

Implementation and Evaluation of a Semi-Automatic Tumor Segmentation Method

Master's Thesis Final Presentation

Jens Glasbrenner

June 1, 2015

Pattern Recognition Lab (CS 5)

Supervisors: Mario Amrehn M. Sc., Tim Horz M. Sc., Prof. Dr.-Ing. Joachim Hornegger





Outline

Motivation

Methods

Proposed Segmentation Method

Implementation

Results

Outlook

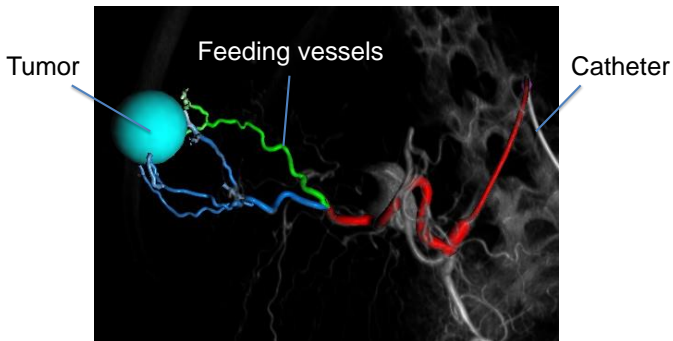
Summary



Motivation

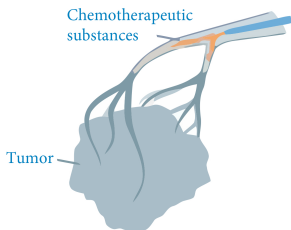
Transarterial Chemoembolization (TACE)

C-arm CT imaging with 3D reconstruction



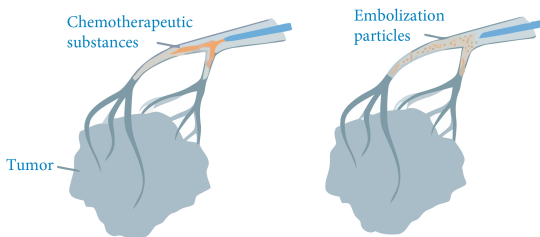
Vessel tree and corresponding ROI (cyan sphere)

Transarterial Chemoembolization (TACE) (cont.)



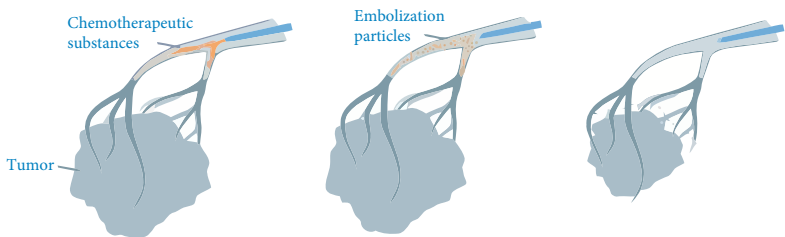
Schematic TACE for hepatocellular carcinoma (HCC)

Transarterial Chemoembolization (TACE) (cont.)



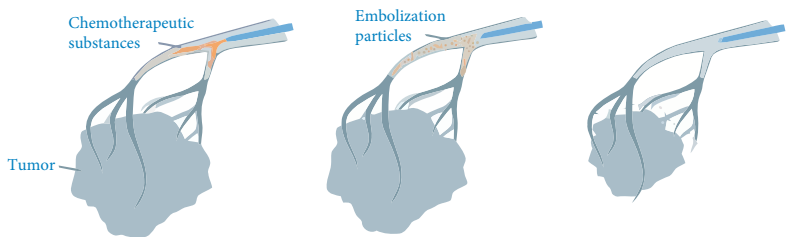
Schematic TACE for hepatocellular carcinoma (HCC)

Transarterial Chemoembolization (TACE) (cont.)



Schematic TACE for hepatocellular carcinoma (HCC)

Transarterial Chemoembolization (TACE) (cont.)

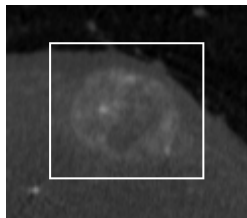
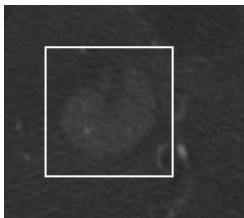
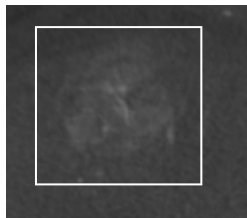


Schematic of the TACE for hepatocellular carcinoma (HCC).

