# DETECTION OF MITOSIS IN BREAST CANCER HISTOLOGY IMAGES USING WAVELET SCATTERING REPRESENTATIONS

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## ABSTRACT

Efforts are ongoing worldwide towards the goal of automatic detection and staging of Breast Cancer using Histology images. One of the important parameters used by Pathologists in this task is the Mitotic count as it indicates the aggressiveness of the tumor. Multiple competitions have been organized around this task as accurate detection is seen as a challenging task. The use of representations derived from the Wavelet Scattering Convolution Network (ScatNet), with fixed filters from a Wavelet filterbank, as defined in Bruna and Mallat (2013), for this task, is explored. A classifier is trained to detect occurences of Mitosis on small patches of the microscopic images. The results are impressive with the best system giving an accuracy of 99.53%.

***Index Terms***— image invariants, scattering transform, medical image analysis, mitosis detection

## 1. INTRODUCTION

Breast cancer is one of the leading diseases in the world, and it leads to nearly a million deaths a year across the world. The most common method for staging of breast cancer involves microscopic examination of samples of breast tissue. Currently, this is a labor-intensive manual process. Motivated both by cost-saving and by potential elimination of human error, research efforts are ongoing to automate as well as improve the diagnosis process. An important sub-task in these pipelines is determining the occurrences of *mitosis* [1].

Multiple competitions have been organized around this problem, some of the major ones being the ICPR 2012 Challenge and the MICCAI 2013 Grand Challenge. Both of these were won by the team from IDSIA, Switzerland. Some key aspects of their approach were the use of Deep Convolution Networks, dataset augmentation, and a boosting-inspired technique to tackle challenging false positives. [2]

This work borrows the first two of those ideas. Instead of Deep Convolution Networks, it explores the use of ScatNet which instead of finding the filters using training, used fixed ones from a Wavelet Filterbank.[3] And secondly, the dataset is augmented using using not only rotational and flip transformations, but also horizontal and vertical translations.

## 2. DATASET

The publicly available ICPR 2012 challenge dataset [1] is used to test the approach. The dataset includes thirty-five curated High Power Fields (HPFs). These are basically 2084 x 2084 pixel sized interest regions from the magnified digital slide image obtained using an Aperio scanner. The occurrences of Mitosis in these High-Power Fields have been hand-labeled by researchers trained in the task. We divide the HPFs into small *patches* that either contain or lack instances of Mitosis. The derived dataset of patches included 226 Mitotic patches and ~89000 or ~150,000 non-Mitotic patches for patch sizes of 100 x 100 pixels and 80 x 80 pixels respectively. An example of an HPF, a Mitotic patch and a non-Mitotic patch can be found in **Figure 1**.

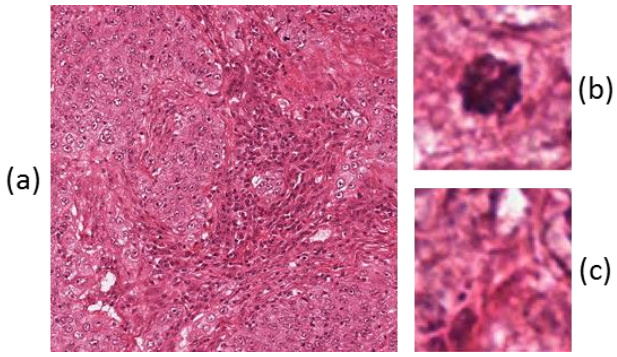


**Figure 1: (a) An example of a High Power Field. (b) An example of an 80 x 80 pixel patch containing Mitosis at the center. (c) An example of an 80 x 80 pixel patch not containing Mitosis**

The full challenge dataset included data from multiple scanners and also separate evaluation datasets, but due to computational limitations, data from only the Aperio scanner was used and 25% of the training dataset itself was held-out for testing. Also, an overwhelmingly large number of non-mitotic patches were available, so these were subsampled to

the exact same number as the mitotic patches. A balanced dataset also being beneficial from the point-of-view of obtaining a high F1-score which is an important metric for the task.

