Segmentation of Brain MR Images

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Abstract—This document is a report for an asignment.

I. Materials

For the assignment we were given t1.raw, t2.raw and pd.raw files corresponding to 3D intensity images of T1-, T2- and PD-weighted MR sequences. We were also given msk.raw file which contains reference contours of brain structures of interest. Reference countours of brain structures were labeled in a standardized way. Namely, the labels of normal (CSF, GM and WM) and pathological (lesions) structures are given as L = {CSF = 1, GM = 2, WM = 3, LESIONS = 10}. All images and masks have dimensions $271 \times 217 \times 36$. Initial dimension of z-axis 181 was reduced o 36 due to time constraints by taking into account every 5th slice of original images and mask.

Asignment was solved using python programming language (jupyter notebook environment).

II. Assignments

A. Determining binary mask M

In this section we determined binary mask M of a region corresponding to brain structures (CSF, GM and WM) based on a given mask reference.
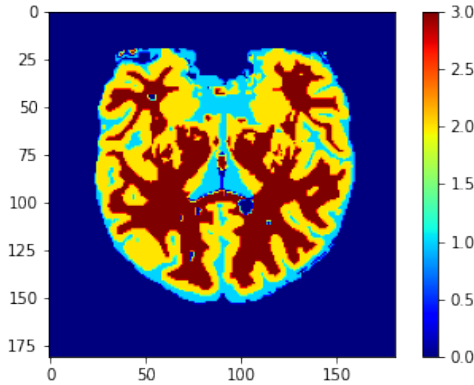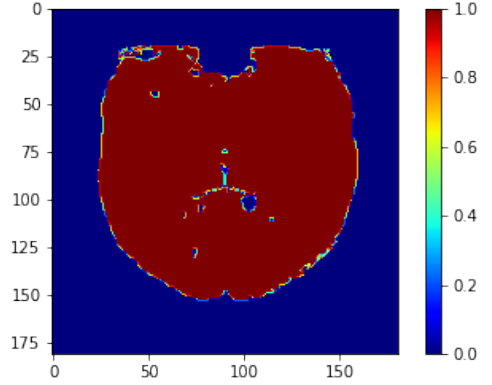

Fig. 2. Axial cross-section x × y × 18 of the binary mask M at modified coordinate $z = 18$, which corresponds to original coordinate $z = 90$.

B. Feature values as points in 3D feature space

Based on 3D intensity images t1.raw, t2.raw and pd.raw intensity values $I_{T_1(x)}$, $I_{T_2(x)}$ and $I_{T_3(x)}$ which lie in the brain mask region M were extracted. We formed a new matrix of features $Y = [I_{T_1(x)}, I_{T_2(x)}, I_{T_3(x)}]$, which has dimensions N × 3. In this case N was 387972.
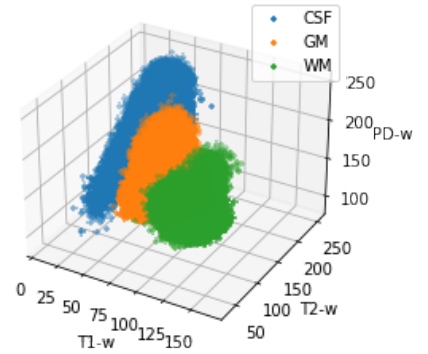

Fig. 1. Axial cross-section x × y × 18 of the mask at modified coordinate $z = 18$, which corresponds to original coordinate $z = 90$.

Fig. 3. Feature values y of Y matrix as points in 3D feature space.

C. Determining initian cluster means

Initial cluster means μ_i were determined using kMeansInit function.

TABLE I
INITIAL CLUSTER CENTERS

Initian cluster centers	I_1	I_2	I_3
μ_1	69	159	209
μ_2	77.59	146.46	190.76
μ_3	96.64	104.83	182.76

D. Cluster analysis based on k-means++

Cluster analysis was performed using kMeansPP function, where the input iY was matrix of feature values of size N × d, iK number of clusters (in this case 3) and iMaxIter maximal number of iterations of k-means++ algorithm. Due to time constraints maximal number of iterations was set to 10. By printing out every iteration of center values in kMeansPP function we can see that the algorithm has not yet converged. For better results would have to increase iMaxIter value.

