

# *CS6240 Multimedia Analysis*

## *3D Tumor Segmentation using Level Set*

*Sima Taheri*  
*04/27/2006*

# Outline

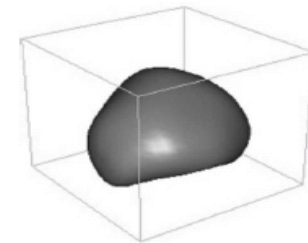
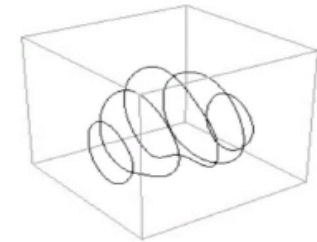
- **Introduction**
- **Objective**
- **Problem Formulation**
- **Problem Solving**
  - ✓ **Initialization**
  - ✓ **Narrow band Solution**
  - ✓ **Speed Function Design**
  - ✓ **Stopping Criterion**
- **Simulation Results**
- **Discussion**
- **Q&A**

# Introduction

- **Two approaches to obtain the 3D tumor surface.**

- **3D reconstruction from its 2D contours**

- ✓ **Using a sequence of 2D contours detected in the parallel cross-sectional images.**
    - ✓ **Disadvantages**
      - ✓ **Broken boundary in one slice usually leads to poor detected results**
      - ✓ **A segmentation of an slice along different axes may lead to different results**
      - ✓ **The reconstruction of the surface and its properties from 2D contours may lead to inaccurate results.**



- **Volume approach**

- ✓ **Carry out the computation in 3D space and detect the 3D tumor surface directly.**
    - ✓ **Advantages**
      - ✓ **More robust and accurate**

# Objective

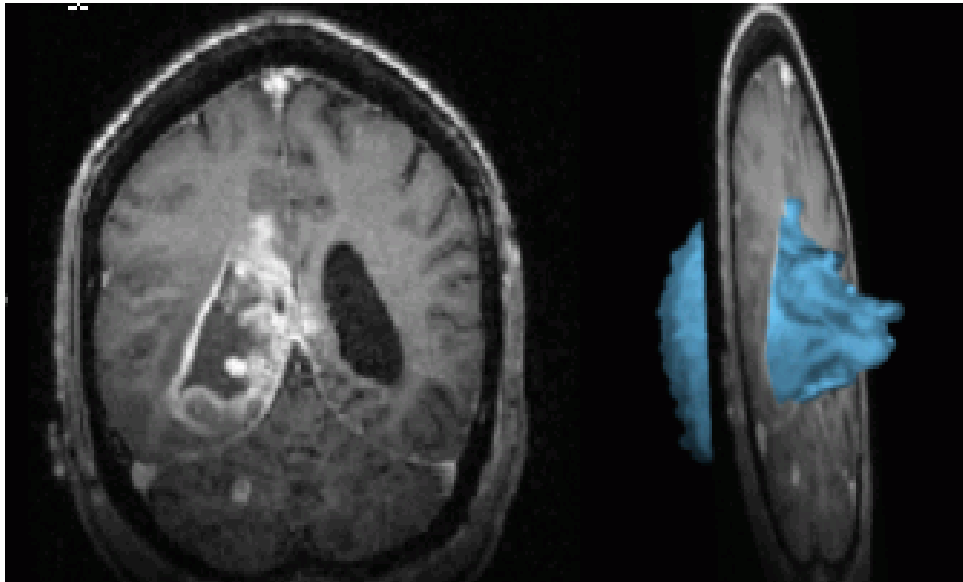
- **Segmentation of 3D tumor in Magnetic Resonance Images using volume approach**
- **We choose the level set as the surface detection mechanism for the following of reasons:**
  - ✓ **Its ability to handle complex geometry and topological changes.**
  - ✓ **No significant differences in tracking fronts in 2D and 3D.**
  - ✓ **Its computational efficiency in 3D by the use of Narrow-Band techniques.**
  - ✓ **Its free initial hypersurface selection which can potentially relieve the user involvement.**
- **Evaluate these methods on a number of clinical cases to establish their feasibilities.**

# *Problem Formulation*

# Inputs

- **Let  $\{I_k\}$  denote the multichannel 3D Magnetic Resonance (MR) images that show different aspects of the tumor region.**
- **We use post-contrast T1-weighted images of the whole head, having an in-plane resolution of  $256 \times 256$  and about 20 slices (depending on the individual dataset), with a voxel resolution of  $1 \times 1 \times 2 \text{ mm}^3$** 
  - ✓ **High resolution T1-weighted MRIs are commonly used for detailed imaging of neuroanatomy, but by themselves do not distinguish tumor tissue well.**
  - ✓ **T2-weighted MRIs do highlight tumor tissue and surrounding edema, but are often difficult to obtain in high resolution.**
  - ✓ **Of great use is a post contrast T1-weighted MRI, where contrast agent has been injected into the bloodstream to highlight the tumor.**

- ***3D surface which shows the tumor volume.***

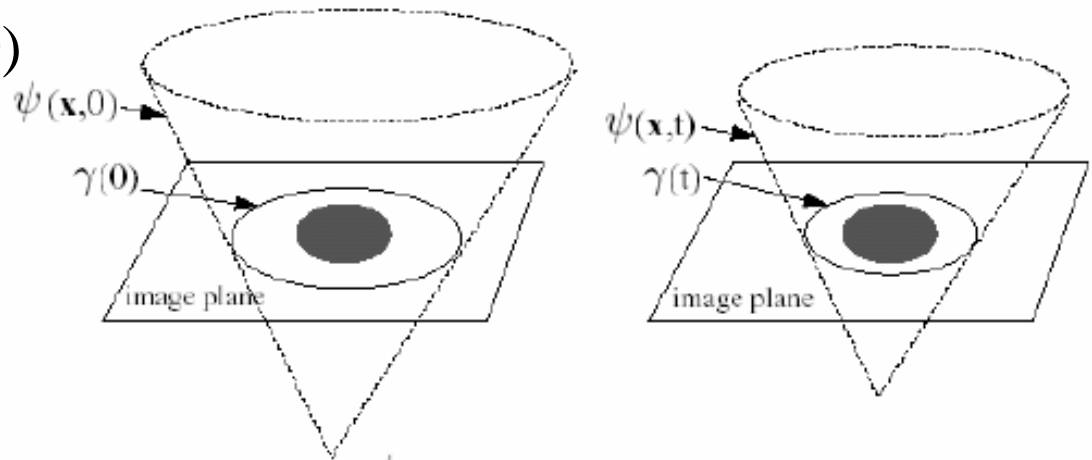


# Problem Definition

- **The volume segmentation problem can be expressed as the computation of a 3D surface  $\gamma(t)$  propagation in time along its normal direction.**
- **The propagating front  $\gamma(t)$  is embedded as the zero level set of a time-varying 4D function  $\psi(\mathbf{p}, t), \mathbf{p} \in \mathbb{R}^3$ .**
- **The evolution equation for  $\psi$  is as follow,**

$$\psi_t + F|\nabla \psi| = 0$$

$$\psi(\mathbf{x}, t = 0) = \gamma(t = 0)$$



$\gamma$  zero isocontour ;  $\psi$  high dimensional surface;  $\bullet$ : object of interest;



# Problem Definition (Contd.)

- **The problem is to find an appropriate initial surface  $\gamma(t = 0)$  and to design an appropriate speed function  $F = f(F_I, S)$  which can drive the evolving front to the desired object surface.**
  - ✓  **$F_I$  is the image force which can be gradient magnitude of the images or the gray levels.**
  - ✓  **$S$  is the smoothness parameter which depends on the front characteristics such as curvature and normal direction.**

