Mitosis Detection using Deep Learning

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Objectives

We attempt to detect mitotic pixels in Breast Cancer histology images by using Deep Learning methods inspired by the technique that won the 2012 ICPR Mitosis Detection competition.

Introduction

Mitosis detection in digital histopathology is a challenging problem because mitotic entities are small objects with a large variety of shapes, and they can thus be easily confused with some other objects or artefacts present in the image. **Mitotic count** is an important parameter in **cancer grading** as it gives an evaluation of the aggressiveness of the tumour.
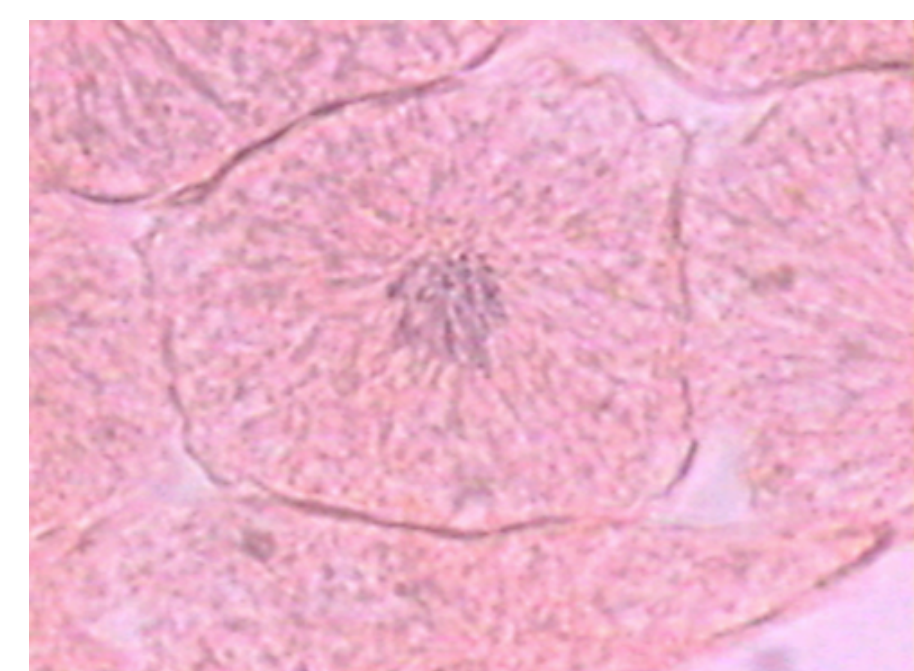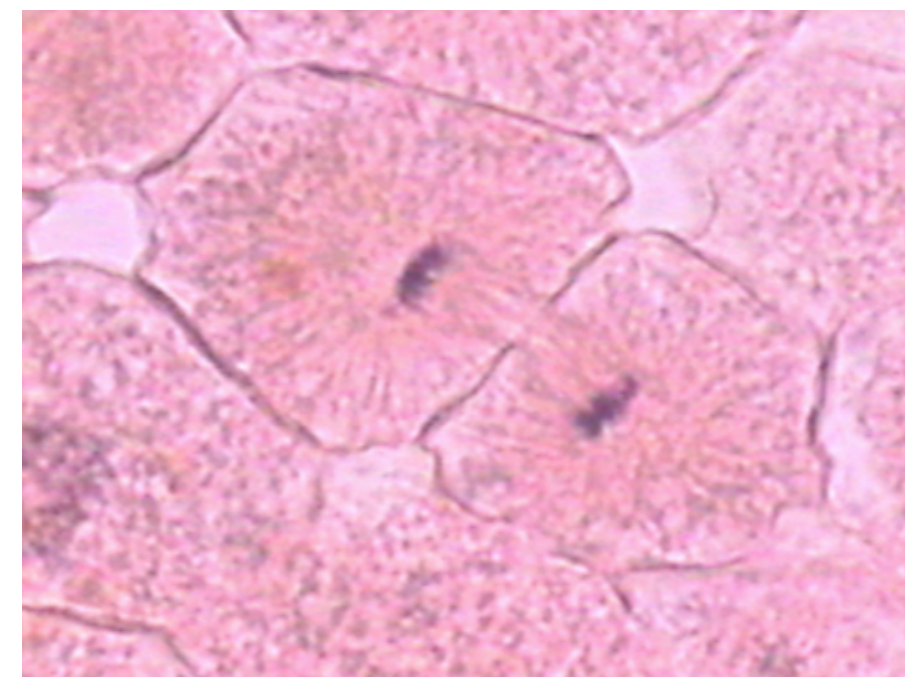
(a) Prophase   (b) Anaphase
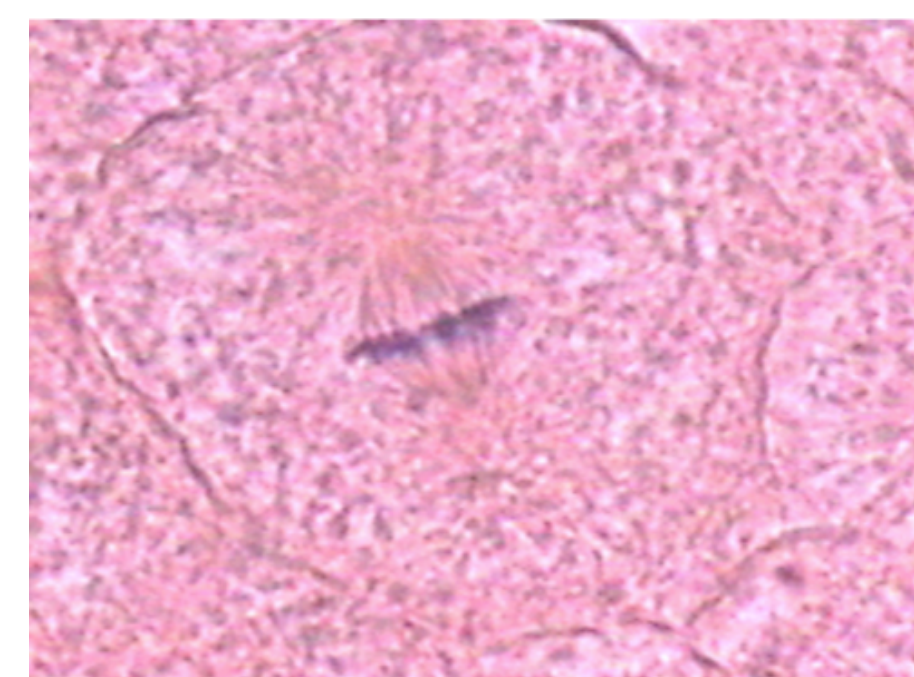
(c) Metaphase   (d) Telophase

