Unsupervised Learning for Analyzing Brain Tumors

Christopher Elamri Guillermo Angeris Teun de Planque

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Abstract

Every year 256,000 new cases of brain cancer are diagnosed worldwide. Early diagnosis and better understanding of the specific types of tumors of brain cancer patients can significantly increase survival rates [1]. We used unsupervised learning algorithms in combination with Gaussian smoothing and Gabor filters to directly analyze 3D MRI brain images in order to discover spatial regions correlated to different types of brain tumors.

1 Introduction

Localized brain tumors are highly treatable when diagnosed in an early stage [1]. According to the National Cancer Institute, the average 5-year survival rate of people with a localized brain tumor (grade I, diagnosed early) is 77% [1]. However, if the brain tumor is diagnosed after metastasis, the 5-year survival rate quickly drops to less than 10% [1]. In other words, an early and accurate diagnosis is essential for full recovery. Thus, it is important to develop new methods to improve existing imaging methods. We propose using unsupervised learning algorithms such as k-medoids clustering, and k-means clustering in combination with 3-dimensional Gabor filters and Gaussian blur to directly analyze MR brain images in order to find clusters related to specific types of brain tumors. Since some types of brain tumors are less responsive to specific kinds of treatments that are highly effective for other types, the classification of different types of brain tumors can help doctors find more effective treatments. Hence, our classifications may prove to be helpful not only in early detection but also in improving cancer treatments of brain tumors.

2 Dataset

We use the 2013 BraTS dataset[1] containing four types of magnetic resonance 3D images (MRI) of the brain of each cancer patient. Each image has four modalities (FLAIR, T1 pre-contrast, T1 post-contrast, and T2 weighted).[2] An additional segmentation file has labels for different parts of the tumor (1: necrosis, 2: edema, 3: nonenhancing, 4: enhancing), created by a medical professional for the explicit purpose of classification. All the meta-image files contain a 3-dimensional matrix of pixel values representing the consolidated slices of a single MRI scan which have been co-registered; that is, the value of a pixel (x, y, z) of one brain corresponds to the (x, y, z) pixel of another (pixel here is interchangeable with voxel[3]) in terms of relative location in the brain.

3 Analysis and Methods

3.1 Classification Techniques

We use different unsupervised learning algorithms including k-means and k-medoids clustering [2]. We cluster the described images in order to meaningfully correlate spatial regions to tumor areas. In particular, we cluster each voxel based on its z-score relative to the mean and variance of the distribution of pixels, as a means of standardizing over several different scans. Both k-means and k-medoids are sensitive to initializations; however, we use MATLAB software which runs k-means++, a version of k-means that uses a heuristic to find centroid seed for k-means clustering [2]. k-means++ improves both the running time and the quality of the final optimum. We use k-medoids because of both its usefulness for clustering categorical data where a mean is impossible to define

[1] Found at http://martinos.org/qtim/miccai2013/.

[2] FLAIR (Fluid-attenuated inversion recovery): provides better delineation of the lesions adjacent to the ventricles and gives better definition for edema and tumors. T-modalities enable different imaging contrasts that differentiate parts of the tumor and normal adjacent cells.

[3] A voxel represents a value on a regular grid in three-dimensional space.

or interpret, and its increased robustness to outlier data compared to k-means++ [2].

3.2 Gaussian Blur

We first preprocess the voxels by convolving with a Gaussian kernel. This kernel produces a distribution of which the mean is at the kernel's center [3] [4] and that then decays outwards by the euclidean norm. In particular, we convolve our pixel values with a kernel of the form

$$g(x,y,z) = \frac{1}{(2\pi)^{3/2}\sigma^3} \exp\left(-\frac{x^2+y^2+z^2}{2\sigma^2}\right).$$

The resulting smoothing spatially correlates pixels in the image according to the given Σ matrix [5], *e.g.* the larger the value of σ, the larger the bandwidth and the more correlation induced between spatially more separated pixels. In the current application, the bandwidth of the Gaussian convolution kernel was found using cross-validation.

