Bioimage Informatics

Lecture 13, Spring 2012

Bioimage Data Analysis (IV)

Image Segmentation (part 2)



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Outline

- Review: Steger's line/curve detection algorithm
- Intensity thresholding based image segmentation
- A brief introduction to ITK
- Image segmentation performance evaluation

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Steger's Curve Detection Algorithm (I)

 Step 1: Identify maximal line width. Convolve image with a Gaussian kernel whose size satisfies:

$$\sigma \ge \frac{w}{\sqrt{3}}$$



Steger's Curve Detection Algorithm (II)

 Step 2: For each pixel, calculate the direction (n_x, n_y) with the maximal second directional derivative, which is the eigenvector corresponding to the largest eigenvalue of the Hessian matrix.

$$Hf = \begin{bmatrix} \frac{\partial^2 f}{\partial x^2} & \frac{\partial^2 f}{\partial x \partial y} \\ \frac{\partial^2 f}{\partial y \partial x} & \frac{\partial^2 y}{\partial y^2} \end{bmatrix}$$

Steger's Curve Detection Algorithm (III)

• Step 3: Calculate the first and second directional derivative

$$r' = \begin{bmatrix} n_x & n_y \end{bmatrix} \begin{bmatrix} f_x \\ f_y \end{bmatrix}$$
$$r'' = \begin{bmatrix} n_x & n_y \end{bmatrix} H \begin{bmatrix} n_x \\ n_y \end{bmatrix}$$
$$= f_{xx}n_x^2 + 2f_{xy}n_xn_y + f_{yy}n_y^2$$

• Step 4: Determine location of the local intensity maximum

$$p(x) = r + r'x + \frac{1}{2}r''x^2 \qquad x^* = -\frac{r'}{r''} = -\frac{f_x n_x + f_y n_y}{f_{xx} n_x^2 + 2f_{xy} n_x n_y + f_{yy} n_y^2}$$

Steger's Curve Detection Algorithm (IV)

• Step 5: Test whether it is a center line point

$$\begin{cases} \text{if } x^* \in \left[-\frac{1}{2} \quad \frac{1}{2} \right], \text{ the pixel is on the center line} \\ & \text{otherwise} \end{cases}$$

• Step 6: Link individual center line pixels into a line/curve

Steger's Line Detection Algorithm (V)

• Step 7: Correct for intensity imbalance if necessary



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Overview: Image Segmentation (I)

Definition

Segmentation is the process of separating objects from background (Snyder & Qi in "Machine Vision)

Segmentation is the partitioning of a dataset into continuous regions (or volumes) whose member elements have common, cohesive properties (Yoo in "Insight into Images").

Image segmentation is the task of finding groups of pixels that "go together" (Szeliski in "Computer Vision").

 Segmentation is an essential process in bioimage analysis that is critical for many subsequent processes such as object recognition and shape analysis.



Overview: Image Segmentation (II)

- There are many types of segmentation techniques:
 - Threshold-based segmentation
 - Region-based segmentation
 - Boundary/surface-based segmentation
 - Motion-based segmentation
 - Color-based segmentation
 - Others...



- It is often very useful to combine multiple techniques for image segmentation.
- For bioimage analysis, accuracy in segmentation is essential.

Thresholding-Based Segmentation (I)

• Revisit the definition

"Segmentation is the partitioning of a dataset into continous regions (or volumes) whose member elements have common, cohesive properties".

- Intensity is the most frequently used property.
- Multiple continuous regions of cohesive intensities will result in multiple peaks in intensity histogram.

Thresholding-Based Segmentation (II)

- Thresholding-based segmentation is usually among the first options to be considered.
 - Simple; can be quite reliable
 - Easy to implement.
- There are many refinements to the basic idea that work remarkably well.

Basic Ideas of Thresholding-Based Segmentation (I)



Basic Ideas of Thresholding-Based Segmentation (II)



FIGURE 10.36 (a) Noiseless 8-bit image. (b) Image with additive Gaussian noise of mean 0 and standard deviation of 10 intensity levels. (c) Image with additive Gaussian noise of mean 0 and standard deviation of 50 intensity levels. (d)–(f) Corresponding histograms.

How to Set Thresholds (I)

• There are several ways to set the thresholds.

- Using local minima in the intensity histogram.
- Use intensity histogram fitting with a mixture of Gaussians.

• Example:

Example Results



Region Growth After Thresholding

• Thresholded pixels need to be connected into regions, often through recursive region growth.

• Morphological image processing is often required to remove noise-related irregularities.



How to Set Thresholds (II)

• One way to fit multiple Gaussians

Reference: C. Fraley and A. E. Raftery. *Model-based clustering, discriminant analysis and density estimation*. Journal of the American Statistical Association, 97:611–631, 2002.

