Mitosis Detection in Breast Cancer Histological Images Based On Texture Features Using AdaBoost

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Abstract

Counting mitotic figures present in tissue samples from a patient with cancer, plays a crucial role in assessing the patient's survival chances. In clinical practice, mitotic cells are counted manually by pathologists in order to grade the proliferative activity of breast tumors. However, detecting mitoses under a microscope is a labourious, time-consuming task which can benefit from computer aided diagnosis. In this research we aim to detect mitotic cells present in breast cancer tissue, using only texture and pattern features. To classify cells into mitotic and non-mitotic classes, we use an AdaBoost classifier, an ensemble learning method which uses other (weak) classifiers to construct a strong classifier. 11 different classifiers were used separately as base learners, and their classification performance was recorded. The proposed ensemble classifier is tested on the standard MITOS-ATYPIA-14 dataset, where a 64×64 pixel window around each cells center was extracted to be used as training data. It was observed that an AdaBoost that used Logistic Regression as its base learner achieved a F1 Score of 0.85 using only texture features as input which shows a significant performance improvement over status quo. It is also observed that "Decision Trees" provides the best recall among base classifiers and "Random Forest" has the best Precision.

Keywords Breast cancer grading; Mitosis detection; Computer Aided Diagnosis; Texture Features; Ensemble learning; Pathology.

1. Introduction

Detecting dividing (ie. mitotic) cells is a challenging problem in the field of digital pathology. Mitotic cells are defined as cells that have basophilic cytoplasm and hairy extensions, while having no visible nucleus membrane. In clinical practice, mitotic cells are counted manually by pathologists in order to grade the proliferative activity of breast tumors[1]. However, this task is laborious, subjective and time-consuming. Using computer-based methods for recognizing and counting mitoses can reduce error rates and inter-observer variation. The challenging problem in classifing cells into mitotic and non-mitotic classes is that mitosis is a complex biological process in witch the cell undergoes various morphological transformations, apearing in a large variety of shape configurations[2]. Variation in appearances may also be caused by other factors like aberrant chromosomal makeup of tumors and imperfections of the tissue preparation process[3]. Figure 1 shows a mitotic cell and some non-mitotic cells as an example.

The World Health Oraganization has recommended the Nottingham Grading System for grading breast cancer (i.e malignant, benign or non-cancerous). This system relies on three factors to grade cancer stages: tubule formation, nuclear atypia and the number of mitotic cells present in the tissue, the latter being of significant importance. A simple way to detect or even grade breast cancer is by counting mitotic cells present in a pre-defined area of tissue samples; if the count of mitotic cells is greater than a specific number, it is possible that the tissue is cancerous . In this research we aim to detect mitotic cells present in breast tissue using their texture features. When classifiying cells into mitotic and non-mitotic cells it is important to select features that are available in mitotic cells throughout the mitotic transformation process. Our results show that, being a rotation-invariant feature, histogram and texture features are appropriate for classifying cells using a supervised learning method.

We use Adaptive Boosting[4] for classification of mitotic cells. Adaptive Boosting, also known as AdaBoost, is an algorithm for constructing a "strong" classifier as a linear combination of "weak" classifiers. Weak classifiers can be thought of as features that are weakly related to classes. AdaBoost tries to create a highly accurate prediction rule by combining many rules that are relatively weak or inaccurate.

There are many types of immunohistochemistry stains used forstaining tissues. Our proposed method only works

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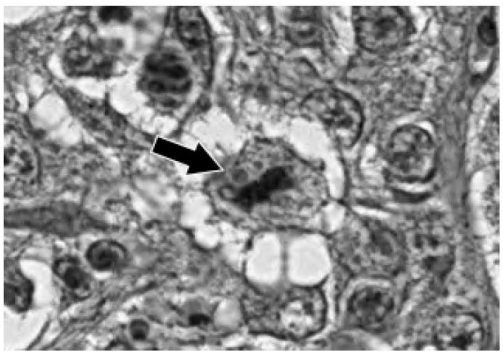
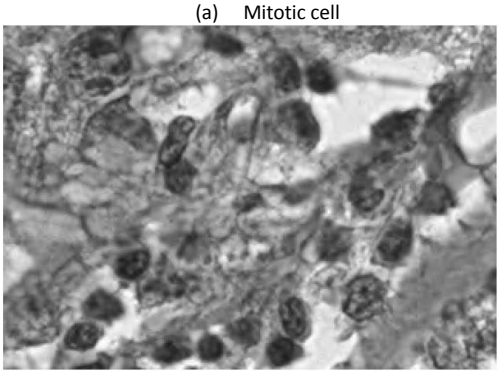


