La modélisation de la flocculation dans le chemostat

Tewfik Sari
EPI MERE INRA/INRIA, Montpellier & Université de Mulhouse
tewfik.sari@uha.fr, tewfik.sari@sophia.inria.fr

En collaboration avec
Jérôme Harmand, Claude Lobry et Alain Rapaport

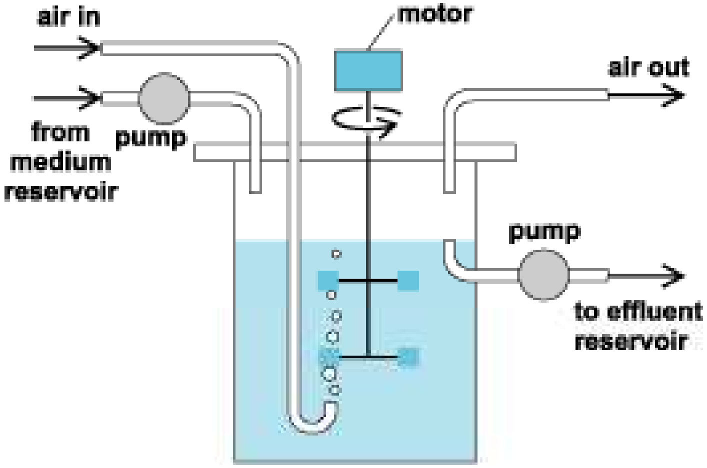
Rencontre TREASURE

Tunis, 23-26/11/2010

LAMSIN – ENIT

Le chemostat : une espèce

$$\left\{\begin{array}{lcl} S'(t) & = & D[S_{in} - S(t)] - k\mu(S(t))X(t) \\ X'(t) & = & [\mu(S(t)) - D]X(t) \end{array}\right.$$



Les inventeurs du chemostat

- Novick A. and Szilard L. (1950), *Description of the chemostat*. Science, 112, 715-716
- Monod, J., *La technique de culture continue theorie et applications*. Ann. Inst. Pasteur, 79, 390-410, 1950



Exemples de cinétiques μ

- Linéaire

$$\mu(S) = \alpha S$$

- Monod

$$\mu(S) = \frac{\mu_{max} S}{K + S}$$

- Haldane

$$\mu(S) = \frac{\mu_{max} S}{K + S + S^2/K_i}$$

The chemostat : equilibrium point

$$\left\{\begin{array}{rcl} S' & = & D(S_{in} - S) - \frac{\mu(S)}{Y}X \\ X' & = & (\mu(S) - D)X \end{array}\right.$$

$$\mu(S) = D \Leftrightarrow S = \mu^{-1}(D)$$

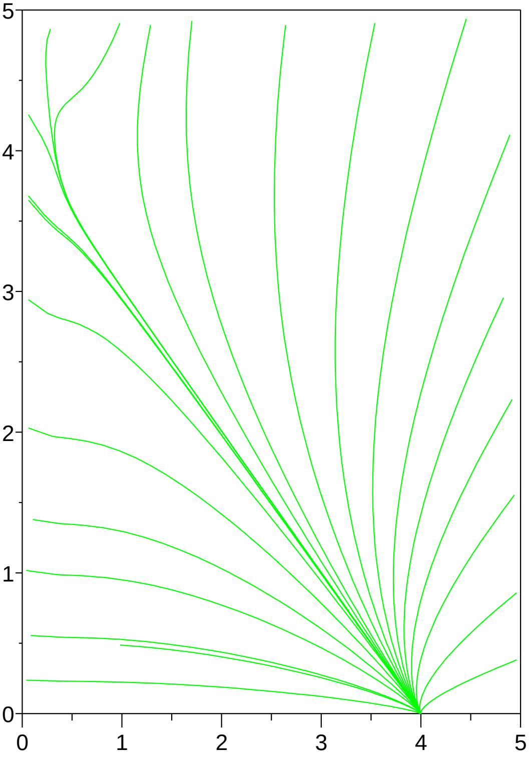
- $E_0 = (S = S_{in}, X = 0)$ (washout)
- $E^* = (S^*, X^*)$, $S^* = \mu^{-1}(D)$ and $X^* = Y(S_{in} - S^*)$
- $\mu^{-1}(D)$ is called the break-even concentration
- E^* exits and is stable if and only if $\mu(S_{in}) > D$

