Individual-Based Modeling of Spatio-Temporal Dynamics

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Outline

Single species ricker logistic model

↓

Extend to the model including spatial structure

↓

IBM simulation & analysis

↓

two species model with spatial structure

↓

IBM simulation & analysis

↓

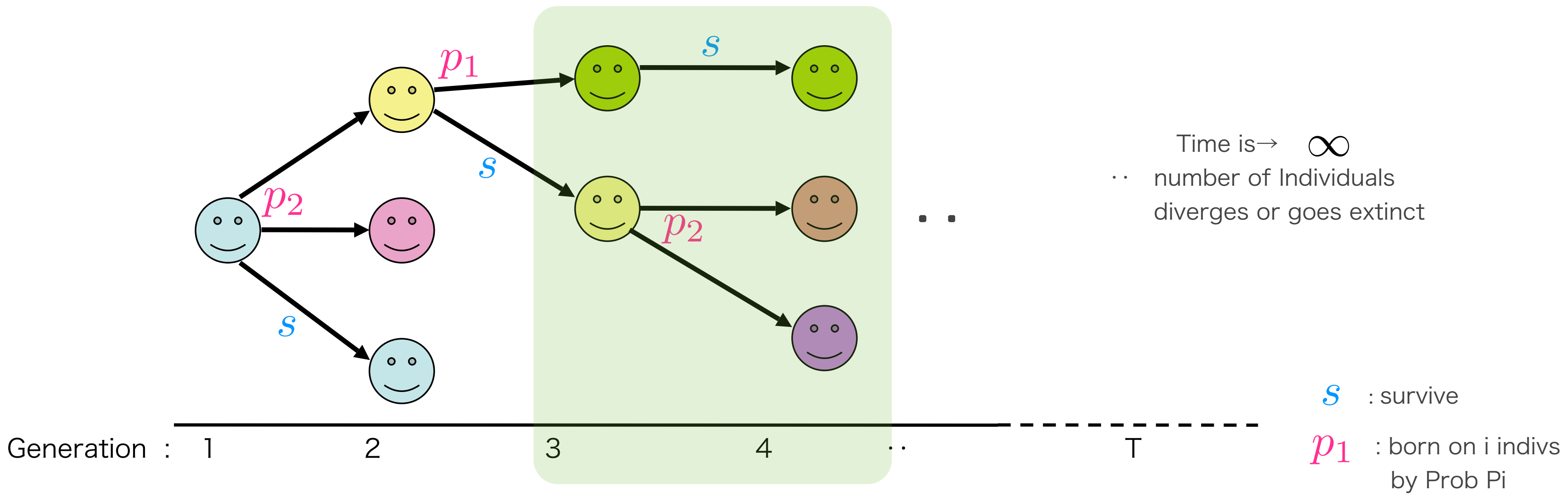
Future work