- Normal vector of the front,  $\bar{n} = \frac{\nabla \psi}{|\nabla \psi|}$

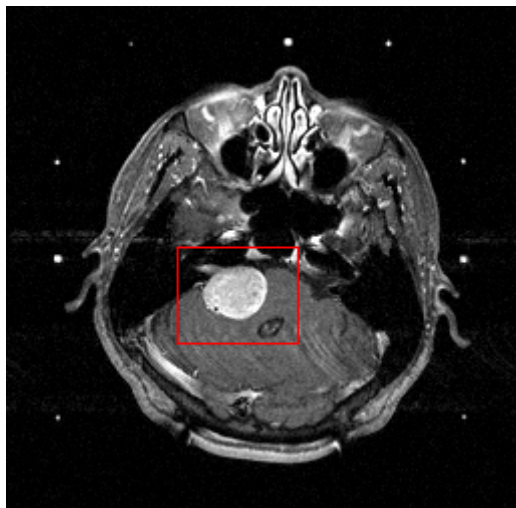
- Curvature of the front,  $\kappa = \nabla \cdot \frac{\nabla \psi}{|\nabla \psi|}$

# *Problem Solving*

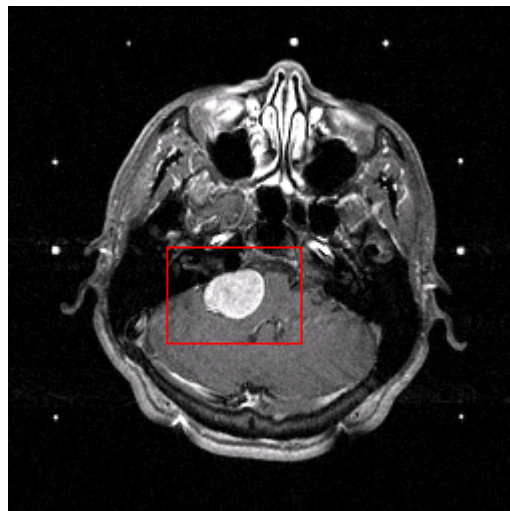
# Initialization

- **Since the level set method is able to handle the change of topology, our initializing surfaces do not need to be placed close to the boundaries of interest and in similar topological form.**
- **We initialize the level set in the region of interest (ROI) which is drawn manually in the reference image.**
- **We have two approaches for initialization,**
  - ✓ **Automatic initialization,**
    - ✓ **We automatically put a small sphere at the center of ROI as the initial zero level set to start the surface detection**
  - ✓ **Semi-automatic initialization**
    - ✓ **Sometimes, automated initialization is improper because the tumor may have irregular shape.**
    - ✓ **So we initial the level set with manually selected centers.**

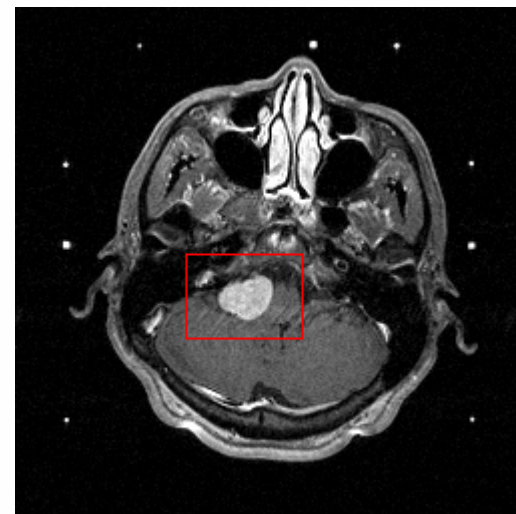
# Automatic initialization



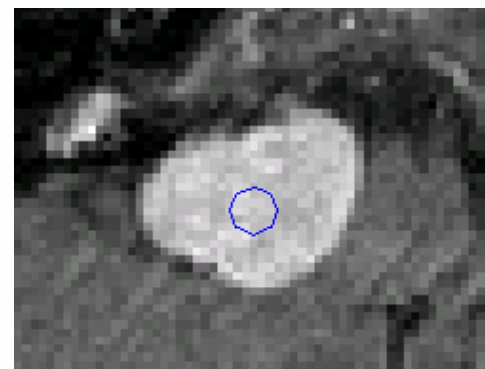
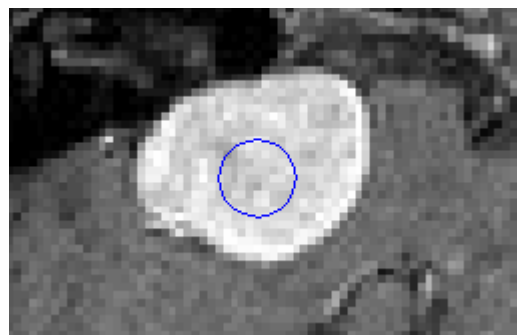
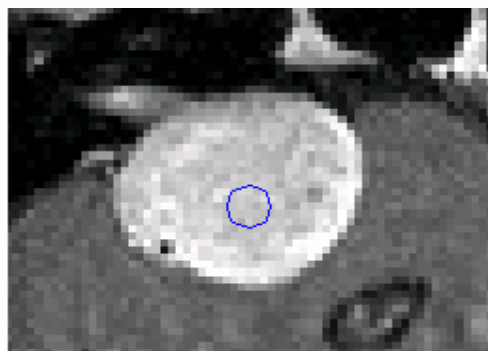
11



13



15



# *Semi-automatic initialization*

- ***A single level set may fail to detect all the desired boundaries due to the intensity inhomogeneity and irregular shape of the tumor.***
- ***We can use multiple level sets to optimize the initialization procedure.***



