

DESCRIPTION FOR THE GENERAL PUBLIC

Research project objectives/ Research hypothesis.

Particle methods are numerical tools used for approximation of certain types of Partial Differential Equations (PDEs), which are frequently modelling systems appearing in fluid mechanics, physics and in general, in applied mathematics.

This project is devoted to the analysis and development of this wide class of particle methods. More specifically, we wish to adapt their main idea and best features to the field of mathematical biology. This task is neither easy nor straightforward: Equations describing problems appearing in biology usually do not preserve mass and are equipped with renewal terms, which (in most cases) are nonlocal. Once such an equation is equipped with nonlocal renewal term, new individuals are absorbed into the system. The new individuals can vary with respect to the structural variable (e.g renewal and differentiation of stem cells).

This difference between equations appearing mathematical physics and mathematical biology, obviously, leads to the necessity of deriving new algorithms. Such methods call for much more effort to obtain satisfactory accuracy (order of the numerical integrator).

In order to improve the rate of convergence of the methods we will resort to *splitting methods*. This will additionally lower the computational cost of the methods.

Within this project we will (i) derive appropriate numerical schemes, (ii) incorporate into those numerical schemes adequate splitting in time, (iii) prove the convergence of those methods delivering the order of the schemes, (iv) present some numerical simulations.

The idea of particle methods was introduced for computational fluid dynamics by Francis Harvey Harlow nearly sixty decades ago, and since then have been extensively explored. The convergence of latest improvements on particle methods has been shown to be optimal.

On the other hand a similar method *Escalator Boxcar Train* was introduced nearly thirty years ago by Andre de Roos for mathematical biology, but the issue of its low convergence has stayed intact.

Nonlinear first order hyperbolic problems with a renewal term are usually used to model the evolution of structured populations, that is populations that are heterogenous with respect to some individual property like size, age, maturity or phenotype. PDEs with nonlocal renewal term for modelling dynamic of populations were applied in 1926 by McKendrick. Later, in 1959, Von Foerster modelled the process of cell division in a similar way. Structured population models are of great importance in natural sciences and appear, for example, in limnology and oceanography, ecology of ontogenetic growth and development in organisms and in biology to describe dynamics of of assemblies of interacting neurons or the process of renewal and differentiation of stem cells.

Higher order methods are useful for numerical simulation of those models, but they are necessary in the inverse structured population models, that is where: (i) the model equation is known, (ii) some measurement data are known, (iii) the aim is to find proper coefficients. Optimization of that problem may be based on Bayesian approach. Then computations have to be performed very accurately and repeatedly, as every step of Metropolis–Hastings algorithm requires solving the system of equations with possibly different coefficients. Because ergodic properties of the Markov processes appear only after extremely huge number of steps of Metropolis–Hastings algorithm, we really need to resort to accurate and computationally cheap methods.