**Medical Image Segmentation using Region-Growing and a Simplified Mumford-Shah Functional**

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**Significance and Aims**

Segmentation is a vital task in modern medical image processing that serves to reduce data analysis only to specific sub-regions that are of clinical interest. Advances in medical imaging technologies have provided the medical and scientific communities with larger datasets of ever-increasing image quality. Thus, there is an inherent need for robust segmentation methods that can extract clinically important information *automatically*, as opposed to performing time-consuming *manual* segmentation which is still done today in some clinical applications. The overarching goal of this project is to successfully implement an algorithm that automatically segments medical images using a region-growing algorithm. This will be accomplished through the following **specific aims**.

**Specific Aim 1**: **Reproduce an existing region-growing segmentation algorithm using a simplified Mumford-Shah functional.**

**Specific Aim 2**: **Develop a novel region-growing algorithm using the same formulation but with added flexibility in initialization conditions and increased efficiency in calculating the cost function.**

With respect to expected outcomes, the work proposed in **specific aim 2** is expected to decrease post-processing times and increase segmentation reproducibility, which will in turn positively impact clinical workflows that currently utilize manual segmentation methods.

**1. Introduction**

Segmentation is an image processing technique that takes advantage of one or more imaging features to partition the image (or set of images) into useful regions of interest. This can analogously be described as assigning certain labels to pixels in an image, thereby grouping pixels that share similar features. This process is very commonly seen in medical image processing, in which a medical image is decomposed into clinically significant segments, which can make the image easier to visualize or can simplify the data analysis procedure (restricting analysis only to a subset of the image). The degree and accuracy to which an object is segmented depends highly on the task being performed, and is thus highly dependent on the specific application. Some applications involve (1) quantification of tissue volume (2) localization of pathology (3) studying tissue structure (4) treatment planning (5) and statistical analysis of tissue regions1. Because of the large diversity in imaging tasks, a large variety of segmentation methods have been developed due to the fact that one method may be better adapted for a certain imaging task. Segmentation techniques range from manual methods, in which a user manually identifies regions of interest, to more automated methods, in which segmentation is performed unsupervised. Manual methods are often time-consuming and are prone to relatively high inter- and intraoperator variability. Additionally, larger and more accurate medical image datasets are being acquired. Thus, there is an inherent need for robust segmentation methods that can extract clinically important information *automatically*, as opposed to performing time-consuming *manual* segmentation which is still done today in some clinical applications.

There are several common methods that are used to automatically or semi-automatically segment images, each with varying degrees of accuracy, efficiency, and simplicity. One relatively simple and popular segmentation technique is region-growing, a method that groups similar pixels into larger subregions based on a predefined condition. This method begins with a “seed” point placed in the image, and the region grows based on the predefined condition, which in most cases is a gray level threshold. Pixels will be advanced outwards from the “seed” and will be added to the region if they are within the range of gray level thresholds. In some cases, manual placement of seeds is not desired, as in fully-automated processing. Perhaps the simplest approach is to select seed points in an iterative pattern throughout the image until every pixel in the image is contained within a subregion. Another approach is to perform the region-growing process on *every* pixel using the same thresholding condition that is be used to assign pixels to regions. If the result of these computations shows clusters, the centroid pixels of these clusters can be used as initial seeds2. The reasoning behind this technique is that the number, size, and shape of segmented regions will depend highly on the seed point locations. Thus, by calculating region-growing for every pixel, one can get a “general idea” of where primary regions should lie. Yet another approach is to subdivide the image initially into a set of arbitrary, disjointed regions and then iteratively merge or split them based on the criteria stated previously2.