12



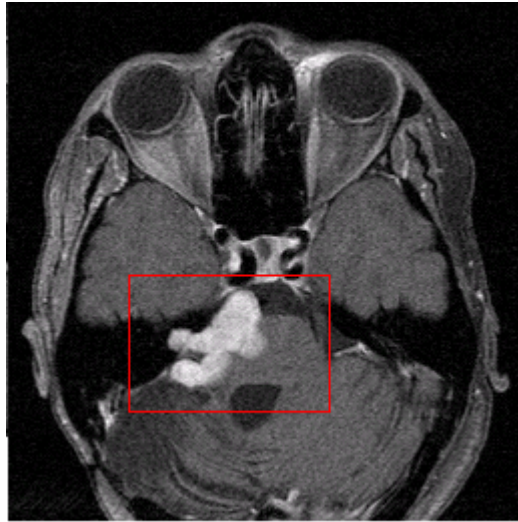
13



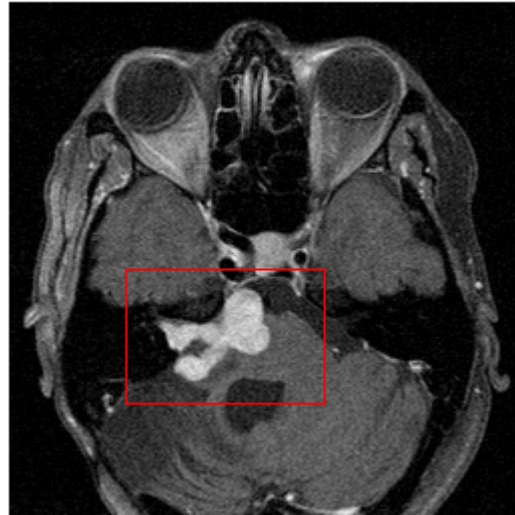
14

***Even though the iteration number is increased, the contours in some slices cannot reach the upper-left corners.***

# *Evolving Bubbles*



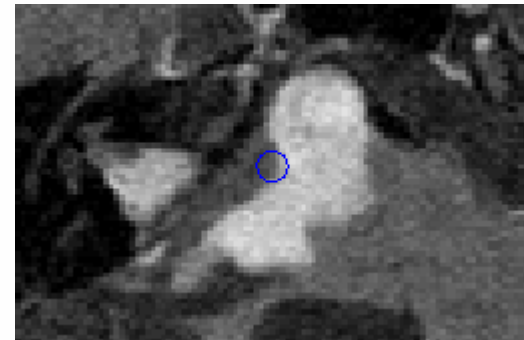
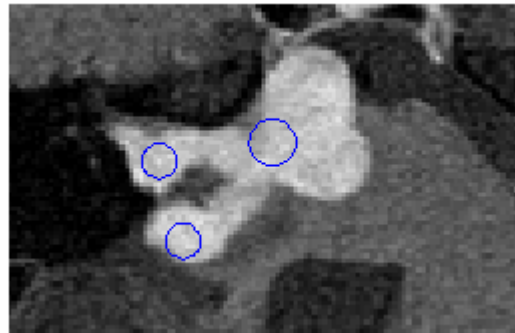
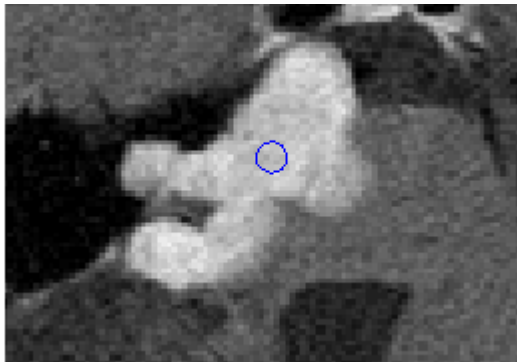
11



13

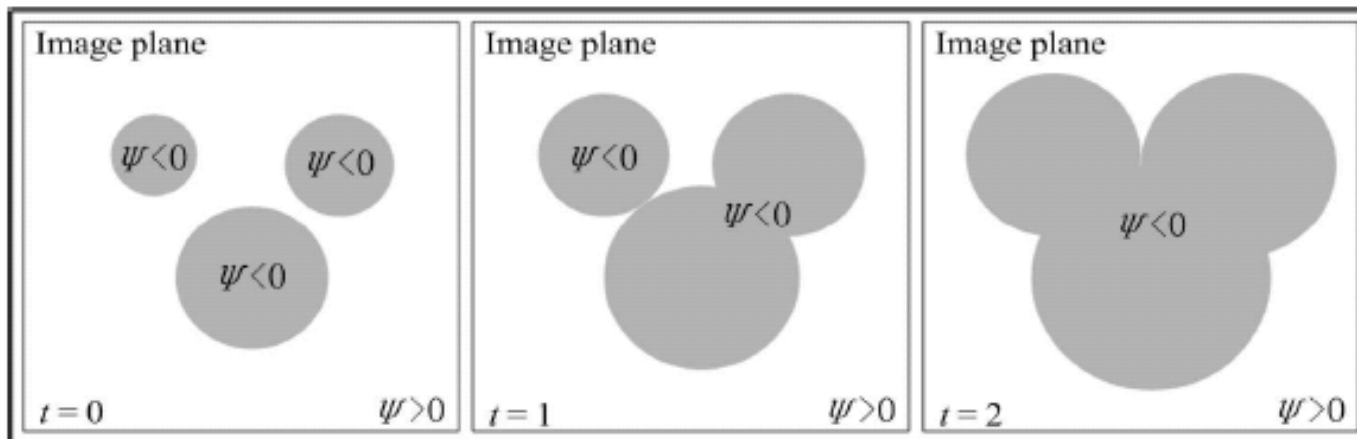


15



# Note

- **Note that one of the initial spheres crosses over the tumor boundaries to the background**
- **We should design the proper speed function to cause that part shrinks and finally is attracted to the desired boundaries**



**Merging of three bubbles when evolving with constant speed along normal direction.**

# *Narrow band Solution*

- ***For a 2D interface evolving in 3-D space, the level set algorithm is at least an  $O(N^3)$  method per time step.***
  - ✓ ***N is the number of points in the spatial direction.***
- ***One drawback of this technique stems from the computation expense.***
- ***Clearly, the disadvantage of heavy computational load is even worse for a 3D level set based approach.***
- ***To overcome this drawback, Adalsteinsson and Sethian proposed a fast level set method for propagating interfaces, named Narrow-Band Method.***
- ***The main idea:***
  - ✓ ***To modify the level set method so it only affects points close to the cells where the front is located.***

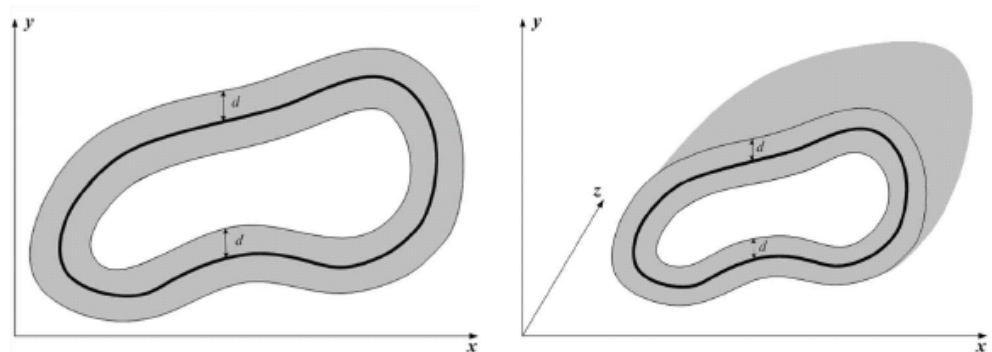


# Narrow band (Contd.)

- **As a consequence of this update strategy, the front can be moved through a maximum distance of  $d$ , either inward or outward, at which point we must rebuild an appropriate (a new) narrow band.**
- **We choose  $l$  as the number of iteration which ensures zero level set doesn't leave the narrow band.**
- **We reinitialize the level set function, in each time step after  $l$  iterations, by treating the current zero level-set configuration, i.e.  $\psi = 0$ , as the initial hypersurface  $\gamma(0)$ .**

$$l = 5$$

$$d = 0.015$$



(a)

(b)

# Speed Function Design

- **The original formulation of speed function is,**

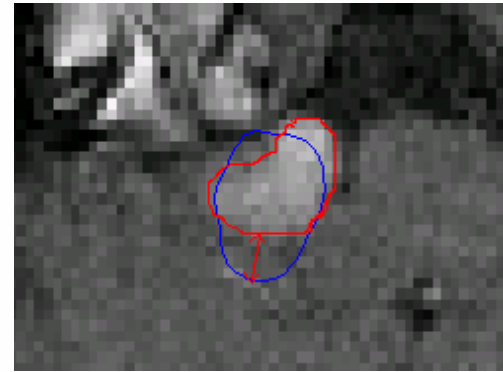
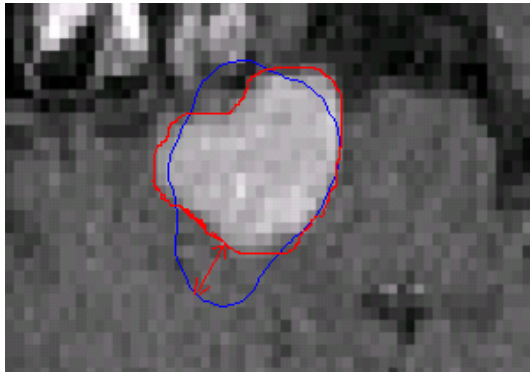
$$F = \underbrace{K_I}_{\text{image force}} \cdot \underbrace{(F_0 - \varepsilon K)}_{\text{internal force}}$$

- ✓  $F_0$  is a constant term (usually taken as 1) which makes the surface contract or expand.
- ✓  $K$  is the mean curvature of the evolving front.
- ✓  $\varepsilon$  is the entropy condition expressing the importance of regularization.
- ✓  $K_I$  is the data consistency term which ensures the propagating front will stop in the vicinity of the desired object boundaries.