supplementary

Pallarel computing using many CPU

Single species individual-based dynamics in the discrete time

- Galton-Watson process



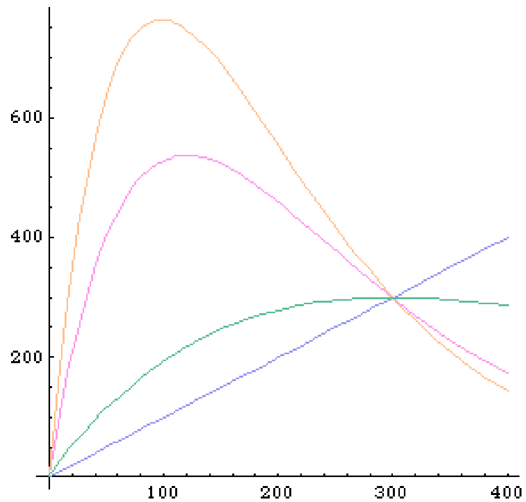
Ricker logistic model

The average number of offspring depends on all individuals

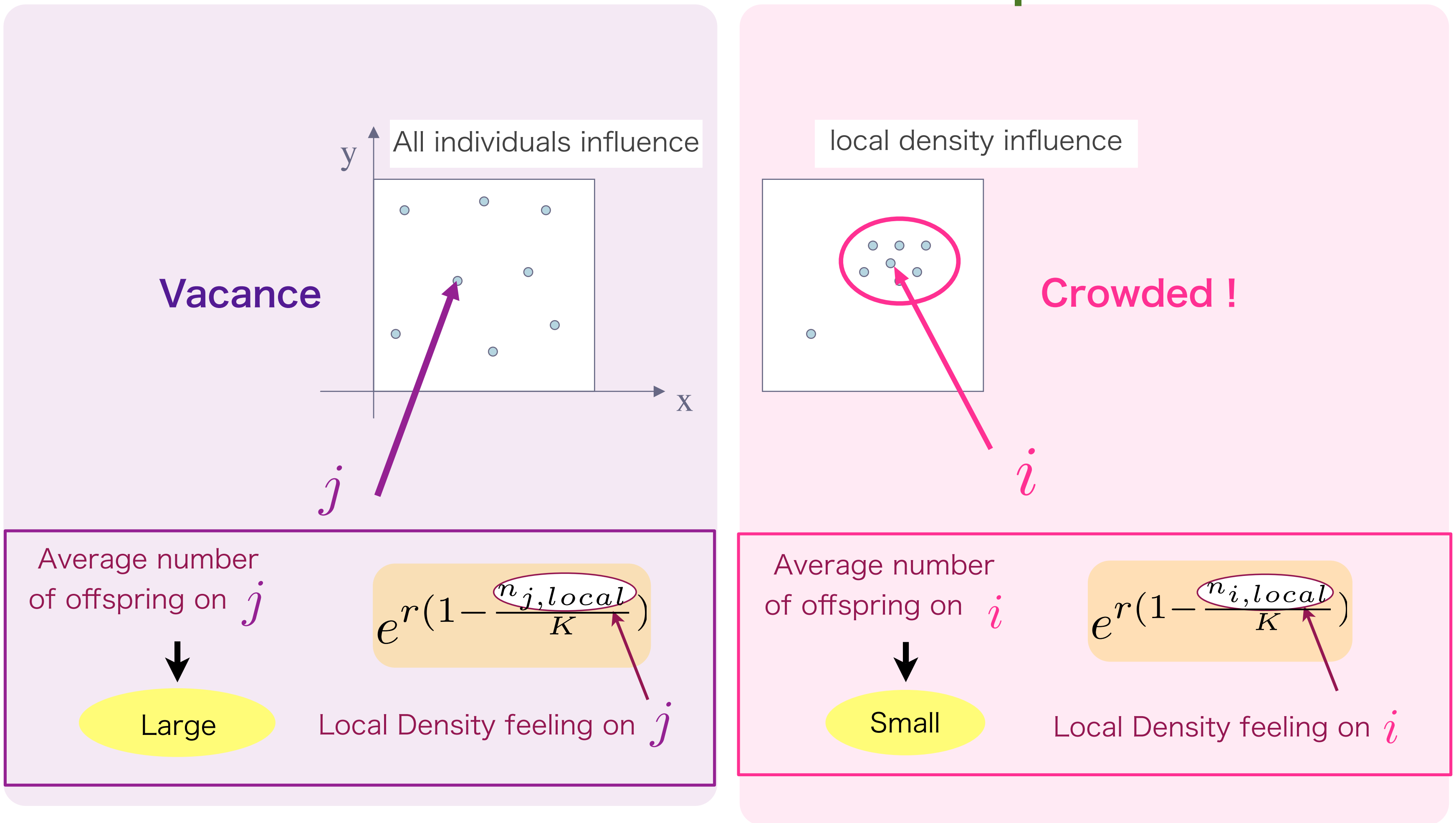
$$n_{t+1} = e^{r\left(1-\frac{n_t}{K}\right)} n_t$$

