



takes a step further, extending the MOSAIC model to include large-scale spatial interactions across the landscape. Related work, using cellular automata, on integrating spatial and temporal dynamics for vegetative models is reviewed by Balzter, et al. [1998].

Section 2 reviews piece-wise deterministic Markov processes and describes how spatial interactions and succession dynamics may be modeled with these processes. Simulation examples derived from the H. J. Andrews Forest in Oregon are given in section 3. Section 4 contains some concluding remarks.

## 2. PIECEWISE DETERMINISTIC MARKOV PROCESSES

A piecewise-deterministic Markov process is a stochastic process that evolves deterministically until a random time when the process jumps to a new (random) state. PDM processes were introduced by Davis [1984]. These processes provide a flexible framework for simultaneously representing spatial interactions and succession dynamics within a forest landscape. Moreover, these processes are readily amenable to large-scale computer simulations. PDM processes have been used in a variety of settings, including storage processes, capacity expansion problems, and financial investment models.

Four basic components define a PDM process: the state space, a description of the deterministic motion between jumps, the rate at which jumps occur, and the distribution of the state after a jump has occurred. Each of these components is described below within the context of forest dynamics. Note that the deterministic motion of the PDM processes given here is only used to keep track of the times that forest plots have been in their current states. So, the processes used here are piece-wise linear, a special case of PDM processes.

### 2.1 State space and deterministic motion

A forest landscape is divided into several cells. Cells range from a fraction of a hectare to several hectares. The area within a cell is assumed to be environmentally homogeneous – for example, all regions within the cell have roughly the same elevation, slope, aspect and soil type. Each cell is then partitioned into gap-sized plots with a two-dimensional grid of  $N$  total plots. The state of a plot is determined by the distribution of tree species within it and the respective functional roles of those species. This paper focuses on modeling the dynamics of plots within a single

selected cell. Forthcoming work investigates “scaling-up” the model to account for cell-to-cell interactions.

Assume that plots may be in any of  $K$  states and denote the set of possible states by  $S$ . It is important to keep track of the amount of time each plot has been in its current state. So, the state space of the cell is defined to be  $E = (S \times [0, \infty))^N$ . The state of the cell at time  $t$  is  $X_t = ((s_1(t), \tau_1(t)), \dots, (s_N(t), \tau_N(t)))$ , where  $s_i(t)$  is the state of plot  $i$  at time  $t$  and  $\tau_i(t)$  is the time that the plot has been in state  $s_i(t)$  since the last time it changed states.

Again, the deterministic portion of the PDM processes is used here only to keep track of how long plots have been in their current state. Thus, between jump times, the state of the each plot remains constant, while the time in that state evolves at unit rate – that is, between jump times  $d/dt \tau_i(t) = 1$ .

### 2.2 Jump rate

The process  $X_t$  jumps when any of the plots in the cell changes states. The overall rate that the process jumps is determined by an intensity function  $\lambda : E \rightarrow \mathbf{R}^+$ . It is assumed that  $\lambda$  is the sum of individual plot intensity functions – that is,  $\lambda = \lambda_1 + \lambda_2 + \dots + \lambda_N$ . Intuitively,  $\lambda_i(x)$  is the instantaneous rate that plot  $i$  changes states given that the current state of the cell is  $x \in E$ . The time  $T_1$  until the first jump has distribution

$$(1) \quad P[T_1 \leq t] = 1 - \exp\left(-\int_0^t \lambda(X_u) du\right) \\ = 1 - \exp\left(-\int_0^t \left(\sum_{i=1}^N \lambda_i((s_1(0), u), \dots, (s_N(0), u))\right) du\right)$$

Once the process has jumped to a new state, the distribution of the next inter-jump time is defined analogously.