(a) Mitotic cell



(b) Non-Mitotic cell

Fig. 1 Examples of mitotic and non-mitotic cells. In Fig. 1(a) the mitotic cell is located in the center of the image, surrounded by non-mitotic cells.

on biopsy images stained with H&E[1]. The input images should have a dimension of 1539×1376 pixels. Currently our mitosis detection method is limited to detecting mitotic cells in 3-channel RGB color images.

This paper also tries to address the problem of classifying highly-imbalanced data of mitotic and non mitotic cells using adaboost. Various weak learners can be used as base estimators in an AdaBoost classifier. We show that it is possible to classify highly imbalanced data of mitotic cells using AdaBoost with Logistic Regression as base estimator. The literature on mitosis detection in biopsy images is briefly reviewed in Section II. In Section III, the selected features used for classification are briefly discussed. In section IV, our results are presented. Our AdaBoost classifer achieves an F1 measure of 0.85, showing improvement over competing methods. Our results are compared with other detection methods in the last section.

2. Related Work

In histography of breast cancer, a paraffinized section of breast tissue is scanned under a microscope to detect the dividing cells. Mitoses are dark cells that have no visible nuclear membrane, and usually appear to have hairy extensions. To detect and count these cells, there are two main approaches. The first approach is to to detect mitotic cells straightly from the tissue image, usually using neural networks[5-8]. The second approach is segment all the cells that are found in the tissue image, and then classify these cells into mitotic and non-mitotic classes[3,9-13].

The first approach is somewhat straight-forward: pixel values are fed into the neural network; the neural network decides if the image belongs to a mitotic cell or not. Neural networks has been used in a number of studies as a means for achieving high detection performance. For example in [6], the authors used Deep Neural Networks to detect mitotic cells in a single step from the input image. Their performance on the standard AMIDA13 dataset was an F1 score of 0.61, the highest score in the 2013 contest of mitosis detection. Similarly, in [5], Wang et al. used a cascade of handcrafted features alongside convolutional neural network features in order to detect mitotic cells faster than the previously mentioned research. The reported training time for this method was 4 days, with yielded an F1 score of 0.734 on a dataset of 35 images. Both of these methods, however, suffer from high computational overhead and very long training/detection times.

The second approach requires several steps to be performed on the input image beore classifying cells, starting with separating cells from the background tissue, or cell segmentation. Before segmenting cells, it is common practice to pre-process the input images. Improper lighting and non-standard staining usually results in blurred images containing artifacts[2]. Gaussian filter has been used for reducing noise[14] and minimizing the effect of variations in tissue staining[15]. ROI[2] selection is sometimes performed on input images to remove unnecessary processing on input data[16]. Histogram equalization has been used to normalize color distribution to that of a chosen image[17]. Intensity stretching after converting color images to grayscale was done in [18].

The method proposed in [8] employs a morphological double threshold operation to segment candidate cells. It then uses rotation-invariant features such as color, binary shape-based, Laplacian and morphological features. For classification, the authors used a cascade ensemble of AdaBoost classifiers and a single AdaBoost classifier. Results favor cascaded ensemble of AdaBoost classifiers with F1 measure of 58% vs 39% for single AdaBoost classifier. Also, the authors concluded that a granular structure may be a strong evidence for mitosis appearance. In [3], the authors extracted histogram features from cells and used random forests with weighted voting to classify the candidates and reported an F1-score of 0.72. To minimize over-segmentation, the authors developed a method that maximizes gray-level scale-space, blurring images while conserving edges. Histogram and intensity features were selected as rotation-invariant features which are necessary for the problem of mitosis detection. Weighted voting discourages trees with poor classification performance during training.