⇒ Goal: Fast and accurate segmentation of various types of tumors

Challenges of Tumor Segmentation

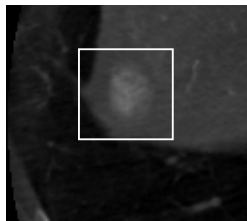
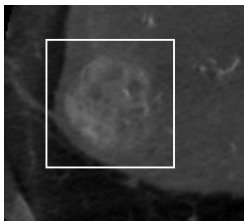
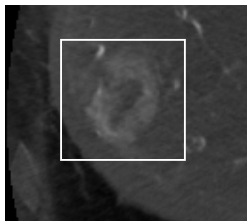
- High diversity - no typical shape
- Intensity overlaps between tumor and surrounding tissue
- Different intensity patches - necrotic regions





Challenges of Tumor Segmentation (cont.)

Appearance of a tumor may even vary within different slices





Automatic vs. Interactive Segmentation

Automatic segmentation

- Requires a large ground truth database
- "Semantic-gap" problem

Interactive segmentation

- Requires a large amount of user interaction
- Interobserver-variability



Automatic vs. Interactive Segmentation

Automatic segmentation

- Requires a large ground truth database
- "Semantic-gap" problem

Interactive segmentation

- Requires a large amount of user interaction
- Interobserver-variability

⇒ Solution: Interactive segmentation with automatic initialization



Methods



GrowCut Segmentation

- ⇒ Based on **cellular automaton theory**
- ⇒ Discrete in space and time
- ⇒ Voxels are treated as **cells**



GrowCut Segmentation

- ⇒ Based on cellular automaton theory
- ⇒ Discrete in space and time
- ⇒ Voxels are treated as cells

A cellular automaton is a quad-tuple

$$A = (P^n, S, N, \delta)$$

- P^n : Cellular space
- S : State set
- N : Neighborhood system
- δ : Local transition rule



GrowCut Segmentation (cont.)

- ⇒ Based on cellular automaton theory
- ⇒ Discrete in space and time
- ⇒ Voxels are treated as cells

State of each cell p in cellular space P^n is a triplet

$$S_p = (l_p, \theta_p, \mathbf{c}_p)$$

- l_p : Label of current cell p
- θ_p : Strength of current cell p
- \mathbf{c}_p : Feature vector



GrowCut Segmentation (cont.)

- ⇒ Based on cellular automaton theory
- ⇒ Discrete in space and time
- ⇒ Voxels are treated as cells

Initialization of the cellular automata (CA)

- Unlabeled voxels: $l_p = 0, \quad \theta_p = 0.0, \quad \mathbf{c}_p = i_p$
- Foreground voxels: $l_p = 1, \quad \theta_p = 1.0, \quad \mathbf{c}_p = i_p$
- Background voxels: $l_p = -1, \quad \theta_p = 1.0, \quad \mathbf{c}_p = i_p$



GrowCut Segmentation (cont.)

⇒ User defined seeds expand over the image



0



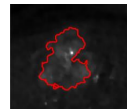
5



10



15



64

GrowCut Segmentation (cont.)

- ⇒ User defined seeds expand over the image
- ⇒ Cells try to occupy their neighbors iteratively

Attacking strength θ of neighboring cell q is weighted by

$$g_{lin}(\mathbf{c}_p, \mathbf{c}_q) = 1 - \frac{\|\mathbf{c}_p - \mathbf{c}_q\|_2}{c_{max}} \geq 0$$



0



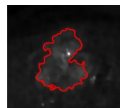
5



10



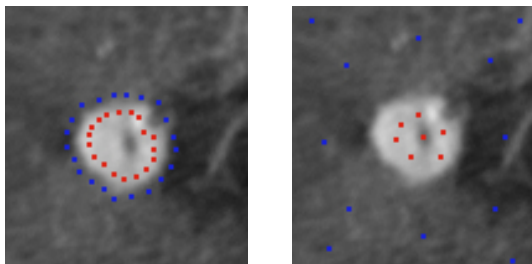
15



64

User Interaction Patterns

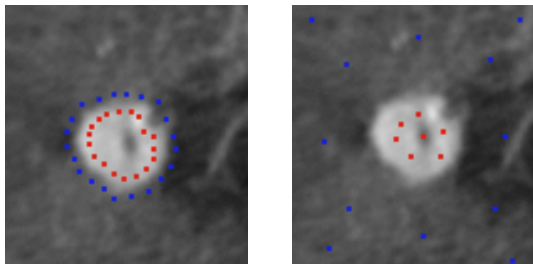
Problem: How to place the seeds efficiently?



