

4D Active Cut: An Interactive Tool for Pathological Anatomy Modeling

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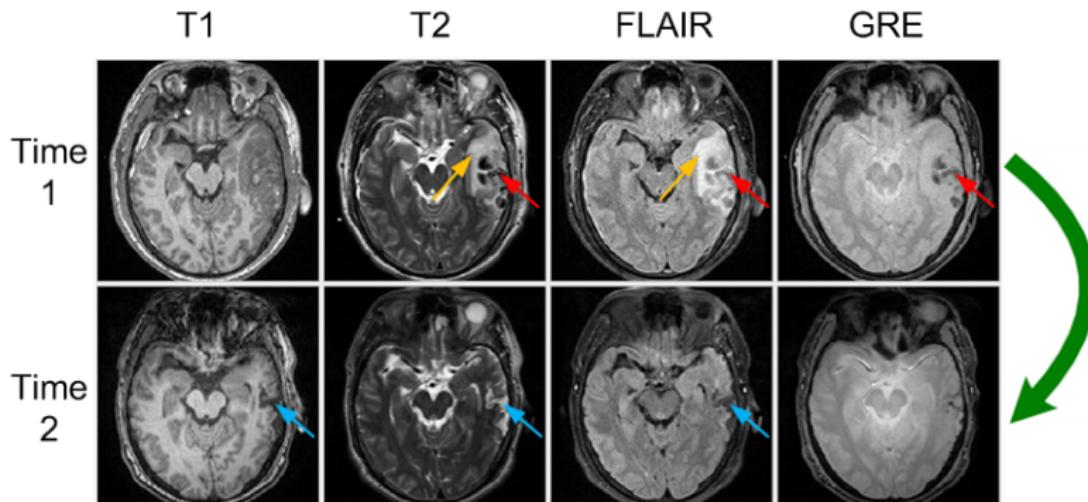
3 Results

- Illustration of the iterative process
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- 4D pathological anatomy modeling is key to understanding complex pathological brain images.
- It is a challenging problem due to the difficulties in detecting multiple appearing and disappearing lesions across time points and estimating dynamic changes and deformations between them.
- Existing interactive segmentation methods passively waits for user to refine the segmentations which is a difficult task in 3D images that change over time.