A segmentation can also be performed using variational methods, which is the process of minimizing a variational model (cost function) that suitably describe a practical segmentation problem. Variational methods can also be solved using a probabilistic approach, often modeled by Markov random fields and optimized with Bayesian estimation (a posteriori estimation)3. One commonly encountered cost function is termed the Pott’s Model. The formulation is given below:

where γ is the regularization parameter, **x** is the output image (segmentation), **y** is the input image, and represents the norm. The first term enforces “flatness” of the segmentation output and the second term enforces data fidelity, with the regularization parameter γ balancing the two terms. This formulation is often quite difficult to minimize, as many algorithms require a derivative of the cost function in order to approach a local or global minimum. Since the Pott’s model contains an norm in the first term, an analytical solution for the gradient of the cost function is not easily solved. However, this can be solved using a convex relaxation approach as noted in many articles4–6. Another closely related formulation is termed the Mumford-Shah model7, which enforces both boundary length sparsity and data fidelity of the segmentation output. This model will be more thoroughly discussed in the methods and theory section. It should be noted that each of these approaches yield non-convex topologies, which are difficult to optimize. Despite this, generally satisfactory images can be found despite the non-convex nature of the problem, and can be further reinforced when multiple segmentation and image processing techniques are used in a multi-stage process8.

Koepfler at al.9 present a novel multi-stage segmentation algorithm that combines both region-growing and variational methods. This technique proposes using region-growing to merge split regions based on a simplified Mumford-Shah functional. In this specific paper, every pixel in an image is assigned a separate region. For every pixel, each adjacent pixel is tested by: (1) evaluating the value of the Mumford-Shah functional for each region separate and (2) evaluating the value of the functional when the two pixels are merged. If the cost function decreases when the pixels are merged, then the two regions are merged. On the other hand, if the cost function increases when the pixels are merged, they are left as separate regions. This is done iteratively for every pixel in the image. Several distinct disadvantages arise from this type of algorithm. Firstly, this method does not calculate the *global* cost function, but rather only the two regions being considered. Additionally, initializing the image by assigning every pixel to a different region can become very computationally expensive, particularly in the case for large image matrices and also for high discontinuous images with many inherent regions.

The purpose of this study is twofold: (1) to successfully reproduce the segmentation algorithm described by Koepfler et al and to (2) develop a new algorithm to alleviate the drawbacks of the aforementioned algorithm as described in **specific aim 1** and **specific aim 2** respectively. Both algorithms will be tested on simulated phantoms and clinical images and the results will be compared qualitatively as well as quantitatively, using several common segmentation performance metrics. The hypothesis is that our novel algorithm will both increase the accuracy and efficiency of the previously described algorithm.

**2. Theory and Methods**

In regards to **specific aim** 1, this project seeks to reproduce an automatic region-growing based algorithm that was discovered during the literature search process. This algorithm iteratively minimizes a simplified Mumford-Shah cost functional and assumes every segmented regions are piece-wise constant values. The performance of this algorithm will first be tested using a modified Shepp-Logan brain phantom in MATLAB (Mathworks, Natick, MA) with varying degrees of zero-mean noise added (σ = 0, σ = 0.002, and σ = 0.005).

**2.1 Mumford-Shah Functional**

Another commonly encountered cost function is the Mumford-Shah functional7, which is given as:

where **f** represents the output image (segmentation) and **g** represents the actual image. The first term is the data fidelity term, in which the absolute the mean square between the segmentation and the image is integrated over the entire image set (). Note that individual regions in the segmentation image () are disjointed connected open subsets of a planar domain each one with a piece-wise smooth *boundary* with K representing the boundary set, such that: . The second term integrates over the relative complement of K in the overall image set, which are all of the non-boundary regions (). This term requires that f does not vary considerably over the each segmentation subregion. Lastly, the third term requires that the boundary set be as small as possible. Regularization parameters and balance the data term and the length of boundaries of all of the segmentation regions respectively.

**3. Results**

**4. Discussion**

**5. Conclusion**

**References**

1. Pham, D. L., Xu, C. & Prince, J. L. Current methods in medical image segmentation. *Annu Rev Biomed Eng* **2**, 315–337 (2000).

2. Gonzalez, R. C. & Woods, R. E. *Digital Image Processing*. (2002).

3. Kato, Z. & Zerubia, J. Markov Random Fields in Image Segmentation. in *Foundations and Trends in Signal Processing* **5**, 1–15 (2011).

