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N. Thommeret, J.S. Bailly, C. Puech

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Thommeret Nathalie
Laboratoire de Géographie Physique - UMR 8591
Université Paris 1 - CNRS
Meudon, France
nathaliethommeret@gmail.com

Bailly Jean-Stéphane
UMR LISAH - UMR TETIS
AgroParisTech
Montpellier, France
bailly@teledetection.fr

Puech Christian
Maison de la télédétection - UMR TETIS
Cemagref
Montpellier, France
puech@teledetection.fr

Abstract— **More and more elevation data and methods are available to automatically map hydrographic or thalweg networks. However, there are few methods to assess the network quality. The most used method to compare an extracted network to a reference network gives global quality information on only geographic criterion. The method proposed in this paper allows a network assessment compared to a reference network whose results can be interpreted more easily and more related to networks morphologies. This method is based on a hierarchical node matching within a graph. Nodes are classified by hierarchical level according to their importance in the tree-structured network. Then, a matching process seeks for nodes pairs between the two networks based on the geographic distance. The hierarchy introduces a priority order in the matching. The relative location of nodes pairs is checked in order to ensure a topological consistency. Finally, similarity statistics based on nodes matching counts are computed. While the usual method only takes into account a geographic criterion, the presented method integrates geographic, geometric and topologic criteria. It is an interactive and object-by-object matching. Moreover, the hierarchical approach helps comparing networks represented at different scales. It provides global statistics but also step-by-step maps that helps characterizing the spatial distribution of network delineation errors.**

INTRODUCTION

The progresses in terrain modeling allow nowadays automatic and systematic mapping of morphological features as drainage or thalweg networks. Various methods make possible the automatic extraction of such networks from DTMs (O'Callaghan et Mark, 1984; Quinn et al., 1991; Lea, 1992; Tarboton, 1997; Molly and Stepinski, 2007; Thommeret et al., 2010; Pirotti and Tarolli, 2010). Consequently, for a given area, numerous representations of networks can be provided from several elevation data and/or from different extraction methods and sometimes from different softwares (Hengl et al., 2009). Usually, main branches of the different representation are similar but greater differences are pointed out for upstream branches. Each result should be compared to a ground-truth to determine which one is the most representative. In addition, another problem is that ground truth data are not always available with same scale which makes the usual accuracy assessments methods (Heikpe et al., 1997) inappropriate.

To assess the quality of a representation, we need a tool that permits to quantitatively and synthetically compare two networks (at different scales). A network assessment should respond to the following questions: how much of the network is over-detected and how much is under-detected (Heikpe et al., 1997)? But other questions seem to be important like: is the network topology correct? What proportion of errors occurred on the main branches of the network compared to those located upstream?

There is no standard method to assess the quality of an extracted network (Molloy and Stepinski, 2007). The automatic method the most used (known as the buffer method) allows for an estimate of the delineation error based on a geographic overlap of the networks (Heikpe et al., 1997). It is a global comparison that focuses on the over and under-detection total lengths. It provides valuable first information on the network's geometric accuracy (Heipke et al., 1997). However this method is based on a single criterion of linear geographic proximity while it seems interesting to take into account the networks' morphology and thus integrate a topological criterion. In the other hand, strictly topological comparisons are possible (Ferraro and Godin, 2003) but not adapted to spatially referenced objects.

This paper deals with the issue of automatic and quantitative network comparison in order to assess extractions. We propose a method that integrates geometric, geographic and topologic criteria and perform accuracy assessment even when ground truth data are not at the same scale.

METHODS

The method presented is based on a hierarchical graph node matching when DTM extracted networks are transform in tree graph objects. It aims at seeking pairs of nodes between the extracted network to test (T) and a reference network (R).

Firstly, nodes are classified by hierarchical level from downstream to upstream for both networks. Then, an iterative matching is processed: first-classes nodes are matched then second-classes nodes up to the source-nodes. Matching can be based on a simple geographic criterion: the geographic distance of the two networks' nodes.

Node labeling

We chose the method to focus on the nodes rather than the edges of the network due to 1- nodes-edges duality and simple nodes geometry and 2- higher edges sensitivity to noise in geographic positioning: for instance, spatial resolution impacts reaches geometry and extent.