TBI images



Baseline Lesions

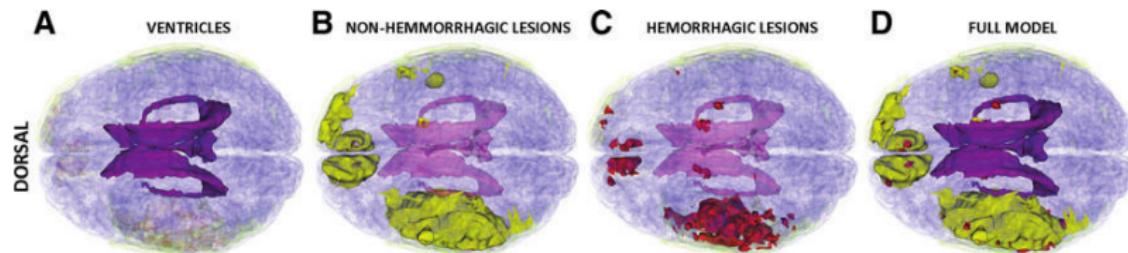
- Swelling (edema)
- Bleeding

Followup Lesions

- Chronic lesion
- Bleed

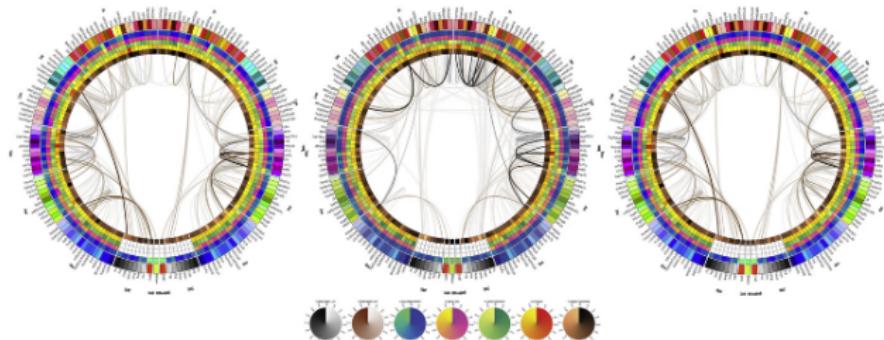
4D modeling enables other analysis

Structural pathology analysis



Andrei Irimia et al., Journal of Neurotrauma, 2011

Brain connectivity analysis



Andrei Irimia et al., NeuroImage: Clinical, 2012

GrabCut, Carsten Rother et al., ACM TOG 2004

- User gives an initial guess of the region of interest (foreground).
- The algorithm estimates globally optimal boundary between the foreground and background regions.
- The user then inspects the segmentation results, and adjusts the boundary by drawing a region as a hard constraint.

This process works well on 2D images, as users can quickly find incorrectly classified regions.

However, such interaction is a huge burden to users once applied to 3D volume data, since one has to visually inspect each slice and correct it.

- User gives bounding box (trimap) to initialize the algorithm which is used for initial α map.

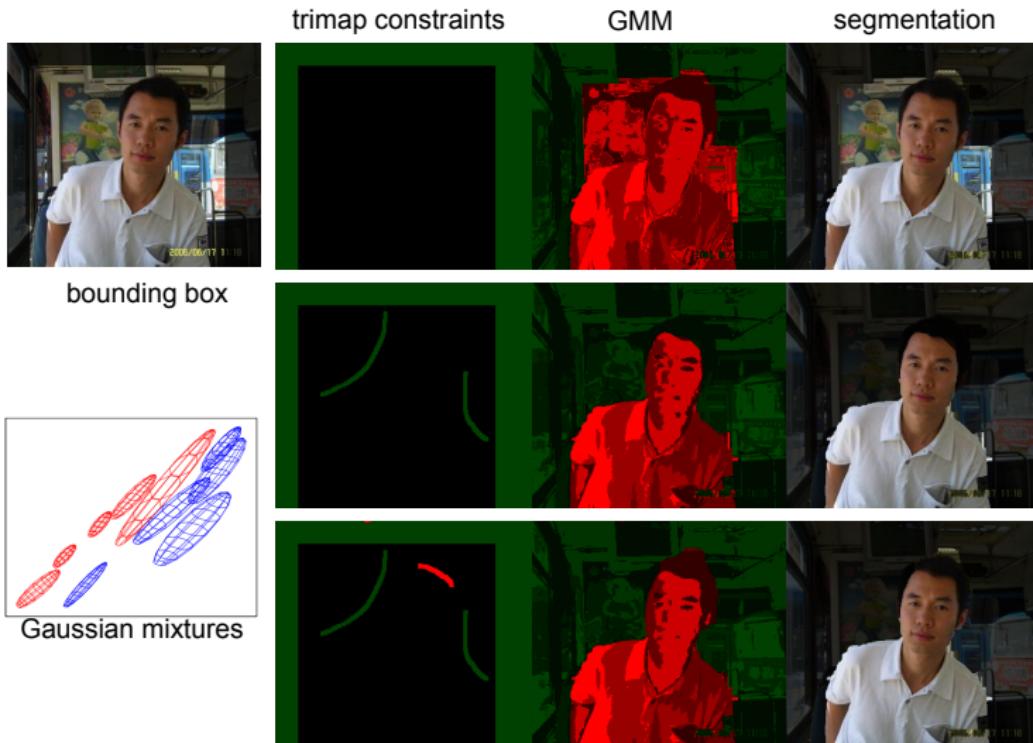
Begin: iterative minimization

- 1 Assign Gaussian mixture models(GMM) components to pixels using current α map.
- 2 Learn GMM parameters from data.
- 3 Estimate Segmentation using the Graph Cut based on the estimated GMM parameters to update α map.
- 4 Repeat 1-3, until convergence.

