HOCHSCHULE FÜR ANGEWANDTE WISSENSCHAFTEN WÜRZBURG-SCHWEINFURT

AUTOMATED CELL COUNTING FOR LABORATORY AUTOMATION IN LIFE SCIENCES

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ABSTRACT

Cell counting has been a vital aspect of life sciences and biological research to date. However, the procedure is done manually and can be tedious, with Hemocytometer (Neubauer Chamber) being the most frequently used manual cell counting method. This method provides a geometrical grid which specifies the region of interest of the count. In this paper, we propose using Convolutional Neural Network based algorithms (Faster RCNN and YOLOv4) to automate cell counting and compare it with the conventional method. This proposed technique employs deep learning and image processing to isolate the chamber grid patterns, recognize each region of interest, and perform the count. It is also necessary to evaluate the results, establishing the accuracy of the proposed method and creating a Graphical User Interface (GUI) for the method that gives the best cell counting benchmark for optimal use of the method in a laboratory.

1.0 INTRODUCTION

Image-based cell counting is essential to a wide range of biological research problems [1], since the growth or decay rate of the cells in any environment, natural or artificial, makes available valuable insights into the behavior of the cell in question.

Usually scientists' resort to manual cell counting by the utilization of the Neubauer Chamber, otherwise known as a Hemocytometer, and microscopes. The Neubauer chamber encloses a section of the solution in a grid of well-known dimensions and, with the help of a microscope which procures pictures of the enclosed grid as shown in the figures below. By counting the cells in each box and the number of boxes or squares used in the cell count, the concentration per milliliter of solution can be estimated.

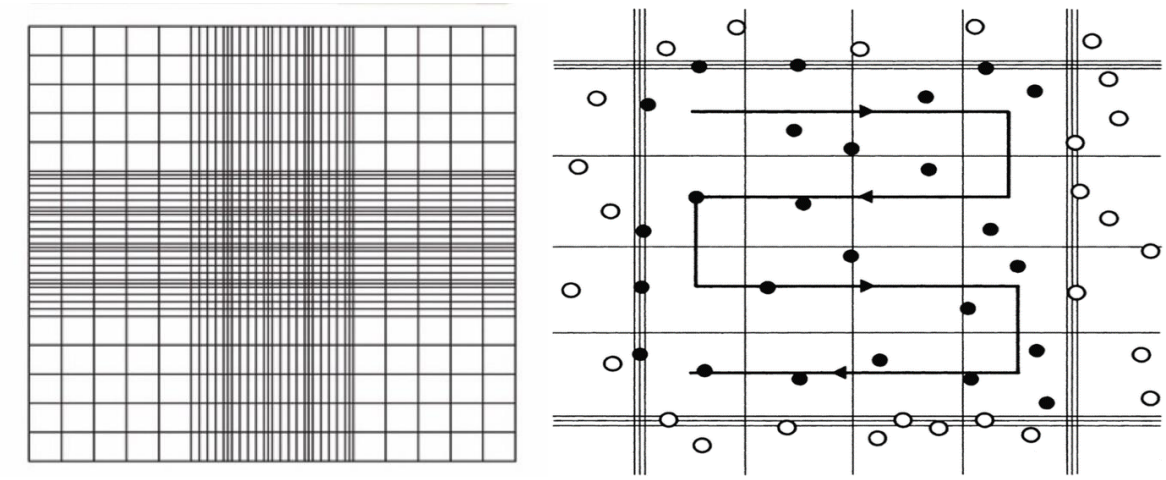

Fig. 1: a) The Neubauer chamber grid. b) Counting the cells using a Neubauer Chamber [2].

This method can be tedious and requires proper training and experience to use. Even with experience it is still error prone as the environment and the physical capacity, eyesight, stress level of the scientist in question can affect the count, making the procedure mostly an estimate.

Therefore, the importance of creating a fast and reliable method of performing cell counting cannot be overstated. Recently, with the advances of Machine Learning and object detection, new innovative methods of cell counting favor the use of Deep Neural Network methods due to their adaptability in various research areas. This method is also not without its own drawbacks but the advantages it offers outweigh the question of automation taking away jobs from people. Instead it enables scientists focus more on the necessary work of solving problems in life sciences.

Object detection and localization have seen much progress in the machine learning community. For example, Region-based Convolutional Neural Networks (R-CNN) [3], Fully Convolutional Networks (FCN) [4] and You Only Look Once (YOLO) [5] have become the state-of-the-art algorithms for the object detection problem.

2.0 RELATED WORK

Object detection and counting is generally realized by training a neural network or by template matching. When training a neural network, the objective is for the network to detect the object and further instantiate the number of times the object was detected. One of the major draw backs and time-consuming part of this method is the data labelling with the area of interest. A different approach consists of forecasting object density instead of precise object locations as proposed by Lempitsky and Zisserman [6] and by Xie et al. [7] for microscopy images.

In this paper, we propose solving the cell detection and counting problem using the precise location data labelling and Faster RCNN training procedure.

3.0 RESEARCH QUESTION AND APPROACH

The main approach would be to train a neural network to recognize cells from a static or dynamic feed and count them. The approach can be classified as a supervised learning one of the two major machine learning classifications [5]. The first step ideal will be to collect and process the datasets in a way that is relatively easy for the computer to understand using image processing among other techniques. Secondly the neural network will be trained with the necessary requirements, a GPU enabled computer and the transformed dataset.

The goal is not limited to comparing this machine learning method with the conventional hemocytometer method but also to ascertain the technicality involved in scaling up the process without the need of someone working directly with it. Although this could be troublesome it is worthwhile to investigate.

TIMELINE

With the time required to collect and label a sufficient dataset, train, compare the methods and create a graphical user interface for a laboratory integration, a timeline of 3-5 months would be recommended before moving to the possible automation of the labelling process for easy scale up.

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