

Research Paper: Machine Learning Application for Brain Tumor Localization in the Repository of Molecular Brain Neoplasia Data (REMBRANDT)

Machine Learning for Health Care (Heinz 95-845) - Lukas Mohs

1. Abstract

Within this paper, I want to present the outcome of the combined application of *Computer Vision* (CV) and *Machine Learning* (ML) to the *Repository of Molecular Brain Neoplasia Data* (REMBRANDT) dataset. This dataset contains pre-surgical *magnetic resonance* (MR) multi-sequence images of 130 patients. Based on a visual analysis and the application of several ML algorithms, I tried to predict the location of the brain tumor and compare it to the evaluation of three Radiologists, which defined the affected brain part and the potential impact on the brain functionality.

2. Introduction and Background

2.1 Brain Cancer

Among all types of cancer, brain cancer is one of the deadliest even if it's not one of the most common ones. With a so-called *5-Year Relative Survival Rate* of 32 % for white people and 39 % for black people it ranks on place 7 out of 26 for the lowest survival rate. Specific cancer types like *Glioblastoma*, a very fast growing type of tumor, even has a rate of 5%. Especially in the later years of life, this rate decreases heavily for all types of brain cancer. (American-Cancer-Society) The high variance in the survival rate is given by many factors such as the type of tumor, the location and of course whether it was treated. Especially the latter ones formed a major part of scientific studies that included ways of scanning the human brain for malignant tissue as well as the way of stopping the growth of the tumor cells. (World-Health-Organization)

2.2 Magnetic Resonance Imaging (MRI)

Magnetic Resonance Imaging (MRI) addressed the challenge of *scanning* the human body by using *radiology* to see different layers of the inner tissue or organs. These different layers can be combined together to construct a 3-dimensional model of any part of the body. Mainly a strong *magnetic fields* is used in combination with *radio waves* and so-called *field gradients*. In comparison to *Computer Tomography* (CT), MRI doesn't rely on *X-radiation*, which qualifies it as a less harmful method. It should be mentioned that the magnetic waves of MRI can affect *cardiac pacemakers* so that exceptions apply. (Edelman and Warach, 1993)

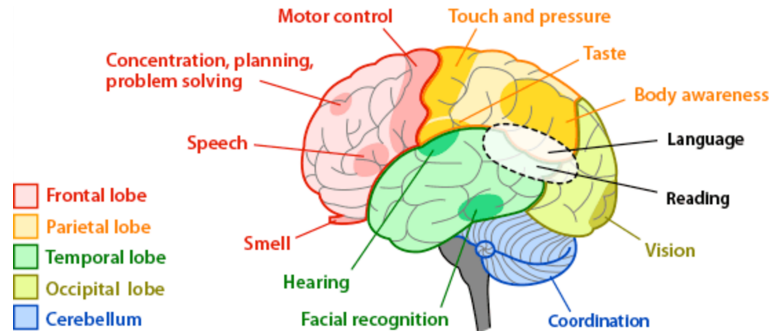


Figure 1: Brain Areas (source: Arizona State University)

2.3 The Human Brain

Especially the development and refinement of the MRI technology favored advanced studies about the structure and functionality of the human brain. In order to understand the classification task of the presented algorithm, the major parts of the human brain are shortly described and visualized in Figure 2.3:

- *Frontal Lobe*: resides in the front of the head and is the only lobe on the lateral surface and separated from the other ones. It is responsible for problem solving, planning but also processes stimuli from the nose.
- *Temporal Lobe*: caudally joins the parietal and occipital lobe without a clear boundary. Researchers could show that it hosts the function of recognizing faces.
- *Parietal Lobe*: is Clear separated from frontal lobe but merges into temporal and occipital lobe. It is important for the control of the body including the sense of touch.
- *Occipital Lobe*: has also no clear boundary to its neighbours (parietal and temporal lobe). The stimuli of the eye are for example processed by this lobe.
- *The Insula*: is a small portion of the cerebral cortex and hidden by the other outer lobes. It is believed to be responsible for consciousness.
- *The Cerebellum*: is placed on the back of the head below the occipital lobe and next to the *brain stem*. It could be shown that it is responsible for fine motoric controls and languages.