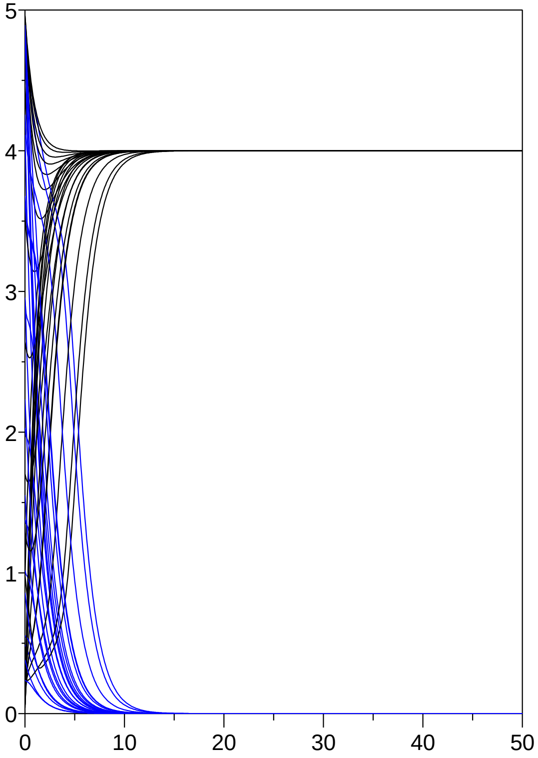
Inhibition by the substrate

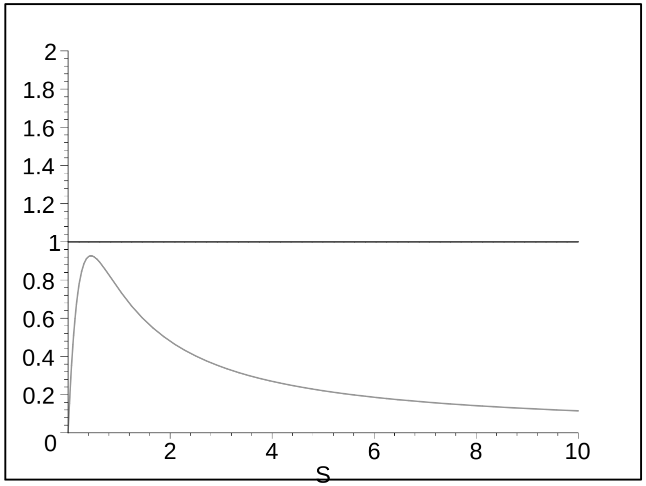
$$\left\{\begin{array}{rcl} S' & = & D(S_{in} - S) - \frac{\mu(S)}{Y} x \\ x' & = & (\mu(S) - D)x \end{array}\right.$$

- $\mu(S) = \frac{mS}{K+S+S^2/K_i}$ is a Haldane function
- equation $\mu(S) = D$ can have two solutions $S_1^* < S_2^*$
- $E_1^* = (S_1^*, Y(S_{in} - S_1^*))$ exists if and only if $S_1^* < S_{in}$. It is stable.
- $E_2^* = (S_2^*, Y(S_{in} - S_2^*))$ exists if and only if $S_2^* < S_{in}$. It is unstable and E_0 is stable.

