

Transport on river networks: A dynamical approach

Ilya Zaliapin

Department of Mathematics and Statistics, University of Nevada, Reno

Efi Foufoula-Georgiou

St. Anthony Falls Laboratory and National Center for Earth-surface

Dynamics, Department of Civil Engineering, University of Minnesota

Michael Ghil

Geosciences Department and Laboratoire de Météorologie Dynamique

(CNRS and IPSL), Ecole Normale Supérieure and Department of

Atmospheric and Oceanic Sciences and Institute of Geophysics and

Planetary Physics, University of California, Los Angeles

I. Zaliapin, Department of Mathematics and Statistics, University of Nevada, Reno, USA.

E-mail: zal@unr.edu.

E. Foufoula-Georgiou, St. Anthony Falls Laboratory and National Center for Earth-surface

Dynamics, Department of Civil Engineering, University of Minnesota, 2 Third avenue SE, Min-

neapolis 55414, USA. E-mail: efi@umn.edu.

M. Ghil, Geosciences Department and Laboratoire de Météorologie Dynamique (CNRS and

IPSL), Ecole Normale Supérieure, Paris, FRANCE, and Department of Atmospheric and Oceanic

1 **Abstract.** This study is motivated by problems related to environmen-
2 tal transport on river networks. We establish statistical properties of a flow
3 along a directed branching network and suggest its compact parameteriza-
4 tion. The downstream network transport is treated as a particular case of
5 nearest-neighbor hierarchical aggregation with respect to the metric induced
6 by the branching structure of the river network. We describe the static ge-
7 ometric structure of a drainage network by a tree, referred to as the *static*
8 *tree*, and introduce an associated *dynamic tree* that describes the transport
9 along the static tree. It is well known that the static branching structure of
10 river networks can be described by *self-similar trees* (SSTs); we demonstrate
11 that the corresponding dynamic trees are also self-similar. We report an un-
12 expected *phase transition* in the dynamics of three river networks, one from
13 California and two from Italy, demonstrate the universal features of this tran-
14 sition, and seek to interpret it in hydrological terms.

Sciences and Institute of Geophysics and Planetary Physics, University of California Los Angeles,
USA. E-mail: ghil@atmos.ucla.edu.

1. Introduction

15 The topology of river networks has been extensively studied over the past decades and
16 stream ordering schemes, as well as statistical self-similarity concepts, have been explored
17 to a considerable extent [see *Horton*, 1945; *Strahler*, 1957; *Shreve*, 1966; *Tokunaga*, 1978;
18 *Mandelbrot*, 1983; *La Barbera and Rosso*, 1987; *Marani et al.*, 1991; *Rodriguez-Iturbe et*
19 *al.*, 1992; *Peckham*, 1995; *Badii and Politi*, 1997; *Rodriguez-Iturbe and Rinaldo*, 1997;
20 *Turcotte*, 1997; *Sposito*, 1998; *Peckham and Gupta*, 1999; *Pelletier and Turcotte*, 2000;
21 *Burd et al.*, 2000; *Dodds and Rothman*, 2000; *da Costa et al.*, 2002; and references therein]

22 What has been less studied, however, is how the static topology of a river network affects
23 and is affected by the dynamical processes operating over this network. For example,
24 consider a directed tree that represents a river network, and assume we are interested in
25 the mixing of water, solutes and sediments as they move downstream in reaches of variable
26 lengths and merge at junctions of the river network. One might want then to attach a
27 “metric” to the nodes of this tree, such as the distance to the nearest source, and consider
28 the notion of a *dynamic tree*, superimposed on the template of the underlying *static tree*.

29 This dynamic tree is likely to have a different hierarchy and topology than the static
30 one. Depending on the dynamics, for example, some of the static-tree branches might be
31 completely cut off, either due to a blockage that prevents transport along these branches
32 or due to the absence of conditions to generate sediment or nutrient for downstream
33 transport. In this case, the dynamic tree will have a different hierarchy than the static
34 one, and this difference might affect the scaling of fluxes that participate in defining the
35 envirodynamics on the network of interest. In general, a static tree of a given Horton-

36 Strahler order could become a dynamic tree of a lesser or higher order, depending on the
37 superimposed dynamics.

38 The purpose of this paper is to study the dynamic topology of directed trees, starting
39 with several simple cases, first synthetic and then realistic. The direction we use is obvi-
40 ously “downstream,” *i.e.*, from the leaves to the root of the tree. We focus on a dynamic
41 hierarchy built on the concept of “connectivity”: once two streams are connected, they
42 both influence the downstream dynamics. One can thus imagine that two order-1 streams
43 of different lengths, l_1 and l_2 , merge at a node but do not automatically give rise to an
44 order-2 stream, as would be the case in the standard Horton-Strahler ordering scheme;
45 instead, we keep track of length and the assigned order becomes 2 only when the running
46 index of length becomes $\max(l_1, l_2)$.

47 Alternatively, one might keep track of time, rather than length: the two are equivalent
48 if the flow velocity is constant along all the branches, which we will assume in the present
49 paper, for simplicity’s sake. In other words, a dynamical node of order 2 is created
50 only when the fluxes from both order-1 streams do reach the connecting node. Such
51 considerations will result in a different ordering of the dynamic tree compared to the
52 static one. Moreover, the newly created dynamic tree will be *time-oriented*, a property
53 that is absent in conventional static trees.

54 We approach the problem of hierarchical dynamics of river networks using general
55 concepts of *hierarchical aggregation*, which studies how multiple individual particles
56 (molecules, species, individuals, *etc.*) merge (aggregate, collide) with each other to form
57 clusters in different physical, chemical, biological, or sociological settings. A major role
58 in such studies is played by the notion of *cluster dynamics*. This concept refers to the

59 situation when a system that contains an infinite number of interacting particles can be
60 decomposed into *finite* clusters that move independently of each other for some random
61 interval of time. After this time, the particle interactions give rise to infinite-range cor-
62 relations, although the system can be decomposed into another set of finite independent
63 clusters, and so on.

64 In the 1970s, Ya. G. Sinai developed a self-consistent mathematical formalism and
65 proved the existence of cluster dynamics for some particle systems in statistical mechanics
66 [Sinai, 1973, 1974]. The ideas of cluster dynamics have been applied to plasma physics,
67 economics, and the study of precursory patterns for extreme events in geophysics [Rotwain
68 *et al.*, 1997; Molchan *et al.*, 1990; Keilis-Borok and Soloviev, 2003]. Recently, Gabrielov
69 *et al.* [2008] evaluated numerically the cluster dynamics of elastic billiards, leading to the
70 detection of what appear to be the first genuine *phase transitions* and *scaling phenomena*
71 that develop in time, rather than with respect to a control parameter, such as temperature
72 T or density; *i.e.*, a transition occurs and scaling develops as time t evolves toward a critical
73 value t^* , rather than as the parameter T crosses a critical value T^* .

74 In this paper, we adapt the concept of cluster dynamics to environmental transport on
75 river networks. Notably, we obtain a remarkably similar, and equally unexpected, phase
76 transition in the cluster dynamics of river networks and attempt to interpret it in this
77 context. We also study the statistical properties of the dynamic trees introduced herein.
78 It is well known that the static branching structure of river networks can be described
79 by *self-similar trees* (SSTs); we demonstrate, using three actual river basins, that the
80 corresponding dynamic trees are also self-similar.

81 This paper is structured as follows. We review in Section 2 the terms and concepts
82 relevant to the hierarchical analysis of branching structures, including the Horton-Strahler
83 and Tokunaga branching taxonomies. Section 3 introduces the concept of a *dynamic tree*
84 that is associated with a given *static tree*, by using two examples from river transport.
85 Section 4 describes two types of static trees analyzed in this study. The first type reflects
86 the well-formed “river network” of a basin. The second type reflects the “unchannelized
87 drainage network”; this network is composed of drainage paths that are not permanent
88 channels but are perpendicular to the topographic contour lines and follow the steepest
89 downstream gradient. In other words, this drainage network is formed by paths of “zero-
90 order” basins or hillslopes. Hierarchical aggregation is described in greater depth, and
91 with additional examples from several fields, in Section 4, along with an abstract metric
92 space setup. Three actual river networks, from California and Italy, are analyzed in
93 Section 6. A summary and discussion follow in Section 7.

2. Main concepts and definitions

94 This section introduces the main concepts used in the analysis of branching structures,
95 along with their definitions and illustrative examples.

2.1. Trees

96 A *tree* \mathbb{T} is a set of *nodes* connected by *vertices* (also called *edges* or *links*) in such a
97 way that there are no loops, *i.e.* there are no closed paths formed by distinct edges (see
98 Fig. 1). A *rooted tree* has one special node designated as a *root*. In a rooted tree each
99 connected pair of nodes has a parent-child relationship, with the parent being the element
100 that is closest to the root [Athreya and Ney, 1972]. The nodes with no children are called

101 *leaves*. The *depth* d_i of a node i in a rooted tree is defined as the number of edges between
102 this node and the root. The depth D of a tree is the maximum of the depths d_l over all
103 the leaves l .

104 In this study we will work with *binary trees*. In a binary rooted tree, each node may
105 have either two or no children. This means that each internal node i (every node except
106 for the root and the leaves) is connected to three other nodes: one is a parent of i , and
107 the other two are its children. The root is only connected to two children, and each leaf
108 is connected to a single parent. A *complete binary tree* is a rooted tree such that all its
109 leaves have the same depth. Our interest for binary trees is motivated by the observation
110 that many natural phenomena exhibit binary branching. For example, in river networks,
111 it is unlikely for three or more streams to merge at exactly the same point, while in gas
112 dynamics it is unlikely that more than two molecules will collide at the same time.

113 In our study of river transport, the tree \mathbb{T} will represent a drainage network; see Fig. 1.
114 Hence the nodes correspond to the merging points of streams and vertices to the stream
115 segments between these points, while the network's sources are the leaves, and the outlet
116 is the root of the tree.

2.2. Branching-order taxonomies

117 In many applications, there is a need to order the nodes according to their importance
118 in forming the entire hierarchy; this importance often corresponds also to relative size.
119 For instance, in a botanical tree the leaves are the most delicate, smallest elements; the
120 intermediate levels are formed by consecutively wider branches, while the most heavy,
121 robust element of the plant is its trunk. Likewise, one naturally distinguishes in a river

122 network between minor and major tributaries, according to the amount of water that they
 123 are able to carry.

124 In a complete tree, the node ordering task is quite straightforward since a node's order
 125 can be chosen to be inversely proportional to its depth: "the deeper, the smaller". The
 126 problem, however, becomes more complicated when one deals with an incomplete tree; in
 127 this case, the depth can no longer serve as a proxy for size, since the leaves, while being
 128 the smallest elements, will often be assigned indices that are as large as those of much
 129 heavier internal nodes.

130 *Horton* [1945] developed a convenient way to order hierarchically organized river tribu-
 131 taries; this method was later refined by *Strahler* [1957] and further expanded by *Tokunaga*
 132 [1978]. Currently, the so-called Horton-Strahler and Tokunaga ordering schemes are stan-
 133 dard tools of branching analysis.

134 2.2.1. Horton-Strahler ordering

135 Each leaf in a binary rooted tree is assigned a Horton-Strahler (HS) *order* $r(\text{leaf}) = 1$;
 136 see Fig. 2a. Each node p , which is the parent of nodes c_1 and c_2 , is assigned a Horton-
 137 Strahler order $r(p)$ according to the following rule [*Horton*, 1945; *Strahler*, 1957; *Newman*
 138 *et al.*, 1997]:

$$r(p) = \begin{cases} r(c_1) + 1 & \text{if } r(c_1) = r(c_2) \\ \max(r(c_1), r(c_2)) & \text{if } r(c_1) \neq r(c_2). \end{cases} \quad (1)$$

139 A *branch* is defined as a union of connected nodes with the same order. We will denote by
 140 N_r the total number of branches of order r . Notice that each branch has *linear* structure:
 141 two children of the same parent can not belong to the same branch.