Figure: Stages of Mitosis: Structure to be detected by DNN

Detecting mitotic nuclei is a hard problem because they appear in variable shapes and sizes in the histology images. As the dataset contains both the challenging negative cases and the strongly negative cases, it becomes extremely difficult for a classifier to learn the complex features that differentiates them from the positive cases.

Architecture

We first filter out the strongly negative cases with the help of a Base CNN and then train a two CNN ensemble with different sizes of filters to learn the differences between the challenging negative cases and the positive mitotic cases. The architecture of our model is inspired from [1], except for the Base CNN, which we have obtained through experimentation.

Table: Base CNN

	Type	Maps & Neurons	Size
0	Input	3 x 101 x 101	-
1	Convolutional	16 x 96 x 96	6 x 6
2	Max Pooling	16 x 48 x 48	2 x 2
3	Convolutional	16 x 44 x 44	5 x 5
4	Max Pooling	16 x 22 x 22	2 x 2
5	Convolutional	16 x 20 x 20	3 x 3
6	Max Pooling	16 x 10 x 10	2 x 2
7	Fully Connected	200	1 x 1
8	Fully Connected	100	1 x 1
9	Fully Connected	2	1 x 1

Table: First CNN Model

	Type	Maps & Neurons	Size
0	Input	3 x 101 x 101	-
1	Convolutional	16 x 100 x 100	2 x 2
2	Max Pooling	16 x 50 x 50	2 x 2
3	Convolutional	16 x 48 x 48	3 x 3
4	Max Pooling	16 x 24 x 24	2 x 2
5	Convolutional	16 x 22 x 22	3 x 3
6	Max Pooling	16 x 11 x 11	2 x 2
7	Convolutional	16 x 10 x 10	2 x 2
8	Max Pooling	16 x 5 x 5	2 x 2
9	Convolutional	16 x 4 x 4	2 x 2
10	Max Pooling	16 x 2 x 2	2 x 2
11	Fully Connected	100	1 x 1
12	Fully Connected	2	1 x 1

