

# Numerical Stability of the Escalator Boxcar Train under reducing System of Ordinary Differential Equations

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- Physiologically structured population models (PSPMs) describes the dynamics of an arbitrary number of biological populations. Examples include models of fishes in lakes and trees in forests.
- PSPMs investigate the study of change in populations in which individuals differ physiologically in one or more ways, e.g., in their size.

- For the dynamics of PSPMs, the density  $n(x, t)$  of individuals of state  $x$  at time  $t$  satisfies

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Here,  $g$  is the growth rate,  $\mu$  is the mortality rate, and  $b$  is the fecundity rate.

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- The cohorts clarify internal cohorts and boundary cohorts because of reproduction. The new born individuals are assumed to have the same physiological properties and are accumulated in the boundary cohorts.
- The number of individuals in the  $i^{th}$  cohort is denoted by  $N_i(t)$  and the mean individual state will be used and denoted as  $X_i(t)$ .

- The dynamics of the internal cohorts and boundary cohort for non reproduction are defined by

$$\frac{dN_i}{dt} = -\mu(X_i, E)N_i \quad (1)$$

$$\frac{dX_i}{dt} = g(X_i, E) \quad (2)$$

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- If reproduction does occur, the dynamics of the boundary cohorts for the reproduction case follow

$$\frac{dN_0}{dt} = -\mu(X_0, E)N_0 + \sum_{i=0}^M b(X_i, E)N_i$$

$$\frac{dX_0}{dt} = g(X_0, E)$$

## Process of internalizing the boundary cohort

- In the course of time, both the number and size of individuals in the boundary cohort increase according to the reproduction of individuals and the environment.
- The boundary cohort must be internalized sufficiently often since an applicable large approximation error can be occurred because of above properties.
- The number of internal cohorts will be increased due to internalization

# Process of merging internal cohorts

- We merge the two cohorts together if the number of individuals in an internal cohort falls below a certain threshold and that the size of the internal cohort closet to this one, is close enough
- The number of offsprings stays the same, compared to if we had not merged the cohorts



# The Daphnia's Life History Model

- To illustrate the formulation of an EBT-model, the objects for the PSPMs is the waterflea *Daphnia pulex*.
- *Daphnia* behaviour is extremely influenced by the size of an individual.
- Larger individuals have higher food consumption, basal metabolism and reproduction rate.
- The mature *Daphnia* can shrink under particular conditions.

## Error bounds when merging two cohorts

We consider two cohorts  $(X_a, N_a)$  and  $(X_b, N_b)$ .

The difference,  $\Delta x = X_b - X_a$ , between the sizes of these cohorts is assumed to be sufficiently small. The food available in the system will be assumed to be constant.

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From Equation (1), we have  $N'(t) = -\mu N(t)$ .

According to the Equation (2) and the growth rate of Daphnia, the dynamics of cohorts for  $X(t)$ :

$$X'(t) = c_1 \left(1 - \frac{X(t)}{K}\right)$$

For non-merging cohort, the dynamics of the population fecundity  $b_w(t)$  from the growth rate of Daphnia is

$$b_w(t) = c_2 N_a(t) X_a^2(t) + c_2 N_b(t) X_b^2(t). \quad (3)$$

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In view of Equation (3), we initialize the merged cohort size to

$$X_{m_0} = \sqrt{\frac{N_{a_0} X_{a_0}^2 + N_{b_0} X_{b_0}^2}{N_{a_0} + N_{b_0}}}$$

# Theorem

Under the above assumptions we get

$$b_m = b_w + O(\Delta x_0 \cdot \Delta t)$$



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Proof: For merging cohort, we can also get newborn individuals by using Taylor's expansion and above equations.

$$\begin{aligned} b_m &= c_2(N_{a_0}X_{a_0}^2 + N_{b_0}X_{b_0}^2) - c_2\mu(N_{a_0}X_{a_0}^2 + N_{b_0}X_{b_0}^2)\Delta t \\ &\quad + 2c_1c_2N_{a_0}\sqrt{\frac{N_{a_0}X_{a_0}^2 + N_{b_0}X_{b_0}^2}{N_{a_0} + N_{b_0}}}\Delta t \\ &\quad + 2c_1c_2N_{b_0}\sqrt{\frac{N_{a_0}X_{a_0}^2 + N_{b_0}X_{b_0}^2}{N_{a_0} + N_{b_0}}}\Delta t \\ &\quad - \frac{2c_1c_2}{K}(N_{a_0}X_{a_0}^2 + N_{b_0}X_{b_0}^2)\Delta t + O(\Delta t^2) \end{aligned}$$