[1] Hematoxylin and Eosin, fluorescent acidic compounds widely used for staining tissues

[2] Region of Interest

Fig 2. Our proposed method for classifying cells into mitotic and non-mitotic classes

Support Vector Machines has been used in order to detect mitotic cells based on objective and pixel-wise textural features in [12]. Regions of interest were selected using maximum likelihood classification and object-wise local binary pattern features were extracted from the input cells afterwards. The input cells were segmented using morphological operations. The result was a F1 score of 0.71. In another research, SVM was used to classify mitotic cells using a set of 1050 features extracted from grayscale input images[18].

Steps of our proposed method performed on a sample tissue image. The original image is shown in figure (a). In figure (b), pre-processing is performed on previous image. Following this, the blue-ratio image is calculated from the previous step; the image is blurred, then a morphological openning action is performed on the image, removing smaller blobs (figure (c)). The center point of each blob is then taken as the seed point (figure (d)), and a 64×64 window over each center point is extracted, which is shown in figure (e). The extracted cells are then fed to the classifier, classifying each cell as mitotic or non-mitotic, shown in figure (f).

Methods that rely on separating cells before training their classifier usually suffer from failures in their segmentation step. As performing morphological operations on histology images to separate cells often results in false cell boundaries and cells that are not segmented correctly, features extracted from them are not reliable. Thus, we do not segment cells from the background tissue. When segmenting cells, we select a 64×64 pixels window centering the cell, which holds the cell and the background image intact. Moreover, our AdaBoost classfier which uses Logistic Regression as its base estimator, does not need to assign weights to input data, to compensate for class imbalance between mitotic and non-mitotic cells. In the next section our proposed method is presented.

3. Methods

In this study, we use a fully-texture-based strategy for detecting mitoses in breast histopathology images stained with H&E, aiming to improve Precision and Recall of mitosis detection at the same time. Our emphasis is on extracting texture features as rotation-invariant features, while using a simple form of AdaBoost classifier that can classify unbalanced data. In the problem of detecting mitoses in histopathology images, class distribution for mitotic and non-mitotic cells is highly unbalanced, as there are usually very few mitoses against thousands of non-mitotic cells present in a sample tissue.

Mitotic cells usually appear as dark cells with hairy extentions and a granular texture in biopsy images. These cells do not have a specific orientation in the tissue when the cross section of breast tissue is being imaged. Thus, our classification method should be based on rotation invariant features which tend to remain almost unchanged throughout cell division phases. The pipeline diagram of our proposed method is shown in Fig. 2.

3.1 Pre-Processing

The slides from different patients's tissue samples differ in staining conditions and tissue appearance. Non-standard staining leads to unwanted artifacts in the images. Moreover, each batch of slides appears with a different lighting and contrast when scanned under a microscope[2], sometimes leading to noisy, blurred images. Adaptive Histogram Equalization[19] is employed to imporve contrast of the input images. Adaptive histogram equalization is a contrast enhancement method that works by applying to each pixel, the histogram equalization mapping regarding the pixels in a region around it.

Afterwards, the blue ratio image is calculated from each input image. Hematoxylin, which is a dark blue-purple substance, has more concenteration in cell nuclei. Eosin, on the other hand, stains proteins with a pink color. In a stained tissue sample, sometimes the tissue is not stained homogenously, so using blue channel The contrast between mitotic cells and background tissue is enhanced in the blue ratio image. Blue ratio image is defined in equation 1:

$$\text{BRatio} = \frac{B}{1+R+G} \times \frac{256}{1+R+G+B} \qquad (1)$$

where R, G and B are values from Red, Blue and Green channels, for each pixel of the image. This transformation converts an RGB image to a single channel image. Fig. 3(b) shows the effect of pre-processing on a sample image.

