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Direct and inverse analysis of diffusive logistic population evolution with time delay and impulsive culling via integral transforms and hybrid optimization

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ABSTRACT

Motivated by the fact that several species act as a vector in the spread of human or livestock diseases, many works propose mathematical formulations for the modeling of these populations, most of them considering Fickian dispersion and logistic like growth rates. For the best use of these models in a real application of optimal population control, the model parameters should be identified as accurately as possible for a given species population. In this work, this parameter identification problem is formulated as an inverse problem, which is tackled with a combination of the Generalized Integral Transform Technique (GITT), for the direct problem solution, and a hybrid stochastic–deterministic procedure for the minimization of the defined objective function in the inverse analysis, employing the Differential Evolution and the Levenberg–Marquardt methods. The direct problem solution with GITT and the inverse analysis are critically investigated. In order to improve the computational performance of the inverse problem solution, a second order semi-analytical integration and a solution refinement scheme are proposed.

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1. Introduction

Since the pioneering works of Holling [1] and Segel and Jackson [2] many works have been proposed towards the modeling of populations growth [3–13], most of them considering Fickian dispersion and logistic like growth rates, seeking to take into account different aspects that play some role in the population dynamics, such as the migration to less populated areas, presence of predators and preys, toxicant, culling sites and several other parameters that affect the birth and death rates. Most of these papers are concerned with the proposition of different models and their stability analysis, presenting some analytical solution results to some oversimplified models or numerical solutions obtained with classical numerical methods. Indeed, all these models have potential to be very useful in practical applications, such as in the population control of species that act as a vector in the spread of diseases, for example when one seeks to optimize the locations of culling sites and their intensities in order to guarantee an acceptable population level, with no epidemic risk, and avoiding interference in the surrounding environmental elements. Nevertheless, very little has been done in the integration of theory and practice regarding these population dynamics models. In order to bridge that gap, one first step is the establishment of an inverse

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Nomenclature

u	population density
u_0	initial population density
x	dimensionless space variable
t	dimensionless time variable
D	population dispersion parameter
$b(u)$	birth rate
$d(u)$	death rate
x_j	culling sites locations
B_j	culling sites intensities
P, K, C	parameters of the logistic like growth rate model
N	truncation order in the solution expansion
M	number of subregions in the semi-analytical integration
N_i	normalization integrals in the eigenvalue problem
N_{cs}	number of culling sites
N_{un}	number of unknown parameters to be estimated
\mathbf{P}	vector of unknowns
\mathbf{Y}	vector of measurements
\mathbf{U}	vector of calculated quantities at the same positions and times as the experimental measurements
\mathbf{W}	covariance matrix of the errors
S	objective function
\mathbf{J}	Jacobian matrix

Greek letters

τ	reproduction time delay
μ	per capita premature death rate
β	eigenvalues of the direct problem
ψ	eigenfunctions of the direct problem
σ_e	standard deviation of the experimental data measurement errors
Φ	modified information matrix, Eq. (15)

Subscripts & superscripts

$-$	integral transform
\sim	normalized eigenfunction

analysis methodology [14,15], for the estimation of the model parameters for a given species population, aimed at achieving the best prediction performance of the proposed model. In fact, one of the first works appearing in the literature focusing on this issue is quite recent [16].

In general, such inverse methodologies require accurate and computationally fast direct problem solution methodologies, so as to allow for the computational intensive iterative analysis often required by the inverse problem solution. In this context, the Generalized Integral Transform Technique (GITT), a hybrid numerical–analytical approach, must be placed among the most adequate techniques for the solution of convection–diffusion problems [17–20]. The hybrid nature of this methodology permits the obtention of analytical expressions which are very suited for intensive tasks [21]. The GITT approach is based on extending the classical integral transform method [22] to overcome barriers posed by different classes of problems such as nonlinear coefficients, moving boundaries and nonlinear convective terms. The relative merits of such an approach over purely numerical procedures include the automatic global accuracy control capability and the mild increase on computational cost for multidimensional nonlinear situations. On the other hand, while modern numerical methods may readily handle problems in complex geometric configurations, such as irregularly shaped domains, the analytical approaches are known for their relative limitations in dealing with such problems and, in fact, this issue is currently one of the main research fronts concerning the GITT methodology [23].

One first contribution of the present work is thus the investigation of the GITT application for the solution of the nonlinear diffusive equations often employed to model the diffusive population growth with time delay and impulsive culling. In order to improve the direct problem solution computational performance, which is critical due to the intensive iterative analysis required by the inverse methodology, a second order semi-analytical integration is implemented, which is aimed at providing an analytical evaluation of the oscillatory behavior of the eigenfunctions within each subregion. After a critical examination of the direct problem solution so obtained, we proceed to the inverse analysis in order to illustrate the identification of the model parameters and provide a complete methodology which can be extended to other diffusive population growth models.

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