

Tree-like Shapes Distance Using the Elastic Shape Analysis Framework

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The analysis and comparison of tree-like shapes is of great importance since many structures in nature can be described by them. In the field of biomedical imaging, trees have been used to describe structures such as neurons, blood vessels and lung airways. Since it is known that their morphology provides information on their functioning and allows the characterization of pathological states, it is of paramount importance to develop methods to analyze their shape and to quantify differences in structures. At present, there are a number of methods for the comparison of trees. Some only take into account the topology of the trees (such as [1], [2]), while others consider both topological and geometrical information (such as [3], [4]).

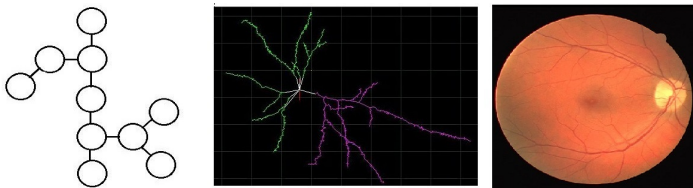


Figure 1: Diagram of a rooted tree (left) and examples of tree-like structure found in nature: neuron (middle) and blood vessels (right). Taken from <http://neuromorpho.org/> and <http://www.isi.uu.nl/Research/Databases/DRIVE/>

In this paper, we present a new method for comparing tree-like shapes that takes into account both topological and geometrical information. It is based on the Elastic Shape Analysis Framework, a framework originally designed for comparing shapes of 3D closed curves in Euclidean spaces [5]. The idea behind this approach is the following. A 3D open curve is parameterized in a special way called SRVF (squared root velocity function). The set of all the SRVF parameterized curves in \mathbb{R}^3 defines a manifold called the preshape space. In order to only compare the shape of the curves, all shape preserving transformations are removed from the representation (translation, rotation, scale and parametrization). This forms a quotient space of the original manifold called the shape space. This framework was later extended to include additional information in the shape analysis. This is achieved by including an additional function $\beta_C : [0, 1] \rightarrow \mathbb{R}^k$ (where k is an arbitrary dimension) to the original representation of the curve. The two components are combined to form a new curve in \mathbb{R}^{3+k} . Finally, one can define geodesics in the resulting space that can later be used to define distances and to compute averages of sets of curves.

In this paper we extend the Elastic Shape framework to define a metric between trees. We consider two trees T_1 and T_2 , each consisting of a main curve and several branches (and possibly sub branches). All are represented by 3D open curves in \mathbb{R}^3 .

A matching function that assigns the branches of one tree to the other is defined, along with a branch function C which indicates, for a given point on curve β , how many branches remain after it. We only take into account branches which have a match in the other tree. Finally, we define the distance between two trees T_1, T_2 as:

$$D(T_1, T_2) = \min_M [d((\beta_1(t), C_1(t, M)), (\beta_2(t), C_2(t, M))) + \sum_{(i,j)} \alpha_{i,j} M(i, j) D(T_1(i), T_2(j))] \quad (1)$$

where β_k is the main curve of tree k , C_k its branch function, M the matching function, $\alpha_{i,j}$ a weight parameter and $D(T_1(i), T_2(j))$ the distance between the matched branches (sub trees) of the two trees.

The first term of the distance definition embeds some geometrical information on the main branch by matching segments between branching points. Topological information is taken into account through the C function. Sub branches are taken into account in a recursive way in the second

term. Note that the coefficients weight the different order of sub branches with respect to the main branch. Moreover, $\alpha_{i,j}$ controls how non matched branches ($M(i, 0) = 1$ or $M(0, j) = 1$) are penalized. Typically, $\alpha_{i,j}$ equals a_1 if $i \neq 0, j \neq 0$ and it equals a_2 otherwise.

The formulation for the distance between the two main curves, two matched branches and unmatched branches is described in the paper.

As a first application, we used our method for the comparison of axon morphology. We have labeled single neurons within intact adult *Drosophila* fly brains and have acquired 3D fluorescent confocal microscopy images of their axonal trees. Both normal neurons and neurons in which a gene related to neurological diseases in humans was inactivated have been imaged (20 normal and 24 mutant). Each 3D image contains a single axonal tree that was manually segmented by an experienced biologist (see Figure 2) and the result converted to 3D open curves in \mathbb{R}^3 .

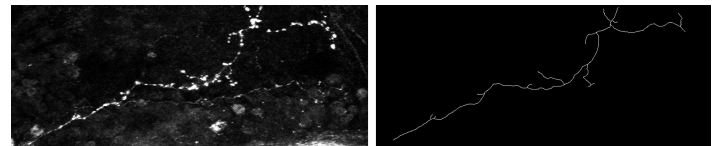


Figure 2: Original confocal microscopy image of a normal axonal tree (left) and its manual tracing (right) (maximum intensity projections).

For the validation of our method we have compared our results with the ones obtained by RTED [6], an efficient solution for the tree edit distance problem. We have calculated inter and intra class distances between normal and mutant populations and implemented a basic classification scheme. Results showed that the proposed method better distinguishes between the two populations than a pure topological metric.

Furthermore, our method allows us to compute mean shapes between two axonal trees by taking the middle point along the geodesic between the two trees (Figure 3). This is something that TED and other methods are unable to do. This will allow us to derive more complex classification scheme such as the K-means algorithm.

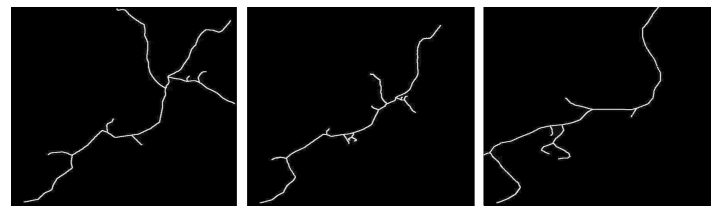


Figure 3: Two axonal trees (left and right) and their mean shape (middle) (2D projections).

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