EVOLUTION RULES OF DETERMINISTIC CELLULAR AUTOMATA FOR MULTICHANNEL SEGMENTATION OF BRAIN TUMORS IN MRI

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Abstract: *Image segmentation is the process of partitioning an image in groups of pixels or voxels that share a common characteristic. High sensitivity and high precision segmentations of cerebral tumors in magnetic resonance images are necessary for the safe planning of radiosurgical treatment. GrowCut is an image segmentation method based in a cellular automaton that simulates the competitive growth of various bacteria colonies in the image space. We present a group of automata evolution rules for image segmentation that are derived from GrowCut, and a quantitative comparison of the segmentations of brain tumors in multichannel magnetic resonance images achieved through these rules in GPU implementations.*

Keywords: Cellular Automata, Computer Vision, Segmentation, GPU, Image Processing

1. INTRODUCTION

A deterministic cellular automaton is a dynamic model represented by an array of cells that evolve through a succession of states *t*. In the automata considered, each one of these cells is in a particular state *S*, characterized by a strength level θ, a label *L*, and a digital level descriptor $\vec{I}$ [1]. The automaton evolves in the space of an *N* dimensional image. In the case of coregistered multimodal volumes of magnetic resonance images, the vector $\vec{I}$ is constituted by various image channels at each voxel. At each evolution step, a function is applied simultaneously in all of the automaton's cells. This function evaluates each cell to determine its next state, considering the current states of its neighboring cells. Neighborhood systems considered are the 3D Von Neumann and 3D Moore neighborhood. The automaton's evolution can be described as the competitive colonization of the cell space in the image, where each cell is attacked by its neighbors, with strength of attack equal to the product of the neighbor's current strength and a term that's inversely proportional to the digital level distance between the current cell and its attacking neighbor. The manner in which strength of attack is calculated makes regions with high homogeneity in their digital level descriptors highly likely to be colonized by the same label. The automaton starts its evolution through the definition of a set of cells with label and strength, called seeds, which can be determined in a supervised, or unsupervised manner, as described in other works by the authors [2], [3]. After a set of seed cells have been defined, the automaton starts its evolution as defined in Fig. 1a. We present a modification to this algorithm (see Fig. 1b) that reduces computation time, and modifications to attack strength penalization rules [4], with a quantitative comparison of segmentation quality achieved.

```
// for each cell in the automaton
for ∀p ∈ P
        // copy previous state
        L_p^{t+1} = L_p^t
        θ_p^{t+1} = θ_p^t
        // neighbors attack currently evaluated cell
        for ∀q ∈ N(p)
            if g(‖I_p − I_q‖_2) · θ_q^t > θ_p^t
                L_p^{t+1} = L_q^t
                θ_p^{t+1} = g(‖I_p − I_q‖_2) · θ_q^t
            end if
        end for
end for
```

(a)

```
E = true
while (E)
    E = false
    // for each cell in the automaton
    for ∀p ∈ P
        // copy previous state
        L_p^{t+1} = L_p^t
        θ_p^{t+1} = θ_p^t
        // neighbors attack currently evaluated cell
        for ∀q ∈ N(p)
            if g(‖I_p − I_q‖_2) · θ_q^t > θ_p^{t+1}
                L_p^{t+1} = L_q^t
                θ_p^{t+1} = g(‖I_p − I_q‖_2) · θ_q^t
                E = true
            end if
        end for
    end for
end while
```

(b)

Figure 1 – Automaton's Evolution Rule. a) "GrowCut", as defined by Vezhnevets et al. [1]. The criterion to determine which conquering neighbor cell *q* assigns label to the currently evaluated cell *p* in *t* +1 is $g(\|\vec{I}_p - \vec{I}_q\|_2) \cdot \theta_q^t > \theta_p^t$, which makes the *last* conquering cell evaluated be the one that assigns label and strength to the cell *p*. b) "Corrected GrowCut". The evaluation criterion to determine conquering cell is replaced by $g(\|\vec{I}_p - \vec{I}_q\|_2) \cdot \theta_q^t > \theta_p^{t+1}$, which makes the *strongest* conquering cell evaluated be the one that assigns label and strength to the cell *p*. A convergence criterion is expressed as the state where no cell in the automaton updates its strength and label.