142 In a tree with n leaves, the longest branch can be formed by $(n - 1)$ nodes; this is the
 143 case when two leaves merge together to form an order-2 branch and then all other leaves

144 join this branch one by one. We refer to this situation as *exhaustive branching*. It is
 145 readily seen that each leaf is always an order-1 branch. An order-2 branch is created by
 146 merging two leaves and can consist of more than one node, depending on the leaves that
 147 join it; an order-2 branch that consists of two nodes is highlighted in Fig. 2a. The order
 148 Ω of a tree is the maximal order of its branches (or nodes).

149 In a complete tree, each branch consists of a single node since the children of an order-
 150 r node always have the same order ($r - 1$). In such a tree, the HS order is uniquely
 151 determined by the node depth d via $r = D - d + 1$, where the tree depth is $D = \Omega$.

152 2.2.2. Tokunaga indexing

153 Tokunaga indexing [Tokunaga, 1978; Peckham, 1995; Newman et al., 1997] extends
 154 upon the Horton-Strahler orders; it is illustrated in Fig. 2b. This indexing focuses on
 155 incomplete trees by cataloging the merging points between branches of different order.
 156 A first-order branch that merges with a second-order branch is indexed by “12” and the
 157 total number of such branches is denoted by N_{12} . A first-order branch that merges with a
 158 third-order branch is indexed by “13” and the total number of such branches is N_{13} , and
 159 so on. In general, N_{ij} for $j > i$ denotes the total number of order- i branches that join an
 160 order- j branch.

161 The Tokunaga index T_{ij} is the number of branches of order i that merge with a branch
 162 of order j , normalized by the total number of branches of order j ; in other words, T_{ij} is
 163 the average number of branches of order $i < j$ per branch of order j :

$$T_{ij} = \frac{N_{ij}}{N_j}. \quad (2)$$

164 Merging of branches of different orders is referred to as *side branching*. It is easily
 165 seen that side branching is absent in a complete tree, and “a tree with side branching”

166 is synonymous to “an incomplete tree.” For incomplete trees, the side-branching indices
 167 become increasingly important as they help to define a tree’s structure, possibly indicating
 168 properties that are unique to specific classes of trees.

169 For consistency, we denote the total number of order- i branches that merge with other
 170 order- i branches by N_{ii} and notice that in a complete binary tree $N_{ii} = 2N_{i+1}$. This
 171 allows us to formally introduce the additional Tokunaga indices:

$$T_{ii} = \frac{N_{ii}}{N_{i+1}} \equiv 2.$$

172 The set $\{T_{ij} : 1 \leq i, j \leq \Omega\}$ of Tokunaga indices provides a complete statistical description
 173 of the branching structure of an order- Ω tree.

174 2.2.3. Other node statistics

175 We introduce here two node statistics relevant to our river transport study:

- 176 • the *number of nodes* (or links) within a branch i is denoted by c_i ; and
- 177 • the *magnitude* m_i of a node i is the number of leaves that descend from i ; in other
 178 words, the magnitude of a branch is the number of the sources upstream of it.

179 Magnitude measures the complexity of the river structure upstream from a given branch.
 180 We notice that each leaf (source) has unit magnitude, $m_{\text{leaf}} = 1$, and the magnitude of a
 181 parental node p is the sum of the magnitudes of its children c_1 and c_2 :

$$m_p = m_{c_1} + m_{c_2}. \quad (3)$$

182 Accordingly, a node or order r has magnitude $m \geq 2^{r-1}$, with equality being attained
 183 only for a complete binary tree. The average number of nodes and average magnitude of
 184 an order- r branch are denoted by C_r and M_r respectively.

2.3. Self-similar trees

185 The concept of *self-similarity* provides a powerful tool for describing and studying trees.

186 A self-similar tree (SST) is defined by the constraint

$$T_{i,i+k} = T_k \text{ for } k = 1, 2, \dots \quad (4)$$

187 E. Tokunaga was probably the first to study SSTs, and considered an additional con-

188 straint on the branching indices [*Tokunaga, 1978*]:

$$\frac{T_{k+1}}{T_k} = c, \quad \text{or} \quad T_k = a c^{k-1} \text{ for } a, c > 0. \quad (5)$$

189 The SSTs that satisfy (5) are called *Tokunaga trees*.

2.4. Horton laws

190 Empirically, the average values of branching statistics for the observed river basins

191 depend exponentially on the order r :

$$N_r = N_0 R_B^{\Omega-r}, \quad (6)$$

$$M_r = R_M^{r-1}, \quad (7)$$

$$C_r = C_0 R_C^r \quad (8)$$

192 for some positive constants N_0 and C_0 . Such relationships are called *Horton laws*; the

193 bases R_B , R_M , and R_C of the exponential relationships are called *stream ratios*.

194 *McConnell and Gupta* [2008] showed that the Horton laws (6), (7) hold asymptotically,

195 *i.e.* for $r \rightarrow \infty$, in a self-similar Tokunaga tree; they also proved that $R_B = R_M$. Moreover,

196 *Zaliapin* [2009] demonstrated the stream ratio inequality

$$R_B = R_M < R_C, \quad (9)$$

197 that had been conjectured by *Peckham* [1995]. In addition, *Zaliapin* [2009] demonstrated
 198 that the Horton laws hold, under some additional assumptions on the Tokunaga indices
 199 T_k , for self-similar trees that do not necessarily satisfy the Tokunaga condition (5).

3. Static vs. dynamic trees: Network envirodynamics

200 The topological structure of a river network is well described by a tree, which we denote
 201 by \mathbb{T}_S and call the *static tree*. To describe the downstream transport on \mathbb{T}_S we now
 202 introduce a *dynamic tree* \mathbb{T}_D , which can be interpreted as follows. Imagine that we inject
 203 a dye simultaneously into all the sources of our river network, represented by the leaves of
 204 \mathbb{T}_S , and the dye starts propagating down the river, from the sources to the outlet, with the
 205 same constant velocity along all the streams. The tree \mathbb{T}_D describes the time-dependent
 206 history of the mergings of the colored streams.

207 Next, we consider two detailed examples that will clarify this important concept. We
 208 restrict ourselves to the simplest case of constant velocity along all the streams; taking this
 209 velocity to be unity, time and length scales can be interchanged. An extension to spatially
 210 or temporally variable velocities is straightforward: we shall see that the dynamic tree \mathbb{T}_D
 211 is completely determined by the static tree \mathbb{T}_S and the set of time *delays* τ_i necessary for
 212 the dye to propagate from a node i to its parent.

3.1. Synthetic example

213 Figure 3 shows how to construct the dynamic tree for a basin with four sources **a**, **b**,
 214 **c**, and **d**. The static tree for this basin is a complete binary tree shown in the top right
 215 panel. The same tree with the link lengths explicitly shown is placed in the top row of
 216 panels; the top left panel indicates the values of these lengths.

217 The consecutive phases of construction of the dynamic tree are shown in the bottom
218 row of panels. At step 0 (the leftmost top and bottom panels), all the links in the tree
219 are “empty” (dashed lines) and the dye is injected into the sources **a**, **b**, **c**, and **d**.
220 Accordingly, we have four disconnected clusters of colored flux; they correspond to four
221 disconnected nodes in the lower left panel. Each step in the figure is a snapshot of the
222 process after a unit time interval; recall that we only use constant velocity in this paper
223 and, without loss of generality, this velocity equals unity.

224 At step 1 the dye has propagated a unit length along each stream, which is depicted by
225 solid lines in the top panel. Since all four streams are disconnected so far, the dynamic
226 tree still consists of four disconnected branches, each of which corresponds to a colored
227 stream of unit length. At step 2 the streams **a** and **b** merge. This is reflected in the
228 dynamic tree, where the nodes **a** and **b** are now connected into a single cluster. Notice
229 that the leaves **a** and **b** are not directly connected in the static tree; this connection
230 reflects a special property of the dye’s downstream propagation.

231 At step 3 stream **c** reaches stream **a**. Since stream **a** by that time is already merged with
232 stream **b**, we say that the stream **c** merges with the cluster of **a** and **b**; this is reflected
233 in the dynamic tree in the lower panel for this step. Hence, at step 3 there exist two
234 connected clusters of the colored flux: one cluster is formed by the streams **a**, **b**, and **c**,
235 while stream **d** alone forms the second cluster. Finally, at step 4, all the colored fluxes
236 merge together. The conventional representation of both static and dynamic trees, which
237 does not show the link lengths, is given in the two rightmost panels.

238 This example shows that the dynamic tree \mathbb{T}_D can be very different from the correspond-
239 ing static tree \mathbb{T}_S . We notice in particular that in this example the static tree is a tree

240 with no side branching; it has the largest possible Horton-Strahler order, $\Omega = 3$, for a tree
241 with four leaves. At the same time, the dynamic tree exhibits exhaustive side-branching;
242 accordingly, it has the smallest possible order, $\Omega = 2$, for a four-leaved tree.

3.2. Realistic example

243 Here we illustrate the dynamic tree for an order-3 subbasin of the Noyo basin; this basin
244 is located in Mendocino County, California, USA, and is described by *Sklar et al.* [2006].
245 The stream network for this subbasin is shown in Fig. 4; its fifteen sources are marked
246 by numbers 1 to 15 and fourteen stream joints by letters **a** to **n**. The static tree \mathbb{T}_S for
247 this stream network is shown in Fig. 5a; it has the Horton-Strahler order $\Omega = 3$.

248 The time-oriented dynamic tree \mathbb{T}_D is shown in Fig. 5b against the time axis (on the
249 ordinate); notice that time can also be interpreted as the distance traveled by the dye
250 from each source. This interpretation has a direct connection to the metric properties of
251 the basin and we will use it in the subsequent analysis. The order of the dynamic tree is
252 $\Omega = 4$. The letter and number marks in Fig. 5 match those in Fig. 4.

253 Four snapshots of the dye propagation — at times $t = 1, 20, 39$, and 60 — are shown
254 in Fig. 6. In this example, the dynamic tree shows a larger degree of side-branching
255 compared to the static tree; this larger degree is reflected in its larger HS order. We shall
256 see in other realistic examples, further below, that this seems to be the case for most
257 actual river networks.

4. Stream vs. hillslope networks

258 In an actual landscape, channels are initiated when the area upstream suffices to create
259 a sustainable source of streamflow and this source imprints a permanent channel on the

260 terrain. Although these channels are typically detectable by field observations, the extrac-
261 tion of the channel initiation points, or “channel heads,” from Digital Elevation Models
262 (DEMs) has been a subject of intense study. Most commonly, channels are assumed to be
263 initiated when the upstream area, or area times a typical slope, exceed a given threshold;
264 the parameters of such relationships are field-calibrated. More recently, the availability of
265 high-resolution, 1-m elevation data from LIght Detection and Ranging (LIDAR) instru-
266 mentation has initiated a new generation of methodologies for the automatic detection of
267 channels as “edges” or “features” in the terrain [*e.g.*, *Lashermes et al.*, 2007; *Passalaqua*
268 *et al.*, 2009].

