MODEL OF SPATIAL ORGANIZATION OF VEGETATION IN RIVER FLOODPLAINS

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ABSTRACT

In the framework of landscape ecology, we propose to modelize the spatial organization of vegetation in river floodplains. This model is based on the generation of non-homogeneous, anisotropic random patterns defined on a square lattice given the knowledge of the ecological functioning of these ecosystems. This model proceeds in two steps.
First, geographic information is computed (distances to the nearest dead arm and to the nearest active channel, convexity and concavity,...) using information about whole hydrographic network of channels (presently and pastly created by the fluvial dynamic). This leads to a first tesselation of the image.Then a set of probabilities of occurrence of each vegetation type is assigned to each site.
Second, a random number, weighted by the probability of the observed vegetation, is assigned to each site; then the consolidation can process. The weakest sites are eliminated while the strongest, called the survivors, extend their frontiers and incorporate the sites just deleted. The two processes, decimation and expansion, are recursive and parallel.
At every hierarchical level, islands and channels contents are updated; this allows or not the expansion of vegetation, with respect of the probabilities. Each vegetation of each element has its own expansion criteria (vegetation, geographical proximity or random choice).
The resulting patterns are not segmentations of the tesselation defined by initial geographic information. On the contrary, they present a stochastic appearance which reflects both the stochastic appearance and the spatial determinism of vegetation spatial organization in river floodplains due to the fluvial dynamic.

Key words: stochastic pyramid, spatial pattern, modelization, river floodplain.

INTRODUCTION

The spatial organization of vegetation in given areas can be viewed as the spatial organization of different colors in images, each color being associated to a vegetation type, called more precisely functional unit. We propose a modelization to describe such patterns that will be elaborated and tested on the vegetation of a large river floodplain, the Rhône river, characterized by the diversity of its components. Indeed, the fluvial dynamic determines the habitat diversity by the erosion-deposition processes that create biotopes (Bravard et al., 1986). Then each fluvial landform may be colonized by different vegetation types that may replace each other over time (Amoros et al., 1987). Consequently the real patterns are containing both a stochastic appearance and a spatial determinism. We will try to create them on synthetic images.
This model is based on a recent generation of non homogeneous, anisotropic random patterns defined on a square lattice, the stochastic pyramid (Meer et Connelly, 1989), that we have

constrained by the knowledge of the ecological functioning of these ecosystems. It proceeds in two steps, which are iterated until stabilization: the first process is called decimation and the second one expansion. The principle consists in eliminating some of the sites and in expanding the others. The data structure used is an image pyramid (Jolion et Rosenfeld, 1993) that represents, at each level of its hierachy, the state of the survivors expansion.

THE STOCHASTIC PYRAMID

The stochastic pyramid (Meer et Connelly, 1989; Meer, 1989) is based on a hierarchy of seed structures. Its base, the first level, is represented by the lattice. The neighborhood of each site is defined by the allowed connectivity type (4 or 8), and consequently each site has 4 or 8 neighbors. Each site (i,j) of level l, say (i,j,l), is called seed, and we define its support $S_{ij}(l)$ as the set of seeds formed by (i,j,l) and all the adjacent seeds connected to it. These connected seed structure can be regarded as a realization of a regular graph defined on the lattice, with the site as vertices and the connections defining the supports as edges.

During the upper levels, a local decimation process eliminates some of the sites, which are all incorporated by the remaining seeds. These survivors are growing and becoming cells of various sizes, and only they keep the appellation of seeds. This second process is called expansion. Two seeds are neighbor if and only if the cells derived from them are adjacent, $i.e.$ these cells have a common border. So the support $S_{ij}(l)$ is always defined as the set of seeds formed by (i,j,l) and all the adjacent seeds (n,m,l) connected. The new graphs are not regular, because of the stochastic functionning of the decimation and expansion processes: we can say they are random graphs.

The same algorithms can be applied to each level of the hierarchy l, $l \in [0,L]$, the random graph of level 1 deriving from level $l-1$. The seeds always correspond to locations on the initial square lattice, and their density decreases with level. The connected seed structure at every level is a random graph constrained to local connections.

The decimation process

The decimation process is local, based on information available in a small, compact neighborhood: the support $S_{ij}(l)$. Each seed (i,j,l) is characterized by three variables, $p_{ij}(l)$, $q_{ij}(l)$ and $x_{ij}(l)$.