End: iterative minimization

- User editing

GrabCut interactive segmentation method



The disadvantages of GrabCut or similar methods:

- The algorithm is in a passive learning state.
- Its performance entirely depends on user's active inspection and correction.
- The passive learning process is the bottleneck when applied to 3D data.
- It is designed for segmenting single object.

Active learning

Active learning is one type of supervised/semi-supervised machine learning. This kind of learning algorithms are able to interactively query the user (or some other information source) to obtain the desired outputs at new data points.

Algorithms for determining which data points should be labeled (query users) can be organized into a number of different categories

- Uncertainty sampling: label those points for which the current model is least certain
- Expected model change: label those points that would most change the current model
- Variance reduction: label those points that would minimize output variance, which is one of the components of error.
- ...

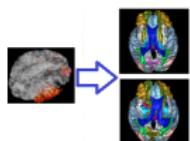
[Wikipedia, Active learning \(machine learning\).](#)

Several researchers have applied active learning to 3D image segmentation:

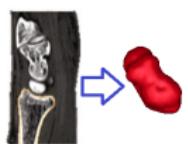
- Top et al. proposed to query users the most uncertain 2D slices. [Top et al., MICCAI 2011](#)
- Veeraraghavan et al. used grow cut for segmentation and estimated the uncertainty using a support vector machine classifier. [Veeraraghavan et al., IEEE ISBI 2011](#)
- Iglesias et al. used active learning for constructing manually labeled dataset for training supervised classifiers. [Iglesias et al., IPMI 2011](#)

Other active learning based segmentation methods

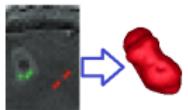
Our method is different from them in that:



It solves both segmentation and registration in a unified 4D framework.