269 The channelized paths, *i.e.* the branches of the river network, are not the only parts
270 of the basin by which water or other fluxes — *e.g.*, sediments, nutrients, or pollutants —
271 are transported downstream. The unchannelized part of the basin, often called *zero-order*
272 *basins* or *hillslopes*, is drained by pathways that have their own topology. In this work,
273 we extract (i) *stream networks* from DEMs by using a critical threshold area A_c , and (ii)
274 *hillslope networks* by assuming that A_c is as small as the DEM resolution.

275 Clearly, each stream network is a part of the corresponding hillslope network. For a
276 generic river basin, though, the total length of channelized paths is much smaller than
277 the total length of unchannelized paths. In the present study, we assume that stream
278 networks reflect the properties of channelized paths, while hillslope networks reflect the
279 properties of unchannelized paths. The study of unchannelized-path topology below will
280 show that it is quite different from the topology of the channelized paths.

281 Construction of stream and hillslope static trees is illustrated in Fig. 7. Figure 7a
282 shows a small part of a river basin; it is divided into 16 square regions called *pixels*. The

283 well-defined streams occupy some of the pixels (shaded squares), the rest of the pixels
284 (white squares) represent *hillslopes*, *i.e.* unchannelized parts of the basin.

285 The elevation data can be used to figure out the flux direction from each pixel, whether
286 stream or hillslope; this direction is depicted by arrows in Fig. 7b. We assume that there
287 is a unique flux direction away from each pixel; at the same time, fluxes can reach a
288 given pixel from more than one other pixel. This property allows one to represent the
289 directional information by a tree, which is shown in Fig. 7c. Solid nodes and solid lines in
290 the figure represent the stream pixels and the stream flow respectively, while open nodes
291 and dashed lines represent the hillslope nodes and hillslope flow.

292 The final step in creating the static tree of this subbasin is to remove the linear segments
293 (chains), that is to remove the nodes with only two connections (except the tree root).
294 The resulting static hillslope tree is shown in panel (d). The static stream tree is obtained
295 from the hillslope tree by removing the dashed links that represent unchannelized paths,
296 and removing the remaining chains; the stream tree for our example is shown in panel
297 (e).

5. The dynamics of hierarchical aggregation

298 The consecutive merging of river streams discussed in the previous section is a special
299 case of a general phenomenon of *hierarchical aggregation*. This phenomenon is also called
300 *inverse cascading*, and it can be described as follows.

301 Consider a process that starts at time $t = 0$ with N individual *particles*, which can be
302 considered as *clusters* of unit mass. As time evolves, the clusters start to merge with one
303 another, according to a set of suitable rules, thus forming consecutively larger clusters.
304 We assume that only two clusters can merge at the same time; thus after each merging

305 the number of clusters decreases by one. The process continues until all particles have
306 been merged into a single cluster of mass N . The evolution of the above process can be
307 described by a time-oriented binary tree, whose leaves correspond to the initial particles,
308 the root to the final cluster of N particles, and each internal node to the merging of a
309 particular pair of clusters.

5.1. Examples

310 Among the many instances of the above general aggregation scheme, we mention here
311 the following four.

312 **Percolation.:** In the *site percolation* process on an $L \times L$ lattice, the initial $N = L^2$
313 particles correspond to the sites of the lattice, while clusters correspond to connected
314 patches of occupied sites that are formed during the percolation process [*Zaliapin et*
315 *al.*, 2005]. In fact, the same scheme can be applied to bond percolation, as well as to
316 percolation on grids in higher dimensions.

317 **Billiards.:** *Elastic billiard* on a rectangular table can be used to model *gas dynamics*
318 in two dimensions (2-D). Here the initial particles are the N billiard balls (gas molecules)
319 at time $t = 0$. Each of the balls is assigned an initial position and velocity. The clusters
320 at time Δ are formed by balls that have collided during the time interval $[0, \Delta]$ [*Gabrielov*
321 *et al.*, 2008]. Formally, two balls are called Δ -*neighbors* if they collided during the time
322 interval $[0, \Delta]$. Each connected component of this neighbor relation is called a Δ -*cluster*.
323 Notice that within an arbitrary Δ -cluster each ball has collided with at least one other
324 ball during the time interval $[0, \Delta]$. In other words, a Δ -cluster is a group of balls that
325 have affected each other's dynamics during the time interval of duration Δ . The mass of
326 each cluster is simply the total number of balls within that cluster. Upon many collisions

327 of the balls, the whole system will be composed of clusters of different sizes. As time
328 evolves, the number of clusters will decrease and their mass increase.

329 The same scheme can be applied to a system of particles that interact according to some
330 potential $U(\mathbf{x})$. *Bogolyubov* [1960] suggested that when the interaction of particles is short-
331 ranged, the system can be decomposed into finite clusters so that during some random
332 interval of time, each cluster moves independently of other clusters as a finite-dimensional
333 dynamical system. After this time interval, the system can be decomposed again into
334 other dynamically independent clusters and so on. This type of dynamics is called *cluster*
335 *dynamics* and *Sinai* [1974] showed analytically that it exists in a one-dimensional (1-D)
336 system of statistical mechanics. Numerical results of *Gabrielov et al.* [2008] describe the
337 presence and various properties of cluster dynamics in a 2-D system of hard balls.

338 **Phylogenetic trees.:** Probably the best-known application of hierarchical aggre-
339 gation is in constructing phylogenetic trees that describe the evolutionary relationships
340 among biological species [*Maher*, 2002]. Here, a node corresponds to a set of species.
341 Two species are connected if they have a direct common ancestor; the link length from
342 a species to its direct ancestor equals the time it took to develop the descendant species
343 from that ancestor.

344 **River transport.:** The example of interest to us here is the downstream transport
345 along a river network. In this case, the initial particles are the environmental fluxes at
346 the sources of the network, and clusters are formed by consecutive merging of the streams
347 down the river path. That is, new clusters are formed when fluxes from upstream merge
348 at the stream junctions. This scheme of describing dynamics along a static tree was
349 considered in detail in Section 3, albeit without referring to hierarchical aggregation.

5.2. General set-up

350 Hierarchical aggregation can be described in great generality by using the framework of
 351 nearest-neighbor clustering in a metric space. Specifically, consider a set \mathbb{S} with distance
 352 $d(a, b)$ for $a, b \in \mathbb{S}$; the elements of the set will be called *points*. The distance $d(A, B)$
 353 between two subsets of points $A = \{a_i\}_{i=1, \dots, N_A}$ and $B = \{b_i\}_{i=1, \dots, N_B}$ from \mathbb{S} is defined as
 354 the shortest distance between the elements of the sets:

$$d(A, B) = \min_{1 \leq i \leq N_A, 1 \leq j \leq N_B} d(a_i, b_j).$$

355 *Nearest-neighbor clustering* is a process that combines points from \mathbb{S} into consecutively
 356 larger subsets, called *clusters*, by connecting at each step the two nearest clusters; this
 357 process can be described by the *nearest-neighbor spanning tree* \mathbb{T} . Specifically, consider
 358 N points $c_i^0 \in \mathbb{S}$, $i = 1, \dots, N$ with pairwise distances $d_{ij}^0 \equiv d(c_i^0, c_j^0)$. These points,
 359 considered as clusters of unit mass ($m_i = 1$), form N leaves of the time-oriented tree \mathbb{T} .
 360 The first internal tree node is formed at the time $t_1 = \min_{ij} d_{ij}^0$ by merging two closest
 361 points $c_{i^*}^0$ and $c_{j^*}^0$ with $(i^*, j^*) = \operatorname{argmin}_{ij} d_{ij}^0$, where $\operatorname{argmin}_{ij} f(i, j)$ is defined as a pair
 362 (i^*, j^*) such that $f(i^*, j^*) = \min_{ij} f(i, j)$. This merging creates a new cluster of two
 363 points, with a mass of $m_i + m_j = 2$. Hence, at time t_1 , there exist $N - 1$ clusters: $N - 2$
 364 clusters with unit mass and one cluster of mass $m = 2$.

365 We can now reindex the clusters so as to work with clusters c_i^1 , $i = 1, \dots, N - 1$; their
 366 total mass is $\sum_{i=1}^{N-1} m_i = N$ and pairwise distances are $d_{ij}^1 \equiv d(c_i^1, c_j^1)$. The second internal
 367 node of tree \mathbb{T} is formed at time $t_2 = \min_{ij} d_{ij}^1 > t_1$ by merging the two closest clusters
 368 from the set $\{c_i^1\}_{i=1, \dots, N-1}$. Thus, at time t_2 we have $N - 2$ clusters c_i^2 such that their total
 369 mass is N and pairwise distances are $d_{ij}^2 \equiv d(c_i^2, c_j^2)$. We continue in the same fashion,
 370 so the k -th internal cluster, for $1 \leq k \leq N - 2$, is formed at time $t_k = \min_{ij} d_{ij}^k > t_{k-1}$,

371 and at that time we have $(N - k)$ clusters c_i^k , $i = 1, \dots, N - k$ with masses m_i such that
 372 $\sum_{i=1}^{N-k} m_i = N$. Finally, at time t_{N-1} we create a single cluster of mass N that combines
 373 all points c_i^0 ; this cluster forms the root of the tree \mathbb{T} .

374 Consider two nodes a and b from the nearest-neighbor tree and let t_a and t_b be their
 375 time marks; recall that the tree is time-oriented by the definition of the successive times
 376 $t_k = \min_{ij} d_{ij}^k > t_{k-1}$ at which the cluster mergers occur. The *ancestors* of a node are its
 377 parent, the parent of that parent, and so on, all the way to the root. Clearly, the time
 378 mark for an ancestor is larger than that of a descendant. The *nearest common ancestor*
 379 p of nodes a and b is their common ancestor with the minimal time mark t_p .

380 The distance $u(a, b)$ along the the nearest-neighbor tree is defined as the maximum of
 381 the values $u(a, p) \equiv t_p - t_a$ and $u(b, p) \equiv t_p - t_b$. This distance satisfies two of the
 382 usual distance axioms, symmetry and strict positivity, but the triangle inequality can be
 383 replaced by a more stringent one, namely

$$u(a, b) \leq \max[u(a, c), u(c, b)],$$

384 which holds for any three nodes a, b and c . Such a distance function is called an *ultrametric*
 385 [*Rammal et al.*, 1986; *Schikhof*, 2007]. Ultrametric spaces have many peculiar properties;
 386 for instance, one can rename *any* triplet a, b, c of nodes in such a way that

$$u(a, c) = u(b, c).$$

387 These unusual properties give ultrametric spaces considerable flexibility in applications,
 388 and point sets connected via nearest-neighbor clustering are a representative example of
 389 such spaces.

390 In the billiard example of Section 5.1, the space \mathbb{S} is the set of N billiard balls and the
391 ultrametric distance function $u(a, b)$ equals the time before the first collision of the balls
392 a and b . Naturally, their distance depends on the initial positions and velocities of the
393 two balls a and b , but it is affected by the global billiard dynamics: our two balls may
394 be set to collide at a given time t^* in the absence of other balls, but may be hit by some
395 other ball at time $t < t^*$, thus postponing the collision of a with b .

396 In our river transport problem, the space \mathbb{S} is the set of all river sources. The ultrametric
397 distance $u(a, b)$ between two sources is defined as the time necessary for the corresponding
398 fluxes injected into these two sources to meet down the river path. If the static river
399 geometry is described by the tree \mathbb{T}_S — and we assume, as previously stated, that fluxes
400 move with unit speed downstream — the traditional distance $d(a, b)$ between two sources
401 equals the maximal length along the tree to their nearest common parent in \mathbb{T}_S . The
402 nearest-neighbor spanning tree of hierarchical-aggregation theory becomes what we called
403 so far, in the context of river transport, the dynamic tree \mathbb{T}_D . As previously stated, this
404 dynamic tree differs, in general, from the static tree \mathbb{T}_S and depends not only on the
405 topology of the latter, but also on the actual length of the links. If the velocities vary
406 in time or space, then the spanning tree \mathbb{T}_D will depend on the specific dynamics of the
407 processes operating on the static tree.