$$K_I(x, y, z) = \frac{1}{1 + |\nabla G_\sigma * I(x, y, z)|^p}, p = 1, 2$$

# *Speed Function Design (Contd.)*

- In some image slices, the boundary feature of the tumor is not salient enough and the image gradient information is weak.*
- It usually causes the “boundary leaking” problem when we apply the level set method to detect the 3D tumor surface.*

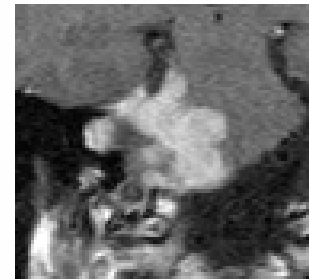
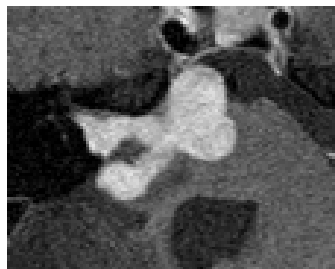
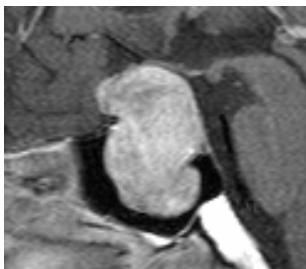
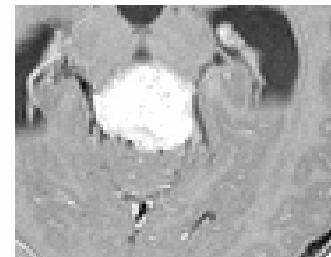
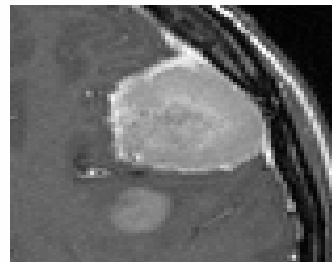
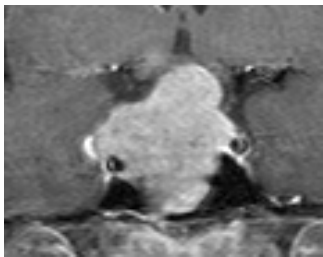


*red contour: drawn manually, blue contour: algorithm result*

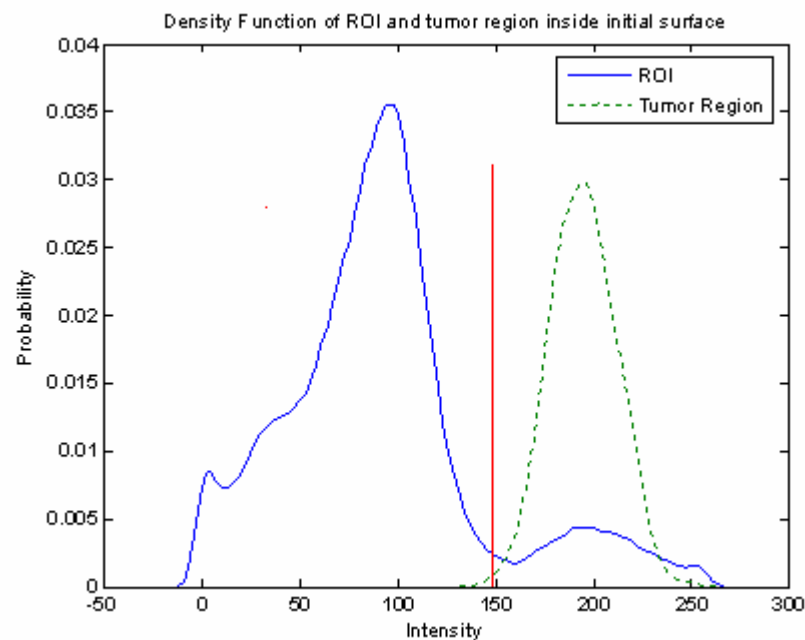
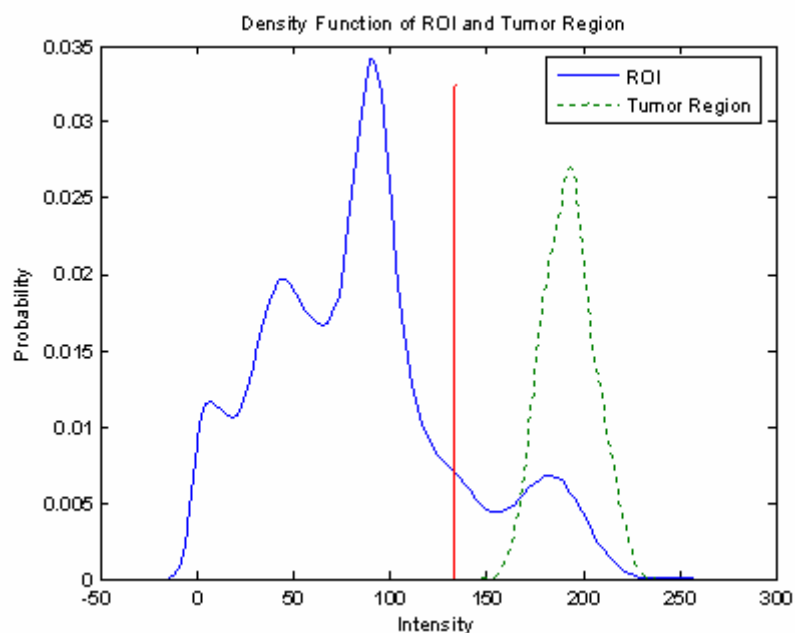
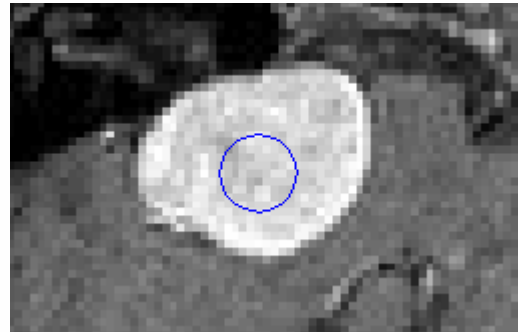
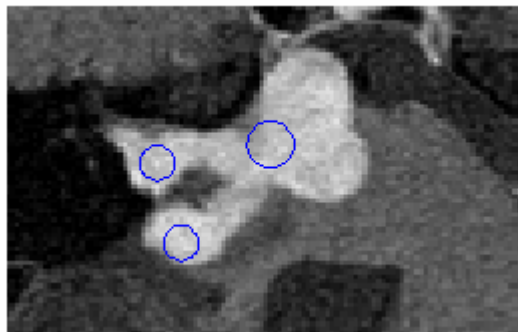
- We integrated the region information instead of the image gradient into the level set method to remedy the leaking problem.*

# Threshold Updating

- *There is a distance between intensity level of tumor part and background.*
- *Therefore, an appropriate threshold can be used to distinguish these two regions.*
- *Since the threshold is unknown at first, we should devise a method to update the threshold so that it converges to the proper value.*



# Density Function

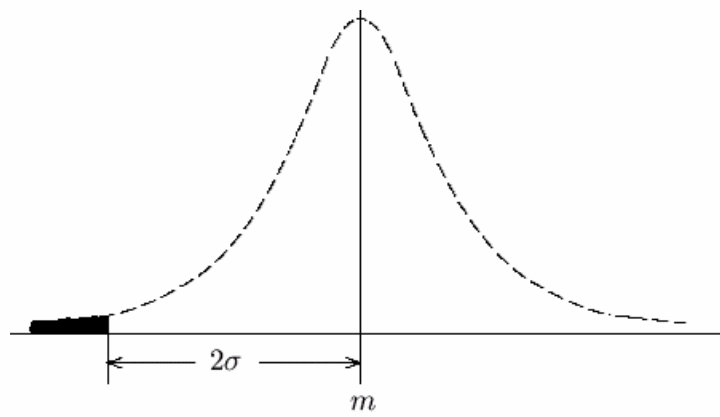


# Confidence Interval

- According to the previous figures normally the tumor intensity distribution is Bell-shaped.
- For a normal distribution, the probability that a measurement falls within  $n$  standard deviations ( $n\sigma$ ) of the mean (i.e., within the interval  $[\mu - n\sigma, \mu + n\sigma]$ ) can be determined.

