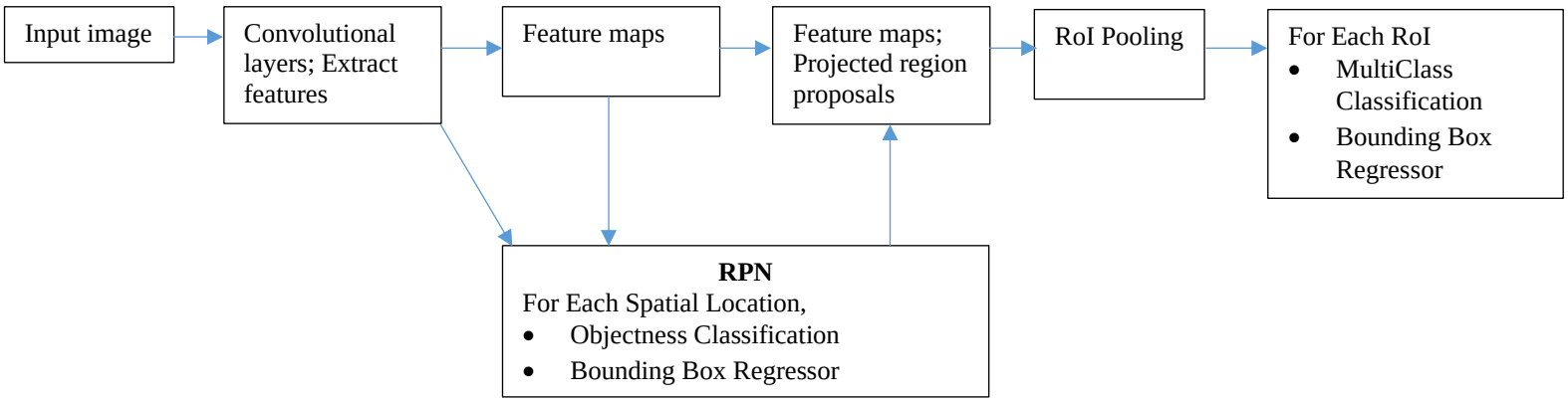


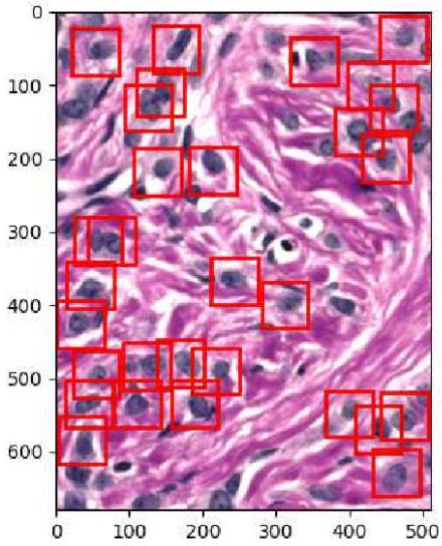
Diagram adapted from (22)

Faster R-CNN, when compared to other region-based CNNs such as R-CNN is highly accurate and entails lower computational complexity thereby cutting down the time consumption. The Faster R-CNN comprised of three sub-networks, the feature-extraction network, region proposal network (RPN) and classification network.
In the feature-extraction network, a feature map known as an activation map is generated, and appropriate deep features are extracted. Different types of CNNs can be used as a feature extractor, and we used a Resnet-50 which includes 50 weighted layers as the feature extraction

network. The produced feature maps are fed to the region proposal network (RPN) which is the second part of the Faster R-CNN. The input and output sizes of the following networks depend on the output of the previous networks. In our study, the outputs are (256, 344), (128, 172), (64, 86), (32, 43).The feature map extracted in step 1 and the region proposals generated in step 2 are input into the classification part of the Faster R-CNN.