- Volume seeds yield better results than surface seeds [Mo10]
- The more seeds the higher the segmentation quality [Mo10]

User Interaction Patterns

- Problem: How to place the seeds efficiently?



- Volume seeds yield better results than surface seeds [Mo10]
 - The more seeds the higher the segmentation quality [Mo10]
- ⇒ Solution: Automatically compute a 3D seed template



Automatic Initialization

⇒ 3D seed template...

- ... maximizes amount of initial seeds
- ... spreads seeds throughout the volume
- ... reduces the uncertainty of the user



Automatic Initialization

⇒ 3D seed template. . .

- . . . maximizes amount of initial seeds
- . . . spreads seeds throughout the volume
- . . . reduces the uncertainty of the user

⇒ Utilize Gaussian Mixture Model

- Calculate an optimal threshold δ_{opt} to compute a seed template



Automatic Initialization

⇒ 3D seed template...

- ... maximizes amount of initial seeds
- ... spreads seeds throughout the volume
- ... reduces the uncertainty of the user

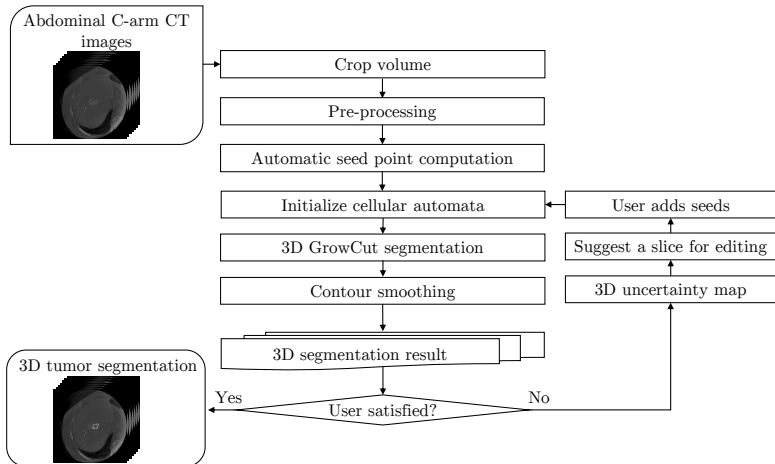
⇒ Utilize Gaussian Mixture Model

- Calculate an optimal threshold δ_{opt} to compute a seed template
- Initialize seeds with plausible strength θ_p



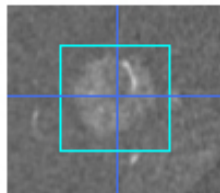
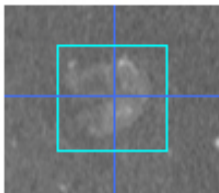
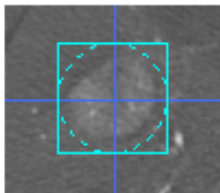
Proposed Segmentation Method

