

# **CS 446 Computer Integrated Surgery II**

## **Paper Critical Review, 21 April 2012**

Mehmet Akif Gulsun

Mentor: Gareth Funka-Lea, Siemens Corporation, Corporate Research, Princeton

### **Introduction**

This is a critical review of the paper “An Airway Tree-shape Model for Geodesic Airway Branch Labeling” written by Feragen et. al. [1]. This paper presents a method for airway branch labeling by computing geodesic deformations between mathematical airway tree-shape models. The authors claim that the labeling results are good taking the large variation in the training set into account. Even though some important points in their experimental validation are not clarified, the proposed method brings novelty to the field with a geodesic deformation which simultaneously considers both airway topology and branch geometry.

### **Relevance**

The technical approach of my project includes the computation of average coronary tree from a population by computing geodesic deformations based on an unique tree-shape metric called Quotient Euclidean Distance (QED). The QED metric was first proposed by the same authors of the reviewed paper [2] who then applied this metric to airway branch labeling. I selected this paper for my review because it assesses the accuracy of QED geodesic deformation with an application to tree matching and it explains this metric to a broader community thoroughly.

### **Paper Summary**

The reviewed paper proposes a novel method for the automated labeling of an unseen airway tree by first finding its correspondence to labeled airway trees in a training set and then assigning a label to each branch of the unseen tree based on a majority vote scheme. It establishes the branch correspondence between two airway trees by a unique geodesic deformation which is the main contribution of the paper. The authors begin their paper by motivating the importance and difficulty of the problem which is followed by related works. They then explain the tree-shape space including a unique geodesic metric and its application to airway trees. The paper is concluded after presenting and discussing the results.

Finding the correspondence between airway trees in a population is a necessary task to monitor progression and variability of diseases at specific anatomical locations. Airway centerlines extracted from Computed Tomography (CT) scans are commonly used for airway tree comparison and branch labeling. However, this comparison is difficult due to spurious or missing branches

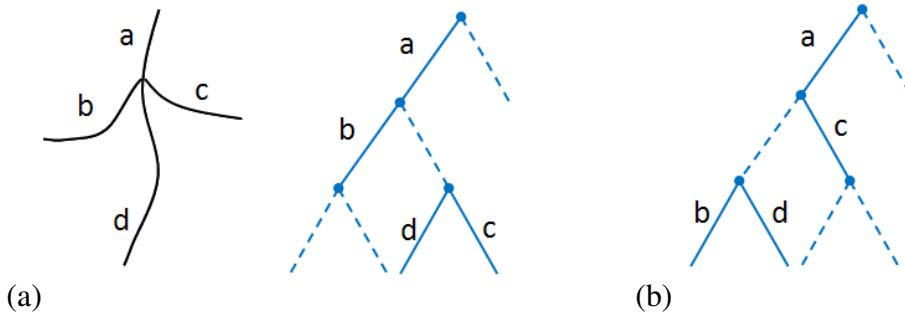


Figure 1: a) Representation of non-binary tree-shapes. Tree-shape is shown on left. Its corresponding binary tree with zero-attributed edges is shown on the right. b) Representation of the same tree-shape in (a) with a different binary tree.

and more importantly anatomical variation. This problem was previously addressed in the literature by methods that use one of the topology or branch geometry features of airway trees. These methods include maximal clique computation on association graphs that only considers topology and has NP hard complexity, implicit recursive labeling during segmentation that is prone to topological changes and path matching that can only label paths and therefore loses topological information. On the other hand, different than these previous methods, the reviewed paper proposes a solution to this problem by computing continuous and morphological geodesic deformations between trees using both topology and branch shape features of airway trees.

The tree-shape space and geodesic metric used in this paper were previously defined by the authors [2]. In their work, any tree-shape corresponds to a point in the Euclidean space and is represented as a pair  $(T, f)$  of an ordered binary tree  $T = (E, r)$  with edges  $E$  and a root point  $r$ , and branch attributes  $f : E \rightarrow \mathbb{R}^{3n}$  where each edge  $E$  is mapped with  $n$  landmark points sampled along the matching branch geometry. The binary tree accounts for the tree-shape topology where non-binary tree-shapes can be represented via binary trees by collapsing their zero-attributed edges, Figure 1a. The Euclidean representation of the tree-shape space then becomes  $X = \prod_{e \in E} \mathbb{R}^{3n}$ . In order to represent natural and continuous deformations between two trees with different topologies, the author defines the quotient space  $\tilde{X}$  where different representations of the same tree-shape are identified. In their definition, two tree representations are identical if the attributed trees are exactly the same after collapsing zero-attributed edges, Figure 1b. In other words, the quotient space  $\tilde{X}$  glues together all points in  $X$  that correspond to the same tree-shape.