(Duvernoy et al., 2012)

2.4 Computer Vision

Computer Vision (CV) is a field of *Computer Science* that focusses on the way of how to digitally process, analyze and understand images. Driven by the development of cheap cameras and computing power, CV is applied in many circumstances to support or replace the human's richest sense: the eye. To provide a highlevel understanding of a CV identification or classification approach, one has to consider the digital representation of an image on the

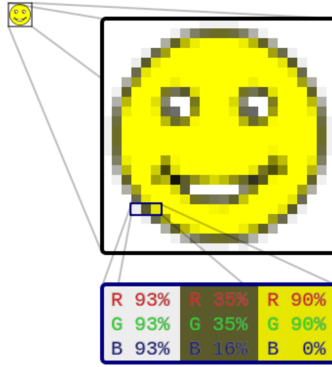


Figure 2: Raster Graphics (source: Wikipedia)

computer. This can be decomposed to a two-dimensional matrix, where each entry holds a tuple of three values: the *Red*, *Green* and *Blue* (RGB) channel. This tuple identifies how the color of one specific *pixel* is composed. These matrix of pixels is often referred to as *raster graphic*. Figure 2.4 demonstrates this representation for three specific pixels within an image. Most common file types represent these three channel values in a range between 0 and 255. The brightness of an image is therefore determined by the average of the sum of each pixel's RGB values. The contrast of an image is referring to the variance of the sum of each pixel's RGB values: the higher the difference, the stronger the contrast. These concepts are important to later understand the image processing algorithm.

2.5 Machine Learning

In the recent years, *Machine Learning* (ML) generated special attention due to its successful application in many fields of industry. Generally, ML can be understood as an automated approach of analyzing and learning specific patterns within a big series of data. For this purpose, statistical principles are implemented on a given *training set* afterwards to predict the class or value of new instances. ML is used in this scenario to evaluate the output of the image processing step and locate the brain tumor within a given sequence of MRI scans. In particular, the probabilistic *Naive Bayes* classifier will be used in combination with a *Decision Tree* due to their simplicity, which allows a solid interpretability.

3. Implementation: ML Prediction based on CV Pattern Matching Outcomes

Within this section I want to describe the setup and implementation of the *ensemble* of CV and ML that is used to locate the brain tumor within the image sequence retrieved from the MRI scan. Ensemble means that a two-step process is used to realize the final prediction:

- First, the images from the REMBRANDT dataset are retrieved, preprocessed and analyzed by the application of several pattern matching methods.
- Then, the output of the analysis is written to *CSV* file to be taken as an input for the ML learning and prediction approach.

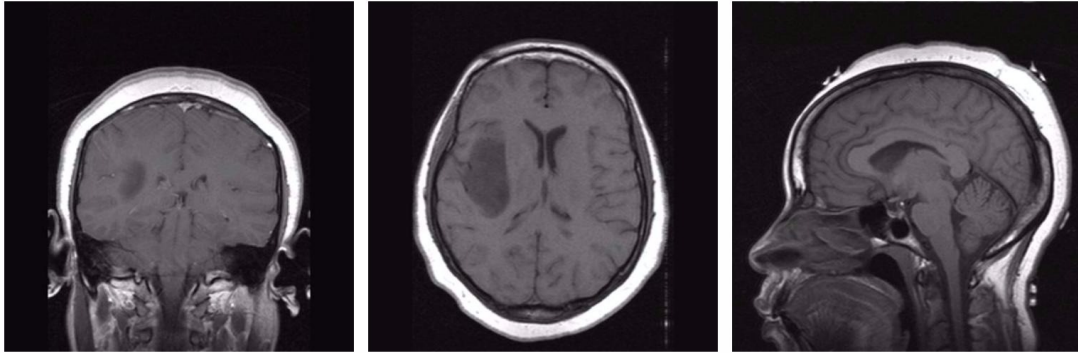


Figure 3: Sequence Comparison (back to front, top to bottom, left to right)

The most recent version of the source code of this project, which is based on *Python* for the image processing and *R* for the ML part, can be found on Github:

<https://github.com/lukasmohs/TumorDetection> .

3.1 REMBRANDT Image Data Set

At this point, the input data in form of a series of image sequences is described: The data of REMBRANDT was generated through the Glioma Molecular Diagnostic Initiative and contains the pre-surgical MR multi-sequence images from 130 patients. This image dataset is enriched by a professional classification of three different radiologists for each individual stating the tumor location within the brain. Each sequence can be defined as one specific direction of slicing, which was used in order to scan the patient’s head. This means that each patient was scanned either horizontally or vertically from different angles. In figure 3.1, one image of each of these sequences for one patient is provided. (Kenneth Clark)

Comparing the images provided from each sequence, we can see that the image on the left (*back to front*) and the one on the right (*left to right*) both contain more *noise* in terms of head parts that don’t belong to the actual brain. The automatic localization within the image is additionally more complex than for the one in the middle (*top to bottom*) due to the fact that images might not be cropped similarly so that a localization would need to be realized relatively to the shape of the skull, which would be more error-prone. Therefore, the *top-down* sequence of each patient was chosen to perform the analysis. It should be mentioned that the sequences of each patient are not of similar length meaning that they contain a different numbers of single images.