Overall Workflow



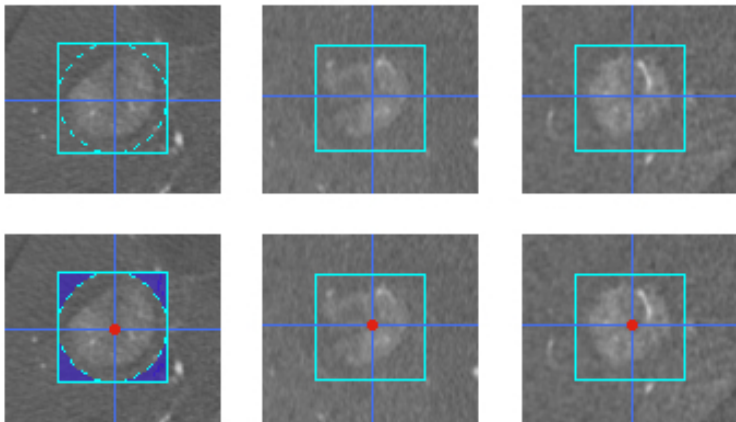


Volume of Interest



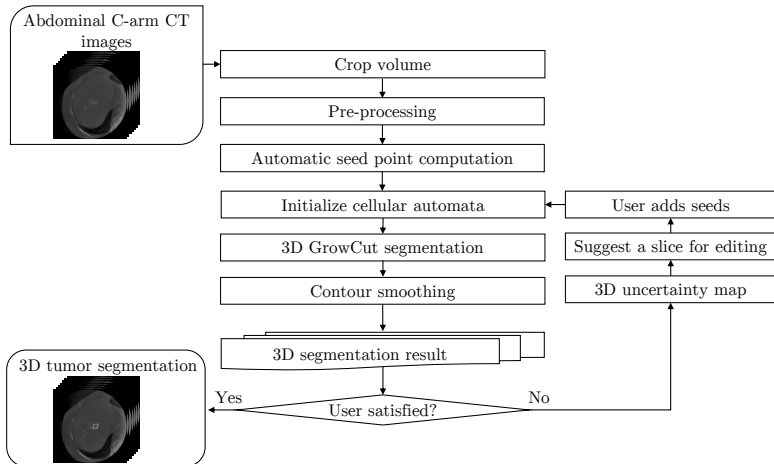


Volume of Interest



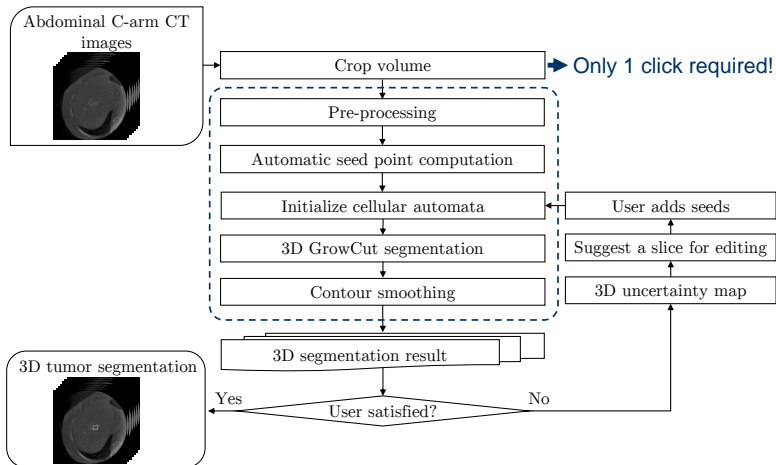


Overall Workflow



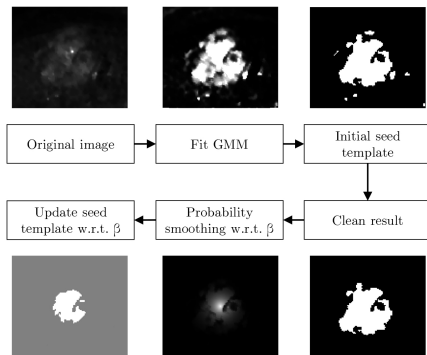


Overall Workflow





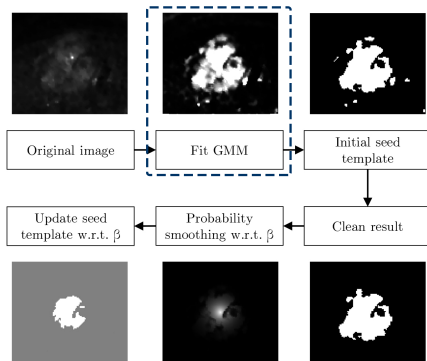
Automatic Initialization - Workflow



2D example of the procedure of automatized seed point calculation



Automatic Initialization - Workflow



2D example of the procedure of automatized seed point calculation



Gaussian Mixture Model

⇒ Weighted sum of Gaussian distributions

⇒ All mixing weights add up to one

$$p(\mathbf{x}_i) = \sum_{k=1}^K p_k \mathcal{N}(\mathbf{x}_i | \mu_k, \Sigma_k)$$

$$\sum_{k=1}^K p_k = 1$$

- p_k : The K mixture weights (priors)
- \mathbf{x}_i : Feature vector
- μ_k : The K means
- Σ_k : The K covariance matrices



Gaussian Mixture Model

⇒ weighted sum of Gaussian distributions

⇒ all mixing weights add up to one

$$p(\mathbf{x}_i) = p_1 \mathcal{N}(\mathbf{x}_i | \mu_1, \Sigma_1) + p_2 \mathcal{N}(\mathbf{x}_i | \mu_2, \Sigma_2)$$

foreground

background

- p_k : the K mixing weights
- \mathbf{x}_i : feature vector ⇒ image intensities
- μ_k : the K means
- Σ_k : the K covariance matrices