Implementation in R : http://www.stat.washington.edu/mclust/

- Determine the number of Gaussians
 - Bayesian information criterion (BIC)

BIC = $2\log p_M(x|M) - N_M \log(n)$

 $M \rightarrow \text{Model}$ log $p_M(x|M) \rightarrow \text{maximized likelihood}$ $N_M \rightarrow \text{Number of parameters in model } M$ $n \rightarrow \text{Number of measurements}$

How to Set Thresholds (III)

Discriminant analysis (supervised classification)

$$P(x \in \text{class } j) = \frac{w_j p_j(x)}{\sum_{k=1}^{M} w_k p_k(x)}$$

Determine the threshold between two neighboring
Gaussian

$$\frac{w_1}{\sigma_1 \sqrt{2\pi}} exp\left(-\frac{(x-\mu_1)^2}{2\sigma_1^2}\right) = \frac{w_2}{\sigma_2 \sqrt{2\pi}} exp\left(-\frac{(x-\mu_2)^2}{2\sigma_2^2}\right)$$

$$\left(\frac{1}{2\sigma_2^2} - \frac{1}{2\sigma_1^2}\right)x^2 + \left(\frac{\mu_1}{\sigma_1^2} - \frac{\mu_2}{\sigma_2^2}\right)x + \left(\frac{\mu_2^2}{2\sigma_2^2} - \frac{\mu_1^1}{2\sigma_1^2} - \log\frac{w_2\sigma_1}{w_1\sigma_2}\right) = 0$$

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Introduction to ITK (I)

- Started in 1999 through funding by the National Library of Medicine to support the Visible Human Project.
- Website: http://www.itk.org/
- ITK: insight toolkit

- Open source software package for image registration and segmentation

 Language: 55% C++; 25% C; XML 11%; Other 9% (as of Feb-27, 2012)

Introduction to ITK (II)

- Scale
 - Approximately 2.2 million lines of code (as of Feb-27, 2012)
 - Initial cost: 718 person years, \$39M (as of Feb-27, 2012)
- Current release 4.0 (as of Feb-27-2012)

Introduction to MAT-ITK

• Website: http://matitk.cs.sfu.ca/

Opcode	Method
SCC	ConfidenceConnectedSegmentation
SCSS	CellularSegmentationSegmentation(Debug)
SCT	ConnectedThresholdSegmentation
SFM	FastMarchSegmentation
SGAC	GeodesicActiveContourLevelSetSegmentation
SIC	IsolatedConnectedSegmentation
SLLS	LaplacianLevelSetLevelSetSegmentation
SNC	NeighbourhoodConnectedSegmentation
SOT	OtsuThresholdSegmentation
SSDLS	ShapeDetectionLevelSetFilter
SWS	WatershedSegmentation

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Reference

Heimann et al, Comparison and Evaluation of Methods for Liver Segmentation From CT Datasets, IEEE TRANSACTIONS ON MEDICAL IMAGING, VOL. 28, NO. 8, pp. 1251-1265. 2009

Medical Imaging Computing and Computer-Assisted Intervention (MICCAI) http://mbi.dkfz-heidelberg.de/grand-challenge2007/index.html

- Liver segmentation: http://www.sliver07.org

- Caudate segmentation: http://www.cause07.org/

Evaluation Strategies

- Option 1: using manual segmentations as references.
- Option 2: relative rating by experts.
- Option 3: rating by consensus.
 - Consensus may not be accurate.

Evaluation Procedure

• Dataset

- A total of 40 images.
- Images are collected under different settings.
- Most images are pathologic (i.e. with abnormal shapes).
- Reference segmentations (ground truth) are generated manually.

• Training versus testing

- 20 images are chosen for training.
- 10 images are chosen for testing.
- 10 images are chosen for on-site competition (no considered in the paper).
- Methods: 10 automated, 6 interactive

Evaluation Criterion

• Five criterion

- Volumetric overlap error
- Relative volume difference
- Average symmetric surface distance
- Root mean square surface distance
- Maximum symmetric surface distance
- Scoring
 - Trained but inexperienced graders are used to set a base score of 75/100.

$$\phi_i = \max\left(100 - 25\frac{\varepsilon_i}{\overline{\varepsilon_i}}, 0\right)$$

Results

TABLE II

OVERVIEW OF RESULTS FOR AUTOMATIC SEGMENTATION METHODS. RESULTS FOR EACH MEASURE ARE REPORTED AS MEAN AND STANDARD DEVIATION OVER ALL TEST IMAGES, TOGETHER WITH MEAN SCORE. ALL SCORES ARE AVERAGED TO A FINAL SCORE GIVEN AS MEAN AND STANDARD DEVIATION OVER ALL IMAGES