3.2 Image Preprocessing

labelimage-preprocessing As the first step of the CV part, the top-down image sequences for the patients were retrieved from the *Cancer Image Archive*:

<https://wiki.cancerimagingarchive.net/display/Public/REMBRANDT> .

An entire sequence of scans is shown in Figure 3.2. In order to better determine the location within one single image and to improve the pattern matching performance, the images should be cropped to the skull in the middle of the image. Hence, the algorithm

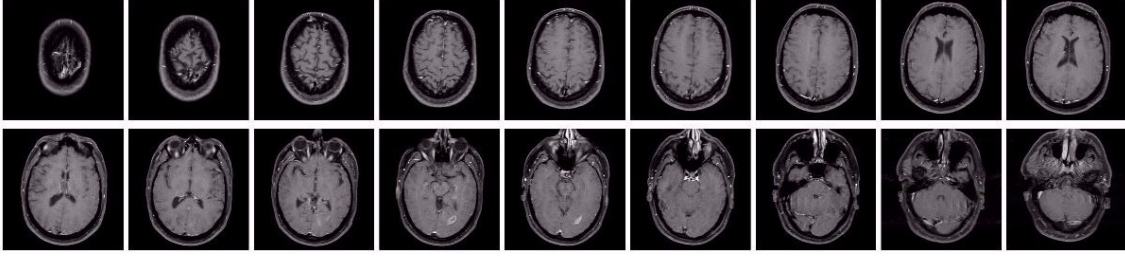


Figure 4: Full Top-down Sequence of Individual

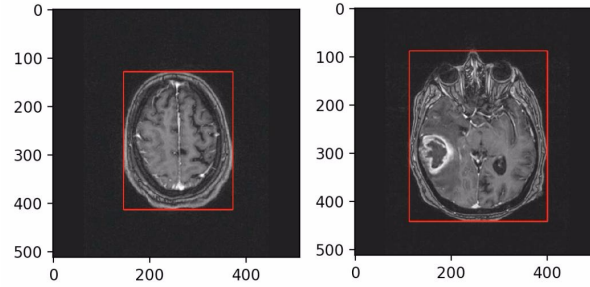


Figure 5: Image Cropping

contained in the *cropImages.py* file was developed that iterates over the *x-axis* and *y-axis* of each image and identifies the important parts of the image based on the brightness (see: section 2.4). Its performance is visualized in Figure 3.2. A new image is written to a file and used for the next processing step.

3.3 Pattern Matching

After preprocessing the images, the main part of the algorithm that extracts features out of the image sequences for the following ML approach can be executed. The major idea of identifying a tumor within each image is based on a *similarity measure* between a so-called *template* and the *target image*. For the actual matching, the *OpenCV* library version 2.4.13.2 for Python was used (Opencv-Dev-Team). In the following, I will explain the development of the matching template as well as the exact matching application.

3.3.1 TEMPLATE DEVELOPMENT

To generate the template as an input for the matching process, I implemented an algorithm that develops a general pattern in form of an image that represents the average of a *training image set*. As explain in section: 2.4, a matrix can be used to represent each pixel of an image. Therefore, I manually selected some input tumor images and applied the algorithm provided in the *generateTemplate.py* file. Each image is stretched to the same size and to then calculate the average template matrix, the algorithm iterates over each pixel of each image and adds together all partial RGB values. This can be formulated as follows:

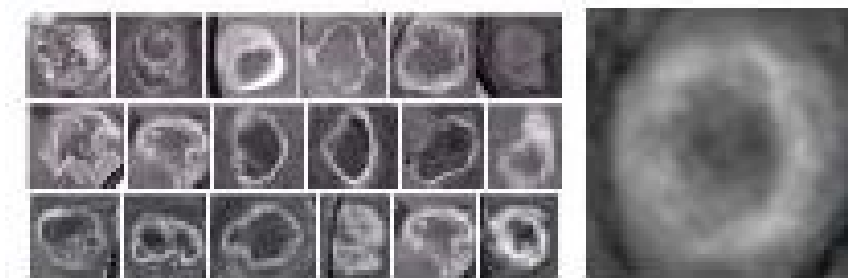


Figure 6: Template Generation (left: input, right: output)

$$\phi_{x,y,c} = \frac{\sum_{i=1}^n A_{x,y,c}^i}{n}$$

where A is the matrix of all sets c :

$$A^i = \begin{bmatrix} a_{1,1} & \dots & a_{1,x} \\ \dots & \dots & \dots \\ a_{y,1} & \dots & a_{y,x} \end{bmatrix}$$

and where c is the set of the color channels RGB:

$$c \in \{r, g, b\}$$

Figure 3.3.1 demonstrates the input and result of this template creation process.

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