

**Semester 6 Mini-Project**  
Report

# **Cancer Detection Using Object Detection**

*Submitted in partial fulfillment of  
the requirements for the award of the degree of*

**Bachelor of Technology  
in  
Information Technology**

Submitted by

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## *Certificate*

This is to certify that this is a bonafide record of the project presented by the students whose names are given below in partial fulfilment of the requirements of the degree of Bachelor of Technology in Information Technology.

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## **Abstract**

Through this report, we aim to expand on the steps involved in detection of cancer through implementation of semantic segmentation in deep learning. The first step being the identification of mitotic cells. After this identification, we need to check if the mitosis is normal or abnormal. If the mitosis is abnormal we can say that the cell undergoing mitosis is cancerous. Through this paper, we walk through the steps in implementation in identifying these cancerous cells in the data set provided to us.

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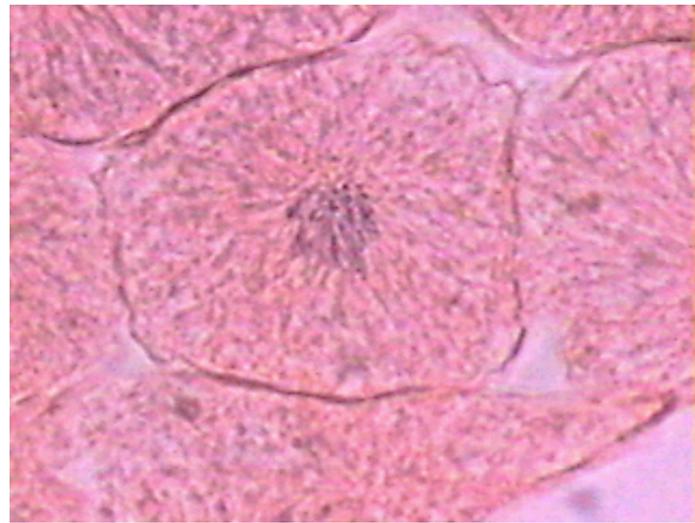
# Chapter 1

## Introduction

Cancer accounts for nearly 70 percent of all deaths in the World. According to World Health Organization, , the three most common cancers in the world in 2008 in terms of incidence were lung (1.52 million cases), breast (1.29 million) and colorectal (1.15 million)[1].

For detection of cancer, tissue samples are collected from a specific part of the body. Histology slides are prepared from these samples. The stain used for these histology slides is Hematoxylin and Eosin stain. The pathologist gives the slide a grade based on either The Scarff, Bloom and Richardson grading system or the The Elston and Ellis grading system[2].

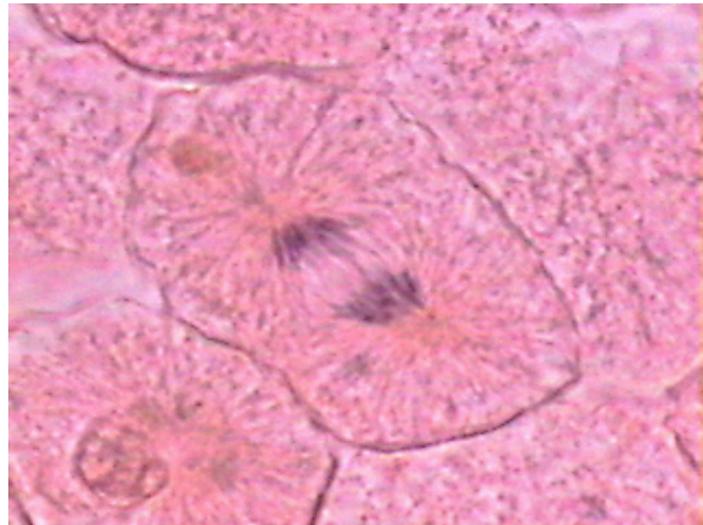
One of the major factors of determining cancer from the histology slides is to check the nuclei is the number of nuclei undergoing cell division also known as mitosis. During cancer, the number of cells undergoing mitosis goes out of control. Several studies have for the creation of automatic tools regarding the same that focus mainly on nuclei or tubule detection. In particular this is a very challenging problem and is not addressed properly, hence is a topic of ongoing research. The main reason behind mitosis being a very challenging task is the fact that the nuclei under mitosis are very small in size and vary quite a lot in their shape. There are four main stages during mitosis namely prophase, metaphase, anaphase, telophase. The shape of the nuclei is different depending on the stage that it is in.