The variables $p_{ij}(l)$ and $q_{ij}(l)$ are binary states variables, and $x_{ij}(l)$ is an outcome of the random variable $X_{ij}(l)$ with continuous probability density function $f(x)$, uniform on $[0,1]$. The first state variable accounts for the afterlife of each seed between each level: $p_{ij}(l)=1$ if and only if (i,j,l) is not decimated.

At the beginning of the local decimation procedure, the first state variable is initialized at 0 for any seed of the lattice. Then a process of search of the locally largest outcome $x_{ij}(l)$ is applied. The following principles must be respected as we want to employ only parallel local processes:

- any decimated seed at level l has at least one survivor in its neighborhood and thus can be allocated to it by a local decision;
- two adjacent seeds on level l cannot both survive at level $l+1$.

A single state variable is not sufficient, that is why the two state variables p and q are used.

The decimation process can be formalized in two steps for the level l. The first is concerned with the search of the real local maxima of every supports, the outcomes $x_{ij}(l)$ being compared with the neighbouring outcomes $x_{nm}(l)$ weighted by a connection weight $\lambda_{nm}(l)$ that we will describe later; the second, once these ones put aside, concentrates on extracting the local sub-maxima.

Algorithm:

$$ 1) \quad p_{ij}(l) = \begin{cases} 1 \Leftrightarrow x_{ij}(l) = \underset{nm \in S_{ij}(l)}{Max} (\lambda_{nm}(l)x_{nm}(l)) \\ 0 \quad otherwise \end{cases} \tag{1} $$

2) *do until stabilization*

a) $q_{ij}(l) = \begin{cases} 1 \Leftrightarrow p_{nm}(l) = 1 & \forall\ nm \in S_{ij}(l) \\ 0 & otherwise \end{cases}$ (2)

b) $p_{ij}(l) = 1 \Leftrightarrow x_{ij}(l) = \underset{\begin{cases} nm \in S_{ij}(l) \\ q_{nm}(l) = 1 \end{cases}}{Max}(\lambda_{nm}(l)x_{nm}(l))$ (3)

These two steps are iterated until no decimation is possible. This stage is reached when only one seed remains on the lattice, and the pattern is formed of a single cell which occupies the whole image.

The expansion process

The expansion process exploits the result of the decimation process: it chooses for every decimated seed the survivor which has the largest outcome $x_{ij}(l)$ and which belongs to its neighborhood: it is noted $NM_{ij}(l)$. We can say that each survivor, in order to define its cell, tries to conquer the decimated seeds close to it. This expansion process is parallel on the random graph but locally sequential for the expanding seeds.
Let (i,j,l) with $p_{ij}(l)=0$, its largest neighbor is:

$$NM_{ij}(l) = Seed\left(\underset{\begin{cases} nm \in S_{ij}(l) \\ p_{nm}(l) = 1 \end{cases}}{Max}(x_{nm}(l))\right)$$ (4)

Heterogeneity and directional preferences

The density of seeds decreases with level, and the size of the survivors increases because of the expansion process. At the beginning, the tessellation is very fine, since each pixel of the lattice is a cell by itself. Next, the level *1* is formed by cells with two or three pixels; and the level *2*, which is a concatenation of the level *1*, has bigger cells. The average size of the new cells increases with the level, and the coarseness of the new patterns is more and more important. At the end of the process, the apex of the pyramid, there is only one seed, and, consequently, only one cell. A hierarchy of random tessellations is obtained.
The random patterns are represented by allocating to each cell one of *256* gray level values. The cells are colored independently, top-down in the hierarchy, in order to preserv parallelism in the processing. A large cell from level *l* can always be represented on the lattice of level *0* as the concatenation of smaller cells taken from any level below *l*. This allows the construction of non homogeneous random patterns in which different regions have different coarseness (Meer and Connelly, 1989).
Anisotropy can be introduced both at the cells delineation stage and at the generation of the seeds structure, with a constant which influences the outcomes in some choosen directions.

CONTROL OF THE STOCHASTIC PYRAMID

In order to control the stochastic pyramid, we propose to precise the weights of the connections between the seeds. We will show that this way is a solution to control isotropy and homogeneity. However, the basis of the processing will be changed. Indeed, instead of using an initial uncolored lattice and coloring cells after decimation and expansion, we will give to each site a color *a priori* which it will try to keep and to expand.
The competition between the sites will still depend on some local rule, but will also depend on some specific local information. This information is determined by the knowledge of the functionning of the floodplain. We assume that the whole hydrographic network of channels, presently and pastly created by the fluvial dynamic, is given. This means that the data is an

image with the drawing of islands, dead arms and active channels, and borders. Geographic information such as distances to the nearest dead arm and to the nearest active channel, distances to upstream and downstream, convexity and concavity,...) are automatically computed. This leads to a partition of each image element in elementary regions, which are characterized by the homogeneity of their geographic locations.

