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## Parameter estimation for growth interaction processes using spatio-temporal information

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#### **1. Introduction**

### a b s t r a c t

Methods for the parameter estimation for a spatio-temporal marked point process model, the so-called growth-interaction model, are investigated. Least squares estimation methods for this model found in the literature are only concerned with fitting the mark distribution observed in the data. These methods are unable to distinguish between models which have the same birth, death, interaction and growth functions and parameters but different arrival strategies for the points. Hence, they are extended such that the spatial structure of a point pattern is also taken into account. The suggested methods are evaluated in a simulation study and applied to a small data set from forestry.

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During the last 20 years the development of techniques such as Global Positioning Systems has facilitated the record of spatio-temporal data. The availability of these data has increased an interest in spatio-temporal modelling. As a consequence, substantial progress has been made in the development of analysis methods involving geostatistical, hierarchical and multivariate time series approaches, together with the implementation of space–time dynamic models and point process models (see, e.g., [Cressie](#page--1-0) [and](#page--1-0) [Wikle,](#page--1-0) [2011,](#page--1-0) [Diggle](#page--1-1) [and](#page--1-1) [Gabriel,](#page--1-1) [2010\)](#page--1-1). Here, we concentrate on the so-called growth–interaction process, which is a spatial marked point process evolving in time (see [Renshaw](#page--1-2) [and](#page--1-2) [Särkkä,](#page--1-2) [2001\)](#page--1-2). New immigrants (points) arrive randomly in time according to a Poisson process, have uniformly distributed locations on the study area, and are assigned some initial marks. In the successive small time intervals, each individual either dies according to a simple death process, or changes its size deterministically. The growth term includes an individual growth function and an interaction function, which depends on the locations and sizes of the neighbouring points. The parameter estimation for the growth–interaction process is discussed in several publications. [Särkkä](#page--1-3) [and](#page--1-3) [Renshaw](#page--1-3) [\(2006\)](#page--1-3) suggest to estimate the immigration and death rates by the maximum likelihood method, and the growth and interaction parameters by a least squares approach. [Cronie](#page--1-4) [\(2010\)](#page--1-4) suggests an improved estimator for the immigration rate, and [Cronie](#page--1-5) [and](#page--1-5) [Yu](#page--1-5) [\(2010\)](#page--1-5) an improved maximum likelihood approach for the immigration and death rates. Furthermore, [Cronie](#page--1-6) [and](#page--1-6) [Särkkä](#page--1-6) [\(2011\)](#page--1-6) add an edge correction to the least squares estimation procedure of the growth and interaction parameters. A separate estimation of one of the growth parameters, namely the carrying capacity (maximal size), is suggested in [Cronie](#page--1-7) [et al.](#page--1-7) [\(2011\)](#page--1-7) when fitting the growth–interaction model to data from a young forest.

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Besides the choice of the growth and interaction functions, the arrival strategy for new immigrants may also influence the spatial arrangement of the points. In the original growth–interaction process the new immigrants are located uniformly and independently of each other in the study region. Given that the locations of mature trees often form a regular pattern, uniform and independent locations may not give the spatial structure that is observed.

[Cronie](#page--1-7) [et al.](#page--1-7) [\(2011\)](#page--1-7) suggest placing new trees according to a hardcore strategy such that the centre of a newly arrived tree is not inside another tree. [Comas](#page--1-8) [\(2009\)](#page--1-8) studies two different forest regeneration strategies through the development of a growth–interaction process. Instead of uniform locations for the new arrivals, he suggests that each tree produces seedlings located according to a Gaussian distribution around the tree. His main purpose is to compare the two regeneration strategies and to study how they affect the size distribution of the trees and timber production. The spatial pattern of the tree locations is not of interest. Here, we will study the effect of different arrival strategies on the spatial structure of a point pattern.