2.2) Dataset: BreCaHAD (23)

In this research, BreCaHAD (breast cancer histopathological annotation and diagnosis dataset) has been used which contains a total of 162 breast cancer histopathology images of 1360 × 1024-pixel, X40resolution stored in uncompressed (.TIFF) image format. These histopathology images have a three channel RGB with 8-bit depth in each channel colour coding scheme. For acquisition of the sample, biopsy slides from breast tissue were stained with **Hematoxylin and eosin** (H&E) and then examined under brightfield illumination with a Zeiss 40× oil objective on a Ziess Axiophot microscope through a 10× magnifier. Then images were digitized using a Spot Pursuit PR3440 camera controlled by Spot v5.2 software which used same acquisition conditions and settings as the dataset BreCaHAD. (0.514 µm × 0.527 µm per pixel at 40×, the camera at 40× objective captures 700 microns by 540 microns of microscopic image with a chip of 1360 × 1024 pixels.). Consultant histopathologists performed the annotations by mutual consent. Input image with annotations, red bounding boxes represent malignant cells.



2.3) Variables:

The primary endpoint of the study was to calculate the classification accuracy of a Faster – RCNN for classifying tumour cells in patients with breast cancer. The secondary endpoint was to assess the factors affecting the classification accuracy score.

2.4) Study Methodology

2.4.1) Experimental Setup

2.4.1.1) Tech Stack

- Ubuntu 20.04
- Python 3.9

- Pytorch 1.6.0
- Torchvision 0.7.0
- Cuda 11.0
- Click 7.1.2
- Numpy
- Matplotlib

2.4.1.2) Hardware

- AMD Ryzen 3900X – 12 Core CPU
- 64 GB DDR4 RAM
- 8 TB HDD
- GeForce RTX 2060 GPU

2.4.2) Training:

1. backbone=resnet50
2. Activation Function = ReLU
3. No of Epochs = 100
4. Batch Size =1
5. Learning Rate = 0.00002, Multiplicative scheduler updated learning rate multiplying learning rate by 0.98. Weight decay of the optimizer set as 0.0005.
6. image_mean= (0.75141764, 0.6385864, 0.8118883)
7. image_std= (0.00398171, 0.00440513, 0.00163838)
8. min_size=1024
9. max_size=1360
10. rpn_fg_iou_thresh=0.9
11. box_fg_iou_thresh=0.9
12. box_nms_thresh=0.8
13. rpn_nms_thresh=0.8,
14. box_bg_iou_thresh=0.1
15. rpn_bg_iou_thresh=0.1
16. box_detections_per_img=200
17. box_roi_pool= MultiScaleRoIAlign (featmap_names=['0', '1'], output_size=21, sampling_ratio=2)
18. num_classes=2

Redundant pixels were eliminated by using compression techniques. Then began the implementation of the deep net by processing the images in the dataset with the help of the OpenCV library in Python 3.9. The aspect ratio of the original slide was preserved as both dimensions were reduced by a factor of 2, giving an image which is 1/4th in area, that is of dimension 512 x 680. Faster R-CNN was trained on the BreCaHAD (breast cancer histopathological annotation and diagnosis dataset). The batch size, learning rate, and weight decay are 1, 0.00002, and 0.0005, respectively. Training images are 512x680 patches which are sampled from 138 images. Input images are interpolated to 1024x1360 before given as input. We performed the training for 100 epochs. So, training uses 13800 patches sampled from training data. Deep-learning networks usually require a sufficient amount of data for complete and efficient training; however, in the majority of cases, a large amount of data is not available. Therefore, a data augmentation technique is used to generate more data from the original data. In our study, flipping in x dimension is randomly applied for data augmentation.

2.4.3) Validation: Validation images are sampled from 12 images, 5 times in each epoch. 60 patches are used in total.

