A Design and Implementation of an Efficient, Parallel Watershed Algorithm for Affinity Graphs

by

Aleksandar Zlateski

Submitted to the Department of Electrical Engineering and Computer Science
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Abstract

In this thesis, I designed and implemented an efficient, parallel, generalized watershed algorithm for hierarchical segmentation of affinity graphs. By introducing four variable parameters the algorithm enables us to use previous knowledge about the input graph in order to achieve better results. The algorithm is very suitable for hierarchical segmentintation of large scale 3D images of the brain tissue obtained by electron microscopy making it an essential tool for reconstructing the brain's neural–networks called connectomes. The algorithm was fully implemented in C++ and tested on a currently largest available affinity graph of size 90GB on which no existent watershed implementation could be applied.

Thesis Supervisor: H. Sebastian Seung
Title: Associate Professor

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Chapter 1

Introduction

The human brain is estimated to contain more than 100 billion neurons. To fully understand the function of neurons and the brain development neuroscientists work on creating the wiring diagram of the brain – map of all neural connections. Recent advances in neural imaging developed at Harvard, and the Max Plank Institute for Medical Research in Heidelberg, Germany has enabled neuroscientists to gather visual data of the brain tissue at previously unobtainable dimensions. Image processing and machine learning algorithms being developed at Massachusetts Institute of Technology instructs the computer to automatically generate and analyze connectivity networks.

A tool visually developed at Seung lab at MIT enables humans to inspect and analyze the resulting networks in 3D as well as fix any possible errors made by the computer.

1.1 Generating Connectomes

Generating neural connectivity networks from raw images of brain tissue is done in three steps. In the first step convolutional networks described by S. Turaga et al. [12] are used to create an affinity graph directly from raw EM[1] images. In the second step a watershed transform is applied on the obtained affinity graphs to obtain

[1]Electron microscopy

a hierarchical segmentation. This thesis describes an algorithm for a generalized watershed transform that is used as the second step. Finally in the third step the hierarchical transformation is examined by humans using a tool called OMNI [14, 10] and all the errors made by the computer are manually fixed. The Figure 1-1 (a) shows a raw image, Figure 1-1 (b) shows a hierarchical segmentation overlayed over the raw image. A 3D view of the final segmentation is shown on Figure 1-1 (c). The OMNI user interface is shown on Figure B-1. A screen shot of editing a hierarchical segmentation using OMNI is shown on Figure B-2

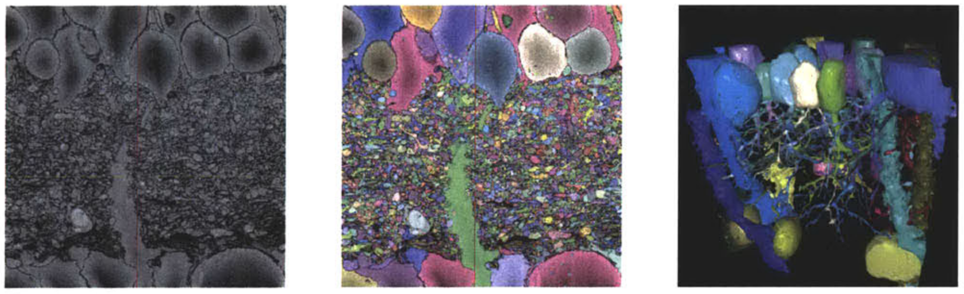

(a) (b) (c)

Figure 1-1: Segmentation of brain tissue

1.2 Motivations for Scalable Parallel Watershed Algorithm

The watershed transform is the method of choice for hierarchical image segmentation. The intuitive idea underlying this method comes from geography: it is that of a landscape or topographic relief which is flooded by water, watersheds being the divide lines of the domains of attraction of rain falling over the region [9].

Many serial and parallel algorithms for the watershed transform of images and affinity graph have been developed in past. However applying any of currently available algorithms on large data is either inefficient or impossible.

Applying the standard watershed transform on the affinity graphs obtained from neural images might not give satisfactory results. In this thesis we propose a generalized watershed transform algorithm that is able to handle an arbitrary large affinity graphs and provides flexibility for obtaining good segmentation of neural images.

1.3 Related Work

In order to compute the watershed of a digital image or an affinity graph, several approaches [1, 13, 5, 6, 7, 2, 3], have been proposed. Many of them consider a gray-scale digital image as an affinity graph. One of the most popular approaches that can be directly applied to affinity graphs consists of simulating a flooding of the topographic surface from its regional minima [13, 5]. We generalize and extend the algorithm described by J. Cousty, G. Bertrand, L. Najman, and M, Couprie [3] in order to support processing arbitrary large data.

1.4 Thesis Outline

The thesis proposes a design of an efficient, parallel watershed algorithm for affinity graphs. It generalizes the standard watershed transform by introducing a set of variable parameters. A serial watershed algorithm is presented in Chapter 2. Chapter 3 proposes a way to efficiently use the serial algorithm for very large affinity graphs. The parallel watershed algorithm is proposed and analyzed in Chapter 4. Chapter 5 provides some result of both the serial and the distributed watershed algorithms.

Chapter 2

Serial Watershed Algorithm

This chapter provides a detailed description of a modified watershed algorithm and a serial implementation based on watershed cuts described by J. Cousty, G. Bertrand, L. Najman, and M, Couprie [3]. Section 2.1 details the notions and notations we use in the rest of the thesis. Section 2.2 introduces a set of paramaterized constraints that generalize the standard watershed transform. The user–defined parameters enable us to use the knowledge about the input in order to achieve better results. Our watershed algorithm is discussed in Section 2.3. Finally, Section 2.4 provides a proof of correctness and an analysis of the running time.

2.1 Basic Notions and Notations

This thesis is settled in the framework of undirected affinity graphs[1]. Following standard notations, we present some basic definitions to handle such kind of graphs.

The standard watershed transform of an affinity graph consists of a segmentation with its segmentation hierarchy. Our algorithm also provides the region graph of the segmentation.

[1]We designed the watershed algorithm keeping in mind a 6–connected affinity graph of a 3D volume. However the described algorithm can be applied to an affinity graph of an arbitrary topology.

2.1.1 Graphs

We define a *graph* as a pair $G = (V, E)$, where V is a finite set and E is a set of unordered pairs of V, i.e., E is a subset of $\{\{x, y\} \mid x, y \in V, x \neq y\}$. In affinity graphs used for image segmentation, V is the set of picture elements (pixels or voxels[2]) and E is any of the usual adjacency relations, e.g., the 4 or 8–adjacency in 2D, 6 or 18–adjacency in 3D. For the rest of the thesis we will assume 4–adjacency for 2D and 6–adjacency for 3D.

