

Modelling of a multi-prey/multi-predator system in a context of parasite transmission ecology

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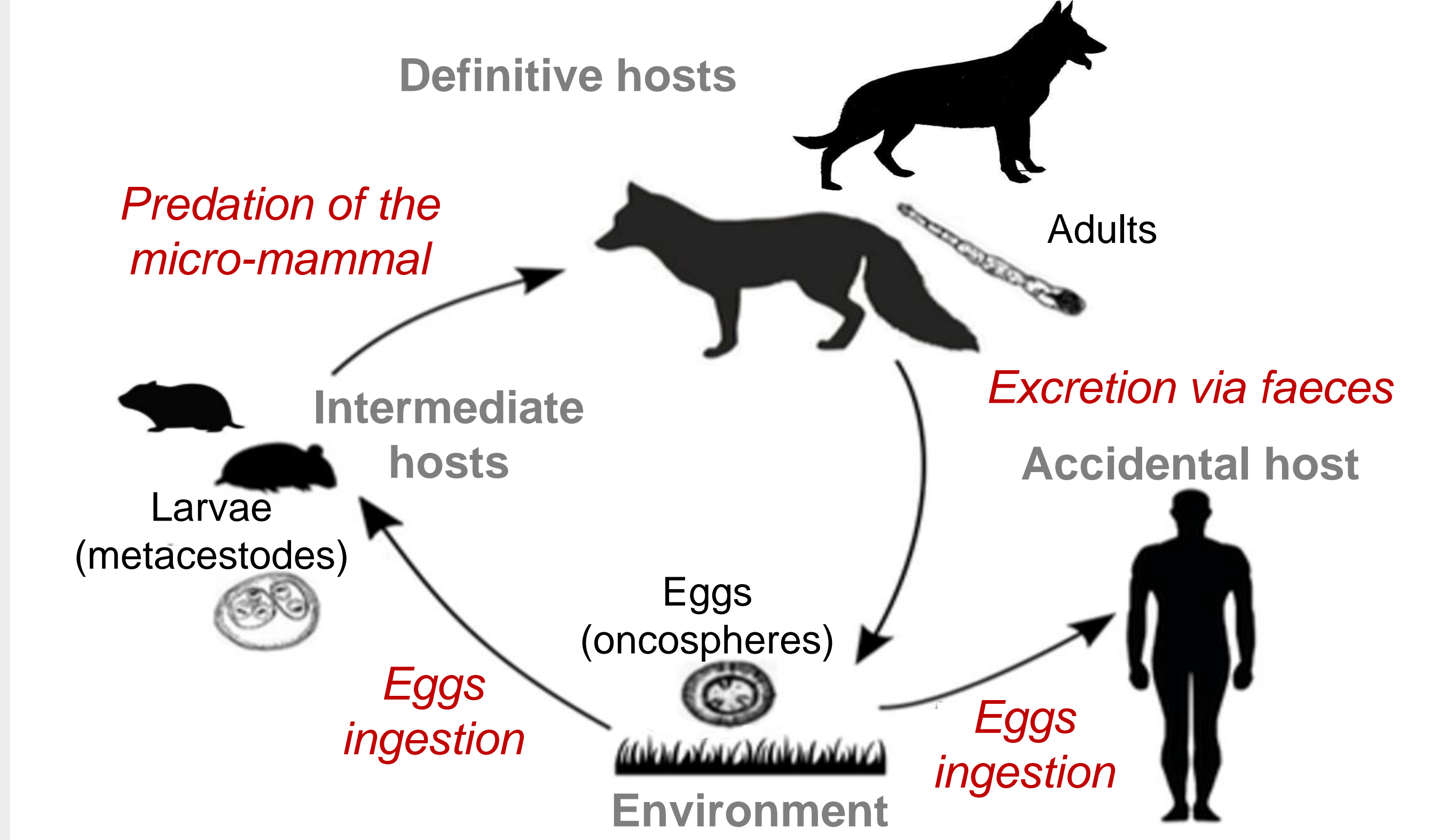
Modelling of a multi-prey/multi-predator system in a context of parasite transmission ecology

