
The usage of variational autoencoders to recognize cancerous changes in MRI images

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Abstract

In this project, I check the effectiveness of using unsupervised learning methods in the problem of locating neoplastic changes in magnetic resonance images. My approach is based on the observation that pathological changes are rare and moreover, they are some deviation from the norm. I used for this purpose a variational autoencoder, which attempts to estimate the lower bound of the probability of occurrence of given observations. Therefore these values were used to classification. I tested the idea with synthetic data, using the MNIST set, with satisfactory results. On medical dataset, the model learned to flag samples based on their brightness, while this observation correlates with the presence of contrast, what is insufficient for precise operations.

1 Introduction

The problem I am considering is locating cancerous changes in magnetic resonance images (MRI) of the head. One of the possible approaches is from the supervised side, which depends on data previously analyzed by specialists, where each case was manually viewed and marked. While this method has many advantages, such as the use of real expert knowledge, the datasets are expensive to prepare and further develop. It can also be limited to a single part of the body because we need to have gathered labels for each part separately. Noting these drawbacks and combining them with the observation that pathological changes are rare and deviation from the norm, the problem can be considered as detecting outliers. I would like to try the unsupervised learning method in which the model would learn to estimate the probability of occurrence of a single sample in a certain context. With this approach, I can mark unlikely observations as pathological ones. Furthermore, the information itself can also help specialists in identifying suspect areas. The model which I decided to use is a variational autoencoder (VAE), combining artificial neural networks with probabilistic modeling.

2 Dataset description

The data comes from Duke University. They are head images made by the magnetic resonance imaging in the FLAIR (fluid-attenuated inversion recovery) technique along with the marked changes area. The images have a size of 256x256x3 pixels, where the first channel corresponds to the moment before entering the contrast, the third after, and the second is the appropriate picture. Masks have a size of 256x256 pixels with 255 value for cancer cells and 0 otherwise. Data are grouped for 110 patients cancer diagnosed. In total, there are 3929 pairs of images in the dataset, with only $\sim 1.02988\%$ pixels identified as pathological cells, which confirms the observation of their rarity.

Table 1: AUC due to the size of the hidden representation at different stages of learning

Model	Epoch					
	1	2	3	20	60	80
VAE 20-d	0.494	0.693	0.655	0.612	0.597	0.590
VAE 50-d	0.552	0.686	0.697	0.616	0.606	0.592
VAE 100-d	0.580	0.685	0.701	0.614	0.595	0.594
VAE 200-d	0.661	0.675	0.668	0.620	0.608	0.597

3 Approach

I divided the pictures into smaller patches with size 22x22. Each piece corresponds to the local neighborhood of its central pixel and I try to predict its class. I chose patches size on the basis of experiments using simple models such as linear regression and CNN to check if they contain enough information for classification. I also removed simple cases from the set, such as nearly whole black images. Then after training the model, I analyze the loss function, which is ELBO in the case of VAE. As this is the lower bound of probability per element, I can categorize samples based on a picked threshold. To this end, I use the ROC curve analysis and the AUC value that indicates the overall quality of the model.

4 Results

The table 1 shows the results. Rapid model overfitting can be noticed, because in most cases results have been worsening since the 3rd epoch. In addition, with time the measurements become almost the same for all sizes. The figure 1 presents the values of reconstruction cost NLL and KLD for test samples. Good separability of some data can be noticed. However, with further analysis, it turns out that these cases are easily categorizable with a simple threshold. For cases without a tumor, these are dark images with a low total sum of pixels. Whereas patches with cancer have a high total sum. It can be deduced from that the model only learned to pay attention to the simple property. That was the brightness of the sample which is correlated with the amount of contrast used during imaging.

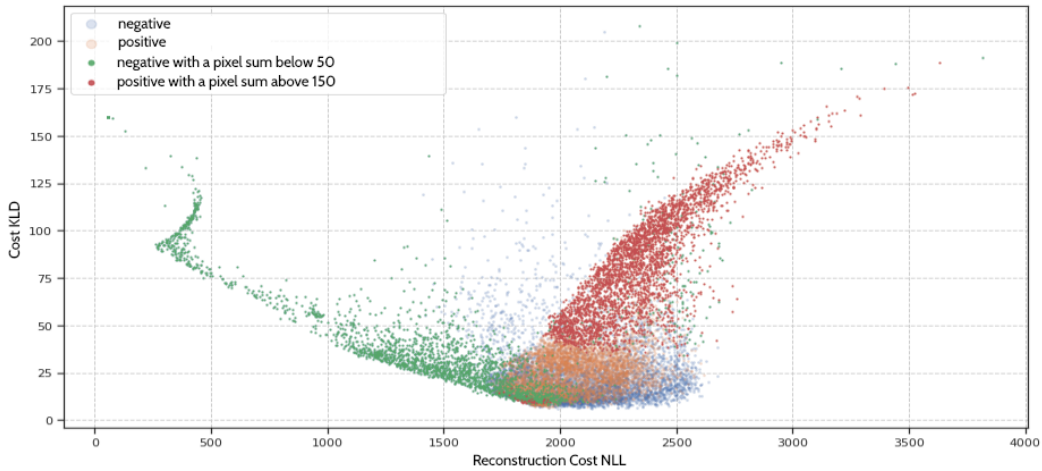


Figure 1: ELBO component costs with the indication of simple cases due to the total sum of pixels

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