2.1.2 Affinity Weights

Let $\mathcal{F}$ be the set of all maps from E to $\mathbb{R}^+$, we say that a map F in $\mathcal{F}$ is an affinity map of G, and F weights the edges in G.

Let $F \in \mathcal{F}$ and $e \in E$, then, $F[e]$ is an affinity or weight of the edge e. For a given $F \in \mathcal{F}$ and $u \in V$, let $F^{\ominus}[v]$ be the maximal value of all $F[e]$ where e is an edge containing v. $F^{\ominus}[v]$ is the value of the strongest edge connecting v with one of its neighbours.

2.1.3 Labels and Segmentations

We denote by $\mathcal{L}$ the set of all maps from V to $\mathbb{N}_0$, and we say that any map L in $\mathcal{L}$ labels the vertices of G with $L[v]$ being the label of v. If $L[v] = 0$ we say that the vertex v is unlabeled.

A given L in $\mathcal{L}$ is a valid segmentation of G iff for any two vertices $u \neq v$ in V that have the same, positive label l there exist a path from u to v that visits only vertices labeled l.

2.1.4 Region Graph and Segmentation Hierarchy

We define a region graph to be a graph obtained by collapsing all the vertices with same labels. Similarly we define region graph's affinities to be the maximal affinities of the corresponding collapsed edges.

[2]Pixel in 3D space

Finally, we define the segmentation hierarchy to be a maximal spanning tree of the region graph. An edges of the segmentation hierarchy (the MST) represent affinity at witch the two segments merge. A subset of a hierarchical segmentation is shown on Figure B-2.

2.2 Additional Constraints

We extend the standard watershed transform by introducing four user–defined constrains. The motivation for generalazing our watershed algorithm comes from the nature of the nature affinity graphs obtained directly from imaged volume by applying CNs[3] as described by S. Turaga at al. [12].

The affinity between two voxels depends on the field of view[4] of the CNs. In simple terms, the the affinity is a function that maps the gray–scale values of the local voxels to $\mathbb{R}$. Due to the noise and exposure difference between slices produced affinity graphs might have slight variations around in the places where the CN is most confident, e.g. near 0 affinity and near 1 affinity. As the watershed transform is based on relative values of the affinities, these small variations might lead to a large number of small segments as depicted on Figure 2-1 (a).

One solution would be to discretize the values of the affinity graph, in which case we would lose powerful property of the real valued affinity graphs which enable us to efficiently implement parallel version of our watershed algorithm without problems related to non–maxima plateaus. This topic is discussed in more detail in Section 4.1.

2.2.1 High Threshold T_h

For a given high threshold value T_h, we mandate that each edge with affinity greater or equal to T_h forces the two vertices to belong to the same segment. We apply this threshold by simply changing the affinity of edges with value higher than T_h to ∞. An example result of applying T_h is shown on Figure 2-1 (b).

[3]Convolutional networks

[4]Values of the local voxels in the original images

2.2.2 Low Threshold T_l

Low threshold T_l simply states that no segment should be *grown* using edges with affinity less than or equal to T_l. By *growing* a segment we consider the first step of the our watershed algorithm described in Section 2.3. The vertices whose all edges have affinity less than or equal to T_l will became single–vertex segments. For such vertices we set $F^{\ominus}(v)$ to ∞. An example result of applying T_l is shown on Figure 2-1 (c).

2.2.3 Size Thresholds T_s and T_e

The role of the last two thresholds T_s and T_e is a bit more elaborate. Once we have obtained a region graph we visit all its edges in decreasing order of affinity. In the case that an edge with affinity greater than T_e connects two segments such that one of them has size[5] lower than T_s we merge the two segments. After we have visited all the edges in the region graph we discard all the segments with the size lower than T_s.

The main motivation for applying the size thresholds is preventing the tiny segments inside and on the borders of the inner–cellular space. Usage of the size thresolds is shown on Figure 2-1 (d).

2.3 The Watershed Algorithm

We present the watershed algorithm by generalizing the drop of water principle approach described in [3]. In addition to vertex labels we also calculate the region graph and the segmentation hierarchy.

The algorithm consist of four steps. In the first step we apply the same approach as desribed in [3] with modified values of $F^{\ominus}$ in order to satisfy constraints T_h and T_l described in Section 2.2. In the second step we generate the region graph. The third step applies the two remaining constraints T_s and T_e. Finally, in the fourth step we generate the segmentation hierarchy.

[5]Number of vertices within the segment

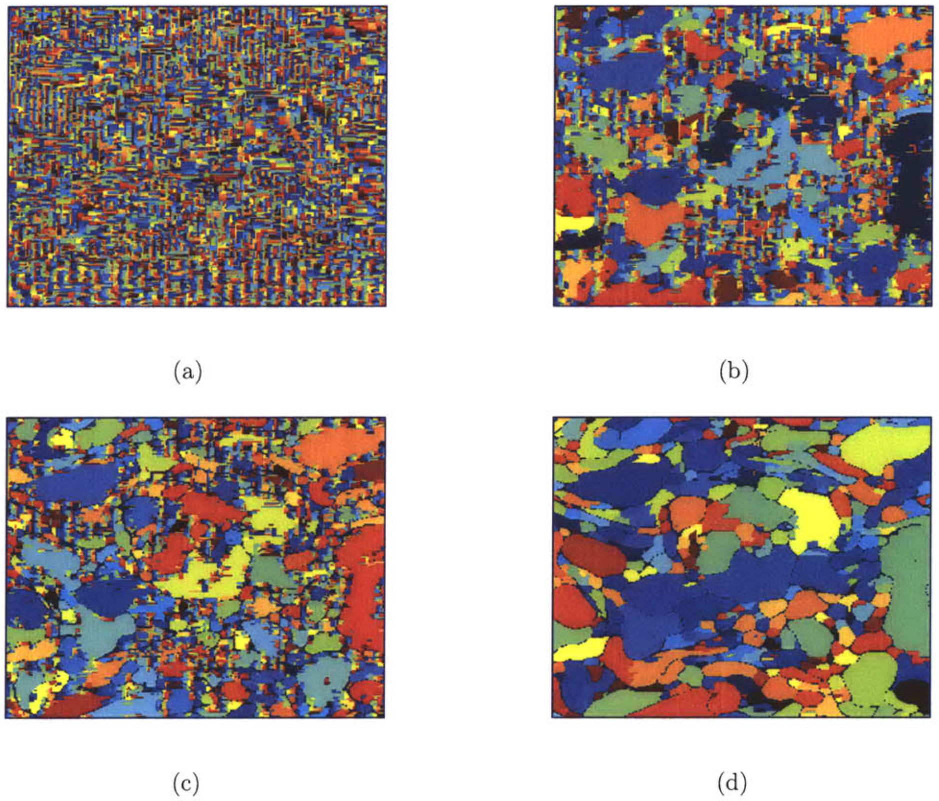


Figure 2-1: Results obtained by using additional constraints (a) Standard watershed transform, (b) Watershed transform using $T_h = 0.98$, (c) Watershed transform using $T_h = 0.98$ and $T_l = 0.2$, (d) Watershed transform using $T_h = 0.98$, $T_l = 0.2$, $T_s = 25$ and $T_e = 0.1$.