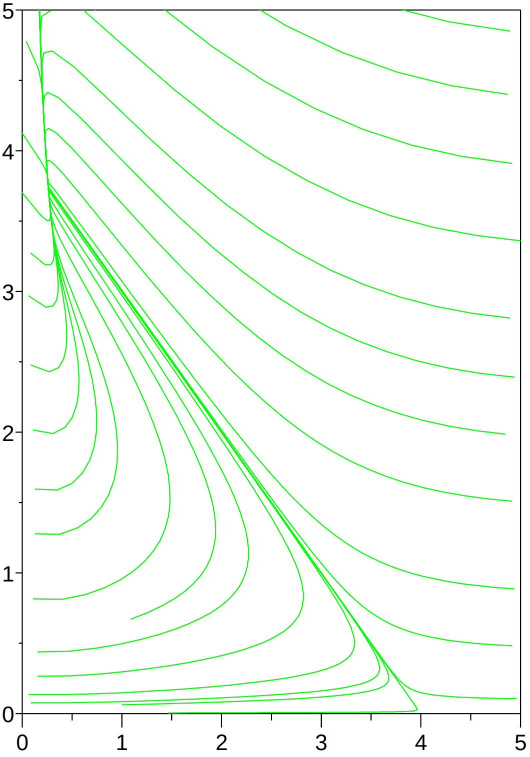
Inhibition : washout

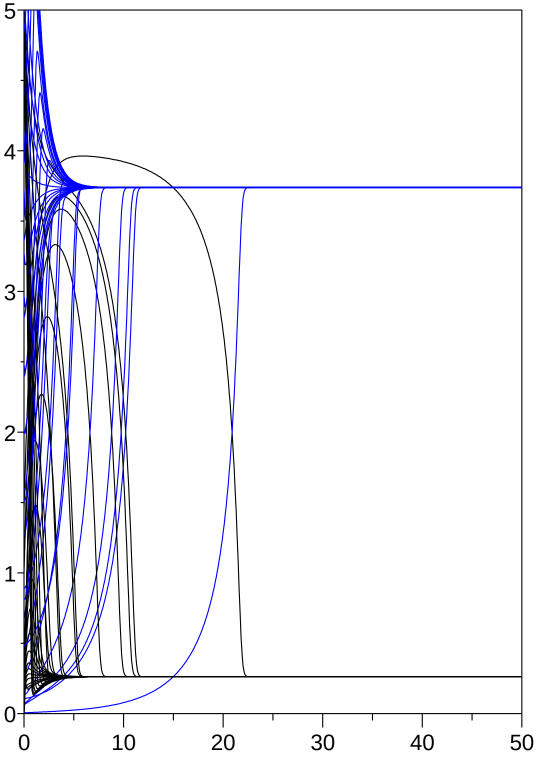


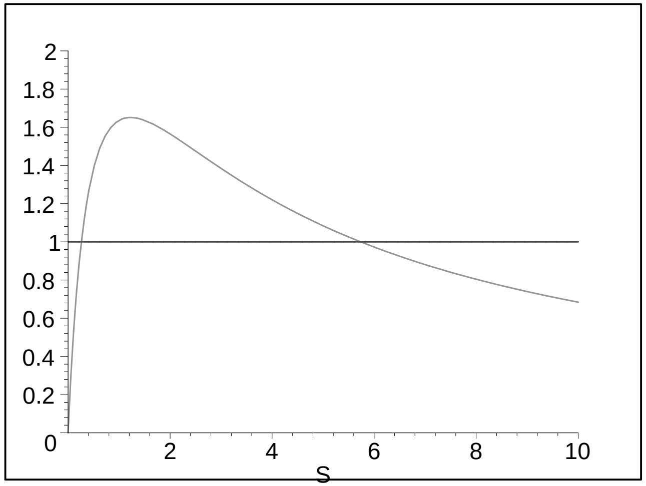




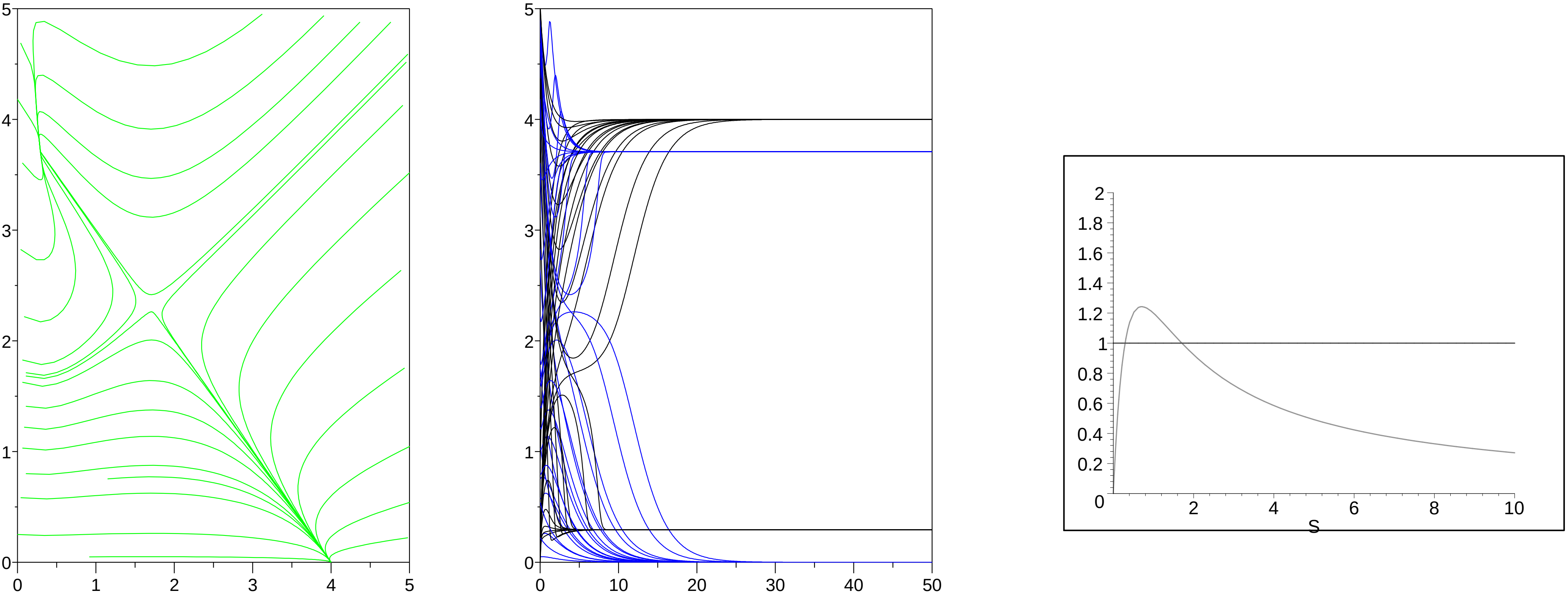
Inhibition : one equilibrium







Inhibition : bistability



La flocculation

The species is present in two forms: isolated bacteria, of density X_L, and flocks of bacteria, of density X_A.
Isolated bacteria and flocks can stick together to form new flocks, with rate $\alpha(\cdot)X_L$, and flocks can split and liberate isolated bacteria, with rate $\beta(\cdot)X_A$:

$$X_L \xrightarrow{\alpha(\cdot)X_L} X_A, \qquad X_L \xleftarrow{\beta(\cdot)X_A} X_A.$$

$$\left\{\begin{array}{lcl} \dot{S} & = & D_S(S_{in}-S) - \mu_L(S)X_L - \mu_A(S)X_A \\ \dot{X}_L & = & (\mu_L(S)-D_L)X_L - \alpha(\cdot)X_L + \beta(\cdot)X_A \\ \dot{X}_A & = & (\mu_A(S)-D_A)X_A + \alpha(\cdot)X_L - \beta(\cdot)X_A \end{array}\right.$$

Attachement (wall growth)

$$\alpha(\cdot) = a, \qquad \beta(\cdot) = b$$

$$\left\{ \begin{array}{lcl} \dot{S} & = & D_S(S_{in} - S) - \mu_L(S)X_L - \mu_A(S)X_A \\ \dot{X}_L & = & (\mu_L(S) - D_L)X_L - aX_L + bX_A \\ \dot{X}_A & = & (\mu_A(S) - D_A)X_A + aX_L - bX_A \end{array} \right.$$

- Pilyugin and Waltman (SIAM Appl. Math., 1999).
- Ce modèle est un cas particulier du modèle de Freter (1983) de l’intestin.