3.3 Gabor Filters

Furthermore, we add features to the image's pixel values using Gabor filtering by convolving with a sinusoid modulated by a Gaussian curve:

$$h(x,y,z) = g(x,y,z)s(x,y,z)$$

where

$$g(x,y,z) = \frac{1}{(2\pi)^{3/2}|\Sigma|^{1/2}} \exp\left(-\frac{1}{2}\bar{q}^T\Sigma^{-1}\bar{q}\right).$$

Here, $\Sigma = \text{diag}(\sigma_x^2, \sigma_y^2, \sigma_z^2)$ is diagonal, $\bar{q} = (x,y,z)$, and

$$s(x,y,z) = \cos(2\pi(vx+uy+wz))$$

is the sinusoid.

Generally speaking, the Gabor filter is a special case of a wavelet basis in which the function that forms the basis minimizes its standard deviations in both the time and frequency domains[4] [6]. Generally speaking, wavelet transforms take the form [7]

$$T(a,b) = \frac{1}{\sqrt{|b|}} \int_{\mathbb{R}} dt\, f(t)\psi\left(\frac{t-a}{b}\right)$$

This is equivalent to (allowing $b = 1$)

$$T(a) = \int_{\mathbb{R}} dt\, f(t)\psi(t-a) = \{f * \psi\}(a)$$

which can be done efficiently given $\psi(t)$, by multiplication in the Fourier domain. This generalized transform is useful and natural in the detection of features such as edges and other rotationally-invariant features due to their similarity to receptive fields in animal experiments [8]. These characteristics make it a desirable choice for experimentation in a high-dimensional space which cannot be visually inspected.

In order to decompose 3-dimensional images into relevant texture features, we generate a large Gabor filter bank to be convolved with the 3-dimensional image for the purpose of classification [8]. These resulting values are then appended to each pixel vector, which is then used to classify each *a priori* into k groups by the algorithms defined in the previous section.

4 Experimental Results

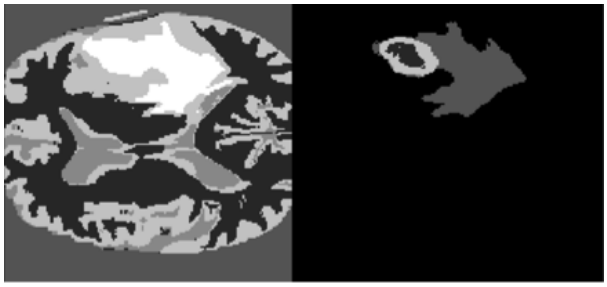

Figure 1: k-means with k = 5

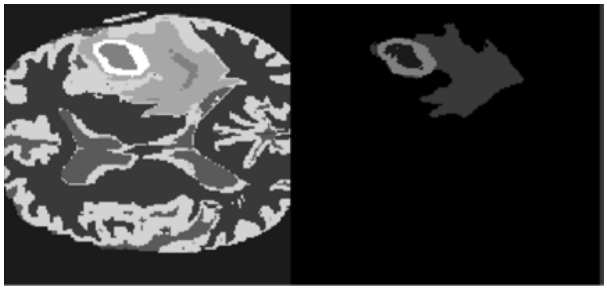

Figure 2: k-means with k = 6

[4] That is, given its width in the frequency domain, Δf and time domains Δt, we have, for any transform $(\Delta f)(\Delta t) \geq \frac{1}{2}$. In this general case, we minimize to the lower bound by finding the function such that $(\Delta f)(\Delta t) = \frac{1}{2}$; this function then becomes our Gabor wavelet.