2.3.1 The Four Watershed Steps

In this subsection we present the pseudo code of the four steps required for our watershed algorithm.

```
INITIAL-WATERSHED($V, E, F$)
 1 for each $u \in V$
 2         $L[u] = 0$
 3 $label_{next} = 1$
 4 for each $u \in V$ such that $label[u] = 0$
 5         $[l, L] =$ STREAM($u, V, E, F, L$)
 6         if $l = 0$
 7                 $l = label_{next}$
 8                 $label_{next} = label_{next} + 1$
 9         for each $x \in L$
10                 $L[x] = l$
11 return $L$
```

```
STREAM($u, V, E, F, L$)
 1 $Q =$ LIST($u$)
 2 $L =$ LIST($u$)
 3 while LIST-LENGTH($Q$) $\neq 0$
 4         $y =$ POP-FRONT($Q$)
 5         while there exist $\{y, z\} \in E$ such that $z \notin L$ and $F(\{y, z\}) = F^{\ominus}(y)$
 6                 if $L[z] \neq 0$
 7                         return $[L[z], L]$
 8                 else if $F^{\ominus}(z) < F^{\ominus}(y)$
 9                                 PUSH-BACK($L, z$)
10                                 $Q =$ LIST($z$)
11                         else PUSH-BACK($L, z$)
12                                 PUSH-BACK($Q, z$)
13 return $[0, L]$
```

The procedure INITIAL-WATERSHED applies the drop of water principle using streams [3]. The output is a valid segmentation labeling of G.

```
CREATE-REGION-GRAPH($V, E, F, L$)
1  $E' = \emptyset$
2  for each $\{u, v\} \in E$ such that $L[u] \neq L[v]$
3      $l_1 = L[u]$
4      $l_2 = L[v]$
5      if $\{l_1, l_2\} \in E'$
6          $F'[\{l_1, l_2\}] = \text{MAX}(F'[\{l_1, l_2\}], F[\{u, v\}])$
7      else $E' = E' \cup \{l_1, l_2\}$
8          $F'[\{l_1, l_2\}] = F[\{u, v\}]$
9  return $[E', F']$
```

The procedure CREATE-REGION-GRAPH creates a region graph of the segmentation L of G. The output is an affinity graph on the set of segmentation labels.

```
APPLY-SIZE-THRESHOLD($L, E_L, F_L, S_L, T_s, T_e$)
1  for each $\{l_1, l_2\} \in E_L$ such that $F_L(\{l_1, l_2\}) \geq T_e$ in decreasing order of $F(\{l_1, l_2\})$
2      $s_1 = \text{FIND-SET}(l_1)$
3      $s_2 = \text{FIND-SET}(l_2)$
4      if $s_1 \neq s_2$ and either $S_L[s_1] < T_s$ or $S_L[s_2] < T_s$
5          $s = S_L[s_1] + S_L[s_2]$
6          $S_L[s_1] = 0$
7          $S_L[s_2] = 0$
8          $S_L[\text{JOIN-SETS}(s_1, s_2)] = s$
9  $newlabel_{next} = 1$
10 for each $l \in L$
11     if $S_L[l] \geq T_s$
12         $S'_l[newlabel_{next}] = S_L[l]$
13         $L'[l] = newlabel_{next}$
14         $newlabel_{next} = newlabel_{next} + 1$
15     else $L'[l] = 0$
16 $E'_L = \emptyset$
17 for each $\{l_1, l_2\} \in E_L$
18     $s_1 = L'[\text{FIND-SET}(l_1)]$
19     $s_2 = L'[\text{FIND-SET}(l_2)]$
20     if $s_1 \neq 0$ and $s_2 \neq 0$ and $s_1 \neq s_2$
21         if $\{s_1, s_2\} \in E'_L$
22             $F'[\{s_1, s_2\}] = \text{MAX}(F'_L[\{s_1, s_2\}], F_L[\{l_1, l_2\}])$
23         else $E'_L = E'_L \cup \{s_1, s_2\}$
24             $F'_L[\{s_1, s_2\}] = F_L[\{l_1, l_2\}]$
25 return $[L', E'_L, F'_L]$
```

The procedure APPLY-SIZE-THRESHOLD applies the size thresholds on the given segmentation L of G. The procedure returns new labels and new region graph. In order to assign new labels to the original set V, for each $v \in V$ we set $L_{new}[v] = L'[L[v]]$.

```
GENERATE-SEGMENTATION-HIERARCHY($E_L, F_L$)
1  for each $\{l_1, l_2\} \in E_L$ in decreasing order of $F(\{l_1, l_2\})$
2      $s_1$ = FIND-SET($l_1$)
3      $s_2$ = FIND-SET($l_2$)
4      if $s_1 \neq s_2$
5          $E_H = E_H \cup \{l_1, l_2\}$
6          JOIN-SETS($s_1, s_2$)
7  return $[E_H]$
```

Given a region graph (E_L, F_L) the GENERATE-SEGMENTATION-HIERACHY generates the segmentation hierarchy.

2.3.2 The Watershed Procedure

Finally we present the main watershed procedure. The procedure SETUP-CONSTRAINTS generates values of F^{Θ} as described in Section 2.2 and CALCULATE-SIZES simply counts the number of vertices per segmentation label.

```
SERIAL-WATERSHED($V, E, F$)
1  SETUP-CONSTRAINTS($T_h, T_l$)
2  $L$ = INITIAL-WATERSHED($V, E, F$)
3  $[E_L, F_L]$ = CREATE-REGION-GRAPH($V, E, F, L$)
4  $S_L$ = CALCULATE-SIZES($L$)
5  $[L', E_L, F_L]$ = APPLY-SIZE-THRESHOLD($L, E_L, F_L, S_L, T_s, T_e$)
6  for each $v$ in $V$
7      $L[v] = L'[L[v]]$
8  $[E_H, F_H]$ = GENERATE-SEGMENTATION-HIERARCHY($E_L, F_L$)
9  return $[L, E_L, F_L, E_H]$
```

2.4 Correctness and Running Time Analysis

A proof of correctness for the the procedure INITIAL-WATERSHED is given in [3]. Assuming correct implementation of the procedures FIND-SET and JOIN-SETS as described in [11] the three remaining parts of our watershed algorithm are correct by design.

