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A Novel Multi-Purpose Tree and Path Matching Algorithm with Application to Airway Trees

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ABSTRACT

Tree matching methods have numerous applications in medical imaging, including registration, anatomical labeling, segmentation, and navigation of structures such as vessels and airway trees. Typical methods for tree matching rely on conventional graph matching techniques and therefore suffer potential limitations such as sensitivity to the accuracy of the extracted tree structures, as well as dependence on the initial alignment. We present a novel path-based tree matching framework independent of graph matching. It is based on a point-by-point feature comparison of complete paths rather than branch points, and consequently is relatively unaffected by spurious airways and/or missing branches. A matching matrix is used to enforce one-to-one matching. Moreover our method can reliably match irregular tree structures, resulting from imperfect segmentation and centerline extraction. Also reflecting the nature of these features, our method does not require a precise alignment or registration of tree structures. To test our method we used two thoracic CT scans from each of ten patients, with a median inter-scan interval of 3 months (range 0.5 to 10 months). The bronchial tree structure was automatically extracted from each scan and a ground truth of matching paths was established between each pair of tree structures. Overall 87% of 702 airway paths (average 35.1 per patient matched both ways) were correctly matched using this technique. Based on this success we also present preliminary results of airway-to-artery matching using our proposed methodology.

Keywords: pulmonary airways, pulmonary arteries, computed tomography, tree matching, path matching, chest CT.

1. INTRODUCTION

Tree matching algorithms can be important components of medical image processing applications. They can be used for the following purposes specifically for lung imaging:

1. Airway-Airway tree matching from imaging studies of the same patient taken at different times
2. Airway-Airway tree matching from different patients
3. Airway-Airway tree matching from one patient to an atlas in order to perform anatomic labeling
4. Artery-Artery matching from imaging studies of the same patient taken at different times
5. Artery-Artery matching from one patient to an atlas or another patient
6. Airway-Artery matching within a single image in order to determine the correspondence between the two tree structures or to assist in detecting additional airway or arteries
7. Matching of Veins to an atlas or to imaging studies of the same patient taken at different times.

Airway-Airway and Artery-Artery matching within the same patient at different times can provide an important basis for image registration and for automated quantitative analysis. For example, automatically measuring changes in bronchial wall thickness over time is possible once airway locations in sequential scans have been matched. Matching to an atlas eases several tasks for radiologists [1, 2]. Typically a radiologist's report identifies abnormalities using precise anatomic labeling: determining this important data could be automated with atlas matching. Matching with different patients

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allows for larger-scale comparisons of multiple patients' data. Airway-Artery matching within the same patients can be used for bronchoscopic navigation [3] or as a basis for improved artery [4] or airway segmentation.

Tree matching algorithms require a tree structure as input. This structure describes the tree as a series of branches interconnected through branch-points. It can be obtained by several different methods including tracking, segmentation, and skeletonization [5]. Once the tree structure is obtained, the matching algorithm operates directly on the structure and any data contained within it. Any non-looping tree structures, such as airways, arteries, and veins, contain an inherent hierarchy of parent and child branches. In fact, a tree structure can be viewed as a directed and branching graph.

There are several approaches to matching Airway-to-Airway trees from the same patient [6, 7] or automated anatomical labeling of the bronchial tree [1, 2]. Recent algorithms generally combine a set of features within the bifurcation points [6, 7, 8, 9], and use a general graph matching algorithm such as finding a maximal clique in an association graph [2, 10], or graph matching by relaxation of fuzzy assignments [11].

These previous tree matching algorithms rely on graph matching techniques and tend to focus on a single application. They exploit the hierarchical structure of the tree to match at a branch-to-branch level. Although graph matching techniques have a firm theoretical background, they may not be the best choice for real-world medical applications where false or missing branches, loops, and differences and changes in anatomy can occur. Since these methods reduce the tree structure into a series of nodes with features compressed from the branch data, false branches can severely reduce the effectiveness of these methods. In addition, some of these methods require a matched starting point of the tree structure, making them ineffective in cases where this information is not available. Depending on the features used, these methods also necessitate a preliminary registration of the two trees for acceptable results. Due to these limitations, these previous methods may require that the tree structures must first be manually generated or edited.