Element partition

Let us define now formally the element e of the image, e is a label, $e \in [1,E]$. How can we have access to each of the elementary regions r ?

First, e is defined by its type t, $t \in [1,T]$. This means that e is an island, a dead arm, a border, etc.. Second e is characterized by its age a, which corresponds to its state of development. The number of possible ages is A_t; it depends on t. We define also a coordinate system which takes into consideration the two dimensions of the floodplain, the longitudinal and the horizontal dimensions. Consequently, each elementary region r is identified by p ($p \in [1,P_t]$) lenghwise and by d ($d \in [1,D_t]$) widthwise. Finally, we can write the elementary region as $r=(e,t,a,p,d)$. The union of all the r is a partition of the image.

Every active (not decimated) seed (i,j,l) is included in such an elementary region r. Before starting the pyramidal process, each seed will take a color c ($c \in [1,C_t]$) compatible with the expected colors of the type t. Then, the seed (i,j,l) is completely defined by (e,t,a,p,d,c), noted sometimes $(e_{ij}, t_{ij}, a_{ij}, p_{ij}, d_{ij}, c_{ij})$.

A priori colors

The choice of c is made *a priori,* with probabilities determined by an ecologist and defined for each region type $z=(t,a,p,d)$, for all the elementary regions $r=(e,t,a,p,d)$, $e \in [1,E]$.
P_z is the probabiliy function which associates to each region type z the probabilities of observing all the possible colors in an element of the type t:

$$\forall t \in T, \; P_z : \left(T \times A_t \times P_t \times D_t \right) \; \rightarrow \; [0,1]^{C_t}$$
$$z = (t,a,p,d) \; \mapsto \; P_z = \left(p_z(1),...,p_z(C_t) \right)$$

where $p_z(c_i)$ is the probability of observing the color c_i in the region type $z=(t,a,p,d)$.
Random coloring is then the simple simulation of a discrete law defined with these weights.

The expansion mode

In the decimation process, each seed (i,j,l) tries to survive and to incorporate some of its neighbours. If we want it to expand itself in a certain direction, because it is "better" in this one and "worse" in the others, in the sense of the local information, we will favour the expansion in the first case and unfavour it in the others. The seed (i,j,l) decides what information must be taken into consideration: this defines the expansion mode. It is a function of local information which produces a constant which weighs the decimation.

Let G be the number of the local informations available on the region type $z=(t,a,p,d)$; G does not depend on t, and $\lambda_z(g)$ the weight associated with the information g. At every region type z, a set of weights can be associated: $\Lambda_z = \left(\lambda_z(1),...,\lambda_z(G) \right)$.

We can compare information on (i,j,l) with these ones of all its neighbors (n,m,l) on the support. Consequently, the weight of the connection between (i,j,l) and (n,m,l) can be seen as the sum of all the positive comparisons and can be written as:

$$\forall \, nm \in S_{ij}(l), \; \lambda_{mode_{ij}}(l) = \sum_{g=1}^{G} \lambda_{z_{ij}}(g_{ij}) \mathbb{1}_{\left\{g_{ij}(l) = g_{nm}(l)\right\}} \qquad (5)$$

where $g_{ij}(l)$ is the gth information available on (i,j,l) defined by $(e_{ij}, t_{ij}, a_{ij}, p_{ij}, d_{ij}, c_{ij})$, noted also (e_{ij}, z_{ij}, c_{ij}).

In order to take account of the relative importance of some of these factors, these weights are not uniform. Each seed (i,j,l) tends to survive and expand itself, *i.e.* it tries to increase the sum of these weights, because the more the weight of the connection, the more chances the seed (i,j,l) survive instead of its neighbor and competitor (n,m,l).

The decimation process

Once the expansion mode is obtained, the decimation process can be formalized in a similar manner as the one used in the stochastic processing. It is just modified. First it suffices to exchange the λ_{nm}, which were characterizing the relative position in the support, with the λ_{mode} which is a dynamic comparison between the seed and its neighbors. Second every outcome x_{ij} is biased by the *a priori* probability, in order to unfavour colors which have only a little occurrence probability, and *vice versa*. So the search of the largest outcome is given as:

$$x_{ij}(l)p_{z_{ij}}(c_{ij}) = \underset{nm \,\in\, S_{ij}(l)}{Max}\left(\lambda_{mode_{ij}}(l)x_{nm}(l)p_{z_{nm}}(c_{nm})\right) \qquad (6)$$

where (i,j,l) is defined by $(e_{ij}, t_{ij}, a_{ij}, p_{ij}, d_{ij}, c_{ij}) = (e_{ij}, z_{ij}, c_{ij})$.
The decimation algorithm is exactly the same, Eq. 6 replacing Eq. 1 and Eq. 3.