For the running time analysis we will assume that $O(v) = O(e)$ which is the case in the standard adjacency relations. The running time of INITIAL-WATERSHED is then $O(v)$ [3]. The worst case running time of CREATE-REGION-GRAPH is dominated by sorting the edges – $O(v \log v)$. Applying size threshold as well as generating segmentation have running time of $O(v \log^* v)$,[6] we make $O(v)$ calls to *union-find* procedures [11].

The worst case running time of the watershed algorithm described in the previous section is then $O(v \log v)$. The expected running time, however, depends on the input graph and given constraints. As shown on Figure 2-1 even a very tight high threshold might decrease the number of segments after the initial watershed stage by a factor much larger than $\log(v)$, bringing the running time much closer to $O(v)$. We could further improve the running time by using parallel sorting rutines described in Section A.1.2.

The memory requirement of the presented algorithm is $O(v)$. We need to store the set of labels, the region graph which is a subset of the original affinity graph and the segmentation hierarchy.

[6]$\log^*$ is the inverse ackermann function

Chapter 3

Watershed Algorithm on Very Large Affinity Graphs

In this chapter we explore a way of using the serial watershed algorithm on very large affinity graphs. Section 3.1 details a way of transparently using the watershed algorithm described in Chapter 2. Some of the bottlenecks of using the serial watershed algorithm are explained in Section 3.2

3.1 Chunk Based Caching

As described in Section 2.4 the memory requirement for the serial watershed algorithm is $O(v)$. Processing a very large affinity graphs would require a computer with large amount of RAM. We propose a solution using on–disk data structures.

The first step of the serial algorithm described in Section 2.3 visits the vertices of the affinity graph and labels them by alternating breath and depth first search. The nodes visited in the STREAM procedure are all reachable from the starting node. If we divide the original affinity graph into chunks[1], we can dynamiclally load only subparts of the graph on demand. Using the most recently used cache algorithms described in Section A.1.5 and implementing wrappers around functions that access the affinity graph we can transparently use the serial watershed algorithm.

[1]Large affinity graph are usually stored in this fashion to provide better data locality

We also change the order in which we examine the vertices. By examining all the vertices in a single chunk we increase the likelihood that the affinity graph chunk required is cached in RAM. We store the vertex labels in similar, chunked fashion.

This approach allows us to process arbitrarly large affinity graphs. There are however some overheads described in the next section, some of which can't be easily overcome. For that reason we develop a parallel version of our watershed algorithm described in Chapter 4.

3.2 Cache Performance

The performance of the serial algorithm with cached data structures depends on number of cache hits/misses. Cache performance strongly depends on the affinity graph processed as well as the constraints described in Section 2.2. Small localized segments lead to more cache hits whereas large non–localized ones might lead to a lot of cache misses. The overheads induced by cache misses as well as the fact that we don't take advantage of multi–core machines are the two major reasons for developing an improved, parallel version of our watershed algorithm.

Chapter 4

Parallel Watershed Algorithm

In this chapter we propose a parallel watershed algorithm analogous to the algorithm presented in Chapter 2. Section 4.1 gives more insight into dealing with non–maxima plateaus. The overview of the algorithm is detailed in Section 4.2. Section 4.3 goes over the required modifications of the serial watershed algorithm. Section 4.4 describes the way we merge the local results. Finally, Section 4.5 analyze the running time and space requirement of the algorithm.

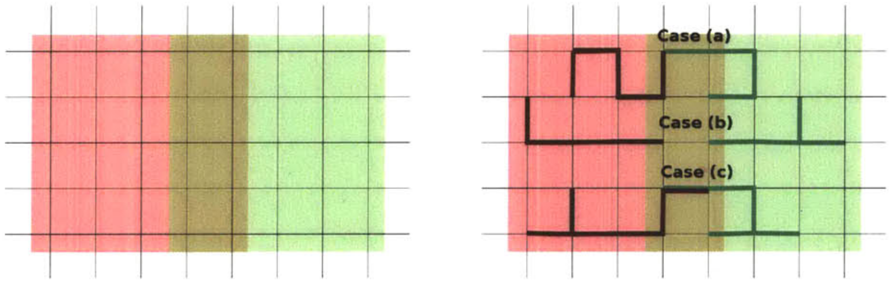
4.1 On Non–Maxima Plateaus

Many authors describe the non–maxima plateaus problem as a major obstacle for developing an efficient parallel watershed algorithm [13, 5, 2, 3]. They further develop methods for dividing the non–maxima plateaus based on either topological or geographical distance. Fortunately, for the reasons described in Section 2.2 we do not have to worry about the non–maxima plateaus as they do not occur in the affinity graphs our watershed algorithm is designed to process. The empirical result from examining a large set of affinity graphs obtained from EM images using CNs support the claim given in Section 2.2. The largest non–maxima plateaus that we find have size of 3, and they occur very rarely. There are only two ways to divide such plateaus, and they can both be considered correct. As described serial watershed algorithm handles non–maxima plateaus correctly based on topological distance, handling large affinity graphs with non–maxima plateaus can be done using the method described in Chapter 3

4.2 Algorithm Overview

The parallel watershed algorithm consists of two steps. In the first step we apply a modified version of the serial watershed algorithm described in Section 4.3 locally. The affinity graph is divided into regions with an overlap of one edge in each dimension (a 2D affinity graph division is shown on Figure 4-1 (a). The result of each region is then stored on disk. In the second step we merge the results of all the regions by examining the overlapping edges.

4.3 Modified Local Watershed



(a) (b)

Figure 4-1: Dividing the afiinity graph with one overlapping edge

There are few modifications that have to be made to the serial watershed algorithm described in Chapter 2 in order to support merging the local results.

The vertices on the borders of the regions are always considered to be local maxima. This can be simply done by setting $F^{\Theta}(v)$ for each border vertex v to be ∞. Also, in the procedure INITIAL-WATERSHED we never examine the border vertices. As we consider the border edges to be local maxima, calling the procedure STREAM on them would simply mark the single vertex as a segment. If a border edge is not reached from some other vertex inside the STREAM method we don't have to create separate segment containing that single vertex, as that vertex will be included in some segment while processing the adjacent region.

Another change has to be made inside the APPLY-SIZE-THRESHOLD method. As we don't know the final size of the segments that touch the border of the region we can't consider them during the stage of merging segments smaller than T_s. We modify APPLY-SIZE-THRESHOLD so that the segments touching the border have *unknown* size. When we encounter an edge between a segment of *unknown* size and any other segment, while looping through the edges of the region graph, we mark both segments as *unknown*. This way we prevent merging any segment for which we don't know its final size.