TABLE II
CLUSTER CENTERS AFTER 10 ITERATIONS

Final cluster centers	I_1	I_2	I_3
μ_1	48.38	189.23	203.55
μ_2	95.05	95.89	186.55
μ_3	128.41	67.12	165.13

E. Non-parametric classification

Non-parametric classification was performed using nonpar-Classification function. Cluster centers were obtained using kMeansPP function from previous section.
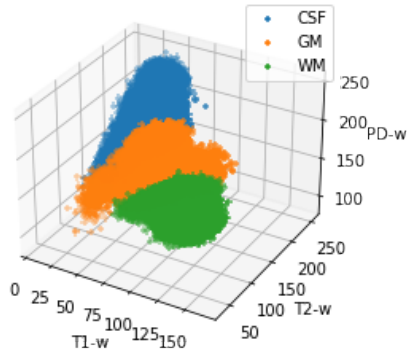

Fig. 4. Non-parametric classification of features using kmeans++.

F. Brain segmentation using T1, T2 and PD images

Brain segmantation was first performed using all T1-,T2- and PD-weighted sequences (d=3). Number of clusters iK was set to 3.
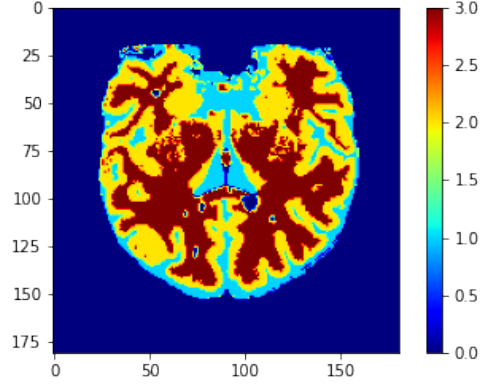

Fig. 5. Cross-section of reconstructed image at modified coordinate z=18.

G. Dice similarity coefficient

Validation of segmentation can be evaluated by computing dice similarity coefficient. Dice similarity coefficient is a quantitive measure of overlap that is widely used. Perfect overlap corresponds to value 1 and no overlap corresponds to value 0. We can use it to compare true and segmented labels of voxels.

Although number of maximal iterations (iMaxIter = 10) was relatively low we score high values of dice similarity coefficient for all types of brain tissue. Results are in Table III.

TABLE III
DICE SIMILARITY COEFFICIENT FOR D=3 SEGMENTATION

Brain tissue	Dice similarity coefficient
CSF	0.957
GM	0.930
WM	0.935

H. Brain segmentation using T2 and PD images

In this segment brain segmentation was performed without the use of T1-weighted image. Only T2-w and PD-w images were included in analysis.

Performance of our algorithm was significantly lower in this assignment (d=2) than in our previous one (d=3). This can be seen by comparing Table III and Table IV.

TABLE IV
DICE SIMILARITY COEFFICIENT FOR D=2 SEGMENTATION

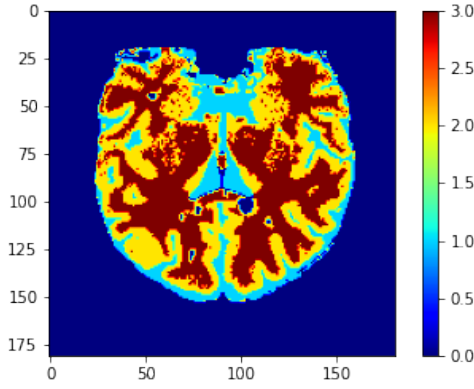| Brain tissue	Dice similarity coefficient
CSF	0.941
GM	0.828
WM	0.842