They call the Euclidean distance in  $\tilde{X}$  as Quotient Euclidean Distance (QED). In this metric, the distance between two different trees is computed from the Euclidean norm of the difference between their points whereas the distance between identical trees is set to zero. The authors show that the geodesic path in this space is a sequence of Euclidean lines which are cut and concatenated after internal topological transitions, Figure 2a. According to the author, the QED based geodesic is suitable for tree registration and also statistics because it is well-behaved and proven to be unique in their previous work [2].

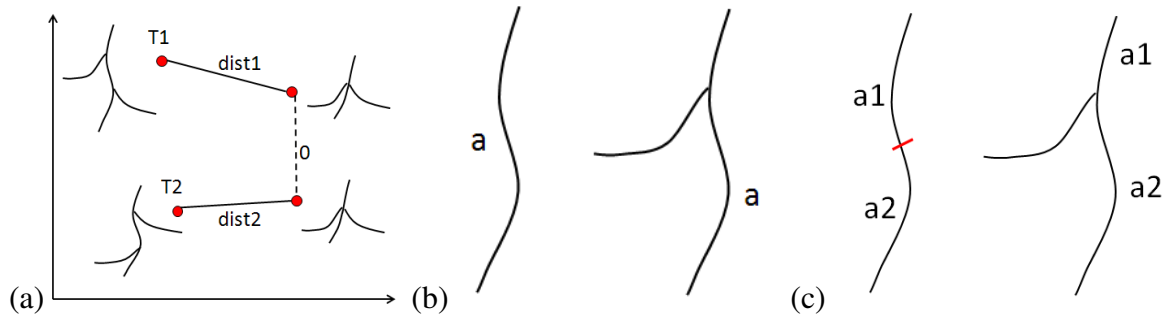


Figure 2: (a) QED path as concatenated Euclidean lines. (b) Missing secondary branch of the left tree causes the main branch of the right tree partially labeled. (c) My implementation using branch partitioning. The main branch of the right tree is fully labeled.

Since airways in this problem are 3D tree-shapes with unknown branch orders, the authors consider all possible branch orderings for the geodesic deformation which, however, increases the computational cost. They overcome this problem by fixing certain identified branches such as right main bronchus (RMB) and left main bronchus (LMB), and perform branch labeling in each of the lobar subtrees separately. Branch labeling is done by propagating labels along the geodesic path between a labeled and unlabeled tree. Their implementation for geodesic deformation lists all possible paths with internal topological changes and chooses the one with minimum distance cost. In order to reduce the complexity of the algorithm, the authors put an upper bound on the total number of internal topological changes along the geodesic path. However, true geodesics between trees with large variations can not be obtained with a limited number of topological changes. The authors address this problem to improve robustness by first labeling a tree from multiple trees in the training set and choosing the branch label has the majority vote.

For the experiments, they used airway trees with large topological variation which were extracted from EXACT'09 segmentation challenge datasets and labeled by a trained image analyst. Small noisy branches were pruned and the remaining branches were sampled with 6 landmark points where the landmark points were translated by aligning the first landmark point with the origin so that large branch differences in low generation do not affect the extent of their subtrees. Each airway tree was normalized by the length of LMB branch which was present and measurable in the training set. The trachea was left out and the fixed branches were detected based on their orientation and extent of their subtrees. The authors only considered branches down to 6-7 generation for labeling. Geodesic deformations were computed in the five lobar subtrees separately by only allowing for one internal topological transition. Each airway tree was matched to entire training set in a leave-one-out fashion and labels were assigned to each branch based on a voting scheme where branch labels with less than 55% consensus or less than 4 votes were not included in the results. Average labeling success rate was 83%.

The authors discuss that 83% success rate was high taking the large variation in the training

set into account and support their claim by presenting a plot showing the number of detected branches for each case. They also discuss that the comparison to other methods (with 97%,90% success rates) was not possible because of different datasets used.

