Identification des paramètres d'une classe de réseaux de régulation de gènes hybrides

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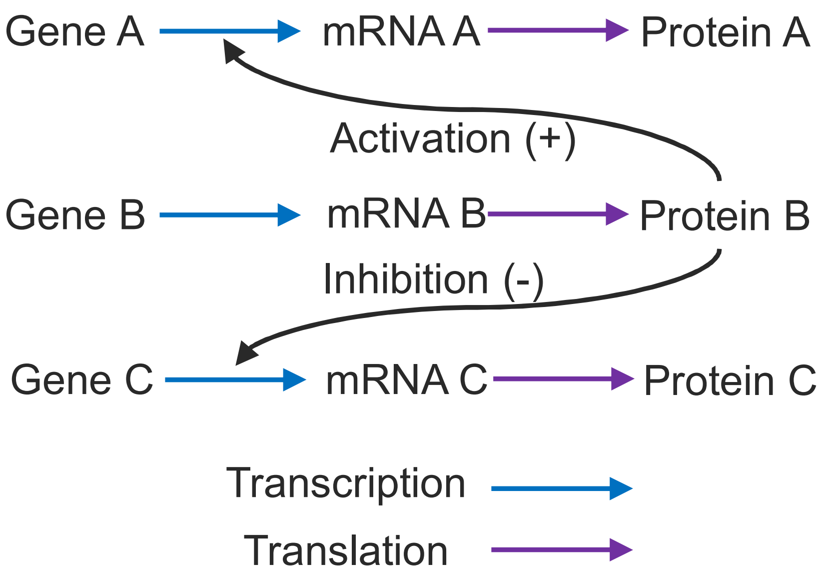
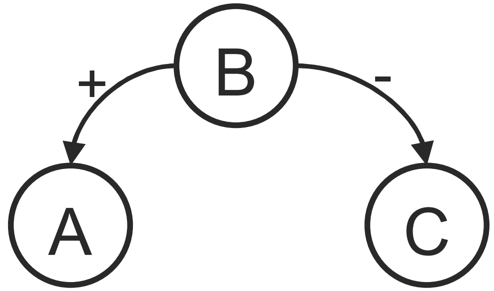
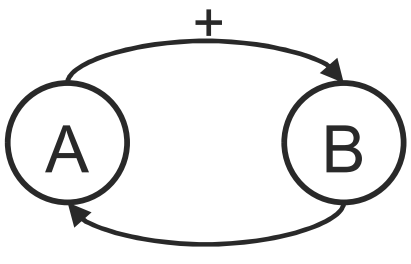
Introduction of gene regulatory networks





Gene regulatory networks (Influence graph)

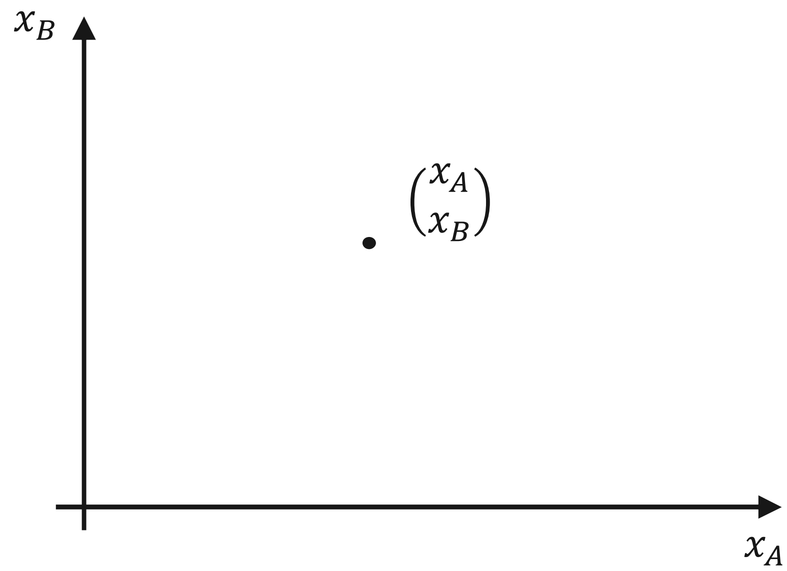
Different formalisms of gene regulatory networks