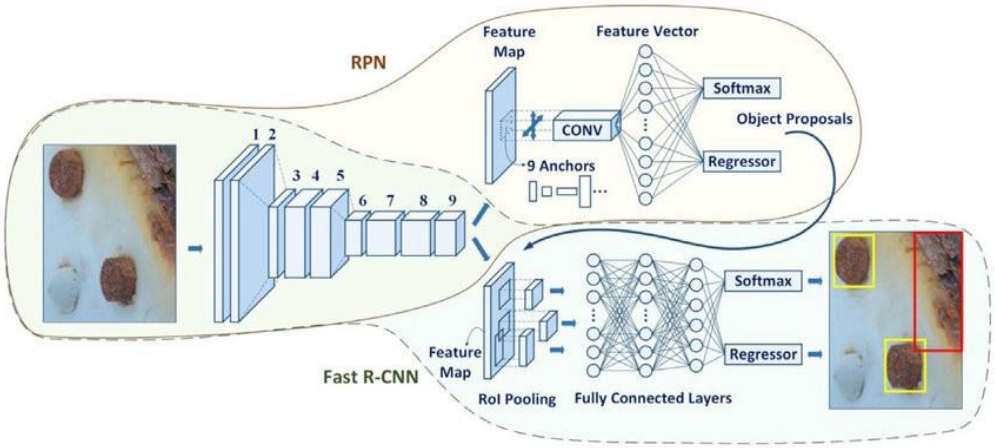
2.4.4) Testing: Test results are obtained from 12 images which are not included in training or validation set. Each image is sampled 10 times. Test set contains 120 patches.

2.5) Tools:

BreCaHAD (breast cancer histopathological annotation and diagnosis dataset) has been used which contains a total of 162 breast cancer histopathology images of 1360 × 1024-pixel, X40resolution stored in uncompressed (.TIFF) image format.

2.6) Algorithm:

Histopathology images include variable number of nucleus and it is hard to localize each nucleus manually, the best solution for this problem is to use Faster RCNN. Because it classifies objects in the image as well as localize them. Structure of Faster RCNN. It contains Feature Extractor Network, Region Proposal Network and Classification Network.



3. Results and discussion

Accuracy on validation data is shown in Fig. 1

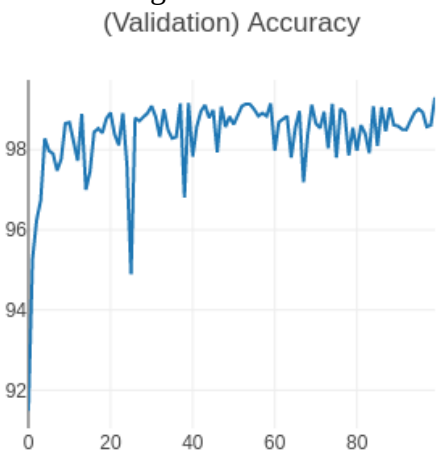


Figure 1

a). Total Loss Training and Validation data are shown in Fig.2 and Fig.3 respectively.

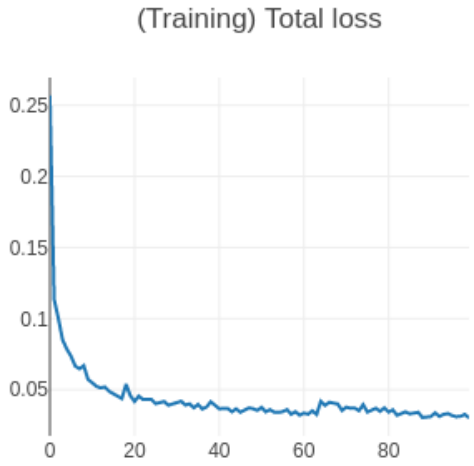


Figure 2

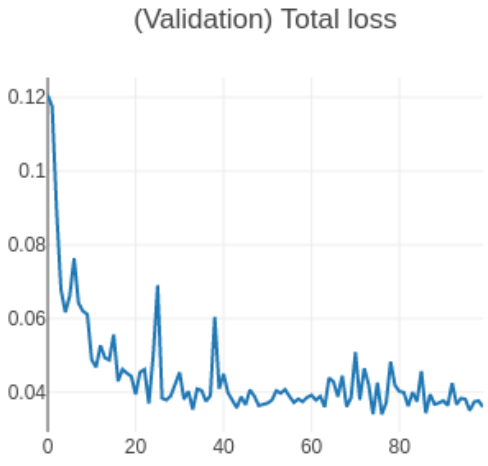


Figure 3

We obtained that classification accuracy for a faster- RCNN on test data is 99.02%.