408 To better understand transport on river networks, we will elucidate in the next section
409 the connection between the statistical properties of \mathbb{T}_S and those of \mathbb{T}_D .

6. Analysis of drainage networks

410 In this section we quantify similarities and differences between the branching topology
411 of static and dynamic trees, both at the stream and hillslope network scale.

6.1. Data description

412 We have analyzed three river basins: Upper Noyo (Mendocino County, California, USA),
413 Tirso (Sardinia, Italy), and Grigno (Trento, Italy). Information about the physiographic
414 and geologic characteristics of these basins can be found in, respectively, *Sklar et al.*
415 [2006], *Pinna et al.* [2004], and *Guzzetti et al.* [2005]. The available DEMs were at a
416 resolution of 10×10 m² for the Noyo basin, 30×30 m² for the Grigno basin, and 100×100
417 m² for the Tirso basin. Since the focus of this study is not the extraction of the most
418 accurate river network from the available DEMs, we felt comfortable adopting a simple
419 criterion for channel initiation as 100 pixels for all basins. Our main conclusions about
420 the comparison between the static and dynamic trees would not be affected by changing
421 the critical threshold areas within reasonable ranges.

422 The static trees we extracted from these DEMs for the three stream networks are shown
423 in Fig. 8. Using the procedure described earlier, we also extracted the static trees for
424 the hillslope networks, which drain every pixel of a basin, by using a steepest gradient
425 algorithm. The corresponding dynamic stream and hillslope trees were then constructed
426 for each basin, assuming a constant unit speed of downstream propagation for the fluxes.
427 Thus, we analyzed four different kinds of tree — static stream, dynamic stream, static
428 hillslope, and dynamic hillslope — for each basin.

6.2. Self-similar properties

429 Figures 9 and 10 show the distributions of the number N_r , average magnitude M_r , and
430 the average number C_r of links for branches of order r . The results in Fig. 9 refer to the
431 stream trees; the results in Fig. 10 to the hillslope trees.

432 Despite the small-sample fluctuations, the figures demonstrate a large degree of con-
433 sistency among the branching indices for the trees from different classes. All considered
434 branching statistics are closely approximated by the Horton laws. Moreover, the results
435 suggest that the relationship (9) holds in all the considered cases. Furthermore, we ob-
436 serve that the values of the stream ratios for static trees are higher than the corresponding
437 values for dynamic trees; and the values of the stream ratios for stream trees are smaller
438 than the corresponding values for hillslope trees.

439 The only indices that considerably deviate from the Horton laws at higher orders are C_r
440 (average number of nodes within an order- r branch) for the Noyo basin and this warrants
441 special investigation in the future. Apart from this discrepancy, overall we conclude that
442 the four classes of trees, dynamic vs. static and stream vs. hillslope, can be closely
443 approximated by the Tokunaga SSTs.

6.3. Phase transition in hierarchical dynamics

444 Here we ask the question as to whether the river network connectivity (in terms of
445 elements of the network participating in transport) exhibits a *phase transition* akin to those
446 found in other systems. Figure 11 shows the fractional magnitudes m_i/N of the branches
447 in the dynamic trees (stream and hillslope trees of the three river basins) as a function
448 of the distance d traveled by the dye. Recall that this distance can also be interpreted as
449 the time t when the node was created by merging of upstream branches. Altogether we
450 consider six cases; in all of them one observes the following scenario. We start at distance
451 $d = 0$ (or time $t = 0$) with N branches (clusters) of unit magnitude corresponding to the
452 most outer nodes of the transport tree. As distance increases (time evolves), the number of
453 clusters decreases while their magnitudes become larger and exhibit prominent variability.

454 In particular, at the small distances the maximal magnitude increases exponentially with
455 distance; this is reflected by an approximately linear form of an upper envelop of the
456 points in the figures (the envelop is not shown). Furthermore, we notice that at the small
457 distances (times) the magnitude distribution is “continuous” in a sense that it does not
458 have significant gaps. However, at some critical time t^* (translated here to distance d^* for
459 easier interpretation), the distribution undergoes a serious qualitative change: a prominent
460 maximal cluster appears, such that its magnitude becomes significantly larger than that
461 of the second larger cluster. Moreover, while the magnitude of the largest cluster keeps
462 growing, the rest of the distribution is fading off so after some time all clusters present
463 at $d = 0$ merge with the largest cluster. An interesting observation is that at the critical
464 distance d^* the magnitude of the largest cluster is just about 10% of the total magnitude
465 N of the system. Notably, this number is universal for all the considered examples.

466 Figure 12 shows the magnitude distribution of the clusters that existed when the dye
467 traveled a given distance d . The analysis is done for the critical distance d^* and a smaller
468 distance $d \approx d^*/2$; they are both indicated by vertical lines in Fig. 11. In all six cases, we
469 see that the magnitude distribution at the smaller distance (squares) has an exponential
470 tail, while at the critical distance (circles) it is a power law. Recall that, in a log-log plot,
471 power-law behavior shows up as a straight line, while exponential behavior becomes a
472 convex curve. This change indicates that a phase transition occurs at the distance d^* .

473 This phase transition is further illustrated in Fig. 13, which shows three snapshots of
474 the dye propagating down the Noyo basin. The distances traveled by the dye at these
475 snapshots are marked by vertical lines in Fig. 14; the figure shows the number of clusters

476 (dotted line) and the magnitude of the largest cluster for the Noyo dynamic tree (solid
477 line), as a function of downstream propagation distance.

478 The values of the six critical distances d^* shown in Fig. 11 vary over two orders of
479 magnitude and depend strongly on the particular network being analyzed. Nevertheless,
480 we notice a very good power-law fit for the value of d^* in terms of the average link length
481 \bar{L} of the corresponding static tree (see Fig. 15):

$$d^* \approx 3.5 \bar{L}. \quad (10)$$

482 This relationship can be interpreted as follows in terms of the transport on river networks:
483 the giant cluster of connected streams is formed when each flux traveled approximately
484 3.5 links downstream from a source. We conjecture that: (a) this is a universal property
485 of downstream transport on Tokunaga trees with rich branching, *i.e.* Tokunaga SSTs
486 with $c > 1$ in Eq. (5); (b) the coefficient of proportionality in (10) may depend on the
487 Tokunaga parameters, but only weakly; and (c) this coefficient is larger than or equal to
488 2 for *any* binary tree. An in-depth investigation of this issue is left for future study.

7. Concluding remarks

7.1. Summary

489 This study focused on the statistical description of environmental transport on self-
490 similar river networks. We approached the problem by considering downstream transport
491 on such a network as a particular case of nearest-neighbor *hierarchical aggregation*; the
492 so-called *ultrametric* induced by the branching structure of the river network provides the
493 distance function with respect to which the downstream flow gives rise to clusters that
494 decrease in number and increase in size with time.

495 We described the static topological structure of a drainage network by the type of
496 tree structure that goes back to the pioneering studies of *Horton* (1945), *Strahler* (1957)
497 and *Shreve* (1966), and referred to it as a *static tree*, to distinguish it from the associated
498 *dynamic tree*. This novel concept introduced herein describes downstream transport along
499 the static tree.

500 We studied the statistical properties of both static and dynamic trees using the Horton-
501 Strahler (HS) and *Tokunaga* (1978) branching taxonomies. Using three river networks —
502 the Noyo, Grigno and Tirso — we showed that both static and dynamics trees can be well
503 approximated by Tokunaga *self-similar trees (SSTs)*. The HS and Tokunaga parameters
504 of these two types of trees differ significantly, though, for each of the three basins. This
505 difference supports the relevance of the dynamic tree concept; its parameter values depict
506 important properties of the transport on a given river network that are not captured by
507 the conventional, static tree.

508 A striking result of this study is the phase transition we found in river network dynamics:
509 as one fills an empty river network through its sources, or injects a dye into a water-filled
510 one, the number of clusters of connected nodes decreases and the size of the largest cluster
511 increases, until a dominant cluster of connected streams forms. During this process, the
512 time-dependent size distribution of the connected clusters changes from an exponential to
513 a power-law function as the critical time approaches.

514 This phenomenon, which may seem rather unexpected in the present, hydrological set-
515 ting, can be better understood within the framework of complex networks. This frame-
516 work has been explored in many natural and socio-economic settings, ranging from the
517 functioning of a cell to the organization of the internet [*Albert and Barabasi*, 2002]. The

518 mathematical theory of complex networks considers a group of nodes that can be con-
519 nected with each other according to some problem-specific rules, thus forming a graph. In
520 the simplest case, the node connections are independent of each other and can be specified
521 by the probability p that two randomly chosen nodes are connected. There exists a critical
522 value p_c such that for $p < p_c$ the network consists of isolated clusters, while a single giant
523 cluster appears as p crosses p_c , and spans the entire network. The appearance of this
524 giant cluster is remarkably reminiscent of infinite-cluster formation in percolation theory
525 [Stauffer and Aharony, 1994]. Albert and Barabasi [2002] provide a comprehensive review
526 of parallels and differences between complex-network theory and percolation theory.

527 It readily follows from the analysis of Section 3 that the transport on river basins fits
528 rather naturally the complex-network paradigm. Formally, each river source is represented
529 by a node and two streams are considered to be connected when their respective fluxes
530 join downstream. This is exactly the scheme we used to define a dynamic tree, with the
531 only difference that we ignored the node connections within already formed clusters. This
532 difference does not affect the process of cluster formation, so all the results of complex-
533 network theory do apply to the envirodynamics of river basins.

534 There is an important difference, though, between complex networks in general and
535 the dynamic trees considered in this study. Our dynamic trees, unlike general networks,
536 are time-oriented, *i.e.*, their nodes can be ordered according in “time” or with respect
537 to a “distance” parameter. The ultrametric distance along such trees satisfies a stronger
538 triangle inequality than ordinary distance (see Section 5.2). Spaces equipped with an
539 ultrametric u , instead of a traditional distance d , have therefore interesting properties [*e.g.*
540 Schikhof, 2007]. As shown in Section 5, hierarchical aggregation via nearest-neighbor

541 clustering provides a common framework for many apparently different processes — e.g.,
542 billiards, river transport, and percolation — in the setting of ultrametric trees, and thus
543 may provide novel insights into these processes.

544 In percolation models, the cluster-size distribution at phase transition is given by a
545 power law, whose index is a function of the system’s dimension alone. In our three river
546 networks, this index differs from the one to the other, and from the river to the hillslope
547 network for the same basin. In our hierarchical aggregation on dynamic trees, different
548 clustering rules may correspond to different effective “dimensions” of the system. At the
549 same time, it is known that the critical percolation indices are universal for systems in high
550 dimensions [*Hara and Slade*, 1990] and trees are a simple model for infinite-dimensional
551 systems [*Albert and Barabasi*, 2002]. Thus, one expects to see the same values of the
552 critical indices when working with percolation on a tree. From this perspective, the fact
553 that our critical exponents vary from basin to basin, and from river to hillslope trees, still
554 needs to be understood.

7.2. Discussion and further work

555 In this study we considered only the simplest clustering rules for the river streams: two
556 streams belong to the same cluster if there is a connected path from one stream to another
557 along the river network. This approach is patterned after percolation studies and allows
558 for a straightforward treatment. It might however result in a situation when two streams
559 belong to the same cluster despite the fact that the respective fluxes are not mixed yet
560 (think of two short streams that merge with a spatially extended cluster at about the
561 same time). Formulating a physically more appropriate set of clustering rules might yield
562 more realistic results for a wealth of river networks with differing properties.