4. Pock, T., Cremers, D., Bischof, H. & Chambolle, A. An algorithm for minimizing the Mumford-Shah functional. in *Proceedings of the IEEE International Conference on Computer Vision* 1133–1140 (2009). doi:10.1109/ICCV.2009.5459348

5. Chambolle, A., Cremers, D. & Pock, T. A Convex Approach to Minimal Partitions. *SIAM J Imaging Sci* **5**, 1113–1158 (2011).

6. Pock, T. & Chambolle, A. A convex relaxation approach for computing minimal partitions. in *Proceedings of the IEEE International Conference on Computer Vision* 810–817 (2009).

7. Mumford, D. & Shah, J. Optimal approximations by piecewise smooth functions and associated variational problems. *Commun Pure Appl Math* **42**, 577–685 (1989).

8. Despotović, I., Goossens, B. & Philips, W. MRI Segmentation of the Human Brain: Challenges, Methods, and Applications. *Comput Math Methods Med* **2015**, 1–23 (2015).

9. Koepfler, G., Lopez, C. & Morel, J. M. A Multiscale Algorithm for Image Segmentation by Variational Method. *SIAM J Numer Anal* **31**, 282–299 (2005).

**Appendix**

Main Script

%% **Region Growing Segmentation Algorithm**

%

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% Built for: MATLAB 2018

%

% Performs region-growing (RG) using a simplified Mumford-Shah functional.

% Initialization is done using region-growing ('grayconnect' function)

% based on a given pixel-value tolerance (tol). Further segmentation is

% done by proposing a merging of two neighboring regions and evaulating if

% this proposed merge decreases the simplified MS functional of the image.

% This process is done iteratively for every initial region. Regularization

% parameter (nu) controls # of regions by weighting region length term.

% Simplified MS: norm(trueImage-approxImage) + length(regions)

% where: approxImage is a piecewise-constant approximation of true image

% based on average pixel value in region, and length of regions is the

% total perimeter length of all regions.

%

% Inspired by: Georges Koepfler and Russell Valentine

% https://coldstonelabs.org/files/science/math/Intro-MS-Valentine.pdf

% http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.53.1631&rep=rep1&type=pdf

%% **Import Data**

% Reads in PNG, MAT, or DICOM files

file = 'brain8.mat'; % Name of image file in current directory

if sum(contains(file,'png'))

rawImage = imread(file); % read png file

elseif sum(contains(file,'mat'))

rawImage = load(file); % load mat file

rawImage = struct2array(rawImage);

elseif sum(contains(file,'dcm'))

rawImage = dicomread(file); % import dcm file

else

disp('Could not recognize file type. Only reads PNG, MAT, and DICOM files');

end

%% **Assign variables and initialize matrices**

nu = 0.1; % regularization parameter

tol = max(rawImage(:))\*0.1; % initial RG tolerance, merge pixels w/in tol

trueImage = double(rawImage); % input image

%% **Initialize Segmentation**

regions = init\_seg(trueImage,tol); % initial set of regions

[approxImage,totaLength] = approximateFull(regions,trueImage); % create initial segmentation

f\_init = approxImage; % grab initial approximation

L = getAllLengths(regions); % array of region edge lengths

E = cost(approxImage,trueImage,totaLength,nu); % compute the cost (mumford shah)

%% **Merge Regions**

labels = unique(regions); % get region labels

N\_regions = length(labels); % number of regions in initial segementation

L\_temp = L;

k = 1;

fig2 = figure(2);

fig2.Position = [50 700 1400 400];

for r = 1:N\_regions

if ismember(r,labels) % if this region still exists

added = [];

for p = 1:N\_regions

added\_p = added; % used to test if no regions are added (break)

[regions\_temp,added] = merge(regions, r, added); % merge adjacent regions

proposedAdd = added(end); % proposed region addition

L\_temp(r) = edgeLength(r,regions\_temp); % set new individual region length

L\_temp(proposedAdd) = 0; % set merged region length to zero

totaLength = sum(L\_temp); % total length

% [approxTemp,~] = approximateFull(regions,trueImage); % approximate image

approxTemp = approximate(r,proposedAdd,regions,approxImage); % create approximate image