2. PENALIZATION TO STRENGTH OF ATTACK

The automaton's evolution rule can be modified to consider the mean and standard deviation in the digital levels of the seed cells. Kim et al. [4] propose an exponential penalization to the strength of an attack performed by a cell whose digital level is more than a standard deviation away from the mean of the digital level of its seed cells. The purpose of this penalization is to make elements considered atypical for their label class less likely to propagate their assigned label. Kim et al. propose applying an exponential penalization to the strength of attack, like the one described in Eq. 1, where the attacking cell q has a digital level that's more than a standard deviation away from its respective mean (n=1, in Kim et al. [4]). The Central Limit Theorem guarantees that at least 31.8% of the cells whose digital levels follow a normal distribution have digital levels that are more than a standard deviation away from their label's mean, making this exponential penalization excessive when cells with high heterogeneity in their digital levels share a label [2]. We propose the alternative criteria to penalize strength of attack, shown in Eq. (1)-(3), $n \in \mathbb{R}$ and represents the number of standard deviations on which to start penalizing strength of attack Eq. (1) shows an exponential penalty, Eq. (2) shows a linear penalty, and Eq. (3) shows a constant penalty, with c_1, $c_2 \in [0,1]$, $c_1 > c_2$.

$$g^*(x, \mu L_q, \sigma L_q) = \begin{cases} 1 - \left(\frac{x}{\max\|\vec{I}\|_2}\right) & if \left\|\vec{I}_q - \mu L_q\right\|_2 < n * \sigma L_q \\ \left(1 - \left(\frac{x}{\max\|\vec{I}\|_2}\right)\right)\left(e^{\left(-n*\left(\left\|\vec{I}_q - \mu L_q\right\|_2\right) - \sigma L_q\right)}\right) & if \left\|\vec{I}_q - \mu L_q\right\|_2 \geq n * \sigma L_q \end{cases} \quad (1)$$

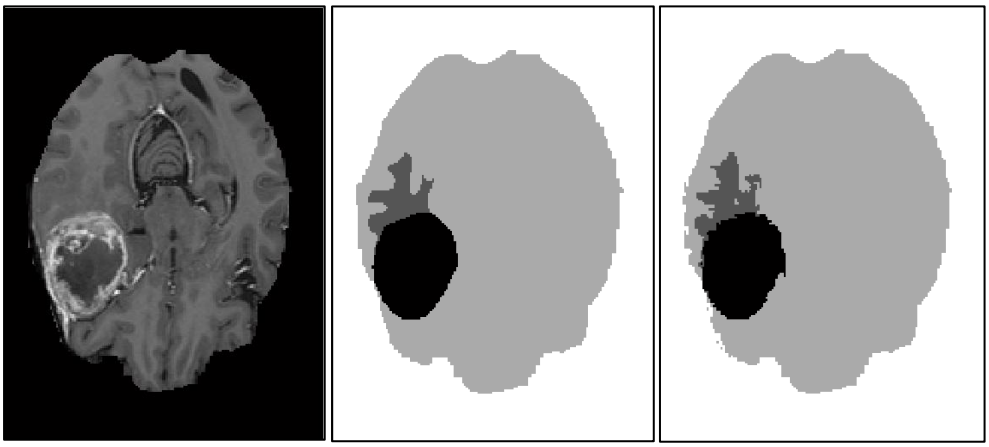
$$g^*(x, \mu L_q, \sigma L_q) = \begin{cases} 1 - \left(\frac{x}{\max\|\vec{I}\|_2}\right) & if \left\|\vec{I}_q - \mu L_q\right\|_2 < n * \sigma L_q \\ \left(1 - \left(\frac{x}{\max\|\vec{I}\|_2}\right)\right)\left(\frac{n*\sigma L_q}{\left\|\vec{I}_q - \mu L_q\right\|_2}\right) & if \left\|\vec{I}_q - \mu L_q\right\|_2 \geq n * \sigma L_q \end{cases} \quad (2)$$

$$g^*(x, \mu L_q, \sigma L_q) = \begin{cases} 1 - \left(\frac{x}{\max\|\vec{I}\|_2}\right) & if \quad \left\|\vec{I}_q - \mu L_q\right\|_2 < n * \sigma L_q \\ 1 - \left(\frac{x}{\max\|\vec{I}\|_2}\right) * c_1 & if \left(\left\|\vec{I}_q - \mu L_q\right\|_2 \geq n * \sigma L_q\right) \wedge \left(\left\|\vec{I}_q - \mu L_q\right\|_2 < (n+1) * \sigma L_q\right) \\ 1 - \left(\frac{x}{\max\|\vec{I}\|_2}\right) * c_2 & if \quad \left\|\vec{I}_q - \mu L_q\right\|_2 \geq (n+1) * \sigma L_q \end{cases} \quad (3)$$

