Mathematical analysis of three species model and introduction of the canonical model.

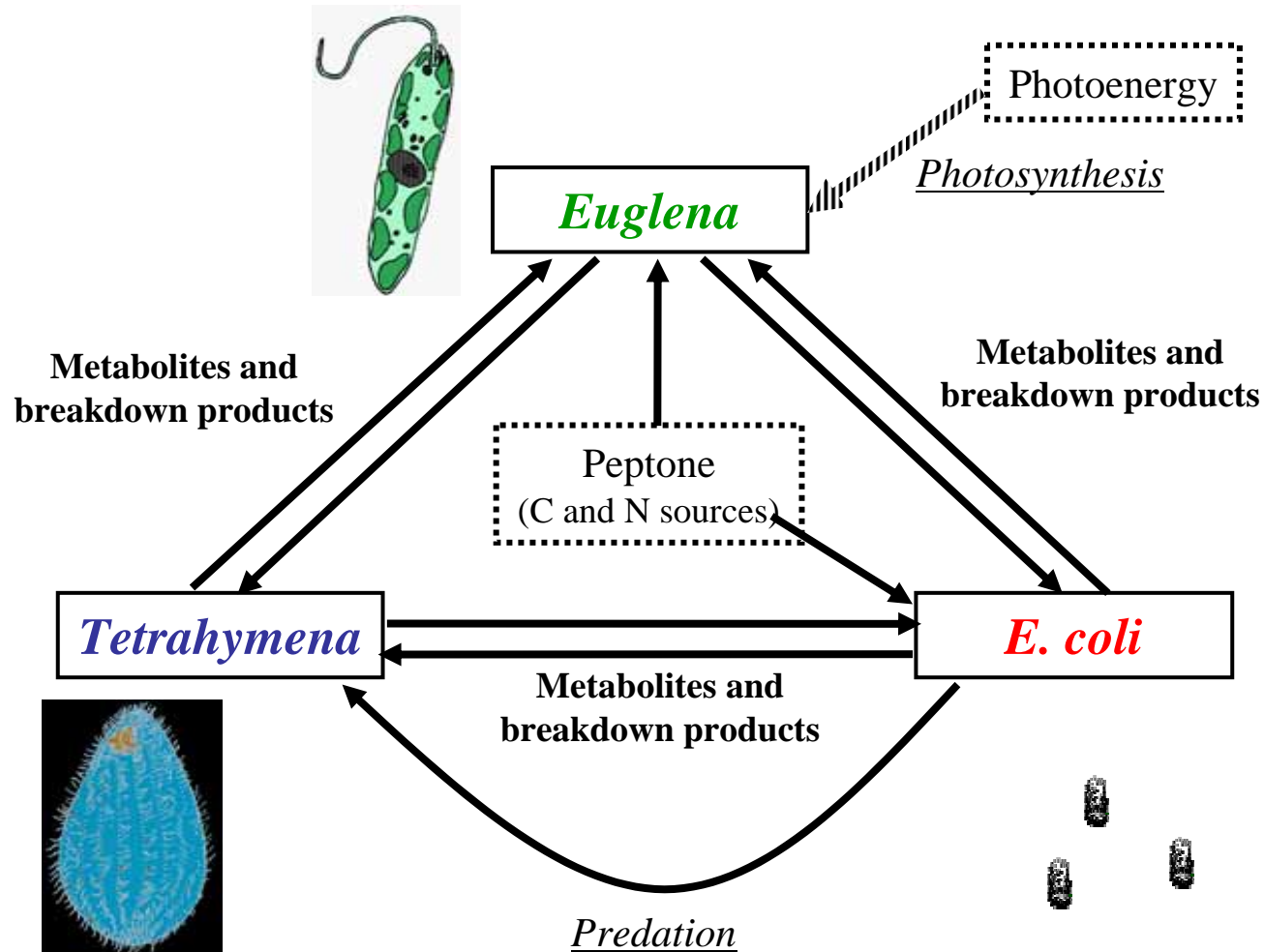Isao Kawaguchi

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Suggestions from Tatiana

- a) could you transform your experimental model into a generic model with competing preys and a predator (all exposed to chronic irradiation)

- b) It would be most interesting to apply the canonical model of population to the case of chronic radiation exposure, could you do it?