## 3. SCATNET

Each image contains a large amount of data, across all the pixels. Often, we care only about certain "important" aspects of the information in the image, which can be represented compactly. These features should be invariant to transformations such as translation, rotation, scale, and so on. For example, in this application, the position at which epithelial cells are located in the image is irrelevant, and their orientation is also irrelevant.

convolving functions at each node. As in Figure 2, at each layer, the input from the previous layer is convolved with wavelets at different scales and orientations. This is essentially doing a complex wavelet transform, where the information from the Image signal is divided in the complex frequency plane. [5] The number of divisions along the radial axis, J, and L, the number of divisions along the rotational axis, are both configurable. Since, the outputs are taken through averaging filters, in order to get the desired invariant properties, some high frequency information is lost. To recover the same, the un-averaged information is passed to the next layer, where it is again convolved with the wavelet filters. All the outputs are finally combined to form a feature vector. More details about the scattering transform are

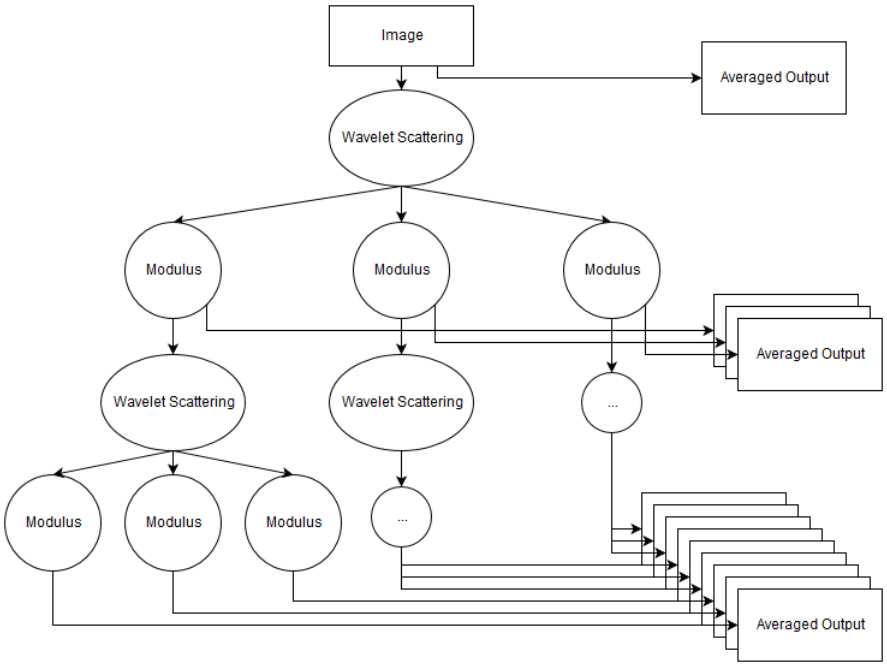


**Figure 2: ScatNet process. The output is the concatenation of all averaged moduli**

Transformations such as SIFT [4] provide some invariant properties and a compact representation of key information. However, in a hypothetical scenario, we may also want to control the degree to which we want our output to be invariant to such transformations. The Scattering Transform, generates a compact representation of the image, and provides control for the degree of invariance desired. Bruna and Mallat [3] suggest that for complex structures over large domains, locally invariant information from SIFT, etc. is insufficient. They say that the Scattering Transform provides not only SIFT-like descriptors at the output of Layer 1, but also higher order information at the further layers, which can help discriminate such complex structures.

The scattering transform is similar to the form of a deep convolution network with wavelets being the

available in Bruna and Mallat [3].

ScatNet also allows configurability of the number of layers, M, the number of scales per octave in the wavelet transform; Q, the amount of oversampling carried out before each layer. To minimize the computational load for calculating the features, the values of the five hyper-parameters were fixed based on previous experience with images at this magnification level, and also apriori knowledge about the invariances at play. The values decided were J = 6, L=1, Q = 1, M = 3 and Oversampling = 1.

