**Background:**

A radiologist is in need of help in their program. They will give me a full set of MRI scans to have a program check for tumor volume. By circling each slide, that the radiologist found a tumor, the program would then find the tumor inside the circle, and calculate its volume. Each slide is roughly 2mm apart from each other. The radiologist marks each slide containing a tumor with a digital pen, circling it in a program.

**Implementation:**

The challenges associated with this feat are thus:

* Tumors have different densities – some are denser than their surroundings, some are less dense
* Tumors have complex shapes, and are not always simply connected regions
* There is the possibility of multiple tumors.

With these problems first laid out, the task of finding the marked region(s) can now be started. Regions are marked on the computer in a color different than the rest of the MRI scan. There are a few ways to find these regions: segmentation, morphology, and thresholding being some of those. With segmentation, the method of region splitting will be discussed. Region splitting allows for segmentation of a specified pixel attribute, for us that is the colored region specified by the radiologist. By splitting each region until a group of regions can be defined by either having the marking color in it, or being in between said marked regions, it can be said these regions encapsulate the tumors. Morphology allows us to segment the tumor filled region(s) out by using the hole. By filling only regions marked with the special color, a mask can be created to allow for image extraction. By cutting this region masked in the masked image out of the original image, a picture consisting only of the marked regions will appear. Thresholding would work very similarly. Simply threshold the image to have the marker color appear white, and everything else black. Any region marked inside the black region(s) would contain the tumor. We can remove these by taking only pixels inside the marked regions to a new image. If there are multiple regions, this can be determined by seeing if there are non-connected regions in the new image. These methods would also work if the radiologist had marked the image without the aid of a computer.

Now that the marked region has been identified, the tumor can be identified. It is assumed that the tumor takes up most of the marked region. Using histogramming, we can tell whether the tumor is denser or less dense than the surrounding cerebral region. To make things easier, tumors will be assumed to be a light region (if they are a darker region, as determined by histogramming, the image can be inverted to comply with this assumption). Now the tumor has to be separated from the accompanying brain matter. We can determine the average color of the surrounding brain matter by taking a histogram of the pixels touching border (it is also assumed that the radiologist leaves some space between the marker and the tumor). Since the color of normal brain matter surrounding the tumor has been obtained, it can be thresholded out of the picture by pushing those values to zero with tumor matter being pushed to white (if the matter was 10% different than that of the tumor, it would be brain matter).

Now that the tumor has been completely segmented, an accurate volume can be calculated. Two tumors become one tumor if two regions of a those tumors on any slide are touching, so this must be checked. A tumor is also the same tumor if it is within 1% of tumor pixel color. If such regions are connected, then the rest of the tumor (the above and below slides to the degree of the before mentioned difference) is then connected. To calculate the volume, the area of the tumor on each slide must be calculated. This can be done by counting the pixels that belong to each tumor on each slide. Because the slides are two mm apart, we can think of the slide as being two mm thick. This gives us a bunch of two mm slices of our tumor. By adding the volume of each of these slices, we can get the total volume of our tumor. This accounts for non-simply connected tumors, too, by only counting regions deemed as tumor cells.