We present a robust tree matching framework that does not rely on graph matching and hence avoids the disadvantages of previous approaches. Our algorithm is robust to false or missing branches and supports irregular tree structures, such as branches with multiple parents or even loops, which are caused by imperfect segmentation and centerline extraction. In addition, our method demonstrates robustness to poorly aligned tree structures. We demonstrate our method with bronchial trees obtained from chest CT scans of the same patient obtained at two time-points.

2. METHODS

The general framework of the proposed method involves comparing a single path derived from one tree structure to another path in a second tree structure. This comparison results in a numeric value, based on features describing the similarity of the two paths. Paths with lower matching values are considered of higher matching probability. The following sections explain the method in more detail.

2.1 Tree Structure

For sake of completeness, we first describe the tree structure itself. A tree T is a collection of doubly linked, directed branches $B = (S_B, P_B, C_B)$ which contains a set of equidistant sites S_B , links to its parents P_B (normally one in airways and arteries), and links to its children C_B (normally two or more in airways or arteries). A branch with no parents, $P_B = 0$, is defined as the *root branch* while branches without any children $C_B = 0$ are defined as *terminal branches*. A set of sites S_B is a vector of ordered, equidistant 3-D coordinates with the first site defined as a *start site* and the last one defined as a *terminal site* of S_B . Note that the tree contains an inherent hierarchy since a branch is always considered to be a child or a parent. Hence, assuming no loops, each branch belongs to a certain generation number.

A *path* p is a series of sites obtained by the combination of one or more directly linked non-repeating branches starting at any site within the first branch and ending at any site of the last involved branch. A *complete path* is defined as a path starting at the root site of the root branch and ending at the terminal site of any terminal branch. Hence, because of this hierarchy, any complete path will always contain the root branch. Note that paths are structures without hierarchical information, i.e. all notions of parent and children branches are eliminated and we are left with a series of sites.

Such tree structures may be obtained from arteries, vessels, or airways. Various methods exist to obtain such structures [5, 6, 7]. This final tree structure may contain false branches, missing branches, and/or unwanted loops. Note that in our definition of complete paths, even if derived from a tree structure with loops, no loops are possible in a complete path. Complete paths from each tree structure are obtained and compared to each other using features to determine a match.

2.2 Features

Features are functions used to obtain a numeric value describing the similarity between two paths. They do not always satisfy all of the properties of a metric, hence the similarity from path a to path b may not be equal to the similarity from path b to path a (commutative property). Therefore, the matching has an associated directionality in which different results may be obtained depending on which path is chosen first. Due to this fact, we refer to the first tree as the original tree, and the second tree as the comparison tree.

We describe three different similarity features to compare the two paths: *Distance*, *Angle*, and *Variance*. The Distance feature depends on the offset between the paths, the Angle feature depends on the differences in path directions, and the Variance feature depends on the variance of the offset between the paths. Other features are possible within this framework. Although the choice of the optimal features depends on the application, these three features work well in the general case. The following paragraphs describe the features in detail. In this description, we refer to the path from the original tree as p and a specific site in that path as p_i . We then refer to the path in the comparison tree as q .

The **Distance feature** describes the mean squared distance between the two paths. It is calculated by summarization of the squared distance between each site of the original path and its closest site within the comparison path. Afterwards this sum is divided by the number of sites of the original path. Since all sites of each branch are equidistant from each other, the number of sites is proportional to the length of the path.

$$d = \frac{1}{i_{\max}} \sum_i (p_i - C(p_i | q))^2 \quad (1)$$

with p_i = site i of the original path and $C(p_i | q)$ = closest site to p_i within the path q of the comparison tree, and i_{\max} is the total number of sites in p .

The **Angle feature** estimates the mean difference of the directions of the two paths. Since a straight line representation of the branches is not used, each site has a direction or heading. The difference between the direction of the tangent at each site of the original path and the direction at the closest site of the comparison path is computed. The sum of the differences for all sites is then divided by the number of points of the original path.

$$a = \frac{1}{i_{\max}} \sum_i \angle(\vec{p}_i, \overline{C(p_i | q)}) \quad (2)$$

with \vec{p}_i = direction at site i of the original path and $\overline{C(p_i | q)}$ = direction of the site closest to p_i in path q .

