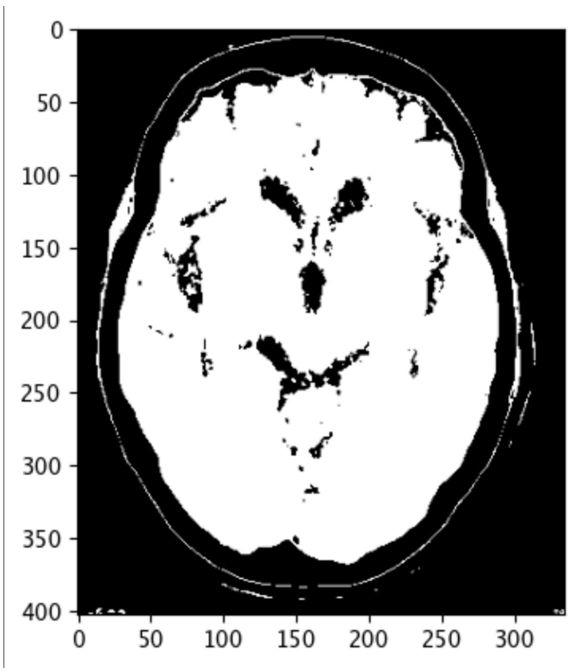
ZSL Report for Lab01

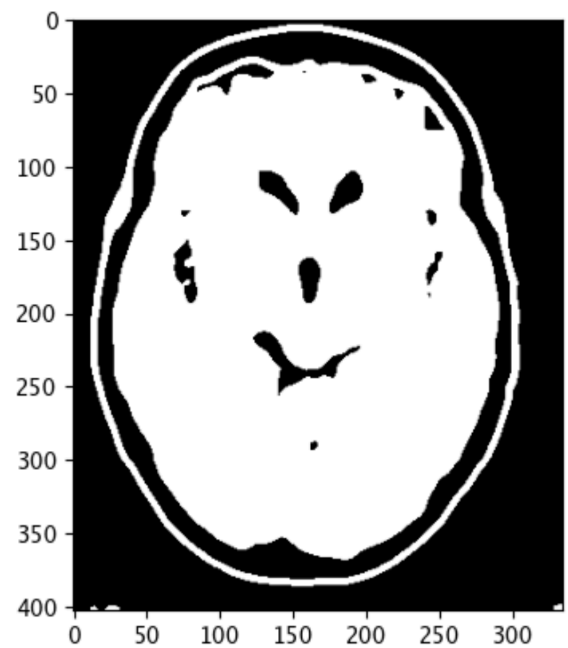
Nguyen Thu Uyen Sarah

Homework 1

Try to improve the binary mask for brain by smoothing the image by Gaussian filter. The Gaussian image filter can be obtained by `fspecial` function, the filtering is performed by the `conv2` function.



a) original brain mask



b) smoothed brain mask using Gaussian filter

In the original image we can see that the boundaries are quite jagged and irregular and the image contains noise and irregularities seen as “speckles” and rough patches in the brain region. The overall shape is good, but the quality for further analysis is very poor. Which is why the smoothed image is better. We can see the boundaries clearly and we got rid of the speckles while preserving the anatomy of the brain.

Homework 2

I implemented the function `my_two_sample_ttest` based on the provided formulas. Using a randomly generated sample, I compared the results of this function with SciPy ttest results as reference. The results of my ttest and Scipy ttest are the same.

Homework 3

In this assignment we were making repeated paired t-test. Where the number of comparisons is equal to number of combinations without repetition, so for our case:

$$C = \binom{n}{k} = \binom{5}{2} = 10$$

Because we are doing this for both variables, we have to multiply C by two, which means that the total number of comparisons is ***twenty***. When we are making this many comparisons repeatedly, we are exposing ourselves to type I. error. Based on FWER (family wise error rate) the probability of randomly aquiring the wanted results (as false positive) grows quite quickly. Since we don't want a false positive, it is suitable to adjust our alpha by using for example Bonferroni correction $\alpha_{adj} = \frac{alpha}{num.test}$. This will lower the probability of getting false positive, but it will also weaken the power of t-test, which means that we are getting more type II. errors (false negatives). That's why for cases like these other methods might be more suitable, for example ANOVA. In our case in particular with 20 total comparisons, the Bonferroni correction is quite strict (α = 0.0025). This conservative approach reduces Type I errors but may increase Type II errors. The fact that 10 out of 17 original significant findings survived suggests genuine group differences rather than random chance.