E2 = cost(approxTemp,trueImage,totaLength,nu); % calculate cost

if (E2-E(k) < 0) % does the cost decrease by merging the new region?

k = k+1;

regions = regions\_temp; % if so, lets change our regions

L = L\_temp;

E(k) = E2; % add result to energy array

labels = unique(regions);

approxImage = approxTemp;

% Updated regions and energy figures

subplot(1,3,1); imagesc(regions); title('Regions')

subplot(1,3,2); plot(1:1:length(E),E); title('Energy'); xlabel('Merging Operations'); ylabel('Energy')

subplot(1,3,3); bar(length(labels)); set(gca,'xticklabel','Number of Regions')

drawnow

% Display outputs

disp(['Iteration: ',num2str(r),'. Region ',num2str(added(end)), ' added to region ', num2str(r),'. attempted merge: ',num2str((p))])

elseif size(added\_p) == size(added)

disp(['Iteration: ',num2str(r),'. There are no more adjacent regions next to region ', num2str(r),'. attempted merge: ',num2str((p))])

break

else

disp(['Iteration: ',num2str(r),'. Region ',num2str(added(end)), ' NOT added to region ', num2str(r),'. attempted merge: ',num2str((p))])

L\_temp = L;

end

end

end

end

f\_final = approxImage;

regions\_final = regions;

N\_regions = length(labels);

figure;

subplot(1,3,1); imshow(trueImage,[]); title('Image')

subplot(1,3,2); imshow(f\_init,[]); title('Initalization')

subplot(1,3,3); imshow(f\_final,[]); title('Final Segmentation')

Ancillary Functions

%% **Initial Segmentation**

% Description:

% Basic region-growing segmentation utilizing 'grayconnected' function

% to connect regions of like pixels. Also fills in small holes.

% Returns:

% regions = basic region segmentation (initialization)

% Arguments:

% trueImage = input image (double)

% tol = threshold for "like pixels" (see 'grayconnected')

% Dependencies:

% NONE

function [regions] = init\_seg(trueImage,tol)

R\_num = 0; % initialize region number

mask = ones(size(trueImage)); % matrix for regions available for merging

regions = zeros(size(trueImage)); % initialize region matrix

while (sum(mask(:)) > 0)

R\_num = R\_num + 1; % update region number

[Rx, Ry] = find(mask == 1,1); % find first instance of new region

temp\_mask = grayconnected(trueImage,Rx,Ry,tol); % connect like pixels

largeRegions = bwareaopen(~temp\_mask, 10); % fill in holes < size 10

temp\_mask = ~largeRegions; % invert to turn region of interest to 1's

regions(temp\_mask) = R\_num; % assign this region to a specific region #

trueImage(temp\_mask) = NaN; % exclude region in trueImage for next grayconnected iter

mask = mask - temp\_mask; % remove already segmented region from mask

imagesc(regions); axis square; title('Unique Region Labels');

drawnow;

end

end

%% **Approximate Image**

% Description:

% Approximates an image based on regions and true image.

% Image approximation is done by averaging true image pixel values in

% each region.

% Returns:

% approxImage = image approximation (double)

% totaLength = sum of total length of each region

% Arguments:

% regions = image of distinct region labels (double)

% trueImage = input image (double)

% Dependencies:

% edgeLength.m

function [approxImage,totaLength] = approximateFull(regions,trueImage)

totaLength = 0;

approxImage = zeros(size(regions));

labels = (unique(regions)); % unique region numbers (labels)

N\_regions = length(labels); % number of total distinct regions

for r = 1:N\_regions

areaR = (regions == labels(r)); % returns 1's in the current region, and zeros elsewhere

approxImage = approxImage + mean(trueImage(areaR))\*areaR; % add approximation of region r to f

totaLength = totaLength + edgeLength(labels(r),regions); % iteratively add region lengths

end

end

%% **Get Each Region Edge Length**

% Description:

% Calculates discrete edge length (perimeter) of each region.