The **Distance Variance feature** is the variance over the distance feature described earlier.

$$v = \frac{1}{i_{\max}} \sum_i [(p_i - C(p_i | q))^2 - d]^2 \quad (3)$$

with p_i = site i of the original path and $C(p_i | q)$ = closest site of p_i in path q of the comparison tree and d is the mean squared distance.

Applying all three features in a comparison yields a distance vector with respect to the original path. To convert a vector into one single value we chose a simple combination method that we call the **Normed combination**, which takes into account the variability of each component. Components with high variability receive less weight than components with low variability. This is obtained by rescaling each component by its variance. So the norm of the distance vector \underline{x} equals:

$$d = \|\underline{x}\|_N = \sqrt{\left(\frac{x_1}{\sigma_1}\right)^2 + \left(\frac{x_2}{\sigma_2}\right)^2 + \dots + \left(\frac{x_n}{\sigma_n}\right)^2} = \sqrt{\underline{x}^t \cdot \underline{V}^{-1} \cdot \underline{x}} \quad (4)$$

where \underline{V} is the diagonal matrix of the variances of the features. \underline{V} is obtained by calculating the variances of each feature over all possible combinations of complete paths within the current pair of trees. In cases where only two paths are compared without considering any further paths, the variances are set to one, which results in a simple **Euclidean combination**. If the variance of a feature equals zero, which means it is constant over all combinations, it is useless for matching purposes, and is excluded from the combination calculation. As a result each complete path of the comparison tree can have a similarity measure to each complete path of the original tree. This similarity measure is used as a basis for the matching framework.

2.3 Complete Tree Matching and Additional Constraints

Simply selecting the minimal similarity measure between two paths as a match results in the potential for many-to-one matching. To match complete trees, existing matching results of the other paths are considered in addition to the minimal similarity measure. A *matching matrix* enforces one-to-one matching within the framework. This matrix consists of all possible paths of the first tree listed in the rows, while all possible paths of the second tree are listed in the columns. Each entry in the matrix contains the similarity measure between two paths. By iteratively selecting the absolute minimal measure, labeling the involved paths as matched, and disregarding these for further matching, a strict one-to-one match constraint is enforced. In the event of equal minimal similarity measures, one is chosen at random. Another possibility to be explored is to select the path with the greater second-lowest measure instead.

Since the original path may have no equivalent in the comparison tree, this strict one-to-one matching may end up in a chain of false labeling if an early match is done incorrectly. To avoid this situation the evaluation of the matching matrix is assisted by a probability matrix, which provides the possibility for many-to-one matching in cases where one-to-one matching is impractical. As a result, previously matched paths are available for future matches. In case the best matching path is already matched, the next best non-matched path with a measurement within tolerance becomes a higher probability than the best match. In case there are no further paths found which fulfill these requirements, a path already matched is labeled as the best match and the probability of this match and the existing matches of this path are decreased by the number of assigned matches.

A tolerance of 0% results in a many-to-one mapping, similar to using no matching matrix and to select for each path within the original tree the one path of the comparison tree with the minimal similarity measurement as the best match. Only in the case of more than one minimal similarity measurement, with exactly the same value for one path of the original tree, prior matches would be used to elect one of these possible best matches, by giving already matched path less attention. A tolerance level of 100% results in the strict one-to-one matching as is the case without the probability matrix. By using the matching matrix, a sort of hierarchy is imposed, by preventing certain matches from being allowed given the score of a previous match. These matrices are one of the ways constraints can be enforced within this framework. Further possibilities are discussed in Section 4.

2.4 Application to Airway Trees

The method introduced above was applied to match airway trees obtained from sequential CT acquisitions. In order to obtain the airway tree model, the airway was first segmented with the tree model subsequently computed from the segmentations. This is described in detail in [5] with an example result shown in Figure 1.

Given the two airway tree models, alignment is done using a simple method. First, the trachea is located by iterating through the first hierarchical levels of the tree and looking for a bifurcation which divides the number of all descendant branches roughly by two and where additionally the number of descendant branches of each child equals roughly half of the total branches of the tree. This bifurcation separates the last branch of the trachea from its children, the left and right main bronchus.