number of offspring depends on all individual influence

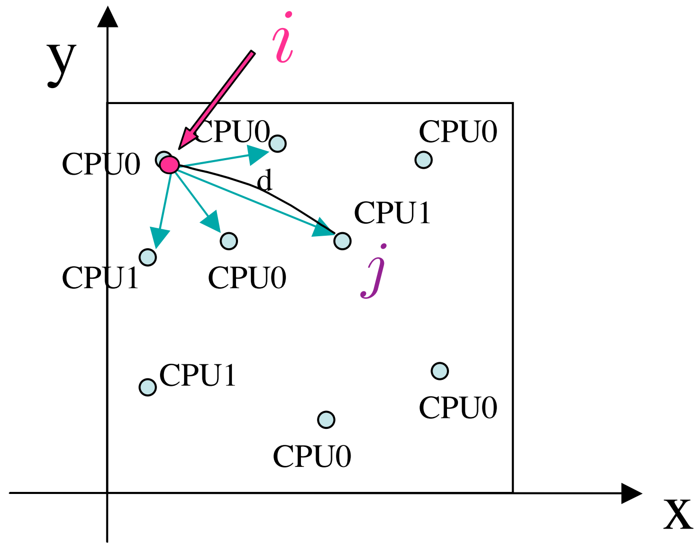
depends on local density



Individual-based Birth and Death in two dimensional space



Local density way of thinking



- Local density feeling on i

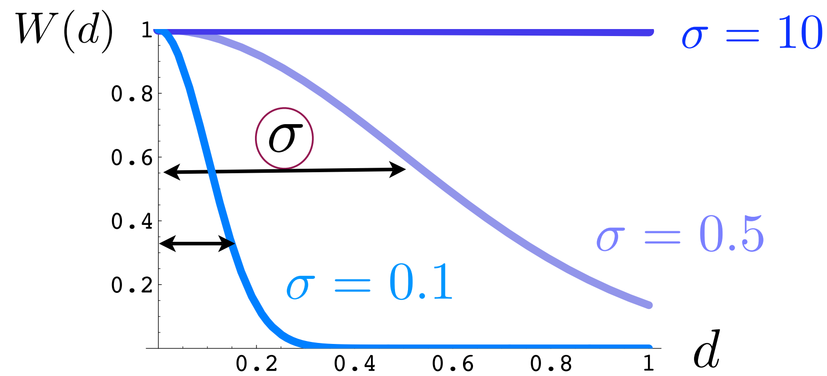
$$n_{i,local} = \sum_{j \neq i} w(d(i,j))$$

distance between i and j

$$w(d) = e^{-\frac{d^2}{2\sigma^2}}$$

σ : distance working on each interaction

the feeling way of individuals



$$\sigma \gg 1 \rightarrow n_{i,local} = n_t$$

$$\sigma \ll 1 \rightarrow n_{i,local} < n_t$$

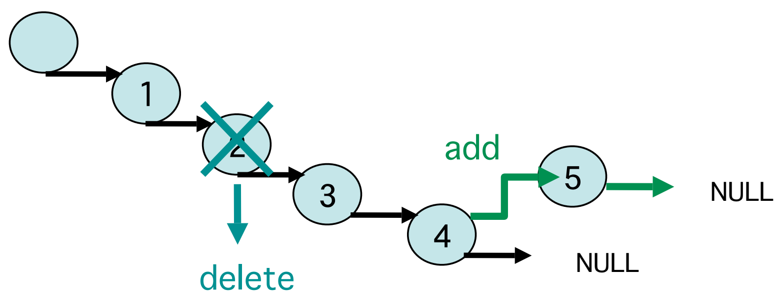
Individual-Based Model

- Model constructed in term of individuals.
- Express individual's birth and death by algorithm.

simulation ↓

Understand how individuals are reproduced and distributed over space.

Express biorogical group using the list structure.