$$p[x \geq \mu - 2\sigma] = 0.977$$

$$p[x \geq \mu - 3\sigma] = 0.998$$

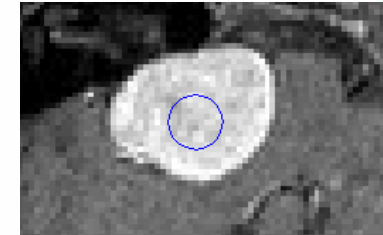
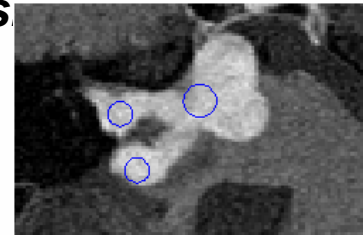


- However for an unknown distribution the Chebyshev bound can be applied. It can be tighter for a symmetric distribution which is not an strong assumption for our case.

$$P[|x - \mu| \leq t\sigma] \leq 1 - \frac{1}{t^2} \quad \Rightarrow \quad P[x \geq \mu - 2\sigma] \leq 1 - \frac{1}{8} = 0.875$$

# Threshold Updating Algorithm

- **Initial threshold,  $T_0 = \mu_0 - 2\sigma_0$** 
  - ✓  $(\mu_0, \sigma_0)$  are the mean and Std. deviation of tumor region inside the initial circles in the reference images



- **In each iteration,**
  - **Samples = image pixels inside zero level set.**
  - **NewSamples = (Samples >  $T_{old} - X$ )**
  - **$\mu = \text{mean}(\text{NewSamples})$ ,  $\sigma = \text{Std. Dev.}(\text{NewSamples})$ ,**
  - **Update threshold,  $T_{new} = \mu - 2\sigma$**
  - **Define the Region Information for grid nodes inside the narrow band,**

$$R = \begin{cases} 1 & I_{g(i,j,k)} > T_{new} \\ 0, (-1) & \text{else} \end{cases}$$

- ***$X$  is a function of the intensity difference between two sides of the tumor edge.***
- ***$X$  is a parameter which ensures that the `NewSamples` only consists of the tumor intensities and there is not any background intensity in it.***
  - ✓ ***In our algorithm we set  $X=30$  for various MR images.***
- ***In the case that initial spheres crosses over the tumor boundaries to the background,***
  - ✓ ***Since the initial threshold is computed only using the reference image, no problem will occur.***



# Speed Function

- **Function  $R$  is then incorporated into the level set method and forms a new speed function as:**

$$F_{new} = F_0(R) - \varepsilon\kappa$$

- **Now  $F_{new}$  is not related to image gradient any more, it only depends on the tumor region and evolving front curvature.**

- **$F_{new}$  has the following properties:**

- ✓  $R=1 \rightarrow F_{new} = F_0 - \varepsilon\kappa$

- **This means inside the tumor region, the evolving front will deform in normal direction and no image constraints are included.**

- ✓  $R=0 \rightarrow F_{new} = -\varepsilon\kappa \quad (R=-1 \rightarrow F_{new} = -F_0 - \varepsilon\kappa)$

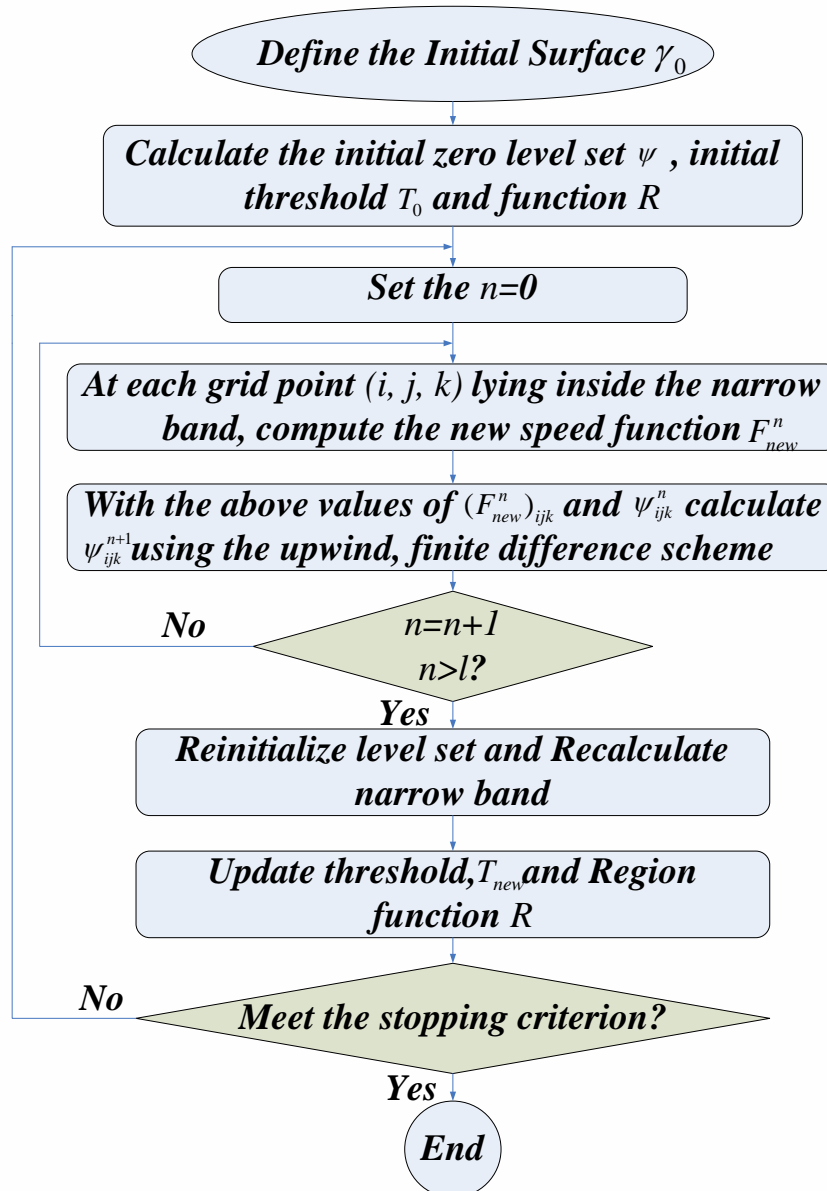
- **This means outside the tumor region, the evolving front will shrink.**

- **Therefore, the interaction of these two properties may make the evolving front eventually attracted to the desired boundaries.**

# Stopping Criterion

- ***If the ratio of new voxels to the total number of voxels on the evolving front in a certain number of consecutive iterations is below a threshold, the surface is thought to reach the desired boundaries already and the iteration stops***
- ***The choice of this threshold value expresses a tradeoff between the accuracy of the detection and the speed of convergence.***
- ***It has been empirically determined from the experiments.***
- ***In our algorithm, 0.003 is finally set as the threshold value for stopping criterion.***