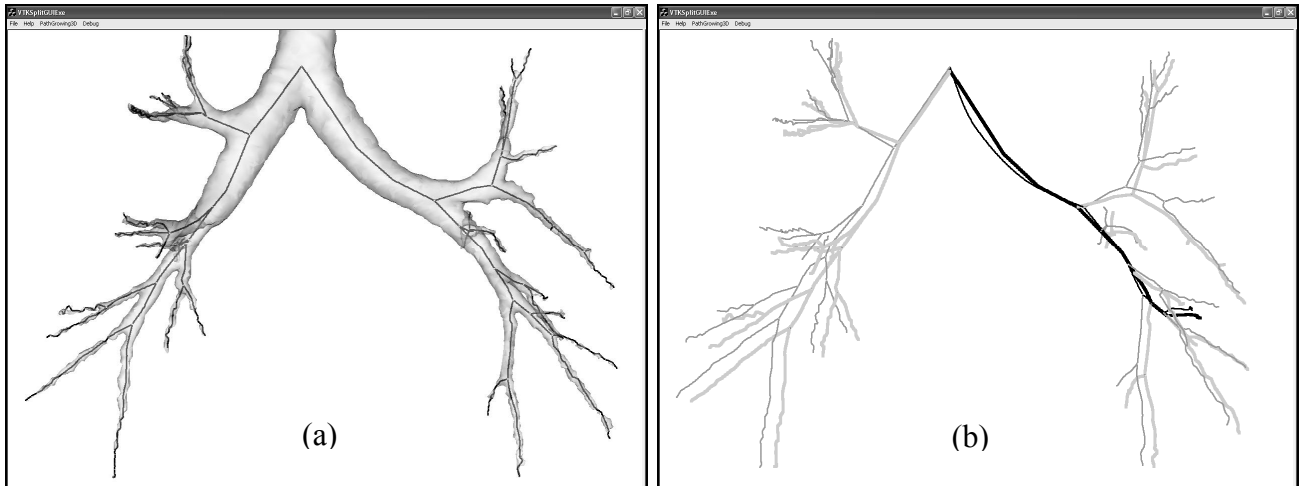


Figure 1: An airway tree matching example. Image (a) shows the segmentation and tree structure of the lung with 36 complete paths containing 69 branches. Image (b) shows two tree structure captured within three month differences and aligned by the simple shifting algorithm. A path is marked in gray and its matched path is highlighted in bold black. The trachea was excluded from the matching since it provides no additional information for the matching method due to the fact that it is part of every path.

After repeating this step for the left and right sub-tree the bifurcation between the right main bronchus and the right upper lobar and intermediate bronchus, and between the left main bronchus and the left upper lobar and lower lobar bronchus were reliably located.

Second, based on these three landmarks the offset between both datasets are calculated by taking the mean of the three individual offsets. Of course, rotational differences or differences caused by different breathing levels cannot be adjusted by this simple alignment, but we will show that even without sophisticated alignment our method will achieve good results. However some of the features, such as angle and variation, are more independent of path location, which opens the possibility to perform a matching without further or even without any alignment whatsoever.

3. RESULTS

We demonstrate that our proposed method for airway tree matching yields excellent results. In addition, initial positive or encouraging results are shown for airway-to-artery matching.

We applied our method to perform an intra-subject matching of the bronchial airways of 10 patients. Two CT images from each patient were obtained by a 4-slice multi-slice CT scanner (Siemens Volume Zoom, Siemens Medical) using slice thicknesses of either 1mm or 1.25mm, and between 15-mAs and 120-mAs with an average of 56.6-mAs. The median inter-scan interval was 11 months, with a range of 3.2 to 17 months. Segmentation and tree capturing was fully automated with a method similar to the one described in [5].

After simple alignment of tree structures, matching was initiated at the first bifurcation. Although beginning at the carina is not mandatory, it helps avoid repeated comparisons of the trachea thereby increasing speed. In addition, it eliminates the influence of the trachea over shorter portions of the path. Matching was performed as described in Section 2 on a path by path basis. The resulting similarity measurements were stored in the matching matrix, with the best matches finally chosen using the probabilistic approach.