Simulation

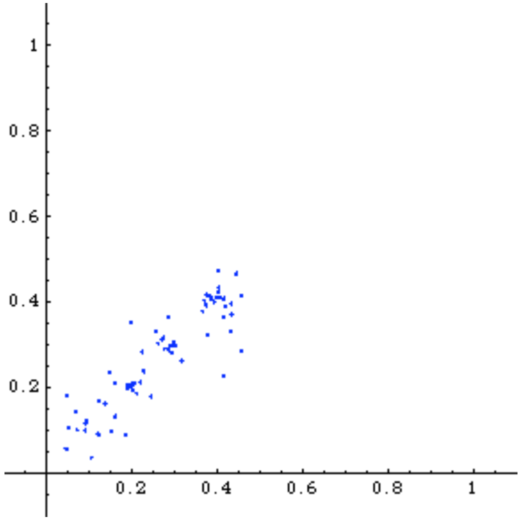
【 Parameter 】

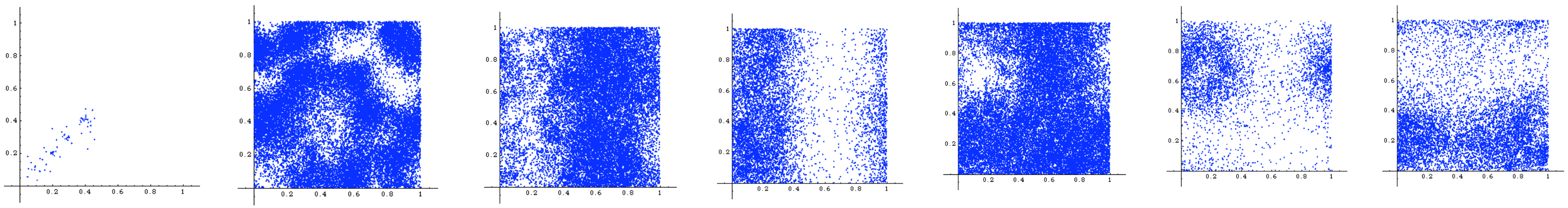
r : 3.0

K : 300

σ : 0.1

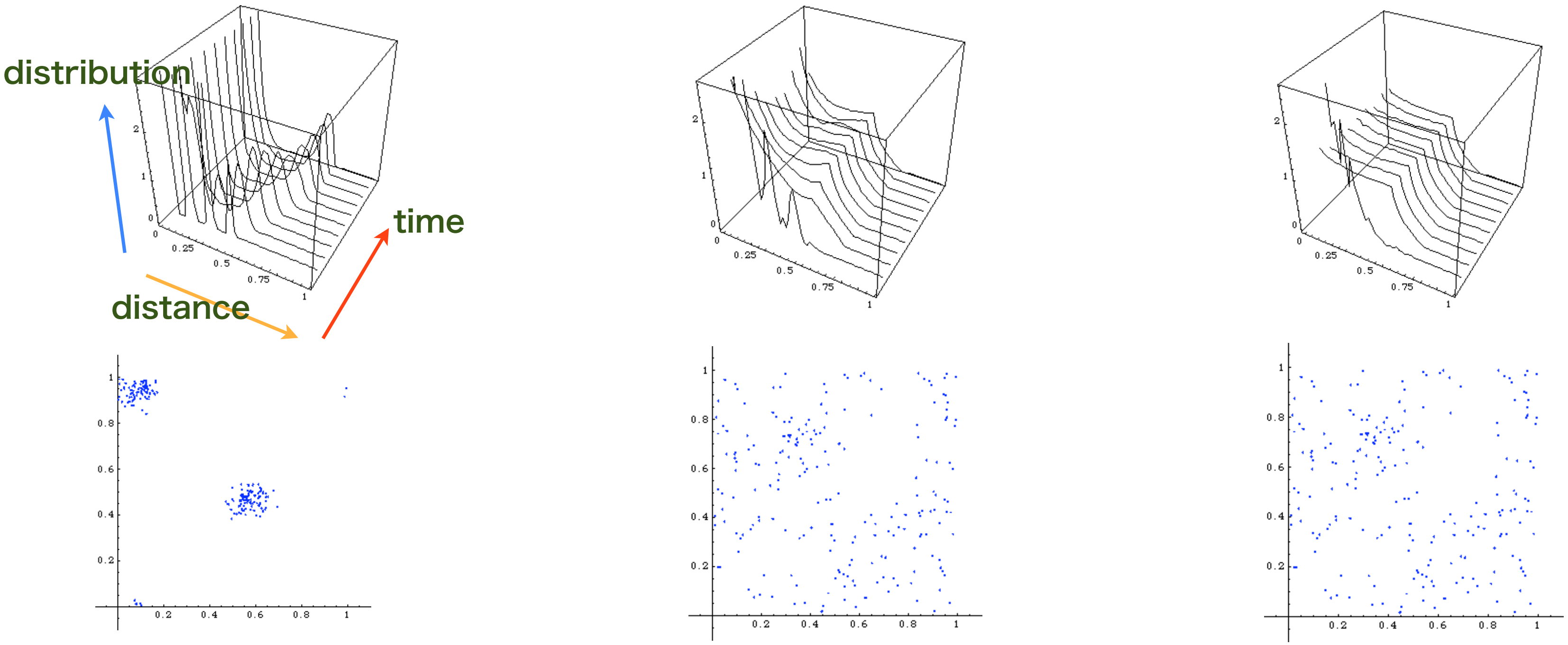
SD-dispersal : 0.05





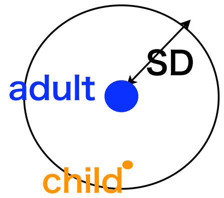
T=1 T=5 T=30 T=50 T=100

Distribution graph of distance between two individuals



SD=0.01 SD=0.03 SD=0.05

SD-dispersal： radius of distance that adult born on offspring



Two species model

Nicholson Bailey model

$$H_{t+1} = RH_t e^{-aP_t}$$
$$P_{t+1} = H_t(1 - e^{-aP_t})c$$

the equilibrium H_t, P_t filled
the next equation

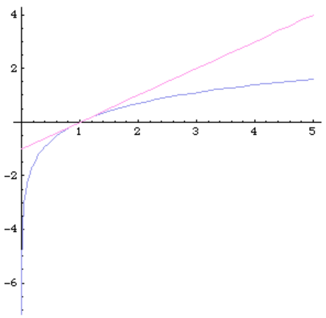
$$\hat{H}_{t+1} = R\hat{H}_t e^{-a\hat{P}_t})$$
$$\hat{P}_{t+1} = \hat{H}_t(1 - e^{-a\hat{P}_t})$$