3.2 Segmentation

Adaptive thresholding[20] is used for cell segmentation. Biopsy images from batches of biopsy samples from different patients can have a wide range of luminance and appear with variable color intensities. It is not feasible to find a single threshold value to separate (darker) cells from

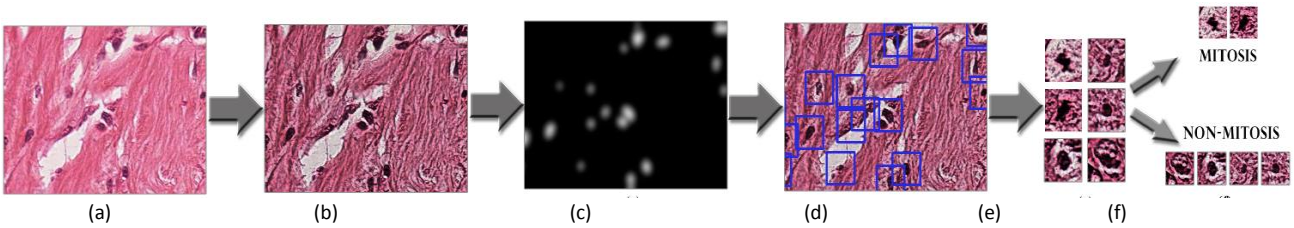


Fig 3. Steps of our proposed method performed on a sample tissue image. The original image is shown in figure (a). In figure (b), pre-processing is performed on previous image. Following this, the blue-ratio image is calculated from the previous step; the image is blurred, then a morphological openning action is performed on the image, removing smaller blobs (figure (c)). The center point of each blob is then taken as the seed point (figure (d)), and a 64×64 window over each center point is extracted, which is shown in figure (e). The extracted cells are then fed to the classifier, classifying each cell as mitotic or non-mitotic, shown in figure (f).

the rest of the tissue. Adoptive thresholding with a block size of 100 pixels and a threshold value of local neighbourhood's mean value was used. The resulting image is noisy, so we perform a morphological openning action on it, removing all blobs smaller than a disk of radius 4 pixels. Seed points located in the center of weight of each cell was then extracted from the resulting binary image. To choose a seed point for each cell, we applied a Gaussian filter so that a dark to bright gradient forms in each blob. Afterwards, center points were detected using regional maximum detection.

Lastly, a 64×64 pixel window around each cells center was extracted to be used as training data. Mitotic and non-mitotic cell nuclei closer than 8μm (approximately 32 pixels) are treated as a single instance, as required by mitosis counting protocol. Thus, if a non-mitotic cells is present in a window containing a mitotic cell, they are treated as a single mitotic cell. Ground truth mitotic cells (annotated by the dataset) were separated from non mitotic cells to be fed to the AdaBoost classifier in the supervised training step. Fig 3(d) shows this step performed on a sample image.

After separating the positive and negative classes, it was observed that there is a high imbalance in the number of two classes. There were about 800 mitotic figures present in the positive class, compared to at least 300,000 non-mitotic cells or dark objects in the negative class. For input images, 60,000 of non-mitotic cell samples where randomly selected to train our classifier. Still, the count of mitotic cells versus non-mitotic cells shows a very high imbalance between the two classes. To mitigate this problem, we rotated each positive class sample that was not located near the edges of the image in 30 degree steps, saving each sample as a new sample. Using this method, the count of positive class was increased to around 9,000, versus 60,000 for negative class. Our data still remained imbalanced, but new instances of positive class result in improved classification performance.

In breast tissue, cells do not have a specific orientation. In other words, a mitotic cell is still counted as a mitotic cell when veiwed from another angle. This idea suggests that features that are rotation-invariant should be selected Performance comparison of AdaBoost classifiers using various base-learners on our un-balanced data.

3.3 Features and Feature Extraction

Mitotic cells are often darker than other cells and appear to have hair like extensions. Mitoses do not take a specific orientation in the tissue, so their shape is captured from various angles in each instance. For features, a total of 112 features that distinguish intensity variations or texture pattern of each cell were selected. To include texture features, Local Binary Patterns, Haralick features and Entropy were selected. Local binary patterns assigns a binary number to each pixel by comparing its neighbour pixels to it[21]. Local binary patterns of input images were calculated. Histograms from the resulting images were calculated over 27 bins. Assuming most cell center points would be located in the center of the 64x64 pixel window. Moreover, another histogram from 32x32 pixel windows centered on each cell seed point was calculated. A vector of 54 float values was created from this feature.