Since both the original and comparison trees are generated without any user interaction, both trees include false positive as well as missing branches. Each false branch in the original tree and each missing counterpart branch in the comparison tree creates an unmatchable path: since by definition they cannot be matched, they are labeled as “N/A” (Not Applicable) in Figure 2.

Beside differences regarding the number of branches, the datasets also show differences in depths of respiration since studies were performed without spirometry to guarantee reproducible levels of inspiration. Therefore, one airway tree might include more peripheral branches than others due to the segmentation method's better performance with increased inspiration. As our matching algorithm is based on features not satisfying the properties of a metric, results cannot be completely independent of the matching direction, i.e. one tree is considered the original tree while the other is the comparison tree. To provide validation results which are independent of the comparison direction we applied our method in both directions so that both trees have a chance of being the original tree. The matching results have been compared to a ground truth, and the validation results in both directions have been combined by calculating the mean classification rates.

The overall results of all 10 patients, matched in both directions, using the matching matrix with a tolerance of 7.5% are shown in Figure 2 and Table 1. There were a total of 702 paths compared over the 10 patients, with an average of 35.1 paths per airway tree. The matching was applied using each of three proposed features *Distance*, *Angle*, and (*Distance*) *Variance* as well as various combinations of these features. A Euclidean combination of two or more features is labeled with the first character of the involved features [D, V, A] and the ending "*Euc*", while the Normed combination has the ending "*Norm*".

Depending on the features chosen, between 61% and 71% of all paths were correctly matched, corresponding to a correct classification rate of 74% to 87% after excluding unmatchable paths. The angle feature and the variance-angle-normed combination provided the best results with an average 25.0 out of 28.7 paths per patient correctly matched. In additional an average of 6.4 paths per patient had no match due to differences in the extracted tree structures.