$$(\hat{H}_t, \hat{P}_t) = (0, 0)$$ → unstable

$$(\hat{H}_t, \hat{P}_t) = (\frac{\log R}{a(1-\frac{1}{R})}, -\frac{1}{a}\log\frac{1}{R})$$

linearization around equibrium $\begin{pmatrix} \frac{\partial f}{\partial H_t} & \frac{\partial f}{\partial P_t} \\ \frac{\partial g}{\partial H_t} & \frac{\partial g}{\partial P_t} \end{pmatrix}$

$$\begin{pmatrix} 1 & -\frac{R\log R}{R-1} \\ 1-\frac{1}{R} & \frac{\log R}{R-1} \end{pmatrix}$$



$$detJ = \left|\frac{RlogR}{R-1}\right| > 1$$

$$|\lambda|^2 > 1$$ unstable

Nicholson Bailey model + Density-dependency

Ricker Logistic multiplation

Innovation local density efficient

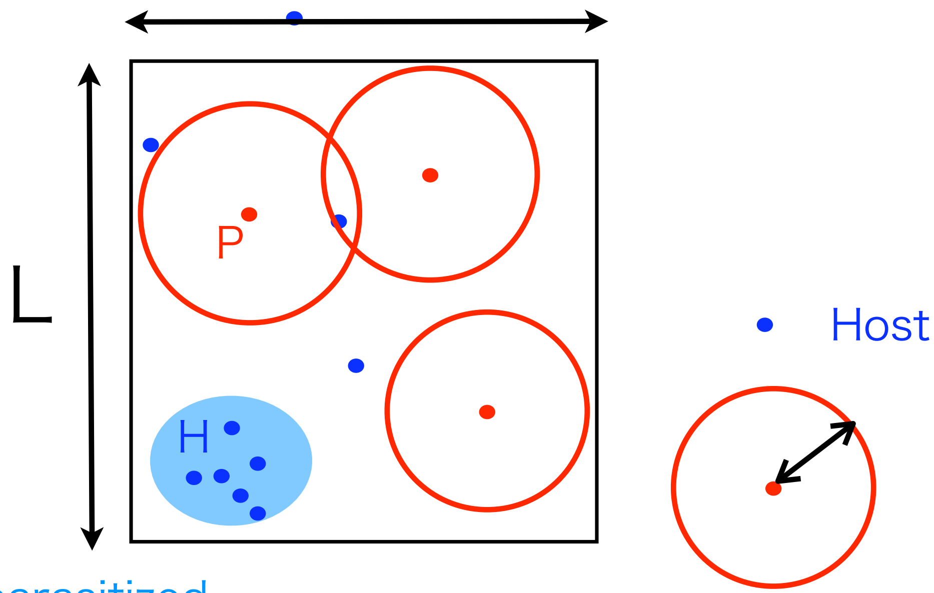
$$H_{t+1} = RH_t e^{-aP_t}$$
$$P_{t+1} = H_t(1 - e^{-aP_t})c$$

$$H_{t+1} = e^{r(1-\frac{H_t}{K})} H_t e^{-aP_t}$$
$$P_{t+1} = H_t(1 - e^{-aP_t})c$$

when “P” equal 0 , ”H” many change depending on “r”

$$H_{t+1} = e^{r(1-\frac{H_t}{K})} H_t$$

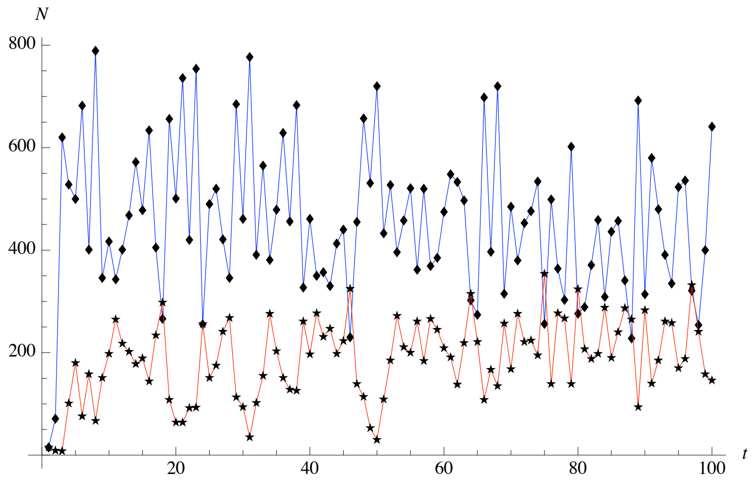
Host and Parasite using Individual-Based Model