(a) **Prophase** is a stage of mitosis in which the chromatin condenses (it becomes shorter and fatter) into a highly ordered structure called a chromosome in which the chromatin becomes visible.



(b) **Metaphase** is a stage of mitosis in the eukaryotic cell cycle in which condensed & highly coiled chromosomes, carrying genetic information, align in the middle of the cell before being separated into each of the two daughter cells.



(c) **Anaphase** is the stage of mitosis when chromosomes separate in an eukaryotic cell. Each chromatid moves to opposite poles of the cell, the opposite ends of the mitotic spindle, near the microtubule organizing centers.



(d) **Telophase** is a stage of mitosis in a eukaryotic cell in which the effects of prophase and prometaphase events are reversed. Two daughter nuclei form in the cell. The nuclear envelopes of the daughter cells are formed from the fragments of the nuclear envelope of the parent cell. As the nuclear envelope forms around each pair of chromatids, the nucleoli reappear.

# **Chapter 2**

## **Problem Statement**

### **2.1 Formal Problem**

We are given very high-resolution scans of HE stained light microscopy cuts showing Undifferentiated Pleomorphic Sarcoma. Our task is to come up with a tool (highly automated technology self-developed or borrowed from elsewhere), that can identify mitoses on those scans with as high accuracy as possible. The project will be divided into two main sub stages namely bounding box based mitosis detection in a given section image and given a mitosis, detect its type, i.e. typical vs atypical mitosis.

### **2.2 Literature Survey**

In the course of the project, we studied several papers to gain a better knowledge and understanding of the concepts we required for this project. However, so far certain works stood out more than others, helping us in the advancement of the project.

Mitotic count is a critical predictor of tumor aggressiveness in the breast cancer diagnosis. Nowadays mitosis counting is mainly performed by pathologists manually, which is extremely arduous and time-consuming. In the paper, 'Deep-Mitosis: Mitosis detection via deep detection, verification and segmentation networks' by Chao Ling and team[3] attempted to solve the problem of mitosis detection in breast tissue images using segmentation and object detection.

The team used two well known datasets for mitosis detection ICPR-2012 and 2014 datasets. They divided their work flow basically into three parts be-

ing segmentation, detection and verification. The segmentation was achieved by the model DeepSeg they developed which was used to create bounding boxes around the mitotic nuclei. In their data, they had two types of annotation - pixel by pixel ground truth and merely centroid of the mitotic nuclei labelled. The Deepseg model used these annotations and further created bounding boxes for the further stages.

The next step was of detection of the nuclei. The DeepDet model was used for that purpose. This is the backbone of their system. They used the model to predict whether a certain region contains a mitotic nuclei or not. Then in the further phase, the verification of the nuclei detected is done. The concept underlying this is that the DeepDet model may detect false positives and false negatives also and the Verification is used to reduce the false positives. The false positives are not considered in the further processes. This increased their accuracy as observed on both the datasets.

In the paper, 'U-Net: Convolutional Networks for Biomedical Image Segmentation' by Olaf and team, [7], the team explored biomedical image segmentation using CNN (Convolutional Neural Networks). They used the concept of up-scaling and down-scaling the image using a series of convolutions and reducing the dimension of the Image. The image is first down-scaled by a series of 3x3 convolutions. Then it is further up-scaled. The network architecture is as follows.

The model is pre trained and used as a basic model for segmentation. The team also used three data sets- nerve cord images, Glioblastoma-astrocytoma U373 cells and HeLa cells on a flat glass recorded by differential interference contrast. They recorded the results.