Modèle de Freter

$$\alpha(\cdot) = a[1 - W], \quad \beta(\cdot) = b + \mu_A(S)[1 - G(W)]$$

avec $W = X_A / X_{A\max}$ et $G(W)$ décroissante

$$\left\{ \begin{array}{rcl} \dot{S} & = & D_S(S_{in} - S) - \mu_L(S)X_L - \mu_A(S)X_A \\ \dot{X}_L & = & (\mu_L(S) - D_L)X_L - a(1 - W)X_L \\ & & +bX_A + \mu_A(S)[1 - G(W)]X_A \\ \dot{X}_A & = & (\mu_A(S)G(W) - D_A)X_A + a[1 - W]X_L \end{array} \right.$$

- Pour $X_{A\max} = \infty$ on a $W = 0$
- si de plus $G(0) = 1$ on a $\alpha(\cdot) = a$, $\beta(\cdot) = b$

Flocs à deux individus

$$\alpha(\cdot) = aX_L, \qquad \beta(\cdot) = b$$

$$\left\{\begin{array}{lcl} \dot{S} & = & D_S(S_{in} - S) - \mu_L(S)X_L - \mu_A(S)X_A \\ \dot{X}_L & = & (\mu_L(S) - D_L)X_L - aX_L^2 + bX_A \\ \dot{X}_A & = & (\mu_A(S) - D_A)X_A + aX_L^2 - bX_A \end{array}\right.$$

- $\mu_A(S) = 0$: Haegeman et Rapaport (JBD, 2008)
- $\mu_A(S) < \mu_L(S)$: Fekih-Salem, Rapaport, Sari

Flocs indiférenciés

$$\alpha(\cdot) = a(X_L + X_A), \qquad \beta(\cdot) = b$$

$$\left\{\begin{array}{rcl} \dot{S} & = & D_S(S_{in} - S) - \mu_L(S)X_L - \mu_A(S)X_A \\ \dot{X}_L & = & (\mu_L(S) - D_L)X_L \\ & & -a(X_L + X_A)X_L + bX_A \\ \dot{X}_A & = & (\mu_A(S) - D_A)X_A \\ & & +a(X_L + X_A)X_L - bX_A \end{array}\right.$$

- C’est l’objet de notre étude. Les détails seront donnés plus tard

Modèle général

$$\left\{\begin{array}{lcl}
\dot{S} & = & D_S(S_{in}-S)-\mu_L(S)X_L-\mu_A(S)X_A \\
\dot{X}_L & = & (\mu_L(S)-D_L)X_L \\
 & & -\alpha(S,X_A,X_L)X_L+\beta(S,X_A,X_L)X_A \\
\dot{X}_A & = & (\mu_A(S)-D_A)X_A \\
 & & +\alpha(S,X_A,X_L)X_L-\beta(S,X_A,X_L)X_A
\end{array}\right.$$

Dynamique réduite

Si on suppose que $\alpha(\cdot)$ et $\beta(\cdot)$ sont “grands”, alors la biomasse totale $X = X_L + X_A$ est donnée par

$$\left\{ \begin{array}{l} \dot{S} = D_S(S_{in} - S) - \mu(S,X)X \\ \dot{X} = \left[\mu(S,X) - D(S,X)\right] X \end{array} \right.$$