ScatNet works with grayscale images and expects the images to be uniformly sized and rectangular. Our data, however, is colored. Further, the staining process causes different components of the tissue to be of a different color, for eg. stromata stain a dull pink, while epithelial cells stain a

deeper purple. The proposed solution involves transforming the image from RGB space to HSV (Hue-Saturation-Value) space, and compute the feature vector independently for each color plane, eventually concatenating the 3 vectors to make the final feature vector.

## 4. DATASET AUGMENTATION

Since the problem of Mitosis detection is Rotation, Flip and Translation invariant, fake additional patches were created using transformations to improve the performance.

Firstly, the problem is translation invariant, but with the initially selected patch size of 80 x 80 pixels, there was very limited scope to set the patch window such that the mitosis is not at the center. This was because some of the mitosis instances were large enough to cover almost the complete area of the patch. Accordingly a larger patch size of 100 x 100 pixels was selected, and random vertical and horizontal translations were applied to the window boundaries such that the centroid of the mitotic region was randomly displaced from the center of the patch.

Secondly, the problem is rotation and flip invariant, so accordingly each patch was converted into a set of 8 patches, one of which being the original patch, second being the 90 degree rotated version, third being the 180 degree rotated version, fourth being the 270 degree rotated version, and the remaining four being horizontally flipped versions of the discussed four.

System (1) is the basic approach wherein the ScatNet features are simply computed for each of the patches and a Radial Basis Function SVM classifier is applied. The scale parameter for the kernel is chosen through MATLAB's heuristic procedure involving subsampling of the data.

System (2) builds on top of System (1). It explicitly addresses the translation invariance property by applying random translations while selecting the window boundaries. The only window size considered here was 100 x 100 pixels because, a smaller size would have negligible margin available for translations in some cases.

System (3) builds on top of System (2). It is the one that further explicitly addresses the rotation and flip invariance properties by carrying out the rotation and flip transformations in addition to the translations of System (2).

| No | Method | 80x80 | 100 x 100 |
|---|---|---|---|
| 1. | ScatNet + RBF SVM | 84.82 | 74.1 |
| 2. | (1) with Random Translations | - | 99.1 |
| 3. | (2) with Rotations and Flips | - | **99.5** |

**Table 1: Accuracies for all systems tested in percentage. Best performer is in bold.**

## 5. RESULTS AND DISCUSSION

Results for each case can be found in **Table 1**. For System (1), 80 x 80 pixel windows performed better. It is felt that since there was limited background, the features could be much more focused on the mitotic activity itself, and the opposite effect took place for the larger windows.

System (2) provided a huge jump in accuracy from System (1), and a whopping 99.1% accuracy was obtained. It is felt that the explicit addressing of translation invariance was really helpful in the detection of mitosis.

System (3) provided a further jump in accuracy to a 99.5%, so clearly, generation of fake rotational and flip transformed variations of the patches was also helpful.

As explained, System (2) and (3) were not deployable on 80 x 80 window sizes. Also, since the sampled dataset and the confusion matrices were balanced, the f1-score values were almost the same as the accuracy fraction.

The author personally finds the results impressive, and regrets the inability conduct further experiments on the full data and to employ the boosting-inspired technique due to lack of more computational power and time. The author expects the f1-score to be lower on the full and unbalanced dataset with more challenging instances, but expects it to be at-least competitive to the top-performing results in [2].

## 6. ACKNOWLEDGEMENT

The idea of employing the Wavelet Scattering Convolution Network (ScatNet) to the Breast Histology images was suggested by Prof. Raghu Machiraju at The Ohio State University. Additionally, the idea of employing ScatNet as an alternative to conventional Deep Convolution Networks for tasks such as the detection of Mitosis was also suggested by Prof. Machiraju.

The MATLAB implementation of ScatNet is credited to Prof. Stephane Mallat's research group at ENS, France.

A course project with ScatNet on a different problem i.e. the classification of Epithelium and Stroma regions in Histology images was done by the author along with Peter Plantinga and Mark Rubeo in the Fall 2015 semester as part of the Advanced Artificial Intelligence course taught by Prof. Eric Fosler-Lussier at The Ohio State University. Figure 2 and the description of ScatNet are adapted from the report prepared for the said project.

## 7. REFERENCES


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