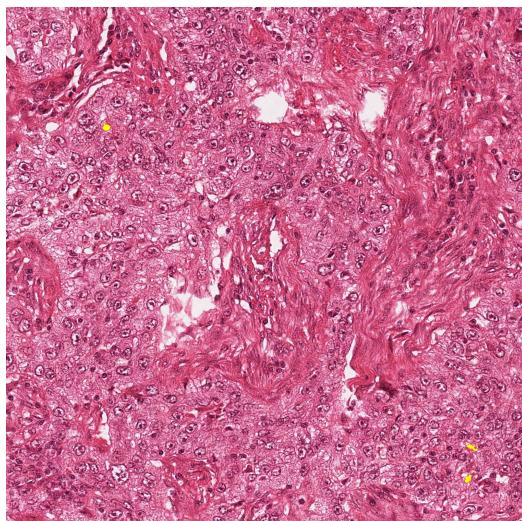
In the paper, 'Fully Convolutional Networks for Semantic Segmentation' by Jonathan and team, [8], the team attempted to create a FCN for the segmentation task. They used pretrained models like VGG Net, Alex Net, GoogLe Net. They fine tuned the parameters and used transfer learning and then trained the model further. They used three datasets - PASCAL VOC, SIFT FFlow and NYUDv2 datasets and found state-of-the-art segmentation on these datasets.

In the paper, 'UNet++: A Nested U-Net Architecture for Medical Image Segmentation', Zongwei Zhou and team [9] attempted to improve the U-Net architecture. The basic model remains the same. UNet++ consists of an encoder and decoder that are connected through a series of dense convolutional blocks. In U-Net model, we have the direct mapping from encoder to

decoder phase. However, in UNet++, they undergo dense convolutions and not a direct mapping with the decoder phase.

## 2.3 Data Set Description

We are using the ICPR 2012 data set. Experienced pathologists have provided a set of 5 breast cancer biopsy slides. The slides are stained with hematoxylin and eosin (HE). In each slide, the pathologists selected 10 high power fields (HPF) at 40X magnification[4].



Slide 1(source: ICPR Dataset 2012)

3 Scanning Equipments have been used:-

An Aperio XT scanner.

A Hamamatsu NanoZoomer scanner.

A 10 bands Multispectral microscope M.

The pathologists have annotated mitosis manually shown in yellow.

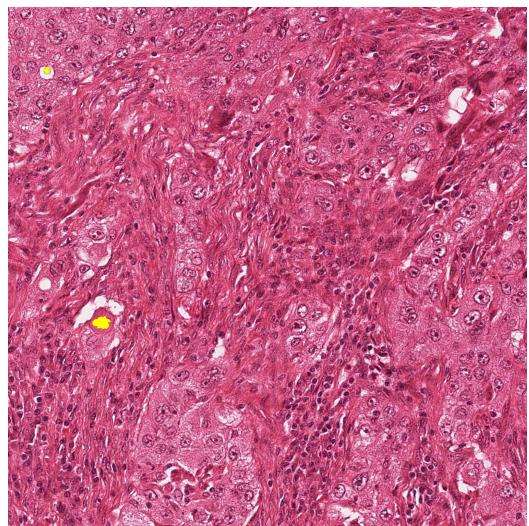
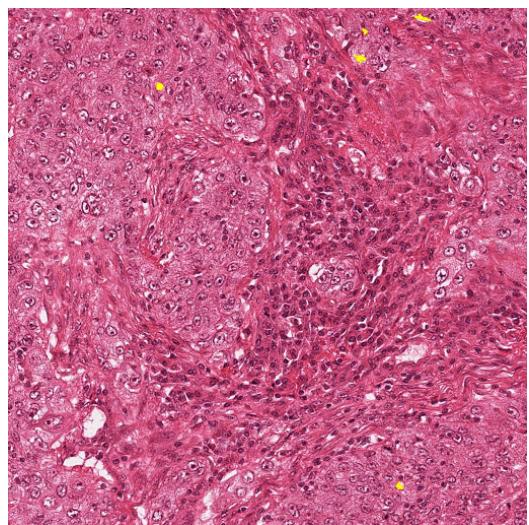