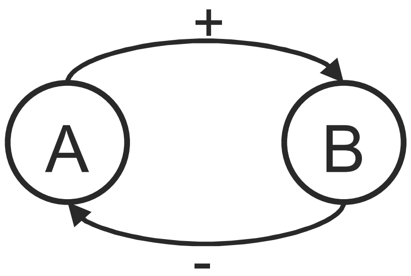
An influence graph

Differential equation

$$\frac{d\,x_A}{d\,t} = -k_1 x_A + K_1 \frac{\theta_B^n}{\theta_B^n + x_B^n}$$
$$\frac{d\,x_B}{d\,t} = -k_2 x_B + K_2 \frac{x_A^n}{\theta_A^n + x_A^n}$$



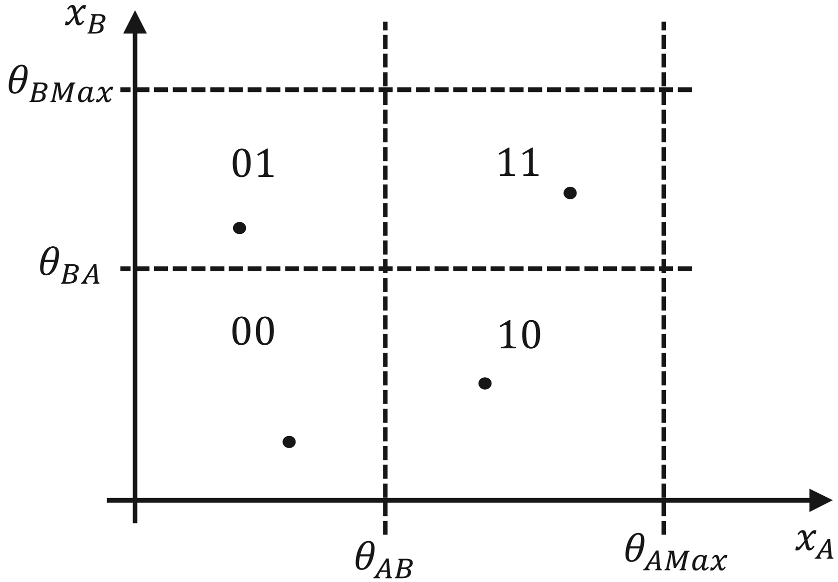
Different formalisms of gene regulatory networks

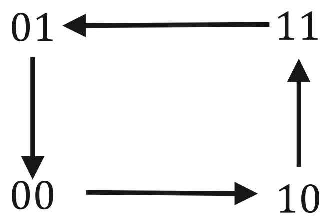


An influence graph

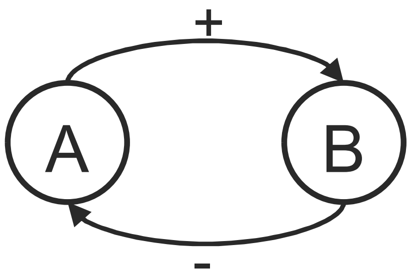
Boolean networks

$$b_A^{t+1} \leftarrow \neg b_B^t$$
$$b_B^{t+1} \leftarrow b_A^t$$





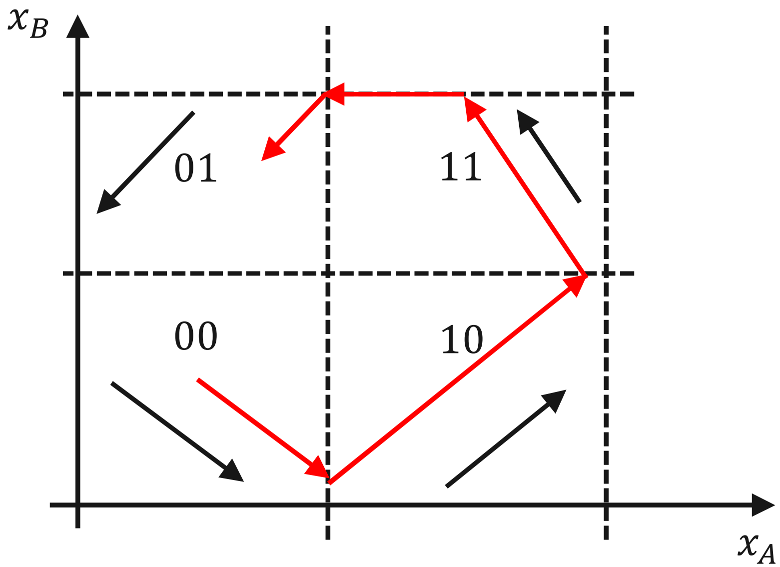
Different formalisms of gene regulatory networks