Finally, we do not have to create the segmentation hierarchy as a global one will be created later.

4.4 Merging Local Watersheds

We merge local results by examining the edges included in adjacent regions. The three possible cases that might occur are shown on Figure 4-1 (b).

In the first case the edge is visited only in one of the two regions. This means that in one of the two regions a local maxima other than the border is found, and in the other the actual overlapping edge is the local maxima. In this case we can simply merge the two segments.

In the second case both regions have local maximas other than the overlapping edge in which case we don't do anything.

In the third case both regions have the overlapping edge as local maxima. In this case we merge the two segments. The overlapping edge might have been on a non–maxima plateau in both the regions in which case we can find an edge e between the resulting segment and some other segment with affinity equal to the one of the overlapping edge. If such an edge exist we merge the two segments connected by e. If there existed more than one edge between the resulting segment with affinity equal to the one of the overlapping edge we use any of them for merging the resulting segment.

This meant that the resulting segment was a part of a plateau.

After all the regions have been merged we apply the size threshold once again. And create the segmentation hierarcy the same way as in the serial watershed algorithm. Note that we don't have to merge local region graphs. As all the local region graphs are already sorted we can use a cache oblivious heap structure described in [8] to visit all the edges of all the region graphs in descending order of affinity.

4.5 Running Time and Space Analysis

Let v be the number of vertices of the affinity graph divided into n equal parts. The running time of processing each part is then $O(\frac{v}{n}\log(\frac{v}{n}))$. Processing all the parts on k CPUs takes $O(\frac{v}{k}\log(\frac{v}{n}))$. The global step of the algorithm visits all the edges of each part's region graph and applies at most constant number of *union-find* operations per visited edge. Extracting a maximum from n pre–sorted lists take $O(\log(n))$ time. The running time of the global step is then $O(v\log(n)\log^*(v))$. The total running time of the parallel watershed is then

$$O\left(\frac{v}{k}\log(\frac{v}{n}) + v\log(n)\log^*(v)\right) = O\left(\frac{v}{k}(\log(v) + k\log(n)\log^*(v))\right)$$

The space requirement for the first part of the algorithm is $O(\frac{kv}{n})$. We assume that the second part of the algorithm is done using only on–disk data structures.

As increasing n increases the running time but decreases the space requirement the value of n should be minimized while making sure that we can fit $O(\frac{kv}{n})$ in RAM.

Chapter 5

Results

This chapter provides some results of both the serial and parallel watershed algorithms. We compare the running time of the standard watershed transform – with no additional constraints and watershed transform with commonly used constraints.

All results are the average of two trials performed on a 16 core Intel Xeon 3.2GHz CPU with 48GB of RAM running Ubuntu Linux 10.10.

5.1 Serial Watershed

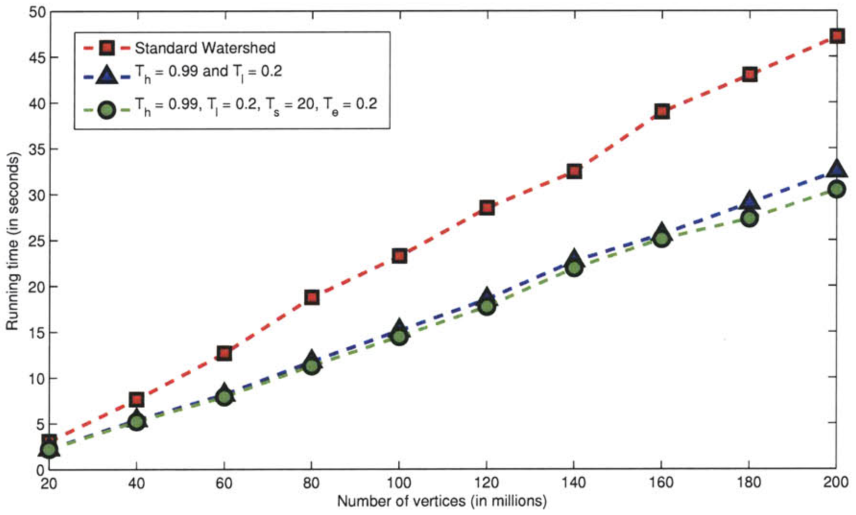


Figure 5-1: Measured running time of the serial watershed algorithm

Figure 5-1 shows results of the serial watershed implementation ran on different size affinity graphs. The introduced constraints result in lower number of segments and smaller region graph. According to the analysis in Section 2.4 this should lead to lower running and is therefore consistent with the measured results.

5.2 Parallel Watershed

In order to minimize RAM usage, the parallel watershed implementation stores intermediate results either on disk or in memory. Storing the intermediate results in memory reduces the i/o overhead but increses the memory usage, and is not possible for very large affinity graphs. In all the tests a chunk size of 256^3 was used.

5.2.1 In Memory

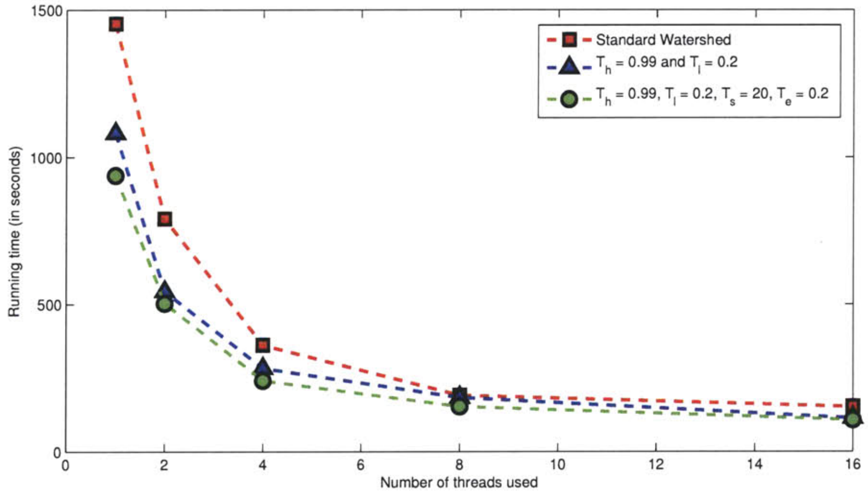


Figure 5-2: Measured running time of the in–memory parallel watershed algorithm

Figure 5-2 shows results of the parallel watershed implementation ran on an affinity graph with 1 billion vertices[1]. The input affinity graph, the output segmentation and

[1] $1000 \times 1000 \times 1000$ volume.

the intermediate results were stored on a *ramfs* partition[2]. Once again we confirm that the introduced constraints result in lower running times.