Gaussian Mixture Model

⇒ **Goal:** Assign each pixel a probability that it belongs to the tumor

- Iteratively with **Expectation Maximization (EM)** algorithm
- Maximizes the likelihood of the data given the GMM

$$\operatorname{argmax}_{\theta} \sum_{i=1}^m \log p(x_i|\theta)$$



Gaussian Mixture Model

⇒ **Goal:** Assign each pixel a probability that it belongs to the tumor

- Iteratively with **Expectation Maximization (EM) algorithm**
- Maximizes the likelihood of the data given the GMM

$$\operatorname{argmax}_{\theta} \sum_{i=1}^m \log p(x_i|\theta)$$

Parameters to fit to image data:

- Mean μ_k
- Covariance Σ_k
- Mixing weight p_k

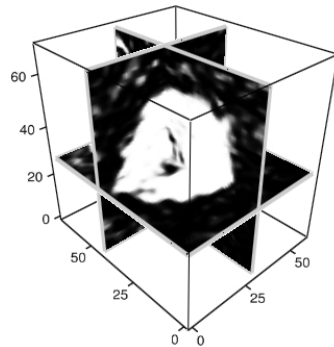
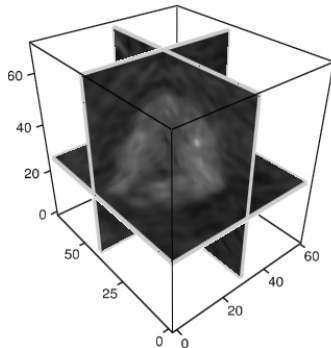


Gaussian Mixture Model: EM

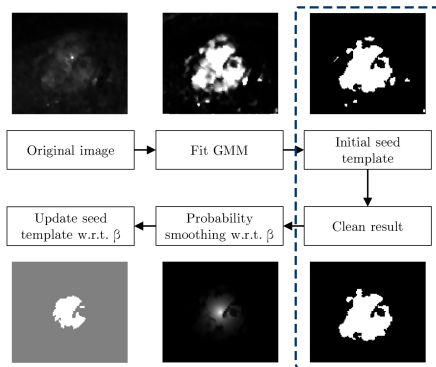
1. Initialize parameters μ_k , Σ_k and p_k
2. Step 1: (E step) Given parameters, assign each pixel x_i a probability for each distribution k
3. Step 2: (M step) Given probabilities, update parameters μ_k , Σ_k , p_k for each distribution k
 - no closed form solution \rightarrow iterative scheme



Initialization - 3D Probability Map

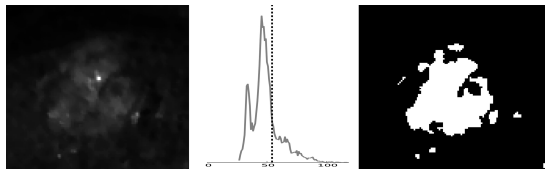


Automatic Initialization - Workflow



2D example of the procedure of automatized seed point calculation

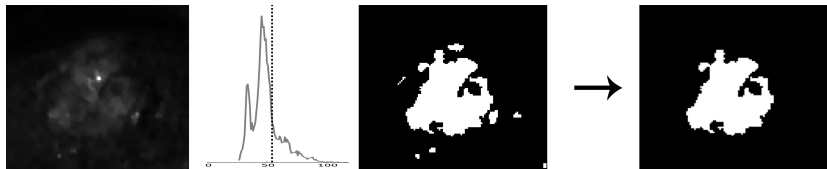
Initialization - Seed Template



Optimal threshold δ_{opt} is the average of the means μ_k

$$\delta_{opt} = \frac{1}{K} \sum_{k=1}^K \mu_k$$

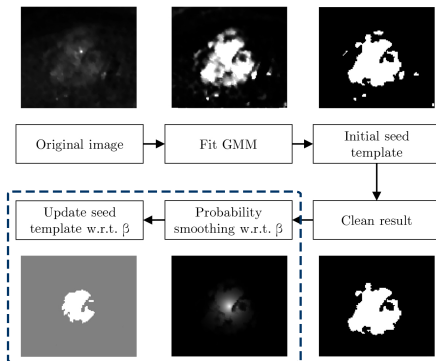
Initialization - Seed Template



- Morphological erosion would erode seed template
- Maximum of extracted regions accounted as tumor
- Remove all outliers smaller than the mean size of all regions