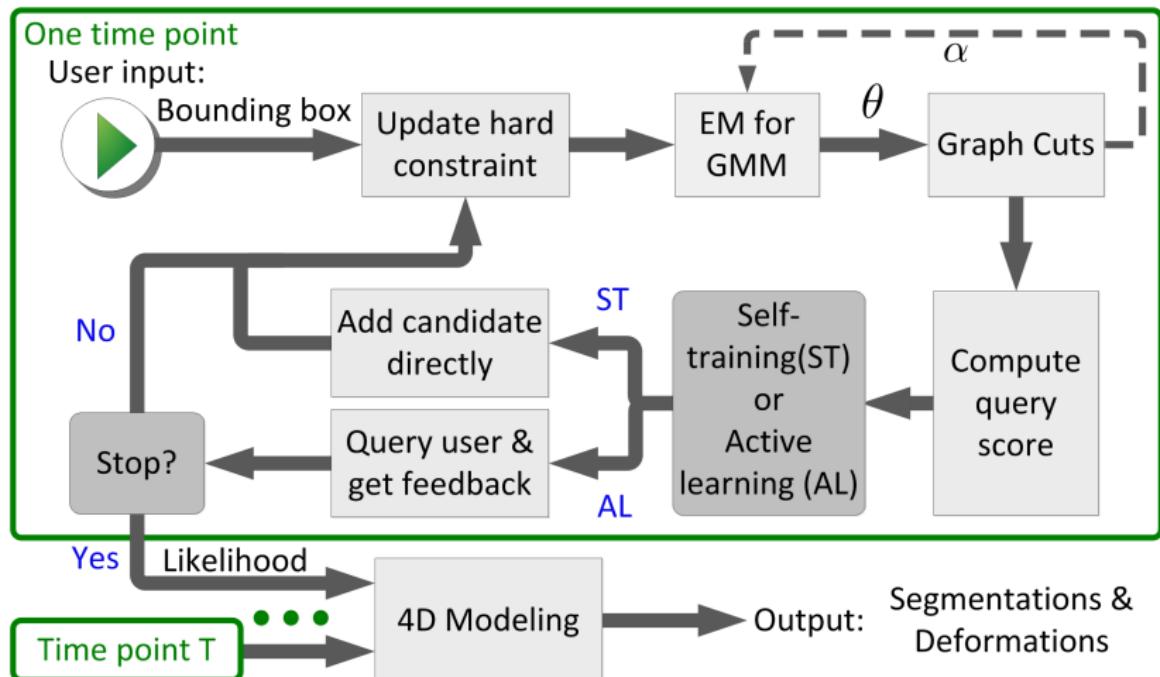


Instead of learning 2D slices, it learns new 3D objects.



Instead of or individual voxels, the 3D objects are better fit human visual perception due to their spatial coherence.

Overview of the proposed algorithm



Within-class model

Prior:

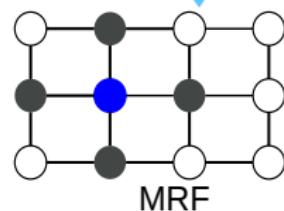
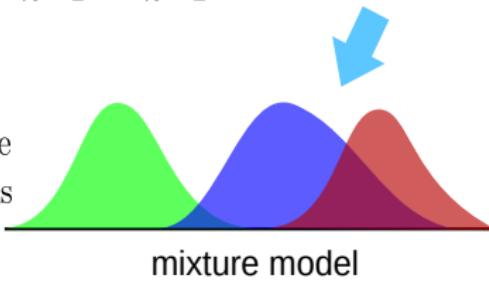
$$p(\mathbf{z}) = \frac{1}{C} \exp\left(\sum_{n=1}^N \sum_{k=1}^K z_{nk} \log \pi_{nk} + \beta \sum_{(n,m)} \langle z_n, z_m \rangle\right)$$

K = 2 (FG)

K = 3 (BG)

z_{nk} : indicator variable

(n, m): neighbor voxels



Likelihood: $p(\mathbf{x}|\mathbf{z}) = \prod_n p(x_n|z_n) = N(x_n; \mu, \sigma^2)$

Consider the case of two classes, the posterior probability for class C_1 can be written as,

$$p(C_1|x) = \frac{p(x|C_1)p(C_1)}{p(x|C_1)p(C_1) + p(x|C_2)p(C_2)} = \frac{1}{1 + \exp(-a)} = \sigma(a)$$

where $\sigma(a)$ is the *logistic sigmoid* function,

$$\sigma(a) = \frac{1}{1 + \exp(-a)}$$

and

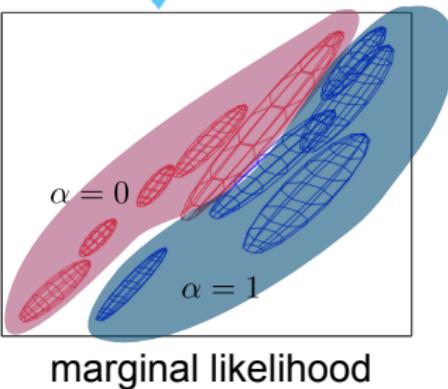
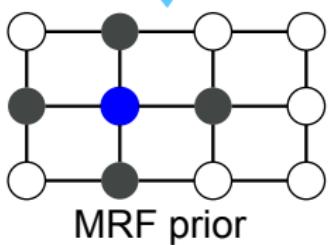
$$a = \ln \frac{p(x|C_1)p(C_1)}{p(x|C_2)p(C_2)}$$