563 So far, we only investigated dynamic trees that have the same set of leaves as the
564 corresponding static tree; this corresponds to injecting a flux through the sources. At the
565 same time, it might happen that a flux of interest is injected into an internal node, *e. g.*,
566 an industrial pollutant from a plant or nutrient production from a local biotic activity.
567 Such situations can be easily modeled by considering a dynamic tree whose set of leaves
568 samples the entire river network.

569 To construct a richer theoretical framework for transport on river networks one may also
570 model the transport along real and synthetic networks by using Boolean delay equations
571 (BDEs). In BDEs, the discrete state variables describe the flux through the river branches;
572 naturally, the rules for updating these variables inherit the child-parent relationship of the
573 stream's static tree. The parent variables are updated based on the values of the children
574 variables, after delays that correspond to time of flux propagation from a child to its
575 parent. *Ghil et al.* [2008] reviewed recently BDEs and their applications to climate and
576 earthquake modeling. We expect such modeling to shed further light on the complex and
577 important problems of river transport.

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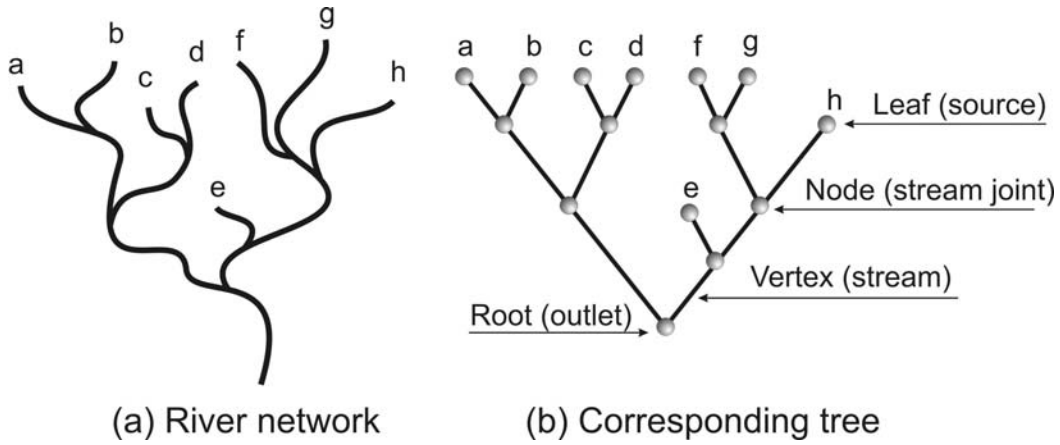


Figure 1. Tree representation of a river network: (a) hypothetical river network; and (b) its representation by a binary tree. The network sources and the respective tree leaves are marked by the same letters in both panels. The figure also illustrates the terminology used in our river transport study.

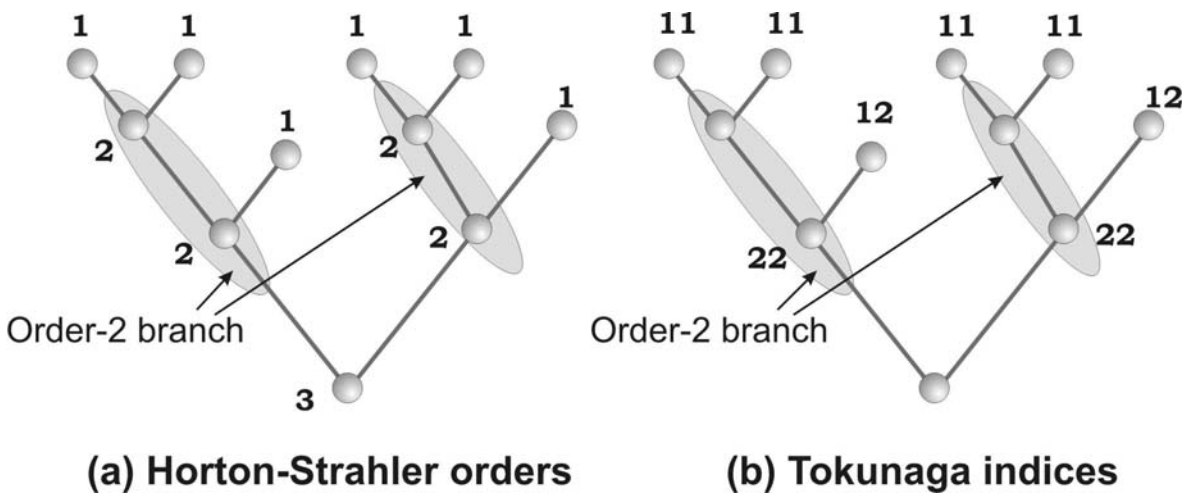


Figure 2. Example of (a) Horton-Strahler ordering, and (b) Tokunaga indexing.

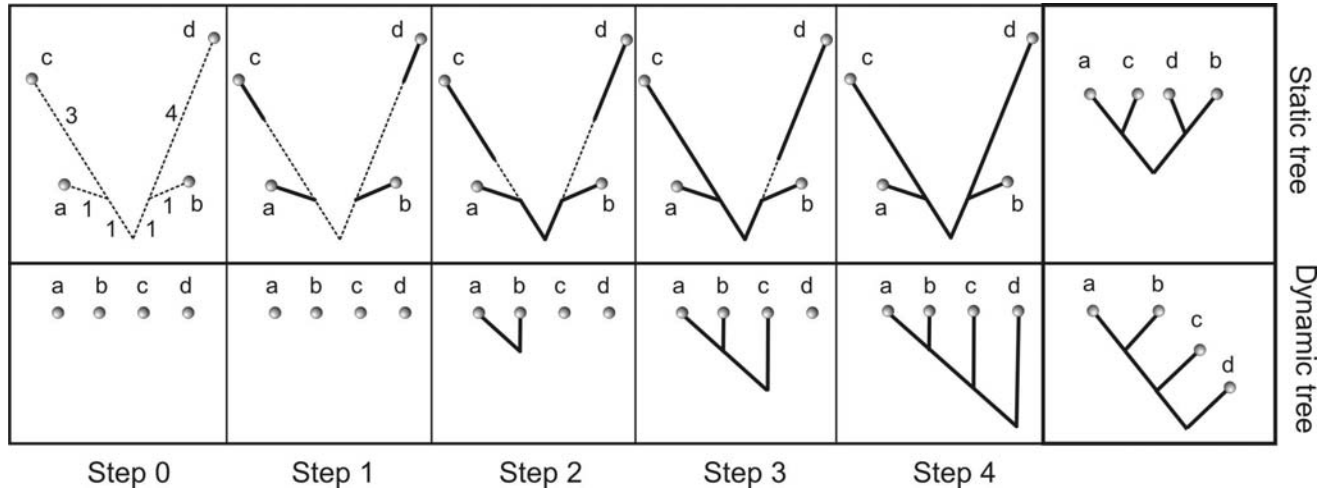


Figure 3. Constructing a *dynamic* tree. The initial static tree and the final dynamic tree are shown in the rightmost pair of panels. The dynamic tree reflects the propagation of a flux from leaves to the root of the static tree at a constant velocity. The top row of panels shows the static tree at different steps of this process; for visual convenience we explicitly show the static tree’s link lengths. The bottom row shows the corresponding phases of the dynamic tree. The top leftmost panel indicates the lengths of the links in the static tree; each step in the figure takes one time unit, that is the flux propagates one unit of length downstream. See Section 3.1 for details.

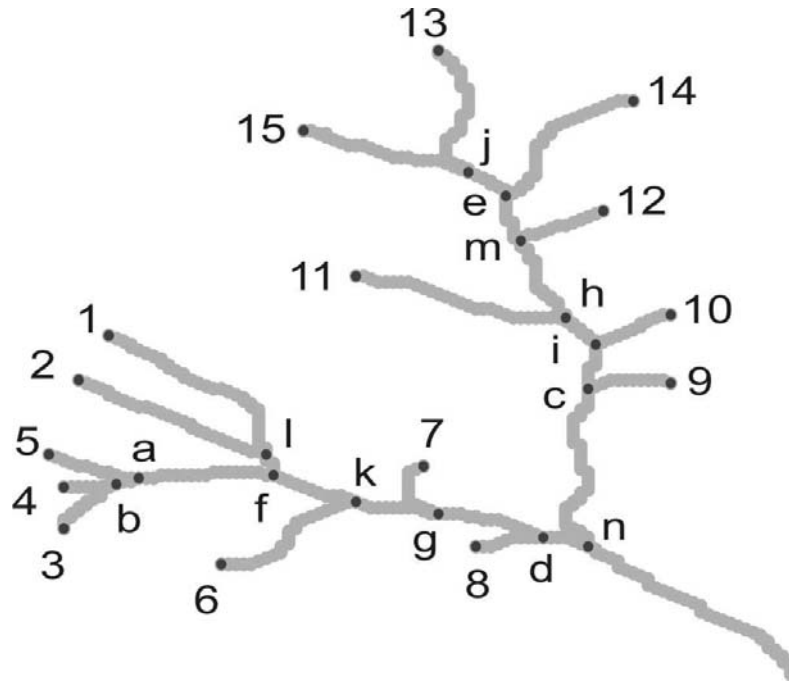


Figure 4. Stream network for an order-3 subbasin of the Noyo river basin, Mendocino county, California. Sources are marked by letters, stream merging points by numbers. The same marks are used in Figs. 5 and 6 that show the static and dynamic trees for this stream.

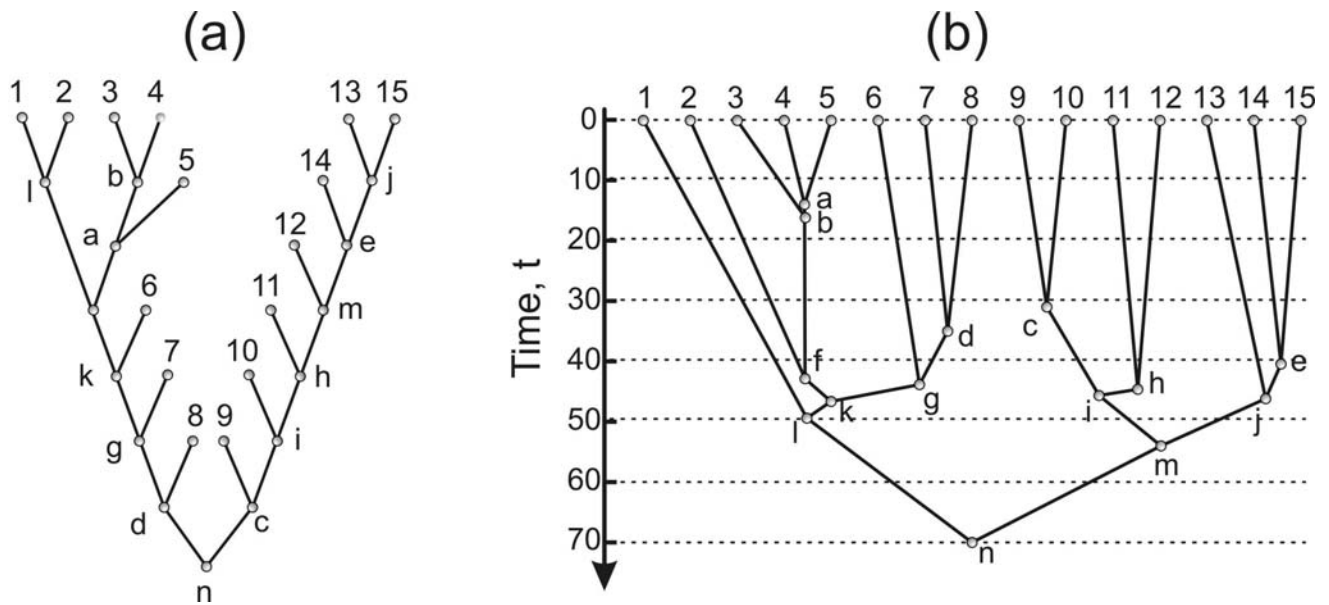


Figure 5. Static and dynamic trees for the Noyo subbasin of Fig. 4. (a) Static tree \mathbb{T}_S and (b) dynamic tree \mathbb{T}_D . Letter and number marks are the same as in Fig. 4.