5.2.2 On Disk

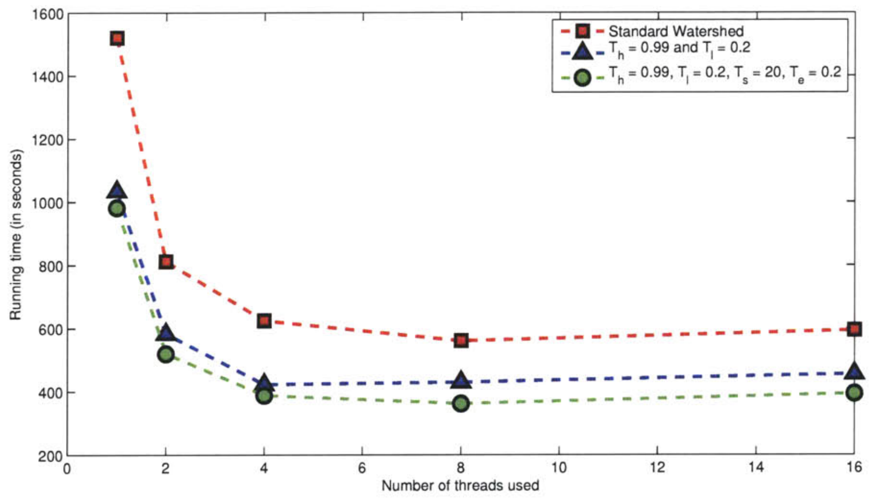


Figure 5-3: Measured Running Time of the On–Disk Parallel Watershed Algorithm

Figure 5-3 shows results performed on the same affinity graph using on–disk storage. Before running the algorithm all system caches were dropped to ensure correct measurements. The runtime includes the time needed to read the input affinity graph from the disk, and store the results on the disk. The results show that when using more than 4 threads the disk i/o becomes the major overhead. The maximal number of threads that improve the overal running time strongly depends on the disk speed.

[2]Virtual disk stored in RAM

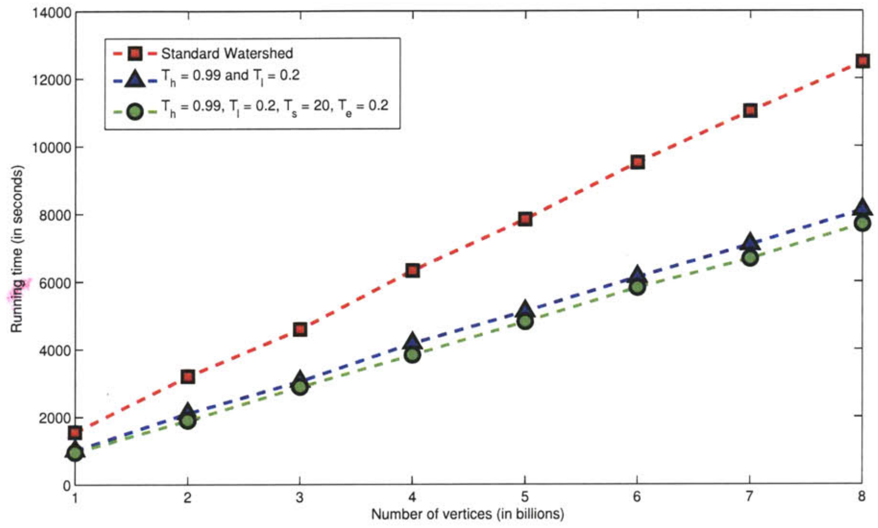


Figure 5-4: Measured running time of the on–disk parallel watershed algorithm using 4 threads

Measured running time of the parallel watershed algorithm using 8 threads ran on very large affinity graphs is shown on Figure 5-4. As the performances are limited by disk i/o speed we see a linear increase running time.

5.3 Segmentation Results

Figure 5-5 shows a 3D representation of a subset of segments obtained by the generalized watershed transform on a 2000^3 volume using our parallel algorithm.