It represents the log of the ratio of probabilities

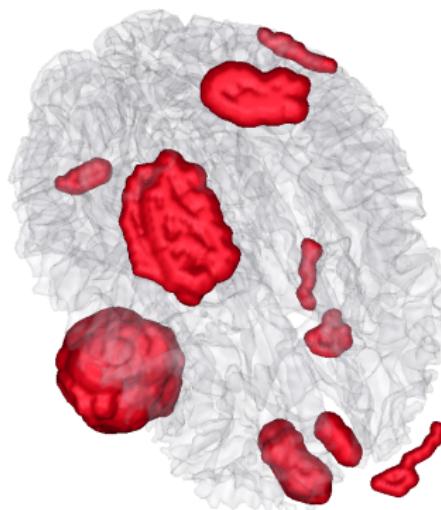
$\ln[p(C_1|x)/p(C_2|x)]$ for the two classes, also known as the *log odds*.

Christopher M. Bishop, PRML

$$a_n = \log p(\alpha_n = 1) + E_{z_n|x_n} [\log p(x_n, z_n; \theta(\alpha_n = 1))] \\ - \log p(\alpha_n = 0) + E_{z_n|x_n} [\log p(x_n, z_n; \theta(\alpha_n = 0))]$$



We obtain a binary map \mathbf{w} by thresholding the predictive map at 0.5, and identify a series of objects R_i by running a connected component detection on \mathbf{w} .





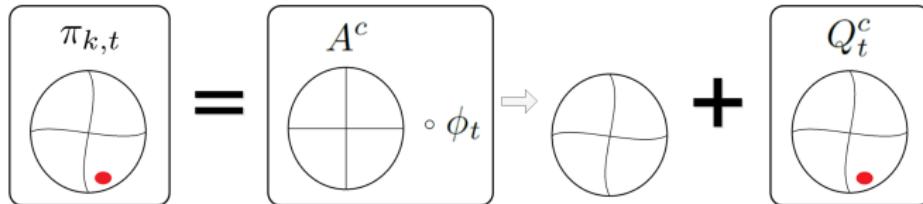
To select the most salient objects, we sort the objects in descending order of the following score:

$$q(R_i) = \left(\sum_{n \in R_i} p(\alpha = 1 | \mathbf{x}_n) \right) / |\{n : n \in \mathcal{B}(R_i)\}|.$$

$q(R_i)$ is the ratio of volume to boundary voxels.

- The above query score prefers objects with larger volumes of posterior probability.
- The score also prefers blob-like objects since such an object has large volume-surface ratio.
- Such criteria reflects our prior knowledge on the lesion object's shape.

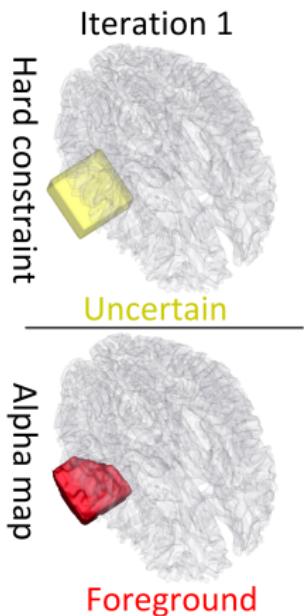
We follow the 4D pathological anatomy modeling framework of our previous work, and define $\pi_{k,t} = A_k \circ \phi_t + Q_{k,t}$,