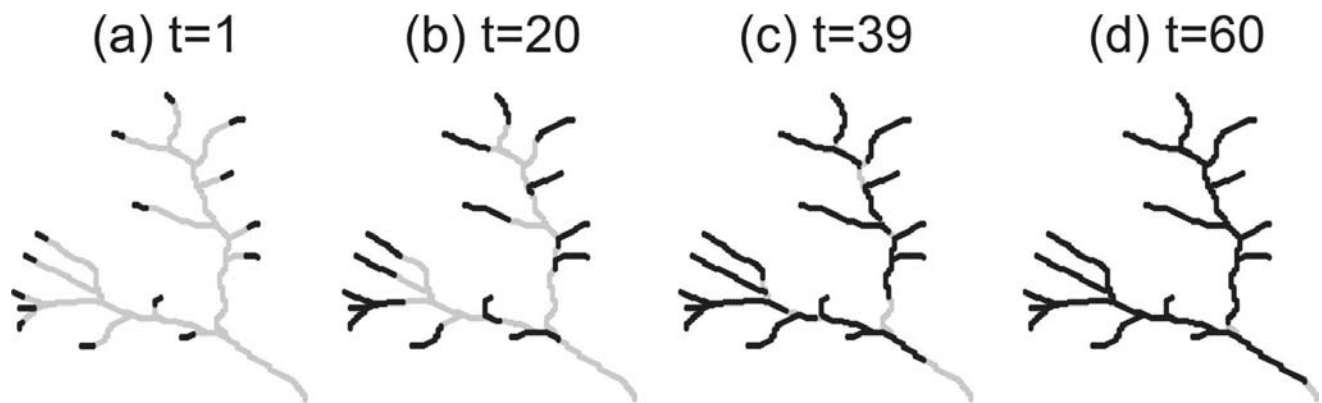


Figure 6. Three snapshots of the evolution of the dynamic tree (heavy solid lines) on the static tree (light solid lines) for the stream of Fig. 4. Letter and number marks are the same as in Fig. 4.

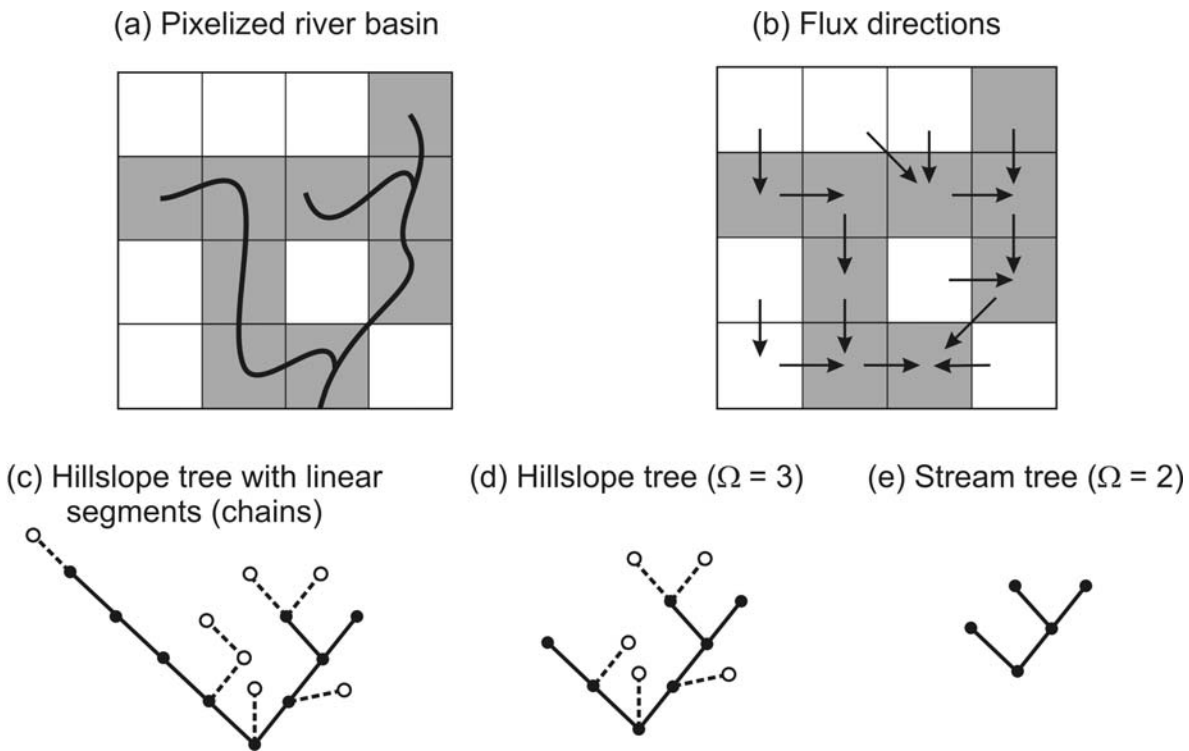


Figure 7. Construction of a *static* tree that represents the topology of hillslope (unchannelized) and stream (channelized) drainage paths. (a) Pixelized river basin; the shaded pixels (cells) correspond to the stream location (solid line), the white pixels – to the valleys or hillslopes. (b) Flux direction obtained from the elevation data. (c) Tree that describes the drainage topology: solid nodes and links correspond to the stream pixels and stream flow; open nodes and dashed links – to the hillslope pixels and hillslope flow. Notice that this tree contains several purely linear segments, with no branching. (d) The same tree, from which the linear segments have been removed: it describes the topology of both hillslope paths and stream paths, and is referred to as the *hillslope tree*. (e) The subset of the tree in panel (d) that describes the topology of the stream paths only; this tree is referred to as the *stream tree*.

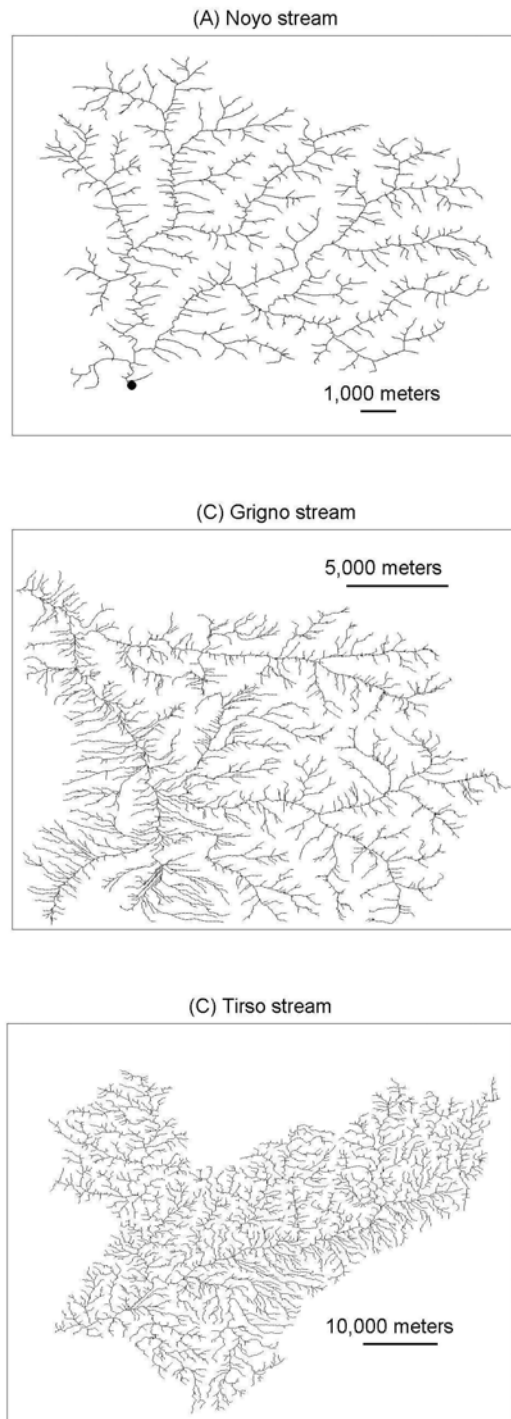


Figure 8. Static trees for the stream networks of the three basins analyzed in this study. a) Noyo, Mendocino County, California, USA; the outlet is marked by a ball; b) Grigno, Trento, Italy; c) Tirso, Sardinia, Italy. See Section 6.1 for details of channel initiation.

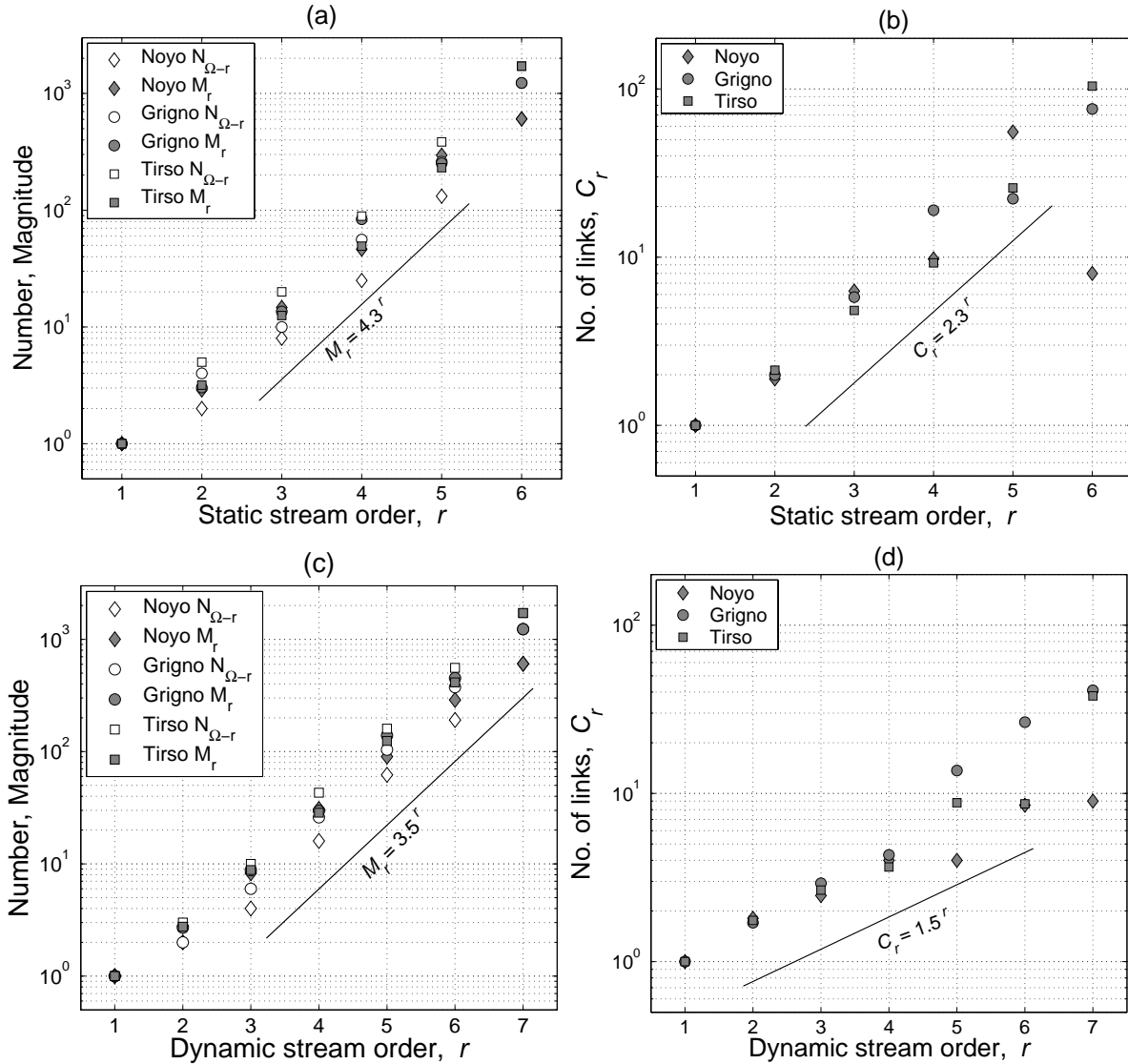


Figure 9. Branching statistics for the stream trees of Noyo, Grigno, and Tirso basins. Number N_r and average magnitude M_r for static (panel a) and dynamic (panel c) trees and average number C_r of links within a branch for static (panel b) and dynamic (panel d) trees.