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Introduction

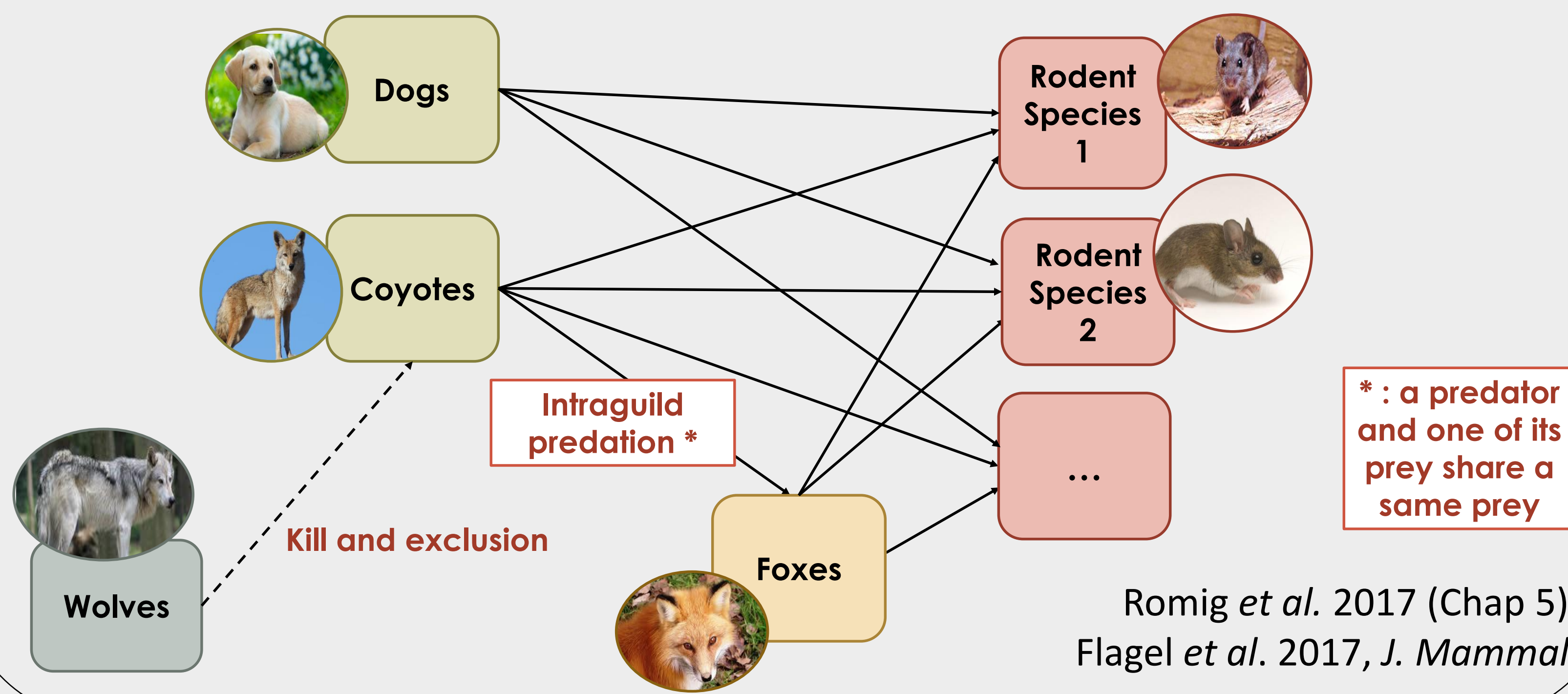
Echinococcus multilocularis (*Em*), a cestode parasite responsible for human alveolar echinococcosis, an emerging zoonosis, completes its life cycle between intermediate hosts (mainly rodents) and definitive hosts (wild and domestic carnivores, mainly generalists predators) by passing from the former to the latter via predation. To predict its transmission dynamics, one should first understand and model dynamics of the community involved in this transmission. In terms of modelling, the generalist character of our predators has been expressed in terms of logistic growth (independent from the presence of a specific prey). We also modelled a multi-predator effect known as intraguild predation (see below). In this context, we aimed to assess the effect of introducing possibility for the predators to adapt its preference of a prey depending on its relative abundance (known as switching) on the coexistence of all species at equilibrium.