A host , if not parasitized, produces X offpring

Parasite & A parasite's area of discovery "r" is patrasitized and produces one parasite offspring

Simulation


N
800
600
400
200
20
40
60
80
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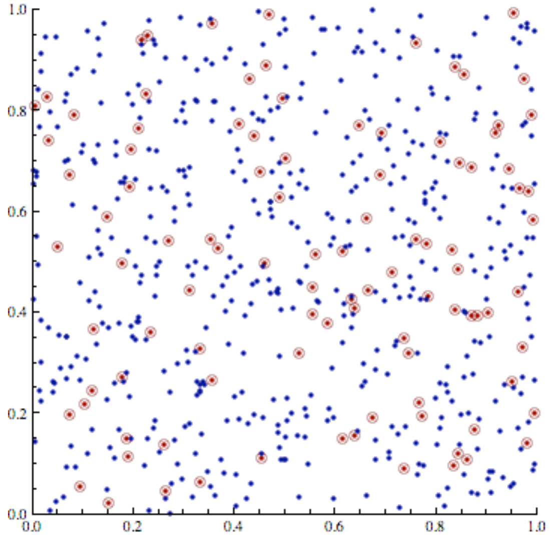
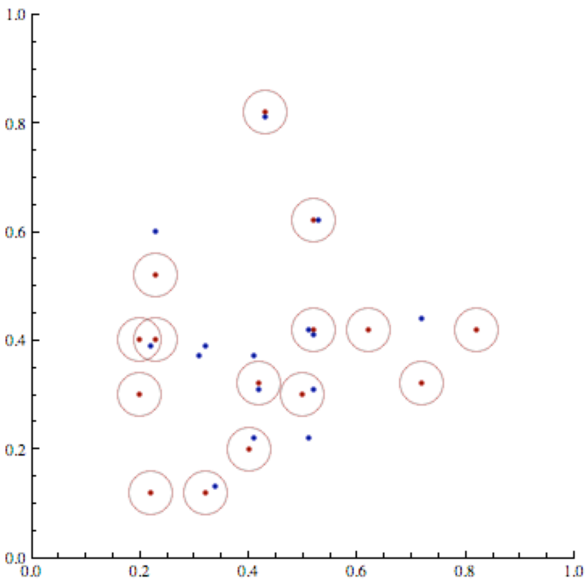
t