Automatic Initialization - Workflow



2D example of the procedure of automatized seed point calculation



Initialization - Probability Smoothing

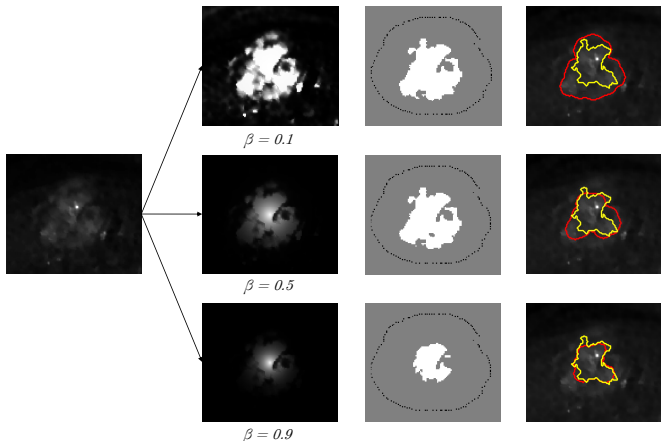
⇒ Probability being tumor proportional to distance from the VOI center

- Smooth probabilities far from the VOI center

$$p_{k_{smoothed}} = \exp(-\beta(\|u - v\|)^2)$$

- u : arbitrary voxel
- v : VOI center

Initialization - Probability Smoothing



Influence of the probability smoothing illustrated for an axial slice



Comparison - Label Propagation



0



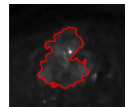
5



10



15



64



0



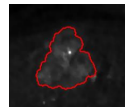
5



10

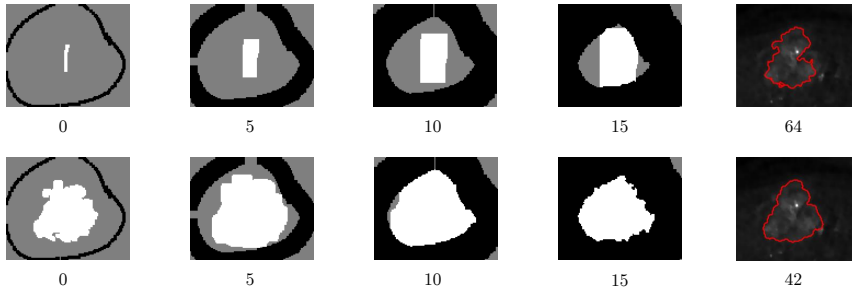


15



42

Comparison - Label Propagation

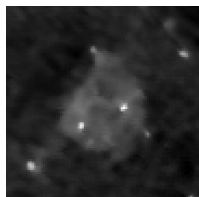


⇒ modified method performs better and converges faster



Number of GMM Components

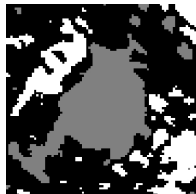
⇒ Empirically set to $K = 2$ components



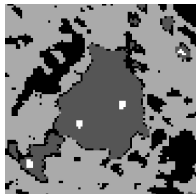
Original
image



$K = 2$
 $t = 4.52$ s



$K = 3$
 $t = 16.17$ s



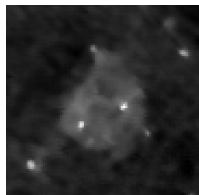
$K = 4$
 $t = 22.66$ s



Number of GMM Components

⇒ Empirically set to $K = 2$ components

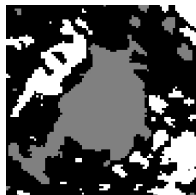
- Computation time increases with K
- Foreground seeds only change slightly



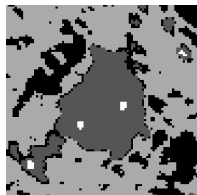
Original
image



$K = 2$
 $t = 4.52 \text{ s}$



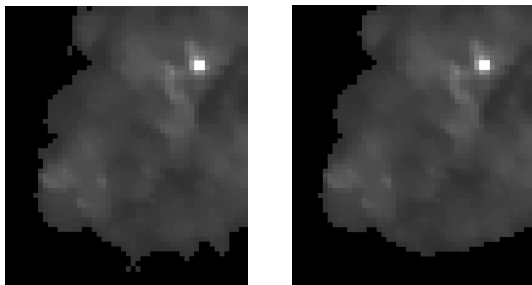
$K = 3$
 $t = 16.17 \text{ s}$



$K = 4$
 $t = 22.66 \text{ s}$

Segmentation Contour Smoothing

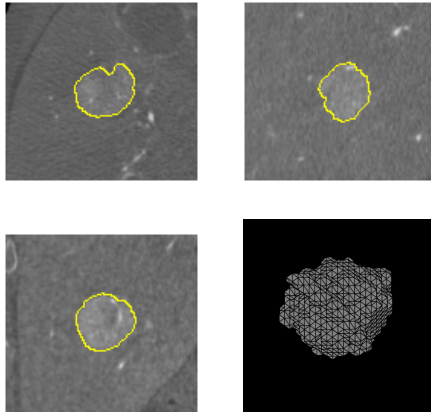
- Smooth ragged segmentation contour
- Morphological operation: binary opening
- Structuring element: 3D sphere