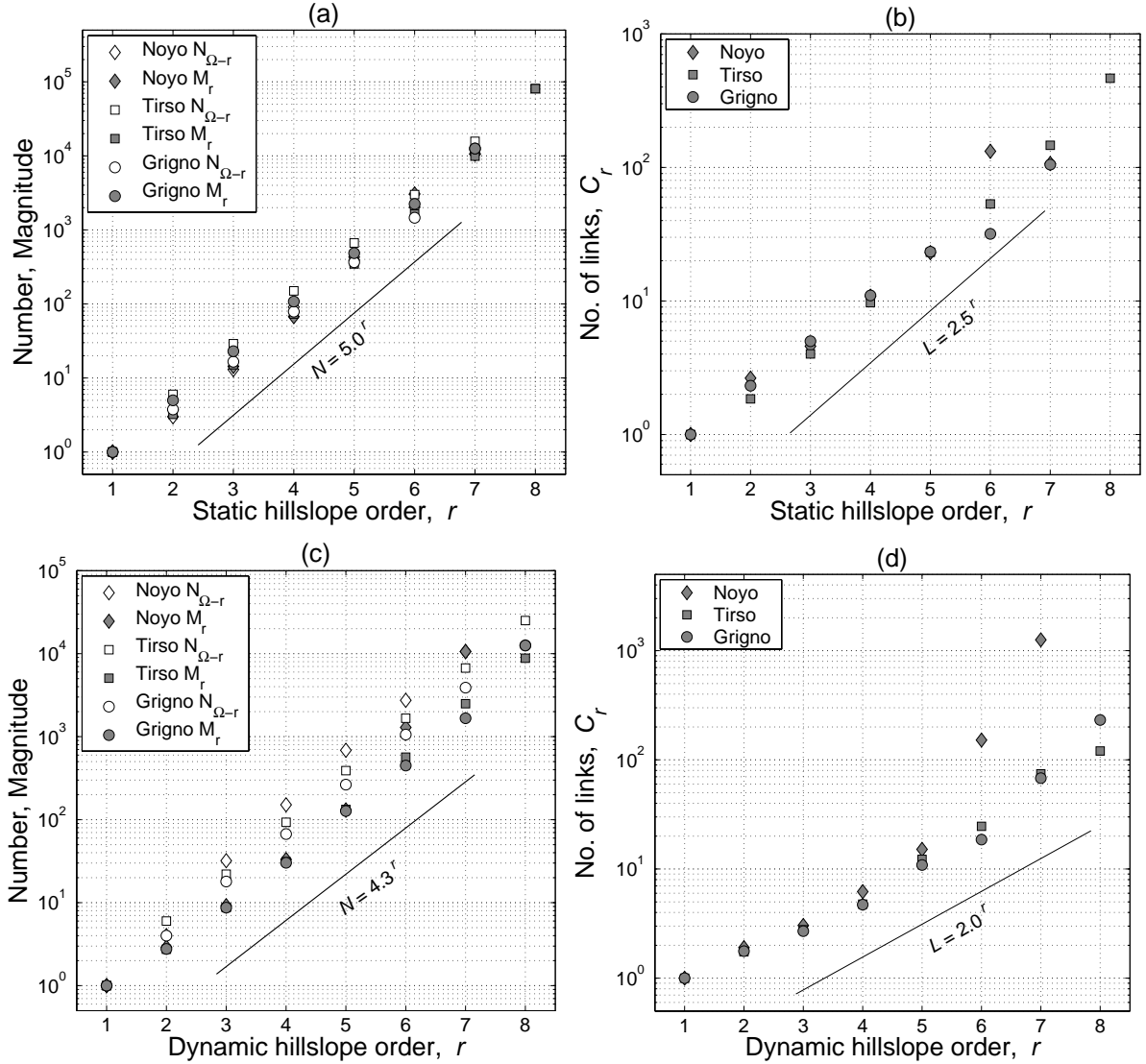


Figure 10. Branching statistics for the hillslope trees of Noyo, Grigno, and Tirso basins. Number N_r and average magnitude M_r for static (panel a) and dynamic (panel c) trees and average number C_r of links within a branch for static (panel b) and dynamic (panel d) trees.

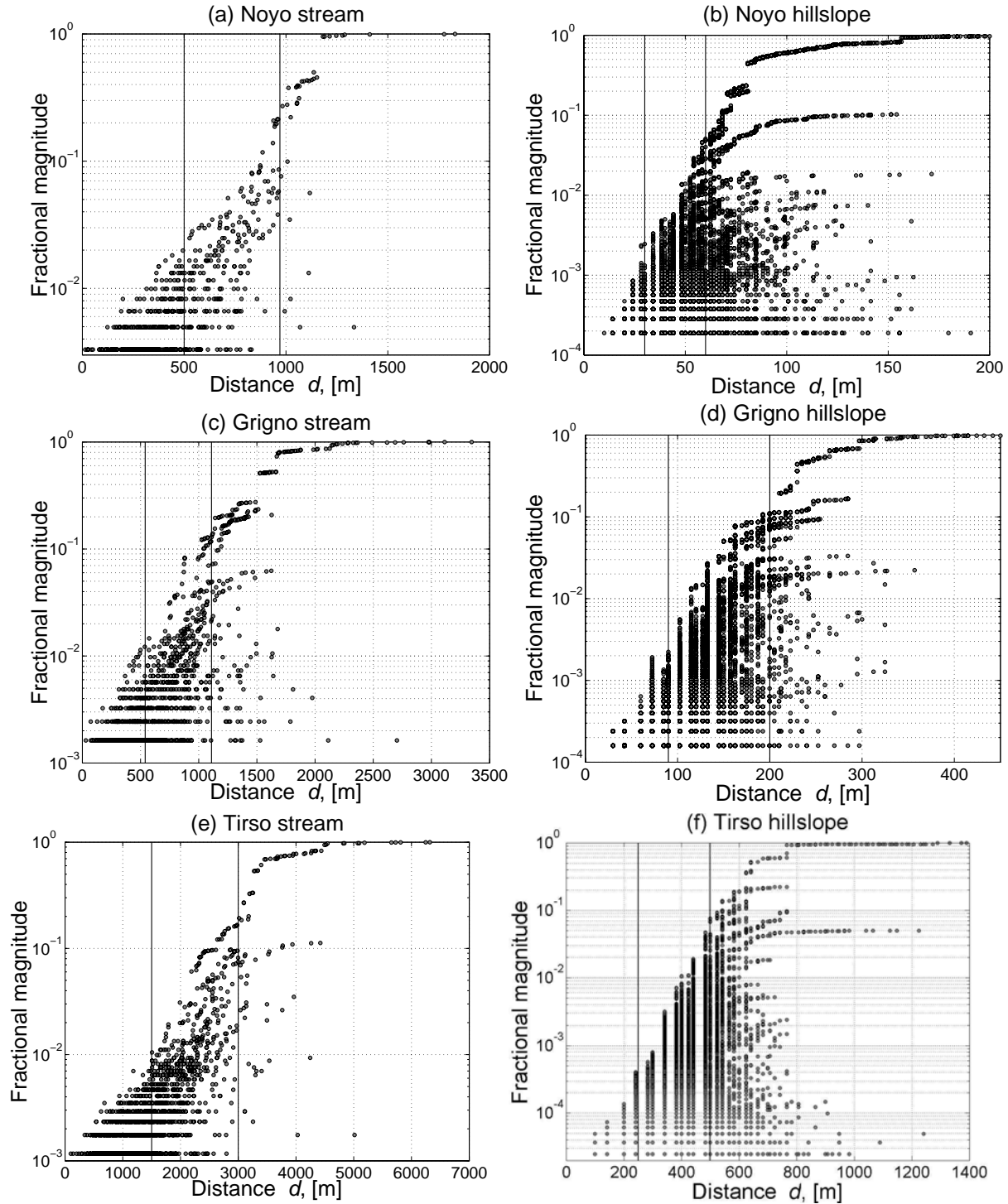


Figure 11. Fractional branch magnitudes m_i/N as a function of the distance d_i traveled by the dye at the branch creation instant. Notice that the distance d_i can be interpreted as the time t_i necessary to create the branch. a) Noyo stream; b) Noyo hillslope; c) Grigno stream; d) Grigno hillslope; e) Tirso stream; f) Tirso hillslope.