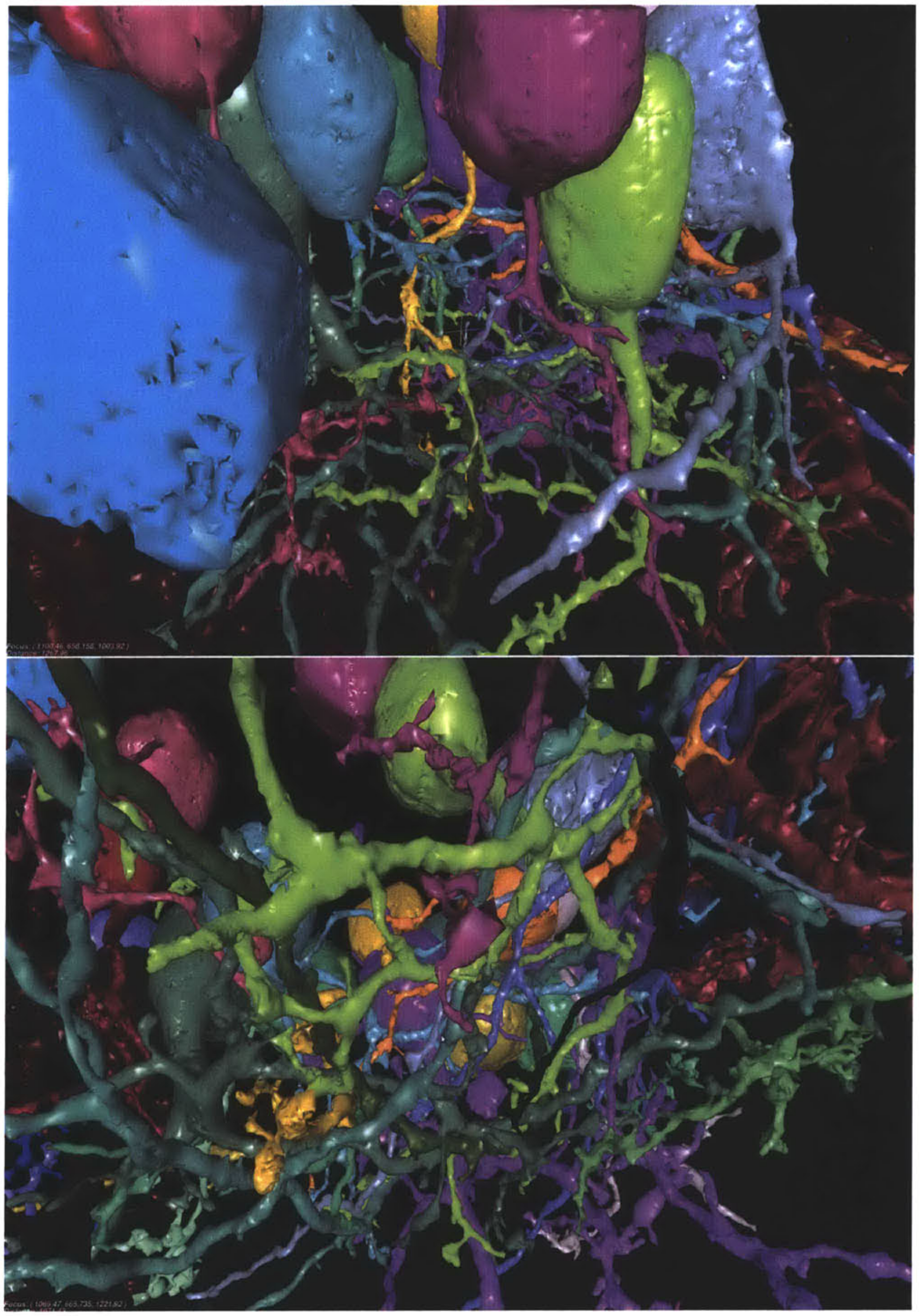


Figure 5-5: Visualization of watershed segmentation on a 2000^3 volume

Appendix A

Implementation Details

The implementation of both serial and parallel watershed are provided as a part of the ZI libraries. The code takes advantage of C++'s templates in order to achieve optimal performance based on the affinity graph sizes and data types. For example, smaller affinity graphs lead to smaller number of labels in which case a smaller integral type is used for labeling the vertices.

A.1 The ZI Library

The ZI libraries provides all the necessary functionality needed for both the serial and parallel versions of the algorithm. Many libraries are extensively used by OMNI to provide real time editing of the hierarchical segmentation obtained by the watershed transform. In the rest of this chapter we describe some of the libraries.

A.1.1 Concurrency

The library enables the use of multiple threads of execution with shared data in portable C++ code. It provides classes and functions for managing the threads themselves, along with others for synchronizing data between the threads.

The Concurrency library also provides some higher level functionality such as prioritized task managers, periodic functions, state managers, et cetera.

A.1.2 Parallel

The Parallel library provides a parallel implementation of many algorithms from the C++ Standard Library. Depending on the platform and compiler flags, the library will either wrap the **gnu parallel** implementations that use OpenMP annotations, or provide an efficient parallel implementation using the Concurrency library described in section A.1.1.

The watershed implementation strongly relies on the Parallel library, especially during the global step of the distributed watershed.

A.1.3 Disjoint Sets

The library provides a fast and memory efficient, generic implementation of the *union-find* data structures as described by R. Tarjan [11].

A.1.4 Heap

The Heap library provides an easy way to create dynamic heaps for arbitrary data structures. The heap elements can be of any type when the key and value extractors are described. An extractor can be any global function, type's member function or type's member variable. The library provides both the standard binary heap implementation as well as the fibonacci heaps as described by M. Fredman and R. Tarjan [4].

A.1.5 Cache

The Cache library provides a set of classes and functions for transparently using external storage for large data containers. It provides a set of caching strategies: most recently used, most commonly used, et cetera.

A.1.6 System

The System library enables us to detect the currently used platform amounts of used/free memory, number of CPUs and many other system parameters.

A.1.7 Time

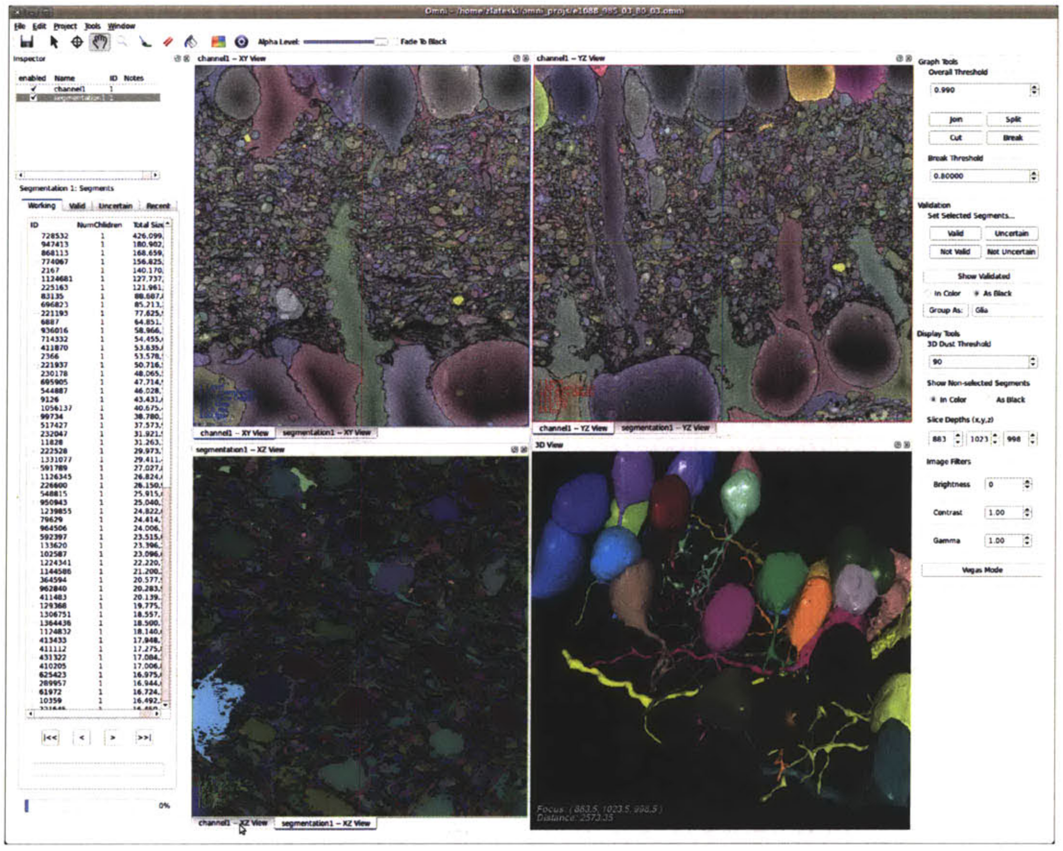
This library provides a set of tools for accurately measuring running time and CPU time. It is an essential tool for performance testing.

A.1.8 Graph

The Graph library provides a large set of graph algorithms including, but not limited to: matchings, topological sorting, dynamic trees, network flows, etc. The library is extensively used in OMNI.