Contour smoothing shown in an axial slice



3D Segmentation Result

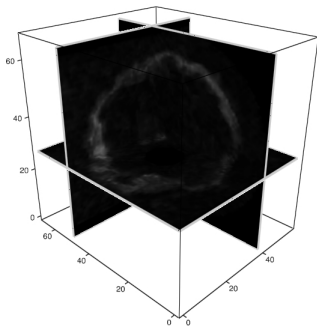


3D segmentation example

Workflow - Editing of the Segmentation

Segmentation uncertainty: number of label changes per cell

- Store # label changes per cell during propagation process
- Normalize to maximum number of label changes

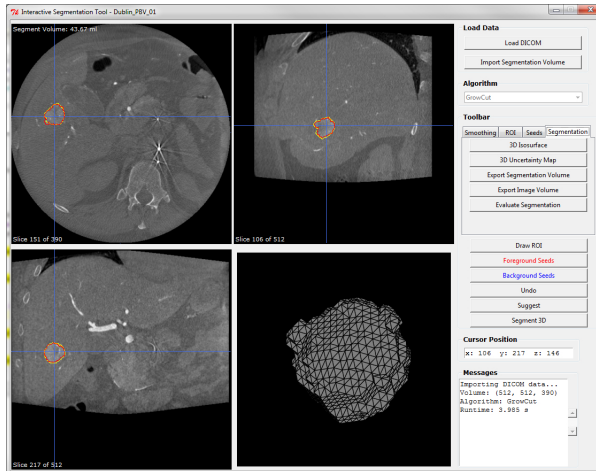




Implementation



Interactive Segmentation Tool - GUI





Implementation

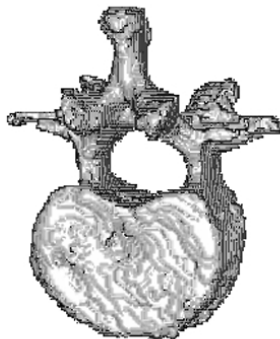
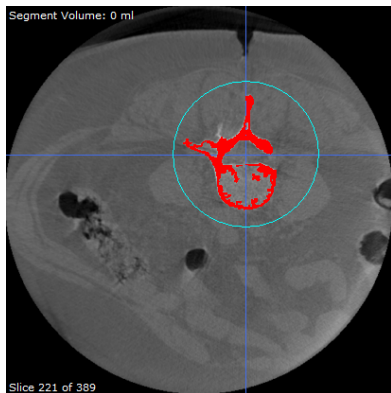
Python

- Concise syntax \Rightarrow Code reuse
- Cython: Interface with fast C/C++ code
- WinPython: Scientific standalone Python distribution

SciPy/NumPy

- NumPy: powerful N-dimensional array object
- Scikit-learn for machine learning algorithms
- Scikit-image for image processing algorithms

Interactive Segmentation Tool - Capabilities



Segmentation of a vertebra



Results



Quantitative Evaluation

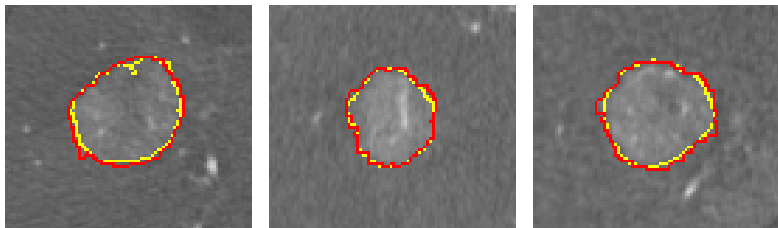
- No manually drawn seeds used
- Ground truth via manual annotation by a clinical expert

Segmentation algorithm	ARI (%)	DC (%)	MI (%)	RAVD (%)
Proposed method	80.58	85.32	68.88	-0.18
Original GrowCut	72.96	78.46	63.00	-0.26
Random Walker	51.12	57.34	45.46	-0.52
Seeded Watershed	53.28	59.44	47.04	-0.46