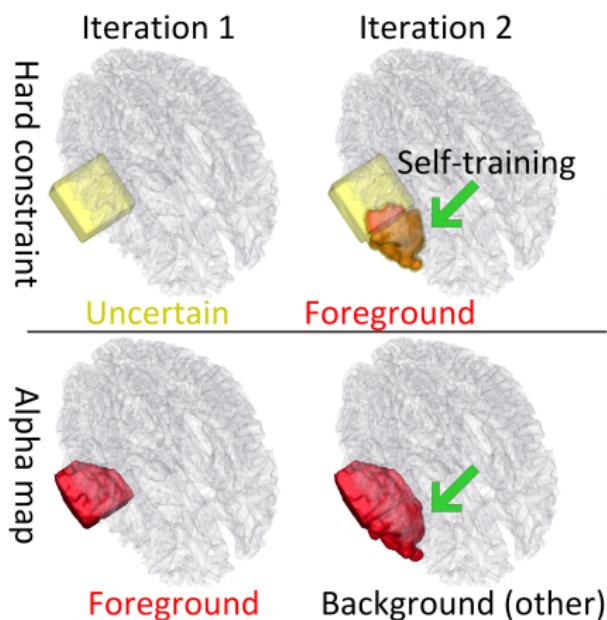
where A is the tissue class probability that is initially associated with the healthy template, ϕ_t is the diffeomorphic deformation from time t to the atlas, and Q_t is the non-diffeomorphic probabilistic change. We use alternating gradient descent to estimate A , ϕ_t and Q_t by optimizing,

$$\begin{aligned}\mathcal{F}(A, \phi_t, Q_t) &= - \sum_{t=1}^T \mathbb{E}_{p(\mathbf{z}|\mathbf{x})} [\log p(\mathbf{z}, \mathbf{x} | \theta, \pi_t)] \\ &= - \sum_{t=1}^T \sum_{i=1}^N \log \left(\sum_{k=1}^K \pi_{i,k,t} p(\mathbf{x}_{i,t} | \theta_t^c) \right)\end{aligned}$$