Table: Second CNN Model

	Type	Maps & Neurons	Size
0	Input	3 x 101 x 101	-
1	Convolutional	16 x 98 x 98	4 x 4
2	Max Pooling	16 x 49 x 49	2 x 2
3	Convolutional	16 x 46 x 46	4 x 4
4	Max Pooling	16 x 23 x 23	2 x 2
5	Convolutional	16 x 20 x 20	4 x 4
6	Max Pooling	16 x 10 x 10	2 x 2
7	Convolutional	16 x 8 x 8	3 x 3
8	Max Pooling	16 x 4 x 4	2 x 2
9	Fully Connected	100	1 x 1
10	Fully Connected	2	1 x 1

Results

❶ Base CNN

Accuracy: 99.77% (pixel-wise classification)

F-score: 0.50 (0.42 precision, 0.63 recall)

❷ Main CNNs

Accuracy: 99.77% (pixel-wise classification)

F-score: 0.51 (0.42 precision, 0.63 recall)
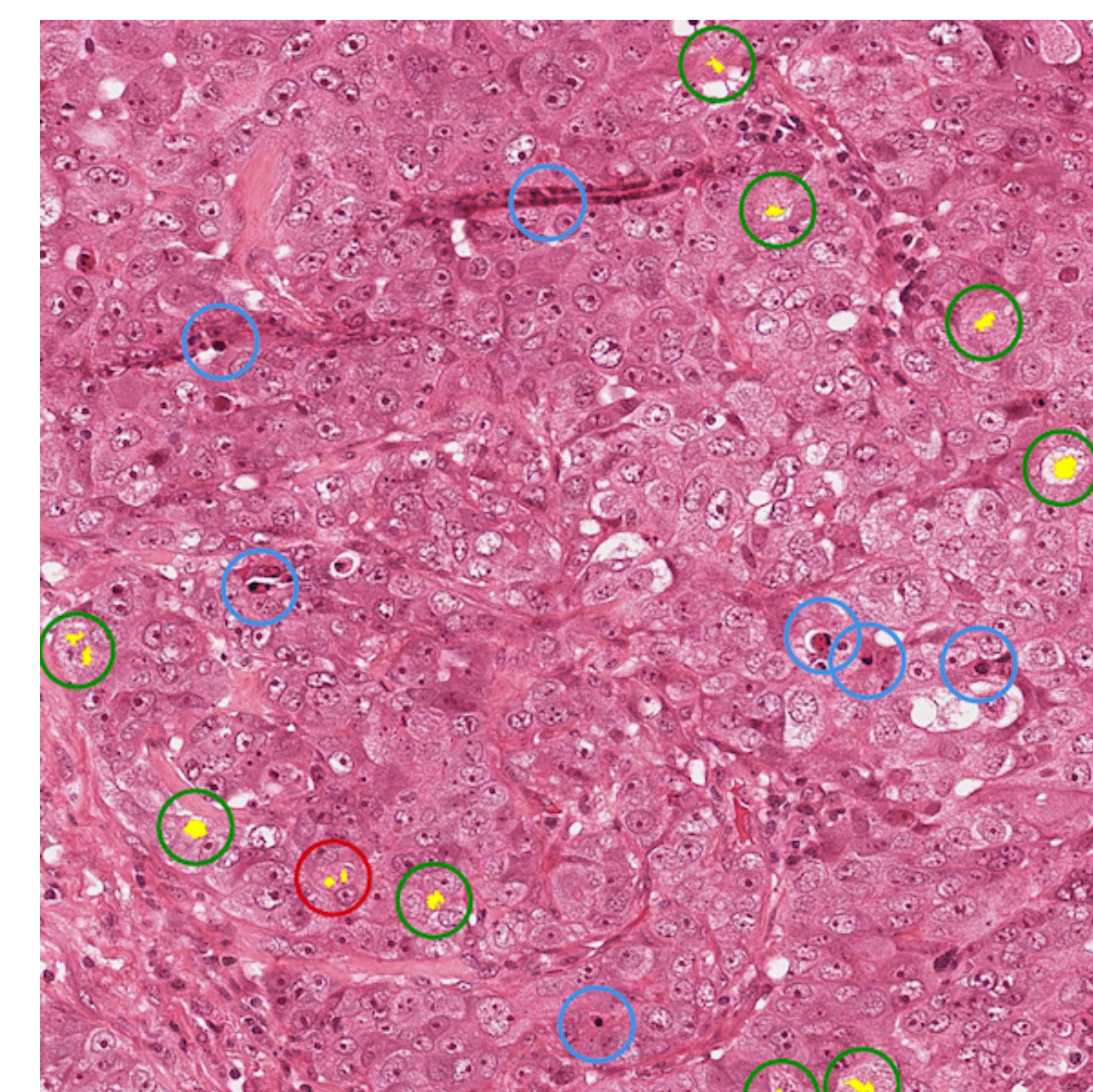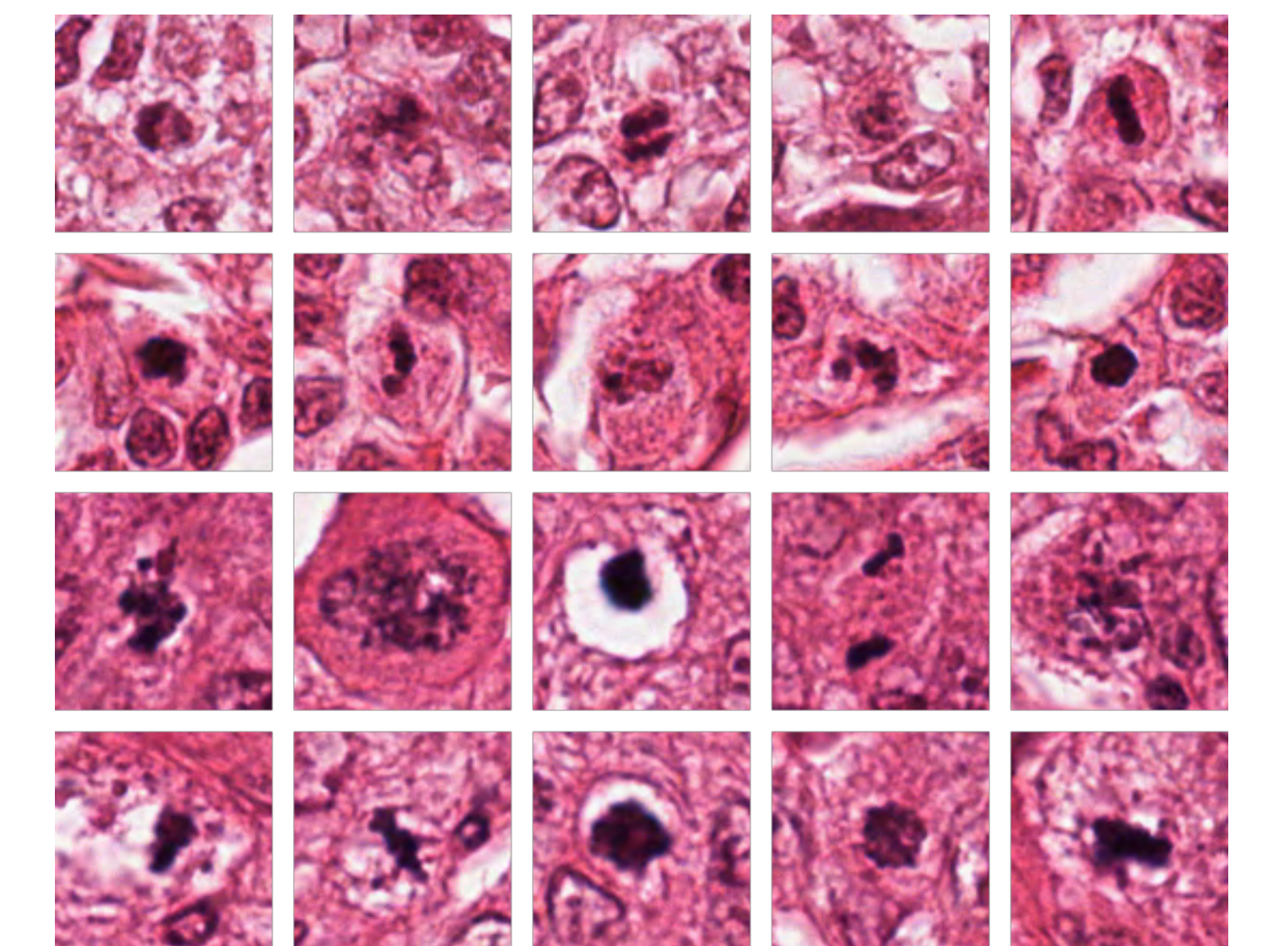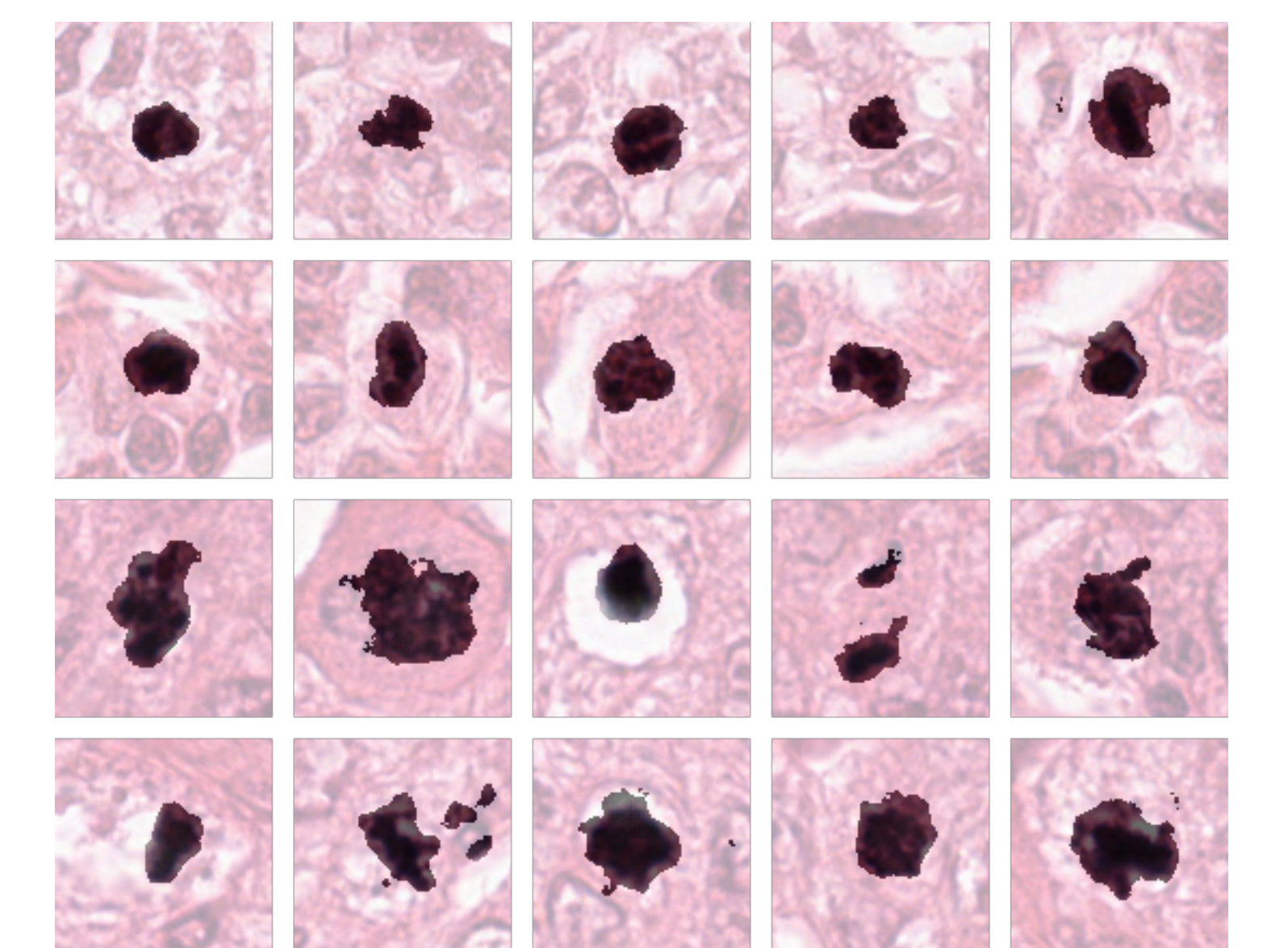
Predictions

Figure: Marked mitotic nuclei. Green: True positive, Blue: False positive, Red: False Negative.

(a) Hand-picked samples of mitotic nuclei

(b) Binary map of predictions

Figure: A collection of challenging mitotic nuclei and their prediction map.

Conclusion

We get almost the same accuracy by taking only the base CNN or taking the base CNN plus the two main CNNs. This occurs because after the filtering of the strongly negative pixels from the image, very few pixels are left for the training of the main CNNs as we have only trained them for about 30 epochs. With more training, the classification will improve as the loss is still going down. But for now, the base classifier gives better results.

References

[1] Cireşan et al.
Mitosis detection in breast cancer histology images with deep neural networks.
In *Medical Image Computing and Computer-Assisted Intervention–MICCAI 2013*, pages 411–418. Springer, 2013.