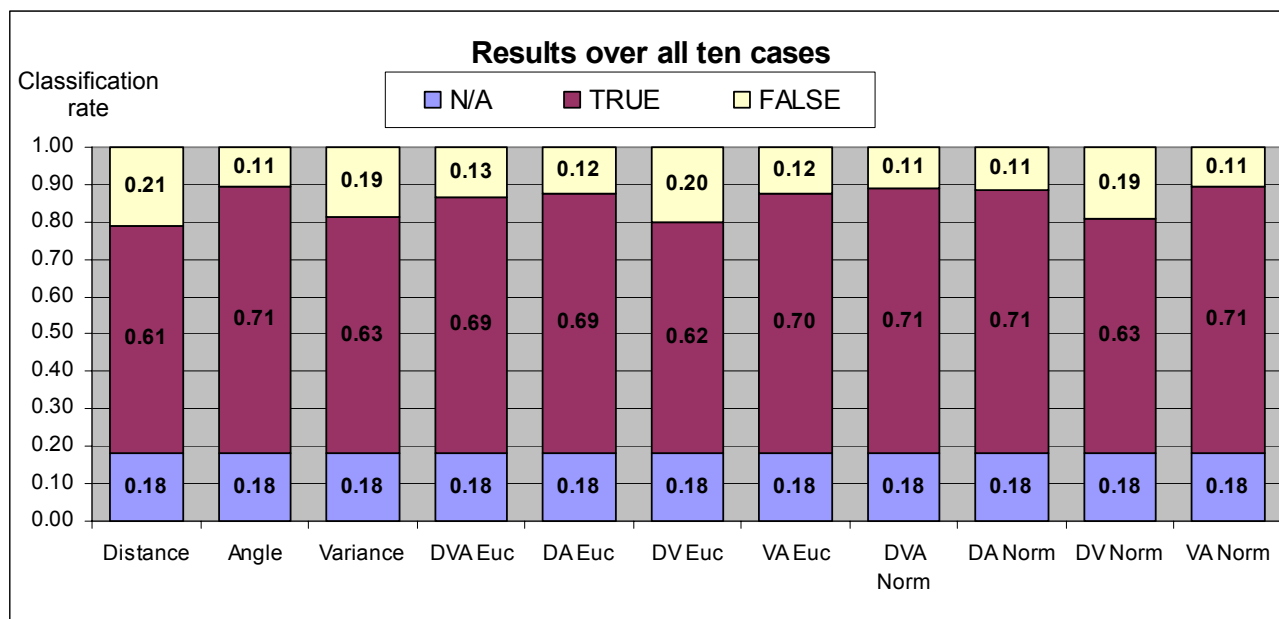


Figure 2: Matching results using the *Distance*, *Angle*, and *Variance* features alone and all possible variations using the described *Normed* and *Euclidean* combinations. The Euclidean combination of the *Distance* and *Angle* features is labeled as "*DAEuc*", while a *Normed* combination of the *Variance* and *Angle* features is labeled as "*VANorm*". The remaining labels follow similarly. Each bar represents all possible paths of the original tree and is divided into regions of correct (true), incorrect (false), and not matchable (N/A) paths.

	<i>MEAN TRUE</i>	<i>MEAN FALSE</i>	<i>VAR TRUE</i>	<i>MIN TRUE</i>	<i>MAX TRUE</i>
<i>Distance</i>	0.74	0.26	0.029	0.42	0.97
<i>Angle</i>	0.87	0.13	0.011	0.57	1.00
<i>Variance</i>	0.77	0.23	0.026	0.45	0.97
<i>DVA Euc</i>	0.84	0.16	0.022	0.45	1.00
<i>DA Euc</i>	0.85	0.15	0.019	0.55	1.00
<i>DV Euc</i>	0.75	0.25	0.029	0.41	0.97
<i>VA Euc</i>	0.85	0.15	0.022	0.48	1.00
<i>DVA Norm</i>	0.87	0.13	0.013	0.57	1.00
<i>DA Norm</i>	0.86	0.14	0.013	0.57	1.00
<i>DV Norm</i>	0.77	0.23	0.025	0.45	0.97
<i>VA Norm</i>	0.87	0.13	0.011	0.65	1.00
	Best results			Worst results	

Table 1: Table of the path matching results for the proposed features and their possible combinations. Unmatchable paths, paths which do not have a counterpart in the equivalent tree structure, caused by false or missing branches, are excluded from these statistics. The mean correct (MEAN TRUE) and the mean false classification rate (MEAN FALSE) are listed for each feature/combination as well as the variance of the correct classification (VAR TRUE) and the minimal/maximal correct classification rate (MIN/MAX TRUE). The results which symbolize the best performance are highlighted in white font with black background, while the worst results are marked by a gray background.

The reason the angle feature provided similar results to a combination of features is due to its greater insensitivity to tree mis-alignments. Since a simple registration method was used for alignment, half of the included datasets had rotational or breathing differences. The superiority of the angle feature in these cases is shown in Figure 3, which divides the ten cases into two subgroups with each 5 cases. The first group (Figure 3a) includes cases where proper alignment was achieved and the second group (Figure 3b) contains poorly aligned cases. The reduced dependency on alignment is reflected in a correct classification rate of 65% of all paths within the second group when using the angle feature, while distance and variance features only achieve results between 48 and 52%. In the properly aligned cases however, all features and their combination provide similar results with correct classifications between 73% and 80% of all paths, or 88% to 95% after excluding unmatchable paths.