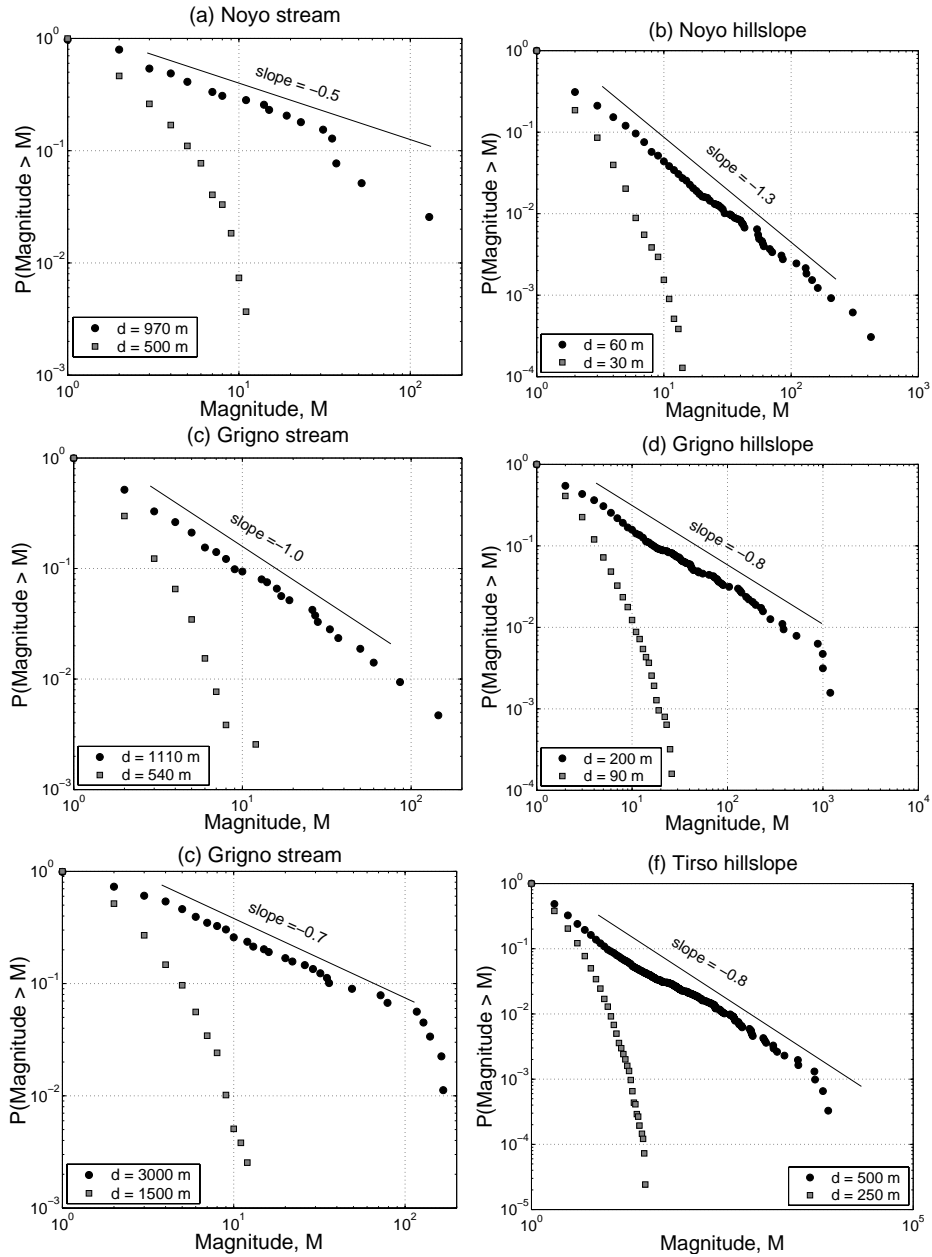


Figure 12. Distribution of branch magnitudes m_i at the critical distance d^* (balls) and at an earlier time (squares) in dynamic trees for the three basins. a) Noyo stream; b) Noyo hillslope; c) Grigno stream; d) Grigno hillslope; e) Tirso stream; f) Tirso hillslope. Each panel shows two distributions, the corresponding distances are depicted by vertical lines in Fig. 11. Notice that the value of the critical distance d^* can be interpreted as the critical time t^* necessary to create the critical cluster. The downward deviations from the pure power laws are due to the finite-size effect.

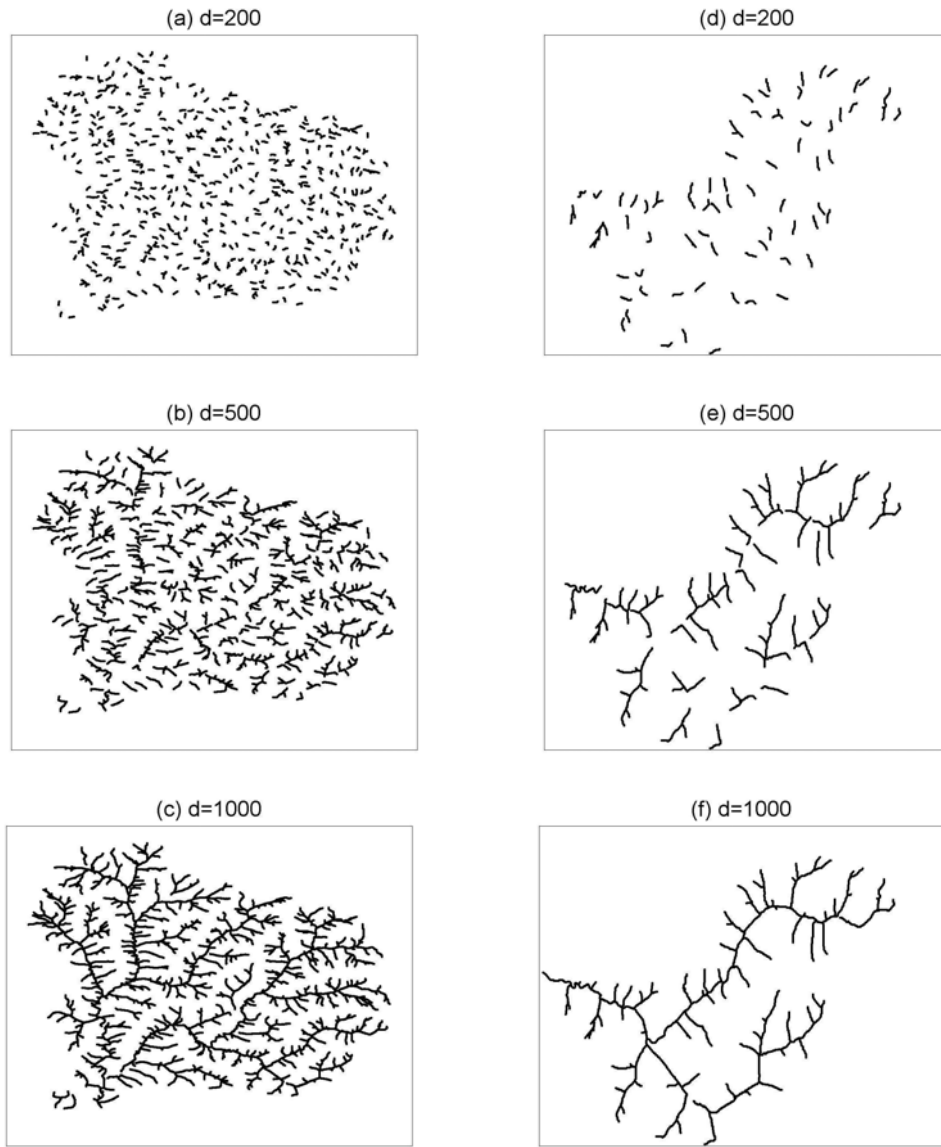


Figure 13. Transport down the Noyo stream network. Three snapshots of flux propagation from the stream sources to the outlet, at (a,d) $d = 200$, (b,e) $d = 500$, and (c,f) $d = 1000$. Panels (a)–(c) show the entire Noyo basin, while panels (d)–(f) zoom onto an order-4 subbasin located in the lower right part of the entire basin. See also Fig. 14.

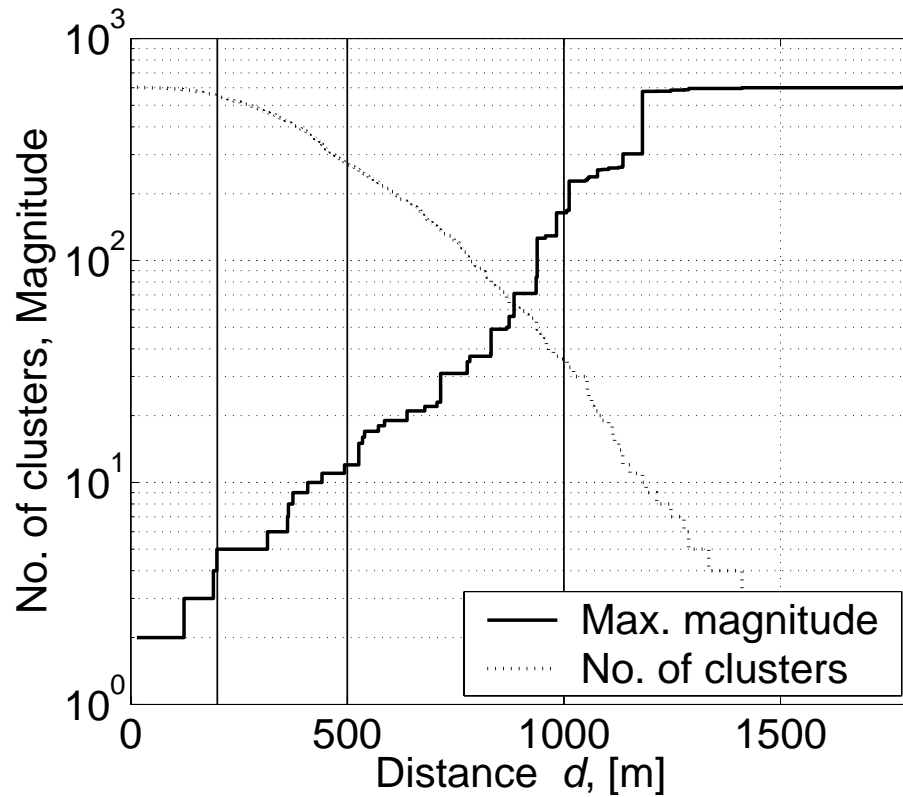


Figure 14. Cluster evolution for the Noyo downstream flux transport: number (dotted line) and largest-cluster size (solid line). Vertical lines correspond to the three snapshots in Fig. 13.

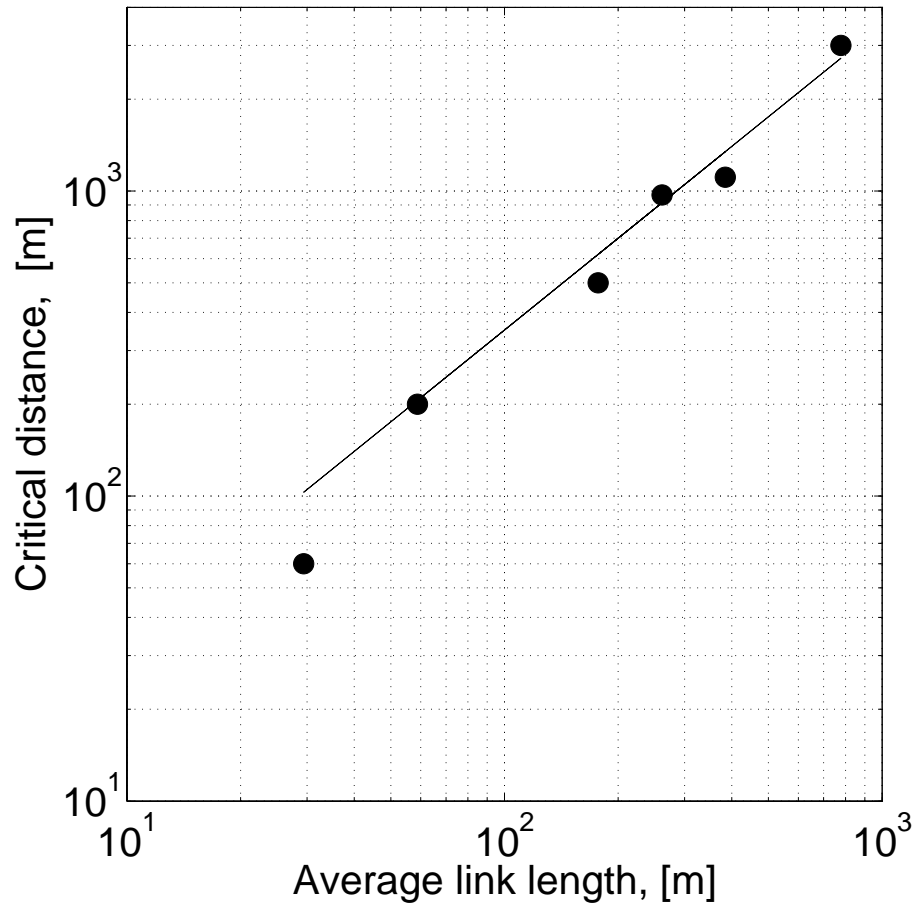


Figure 15. Critical distance d^* as a function of the average link length \bar{L} for the six dynamic trees shown in Fig. 11. The line in the figure corresponds to $d^* = 3.5 \bar{L}$.