Fig. 6. Cross-section of reconstructed image at modified coordinate z=18. Reconstruction was performed using t2- and pd-weighted images.
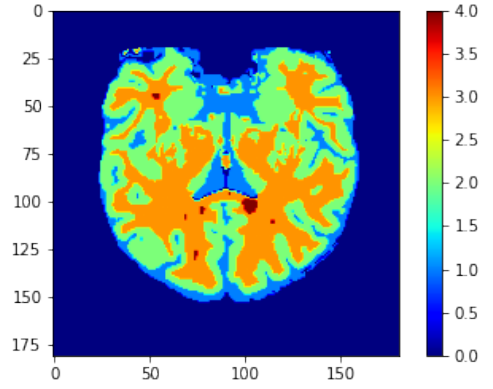

Fig. 8. Axial cross-section x × y × 18 of the mask at modified coordinate $z = 18$, which corresponds to original coordinate $z = 90$. Lesions are included and labeled with value 4.

I. Brain segmentation using T1 image

In this asignment segmentation was performed using T1-weighted sequence.

TABLE V
DICE SIMILARITY COEFFICIENT FOR D=1 SEGMENTATION

Brain tissue	Dice similarity coefficient
CSF	0.946
GM	0.916
WM	0.921

In this asignment maximal number of iterations (iMaxIter) was set at 15 and number of clusters iK at 4. Segmentation was performed using all T1-, T2- and PD-weighted sequences. By comparing results from Table VI and Table III we can conclude that inclusion of lesions has lowered the performance of segmentation for brain structures CSF and GM. Quality of segmentation of WM structures was not significantly affected. Segmentation of pathological tissues (lesions) was very unsuccessful which is reflected in very low value of dice similarity coefficient in Table VI.
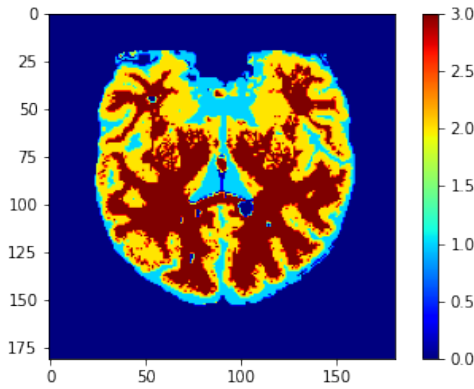

Fig. 7. Cross-section of reconstructed image at modified coordinate z=18. Reconstruction was performed using T1-weighted images.
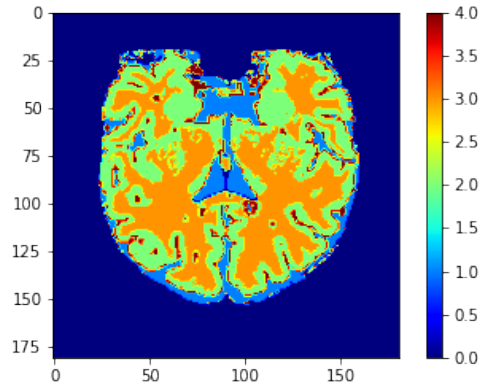

Fig. 9. Cross-section of reconstructed image at modified coordinate z=18.

J. Brain segmentation with lesions

In this asignment we performed segmentation both for normal structures (CSF, GM and WM) and pathological structures (lesions). First step was to update binary mask M so that it includes brain regions corresponding to lesions.

TABLE VI
DICE SIMILARITY COEFFICIENT FOR SEGMENTATION (LESIONS INCLUDED)

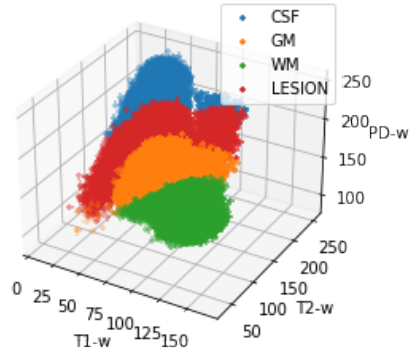| Brain tissue	Dice similarity coefficient
CSF	0.857
GM	0.898
WM	0.923
Lesions	0.065

Fig. 10. Cross-section of reconstructed image at modified coordinate z=18. Points which correspond to pathological tissue lie in feature space between CSF and GM structures. This seems to be the cause of quality reduction of segmentation for CSF and WM structures.