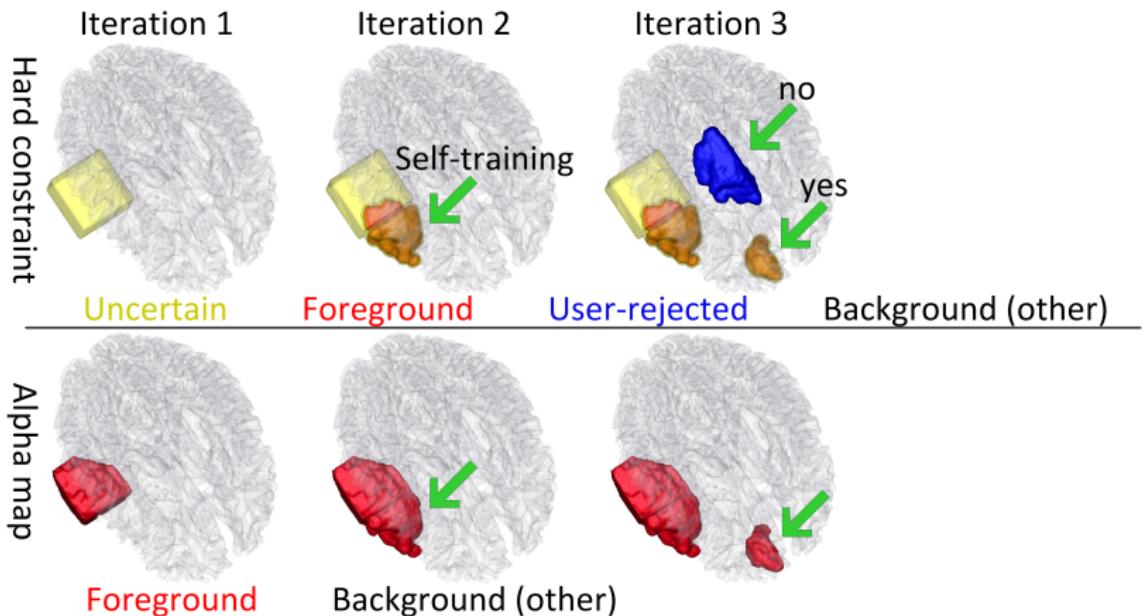
1st iteration - user initialization



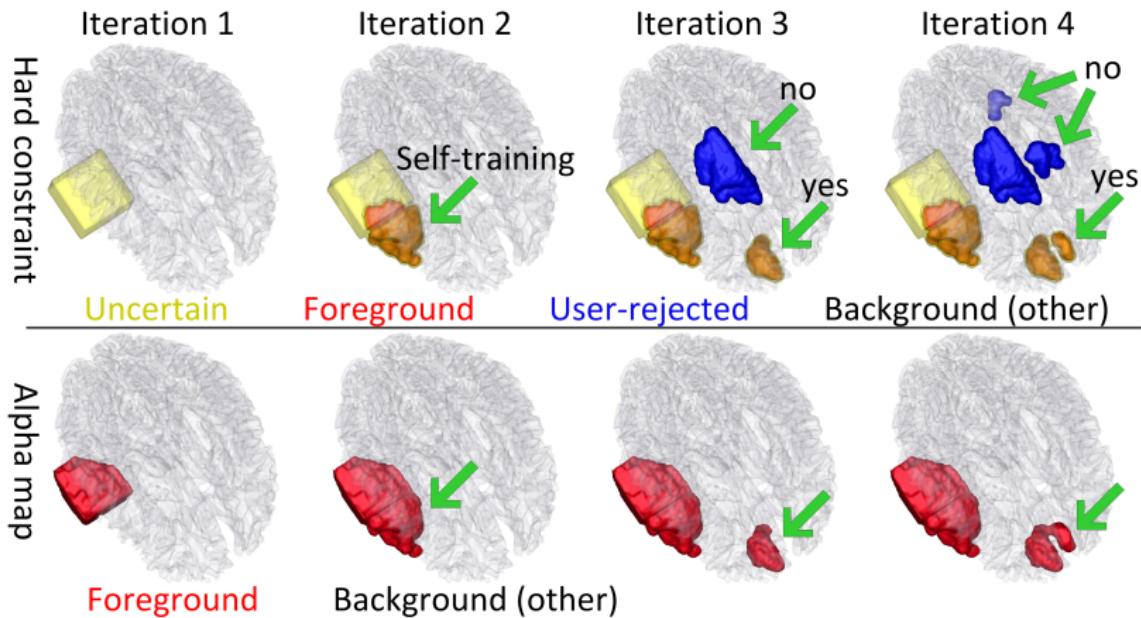
2nd iteration - self training



3rd iteration - active learning

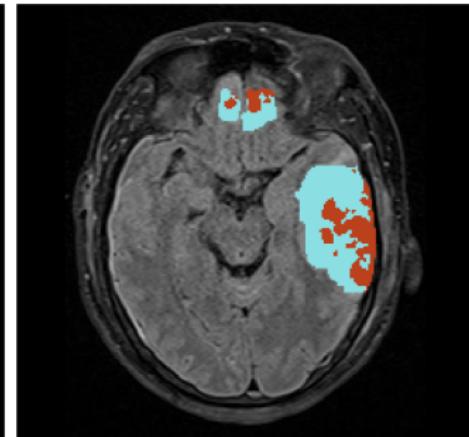
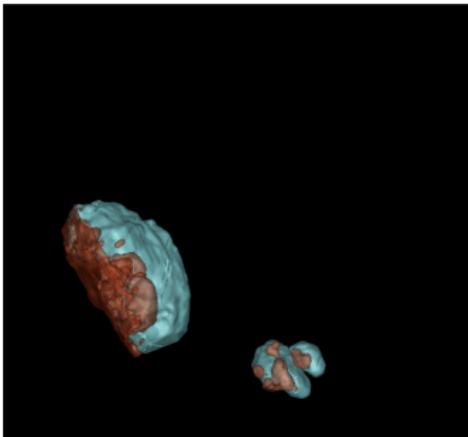