The least squares estimation of the growth and interaction parameters is based on minimising the difference between observed and predicted marks of the points, while the spatial information is not taken into account. Consequently, different arrival strategies cannot be detected by this method. Furthermore, the analysis of a small forest data set in [Cronie](#page--1-6) [and](#page--1-6) [Särkkä](#page--1-6) [\(2011\)](#page--1-6) shows that the spatial structures of the real data and of point patterns simulated from the fitted model do not match. The pattern of tree locations in the real data seems to be more regular than in the simulated data. This may be due to the uniformly located new arrivals in the simulated data. To be able to distinguish between two models with the same birth, death, interaction and growth functions and parameters but different arrival strategies of new points, it may not be enough to base the estimation only on marks, but the spatial structure needs to be included as well.

In this paper we suggest how to estimate the parameters based on both mark information and information on the point locations. This makes the parameter estimation capable of dealing with alternative arrival strategies. In particular, the case of hardcore arrivals is investigated which is considered more suitable for the Scots pine data studied in [Cronie](#page--1-6) [and](#page--1-6) [Särkkä](#page--1-6) [\(2011\)](#page--1-6) than uniform arrivals.

The paper is organised as follows. The growth–interaction process is introduced in Section [2.](#page-1-0) In Section [3](#page--1-9) we recall the estimation approaches presented in [Särkkä](#page--1-3) [and](#page--1-3) [Renshaw](#page--1-3) [\(2006\)](#page--1-3) and [Cronie](#page--1-4) [\(2010\)](#page--1-4), and refine the existing estimation methods by adding spatial information to the procedure. The influence of the arrival strategy and the new estimation approach are investigated by a simulation study in Section [4.](#page--1-10) Finally, in Section [5](#page--1-11) we fit a growth–interaction model to forestry data.

#### <span id="page-1-0"></span>**2. Growth–interaction process**

#### *2.1. Description of the process*

The growth–interaction (GI) process was introduced by [Renshaw](#page--1-2) [and](#page--1-2) [Särkkä](#page--1-2) [\(2001\)](#page--1-2) as a model for tree growth. Trees are modelled by marked points in a given window *W*. The marks are positive real numbers which can be interpreted as sizes.

The GI model starts with an initial, and possibly empty, marked point pattern. New immigrants arrive according to a Poisson process, with rate  $\alpha$ , at uniformly distributed locations  $x_i$ . They are assigned initial marks  $m_i^0$  which are either fixed or follow some distribution. In small time intervals  $(t, t + dt)$ , each individual either dies naturally with probability  $\mu dt$ , or undergoes the deterministic size change

<span id="page-1-1"></span>
$$
m_i(t + dt) = m_i(t) + f(m_i(t))dt + \sum_{j \neq i} h(m_i(t), m_j(t), ||x_i - x_j||)dt,
$$
\n(1)

where *f*(·) is an individual growth function, *h*(·) a spatial interaction function and ∥*x<sup>i</sup>* − *xj*∥ the distance between the locations *x<sup>i</sup>* and *x<sup>j</sup>* . A simulation algorithm for this model is given in [Särkkä](#page--1-3) [and](#page--1-3) [Renshaw](#page--1-3) [\(2006\)](#page--1-3). Note that in [\(1\)](#page-1-1) *h* is a pairwise interaction function since we consider situations, where there is competition between the individuals. However, also higher order interactions, i.e. interactions between more than two points, can be included in the interaction function.

The growth function and the interaction function can be chosen freely. Here, we study the family of so-called logistic power-law functions

$$
f(m_i(t)) = c_1 m_i(t) - c_2 (m_i(t))^{p+1},
$$

where  $c_1$ ,  $c_2$  and *p* are given parameters. As special cases we get the logistic growth function ( $c_1 = \lambda$ ,  $c_2 = \lambda/K$  and  $p = 1$ )

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

and the linear growth function ( $c_1 = -\lambda/K$ ,  $c_2 = -\lambda$  and  $p = -1$ )

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

In these two special cases, the parameter  $\lambda$  is the intrinsic growth rate and *K* is the carrying capacity, i.e. an upper bound for the value of the marks.

There is also a lot of freedom when choosing the interaction function. Here, we will give some examples of pairwise interaction functions. Our first example is the symmetric function

$$
h(m_i(t), m_j(t), ||x_i - x_j||) = -bl(||x_i - x_j|| < r(m_i(t) + m_j(t))),
$$
\n(2)

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