Haralick features[22] was used as a feature that captures texture and tone. Haralick Features First transforms image pixels into a co-occurrence matrix. This matrix is built according to approximity of each pixel with a certain intensity, with pixels that have other intensities. It then calculates a number of statistical features from the matrix. A vector of 56 float values was created from this feature.

Lastly, eight samples from the positive class (mitotic cells) were selected. We selected these cells on the account that their shape represented what a normal mitosis would look like. Similarity to each of these samples was calculated for all training data using template matching method. In template matching, a template image T is slid in over a search image S while its sum of products between coefficients in pixels S(x, y) and T(x, y) is calculated for all pixels of the template image. If the two images were of equal dimentions, a higher sum simply means there two images have more smilarity. Eight float values were extracted as features using template matching with eight representative mitotic cells.

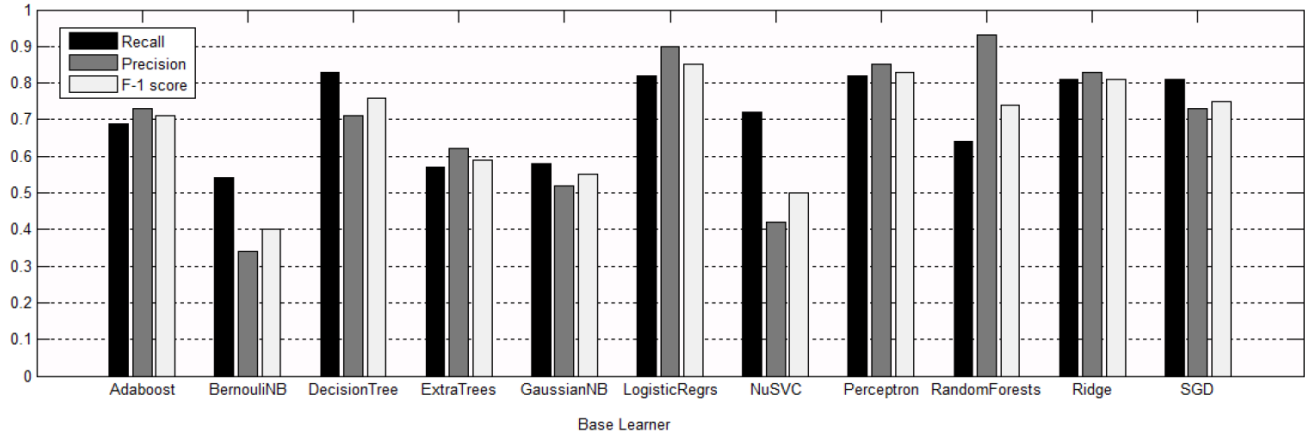


Fig 4. Performance comparison of AdaBoost classifiers using various base-learners on our un-balanced data

3.4 Classification

For classification, every learning algorithm will tend to suit we used AdaBoost[4], an ensemble learning method that combines the performance of many "weak" classifiers, to produce a powerful "commitee" out of them. For mitotic cell classification, various learning algorithms such as Random Forests[3], Cascaded AdaBoost[8] and SVM[18] have been used. AdaBoost's ability to use various weak learners as its base learner makes it a good choice for classifer. An adaboost classifier can also rapidly tweak it's base learners' parameters to fit the dataset, usually without overfitting in practice. For the case of two-class classification with AdaBoost, suppose we have a pool of $n = 2k - 1,\ k \in N$ weak classifiers, each being an expert when classifying a subset of the input data. For a given input xi each classifier kj votes for its opinion $K_j(x_i) \in \{-1,1\}$. The final class decided by this ensemble learning method for xi will be $\mathrm{Sign}(C(x_i))$ where the cost function $C(x_i)$ is defined as [23]:

$$c(x_i) = \alpha_1 K_1(x_i) + \alpha_2(x_i) + \cdots + \alpha_n K_n(x_i) \quad (2)$$

where α denotes the weights that we assign to the opinion of each classifier K. The classifiers K_i -also known as base estimators or weak learners- can be a combination of any types of classifiers. The AdaBoost classifier used in this research, uses only a single type of classifier as the base estimator in each test.