4th iteration - active learning

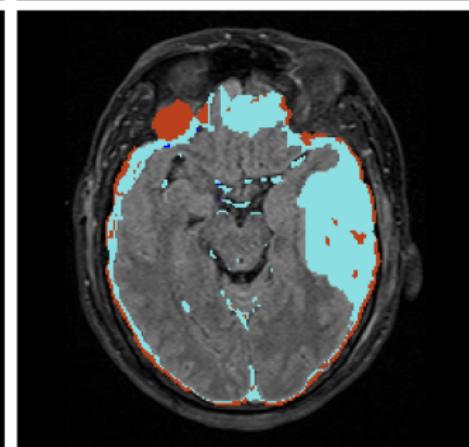
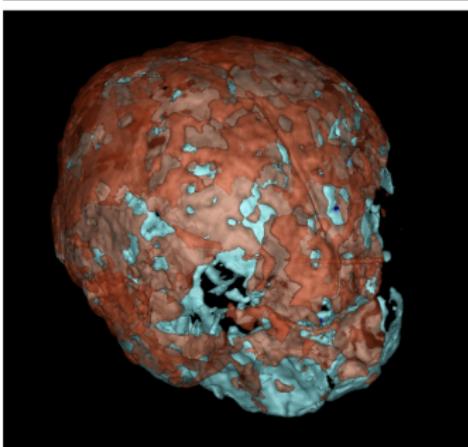


Qualitative comparison

Our
method



GrabCut



Quantitative comparison

Subject	Baseline		4D active cut		
	NHL	HL	NHL	HL	UI
I	0.2503	0.0613	0.6349	0.5698	5
II	0.3269	-	0.6910	-	4
III	0.1311	0.2288	0.4512	0.4840	6
IV	0.0918	0.0998	0.3503	0.1153	5

Table : Dice values comparing *4D active cut* and GrabCut to ground truth. HL and NHL are acute hemorrhagic and non-hemorrhagic lesions. UI denotes the number of interactions a user performed using *4D active cut*. Subject II has no ground truth for HL due to the lack of GRE modality.

Result of 4D modeling

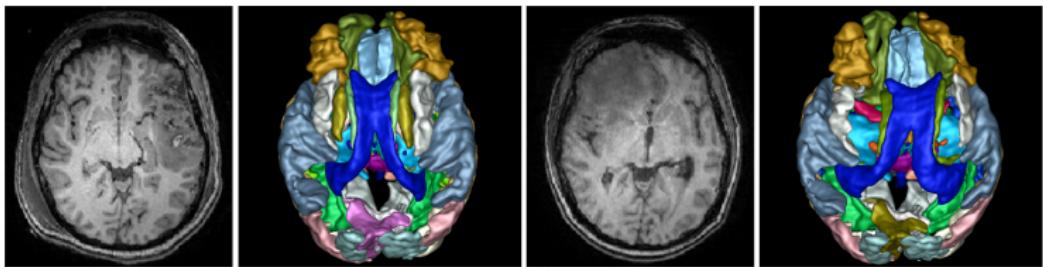


Figure : Result of mapping parcellation labels associated with the healthy template to each time point. The left two images are the T1 reference TBI image at acute stage and mapped parcellations, and the right two images are the same at chronic stage.

Advantages of the proposed framework

- It actively query users candidate patches instead of passively wait for user correction.
- It can detect multiple lesion objects with minimal user input.
- It is robust given inaccurate user initialization.
- It does 4D modeling instead of only 3D segmentation.

- Explore integration of active learning and 4D modeling.
- Validation and verification on other image data presenting pathologies.

Thanks!

Thank you for your attention!

Questions?

- Search $p(z|x)$ in subspace:
$$Q(z) = \prod_n q_n(z_n).$$
- $\log p(z_{nk}) = z_{nk} \pi_{nk} + \sum_{m \in \mathcal{N}(n)} \langle \mathbb{E}(z_m), z_n \rangle + \log \mathcal{N}(x_n; \theta(z_n))$
- $\mathbb{E}(z_{nk}) = p(z_{nk} = 1)$ for binary variable z_{nk} . Save $\mathbb{E}(z_{nk})$ for updateing other nodes.

