

VarVis: Visualizing Anatomical Variation in Branching Structures

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Abstract

Anatomical variations are naturally-occurring deviations from typical human anatomy. While these variations are considered normal and non-pathological, they are still of interest in clinical practice for medical specialists such as radiologists and transplantation surgeons. The complex variations in branching structures, for instance in arteries or nerves, are currently visualized side-by-side in illustrations or expressed using plain text in medical publications.

In this work, we present a novel way of visualizing anatomical variations in complex branching structures for educational purposes: VarVis. VarVis consists of several linked views that reveal global and local similarities and differences in the variations. We propose a novel graph representation to provide an overview of the topological changes. Our solution involves a topological similarity measure, which allows the user to select variations at a global level based on their degree of similarity. After a selection is made, local topological differences can be interactively explored using illustrations and topology graphs. We also incorporate additional information regarding the probability of the various cases. Our solution has several advantages over traditional approaches, which we demonstrate in an evaluation.

Categories and Subject Descriptors (according to ACM CCS): 1.3.8 [Computer Graphics]: Applications—

1. Introduction

Anatomical variations are natural variations in anatomy, which are considered normal and non-pathological. For bones and organs, they consist mainly of geometric differences in size and shape, but branching structures, such as the vascular and nervous system, exhibit more complex differences and include changes in topology. Among these structures, veins vary the most, while nerves are the least variable [MDA*13]. Prominent examples of complex variations are missing structures, extra structures, different connectivity patterns, or different relations to surrounding structures. First introduced by Vesalius in *Humani Corporis Fabrica* (1542), variations are still clinically relevant today [SVP03]. Knowledge of occurrence frequencies is essential in order to correctly diagnose and safely treat patients [WH99]. Understanding vascular variations is important for many interventional procedures and, thus, for radiologists, vascular surgeons, transplantation surgeons, but also neurosurgeons who perform surgeries on aneurysms and malformations in the brain. For example, in hepatic transplant surgery, preoperative knowledge of vascular and biliary anatomical variations is mandatory for surgical planning. It helps reduce post-operative complications for both the organ donor and the recipient [CSU*08]. After initial discussions with collaborating domain experts, we elicited aspects of interest in an educational setting. Relevant knowledge includes the types of variations, their frequency, similarity, and major differences. The current way of presenting knowledge on variations is based on textual information or depiction. The first requires the reader to construct a mental model of the exact variations, which can be challenging. The second often relies on simplified illustrations exemplifying different variations side by side, including the probability percentages of encountering these variations (See Figure 1). In this case, it is difficult to

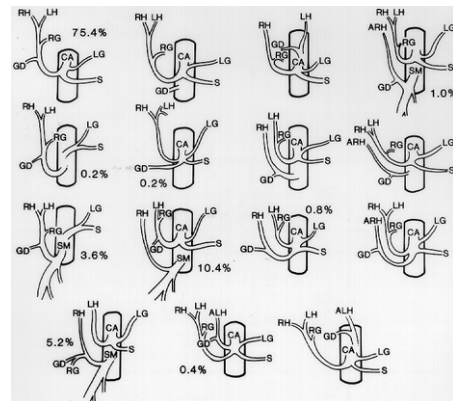


Figure 1: Gastroduodenal artery variation illustrations [DA47].

visualize the complete range of variations when many possibilities exist, as it leads to a significant visual overload. Further, complex anatomical structures result in difficult to interpret illustrations and sequential search is needed to identify differences or similarities between variations. Currently, similarity and dissimilarity between variations is not emphasized. While comparing two variations is already difficult, investigating groups or trying to identify probabilities for common structures is very challenging. Further, the links between topological changes are often hard to detect and too manifold to organize easily in an illustration.

We propose an interactive visualization application for anatomical variations, called VarVis, which allows the user to compare and explore variations of branching structures interactively at a global as well as local level. We use the original anatomical illustrations

as input for our system and enhance these illustrations to facilitate their analysis and understanding. Using our application, users can gain insight into existing variations and their differences and similarities. Specifically, our contributions are: 1) Interactive visualization of the variations and the differences between them. To this extent, we make use of graph representations to which we apply a topology similarity measure to identify the degree of difference. 2) An interactive prototype application to explore and identify local similarities and differences via various linked interactive illustrations.