Table: Averaged segmentation results for all datasets

Segmentation Results

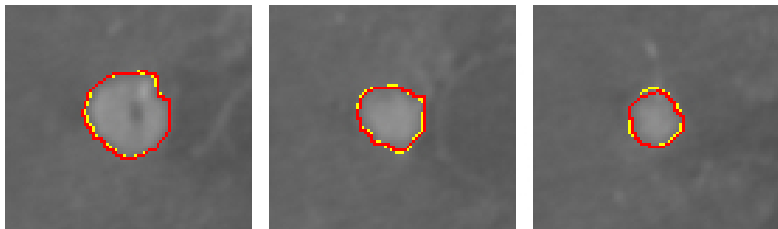
Large intensity overlap between cancerous and healthy tissue



Segmentation result of proposed method (yellow) and ground truth (red)

Segmentation Results (cont.)

Homogenous intensity distribution → clear borders

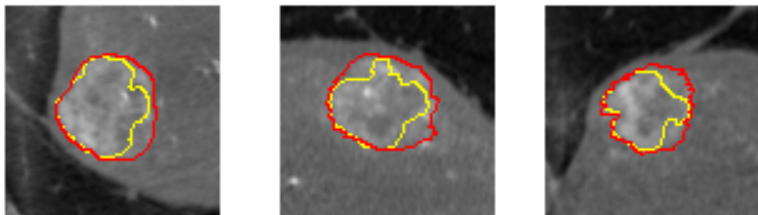


Segmentation result of proposed method (yellow) and ground truth (red)

Segmentation Results (cont.)

Necrotic tumor → inhomogeneous intensities

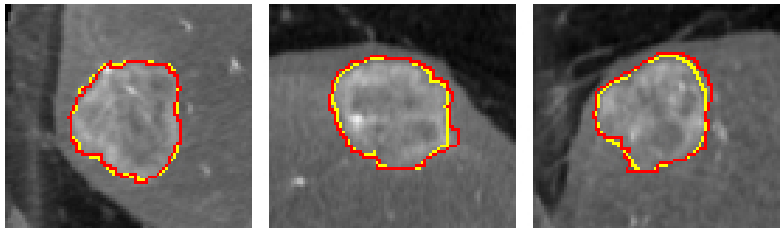
Algorithm might stop label propagation at necrotic borders



Segmentation result of original GrowCut (yellow) and ground truth (red)

Segmentation Results (cont.)

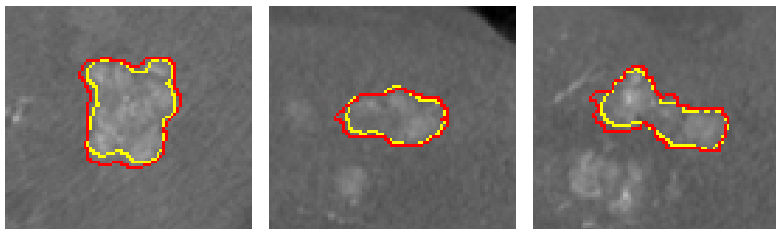
Necrotic tumor, inhomogeneous intensities



Segmentation result of proposed method (yellow) and ground truth (red)

Segmentation Results (cont.)

Arbitrary shape with proliferations



Segmentation result of proposed method (yellow) and ground truth (red)



Outlook



Outlook

Extend segmentation method

- Parallelization of segmentation algorithm on the GPU
- Separate segmentation of necrotic regions for further investigations

Extend evaluation

- Sensitivity to user interaction w.r.t. the VOI placement
- Evaluation on a larger ground truth database



Summary




Summary

Fast and reliable tumor segmentation is important for

- Quantitative therapy monitoring, e.g. after TACE
- Efficient planning of follow-up treatments

An extension of the CA based segmentation algorithm

- Is realized with a probabilistic model: GMM
- Reduces user interaction to a minimum - only one click
- Reduces uncertainty of the user
- Reduces runtime of the overall segmentation process



Thank you for your attention!



Bibliography I



Vezhnevets, Vladimir and Konouchine, Vadim

GrowCut: Interactive multi-label ND image segmentation by cellular automata.

Graphicon, 2005.



Moschidis, E. and Graham, J.

A Systematic Performance Evaluation of Interactive Image Segmentation Methods Based on Simulated User Interaction.

IEEE international conference on Biomedical imaging, 2010.