

Classifying Transmission Electron Microscopy Virus Textures

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Abstract

Determining the identity of a virus sample is of utmost importance in today's medical community. An incorrect classification of the virus can be life-threatening not only to the patient, but to people surrounding him or her. A transmission electron microscopy image of a virus sample can be hard to discern for the human eye and a doctor needs to be positive about the identity of the virus i.e., if it's Influenza or Ebola. Fortunately, machine learning algorithms perform exceedingly well on image classification tasks and don't require expert knowledge to do so. Here we present a successful application of using convolutional neural networks to classify viruses samples into one of 15 categories and compare its performance to previous work done on the same task.

1. Introduction

2. Related Work

In the work of Kylberg et al. [1], texture analysis is performed on the virus samples and the resulting feature vector is fed to a Random Forest classifier. They are comparing the performance of different texture analysers such as Local Binary Patterns and Radial Density Profile along with their respective variants. First, we will briefly explain the feature extractors they used. Then, we will present the results they got.

2.1. Local Binary Profile (LBP)

Given an image, for each pixel p_i in it, sample n equally-spaced points on the circle of radius r with center p_i and construct a vector $v(p_i)$ such that its i th entry is a 1 if the i th sampled pixel has a value bigger than p_i or a 0 otherwise. With its sequence of 0s and 1s, $v(p_i)$ now makes a binary number v_{p_i} , hence the name. Once we have the v_{p_i} for all pixels, we construct a histogram counting the number of appearances of each value v_{p_i} . The histogram is the feature

vector associated with the given image. Kylberg et al. [1] denote this feature extraction method by $LBP_{n,r}$, where n is the number of sampled points and r is the radius, as described above. The resulting histogram is represented in a vector of counts with 2^n elements.

In order to reduce the size of that feature vector, Kylberg et al. [1] mention a modification of LBP in the following sense: instead of creating v_{p_i} by interpreting the vector $v(p_i)$ and using v_{p_i} as is, rotate the number v_{p_i} bitwise until you get the smallest possible number. For example, the number 110 would turn into 011. They name it rotational invariant and denote it with $LBP_{n,r}^{ri}$.

To further reduce the size of the histogram, they also try restricting the values of v_{p_i} to only numbers that have 2 or less transitions from 0 to 1 or from 1 to 0 and they call this variant "uniform binary patterns with at most 2 spatial transitions", denoted $LBP_{n,r}^{u2}$. For example, 01010 has 2 transitions from 0 to 1 and 2 transitions from 1 to 0 which makes 4 transitions in total so this version $LBP_{n,r}^{u2}$ would not count that number. On the other hand, 00111 has only 1 transition from 0 to 1 so it is accepted.

References

- [1] Gustaf Kylberg, Mats Uppström, and Ida-Maria Sintorn. Virus texture analysis using local binary

patterns and radial density profiles. In *Progress in Pattern Recognition, Image Analysis, Computer Vision, and Applications*, pages 573–580. Springer Berlin Heidelberg, 2011.