Figure 2.1: Slide 2(source: ICPR Dataset 2012)



Slide 3(source: ICPR Dataset 2012)

# **Chapter 3**

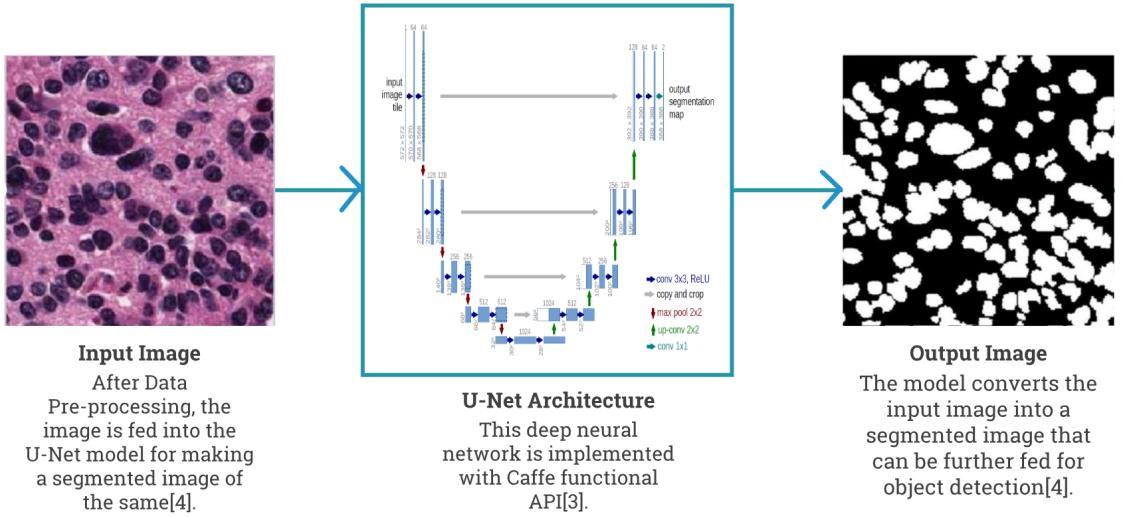
## **Methodology Proposed**

### **3.0.1 Data Prepossessing**

The pre-trained model we use expects a single-channel input image. Hence we used Red, Green and Blue channels individually. Due to loss of stain intensities, we use skimage's `rgb2hed()` function to convert them to Hematoxylin and Eosin channels. As results were not satisfactory, we switched to training the model with the ICPR dataset which is well annotated. For each corresponding image we make a segmentation mask/patch which serves as the target variable/label.

### **3.0.2 Image Segmentation**

The first and foremost task for detecting mitosis in the slides is to create segmentation maps. Image segmentation is the process of partitioning a digital image into multiple segments (sets of pixels, also known as super-pixels). The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyze.[5][6]. We pass tuples of original image and corresponding mask during training. Hence while testing on an unseen image, we receive a segmented image as output.



### 3.0.3 Object Detection

We mark the bounding box co-ordinates for the given mitosis in the slides and create a tuple of the co-ordinates of top left and bottom right points. We also add the count of mitoses in the tuple. Then we apply You-Only-Look-Once(YOLO) algorithm to scan the images and look for mitoses. YOLO will return co-ordinates of all detected mitoses in an unseen image and their count. We pass this data to the classification model.

### 3.0.4 Classification

Our given data contains images of tissues. Each tissue image has some nuclei and we need to classify these nuclei into whether that nucleus is undergoing cancerous or a-cancerous mitosis.

For this, we first need to detect mitotic nuclei using object detection(bounding boxes). After that, to classify whether the mitosis is cancerous or a-cancerous, we will use some parameter like count.

# Acknowledgments

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Thank you.

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