### 2.3 Distribution after a jump

Suppose that a jump occurs at time  $t$ . The probability that it occurred because plot  $i$  changed states is  $\lambda_i(X_t)/\lambda(X_t)$ . Given that plot  $i$  changed states a probability transition measure,  $Q_i$ , specifies the probabilities for the plot transitioning from one state to another. Formally, following a jump at time  $t$  from state  $x = ((s_1, u_1), \dots, (s_N, u_N))$ , the distribution on the next state is given by

$$Q(x) = \frac{\lambda_1(x)}{\lambda(x)} \left( \sum_{s \in S} Q_1(x)(s) \delta_{((s,0), \dots, (s_N, u_N))} \right) + \dots + \frac{\lambda_N(x)}{\lambda(x)} \left( \sum_{s \in S} Q_N(x)(s) \delta_{((s_1, u_1), \dots, (s, 0))} \right), \quad (2)$$

where  $Q_i(x)(s)$  gives the probability of plot  $i$  transitioning to state  $s$  when the cell was in state  $x$ , and  $\delta_y$  denotes the point mass measure at  $y$ . Note that if the process jumps because of a state transition in plot  $i$ , then the time that plot  $i$  has been in its current state is reset to 0.

## 2.4 Independent plots

Acevedo et al. [1995] studied the case for which each cell (or plot) changes according to a semi-Markov process independent from all other cells (plots). All these independent semi-Markov processes (one for each plot) can be integrated into a single PDM process by appropriately defining the intensity functions  $\lambda_i$  and probability transition measures  $Q_i$  as follows. Recall that semi-Markov processes are typically specified by a probability transition matrix and a set of probability distribution functions that give the time to transition from state to state. Let  $P^i = (p_{k,j}^i)$  be the state probability transition matrix for plot  $i$ , where  $p_{k,j}^i$  denotes the probability of the plot transitioning to state  $j$  given it is in state  $k$ . The random time that plot  $i$  spends in state  $k$ , given that its next state is  $j$ , has distribution function  $F_{k,j}^i$  and density  $f_{k,j}^i$ . Since plots evolve independently of one another, each plot has an intensity function that is dependent only on that plot's current state and its time in that state. Specifically,

$$\lambda_i((s_1, u_1), \dots, (s_N, u_N)) = \frac{\sum_j p_{s_i, j}^i f_{s_i, j}^i(u_i)}{\sum_j p_{s_i, j}^i (1 - F_{s_i, j}^i(u_i))}. \quad (3)$$

Likewise, the transition measure for each plot is dependent only on the plot's current state and time in that state. The transition measure is

$$Q_i((s_1, u_1), \dots, (s_N, u_N))(j) = \frac{p_{s_i, j}^i f_{s_i, j}^i(u_i)}{\sum_m p_{s_i, m}^i f_{s_i, m}^i(u_i)}. \quad (4)$$

## 2.5 Spatial interactions between plots

Spatial interactions between plots may be integrated into the MOSAIC semi-Markov processes through both the intensity functions and the transition measures of the PDM framework.

In principle, this means defining  $\lambda_i$  and  $Q_i$  for each plot  $i$  and for all possible states of the cell. Even for a small number of states this would be an arduous task. Standard approaches to making spatial interaction models more tractable include limiting the range of neighboring plots that are assumed to influence a given plot, assuming spatial homogeneity of the spatial effects, assuming functional forms for each  $\lambda_i$  and  $Q_i$ , and applying straightforward transformations to parameters used in independent plot models (cf. Balzter et al. [1998]). All of these techniques are used here.