- c) The concept of metapopulation with extinction of some sub-populations and their repopulation due to migration seems to be very promising, it would be nice if you make a presentation about this concept; will you?

Three species model

Microcosm
(Kawabata microcosm)

Interactions in the three-species microcosm

Photoenergy

Photosynthesis

Euglena

Metabolites and breakdown products

Metabolites and breakdown products

Peptone
(C and N sources)

Tetrahymena

E. coli

Metabolites and breakdown products

Predation

We developed a simulation model of microcosm.s

Chronic exposure on SIM-COSM
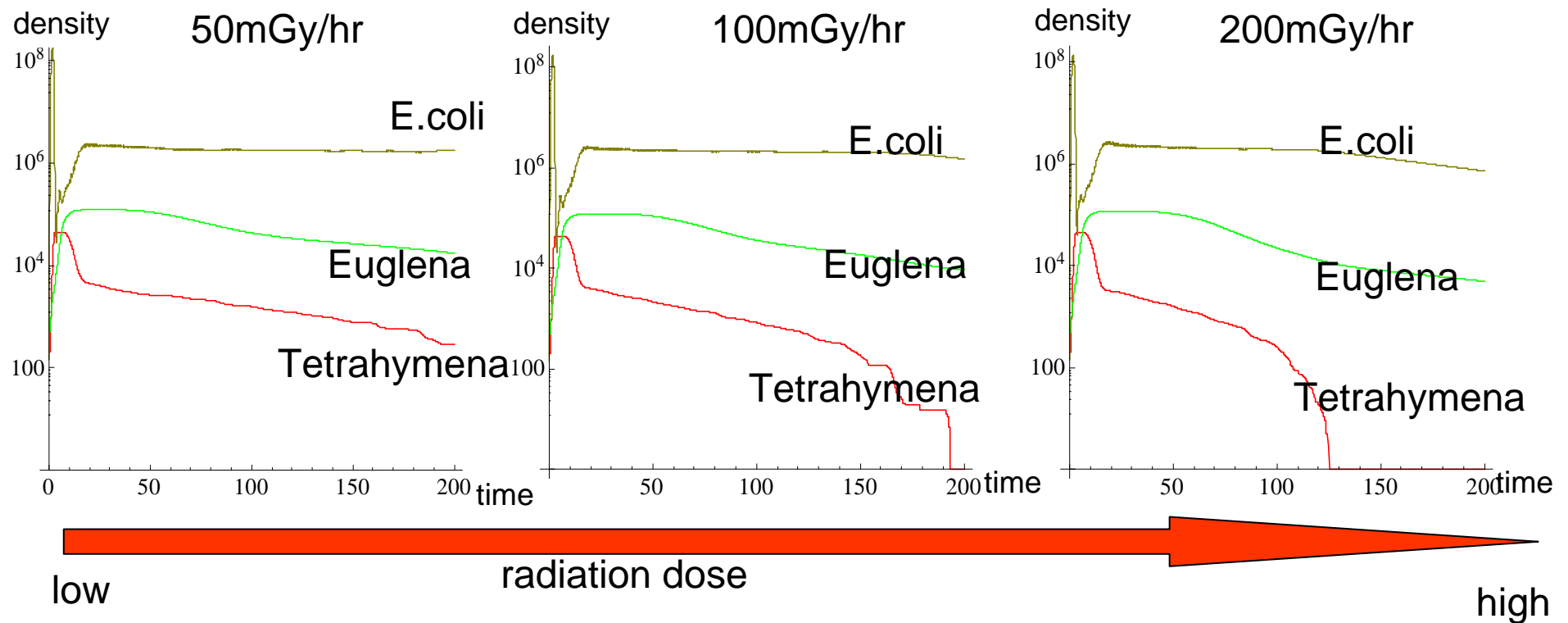
In chronic exposure, Tetrahymena (most resistant species in individual level) is the most sensitive.

Assumptions

- To develop a simple mathematical model, we focused on the direct interaction between species, and indirect interactions are ignored.
  - whereas each species depends on metabolites from the others in microcosm and SIMCOSM.
- The ecosystem is not closed.
  - Microcosm and SIMCOSM are self sustainable system and closed system.
- Spatial effects are omitted.
- Stochasticities are ignored.