The pseudocode for AdaBoost algorithm is as follows[23]:

For a two-class classification problem, we have T input points x_i and T labels yi taking values of {-1, 1} for the two classes respectively.

Initial weights w_i are assigned to all data points x_i. Let W be the sum of weights wi of all data points and Let W_e be the sum of weights of mis-classified inputs for the considered classifier.

To choose M classifiers from a pool of classifiers, we perform M iterations:

At the m-th iteration, the classifier with the lowest rate of weighted error We is chosen and added to the list of chosen classifiers. In each iteration, AdaBoost systematically extracts a classifier from the pool of classifiers by recording how many of the multidimentional xi points it succeeds to classify. At the beginning, all of the base estimators have the same weight. After each iteration, the more difficult xi's remain to be classified correctly, so AdaBoost's algorithm assigns a larger weight to them. The process of drafting classifiers, tries to add new classifiers to the selected classifiers at each iteration, so that the overall performance improves.

for $m = 1$ *to* M

1. *Choose a classifier km from the pool of classifiers, which would minimize*
$$W_e = \sum_{y_i \neq K_m(x_i)} W_i(m)$$
2. *Set* α_m *,the weight of the classifier* k_m *to*
$$\alpha_m = \frac{1}{2} ln(\frac{1 - e_m}{e_m})$$
where $e_m = \frac{W_e}{W}$
3. *Update the weights of each xi for the next iteration. If classifier km successfully classifies* x_i*, set*
$$w_i^{m+1} = w_i^m e^{\alpha_m} = w_i^m \sqrt{\frac{1 - e_m}{e_m}}$$
otherwise set
$$w_i^{m+1} = w_i^m e^{-\alpha_m} = w_i^m \sqrt{\frac{e_m}{1 - e_m}}$$

4. Implementation and Evaluation

A series of tests were performed on 11 AdaBoost classifiers which had various classifiers as their base learner. In each test a different base estimator was used and the classification performance was measured with 5-fold cross-validation tests. The measures evaluated in our tests were Recall, Percision and F1 score. There has been a few mitos detection contests to date, namely ICPR 2012, AMIDA-13 and Mitos-Atypia-2014. Being a weighted average of Percision and Recall, F1 score was used as the main measuring criteria for comparison in

these contests; Accordingly, we too used F1 score to rank our classifiers' performance.

4.1 Dataset

The dataset used in this research is MITOS-ATYPIA-14. This dataset contains a set of breast cancer biopsy slides taken from 16 patients and prepared according to standard laboratory protocols. The images are scanned using two WSI devices: Aperio Scanscope XT and Hamamatsu Nanozoomer 2.0-HT. In this research we only use the 1,136 frames that have X40 magnification, provided from the Aperio device, and stored as 24 bit RGB bitmap images in TIFF format. The slides are stained with standard H&E dyes which stain cell nuclei with a purple-blue hue while staining underlying tissue with a pink color. The slides are from different batches, scanned under various lighting conditions and are not stained uniformly, to be as realistic as possible.

4.2 Implementation and Parameters

Our classifer was implemented in Python 2.7 on a 64-bit Intel(R) Core(TM) i7-4700MQ processor setup with 8GBytes of RAM. The AdaBoost classifier was provided by the Open-Source Scikit-learn library[24].

We use a number of classifiers as base learners for our main AdaBoost classifier. Some of these classifiers are weak classifiers (for this particular problem), others being strong component classifiers. The authors in [25] suggested that using strong component classifiers in AdaBoost is not viable and most likely will result in overfitting. However, findings in [26] show that when SVM (usually considered a strong classifier) is used as a base estimator with only a small subset of training data fed to it, it can act as a weak classifier; The resulting classification performance may even be greater than that of a SVM classifier or an AdaBoost with other component classifiers.