Appendix B

Figures



enabled	Name	ID	Notes
✓	channel1	1	
✓	segmentation1	1	

Segmentation 1: Segments

Working | Valid | Uncertain | Recent

ID	NumChildren	Total Size
728532	1	426,099,
947413	1	180,902,
868113	1	168,659,
774067	1	156,825,
2167	1	140,170,
1124681	1	127,737,
225163	1	121,961,
83135	1	88,687,
696823	1	85,213,
221193	1	77,625,
6887	1	64,851,
936016	1	58,966,
714332	1	54,455,
411870	1	53,635,
2366	1	53,578,
221937	1	50,716,
230178	1	48,065,
695905	1	47,714,
544887	1	46,028,
9126	1	43,431,
1056137	1	40,675,
99734	1	38,780,
517427	1	37,573,
232047	1	31,921,
11828	1	31,263,
222528	1	29,973,
1331077	1	29,411,
591789	1	27,027,
1126345	1	26,824,
226600	1	26,150,
548815	1	25,915,
950943	1	25,040,
1239855	1	24,822,
79629	1	24,414,
964506	1	24,006,
592397	1	23,515,
133620	1	23,396,
102587	1	23,096,
1224341	1	22,220,
1144586	1	21,200,
364594	1	20,577,
962840	1	20,283,
411483	1	20,139,
129368	1	19,775,
1306751	1	18,557,
1364436	1	18,500,
1124832	1	18,140,
413433	1	17,948,
411112	1	17,275,
431322	1	17,084,
410205	1	17,006,
625423	1	16,975,
289957	1	16,944,
61972	1	16,724,
10359	1	16,492,

Graph Tools
Overall Threshold: 0.990
Break Threshold: 0.80000

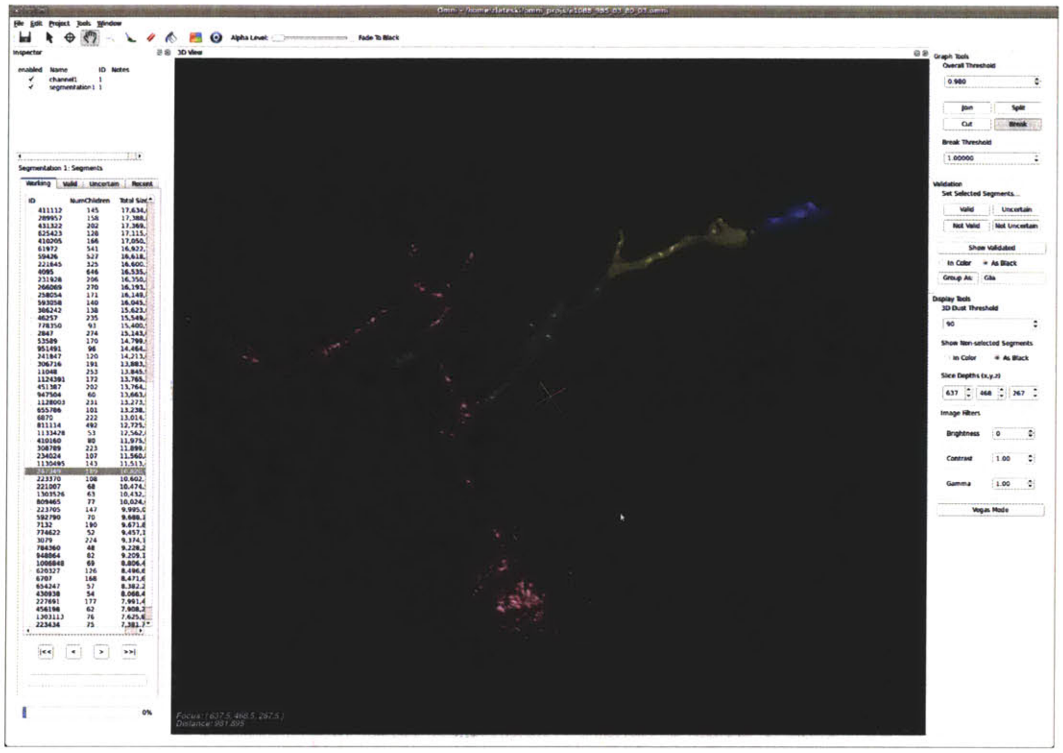
Validation
Set Selected Segments...
In Color [✓ As Black]
Group As: Glia

Display Tools
3D Dust Threshold: 90
Show Non-selected Segments: [✓ In Color] As Black
Slice Depths (x,y,z): 883 1023 998

Image Filters
Brightness: 0
Contrast: 1.00
Gamma: 1.00

Focus: (883.5, 1023.5, 998.5)
Distance: 2573.33

Figure B-1: OMNI user interface



enabled	Name	ID	Notes
✓	channel1	1	
✓	segmentation 1	1	

Segmentation 1: Segments

Working | Valid | Uncertain | Recent

ID	NumChildren	Total Size
411112	145	17,634,
289957	158	17,388,
431322	202	17,369,
625423	128	17,115,
410205	166	17,050,
61972	541	16,922,
59426	527	16,618,
221645	325	16,600,
4095	646	16,535,
231928	206	16,350,
266069	270	16,193,
258054	171	16,149,
593058	140	16,045,
306242	138	15,623,
46257	235	15,549,
778350	93	15,400,
2847	274	15,143,
53589	170	14,799,
951491	96	14,464,
241847	120	14,213,
306716	191	13,883,
11048	253	13,845,
1124391	172	13,765,
451387	202	13,764,
947504	60	13,663,
1128003	231	13,273,
655786	101	13,238,
6870	222	13,014,
811114	492	12,725,
1133428	53	12,562,
410160	80	11,975,
308789	223	11,899,
234024	107	11,560,
1130495	143	11,513,
[illegible]	[illegible]	[illegible]
223370	108	10,602,
221007	68	10,474,
1303526	63	10,432,
809465	77	10,024,
223705	147	9,995,0
592790	70	9,688,1
7132	190	9,671,6
774622	52	9,457,1
3079	224	9,374,1
784360	48	9,228,2
948864	82	9,209,1
1006848	69	8,806,4
620327	126	8,496,6
6707	168	8,471,6
654247	57	8,382,2
430938	54	8,068,4
227691	177	7,991,4
456198	62	7,908,2
1303113	76	7,625,6
223434	75	7,381,7

Graph Tools
Overall Threshold: 0.980
Break Threshold: 1.00000

Validation
Set Selected Segments...
In Color ● As Black
Group As: Glia

Display Tools
3D Dust Threshold: 90
Show Non-selected Segments: In Color ● As Black
Slice Depths (x,y,z): 637 468 267

Image Filters
Brightness: 0
Contrast: 1.00
Gamma: 1.00

Figure B-2: Hierarchical segmentation in OMNI

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