Faster RCNN generates predetermined number of bounding boxes as output which can be either a true positive or a false positive out of which many of them are false positive bounding boxes. Therefore, it uses score threshold value to get rid of false positive bounding boxes. Red circles represent ground truths and green circles represent the predictions when the threshold is set as 0.05.

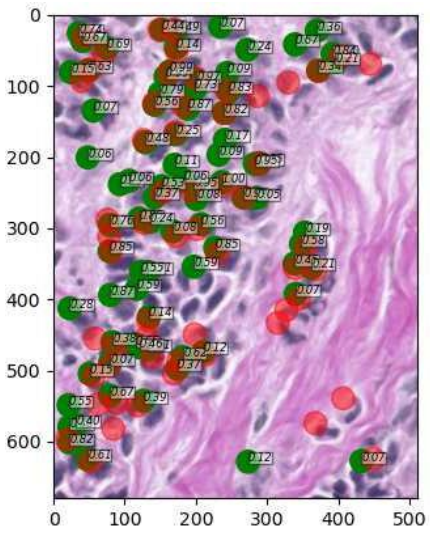


Fig.4 shows the True positive and false discovery rates with respect to threshold values. When the threshold value is lowered, Faster RCNN is able to detect 99.02% of the malignant cells while producing many false positive bounding boxes besides positives. Increasing the threshold can remove more than half of them while removing positive bounding boxes as well.

Figure 4: True positive and False discovery rates with respect to threshold values

4. Conclusion

In the rapid rise in the incidence of breast cancer, histopathological diagnosis and classification cost a lot of human resources as well as man-hours. In order to keep up with this increased demand, we have to look for alternative methods which could potentially automate this process of diagnosis and classification. The best solution we propose for this problem is to use a Faster RCNN for detection and localisation of cancer cells. Results showed that classification accuracy of a Faster - RCNN on the test data is 99.02%.

4.1 Strengths and limitations

Major advantages of a faster R-CNN are its low cost, high accuracy and lower computational complexity when compared to other region-based CNNs such as R-CNN and Fast R-CNN. One of the major drawback of using Faster R-CNN for detection of tumour cells in a histopathological image is that it produces many false positives. Increasing the threshold for box scores can get rid of more than half of the false positives. But it comes at a cost of removing true positives as well. However, different methods can be employed to get rid of false bounding boxes while protecting positive boxes. For example, graph network can be used to remove negative bounding boxes.

4.2 Future Research Direction

We will be implementing the deep learning algorithms on Whole Slide images, using different deep learning architectures.

5) Conflicts of Interest
Authors declared that they have no conflicts of interest

6) Financial Support and Sponsorship
Nil.