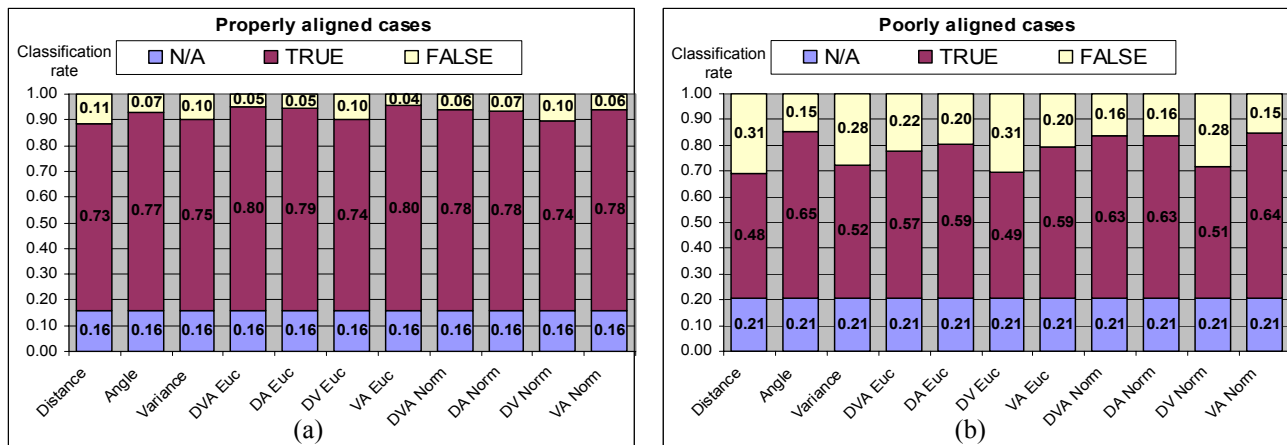


Figure 3: Graphs of matching results with a tolerance level of 7.5% divided by alignment of trees. Graph (a) summarizes the performance of the features and their combination in these five cases where the simple shifting algorithm already achieved a proper alignment, whereas Graph (b) summarizes the remaining five cases where this algorithm was insufficient to provide proper alignment.

The best and worst match statistics shown in Table 1 provide insight into the performance of the features. As shown in the “max true” column, the best datasets provide a correct classification rate of 100% with almost every feature combination. However the “min true” column shows that certain features are more robust for difficult datasets, with individual features giving results between 41 and 65%. Especially remarkable is the variance-angle-normed combination with a ten percent point superior correct classification to all other features/combinations.

The tolerance parameter of the matching matrix was set to 7.5%. Hence, in the event that the best matching result was already matched, only further paths with similarity value not more than 7.5% higher than the value of the best match are taken into account. This specific value was chosen on the basis of empiric examinations. However, the tolerance setting does not heavily influence the results. Experiments with different tolerance level between 0 and 15% showed only a small impact on the mean correct classification rate. Compared to a 0% tolerance, a setting of 7.5% increases the mean correct classification, disregarding unmatchable branches, by about 2 percentage points. Changing the tolerance from 0 to 7.5% increased the minimum correct by 10 percentage points.

Note that in many cases where a path was scored as falsely matched, most of the length was actually correctly matched, since we do not match on the level of single branches. On average, false path matches were correctly matched in over 62% of their length when using a normed angle-variance combination. In other words, in each falsely matched path with a mean length of 5.2 branches, only 1.3 branches were incorrectly matched to one or more branches in the comparison tree on average. To summarize all false classifications the first (so far as the highest hierarchal level is concerned) effective falsely matched branch was located in the 4th generation level, while the trachea was labeled as the 1st level. In 89% of all false classifications however at least the first four generations, and moreover in 39% at least the first five generations were correctly matched.

Finally, in Figure 4 we present preliminary results of the proposed method in the application of matching airway to arterial paths. The automatically extracted airway tree is rendered in thick lines whereas the automatically extracted arterial tree is indicated by thin lines. In this example a starting site, shown by the arrow, is chosen within the bronchial tree. A path from that point to the terminal branch is automatically computed and marked in bold black. Next, vessels near the start site are automatically segmented and captured into a tree structure by selecting a random root site within the vessel segmentation close to the start site. Finally the selected airway path is compared to all complete paths within the vessel tree. The best match of a vessel path to the chosen airway path is indicated by the thin black line.