Method	Runtime	Overlap error		Volume difference		Avg. distance		RMS distance		Max. distance		Final	
	[min]	[%]	Score	[%]	Score	[mm]	Score	[mm]	Score	[mm]	Score	Score	
Kainmüller et al.	15	6.1 ± 2.1	76	-2.9 ± 2.9	85	0.9 ± 0.3	76	1.9 ± 0.8	74	18.7 ± 8.5	75	77 ± 9	
Heimann et al.	7	7.7 ± 1.9	70	1.7 ± 3.2	88	1.4 ± 0.4	65	3.2 ± 1.3	55	30.1 ± 10.2	60	67 ± 11	
Saddi et al.	5.5	8.9 ± 1.8	65	1.2 ± 4.4	80	1.5 ± 0.4	62	3.4 ± 0.8	52	$29.3~\pm~8.4$	62	64 ± 6	
Schmidt et al.	6–20	10.4 ± 1.9	59	$\textbf{-4.9}\pm3.0$	74	1.7 ± 0.4	56	3.1 ± 1.1	57	$24.0~\pm~8.0$	68	63 ± 8	
Chi et al.	34	9.1 ± 2.8	65	2.6 ± 6.3	73	1.7 ± 0.6	58	3.3 ± 1.2	54	$30.8~\pm~9.2$	60	62 ± 11	
Ruskó et al.	0.5	10.1 ± 4.5	61	-3.8 ± 6.4	72	1.7 ± 0.9	58	3.5 ± 2.3	53	26.7 ± 11.7	65	61 ± 21	
Seghers et al.	30	10.7 ± 2.5	58	-6.8 \pm 2.3	64	1.8 ± 0.4	55	3.2 ± 1.1	56	25.2 ± 10.1	67	60 ± 10	
Furukawa et al.	36	10.8 ± 3.7	58	-7.3 ± 4.7	61	1.9 ± 1.1	53	3.7 ± 1.9	49	31.6 ± 12.7	58	56 ± 17	
van Rikxoort et al.	45	12.5 ± 1.8	51	1.8 ± 4.2	80	2.4 ± 0.3	40	4.4 ± 1.5	40	32.4 ± 13.7	57	53 ± 8	
Susomboon et al.	25	26.4 ± 24	31	-11.5 ± 30	42	10.2 ± 13	15	17.1 ± 18	12	74.0 ± 41.5	23	24 ± 22	
Top 5 majority vote		5.0 ± 1.3	81	-0.7 \pm 1.7	93	0.8 ± 0.3	81	1.7 ± 0.8	77	$19.1~\pm~8.4$	75	81 ± 8	

TABLE III

OVERVIEW OF RESULTS FOR INTERACTIVE SEGMENTATION METHODS. RESULTS FOR EACH MEASURE ARE REPORTED AS MEAN AND STANDARD DEVIATION OVER ALL TEST IMAGES, TOGETHER WITH MEAN SCORE. ALL SCORES ARE AVERAGED TO A FINAL SCORE GIVEN AS MEAN AND STANDARD DEVIATION OVER ALL IMAGES. THE AMOUNT OF REQUIRED INTERACTION IS INDICATED IN PARENTHESES

Method	Runtime	Overlap error		Volume difference		Avg. distance		RMS distance		Max. distance		Final	
	[min]	[%]	Score	[%]	Score	[mm]	Score	[mm]	Score	[mm]	Score	Score	
Beichel et al. MBR (high)	36	5.2 ± 0.9	80	1.0 ± 1.7	91	0.8 ± 0.2	80	1.4 ± 0.4	80	15.7 ± 3.5	79	82 ± 2	
Beck and Aurich (high)	7	6.6 ± 1.6	74	1.8 ± 2.5	88	1.0 ± 0.3	74	1.9 ± 0.4	73	18.5 ± 4.1	76	77 ± 4	
Dawant et al. (med)	20	7.2 ± 1.2	72	2.5 ± 2.3	86	1.1 ± 0.2	73	1.9 ± 0.5	74	17.1 ± 5.4	77	76 ± 5	
Second rater		6.4 ± 1.0	75	4.7 ± 1.8	75	1.0 ± 0.2	75	1.8 ± 0.5	75	19.3 ± 5.6	75	75 ± 4	
Lee et al. (low)	7	6.9 ± 1.4	73	1.3 ± 2.9	88	1.1 ± 0.3	73	2.1 ± 0.5	71	21.3 ± 4.0	72	75 ± 5	
Beichel et al. CBR (med)	31	6.5 ± 1.1	74	1.1 ± 1.9	90	1.1 ± 0.4	72	2.5 ± 1.2	66	23.4 ± 10.5	69	74 ± 9	
Wimmer et al. (med)	4-7	8.1 ± 1.1	68	6.1 ± 2.6	68	1.3 ± 0.2	67	2.2 ± 0.4	69	18.7 ± 4.6	75	69 ± 5	
Slagmolen et al. (med)	60	10.4 ± 3.1	59	3.7 ± 6.2	70	2.0 ± 0.7	50	5.0 ± 2.4	34	40.5 ± 18.2	47	52 ± 19	
Beichel et al. GC (low)	30	14.3 ± 9.4	48	3.1 ± 10.7	62	3.6 ± 3.1	34	7.9 ± 5.9	24	49.2 ± 20.4	38	41 ± 27	

Questions?