Classifiers that can be used in an AdaBoost are those that can assign weights to their input data, as this function is essential to AdaBoost's boosting algorithm. The classifiers that were used as base learners are:

1. AdaBoost (as base-learner)
2. Bernouli Naive Bayes
3. Decision Trees
4. Extra Trees
5. Gaussian Naive Bayes
6. Logistic Regression
7. NuSVC
8. Perceptron
9. RandomForest (as base-learner)
10. RidgeClassifier
11. SGDclassifier

The main AdaBoost classifier used 400 base estimators; i.e the main AdaBoost classifier used 400 Perceptrons when using Perceptrons as base estimators. Classifying performance of each resulting classifier was measured and compared, which is presented in TABLE 1. Of the mentioned classifiers, some are based on decision trees, some on neural networks and some others are regressors which can be used as classifiers.

4.3 Evaluation

When test cells are classified into mitotic (positive) or non-mitotic (negative) classes, we can evaluate our classifier's performance. To evaluate the problem of two-class classification, we use three evaluation criteria:

- Precision: The fraction of instances detected by the classifier to those that are relavant. Precision is defined as:
$$\mathrm{Pr} = \frac{\mathrm{TP}}{\mathrm{TP+FP}} \quad (3)$$
- Recall: The fraction of relavant instances to those that are detected by the classifier. Recall is defined as:
$$\mathrm{Re} = \frac{\mathrm{TP}}{\mathrm{TP+FN}} \quad (4)$$
- F1 Score: harmonic mean of Recall and Precision. F1 score is defined as:
$$\mathrm{F}_1 = \frac{2\,\mathrm{Pr.\,Re}}{\mathrm{Pr+Re}} \quad (5)$$

where TP (True Positives) is the count of cells correctly classified as mitotic. Respectively, FP (False Positives) is the count of cells that are wrongly classified as mitotic. True Negatives (TN) are cells correctly classified as non-mitotic. False Negatives (FN) are in fact mitotic cells, but are wrongly classified as non-mitotic.

The performance of our main AdaBoost classifiers varied based on the type of base estimators the main classifier used. It was observed that, without tweaking parameters or assigning any weights to classes, an AdaBoost classifier that used Logistic Regression as its base estimator had the best performance when classifying highly imbalanced data of mitotic cells. The mentioned classifier achieved an F1 score of 0.85, Recall of 0.82 and Precision of 0.90.

The best recall among our classifiers belongs to an AdaBoost that uses Decision trees as its base estimator, with a recall score of 0.83. The best precision belongs to an AdaBoost that uses Random forests as its base estimator, with a precision score of 0.93. We compared the peformance of our classifier with the reported F1 scores from a number of competing methods. The results are shown in Fig. 5, 6 and 7. We compared our average F1Score from 5-fold cross-validation on the input images. Using cross-validation, we ensure that the test data used for measuring performance is not known to our classifier beforehand, thus, measuring the accuracy of our perdictive model in practice.

An AdaBoost classifier using Logistic Regression as base estimator achieved the highest performance when classifying highly imbalanced data of mitotic cells, without tweaking parameters. It was also observed that tweaking parameters, i.e changing estimators count, tweaking class weights or running iteration had little influence (less than 5%) on classification performance.

Table 1: Performance measures showing Recall, Precision and F1 Score for AdaBoost classifers with various base learners

Base Learner	Recall	Precision	F1Score
AdaBoost	0.69	0.73	0.71
Bernouli Naive Bayes	0.54	0.34	0.40
Decision Trees	**0.83**	0.71	0.76
Extra Trees	0.57	0.62	0.59
Gaussian Naive Bayes	0.58	0.52	0.55
Logistic Regression	0.82	0.90	**0.85**
NuSVC	0.72	0.42	0.50
Perceptron	0.82	0.85	0.83
Random Forest	0.64	**0.93**	0.74
Ridge Classifier	0.81	0.83	0.81
SGD Classifier	0.81	0.73	0.75

5. Conclusion and Future Work

Using adaptive thresholding on blue-ratio images of H&E stained breast tissue scanned images, candidate cells were segmented from underlying background tissue. A feature vector of length 144 was then extracted from each input cell image. The extracted features were a number of texture and pattern features. Finally, the input cells were classified using AdaBoost, an ensemble learning method based on boosting. Input data formed two classes: Mitotic and Non-mitotic. There was a high imbalance between the number of the two classes in our training data. To mitigate class unbalance, rotated versions of mitotic cells were also added to the positive class. We tested a number of classifiers as base learners for our main AdaBoost classifier and compared their performance. It was observed that, an AdaBoost classifier that used Logistic Regression as base learner had the best performance when classifying our highly imbalanced set of data. Our results show a significant improvement over similar existing methods.