Spatial interactions between neighboring plots are introduced into the MOSAIC model by adjusting the state transition probabilities of the semi-Markov processes as a function of the current state of the cell. Only the second order neighborhood of a plot is assumed to influence its dynamics (the second-order neighborhood of a plot consists of the eight surrounding plots). For plot  $i$ , define a neighborhood counting function such that  $n_i^t(s)$  is the number of plots within the second-order neighborhood of plot  $i$  that are in state  $s$  at time  $t$ . The composition of the neighborhood of plot  $i$  is given by the vector  $\mathbf{n}_i^t = (n_i^t(1), n_i^t(2), \dots, n_i^t(K))$ . Let  $P^i = (p_{k,j}^i)$  and  $\{F_{k,j}^i\}_{k,j \in S}$  be the transition probability matrix and transition time distributions, respectively, for the MOSAIC semi-Markov model for the succession dynamics of plot  $i$ . Define an influence array  $P^{i*} = (p_{k,j,h}^{i*})$ , where  $p_{k,j,h}^{i*}$  represents the probability that given plot  $i$  is in state  $k$  it would transition to state  $j$  if all its neighbors were in state  $h$ . For fixed  $h$ , the matrix  $P^{i*} = (p_{k,j,h}^{i*})$  is a probability matrix. Intuitively,  $p_{k,j,h}^{i*}$  represents the maximal influence state  $h$  could have on plot  $i$  transitioning from state  $k$  to  $j$ . To tractably extend the influence model to all possible neighborhood configurations, it is assumed that a plot's state transition probabilities are weighted averages of these maximal values. The weights are given by the proportion of neighboring plots in a given state. Given the state of the cell at time  $t$ , plot  $i$ 's transition probabilities are given by

$$\tilde{p}_{k,j}^i(\mathbf{n}_i^t) = \sum_h p_{k,j,h}^{i*} \left( \frac{n_i^t(h)}{\sum_s n_i^t(s)} \right). \quad (7)$$

## 2.6 Simulation of PDM processes

Simulating the spatial interaction/succession dynamics model described above is accomplished as follows. Starting at the initial state of the cell, the state of each plot remains constant and the time in that state evolves at unit rate until the first

plot changes states. The time until the first plot changes states has distribution

$$P[T_1 \leq t] = 1 - \exp \left( - \int_0^t \left( \sum_i \sum_j \frac{\tilde{p}_{s_i(0),j}^i(\mathbf{n}_u^i) f_{s_i,j}^i(u)}{\sum_m \tilde{p}_{s_i(0),m}^i(\mathbf{n}_u^i) (1 - F_{s_i,m}^i(u))} \right) du \right) \quad (8)$$

Until the first plot changes states (and, more generally, between plot state transitions),  $\mathbf{n}_t^i$  is constant for all plots. It is straightforward using the hazard rate method (see Ross [1997]) to simulate the random time until the first plot changes states. Given that a plot has changed states at time  $t$ , the plot that changed states and the state to which it transitioned is selected according to the distribution given in (2) with

$$Q_i((s_1, u_1), \dots, (s_N, u_N))(s) = \frac{\tilde{p}_{s_i,s}^i(\mathbf{n}_t^i) f_{s_i,s}^i(u_i)}{\sum_m \tilde{p}_{s_i,m}^i(\mathbf{n}_t^i) f_{s_i,m}^i(u_i)} \quad (9)$$

The time until the next state change is determined similarly to the time for the first plot state change, then the new state for the plot changing states is selected, and so on.

### 3. EXAMPLES

The examples given in this section are derived from a MOSAIC model of a cell in the ecotonal area of the H. J. Andrews Forest in the Oregon Cascades. The cell is assumed to be located at 1000 m elevation, with 30% slope and aspect 90°. The MOSIAC semi-Markov model parameters given below are part of a series of FACET runs over 300 terrain types (Acevedo et al. [2001]). Parameters used in the FACET runs were derived from models that had previously been calibrated, evaluated and applied for Pacific Northwest conditions (Urban et al. [1993], Garman et al. [1995]). The cell is divided into a 15 x 15 grid of 225 equal sized plots. Table 3.1 specifies the five cover types or states defined by species dominance and tree height.