The expansion process

The expansion process will use also the λ_{mode} we just defined. We want it to influence, to remain neutral or to unfavour the expansion of the largest survivor (n,m,l) to the detriment of the dead seed (i,j,l). Be careful, the mode of expansion is always specific of the survivor, so we must consider this one of (n,m,l) instead of this one of (i,j,l).
Let (i,j,l) with $p_{ij}(l)=0$, its largest neighbour is:

$$NM_{ij}(l) = Seed\left(\begin{array}{c} \underset{\left\{\begin{array}{l} nm \,\in\, S_{ij}(l) \\ p_{nm}(l) = 1 \end{array}\right.}{Max} \left(\lambda_{mode_{nm}}(l)x_{nm}(l)\right) \end{array}\right) \qquad (7)$$

Non-homogneous and anisotropic patterns are not obtained explicitly. Each cell expands its frontiers in directions according to its expansion mode, *i.e.* in the directions which correspond to the positive comparisons of geographic information. Consequently, the zones in which the expansion is authorized only with the seeds owning to the same zone (the same region in fact) will provide patterns respecting the geographic information, and therefore, the structure already present in the image. Indeed expansion is stopped as soon as some colors tend to expand in zones where there are not expected.
On the contrary, random expansions will not respect directional preferences and the resulted patterns will be random.

The only problem is to stop the expansion without reaching the stage in which some prevailing colors have asserted themselves in every regions, the weakest colors being eliminated. The *a priori* probabilities are then not respected, and the resulting pattern is without any ecological
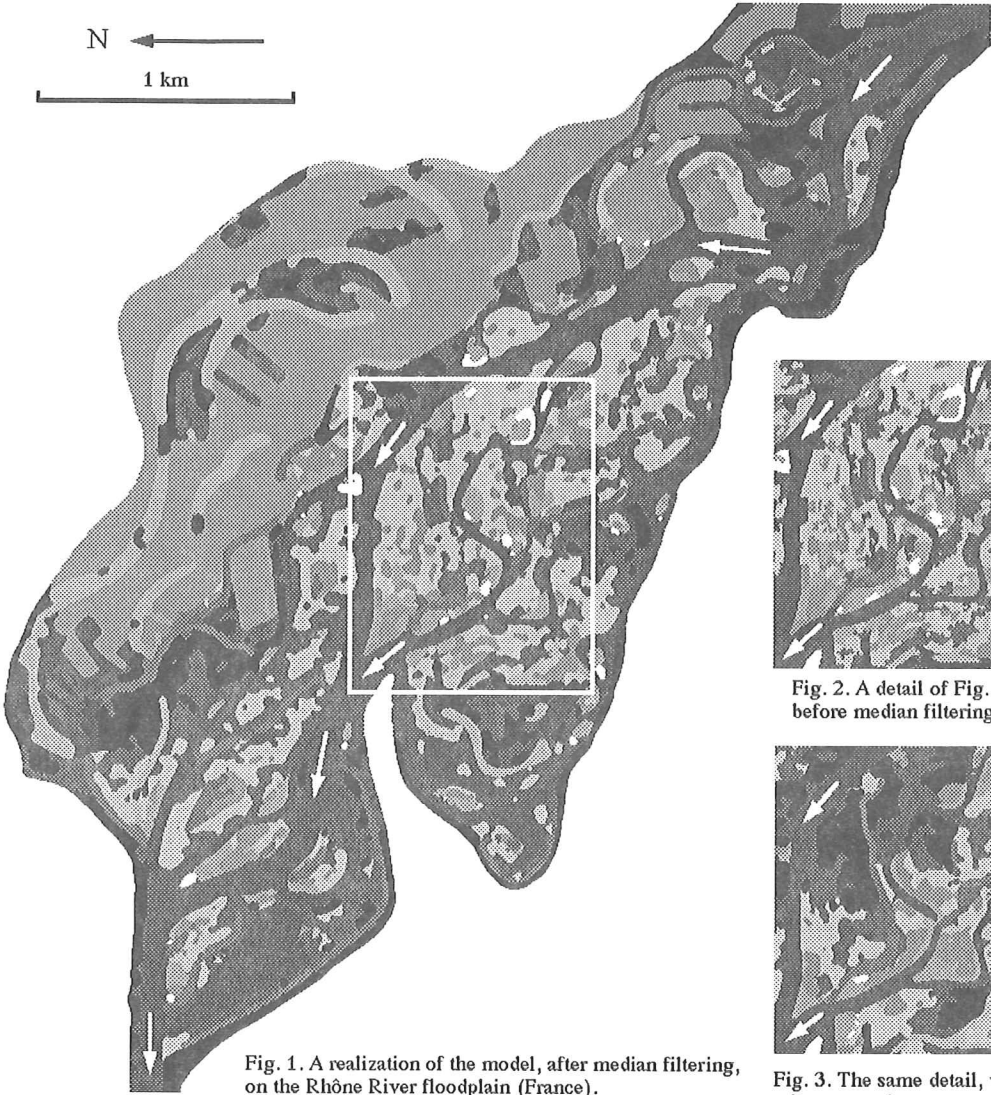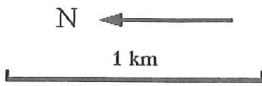
N ←