1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0


1.0
0.8
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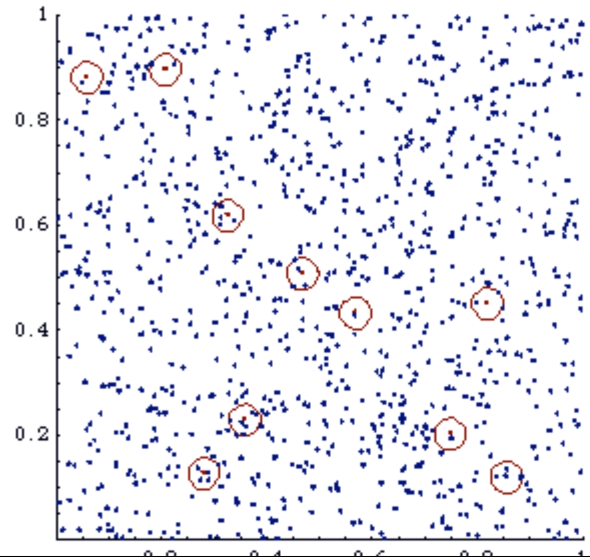
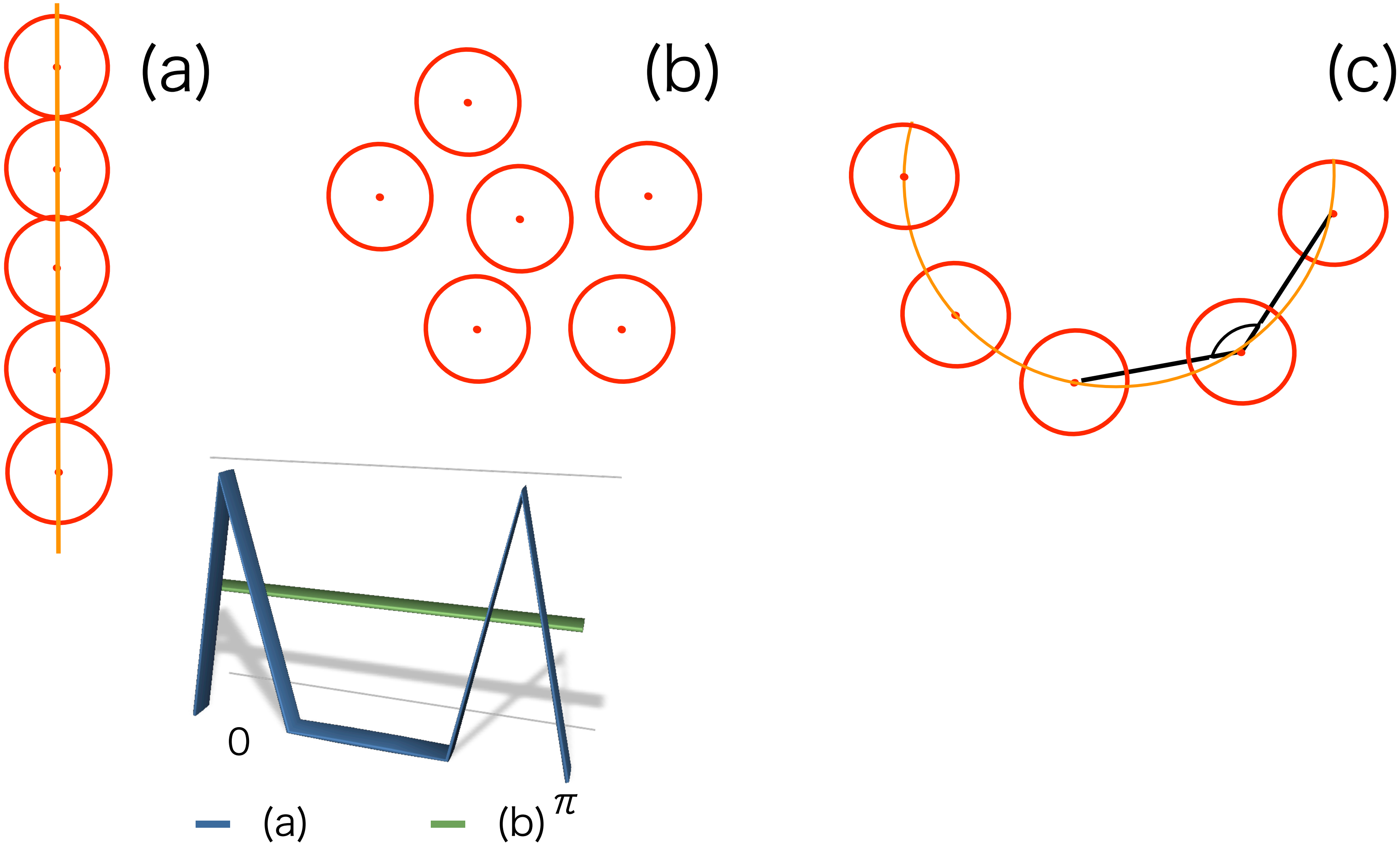
0.2
0.4
0.6
0.8
1.0


1
0.8
0.6
0.4
0.2

One idea to detect spiral in spatial IBM



Future Works

- I have been applied the framework to multiple species system like host-parasite population dynamics
- Analyze 1st, 2nd and 3rd order of spatial statistics (Indexes measuring crowding and specific patterns like spirals)

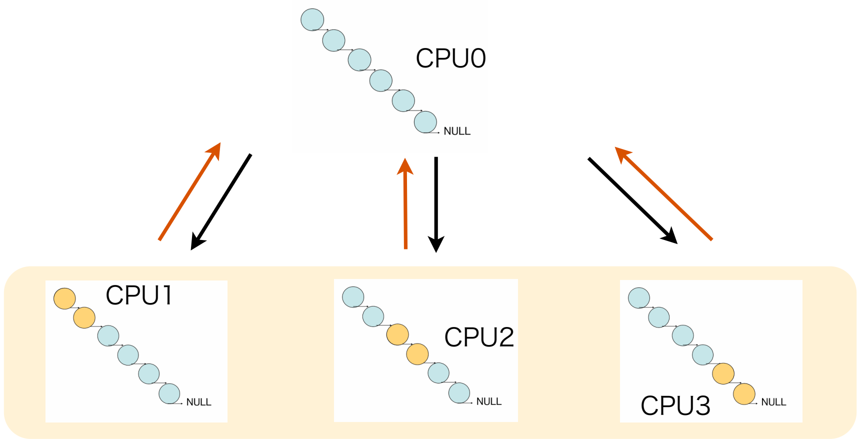
Parallel computing of IBM

MPI (Message-Passing-Interface) :