**Table 3.1.** Cover types and state numbers.

State Number	Cover Type
1	Gap
2	Young Douglas Fir
3	Old Douglas Fir/Hemlock
4	Seral True Fir
5	Mature True Fir

### 3.1 Independent plots

Assuming the plots evolve independently, the MOSAIC semi-Markov processes have transition matrix

$$P^i = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .74 & .26 & 0 \\ .006 & 0 & .53 & 0 & .464 \\ 0 & .692 & 0 & 0 & .308 \\ 0 & 0 & .39 & 0 & .61 \end{pmatrix}, \quad (10)$$

for each plot. Given a plot transitions from state  $k$  to state  $j$ , the time until transition has density function

$$f_{kj}^i(t) = \begin{cases} 0 & \text{for } t < d_{k,j} \\ \frac{1}{\Gamma(\alpha_{k,j})\beta_{k,j}} (t - d_{k,j})^{\alpha_{k,j}-1} e^{-t/\beta_{k,j}} & \text{for } t \geq d_{k,j} \end{cases} \quad (11)$$

where

$$(\alpha_{k,j}) = \begin{pmatrix} 0 & 10 & 0 & 0 & 0 \\ 0 & 0 & 10 & 3 & 0 \\ 1 & 0 & 1 & 0 & 3 \\ 0 & 1 & 0 & 0 & 2 \\ 0 & 0 & 3 & 0 & 1 \end{pmatrix}, \quad (12)$$

$$(\beta_{k,j}) = \begin{pmatrix} 0 & .1458 & 0 & 0 & 0 \\ 0 & 0 & 2.925 & 8.421 & 0 \\ 1 & 0 & 1 & 0 & 39.416 \\ 0 & 9.982 & 0 & 0 & 16.327 \\ 0 & 0 & 24.524 & 0 & 1 \end{pmatrix},$$

and

$$(d_{k,j}) = \begin{pmatrix} 0 & 5 & 0 & 0 & 0 \\ 0 & 0 & 58 & 24 & 0 \\ 374 & 0 & 407 & 0 & 13 \\ 0 & 7 & 0 & 0 & 12 \\ 0 & 0 & 46 & 0 & 413 \end{pmatrix}.$$

Note that, for each feasible transition from state  $k$  to  $j$ , there is a lag of  $d_{k,j}$  years and then the transition time follows a gamma distribution. Starting each plot in state 2 (young Douglas fir cover type), Figure 1 shows the proportion of plots in each state as a function of time. At approximately 300 years, these proportions reach a stationary distribution with ~63% of the plots in state 3 and ~36% in state 5.

### 3.2 Neighborhood interaction

Two sets of influence matrices are considered. In the first, a plot is strongly influenced by the states' of its neighbors. For instance, if a plot in state 3 is surrounded by plots in the same state, then the plot is assumed to stay in that state with probability 1. These "strong influence" matrices are given by (13).

$$\begin{aligned}
 (p_{k,j,1}^{i*}) &= \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .87 & .13 & 0 \\ .5 & 0 & .28 & 0 & .22 \\ 0 & .85 & 0 & 0 & .15 \\ 0 & 0 & .7 & 0 & .3 \end{pmatrix} \\
 (p_{k,j,2}^{i*}) &= \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .87 & .13 & 0 \\ .006 & 0 & .765 & 0 & .229 \\ 0 & .846 & 0 & 0 & .154 \\ 0 & 0 & .7 & 0 & .3 \end{pmatrix} \quad (13) \\
 (p_{k,j,3}^{i*}) &= \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \end{pmatrix} \\
 (p_{k,j,4}^{i*}) &= \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .37 & .63 & 0 \\ .006 & 0 & .262 & 0 & .732 \\ 0 & .346 & 0 & 0 & .654 \\ 0 & 0 & .195 & 0 & .805 \end{pmatrix} \\
 (p_{k,j,5}^{i*}) &= \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 & 1 \end{pmatrix}
 \end{aligned}$$

The second set of influences matrices maintains the same qualitative influences of the first set, but decreases the strength of the influence. These "weak influence" matrices are closer to the independent-plot transition matrix given in (10). These matrices are given by (14).

