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**Course Information**

Course Title: Digital Image Processing

Section: 1

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Department of Computer Science & Engineering

**Lab-08**

**Student’s Information**

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***(Show input and output side by side for all problems****)*

1. Segment the tumor from Figure 1 by using:

i. Region growing approach

function J=regiongrowing(I,x,y,reg\_maxdist)

if(exist('reg\_maxdist','var')==0), reg\_maxdist=0.2; end

if(exist('y','var')==0), figure, imshow(I,[]); [y,x]=getpts; y=round(y(1)); x=round(x(1)); end

J = zeros(size(I));

Isizes = size(I);

reg\_mean = I(x,y);

reg\_size = 1;

neg\_free = 10000; neg\_pos=0;

neg\_list = zeros(neg\_free,3);

pixdist=0;

neigb=[-1 0; 1 0; 0 -1;0 1];

diff = 01;

while(pixdist<reg\_maxdist && reg\_size<numel(I) && diff ~=0)

num1 = sum(sum(reg\_size));

% Add new neighbors pixels

for j=1:4,

% Calculate the neighbour coordinate

xn = x +neigb(j,1); yn = y +neigb(j,2);

% Check if neighbour is inside or outside the image

ins=(xn>=1)&&(yn>=1)&&(xn<=Isizes(1))&&(yn<=Isizes(2));

% Add neighbor if inside and not already part of the segmented area

if(ins&&(J(xn,yn)==0))

neg\_pos = neg\_pos+1;

neg\_list(neg\_pos,:) = [xn yn I(xn,yn)]; J(xn,yn)=1;

end

end

if(neg\_pos+10>neg\_free), neg\_free=neg\_free+10000; neg\_list((neg\_pos+1):neg\_free,:)=0; end

dist = abs(neg\_list(1:neg\_pos,3)-reg\_mean);

[pixdist, index] = min(dist);

J(x,y)=2; reg\_size=reg\_size+1;

reg\_mean= (reg\_mean\*reg\_size + neg\_list(index,3))/(reg\_size+1);

x = neg\_list(index,1); y = neg\_list(index,2);

neg\_list(index,:)=neg\_list(neg\_pos,:); neg\_pos=neg\_pos-1;

num2 = sum(sum(reg\_size));

diff = num2-num1;

end

J=J>1;

%1. Segment the tumor from Region growing approach

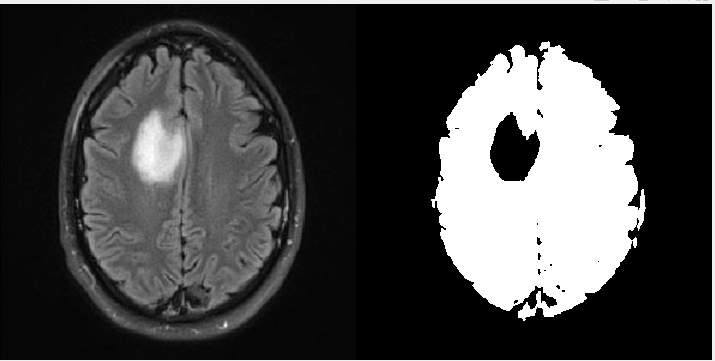
I = rgb2gray(im2double(imread('Tumor.png')));

J=imadjust(I,[],[],0.5);

J=imgaussfilt(J);

J= regiongrowing(J,0.2);

imshowpair(I,J,'montage')



ii. Region Splitting and Merging approach

function g = splitmerge(f, mindim, fun)

Q = 2.^nextpow2(max(size(f)));

[M, N] = size(f);

f = padarray(f, [Q - M Q - N], 'post');

S = qtdecomp(f, @split\_test, mindim, fun);

Lmax = full(max(S(:)));

g = zeros(size(f));

MARKER = zeros(size(f));

for K = 1:Lmax

[vals, r, c] = qtgetblk(f, S, K);

if ~isempty(vals)

for I = 1:length(r)

xlow = r(I); ylow = c(I);

xhigh = xlow + K - 1; yhigh = ylow + K - 1;

region = f(xlow:xhigh, ylow:yhigh);

flag = feval(fun, region);

if flag

g(xlow:xhigh, ylow:yhigh) = 1;