Labels that will be used to classify and match nodes are attributed to T and R nodes based on geometric and topologic attributes; simple geometric labels: x and y coordinates of the nodes and topologic labels mainly based on Shreve magnitude of each node(Shreve, 1966). We chose the shreve taxonomy rather than Strahler's one for a simple reason: for Shreve's, source-nodes have the same weight along the tree whereas for Strahler's they have not the same impact on the ordering increase. Each node magnitude (S) is normalized by the whole network magnitude (S_T) in order to allow comparison between R and T networks at different scales.

The hierarchical nodes classification

The second step consists in a hierarchical node classification for both networks based on the node importance in the tree. It aims to introduce a priority in the pairs' research.

Node importance is determined from the normalized Shreve magnitude that expresses a node relative upstream/downstream position in the tree. The first level of the hierarchy includes the greater junctions of the networks; at the opposite, the last level corresponds to source-nodes. Outlets are matched by definition so they are not taken into account in the classification.

The number of classes (N) is directly related to the scale representation of the network: the more the network is detailed (great values of $S_{T)}$, the more N is high. A theoretical hierarchical level number (N_T) can be obtained by reasoning on a perfect binary tree (Eq. 1). However, studied networks are not perfect binary trees, this number is a maximum. Thus, we introduce an arbitrary correction factor of 2 (related to the two first obvious classes: sources and outlet) in order to obtain a less restricting number of classes given by Eq. 2.

$$S_T = 2^{N_T} \tag{1}$$

$$N = floor\left(\frac{\log(S_T)}{\log(2)}\right) - 2 \tag{2}$$

At the end of this step, the two set of nodes (extracted and reference) are classified by comparable hierarchical level.

The matching of nodes by class

In the third step, we seek for nodes pairs for the different hierarchical levels. The matching is an iterative process starting with the first class of nodes up to the source class.

Geographic proximity rules the matching: a distance matrix is performed from the two node subsets for each hierarchical level. Then each node of the extracted network is related to the closest node of the reference. A distance threshold determines if the pair is acceptable or not. We set the threshold considering the base DTM's resolution, the network extraction accuracy and the length of the shortest distances between nodes in the network.

To adjust the matching to other networks or other terrains, more geometric can be easily integrated in the distance matrix calculation.

Unmatched nodes are put back into play at the next step. It permits to soften strict class limits.

Topological consistency checking

Once a set of node pairs (T,R) is obtained, we check their topological consistency. Each pair represents the same physical node but in two different trees (T and R): these two representations must have the same topological location (upstream-downstream position) in their respective tree. Else, inconsistent node pairs are rejected. The number of topologically consistent pairs provides a quality criterion of the matching process: if all pairs are topologically correct then the matching completely succeeded. In the algorithm implemented, only the topological consistency with the nearest neighbor was tested.

Global similarity statistics

Finally, simple global statistics are computed from the matching. By analogy to Heikpe (1997), we count ratios of matched nodes in T, and ratio of unmatched nodes for both the extracted and the reference networks. In addition to global analysis, these statistics can be computed for each matching step what provide valuable arguments for the networks comparison.

RESULTS

Material

The method is applied to compare two extracted networks (T1 and T2) to a detailed reference network R (fig. 1) on a test-area of the Draix experimental basins in French Prealps. The study area corresponds to badlands area meaning that terrains are highly dissected. Networks are extracted from a one-meter-resolution airborne LiDAR DTM. The reference is a field-mapped network.

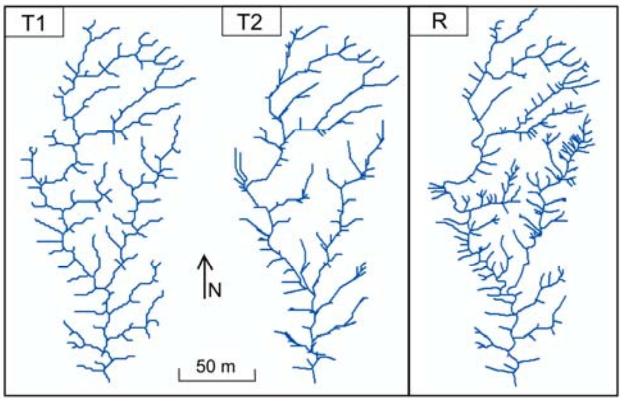

Figure 1. Comparing extracted networks (T1 and T2) to the ground-truth network (R)

The extracted networks result from different extraction method: T1 was extracted using Thommeret et al. (2010) method that combines a morphological index and a drainage algorithm (CI based network); T2 was obtained using the classical D8 algorithm (O'Callaghan et Mark, 1984).

