

Survey on Breast Cancer Detection using Deep Neural Network Techniques

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Abstract— Recent technological advancements in life sciences have opened up possibilities not only to study biological systems from a holistic perspective, but provided unprecedented access to molecular details of living organisms. Medical imaging techniques have widely been in use in the diagnosis and detection of breast cancer. The drawback of applying these techniques is the large time consumption in the manual diagnosis of each image pattern by a professional radiologist. Automated classifiers could substantially upgrade the diagnosis process, in terms of both accuracy and time requirement by distinguishing benign and malignant patterns automatically. Neural network (NN) plays an important role in this respect, especially in the application of breast cancer detection. In this we propose techniques deep neural networks by integrating the predicting the prognosis of women breast cancer.

Keywords: Neural Network, Breast Cancer, Deep Neural network and Images.

I INTRODUCTION

A major current challenge and opportunity in biology is interpreting the increasing amount of information-rich and high-throughput single-cell data. Here, we consider 46 imaging data from fluorescence microscopy [1], 1 particular from imaging flow cytometry [2]. Imaging flow cytometry (IFC) combines the fluorescence sensitivity and 48 high-throughput capabilities of flow cytometry with single-cell imaging. Relevant 49 fluorescent labels are chosen to assess certain phenotypes of interest. The large number 50 of single cells analyzed per sample often hundreds of thousands makes imaging 51 flow cytometry unusually well-suited to deep learning, which demands very large 52 training sets.

The need for novel healthcare solutions and continuous efforts in understating the biological bases of pathologies has pushed extensive research in biological sciences over the last two centuries. Recent technological advancements in life sciences have opened up possibilities not only to study biological systems from a holistic perspective, but provided unprecedented access to molecular details of living organisms. Novel tools for DNA sequencing, gene expression (GE), bio imaging, neuroimaging, and brain-machine interfaces are now available to the scientific community.

Breast cancer is one of the main causes of death among women and the most frequently diagnosed non-skin cancer in women. Breast cancer occurs when the cell tissues of the breast become abnormal and uncontrollably divided. These abnormal cells from large lump of tissues, which

consequently becomes a tumor. Such disorders could successfully be treated if they are detected early. Thus, it is of importance to have appropriate methods for screening the earliest signs of breast cancer.

Automated classifiers may be useful for radiologists in distinguishing between benign and malignant patterns. Thus, in this paper, an artificial neural network (ANN) which can be served as an automated classifier is investigated. In medical image processing, ANNs have been applied to a variety of data-classification and pattern recognition tasks and become a promising classification tool in breast cancer [4]. ANN applications in mammography, ultrasound, and MRI and IR imaging for early detection of breast cancer are reviewed in this paper. Image features can be distinguished in many aspects, such as texture, color, shape, and spatial relations. They can reflect the subtle variance in many degrees. Thus, different selections of image features will result in different classification decisions. These classifications can be divided into three types: first, the method based on statistics, such as Support Vector Machine; second, the method based on rule, such as decision tree and rough sets; and third, artificial neural network

II LITERATURE SURVEY

In one important problem is automatically detecting the cellular compartment where a fluorescently-tagged protein resides, a task relatively simple for an experienced human, but difficult to automate on a computer. Here, they train an 11-layer neural network on data from mapping thousands of yeast proteins, achieving per cell localization classification accuracy of 91%, and per protein accuracy of 99% on held-out images. In this they confirm that low-level network features correspond to basic image characteristics, while deeper layers separate localization classes. Using this network as a feature calculator, they train standard classifiers that assign proteins to previously unseen compartments after observing only a small number of training examples [1].

In this paper [2] they present Deep Flow, a data analysis workflow for imaging flow cytometry that combines deep convolutional neural networks with non-linear dimension reduction. DeepFlow uses learned features of the neural network to visualize organize and biologically interpret single-cell data. Dissecting the cell cycle as a source of cell-to-cell variability is crucial for quantitative single-cell biology. They demonstrate Deep Flow for a large dataset of cell-cycling Jurkat cells. First, they reconstruct the cells' continuous progression through cell cycle from raw image data. This shows that DeepFlow can learn a continuous distance measure between categorical phenotypes. Second, they are able to detect and separate a subpopulation of dead cells, although the data set had been cleaned using established approaches. DeepFlow detects

this morphologically abnormal subpopulation in an unsupervised manner

In this paper [3] they develop an approach that combines deep convolutional neural networks (CNNs) with multiple instances learning (MIL) in order to classify and segment microscopy images using only whole image level annotations. Results: They introduce a new neural network architecture that uses MIL to simultaneously classify and segment microscopy images with populations of cells. This proposed approach on the similarity between the aggregation function used in MIL and pooling layers used in CNNs. To facilitate aggregating across large numbers of instances in CNN feature maps they present the Noisy-AND pooling function, a new MIL operator that is robust to outliers.