avec

$$\mu(S,X) = p(S,X)\mu_L(S) + (1 - p(S,X))\mu_A(S),$$

$$D(S,X) = p(S,X)D_L + (1 - p(S,X))D_A.$$

où $p(S,X)$ dépend des fonctions $\alpha(.)$ et $\beta(.)$

Deux échelles de temps

$$\left\{ \begin{array}{lcl} \dot{S} & = & D_S(S_{in} - S) - \mu_L(S)X_L - \mu_A(S)X_A \\ \dot{X}_L & = & (\mu_L(S) - D_L)X_L - \alpha(\cdot)X_L + \beta(\cdot)X_A \\ \dot{X}_A & = & (\mu_A(S) - D_A)X_A + \alpha(\cdot)X_L - \beta(\cdot)X_A \end{array} \right.$$

$$\dot{X} = (\mu_L(S) - D_L)X_L + (\mu_A(S) - D_A)X_A$$

où $X = X_L + X_A$ est la biomasse totale.

- Les équations de X_L et X_A sont rapides,
- celles de S et de $X = X_L + X_A$ sont lentes
- On fait comme si $\dot{X}_L = 0$ et $\dot{X}_A = 0$

Etat quasi-stationnaire

$$\alpha(S, X_L, X_A)X_L = \beta(S, X_L, X_A)X_A,$$

$$X_L + X_A = X$$

On écrit la solution sous la forme

$$X_L = p(S, X)X, \qquad X_A = (1 - p(S, X))X$$

que l'on remplace dans les équations de S et de X pour trouver

$$\begin{cases} \dot{S} = D_S(S_{in} - S) - \mu(S, X)X \\ \dot{X} = [\mu(S, X) - D(S, X)]\, X \end{cases}$$

Exemples

- Flocs à deux individus :

$$\alpha(\cdot) = \frac{a}{\varepsilon} X_L, \qquad \beta(\cdot) = \frac{b}{\varepsilon}$$

$$p(X) = \frac{2}{1 + \sqrt{1 + 4a/bX}}$$

- Flocs indiférenciés :

$$\alpha(\cdot) = \frac{a}{\varepsilon} X, \qquad \beta(\cdot) = \frac{b}{\varepsilon}$$

$$p(X) = \frac{b}{b + aX}$$

Modèle réduit

$$\begin{cases} \dot{S} = D_S(S_{in} - S) - \mu(S,X)X \\ \dot{X} = \left[\mu(S,X) - D(X)\right]X \end{cases}$$

$$\mu(S,X) = p(X)\mu_L(S) + (1 - p(X))\mu_A(S),$$

$$D(X) = p(X)D_L + (1 - p(X))D_A.$$

- $\mu_L(S)$ et $\mu_A(S)$ croissantes et $\mu_L(S) \geq \mu_A(S)$
- $D_L \geq D_A$ (on peut prendre $D_L = D_S$).
- $0 \leq p(X) \leq 1$, $p(0) = 1$, $p(\infty) = 0$, $p'(X) < 0$.

Les équilibres

$$\begin{cases} D_S(S_{in} - S) - \mu(S,X)X = 0 \\ \left[\mu(S,X) - D(X)\right] X = 0 \end{cases}$$

- Si $X = 0$ alors $S = S_{in}$: $E_0 = (S_{in}, 0)$.
- Si $\mu(S,X) = D(X)$, alors $D_S(S_{in} - S) = XD(X)$. On obtient

$$S = G(X) := S_{in} - \frac{XD(X)}{D_S}.$$

La fonction $G(X)$ est décroissante.