In future, we plan to employ neural networks to add more features to our classifier. We are also considering using neural networks as a filter applied to the input images, for the task of segmenting cells from background tissue. Classic methods such as thresholding or morphological operations tend to miss some cells when the H&E staining process is not performed uniformly on the tissue, or when lighting conditions are not the same when biopsy slides are scanned.

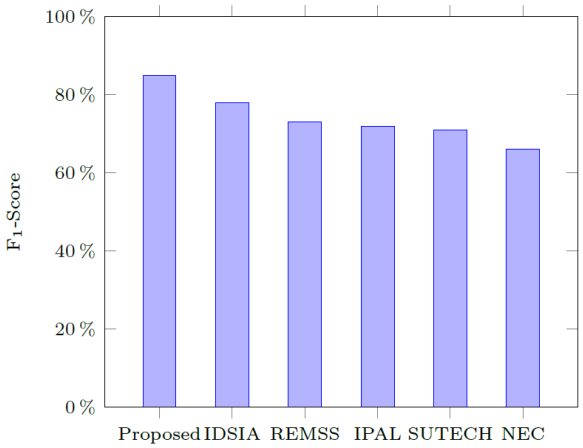


Fig 5. Performance results: F1-Score of our method compared with competing methods from MITOS-14, ICPR2012, AMIDIA-13 contests. IDSIA[6], REMSS[3], IPAL[27], SUTECH[12], NEC[7].

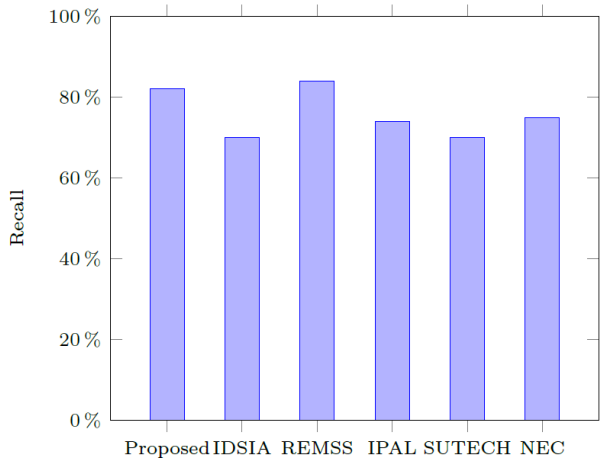


Fig 6. Performance results: Recall of our method compared with competing methods from MITOS-14, ICPR2012, AMIDIA-13 contests. IDSIA[6], REMSS[3], IPAL[27], SUTECH[12], NEC[7].

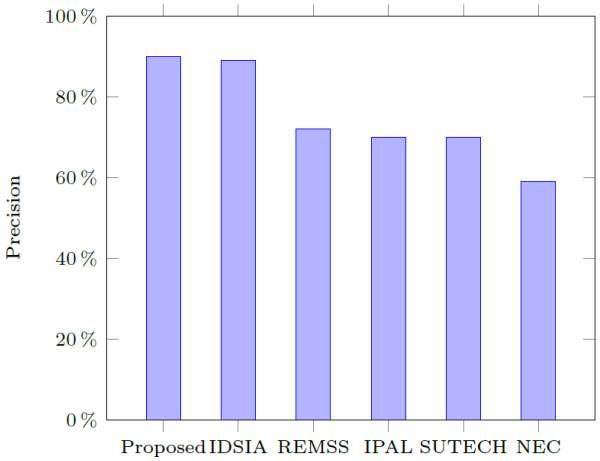


Fig 7. Performance results: Precision of our method compared with competing methods from MITOS-14, ICPR2012, AMIDIA-13 contests. IDSIA[6], REMSS[3], IPAL[27], SUTECH[12], NEC[7].

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