In this paper [4], they propose a solution which adopts Convolutional Neural Networks (CNN) for counting the number of colonies contained in confluent agglomerates that scored an overall accuracy of the 92.8% on a large challenging dataset. The proposed CNN-based technique for estimating the cardinality of colony aggregates outperforms traditional image processing approaches, becoming a promising approach to many related applications.

In this proposed [5] approach won the ICPR 2012 mitosis detection competition, outperforming other contestants by a significant margin. Mitosis detection is very hard. In fact, mitosis is a complex process during which a cell nucleus undergoes various transformations. In addition, different image areas are characterized by different tissue types, which exhibit highly variable appearance. A large amount of

different structures can be observed in histology images stained with Hematoxylin & Eosin, and in particular many dark-blue spots, most of which correspond to cell nuclei.

The Nottingham Histologic Score system is highly correlated with the shape and appearance of breast cancer nuclei in histopathological images. However, automated nucleus detection is complicated by (1) the large number of nuclei and the size of high resolution digitized pathology images, and (2) the variability in size, shape, appearance, and texture of the individual nuclei. Recently there has been interest in the application of “Deep Learning” strategies for classification and analysis of big image data. Histopathology, given its size and complexity, represents an excellent use case for application of deep learning strategies. In this paper, a Stacked Sparse Auto encoder (SSAE), an instance of a deep learning strategy, is presented for efficient nuclei detection on high resolution histopathological images of breast cancer [6].

In this paper [7], they address a central problem of neuroanatomy, namely, the automatic segmentation of neuronal structures depicted in stacks of electron microscopy (EM) images. This is necessary to efficiently map 3D brain structure and connectivity. To segment biological neuron membranes, they use a special type of deep artificial neural network as a pixel classifier. The label of each pixel (membrane or nonmembrane) is predicted from raw pixel values in a square window centered on it. The input layer maps each window pixel to a neuron. It is followed by a succession of convolutional and max-pooling layers which preserve 2D information and extract features with increasing levels of abstraction. The output layer produces a calibrated probability for each class.

Table I. Survey Table

| Sr. No. | Paper Name | Authors Name | Technique Used | Disadvantages |
|---------|--|---|--|---|
| 1 | Accurate Classification of Protein Subcellular Localization from High-Throughput Microscopy Images Using Deep Learning | Tanel Parnamaa and Leopold Parts | DeepYeast used for other image analysis experiments with the same marker proteins and magnification. | Experimental result shows that the performance of this system is weak. |
| 2 | Deep Learning for Imaging Flow Cytometry: Cell Cycle Analysis of Jurkat Cells | Philipp Eulenberg, Niklas Klsohler, Thomas Blasi1, Andrew F. Alexander Wolf | DeepFlow, a data 21 analysis workflow for imaging flow cytometry that combines deep convolutional neural 22 networks with non-linear dimension reduction. | They could not detect even a slight indication of bleed through in the Jurkat 336 cell data |
| 3 | Classifying and segmenting microscopy images with deep multiple instance learning | Oren Z. Kraus, Jimmy Lei Bai and Brendan J. Frey | Deep convolutional neural networks (CNNs) with multiple instance learning (MIL) in order to classify and segment microscopy images using only whole image level annotations. | Classification performance of this techniques is weak. |
| 4 | Bacterial Colony Counting by Convolutional Neural Networks | Alessandro Ferrari, Stefano Lombardi, Alberto Signoroni | Convolutional Neural Networks (CNN) for counting the number of colonies contained in confluent agglomerates | Improvements in the performance. |
| 5 | A Multimodal Deep Neural Network for Human Breast | Dongdong Sun, Minghui Wangand | Prognosis prediction of women breast cancer, they | The worst performance of the system occurs due to small |

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| | Cancer Prognosis Prediction by Integrating Multi-Dimensional Data | and Ao Li | proposed multimodal deep neural networks by integrating multi-dimensional data. | sample size and high dimensional data are used. |
| 6. | Breast cancer detection without removal pectoral muscle by extraction turn counts feature | F. K. Nezhadian, and Saeid Rashidi | Extracting the feature of the mammography image without removing pectoral muscle in the preprocessing stage. | Accuracy of this method for diagnosis normal and abnormal. Additional extraction of features can increase accuracy for diagnosis with benign and malignant cancer |

III CONCLUSION

Breast cancer is the most common disease and is usually associated with poor prognosis. Thus there is an urgent need to develop effective and fast computational methods for breast cancer prognosis prediction. The success stories of ANN, deep architectures, and reinforcement learning in making machines more intelligent are well known. Furthermore, computational costs have dropped, computing power has surged, and quasi-unlimited solid-state storage is available at a reasonable price.

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