2. Related Work

To the best of our knowledge, there is no prior work in developing interactive tools to explore anatomical variations in branching structures. Morphological organ variations, however, were represented and visualized in the context of the VOXEL-MAN project [HH06, HH09]. The prior art closest to our work was presented by Al-Awami et al [AABS*14]. In their NeuroLines work, they successfully apply a subway metaphor to visualize complex neuronal connectivity data. They focus on scalable interactive visualizations for large data sets, but do not attempt to summarize topological variations, nor establish relationships between variations. Kruszynski et al. [FKP*10, KKL07, KvLK06] applied graph representations in biology in order to quantitatively compare coral colonies, using morphological measures to quantify the variation based on skeletonized CT-scans of corals. The output of their approach is a statistical distribution of the morphological features visualized in histograms. None of these methods provide a way to locally compare topological variations. Crippa et al. [CMLR11] used graph averaging to compare multichannel EEG coherence networks quantitatively by computing the distance to an application-specific mean graph. Perez et al. [PHS*02] measured and quantified geometric and topological properties of vascular trees in fundus images of the human eye. Unfortunately, these quantitative measures do not help the anatomical understanding of the topological differences or similarities between the graphs.

In order to identify corresponding local variations, we require a special form of graph matching. Exact graph matching is an NP-hard problem [ZDIT13], but heuristic approaches have been proposed such as inexact graph matching [BA83]. In his survey on tree matching, Bille [Bil05] describes methods for comparing labeled trees and discusses the concept of a tree edit distance, based on simple local operations of deleting, inserting and relabeling nodes. Closely related to graph matching is graph averaging, or finding the mean of a set of graphs. For this, the concept of a graph edit distance is used, which can be defined as the number of operations needed to turn one graph into another. Bunke and Kandel [BG01, BK00] describe the mean of a pair of graphs as a graph that minimizes the sum of graph edit distances between them. Jiang et al. [JMB01] propose the concept of a median graph among a set of graphs, which minimizes the graph edit distances to the whole set of graphs. For our specific local anatomical variation visualization, we are looking for an algorithm that can guarantee anatomical correctness and match corresponding nodes and edges from different trees. The previous work in graph matching does not consider anatomical information, and does not preserve its correctness. The concept of a graph edit distance, however, is a good candidate for a similarity measure and to define the distance between graphs for a global overview of the variations.

3. VarVis

VarVis builds upon illustrations of variations. From these, we create graphs by manually defining nodes for every endpoint and junction

and encode connectivity by placing edges between these nodes. In our context, the resulting structure will form a cycle-free tree. Vascular structures always exhibit a source (main vessel) that is branching to reach specific regions. We assume that each endpoint of the graph will be feeding one specific organ or region, except for the source, which we make the root node of the tree. In this way, an endpoint correspondence between different trees is established. Finally, we make the tree edges directed going from the endpoint nodes towards the root node. The resulting tree encodes vessel connectivity and the topological branching. To facilitate the matching process, we store labels in every node, which indicate the endpoints they feed, e.g., indicating the organs that are provided with a blood supply by arteries.

Our system offers various views for variation comparison. First, we discuss the global view, which allows selection of variations based on global similarities to explore the types of variations and their frequencies. Afterwards, we discuss the local view, which can highlight local similarities and differences in individual variations. To this extent, a tree matching algorithm, interactive enhancement of the illustrations and tree visualization are discussed.

Global view: To help the user determine which anatomical-variation trees are similar, and which are different, we create a topology similarity weighted graph, where each node represents a variation instance. The graph connectivity indicates similarity between variations (i.e., disconnected nodes indicate outliers different from all others). An edge indicates that the similarity of the corresponding trees is above a user-defined threshold. To calculate the similarity between two trees t_1 and t_2 , we find the intersection of the sets of all node labels in each tree, s_1 and s_2 , and normalize this measure by dividing it by the maximum number of nodes:

$$\text{similarity}_{t_1, t_2} = \frac{s_1 \cap s_2}{\max(|s_1|, |s_2|)} \quad (1)$$

This similarity measure is 1 when trees are identical and 0 when the labels of all nodes are different. The Euclidean distances are not taken into account in this measure, as node locations are determined by the artist and not indicative of anatomical location. Other definitions could be used if desired, such as the graph edit distance [Bil05].