1 km

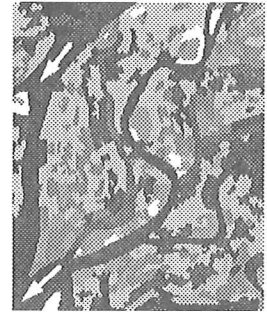Fig. 1. A realization of the model, after median filtering, on the Rhône River floodplain (France).

Fig. 2. A detail of Fig. 1 before median filtering

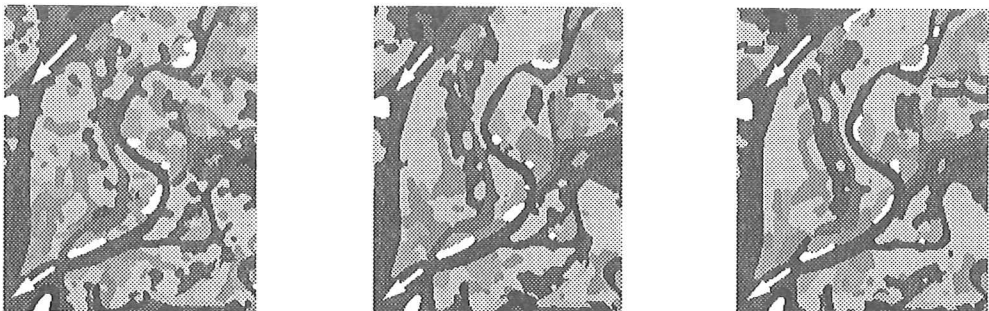Fig. 3. The same detail, with other vegetation types.

Fig. 4. Three different realisations of the model, for which the proximity of the river is gradually more important.

meaning. To avoid this default, which characterises the stochastic pyramid since its apex is formed with only one seed, a controller draws up a balance sheet of every colors at every level. Consequently, the expansion algorithm has to be modified.

At every level l, the percentages of every colors c_i are calculated in all elementary regions r, we denote it as $\hat{p}_r(c_i)$. Then a decimated seed (i,j,l) will not be eliminated if its color is not sufficiently represented in the region type z, *i.e.* the *a priori* probability is not respected.

$$\hat{p}_r(c_i) < p_z(c_i) \qquad (8)$$

Some illustrations

We present some pictures that show different patterns obtained with the same hydrographic network. Fig. 1 is a realization of the model, with a set of *a priori* probabilities. A detail with the same set of probabilities but with different sets of expansion mode, for which the criteria "proximity of a channel" is more and more important is given (Fig. 4a, 4b, 4c). Another realization of the model, with another set of probabilities is used on Fig. 3. All these pictures are presented after median filtering. Only Fig. 2, which is a detail of Fig.1, is shown before applying this filter.

CONCLUSION

We proposed a new way for the generation of random patterns in images with strong constraints. All the realisations of the model can be analysed by an ecologist. He will decide for rejection or acceptation. However, we think that there are so many parameters that the best manner to evaluate the model efficiency is to use the tools of the mathematical morphology approach of random structures: the covariance function and the dilatation operator (Serra, 1982). Both of them summarize the spatial pattern of each color and pair of colors.

A Monte Carlo test can be done (Ripley, 1988); this leads to acceptation or rejection of the model for each color or pair of colors. In order to keep the whole image, we propose to analyse one of the operator with data analysis, and particularly with the 3-modes PCA (Tucker, 1963), since the data are 3-D (colors x distances x images). This will be soon proposed in another paper.

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