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ANNEXES

Annexure I: Architecture of the Faster-RCNN

Backbone	Input	Output	Parameters
(backbone): BackboneWithFPN(			
(body): IntermediateLayerGetter(			
(conv1): Conv2d(3, 64, kernel_size=7, stride=2, padding=3, bias=False)	(1024x1360)	(512x688)	9408
(bn1): FrozenBatchNorm2d(64)			256
(relu): ReLU(inplace=True)			
(maxpool): MaxPool2d(kernel_size=3, stride=2, dilation=1)	(512x688)	(256x344)	0
(layer1): Sequential(			
(0): Bottleneck(			
(conv1): Conv2d(64, 64, kernel_size=1, bias=False)	(256x344)	(256x344)	4096
(bn1): FrozenBatchNorm2d(64)			256
(conv2): Conv2d(64, 64, kernel_size=3, bias=False)	(256x344)	(256x344)	36864
(bn2): FrozenBatchNorm2d(64)			256
(conv3): Conv2d(64, 256, kernel_size=1, bias=False)	(256x344)	(256x344)	16384
(bn3): FrozenBatchNorm2d(256)			1024
(relu): ReLU(inplace=True)			
(downsample): Sequential(			
(0): Conv2d(64, 256, kernel_size=1, bias=False)	(256x344)	(256x344)	16384
(1): FrozenBatchNorm2d(256)			1024
)			
)			
(1): Bottleneck(			
(conv1): Conv2d(256, 64, kernel_size=1, bias=False)	(256x344)	(256x344)	16384
(bn1): FrozenBatchNorm2d(64)			256
(conv2): Conv2d(64, 64, kernel_size=3, bias=False)	(256x344)	(256x344)	36864
(bn2): FrozenBatchNorm2d(64)			256
(conv3): Conv2d(64, 256, kernel_size=1, bias=False)	(256x344)	(256x344)	16384
(bn3): FrozenBatchNorm2d(256)			1024
(relu): ReLU(inplace=True)			
)			
(2): Bottleneck(			
Same with Bottleneck 1	(256x344)	(256x344)	
)			
)			
(layer2): Sequential(			
(0): Bottleneck(			
(conv1): Conv2d(256, 128, kernel_size=1, bias=False)	(256x344)	(256x344)	32768
(bn1): FrozenBatchNorm2d(128)			
(conv2): Conv2d(128, 128, kernel_size=3, stride=2, bias=False)	(256x344)	(128x172)	147456
(bn2): FrozenBatchNorm2d(128)			

(conv3): Conv2d(128, 512, kernel_size=1, bias=False)	(128x172)	(128x172)	65536
(bn3): FrozenBatchNorm2d(512)			2048
(relu): ReLU(inplace=True)			0
(downsample): Sequential(			
(0): Conv2d(256, 512, kernel_size=1, stride=2, bias=False)	(256x344)	(128x172)	131072
(1): FrozenBatchNorm2d(512)			1024
)			
)			
(1): Bottleneck(			
(conv1): Conv2d(512, 128, kernel_size=1, bias=False)	(128x172)	(128x172)	32768
(bn1): FrozenBatchNorm2d(128)			512
(conv2): Conv2d(128, 128, kernel_size=3, bias=False)	(128x172)	(128x172)	147456
(bn2): FrozenBatchNorm2d(128)			512
(conv3): Conv2d(128, 512, kernel_size=1, bias=False)	(128x172)	(128x172)	65536
(bn3): FrozenBatchNorm2d(512)			2048
(relu): ReLU(inplace=True)			0
)			
(2): Bottleneck(			
Same with Bottleneck 1	(128x172)	(128x172)	
)			
(3): Bottleneck(			
Same with Bottleneck 1	(128x172)	(128x172)	
)			
)			
(layer3): Sequential(			
(0): Bottleneck(			
(conv1): Conv2d(512, 256, kernel_size=1, bias=False)	(128x172)	(128x172)	131072
(bn1): FrozenBatchNorm2d(256)			1024
(conv2): Conv2d(256, 256, kernel_size=3, stride=2, bias=False)	(128x172)	(64x86)	589824
(bn2): FrozenBatchNorm2d(256)			1024
(conv3): Conv2d(256, 1024, kernel_size=1, bias=False)	(64x86)	(64x86)	262144
(bn3): FrozenBatchNorm2d(1024)			4096
(relu): ReLU(inplace=True)			
(downsample): Sequential(			
(0): Conv2d(512, 1024, kernel_size=1, stride=2, bias=False)	(128x172)	(64x86)	524288
(1): FrozenBatchNorm2d(1024)			4096
)			
)			
(1): Bottleneck(			
(conv1): Conv2d(1024, 256, kernel_size=1, bias=False)	(64x86)	(64x86)	262144
(bn1): FrozenBatchNorm2d(256)			1024
(conv2): Conv2d(256, 256, kernel_size=3, bias=False)	(64x86)	(64x86)	589824
(bn2): FrozenBatchNorm2d(256)			1024