# Algorithm Implementation

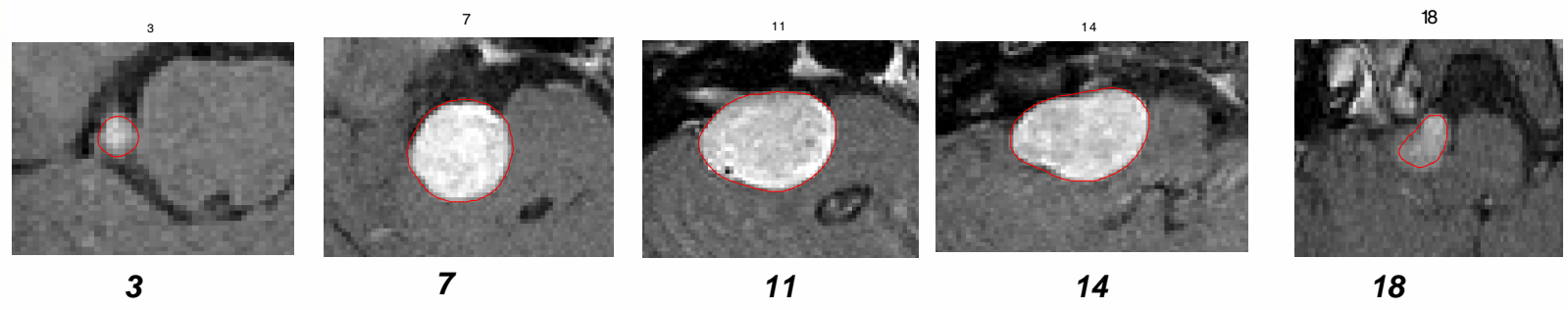
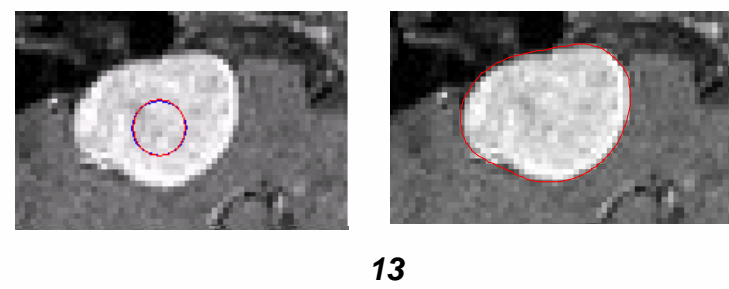


# *Simulation Results*

# Tumor With Regular Shape

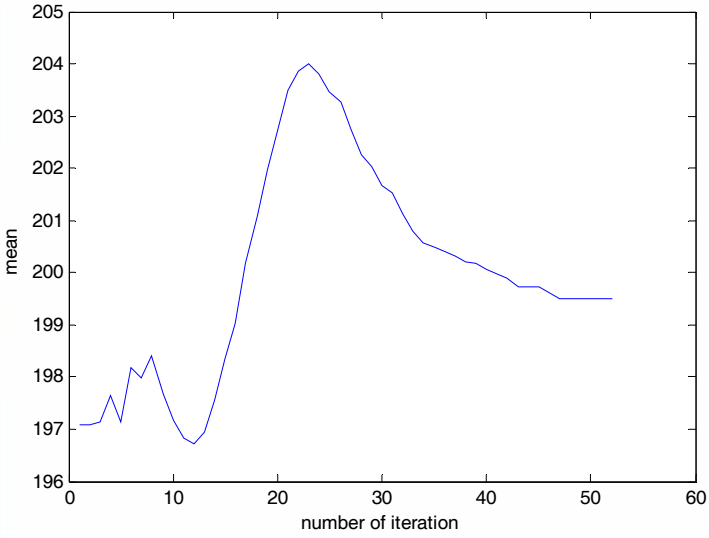
- We have 26 2D slices (2mm width). The slides #3 to #18 consist tumor region.
- Level set is initialized automatically in slide #13 inside the manually drawn ROI.
- Parameters:  $F_0 = 1$      $\varepsilon = 0.01$
- Running time: 2.15 min

$$R = \begin{cases} 1 & I_{g(i,j,k)} > T_{new} \\ 0 & \text{else} \end{cases}$$

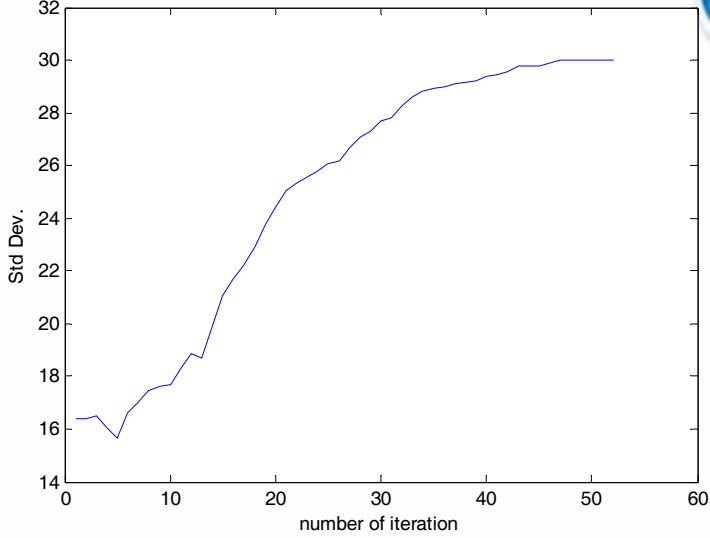


# Threshold Curve

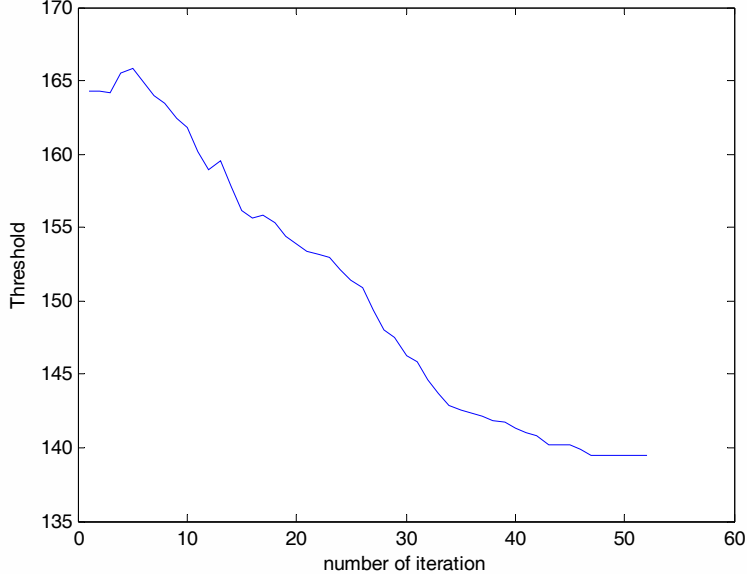
Average intensity of tumor region vs. number of iteration