% Note this does not count outside edge of image as a border

% Returns:

% L = array of region length

% Arguments:

% regions = image of distinct region labels (double)

% Dependencies:

% NONE

function L = getAllLengths(regions)

[m,n] = size(regions);

labels = unique(regions); % unique region numbers (labels)

N\_regions = length(labels); % number of total distinct regions

L = zeros(N\_regions,1); % initialize length array

for r = 1:N\_regions

for i = 1:m

for j = 1:n

if regions(i,j) == r

if (i > 1 && regions(i-1,j) ~= r) % if there is a border b/w pixel of interest and next pixel

L(r) = L(r) + 1; % add 1 to the length

end

if (i < m && regions(i+1,j) ~= r)

L(r) = L(r) + 1;

end

if (j > 1 && regions(i,j-1) ~= r)

L(r) = L(r) + 1;

end

if (j < n && regions(i,j+1) ~= r)

L(r) = L(r) + 1;

end

end

end

end

end

end

%% **Cost Function**

% Description:

% Calculates cost function (simplified mumford-shah functional) value.

% Simplified MS: L2-norm(trueImage-approxImage) + length(regions)

% where: approxImage is a piecewise-constant approx of true image

% based on average pixel value in region, and length of regions is

% total perimeter length of all regions.

% Returns:

% E = cost function value

% Arguments:

% approxImage = approximation of true image (double)

% trueImage = input image (double)

% totaLength = sum of length of all regions

% nu = regularization parameter

% Dependencies:

% NONE

function E = cost(approxImage,trueImage,totaLength,nu)

data\_term = norm(approxImage-trueImage); % data consistency (L2-norm)

edge\_term = nu\*totaLength; % regularization limiting length of region edges

E = data\_term + edge\_term; % cost function value

end

%% **Edge Length**

% Description:

% Calculates discrete edge length (perimeter) of a region.

% Returns:

% regions = new map of distinct region labels

% added = new proposed region to merge

% Arguments:

% regions = image of distinct region labels (double)

% R = region of interest

% added = regions which have already been tested

% Dependencies:

% NONE

function [regions,added] = merge(regions, R, added)

flag = 0;

[m,n] = size(regions);

for i = 1:m

for j = 1:n % iterate left to right

if (regions(i,j) == R)

if (i > 1 && regions(i-1,j) ~= R && sum(eq(regions(i-1,j),added))==0) % check row above

% if there is a border between the region of interest

added = [added, regions(i-1,j)]; % region of proposed merge

mask = (regions == regions(i-1,j)); % create mask of region to be added

regions(mask) = R; % merge regions

flag = 1;

break

end

if (i < m && regions(i+1,j) ~= R && sum(eq(regions(i+1,j),added))==0) % check row below

added = [added, regions(i+1,j)];

mask = (regions == regions(i+1,j));

regions(mask) = R;

flag = 1;

break

end

if (j > 1 && regions(i,j-1) ~= R && sum(eq(regions(i,j-1),added))==0) % check column to the left

added = [added, regions(i,j-1)];

mask = (regions == regions(i,j-1));

regions(mask) = R;

flag = 1;

break

end

if (j < n && regions(i,j+1) ~= R && sum(eq(regions(i,j+1),added))==0) % check column to the right

added = [added, regions(i,j+1)];

mask = (regions == regions(i,j+1));

regions(mask) = R;

flag = 1;

break

end

end

end

if (flag == 1) % break if a proposal is found

break

end

end

end

%% **Approximate Image**

% Description:

% Approximates an image based on regions and true image.

% Image approximation is done by averaging true image pixel values in

% each region. Time is saved by importing an already approximated image,

% only merging new regions.

% Returns:

% approxImage = image approximation (double)

% Arguments:

% r = current region

% proposedAdd = region of proposed merge

% regions = image of distinct region labels (double)

% approxImage = initial image approximation (double)

% Dependencies:

% NONE

function approxImage = approximate(r,proposedAdd,regions,approxImage)

maskR = regions==r; % mask area of current region

maskP = regions==proposedAdd; % mask area of proposed region

mask = maskR | maskP; % create mask of combined region

newMean = mean(approxImage(mask)); % calculate mean of combined region

approxImage(mask) = newMean; % make new approximate image

end