Deterministic model

$$\dot{E} = r_E E \left(1 - \frac{E}{K_E} \right) - \alpha_E E$$

E: population density of Euglena

$$\dot{P} = sE - \frac{axP}{1 + h_x P}$$

P: density of photosynthesis production

$$\dot{x} = r_x \frac{axP}{1 + h_x P} - \frac{bxy}{1 + h_y x} - \alpha_x x$$

x: population density of E. coli

$$\dot{y} = r_y \frac{bxy}{1 + h_y x} - \alpha_y y$$

y: population density of Tetrahymena

r_i: growth rate of organism i
h_i: handling time of species i
α_i: mortality of organism i

a: predation rate of E. coli
b: predation rate of Tetrahymena

Analytic results

- The model has four equilibria
  - All of species were extinguished.
  - Euglena (producer species) was only existing.
  - Only predator species (Tetrahymena) was extinction.
  - All species were coexisted.
- Hysterisis (or resume shift) was not existed (No bistable cases were existed).
- Prey and predator populations were dynamically fluctuated when handling time of prey species is long.

Chronic irradiation

- LD_{50} values with single species cultured are 4000Gy for Tetrahymena, 330 Gy for Euglena and 13 Gy for E. coli.

- From the analysis of the model, in chronic low dose rate irradiation, Tetrahymena who is the most resistant species in individual level is the most sensitive species.

- The analytical result is consistent with simulation results.

the canonical model

The canonical model

The canonical model is developed to calculate
the extinction risk of stable population

$$\frac{dX}{dt} = rX\left(1 - \frac{X}{K}\right) + \sigma_e \xi_e(t) \circ X + \sigma_d \xi_d(t) \bullet \sqrt{X}$$

logistic growth   environmental stochasticity   demographic stochasticity

r: intrinsic growth rate,

K: carrying capacity,

σ_e: intensity of the fluctuation of growth rate by environmental stochasticity,

σ_d: intensity of the fluctuation of growth rate by demographic stochasticity
(can be set as 1)

ξ_e and ξ_d: white noise which corresponding to fluctuation of environment
and demographic process,

Environmental stochasticity: the environment quality fluctuates year-to-year
and the effects of fluctuation is common among the population.

Demographic stochasticity: number of offsprings is different between
individuals.

Estimation of parameters of the canonical model

- Time unit is mean generation time.
- Intensity of demographic stochasticity(σ_d) can be set as 1 if number of offspring per female follows a Poisson distribution.
- Intensity of environmental stochasticity(σ_e) is estimated from time series data.
- Carrying capacity K is equivalent to mean population density.
- Intrinsic growth rate r should be obtained from other source, because growth rate is small when population at equilibrium.

$$K=E[X]$$

$$\sigma_e^2=2r\mathrm{Var}[X]/E[X]^2$$

$$AC_X(\tau)=(\sigma_e^2 K^2+K)e^{-r|\tau|}/(2r)$$
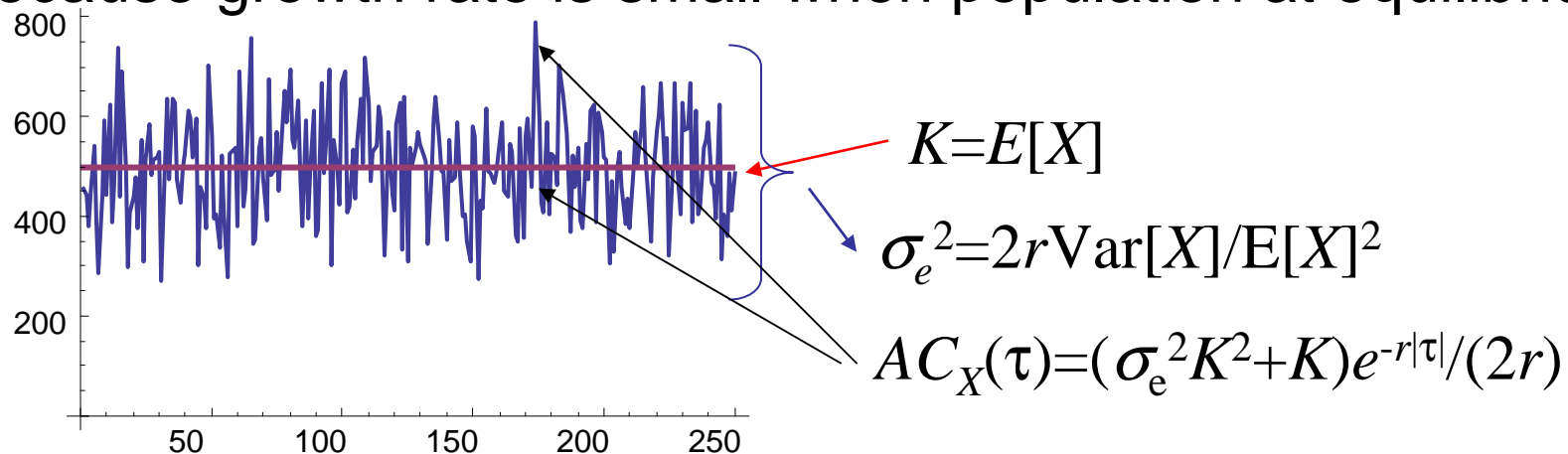
Estimation of intrinsic growth rate r of the population which is consisted of multiple age.