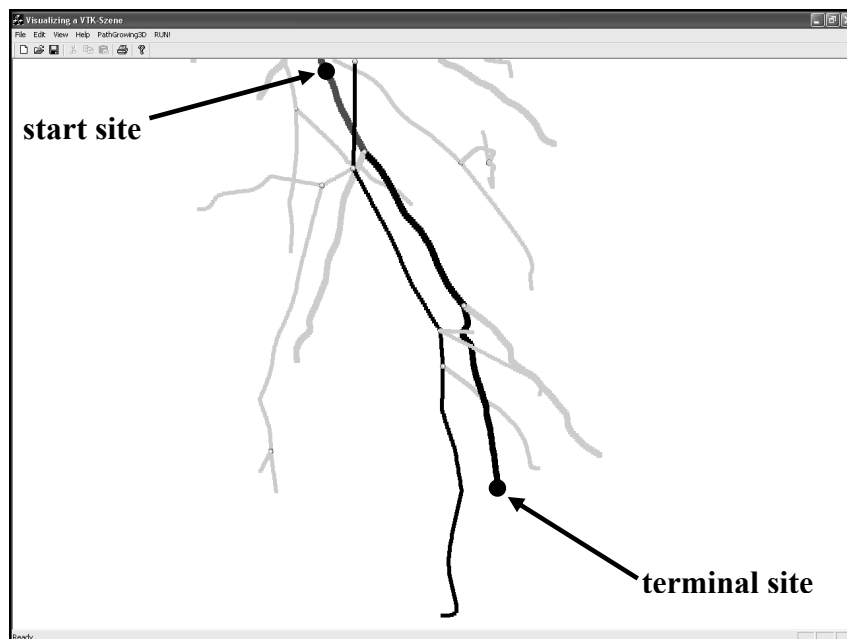


Figure 4: Airway-to-artery matching. The matching airway and arterial path are both shown in black. The root site for the airway path was manually selected. The arterial tree in the region was computed automatically.

4. CONCLUSIONS AND FUTURE WORK

We present a novel tree-matching algorithm and framework that is applicable to a wide variety of tree-matching problems. Existing methods rely on graph matching techniques, which have stricter requirements and are more easily hampered by false branches. Our proposed framework allows the flexibility of using root branches at different portions of the tree while still yielding successful matches. Our method also allows for the possibility of two branches in one tree matching to a single branch in a comparison tree to obviate the problem of a false middle branch. Such potentialities are difficult to realize using a standard node-based matching method.

Although the angle feature alone provides us with the same mean classification rate as the angle-variance-normed combination, the combination of features offers better performance in the worst cases, as shown in Table 1. The distance feature and its combination with other features are heavily influenced by alignment of the two trees. Although this eliminates it from being used in cases where proper alignment is not possible or too costly, it is still valuable as a first estimate of similarity due to its low computational cost. On this basis, computation of more time-consuming similarity values could be reserved for only those cases where a match is more likely.

We propose several ideas for improving our method including: a discussion of ideas involving features followed by changes in the method itself by adding the concept of hierarchy, and ending with a consideration of means of optimization. Regarding features of two paths being matched, it is possible to determine transforms between the two curved 3D lines to determine a similarity measure as well. Features such as curvature and any other measure derived from a function of a series points can be used. For example, a high-order polynomial can be fit to the path and its equation can be used for comparison. Features less sensitive or immutable to affine transformations are necessary to completely avoid any alignment requirements. However, such features would most likely require additional constraints since they allow for many possible matches. For example, they may allow matching of airway paths in the left lung to those in the right lung. Adding further constraints through the matching and probability matrices or through hierarchy is a way to avoid this problem.

The matching matrix, used to enforce one to one matching, increased performance in the worst cases, but did not significantly increase the mean classification rates. However there are other possibilities for using previous matching results to increase performance. Hierarchical constraints can be imposed by determining branch correspondences within matched paths. Hence, a branch-to-branch matching can be derived from the results. One possibility is to create *match votes* for each branch or series of points that are matched via the matched paths. Branches that are matched more often by paths receive more votes. These votes provide confidence level between possible branch matches, allowing for the matching of branches. They can also be used to influence further processing steps by introducing hierarchy constraints.

Two branches that are matched with high confidence can dictate that all other possible paths containing these branches must match at their sites. Also, once branches are matched, a recursive process is possible such that the ends of the matched branches function as root sites for the procedure repeated again. This recursive method allows for the use of the hierarchical constraints while at the same avoiding the disadvantages of graph-matching based methods.

Finally, although classical graph matching may be innately faster than the framework we present for tree matching, there are several methods for possible further optimizations. For example distant or very unlikely matched paths can be easily identified, e.g. by using the distance feature as already mentioned, to avoid more costly comparison steps. Beyond this, the hierarchy constraints can also predict which paths should not be compared. In addition, for applications requiring only matches of a single path (as in bronchoscopy planning), the method can easily outperform graph-matching approaches since the entire tree matching process need not be performed.

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