Echinococcus multilocularis life cycle



Adapted from Baudrot et al. 2016, PhD thesis

Food web implicated in the transmission of *Em* in North America



Model

Adapted from Wei et al., 2019, *Math Comput Simul*, for two generalist predators with intraguild predation and n preys.
For the moment, wolves and dogs compartments are not modelled.

Logistic growth

Predation of foxes on prey k

Predation of coyotes on prey k

Intraguild predation of coyotes on foxes

Prey k
$$\dot{x}_k(t) = r_k x_k(t) \left(1 - \frac{x_k(t)}{K_k}\right) - \phi_{F,k} F(t) - \phi_{C,k} C(t)$$

Foxes
$$\dot{F}(t) = r_F F(t) \left(1 - \frac{F(t)}{K_F}\right) + \sum_{k=1}^n b_{1,k} \phi_{F,k} F(t) - I_{C,F} C(t)$$

Coyotes
$$\dot{C}(t) = r_C C(t) \left(1 - \frac{C(t)}{K_C}\right) + \sum_{k=1}^n b_{2,k} \phi_{C,k} C(t) + b_3 I_{C,F} C(t)$$

$b_{i,k}$ = conversion efficiencies

Each functional response is of Beddington DeAngelis form.

Depending on its expression, each functional response could show switching or no.

For instance, intraguild predation functional response is written as:

Attack rates

Holling II type
$$I_{C,F} = \frac{p_3 F(t)}{H_2 + \sum_{k=1}^n \alpha_{2,k} p_{2,k} x_k(t) + \beta_2 p_3 F(t) + \gamma C(t)}$$

or

Half saturation constant

Handling times

Interference between coyotes

Holling III type
$$I_{C,F} = \frac{p_3 F(t)^2}{H_2 + \sum_{k=1}^n \alpha_{2,k} p_{2,k} x_k(t)^2 + \beta_2 p_3 F(t)^2 + \gamma C(t)}$$