Using Leslie matrix which describes life cycle of the organisms

$$\begin{pmatrix} n_0(t+1) \\ n_1(t+1) \\ \vdots \\ n_w(t+1) \end{pmatrix} = \begin{pmatrix} f(0) & f(1) & \cdots & f(a) & & f(w) \\ p_1 & 0 & & \cdots & & 0 \\ & p_2 & & & & \\ \vdots & & \ddots & & & \vdots \\ & & & p_{a-1} & & \\ 0 & & & & p_w & 0 \end{pmatrix} \begin{pmatrix} n_0(t) \\ n_1(t) \\ \vdots \\ n_w(t) \end{pmatrix}$$

$n_a(t)$: population density of age a at time t

$f(a)$: fertility at age a

p_a: survival rate per year at age a

Averaged growth rate r of the population is obtained from solution of Euler-Lotka equation
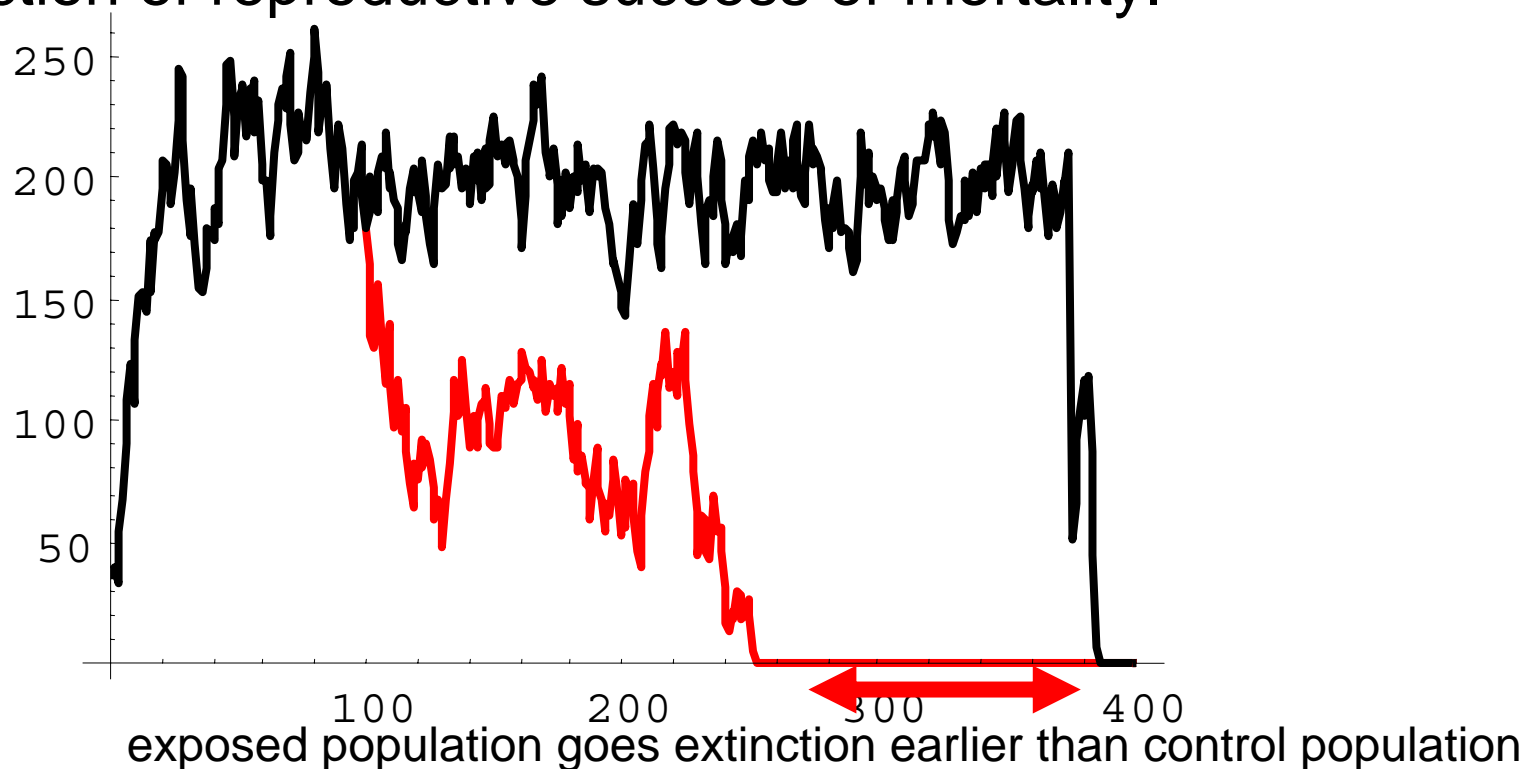
$$1 = \sum_{a=0}^{w} e^{-(a+1)r} f(a) p_1 \cdots p_a$$