Hierarchical matching results

In this particular case study, the distance threshold chosen is 2 m, considering that twice the resolution of the base DTM approaches the data's planimetric noise. The extracted networks have the same number of classes. Every node pairs of both networks are topologically consistent.

The matching progression for CI based network and reference is shown figure 2. We can distinguish for each step of the matching the extracted nodes that find a reasonable pair (in red) and those that are not matched (in green).

The hierarchical matching process provides step-by-step results. Thus the results are sharper than with the global buffer approach. Step-by-step results for the two extracted networks show different extraction quality (fig. 2). For the CI based network, unmatched nodes are localized in specific areas where the DTM is less accurate. While unmatched nodes of the D8 network are dispersed in the space.

Global ratios coming from the matching are presented TABLE 1. For the CI based network, the matched nodes represent 87% of the total number of nodes. For the D8 network, they represent 76%. Thus, the D8 network shows more over-detected nodes than the other network.

TABLE I. QUANTITATIVE MATCHING RESULTS

Networks	**Total node number**	**Pairs**	**Unmatched nodes**	
			Extracted	Reference
T1	200	174	26	170
T2	238	181	56	162

DISCUSSION AND CONCLUSION

In this paper, we propose an interactive method to quantitatively and automatically compare two networks of a same area. The method aims to help assessing networks extracted from DTM to a reference since more and more elevation data and methods are available to automatically extract thalweg networks.

This method relies on hierarchical node matching. It is based on an object-by-object approach which provides more controlled results. The hierarchical approach helps comparing networks represented at different scales. It helps distinguishing extraction artifacts from unmatched nodes resulting from a scale difference between the networks.

Results are satisfying and compliant to visual comparison. This method provides results with clear significations that can be directly interpreted: while the buffer method provides global results based on the network overlap, the proposed method supplies more significant and detailed results. Step-by-step matching maps observation helps qualifying the spatial distribution of extraction errors. The matching progression through the steps can be used to better characterize the networks adequacy along the network hierarchy. It provides another key to the assessment and the interpretation of the differences between the networks.

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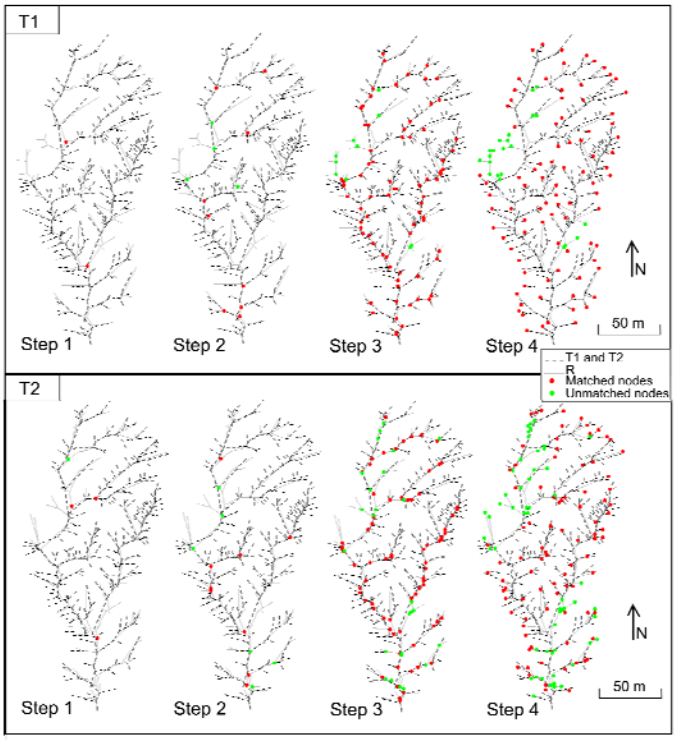

Figure 2. Matching progression through the different steps for the two extracted networks (T1 and T2)