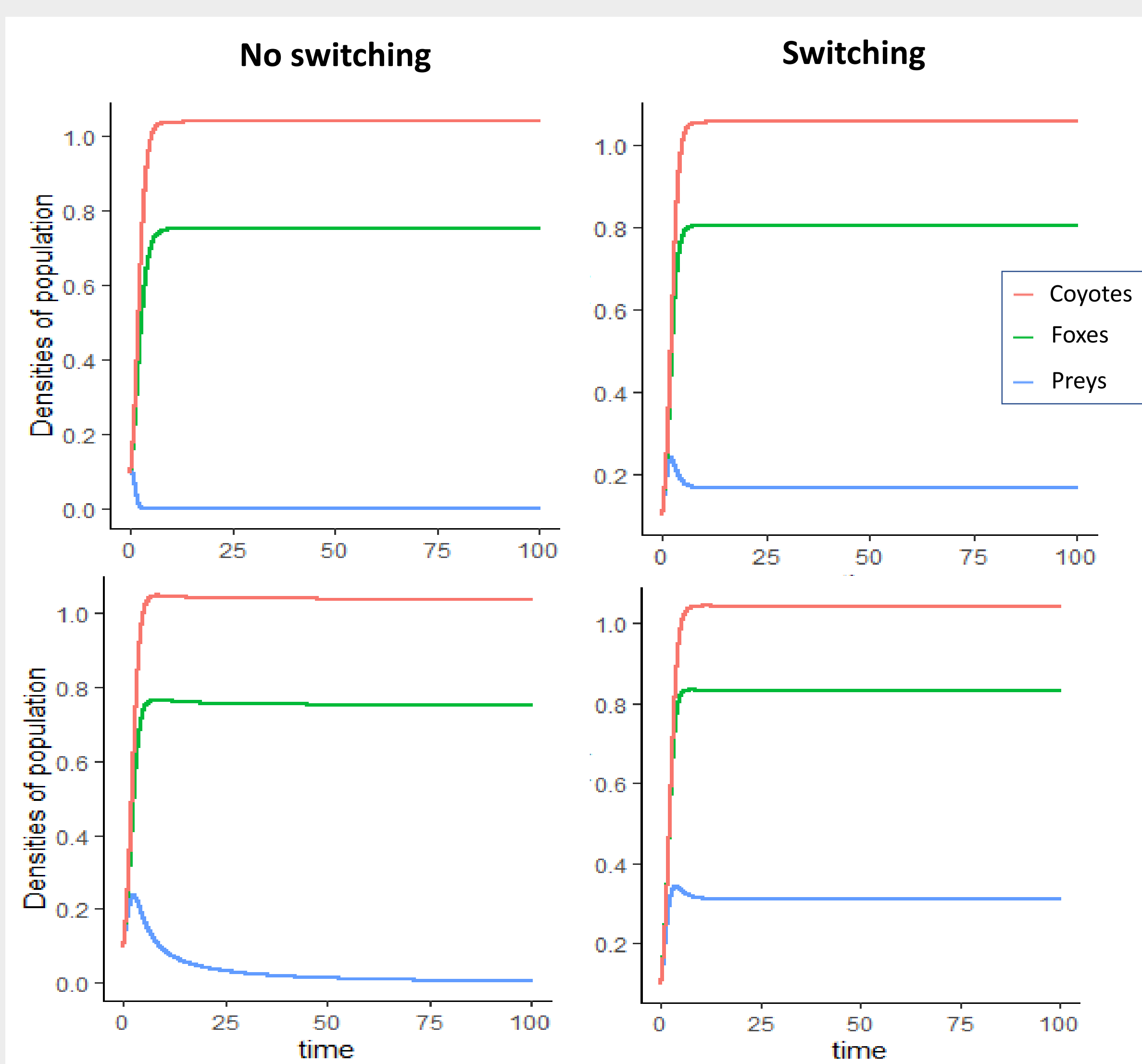
Results

- Simulations with one prey ($n=1$) show that, with logistic growth (corresponding to generalist predators), we obtain coexistence of the three species even without switching behavior and predators can subsist without prey.
- With switching for coyotes functional responses, coexistence of the three species occurs with a biggest range of attack rates from foxes and coyotes on the prey than without switching. Switching has therefore a stabilizing effect.

Figure Simulations with one prey and no switching for $\phi_{F,1}$.

Left. $I_{C,F}$ and $\phi_{C,1}$ exhibit no switching. Right. $I_{C,F}$ and $\phi_{C,1}$ exhibit switching.

Top. Attack rate of foxes on prey = 0.2 and attack rate of coyotes on prey = 9. Bottom. Attack rate of foxes on prey = 1.2 and attack rate of coyotes on prey = 1. All other parameters are the same for both models.



Perspectives

Models will be first extended by adding other predators (dogs and wolves). We will then assess the effect of switching in this context of several predators and n preys. Depending on data and collaborations, this work would be done by bayesian statistics to select the best model and/or by numerical analysis.

Best models will be then implemented with epidemiologic states (SI models) in order to evaluate the impact of biodiversity on epidemiological dynamics for the transmission of *Em* (e.g. dilution or amplification phenomena).