## Critique

The authors state that when the large structural differences between the airway trees in the training set are taken into account, their success rate 83% can be considered high and the large variance in their results is expected. They present a plot showing the number of detected branches in each case. However, the authors do their experiments only down to 6th generation. So, it would be very supportive to show a plot for detected branches down to 6th generation in order to realize the large variation in the part of the airway trees which authors did actually run their method on.

In their problem statement, the authors emphasize that airway trees may have missing branches that can cause topological variations. However, they discard this important point while explaining their method. Their definition of “same tree-shape” does not account for missing branches.

Since the LMB branch was used to normalize each airway tree in the population, the authors should have commented on the variability of the LMB branch relative to the overall size of airway tree. In other words, is the size of LMB branch always linearly proportional to the size of airway tree? For example, a short LMB branch in a large airway tree should not be used for the normalization if a same sized or longer LMB branch exists in a smaller airway tree.

The authors showed the missing upper lobes of the airway subtree as a reason for very low success rate in CASE39. However, in their experiments, branches in each of the lobes were labeled separately. So, why does the missing upper lobes affect the labeling accuracy of other lobes? It is also not clear whether the fixed branches were included in the results or not, i.e., from correctly labeled branches, how many of them are fixed branches? As the main contribution of this paper is the novel unique geodesic metric, another table that only reports the results from each lobe could have been included to see the accuracy of labeling via geodesic deformation.

In addition, even though the authors discuss about the computational complexity of their QED method, they should have provided with some number on the runtime, i.e., does it take hours, days, weeks on a standard PC for allowing one, two, ... internal topological transition? They claim that this method is applicable to vascular structures, however only one internal topological change may not be enough to deform one vascular tree to another.

Finally, the authors do not compare their method to tree edit distance method (TED) which was previously applied to cerebral vessel matching [3]. The authors should have commented on possible differences in the results if TED was applied to the same problem. Because TED metric can be computed efficiently using dynamic programming approaches and would allow for more than one topological changes along the geodesic path.

In spite of the points that are mentioned above, the presented method is novel in the sense that it uses a geodesic tree metric that can account for both topology and branch geometry. The geodesic computed by this metric is also unique which makes it suitable for statistical analysis such as computing mean of a tree set and classifying trees. And the idea of determining branch labels through majority vote is simple but effective when there is structural noise in the training set. The presented method also allows for imposing additional continuous attributes other than only branch geometry such as airway radii. Finally, this paper gives a thorough explanation of the underlying novel tree-shape space to a broader community.

## Conclusion

The reviewed paper presents a novel method for automated labeling of airway branches. While the cases with missing branches and some validation aspects are not explained thoroughly, this method is an application of an unique geodesic metric which is a big contribution to the field. This paper could have been improved by several means. First, the authors could have demonstrated their method on an example where a branch is missing, Figure 2b. One way of dealing with missing branches could be to further divide airway branches into partitions and map them onto consecutive edges on the binary tree, Figure 2c. Second, success rates could have been included in the results table with and without counting fixed branches, and the method for detecting fixed branches could have been explained in more detail. Another improvement could be to support their statement of high variation in topology by showing a plot for detected branches only down to 6th generation instead of the whole airway tree. Finally, they could have explained what makes this method different than TED for branch labeling since TED is a well known method to compute geodesic paths between trees and was previously used for branch labeling.

In my project, there is a large variation in coronary tree topology due to the anatomical variability. This large variation as well as imaging related problems may cause some of the tiny but considerably long branches be missing in the data. Therefore, my QED metric implementation should be able to account for missing branches which will increase the computational time. However, the aligned coronary trees in my project lie on a 2D manifold and the branches are ordered unlike the airway problem in this reviewed paper. So, I can make use of this prior information about branch orderings to compensate for the computational overhead of handling missing branches. In addition, I can use the same idea of fixing branches and computing geodesic deformations in certain subtrees, e.g., by fixing left anterior descending (LAD) and circumflex (CX) branches and apply QED to the extent of their subtrees separately because LAD and CX subtrees exist in the entire training set. Similar to their method, I can consider pruning small branches and run the algorithm down to a certain tree depth.

One of the tasks of my project is to apply TED metric for coronary tree matching. As a future work after my project, I can apply my QED implementation to coronary tree matching and compare it to the TED results.

## References

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