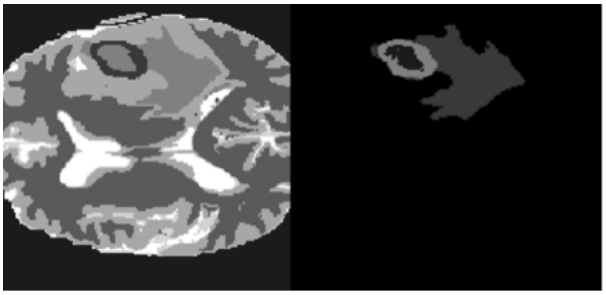

Figure 3: k-means with k = 7

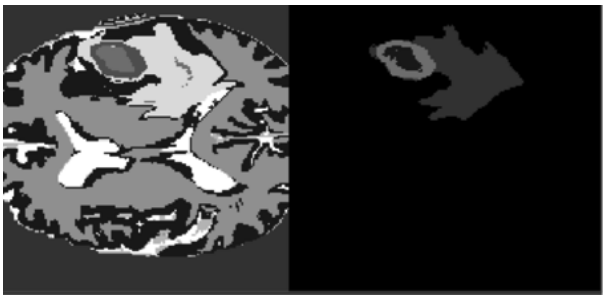

Figure 4: k-means with k = 8

As visible in the above figures, our analysis of the tumor using k-means clustering is similar to that of the doctor. In all figures the right image shows the tumor analysis of a doctor, and the left image shows our analysis. The resulting images for $k = 6$, 7, and 8 clearly indicate the location of the tumor in the brain and show the contours of the tumor; matching the doctor's analysis quite closely.

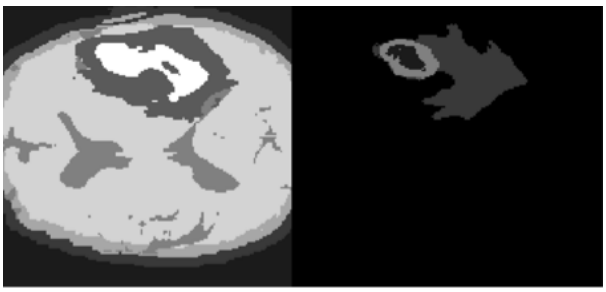

Figure 5: k-means with k = 7 and with convolution Gaussian blur pre-processing

The analysis with Gaussian blur preprocessing gives a different result. We expected the convolution Gaussian blur preprocessing to reduce image noise. Nevertheless, the Gaussian blur preprocessing significantly reduces the details of the image, and as a result the contours of the tumor as indicated in the image obtained with our analysis are different than the contours of the tumor as indicated by the doctor.

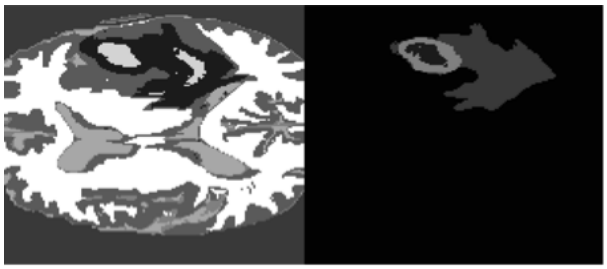

Figure 6: k-medoids with k = 7

Our analysis of the tumor using k-medoids clustering is slightly better than the analysis with k-means clustering. The contours of the tumor as indicated by our analysis with k-medoids clustering are almost identical to the contours of the tumor as indicated by the doctor.

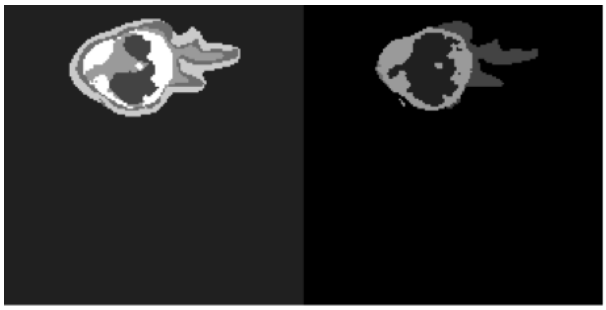

Figure 7: k-means with k = 7 and with Gabor filter (32 filters)

Our analysis of the tumor using k-means clustering and with Gabor filters (32 filters) is better than the analysis of the tumor with k-means clustering but without Gabor filters. The resulting image does not only indicate exactly where the tumor is located in the brain, but it also seems to contain even more information about the tumor than the image that was analyzed by the doctor.

5 Conclusion

The notion that we may have general classes of brain tumors is likely to be an extremely helpful one, not only in the identification and prediction of their behavior, but also possibly in the treatment of such abnormalities. It is not difficult to imagine that there may exist several types of brain tumors each with their own idiosyncrasies regarding medical treatment

(e.g. some tumors may be less responsive to specific kinds of treatments that are highly effective for other types) for which automatic classification and description will greatly help patients and doctors in treating them. Overall, our classifications may prove to be helpful not only in early detection but also cancer treatment of brain tumors, thus increasing overall survival rates.

References

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