We can also calculate newborn individuals for non-merging cohort by using Taylor's expansion

$$\begin{aligned} b_w = & c_2 (N_{a_0} X_{a_0}^2 + N_{b_0} X_{b_0}^2) - c_2 \mu (N_{a_0} X_{a_0}^2 + N_{b_0} X_{b_0}^2) \Delta t \\ & + 2c_1 c_2 (N_{a_0} X_{a_0} + N_{b_0} X_{b_0}) \Delta t - \frac{2c_1 c_2}{K} (N_{a_0} X_{a_0}^2 + N_{b_0} X_{b_0}^2) \Delta t \\ & + O(\Delta t^2) \end{aligned}$$

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 & + 2c_1 c_2 (N_{a_0} X_{a_0} + N_{b_0} X_{b_0}) \Delta t - \frac{2c_1 c_2}{K} (N_{a_0} X_{a_0}^2 + N_{b_0} X_{b_0}^2) \Delta t \\
 & + O(\Delta t^2)
 \end{aligned}$$

Using the continuity of the square root function, we get

$$\begin{aligned}
 X_{a_0} &= \sqrt{\frac{N_{a_0} X_{a_0}^2 + N_{b_0} X_{b_0}^2}{N_{a_0} + N_{b_0}}} + O(\Delta x_0), \\
 X_{b_0} &= \sqrt{\frac{N_{a_0} X_{a_0}^2 + N_{b_0} X_{b_0}^2}{N_{a_0} + N_{b_0}}} + O(\Delta x_0)
 \end{aligned}$$

Thus, the number of new born individuals for merging cohorts converges to the number of new born individuals for nonmerging cohort when  $\Delta x_0$  and  $\Delta t$  goes to zero.

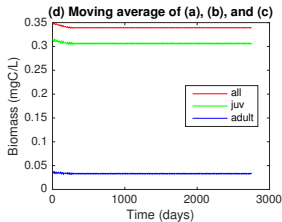
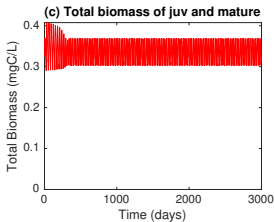
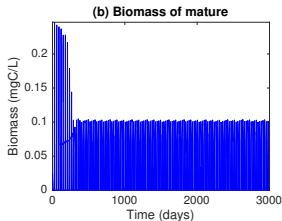
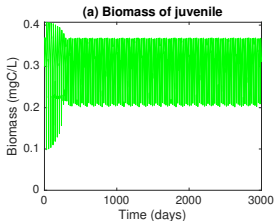
# Simulation of the EBT and Daphnia model

- MATLAB is selected to be used for this project and the function ode45 is chosen to solve the ODEs because of its accuracy and speed.
- We used a least square method to fit the best monomial for the simulation time depending on the number of time steps.
- We found that the relationship between the simulation time and the number of time steps was linear.

# Result of the simulation




Time Span(days)	Merging	Elapsed Time(seconds)	Internal Co-horts	$j(\text{mgC/L})$	$m(\text{mgC/L})$	$v(\text{mgC/L})$
2	Yes	14	45	0.3088	0.0330	0.3418
1	Yes	26	57	0.3072	0.0326	0.3398
1/2	Yes	47	72	0.3137	0.0382	0.3518
1/4	Yes	95	120	0.3132	0.0391	0.3523
2	No	21	749	0.3088	0.0330	0.3418
1	No	53	1367	0.3062	0.0335	0.3398
1/2	No	128	1681	0.3137	0.0382	0.3519
1/4	No	467	3165	0.3132	0.0392	0.3523

# Biomass of juvenile and mature for merging cohorts



## Conclusion and Future Work

- In this paper, we merge cohorts that are sufficiently close together.
- The reduced system of ODE's will not give rise to large changes in the general solution.
- The running time of the simulation, when merging, is proportional to the time step.
- In future work, we aim to build EBT-solver which includes the automatic feature of merging and splitting for more general models.

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Thank you for your attention.