Modelling growth of trees by space-time growth-interaction processes

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Abstract: Our aim is to find models for growth of trees in a forest. We suggest stochastic immigration-death processes and deterministic growth-interaction processes as models. Estimation of parameters of the models is discussed and the models are fitted to a Swedish pine data set.

Keywords: growth-interaction model, immigration-death, least squares, pines

1 Introduction

Growth and yield models are important in order to capture and describe essential elements of forest dynamics, such as stand establishment, growth, and mortality under various conditions and actions over time (Vanclay 1994, Peng 2000). They can be used for example in inventory updating, and planting and management planning (e.g. Burkhart 1990).

A large number of growth-yield and ecological models has been developed to describe and model forest dynamics assuming individual tree information (see e.g. Botkin et al. 1972, Shugart and West 1977, Pacala et al. 1993) but only few of them take distance-dependent spatial tree information into account in their basic formulation. Some simulation models for generating theoretical even aged stands and some spatial growth models to predict these stands are developed for Scots pine (e.g. Pukkala 1989a, 1989b), and for Norwegian spruce (e.g. Pukkala and Kolström 1991). The drawback of these models is that the locations of trees are generated first, and given the locations, the trees are first given sizes and then let grow. The locations and tree sizes are not allowed to develop simultaneously. Furthermore, the spatial growth models are based on so-called competition indices which are computed separately and which take into account only the size and number of competing neighbours.

We consider models where location and size of the trees are developing simultaneously allowing new arrivals and death of trees. Renshaw and Särkkä (2001) introduce some growth-interaction processes and apply Gibbs processes in order to explain the generating mechanism of them. They look at the process at specific time points separately and without taking into account the time dependence and development. Särkkä and Renshaw (2006)

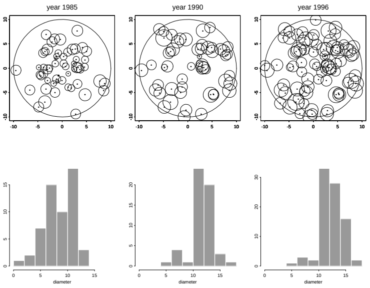

FIGURE 1. Swedish pine data and diameter histograms in 1985 (left), 1990 (middle) and 1996 (right); circle radius is proportional to tree diameter.

suggest to using the method of least squares to estimate the parameters of the full space-time model. The models and estimation procedure are discussed and applied to a Swedish pine data set.

2 Data

We study Swedish pine forest data in a developing woodland near Stockholm (see Figure 1). Tree species, location and diameter at breast height (cm) are measured for all trees of at least 10 cm in diameter or 1.3 m in height on the plot of radius 10m on three different occasions in 1985, 1990 and 1996. No change in soil structure is believed to have occurred during this 11-year period.

3 Model and estimation

Models we suggest for the Swedish pine data are immigration-growth-spatial interaction processes by Renshaw and Särkkä (2001), which are defined as follows. The ith tree that enters the system is of diameter (at breast height) $m_i(t)$, and is located at x_i. New immigrants arrive randomly in time according to a Poisson process, with rate α, have uniformly distributed locations on the study area, and are assigned diameters from $U(0,\epsilon)$ for appropriately small $\epsilon > 0$. In the successive small time intervals $(t, t+dt)$, each individual either dies ‘naturally’ with probability μdt, or else it undergoes the deterministic incremental size change

$$m_i(t+dt) = m_i(t) + f(m_i(t))dt + \sum_{j\neq i} h(m_i(t), m_j(t); \|x_i - x_j\|)dt \; .$$

Here $\|x_i - x_j\|$ denotes the distance between trees i and j, $f(\cdot)$ denotes the individual growth function in the absence of spatial interaction, and $h(\cdot)$

is an appropriate spatial interaction function taken over all trees $j \neq i$. If $m_i(t+dt) \leq 0$ then the individual is deemed to have died 'interactively' and the tree i is deleted, as also happens for natural death.

We consider two models: The first model has the symmetric interaction function

$$h(m_i(t), m_j(t); \|x_i - x_j\|) = -bI(\|x_i - x_j\| < r(m_i(t) + m_j(t)),$$

where $b > 0$ and $I(x)$ denotes the indicator function, and the logistic growth function

$$f(m_i(t)) = \lambda m_i(t)(1 - m_i(t)/K)$$

with intrinsic growth rate λ and (non-spatial) carrying capacity K. The second model has the non-symmetric interaction function

$$\begin{aligned} &h(m_i(t), m_j(t); \|x_i - x_j\|) \\ &\qquad = -b \text{ area}\{D(x_i, rm_i(t)) \cap D(x_j, rm_j(t))\}/\pi r^2 m_i^2(t) \end{aligned}$$

and the linear growth function

$$f(m_i(t)) = \lambda(1 - m_i(t)/K).$$

Here, $D(x_i, s)$ denotes a disc with centre x_i and radius s. The first, symmetric model is appropriate for even aged and planted forests, where trees are about of the same size, and the second, non-symmetric model for mixed aged and naturally grown forests.

The birth rate α and death rate μ can be estimated separately by using the maximum likelihood estimates which can be computed analytically. These estimators are, however, biased downwards possibly due to the fact that some individuals arrive and die within the same unit time interval and are therefore not observed. To estimate intrinsic growth rate λ, carrying capacity K, interaction parameter b and range of interaction r we suggest using the method of least squares since it is far more mathematically and computationally tractable than the maximum likelihood method.

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