Study of efficiency in the numerical integration of size-structured population models: error and computational cost

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We consider the numerical integration of the following nonlinear size-structured population model
\begin{align}
 u_t + (g(x, I_g(t), t) u)_x &= -\mu(x, I_\mu(t), t) u, \quad 0 < x < 1, \ t > 0, \\
 g((x, I_g(0), 0) u(0, t) &= \int_0^1 \alpha((x, I_\alpha(t), t) u(x, t) \, dx, \quad t > 0, \\
 u(x, 0) &= \phi(x), \quad 0 \leq x \leq 1,
\end{align}

where
\begin{align}
 I_g(t) &= \int_0^1 \gamma_g(x) u(x, t) \, dx, \quad I_\mu(t) = \int_0^1 \gamma_\mu(x) u(x, t) \, dx, \\
 I_\alpha(t) &= \int_0^1 \gamma_\alpha(x) u(x, t) \, dx, \quad t > 0.
\end{align}

This model describes the evolution with time $t$ of a population structured by its size $x$. It is determined by the vital functions which include dependencies on both variables and on the total amount of individuals of the population by means of the functions $I_g(t)$, $I_\alpha(t)$ and $I_\mu(t)$, which represent a way of weighting the size distribution density to model the different influence on the condition of life due to individuals of different size. We have considered different numerical methods introduced in [1, 2] and we have described the expression of the principal error terms and its computational cost in terms of the size of the problem. We have considered both theoretical and biological problems.

References


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