MARKER(xlow, ylow) = 1;

end

end

end

end

g = bwlabel(imreconstruct(MARKER, g));

g = g(1:M, 1:N);

function v = split\_test(B, mindim, fun)

v(1:k) = false;

for I = 1:k

quadregion = B(:, :, I);

if size(quadregion, 1) <= mindim

v(I) = false;

continue

end

flag = feval(fun, quadregion);

if flag

v(I) = true;

end

end

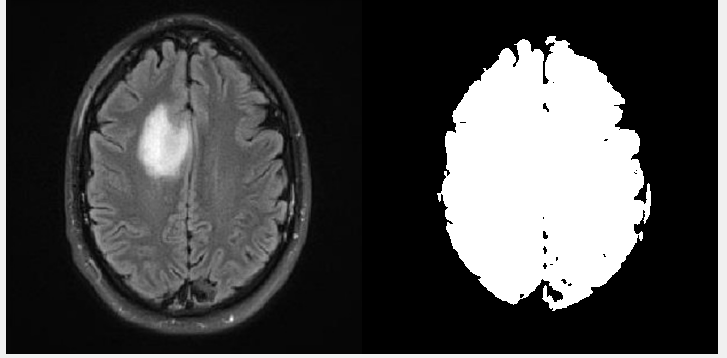
%split&merge

I2 = imread('Tumor.tif');

g = splitmerge(I2,8,@predicate);

figure,subplot(1,2,1);imshow(I2,[]);

subplot(1,2,2);imshow(g,[]);



1. Examine the differences between the methods from Question 2 to highlight their differences in quality and accessibility.

As we can see in the given segmented image in Question 1. We can see in region growing method the tumor is well segmented and highlighted in black form. As it creates a mask also. Whereas in split merge method the brain in well segmented but not the tumor. So region growing method works well segmentation.

1. Segment the tumor from Figure 1 by using Marker Controlled Watershed segmentation.

%watershed

x=imbinarize(rgb2gray(imread('Tumor.png')));

subplot(2,2,1);

imshow(x);

title('Original Image');

a=x;

x=~x;

ms=bwdist(x);

ms=255-uint8(ms);

subplot(2,2,2);

imshow(ms);

title('Image after applying Distance Transformation');

hs=watershed(ms);

ws=hs==0;

subplot(2,2,3);

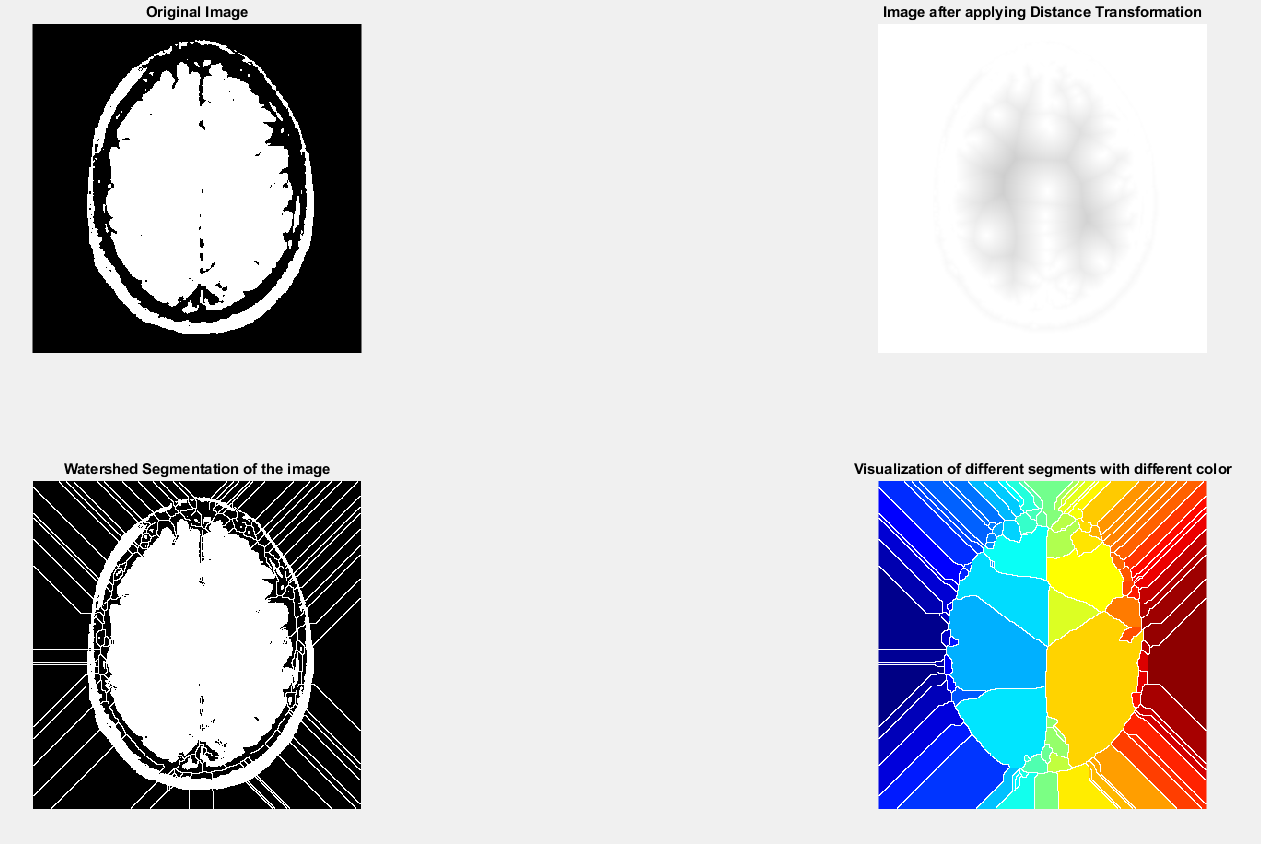
imshow(a | ws);