Standard deviation of tumor intensity region vs. number of iteration



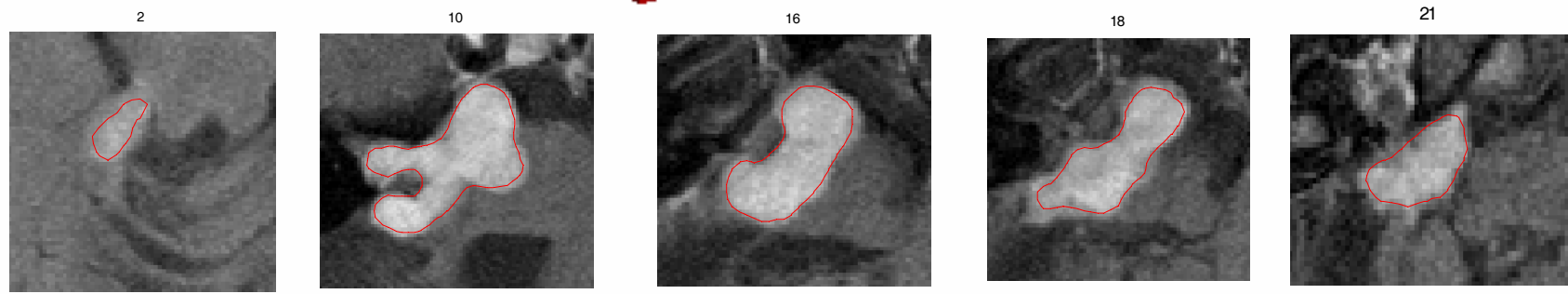
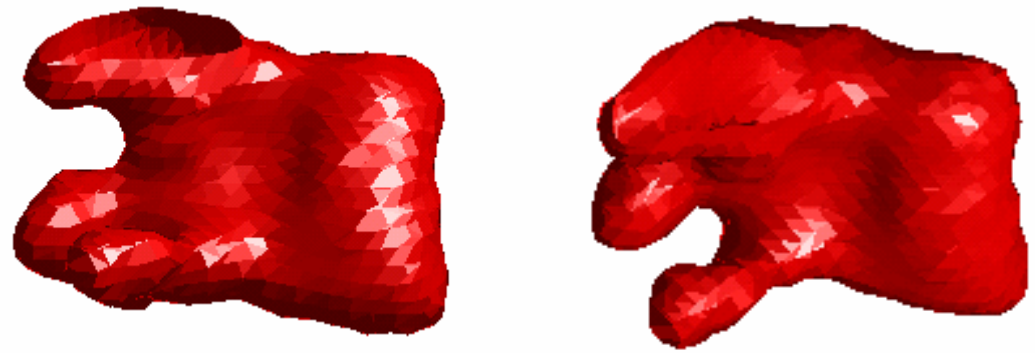
Threshold value vs. number of iteration



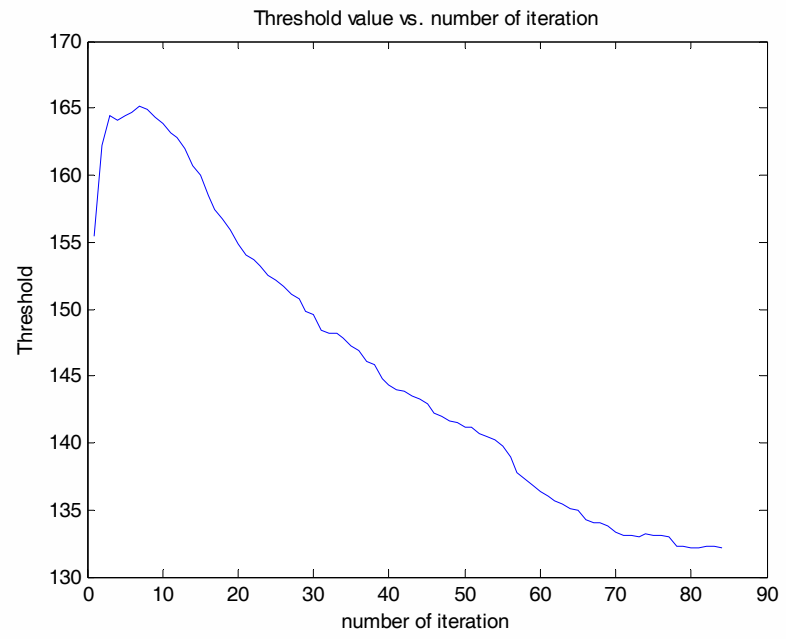
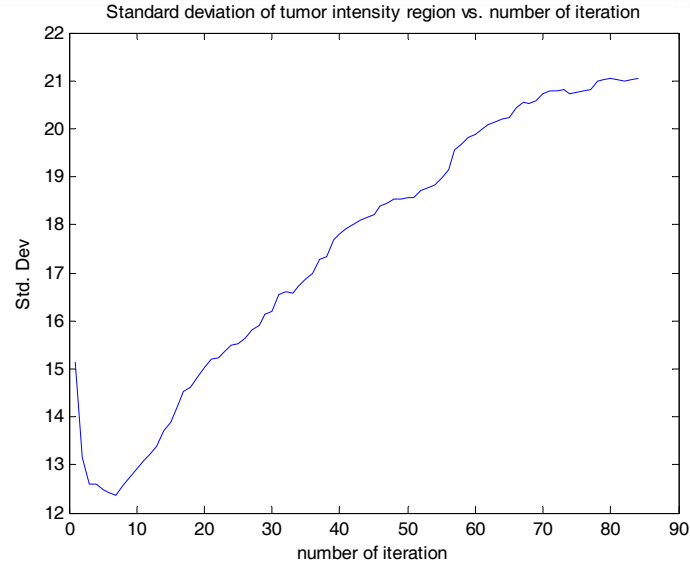
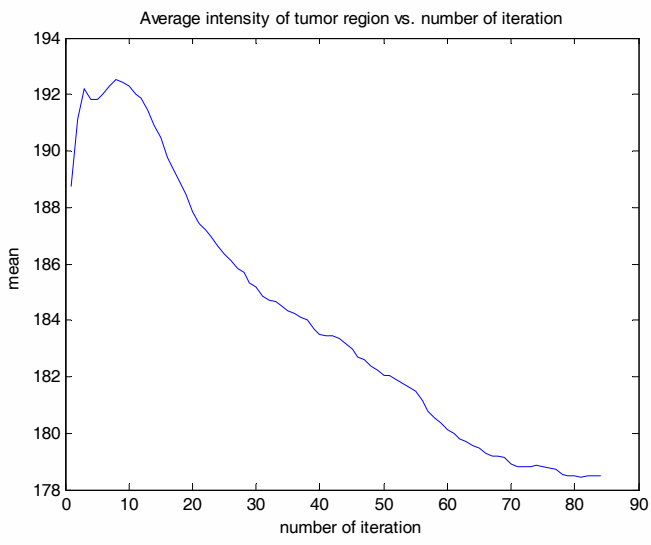
$$T = \mu - 2\sigma$$

# Tumor With Irregular shape

- We have 11 2D slices (3mm width). We obtain one new slice between each two slices using linear interpolation.
- Slides #3 to #21 consist tumor.
- Level set is manually initialized in slide #13 inside the manually drawn ROI.
- Parameters:  $F_0 = 2$      $\varepsilon = 0.01$      $R = \begin{cases} 1 & I_{g(i,j,k)} > T_{new} \\ (-1) & \text{else} \end{cases}$
- Running time: 5 min



# Threshold Curve



$$T = \mu - 2\sigma$$



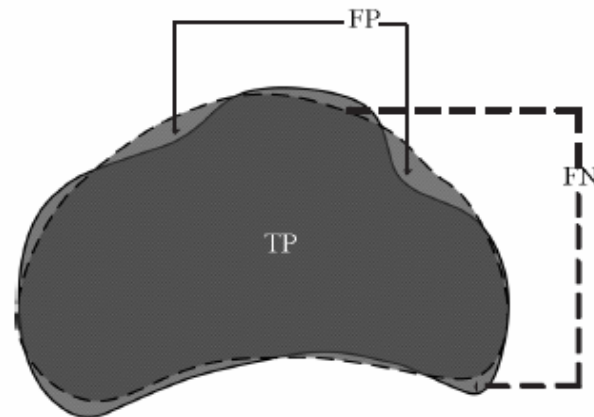
# Evaluation

- ***We compare our results with results of 2D tumor segmentation using SVM.***
- ***SVM method uses the training samples from tumor region and background to segment tumor in each 2D slice.***
- ***However this comparison is not fair because:***
  - ✓ ***We compare the 2d contours of our method with the results of 2D SVM segmentation. Definitely, SVM should performs better.***
  - ✓ ***Our method is (semi)-automatic while SVM needs more user involvement.***
- ***If the error between two results was small, this shows that our algorithm performs well.***