$$(p_{k,j,1}^{i*}) = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .79 & .21 & 0 \\ .21 & 0 & .43 & 0 & .36 \\ 0 & .75 & 0 & 0 & .25 \\ 0 & 0 & .51 & 0 & .49 \end{pmatrix}$$

$$(p_{k,j,2}^{i*}) = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .79 & .21 & 0 \\ .006 & 0 & .624 & 0 & .37 \\ 0 & .75 & 0 & 0 & .25 \\ 0 & 0 & .51 & 0 & .49 \end{pmatrix} \quad (14)$$

$$(p_{k,j,3}^{i*}) = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .87 & .13 & 0 \\ 0 & 0 & .77 & 0 & .23 \\ 0 & .85 & 0 & 0 & .15 \\ 0 & 0 & .7 & 0 & .3 \end{pmatrix}$$

$$(p_{k,j,4}^{i*}) = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .59 & .41 & 0 \\ .006 & 0 & .423 & 0 & .571 \\ 0 & .55 & 0 & 0 & .45 \\ 0 & 0 & .31 & 0 & .69 \end{pmatrix}$$

$$(p_{k,j,5}^{i*}) = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & .37 & .63 & 0 \\ 0 & 0 & .26 & 0 & .74 \\ 0 & .35 & 0 & 0 & .65 \\ 0 & 0 & .2 & 0 & .8 \end{pmatrix}$$

Figures 2 and 3 show the proportion of plots in each state as a function of time for the two sets of influence matrices. For the strong influence case, state 3 becomes the overwhelming dominant state after 180 years. For the weak influence case, state 3 again dominates more of the cell than in the independent case. Although this dominance subsides around 250 years, it starts to increase again after 300 years. In fact, unlike the stable distributions seen in the independent and strong influence cases, the distribution in the weak influence is fairly dynamic as the time horizon increases.

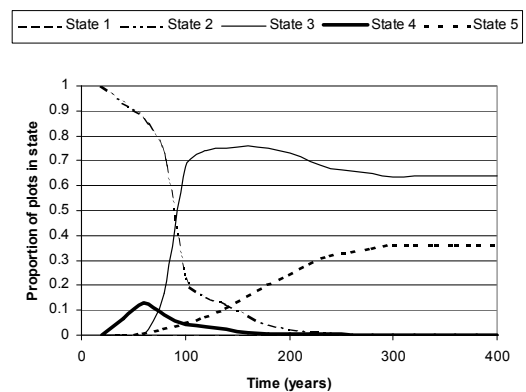
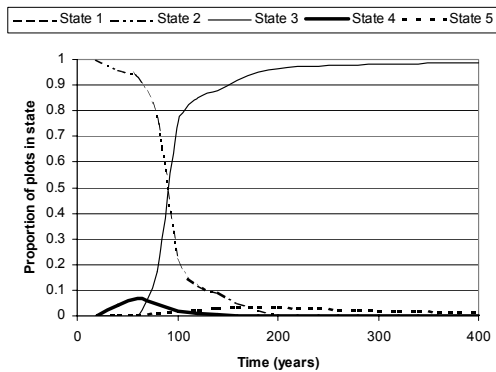
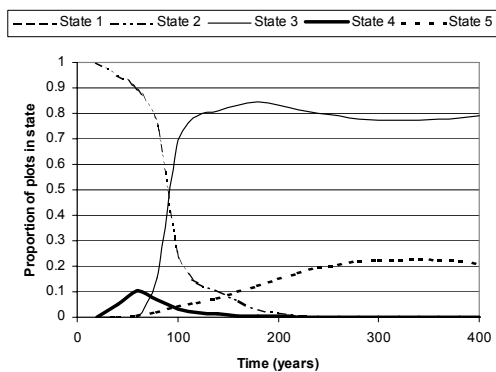


Figure 1. Proportion of plots in each state as function of time for independent model.



**Figure 2.** Proportion of plots in each state as function of time for strong influence model.



**Figure 3.** Proportion of plots in each state as function of time for weak influence model.

#### 4. CONCLUSIONS

Integrating spatial and temporal processes in forest landscape dynamics models is important for effectively using these models in ecosystem science and management. PDM processes provide a flexible framework for combining the succession dynamics modeled by MOSAIC semi-Markov processes with spatial interactions between plots. Moreover, the simulations indicate that significant differences may occur between the dynamics predicted by a MOSAIC model without spatial interactions and an integrated model with both temporal and spatial effects.

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