(conv3): Conv2d(256, 1024, kernel_size=1, bias=False)	(64x86)	(64x86)	262144
(bn3): FrozenBatchNorm2d(1024)			4096
(relu): ReLU(inplace=True)			0
)			
(2): Bottleneck(			
Same with Bottleneck 1	(64x86)	(64x86)	
)			
(3): Bottleneck(			
Same with Bottleneck 1	(64x86)	(64x86)	
)			
(4): Bottleneck(			
Same with Bottleneck 1	(64x86)	(64x86)	
)			
(5): Bottleneck(			
Same with Bottleneck 1	(64x86)	(64x86)	
)			
)			
(layer4): Sequential(			
(0): Bottleneck(			
(conv1): Conv2d(1024, 512, kernel_size=1, bias=False)	(64x86)	(64x86)	524288
(bn1): FrozenBatchNorm2d(512)			2048
(conv2): Conv2d(512, 512, kernel_size=3, stride=2, bias=False)	(64x86)	(32x43)	2359296
(bn2): FrozenBatchNorm2d(512)			2048
(conv3): Conv2d(512, 2048, kernel_size=1, bias=False)	(32x43)	(32x43)	1048576
(bn3): FrozenBatchNorm2d(2048)			8192
(relu): ReLU(inplace=True)			0
(downsample): Sequential(			
(0): Conv2d(1024, 2048, kernel_size=1, stride=2, bias=False)	(64x86)	(32x43)	2097152
(1): FrozenBatchNorm2d(2048)			8192
)			
)			
(1): Bottleneck(			
(conv1): Conv2d(2048, 512, kernel_size=1, bias=False)	(32x43)	(32x43)	1048576
(bn1): FrozenBatchNorm2d(512)			2048
(conv2): Conv2d(512, 512, kernel_size=3, bias=False)	(32x43)	(32x43)	2359296
(bn2): FrozenBatchNorm2d(512)			2048
(conv3): Conv2d(512, 2048, kernel_size=1, bias=False)	(32x43)	(32x43)	1048576
(bn3): FrozenBatchNorm2d(2048)			8192
(relu): ReLU(inplace=True)			0
)			
(2): Bottleneck(			
Same with Bottleneck 1	(32x43)	(32x43)	
)			

)			
)			
(fpn): FeaturePyramidNetwork(			
(inner_blocks): ModuleList(			
(0): Conv2d(256, 256, kernel_size=1, stride=1)	(256x344)	(256x344)	65536
(1): Conv2d(512, 256, kernel_size=1, stride=1)	(128x172)	(128x172)	131072
(2): Conv2d(1024, 256, kernel_size=1, stride=1)	(64x86)	(64x86)	262144
(3): Conv2d(2048, 256, kernel_size=1, stride=1)	(32x43)	(32x43)	524288
)			
(layer_blocks): ModuleList(			
(0): Conv2d(256, 256, kernel_size=3, padding=1)	(256x344)	(256x344)	589824
(1): Conv2d(256, 256, kernel_size=3, padding=1)	(128x172)	(128x172)	589824
(2): Conv2d(256, 256, kernel_size=3, padding=1)	(64x86)	(64x86)	589824
(3): Conv2d(256, 256, kernel_size=3, padding=1)	(32x43)	(32x43)	589824
)			
(extra_blocks): LastLevelMaxPool()			
)			
)			

Region Proposal Network	Parameters
(rpn): RegionProposalNetwork(	
(anchor_generator): AnchorGenerator()	
(head): RPNHead(	
(conv): Conv2d(256, 256, kernel_size=3, padding=1)	590080
(cls_logits): Conv2d(256, 1, kernel_size=1, stride=1)	257
(bbox_pred): Conv2d(256, 4, kernel_size=1, stride=1)	1028
)	
)	

ROI Head	Parameters
(roi_heads): RoIHeads(	
(box_roi_pool): MultiScaleRoIAlign()	
(box_head): TwoMLPHead(	
(fc6): Linear(in_features=112896, out_features=1024, bias=True)	115606528
(fc7): Linear(in_features=1024, out_features=1024, bias=True)	1049600
)	
(box_predictor): FastRCNNPredictor(	
(cls_score): Linear(in_features=1024, out_features=2, bias=True)	2050
(bbox_pred): Linear(in_features=1024, out_features=8, bias=True)	8200
)	