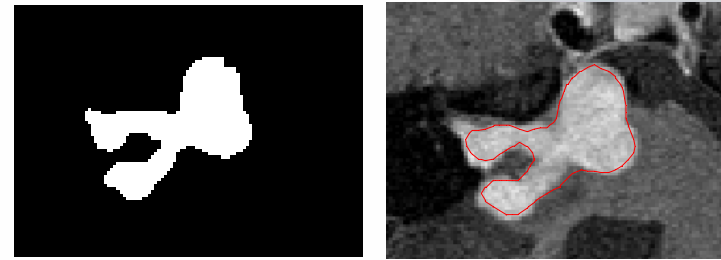
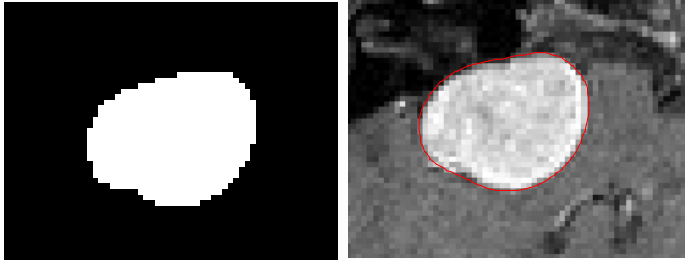
# Area Error

- We used overlap areas defined by two corresponding contours to tell the disagreement between two method.
- The area difference (AD) in each slice is defined as the number of different pixels between SVM result and our algorithm result.
  - ✓ True positive (TP) area: the common pixels contained by both method.
  - ✓ False positive (FP) area : the area enclosed by our algorithm but outside of the result of SVM method.
  - ✓ False negative (FN) area : the area enclosed by the result of SVM method that is missed by our algorithm.

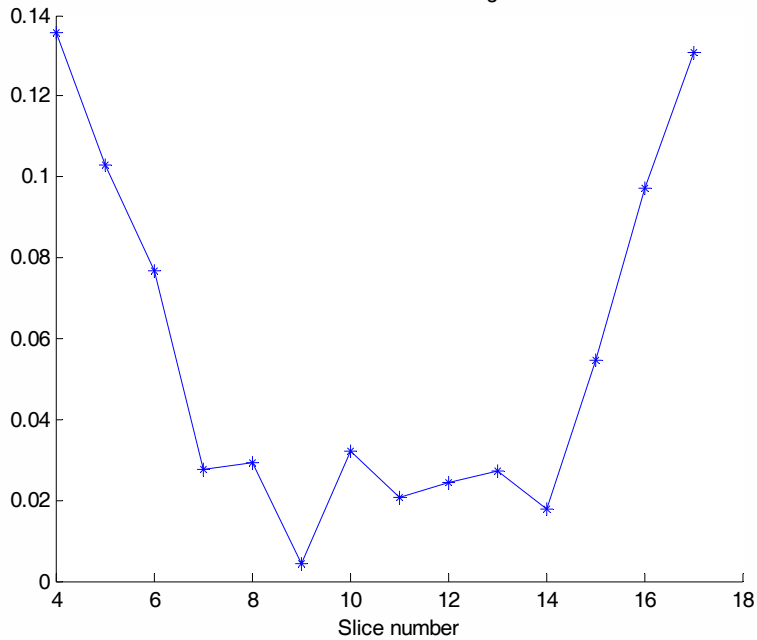
$$AD = \frac{FP + FN}{TP + FP + FN}$$



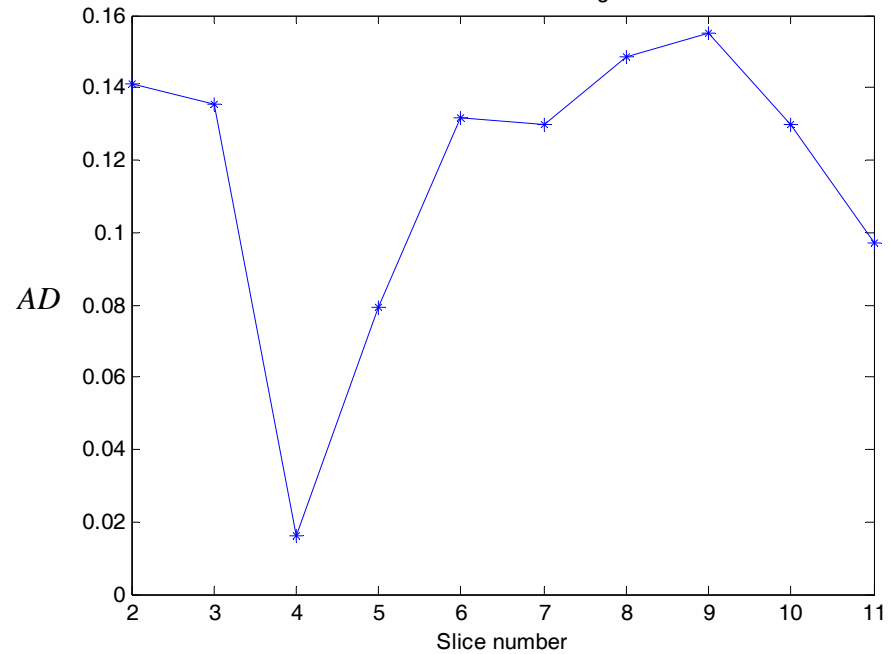
# Evaluation



Volume Difference between results using Levelset and SVM



Volume Difference between results using Levelset and SVM



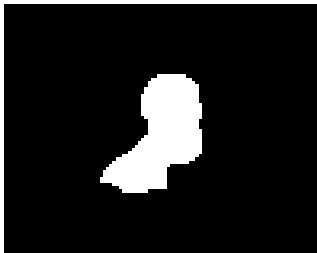
# Evaluation (Contd.)

- **Regular tumor**

- ✓ SVM can not segment tumor in slice#3 and #18, because the tumor region is very small. However, our method performs segmentation in these two slices.
- ✓ The error is small for slices #7 to #14.
- ✓ The highest error is for first and last slice and
- ✓ The mean of the error on various slices is 0.06

- **Irregular tumor**

- ✓ The error for this tumor is higher than error of regular shape tumor.
- ✓ The lowest error is for slice #4.
- ✓ The highest error is for slice #9 and it is because SVM does not consider the separated tumor part.
- ✓ The mean of the error on various slices is 0.11



# Discussion

- **Advantages of our algorithm**

- ✓ **The user involvement is few.**
- ✓ **The running time of algorithm is small.**
  - ✓ **Running time is dependent to the size of tumor, larger tumor → higher running time.**
- ✓ **The algorithm is able to perform 2D tumor segmentation very well for regular or irregular tumor shape.**
- ✓ **The algorithm is able to segment the 3D regular tumor well.**
- ✓ **The algorithm is able to segment the 3D irregular tumor with acceptable accuracy.**
  - ✓ **For higher accuracy, we need more user inputs and more slices which consist tumor region (higher resolution).**

# Discussion

- **Limitation of our algorithm**

- ✓ ***Since this method is based on threshold, the probability density functions of tumor and background should be separated otherwise the threshold will be small and algorithm never stop.***
- ✓ ***The intensity distribution of tumor should be Bell-shaped,***

# References

- **Stanley Osher, James A. Sethian**, “Fronts Propagating with Curvature Dependent Speed: Algorithms Based on Hamilton-Jacobi Formulations “, **Journal of Computational Physics.79, 12-49, 1988.**
- **Malladi, Sethian and Vemuri**, ”Shape Modeling with Front Propagation: A level Set Approach”, **IEEE Transaction on Pattern Analysis and Machine Intelligence, Vol 17, No. 2, Feb 1995.**
- **David Adalsteinsson, James A. Sethian**, “A Fast Level Set Method for Propagating Interfaces” , **Sep 1994.**
- **Sean Ho, Elizabeth Bullitt, Guido Gerig**, “Level Set Evolution with Region Competition: Automatic 3-D Segmentation of Brain Tumors”, **2002.**
- **Level Set toolbox in Matlab.**

*Thank you*

Q & A