An influence graph

Hybrid gene regulatory networks (HGRN)

[Cornillon et al., advances in Systems and Synthetic Biology, 2016]



01

$$\frac{d\,x_A}{d\,t} = V_{ab1a0}$$
$$\frac{d\,x_B}{d\,t} = V_{ba0b1}$$

11

$$\frac{d\,x_A}{d\,t} = V_{ab1a1}$$
$$\frac{d\,x_B}{d\,t} = V_{ba1b1}$$

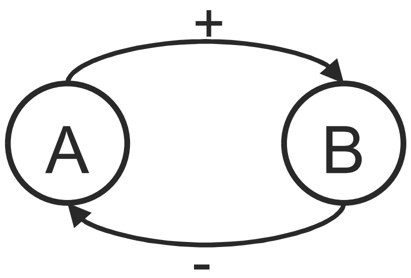
00

$$\frac{d\,x_A}{d\,t} = V_{ab0a}$$
$$\frac{d\,x_B}{d\,t} = V_{ba0b0}$$

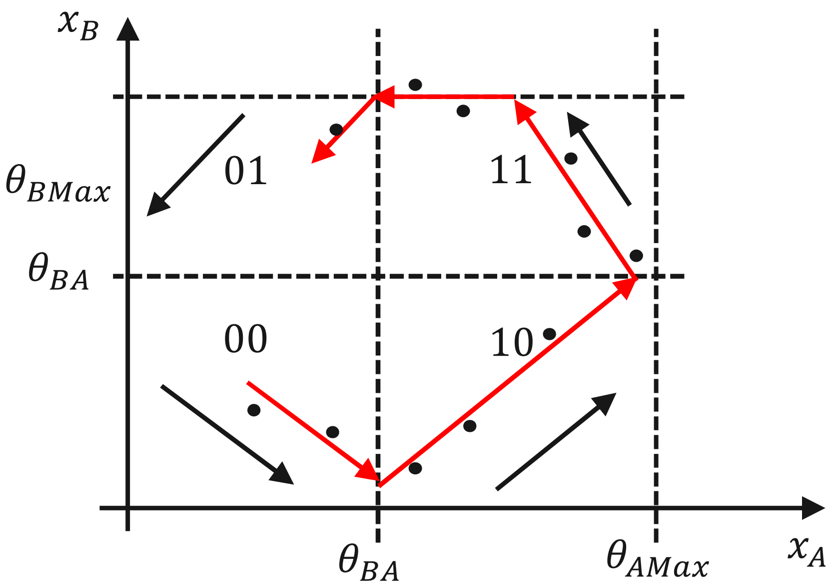
10

$$\frac{d\,x_A}{d\,t} = V_{ab0a1}$$
$$\frac{d\,x_B}{d\,t} = V_{ba1b0}$$

Objective



An influence graph



01

$$\frac{d\,x_A}{d\,t} = V_{ab1a0}$$
$$\frac{d\,x_B}{d\,t} = V_{ba0b1}$$

11

$$\frac{d\,x_A}{d\,t} = V_{ab1a1}$$
$$\frac{d\,x_B}{d\,t} = V_{ba1b1}$$

00

$$\frac{d\,x_A}{d\,t} = V_{ab0a0}$$
$$\frac{d\,x_B}{d\,t} = V_{ba0b0}$$

10

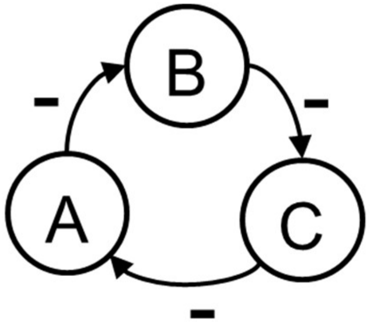
$$\frac{d\,x_A}{d\,t} = V_{ab0a1}$$
$$\frac{d\,x_B}{d\,t} = V_{ba1b0}$$