Chronic radiation

$$\frac{dX}{dt} = \left(r - \Delta r(D)\right)\left(1 - \frac{X}{K}\right)X + \sigma_e \xi_e(t) \circ X + \xi_d(t) \bullet \sqrt{X} - \alpha(D)X$$

$\Delta r(D)$: reduction of reproductive success.

$\alpha(D)$: mortality per capita

morbidity and genomic damage should be converted to reduction of reproductive success or mortality.

exposed population goes extinction earlier than control population

Risk evaluation of the radiation

"average sustainable time (extinction risk)" can be calculated.

$$T_{control} = \frac{2}{\sigma_e^2} \int_0^{x_0} \int_x^{\infty} e^{-R(y-x)} \left(\frac{y+D}{x+D} \right)^{R(K+D)} \frac{dy}{(y+D)y} dx$$

$$T_{exposed} = \frac{2}{\sigma_e^2} \int_0^{x_0} \int_x^{\infty} e^{-R'(y-x)} \left(\frac{y+D}{x+D} \right)^{R'(K'+D')} \frac{dy}{(y+D)y} dx$$

$$D = \sigma_d^2 / \sigma_e^2$$

$$R = 2r / \left(\sigma_e^2 K \right)$$

$$R' = 2r_{exposed} / \left(\sigma_e^2 K_{exposed} \right)$$

Endpoint of the population risk is reduced mean extinction time
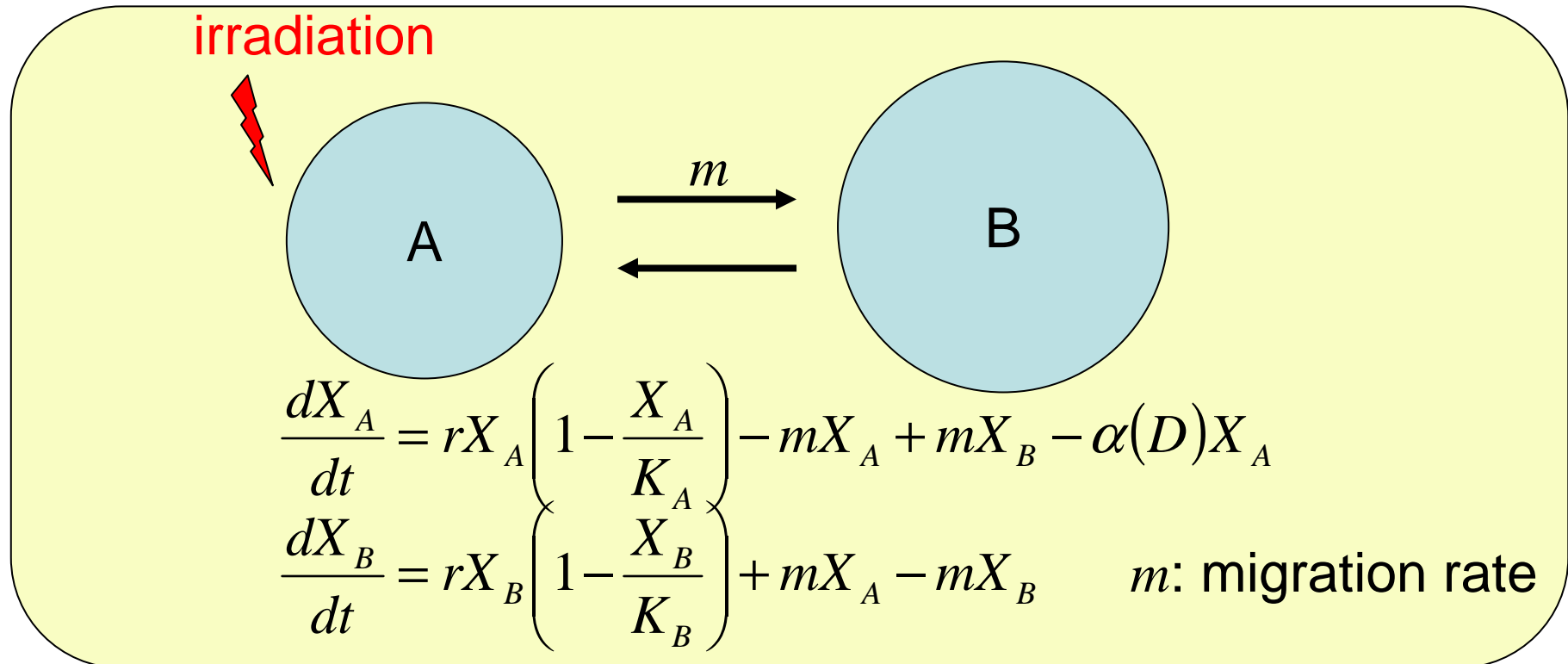
$$\Delta T = T_{control} - T_{exposed}$$

$$\Delta \log T = \log T_{control} - \log T_{exposed} \quad \text{for very large population}$$

$$\Delta 1/T = 1/T_{control} - 1/T_{exposed} \quad \text{for endangered species}$$

Meta-population

Meta population