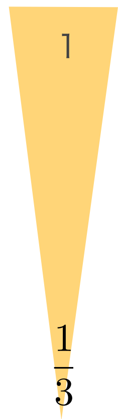
- Use parallel computing of distributed memory
- The library corresponding beteen CPU

CPU 0	CPU 1
send data which calculate to CPU1	receive data from CPU0
	calculate for receiveing data
receive data from CPU1	send calculated data to CPU0
display received data	

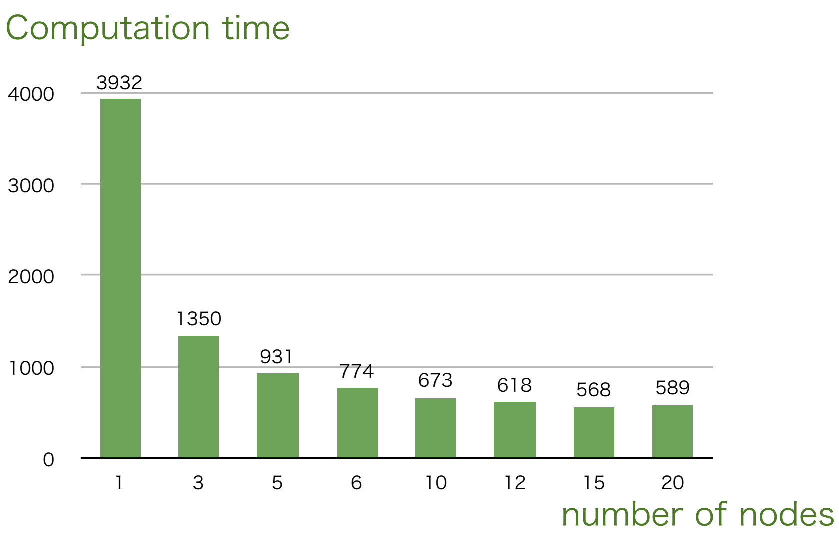
Ex) Using 4 nodes

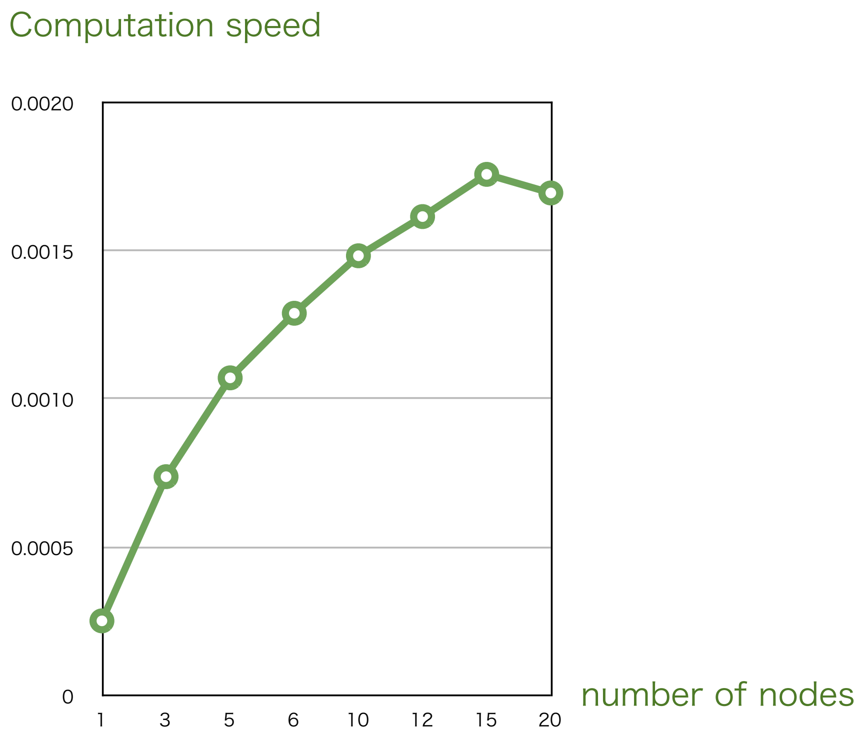


Computation time



Calculation time





Thank you for your attention.