title('Watershed Segmentation of the image');

subplot(2,2,4);

imshow(label2rgb(hs));

title('Visualization of different segments with different color');



1. Segment the tumor from Figure 1 by using Quadtree Segmentation.

I = imread('Tumor.png');

I=rgb2gray(I);

Ifilt = medfilt2(I,[8 8]);

[S] = qtdecomp\_var(I,10);

[Sfilt] = qtdecomp\_var(Ifilt);

blocks = repmat(uint8(0),size(S));

for dim = [256 128 64 32 16 8 4 2 1];

numblocks = length(find(S==dim));

if (numblocks > 0)

values = repmat(uint8(1),[dim dim numblocks]);

values(2:dim,2:dim,:) = 0;

blocks = qtsetblk(blocks,S,dim,values);

end

end

blocks(end,1:end) = 1;

blocks(1:end,end) = 1;

blocks\_filt = repmat(uint8(0),size(Sfilt));

for dim = [128 64 32 16 8 4 2 1];

numblocks = length(find(Sfilt==dim));

if (numblocks > 0)

values = repmat(uint8(1),[dim dim numblocks]);

values(2:dim,2:dim,:) = 0;

blocks\_filt = qtsetblk(blocks\_filt,Sfilt,dim,values);

end

end

blocks\_filt(end,1:end) = 1;

blocks\_filt(1:end,end) = 1;

figure;subplot(221);imshow(I); title('Input image');

subplot(222);imshow(Ifilt); title('Filtered image');

subplot(223);imshow(blocks,[]);title('Quad tree input image with var weight');

subplot(224);imshow(blocks\_filt,[]);title('Quad tree filtered image without var weight');



1. Generate a binary mask of the tumor from Figure 1 using any segmentation method of your choice, then apply:

Binary mask:

rgb = imread('Tumor.png');

I = rgb2gray(rgb);

gmag = imgradient(I);

L = watershed(gmag);

Lrgb = label2rgb(L);

se = strel('disk',20);

Io = imopen(I,se);

Ie = imerode(I,se);

Iobr = imreconstruct(Ie,I);

Ioc = imclose(Io,se);

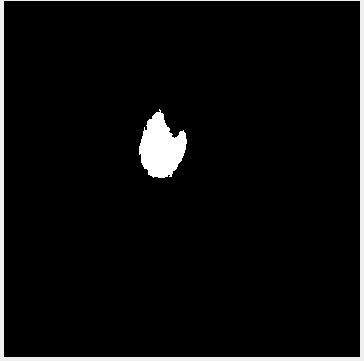
Iobrd = imdilate(Iobr,se);

Iobrcbr = imreconstruct(imcomplement(Iobrd),imcomplement(Iobr));

Iobrcbr = imcomplement(Iobrcbr);

fgm = imregionalmax(Iobrcbr);

figure,imshow(fgm)



i. Morphological Dilation

%dialation

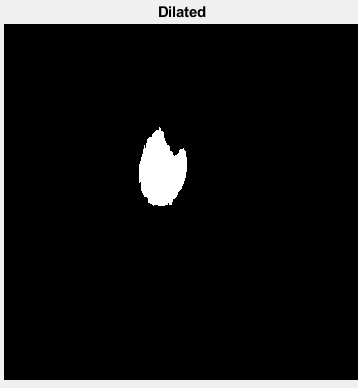
se = strel('line',11,90);

BW2 = imdilate(fgm,se);

imshow(BW), title('Original')

figure, imshow(BW2), title('Dilated')

figure,imshow(fgm)



ii. Morphological Erosion

%erosion

se = strel('line',11,90);

erodedBW = imerode(fgm,se);

figure,imshow(erodedBW), title('Erode')

figure,imshow(fgm)