3. TESTS AND RESULTS

We tested 10 high grade clinical gliomata, and 10 high grade simulated gliomata produced via TumorSim [5], [6]. The human-labeled clinical datasets were curated by adding a fourth class, representing healthy brain tissue, to their ground truth files. This fourth class, represented as light gray in Fig. 2b and Fig. 2c, is added to produce representative means and standard deviations for the classes used to label non-pathological tissue and empty voxels. This fourth class allows the automata to appropriately penalize atypical attacks occurring in these image regions.

The used segmentation seeds are chosen from the ground truth randomly, using the uniform probability distribution. Seed indices, for each dataset, are the same in every automaton variation considered and represent 5% of the true cells corresponding to each label. We consider four labels: tumor, edema, healthy brain tissue, and empty voxels. Tests were performed using the 3D Von Neumann neighborhood. Parameters for constant penalization to strength of attack were c_1 = 0.99, c_2 = 0.95. The automata evolution rules that consider penalties use the conquering cell evaluation criterion shown in Figure 1b.



(a) (b) (c)

Figure 2 - BRATS High Grade Glioma 0001, slice 79. a) T1 channel, with gadolinium contrast agent. b) Ground truth, according to human expert, curated by adding a healthy brain tissue class. This hand-labelled dataset has smooth contours, a common segmentation bias in human raters that is unrepresentative of the real frontiers of tumors, which are characteristically rough. c) Segmentation obtained using automaton evolution rule with constant penalty and n = 3.

Programs were implemented using Matlab 2013a, with Parallel Computing and Image Processing toolboxes. Tests were performed in a computer with an Intel i7 processor, 8 GB of RAM, and an Nvidia GTX 650 GPU. The CUDA implementations of the evolution rules represent each cell in the automaton as a separate thread, and use a 2-kernel schema to resolve race conditions. The complete Matlab code and CUDA kernels used for these tests, alongside curated datasets and descriptive results, can be obtained through the main author's ResearchGate profile [7].

Table 2. Simulation data results: upper rows show mean Dice coefficient for tumor and edema, HG0001 to HG0010, lower rows show mean evolution steps and execution time in seconds.

	Vezhnevets Growcut	Corrected Growcut	Exp. Penalty n=1 (Kim)	Exp. Penalty n=2	Exp. Penalty n=3	Linear Penalty n=1	Linear Penalty n=2	Linear Penalty n=3	Const. Penalty n=1	Const. Penalty n=2	Const. Penalty n=3
Tumor	.9497	.9497	.9081	.9482	.9500	.9307	.9488	.9503	.9508	.9505	.9503
Edema	.8318	.8318	.7735	.8388	.8334	.8052	.8412	.8328	.8422	.8358	.8321
Steps	23.5	14.3	50.9	16.6	15.4	24.8	14.9	14.8	13.7	13.5	13.7
Time	1.27	0.77	4.47	1.43	1.34	2.08	1.26	1.25	1.18	1.16	1.18

Table 2. Clinical data results: upper rows show mean Dice coefficient for tumor and edema, HG0001 to HG0010, lower rows show mean evolution steps and execution time in seconds.