- Population separated sub-populations and sub-Populations are connected each other.

irradiation

m

A

B

$$\frac{dX_A}{dt} = rX_A\left(1 - \frac{X_A}{K_A}\right) - mX_A + mX_B - \alpha(D)X_A$$

$$\frac{dX_B}{dt} = rX_B\left(1 - \frac{X_B}{K_B}\right) + mX_A - mX_B \qquad m: \text{migration rate}$$

Subpopulation A can be sustained due to migration from population B at high dose. However, when migration rate is very high, total population goes extinction

Generic formulation for meta-population

$$\frac{dX_i}{dt} = r_i X_i \left(1 - \frac{X_i}{K_i} \right) - \sum_{i \neq j} m_{ji} \left(X_j - X_i \right)$$

X_i: population density of sub-population i

r_i: intrinsic growth rate of sub-population i

K_i: Carrying capacity of sub-population i

m_{ji}: migration rate from population j to i

Implications for meta-population

- Hakoyama and Iwasa applied the canonical model to meta-population.
- Endpoint is extinction time of total population ($X_{total}=\Sigma X_n$).
- Parameters (r, K, σ_e^2) are estimated from time series data of total population.
- Estimated parameters have many biases, so that the biases are removed by Monte Carlo bias-correction method using approximate maximum likelihood.
- Comparing with computer simulation and estimation from parameter aggregated canonical model, the estimation was very well when migration rate is not low.