The topology similarity is visualized in two views (See Figure 2 on the right). First, as a *node-link graph*, which reveals the connections between the variations that are most similar to each other. This graph visually encodes the probabilities of occurrence for each of the individual trees using a heated body color map for the node color. The similarity between the variations is encoded in the edge color, as well as the position for extra emphasis. Distances between the nodes are preserved in the layout, so that pairs of nodes far away in the topology-similarity graph are dissimilar. The graph can be used to discover groups of similar trees, which will be represented as closely positioned interconnected groups of variations in the topology similarity graph. Second, we include a full *similarity matrix*. Since edges are only generated above a similarity threshold, the distances between all possible pairs are lost in the topology-similarity graph. The matrix representation allows us to answer questions related to the similarity of one tree to all other trees at a single glance. The similarity is quantified in this view, further emphasized by coloring the cells based on the similarity measure. In the matrix view, a blue to red color encoding is used for the cells, where blue represents dissimilar and red represents similar pairs. The matrix can also be re-ordered by different criteria, such as tree id, average similarity and probability. To find the exact similarity values between pairs of variations, the matrix also displays the values inside the corresponding cells.

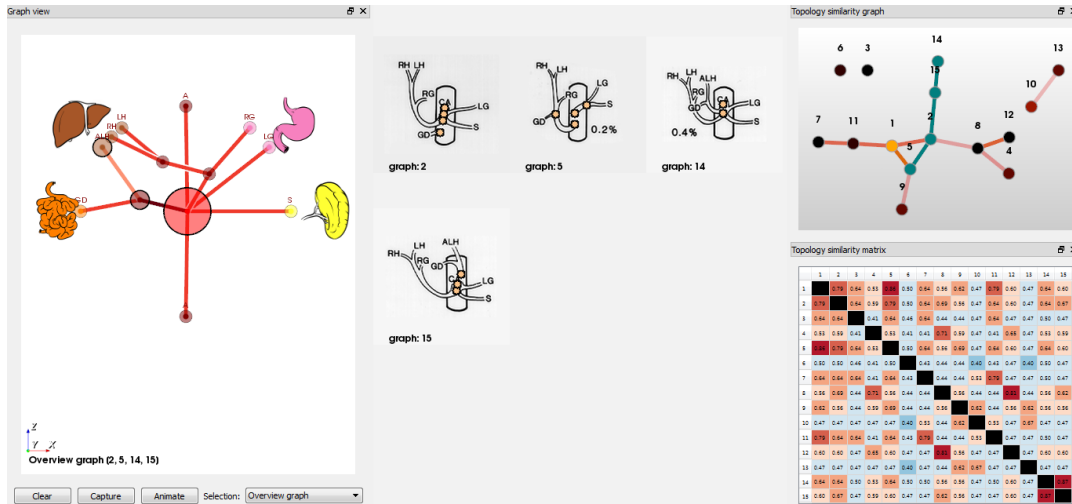


Figure 2: The VarVis interface. In the center view, illustrations of the selected trees can be examined. Top right shows the similarity graph with four variations selected in green. The similarity matrix is visible in the bottom right. The left pane shows the summary tree.

To select variations that are interesting for further exploration into local similarities, the topology-similarity graph can be used (one can select nodes that form a cluster), or by interacting with the matrix (one can select individual variations or groups).

Local view: To be able to identify the exact local differences and similarities between trees, we create a summary tree of the variations for two or more given individual trees. This summary tree will encode a matching between individual tree nodes and can then be used to interactively navigate through the topological differences and similarities. The differences between the trees are collapsed into bigger nodes, while similar nodes and edges are preserved.