	Vezhnevets Growcut	Corrected Growcut	Exp. Penalty n=1 (Kim)	Exp. Penalty n=2	Exp. Penalty n=3	Linear Penalty n=1	Linear Penalty n=2	Linear Penalty n=3	Const. Penalty n=1	Const. Penalty n=2	Const. Penalty n=3
Tumor	.9257	.9257	.8578	.9211	.9237	.8266	.9210	.9236	.9260	.9266	.9259
Edema	.8861	.8861	.7867	.8735	.8778	.7552	.8729	.8777	.8781	.8855	.8848
Steps	25.2	14.4	45.6	24.6	20.9	56.9	22.6	20.1	14.6	14.9	15.9
Time	0.79	0.44	2.25	1.25	1.08	2.78	1.11	1.02	0.71	0.72	0.78

Segmentation quality results in Tables 1-2 are expressed in the Dice Similarity Coefficient, which is equivalent to the F1-measure [2], and represents the harmonic mean of precision and sensitivity scores.

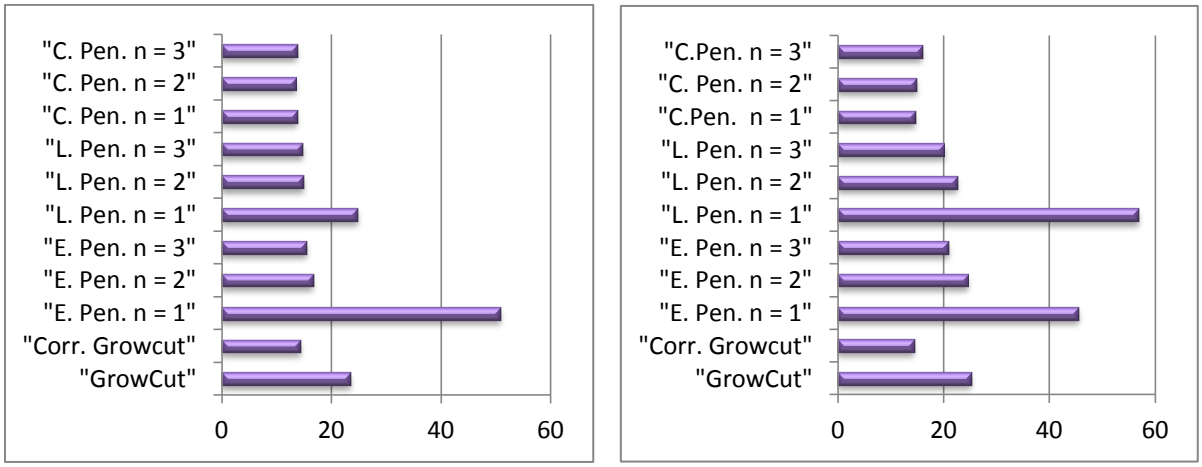


Figure 3 – Mean evolution steps to segment gliomata from BRATS 2012 - HG0001 to HG0010. (a) Simulated data. (b) Clinical data.

The proposed modification to the conquering cell evaluation criterion in the GrowCut evolution rule, shown in Figure 1b, reduces the steps required for the automaton to achieve convergence about 40%, as shown in Tables 1-2 and Fig. 3, for both the simulated and clinical data. Tables 1 and 2 show that the proposed penalized evolution rules improve Kim et al.'s [4] Dice metric result about 5% to 10%, and reduce evolution steps up to 75%, when $n > 1$. In the simulated and clinical datasets, the evolution rule with constant penalty to strength of attack shows a slightly superior Dice metric for tumor with $n \geq 1$. In the simulated datasets, the edema class was best segmented using the evolution rule with constant penalty and n=1, however this doesn't appear reflected in the results for clinical data, probably due to the human rater bias discussed in Figure 2.

4. CONCLUSIONS AND FUTURE WORK

Deterministic cellular automata derived from GrowCut exhibit high segmentation quality of tumoral tissue and cerebral edema in the multichannel MRI high grade gliomata considered. Response time is in the order of seconds in current generation consumer level GPUs, and, in the

tests performed, is improved in about 40% with the proposed modification to the conquering cell criterion. This minimal response time makes the method appropriate for iterative tests, using different parameters, in an unsupervised segmentation task. The proposed penalized automata evolution rules show a notable improvement in segmentation quality (about 5 to 10%) and reduce necessary evolution steps (up to 75%) to the previous method [4]. The proposed automata evolution rules with penalization to strength of attack produce segmentations that are qualitatively and quantitatively different from the ones obtained through unpenalized evolution. Of particular interest is an optimal combination of segmentations obtained through various automata evolution rules using a methodology that estimates rater bias and variance, like STAPLE [8].

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