θ_{BA} θ_{BMax} θ_{BA} θ_{AMax}

V_{ab1a0} V_{ba0b1} ……

Objective

Le graphe d’influence étudié dans ce projet:



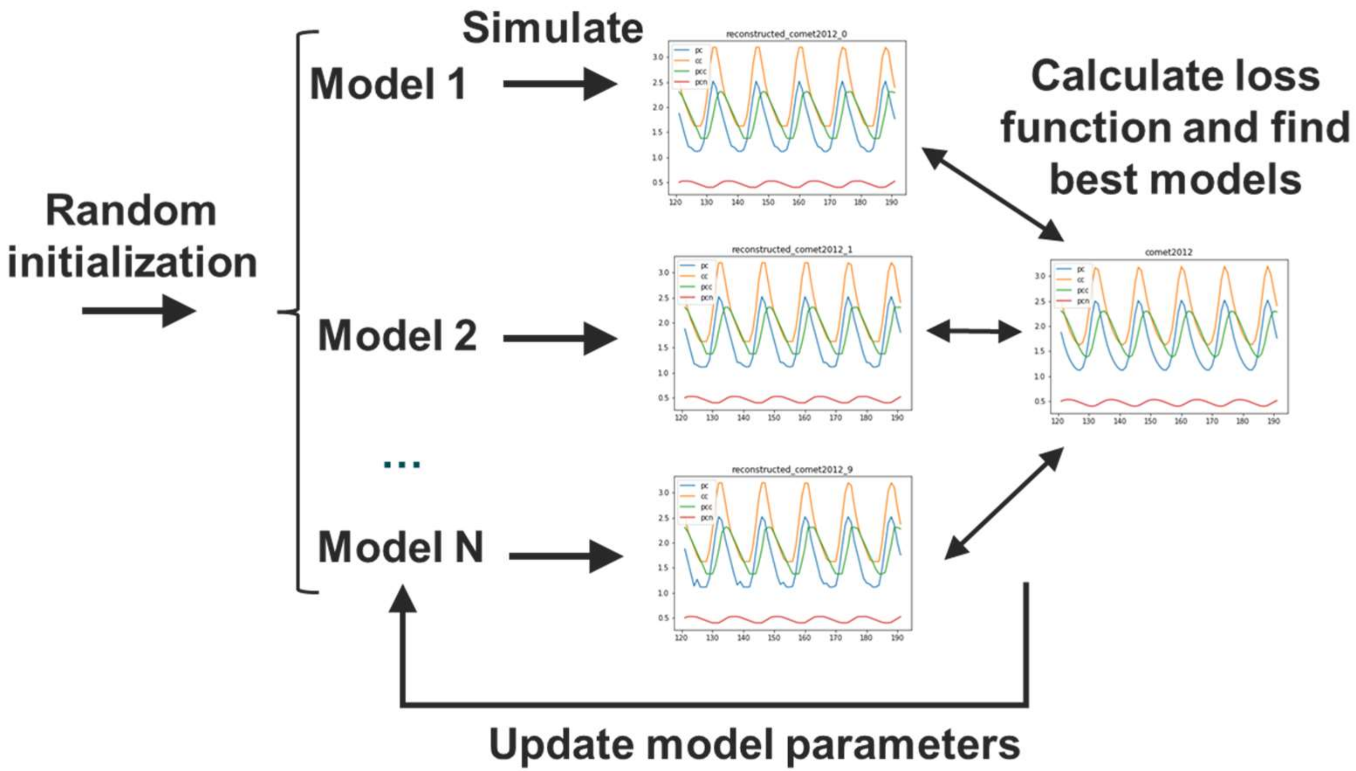
A repressilator

https://github.com/Honglu42/Projet_RetD/blob/main/simulation.ipynb

References about HGRN

[Cornillon, E. et al., advances in Systems and Synthetic Biology., 2016] Cornillon, E., Comet, J. P., Bernot, G., & Enée, G. (2016). Hybrid gene networks: a new framework and a software environment. advances in Systems and Synthetic Biology.

[Behaegel, J. et al., Journal of bioinformatics and computational biology, 2016] Behaegel, J., Comet, J. P., Bernot, G., Cornillon, E., & Delaunay, F. (2016). A hybrid model of cell cycle in mammals. Journal of bioinformatics and computational biology, 14(01), 1640001.



Main idea of Particle swarm optimization