The algorithm starts with an empty summary tree s and then proceeds sequentially over all selected variations. First, endpoint pairs (same organ) in the variation v and s are matched. For each matched endpoint pair, both trees are traversed simultaneously. If the labels of the two corresponding nodes are the same, we move one step up to the root in both trees. If the two label sets differ, we merge the labels and place the new label set at the current position in s . We then proceed with the next matched endpoint. Finally, we process the summary tree and collapse all succeeding nodes in the direction of the root whose label set is a subset of its predecessor. In case additional branches exist in v they need to be added to s separately. Once no more matched endpoints can be found, we take the extra endpoints from v one by one. We traverse up only the tree v until we encounter a node n that is somewhere present in s . We then add the subtree of v below n to its corresponding position in s . Finally, once all endpoints have been processed, we clean up the labels in the summary tree and propagate the labels from the endpoints to the root as before.

After the tree matching is complete, we can highlight local differences and similarities based on the above matching scheme. There are three possibilities. There can be a one-to-one match between nodes, which represents an exact match. There can also be a mismatch, either because a node is not available in the other tree(s) or because the nodes are different. Matched, extra and merged nodes are highlighted in green, purple and orange respectively (see Figure 3).

As an additional component, we visualize the individual and summary tree. We opt for an easy-to-understand 2D representation using a planar layout. We position junction points by a force-

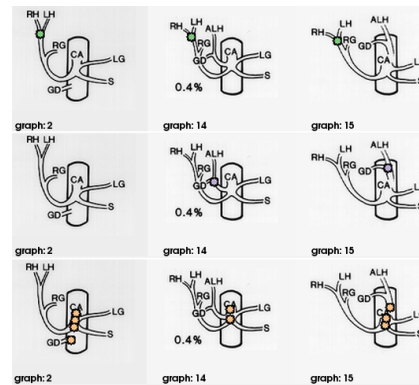


Figure 3: Matching nodes are highlighted in green (top), extra nodes in purple (center) and merged nodes in orange (bottom). directed mechanism to spread the graph, while the endpoints are fixed to maintain a consistent arrangement. We discussed several potential layouts with our domain experts. To keep it intuitive for medical professionals, we fix the root and organ endpoints in a circular layout, which roughly preserves the naturally-occurring organ location, while keeping the tree compact. We also proposed a subway map metaphor similar to the Neurolines work [AABS*14] and a rectangular layout with the organs arranged in two parallel lines. These latter two options were judged too abstract to relate them easily to the anatomy and our experts had a strong preference for a circular layout. While a zero-crossing solution cannot always be found because of the inherent 3D nature of the problem, users can always arrange nodes manually, if needed.

The visual encoding of the summary tree (see Figure 2, left) uses node size and edge coloring to visualize the level of summarization. Bigger nodes indicate that more individual nodes from different trees had to be merged to create the summary tree or extra nodes not available in all trees. The edge coloring further highlights the differences. When the user selects a node in the summary tree, detailed views of the corresponding variations can be explored. In case a selected node consists of many merged nodes, all of the original nodes are highlighted in the associated illustrations (see Figure 2, center). The summary tree can also be used to steer an animation between the summarized variation trees. By fixing matched nodes

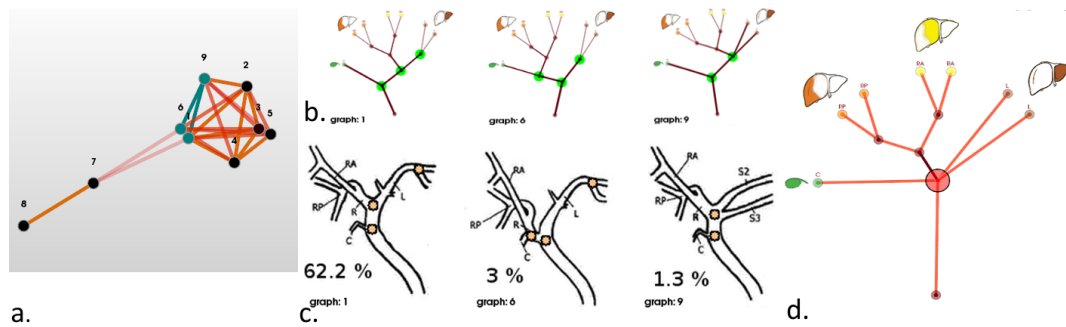


Figure 4: Interacting in the topology similarity graph (a) and illustrations (c) highlights differences in trees (b) and the summary graph (d).

in the same positions and force-directing the merged nodes, initialized at the merged node location, the transitions between individual variations are highlighted.

4. Results

In this section, we present results of our method for two types of anatomical variations. Our application can be seen in Figure 2. The variations in Figure 2 are constructed based on the variations of the gastroduodenal artery, as can be seen in Figure 1. In the original study, 500 cases resulted in 15 variations with various probabilities, indicated as percentages. In Figure 2 (right), the topology similarity graph and matrix are shown. The similarities between the fifteen variations can be explored. The matrix view can be used to see which trees are most similar to all others, and which are most distant. Using the topology similarity graph to select subgroups of trees, we can discover clusters. Trees 4, 8 and 12 for instance, all have an accessory right hepatic artery. In this case, we first selected four trees of interest using the topology similarity graph (top right), causing them to be highlighted in green. In the center view, the selected illustrations are shown, and interaction with these illustrations highlights corresponding nodes in the other illustrations. Furthermore, on the left, we see the summary tree, which can be used to explore the similarities and differences in addition to the illustration. For these trees, we find that the junction nodes vary quite extensively among the selection, as demonstrated by the number of highlighted merged nodes. Furthermore, we find that two of the trees have an accessory right hepatic artery in common, which causes them to cluster together in the topology-similarity graph.

An additional case is presented in Figure 4. Here, we examine variations of the bile ducts [RLSOT12]. First, we selected a cluster of three variations of interest in the topology similarity graph (a). By interacting with the illustrations (c), we highlight the differences in both the individual tree views (b) as well as the illustrations (c). Furthermore, the summary tree (d) can additionally be used for navigation to find these differences at a glance.

5. Evaluation

We performed an informal user study with three domain experts in order to evaluate the potential of VarVis. The participants had diverse medical backgrounds. Two are trained as an MD. The first is involved in developing computer-aided learning techniques, teaching medical subjects. The second expert is currently involved in surgical anatomy research. The third expert is a medical biologist that currently works on e-learning programs within the department of Anatomy for medical students. These experts were selected for their affinity with anatomical education, from the perspective of students as well as teachers. The evaluation consisted of several cycles. In an initial session, we examined the potential of the graph

representation and summary tree. In the followup, we examined the utility of the topology similarity graph and matrix, as well as the relation to medical illustrations. In the evaluations, we used the same datasets that were presented in the results section.

Overall, VarVis was found to be an interesting and promising application by the users. The illustrations linked with the more abstract individual 2D-tree representation provided the users with insight into the topological variations between vascular trees. The abstraction level of the summary tree representation was received with mixed reviews, but all users saw the utility of it in identifying regions that are similar or regions that are different. The users prefer to use the 2D enhanced illustrations over the 2D graph representations, when dealing with questions regarding individual graphs. Furthermore, they were able to quickly spot specific variations using either the individual 2D graphs or the summary tree. The topology similarity graph and matrix were found useful to identify similarities and groups of trees. This task was found especially difficult to achieve with the 2D illustrations alone. All users saw the potential of using VarVis as an educational tool in the future.

6. Conclusions and Future Work

We presented VarVis, a way of visualizing anatomical variations in branching structures that allows the user to compare and explore the global and local characteristics of these variations in an interactive environment. VarVis features a topological similarity graph-based visualization of the variation trees combined with linked enhanced illustrations. The topology similarity graph provides the user with an overview of the existing variations and their similarities at a single glance. Individual variations can be summarized and animated to provide insight into the local differences and similarities. We visualize the graph representations using a semi-automatic force-directed layout algorithm specifically designed to present the graph in a clear and compact overview, while maintaining anatomical structure. We performed an informal evaluation with three domain experts that revealed that VarVis has potential as an educational tool for teaching anatomy. For more conclusive results, a larger follow-up study is needed with medical students. In the future, we would like to extend this work to build patient-specific graph representations based on medical imaging data for anatomical branching structures that have robust automatic segmentation methods available. In this way, the specific variation of the patient could be linked to a 3D anatomical surface representation and analyzed with respect to the most common configurations.

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