Les équilibres

Notons

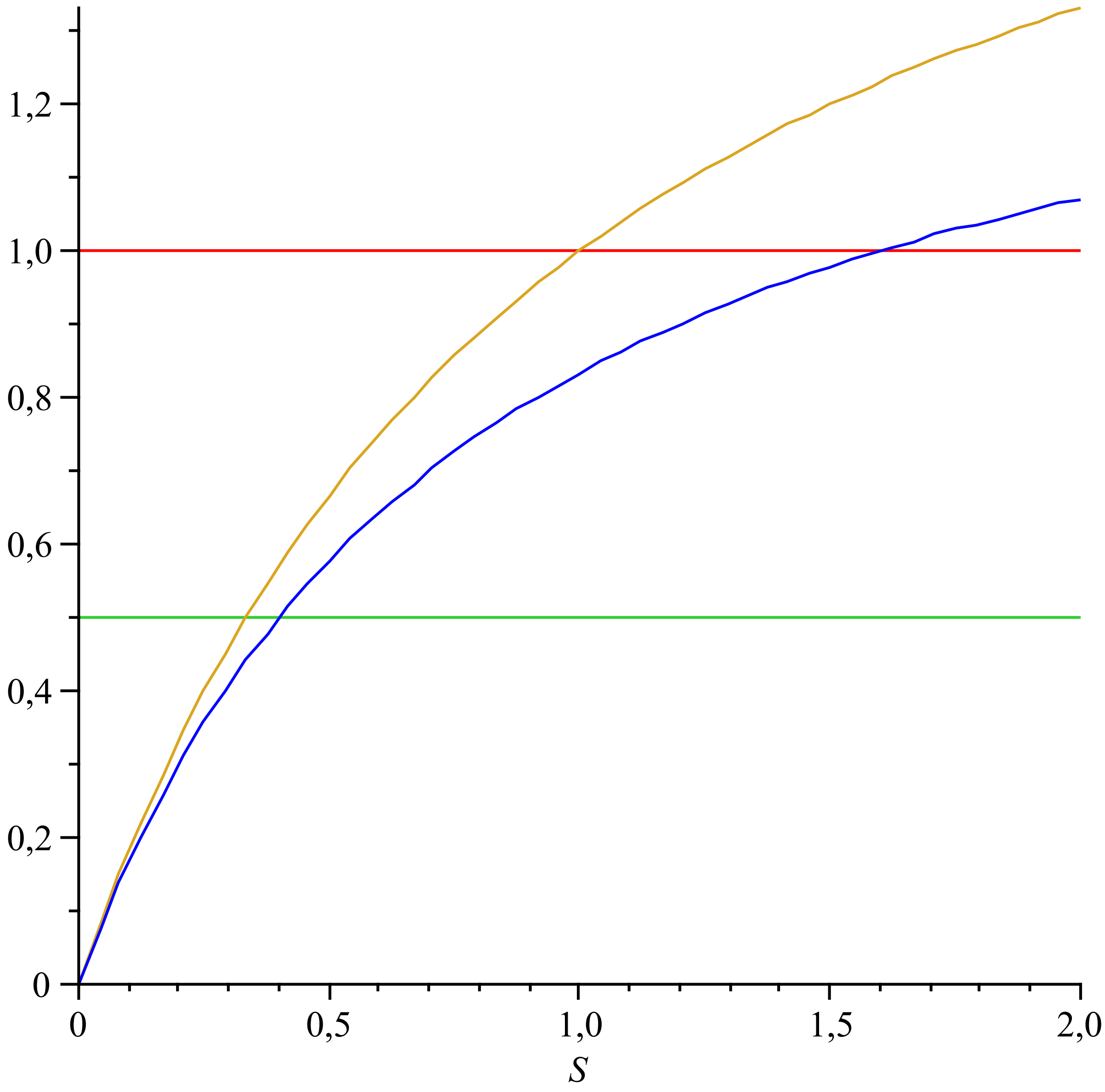
$$\lambda_L = \mu_L^{-1}(D_L), \qquad \lambda_A = \mu_A^{-1}(D_A).$$

- L'équation $\mu(S,X) = D(X)$ définit $S = F(X)$ telle que $F(0) = \lambda_L$ et $F(\infty) = \lambda_A$.
- Si $\lambda_L < \lambda_A$ la fonction F est croissante.
- Si $\lambda_L < S_{in}$, alors il y a un unique équilibre positif. Il est stable.
- Si $\lambda_L > S_{in}$, alors il n'y a pas d'équilibre positif.

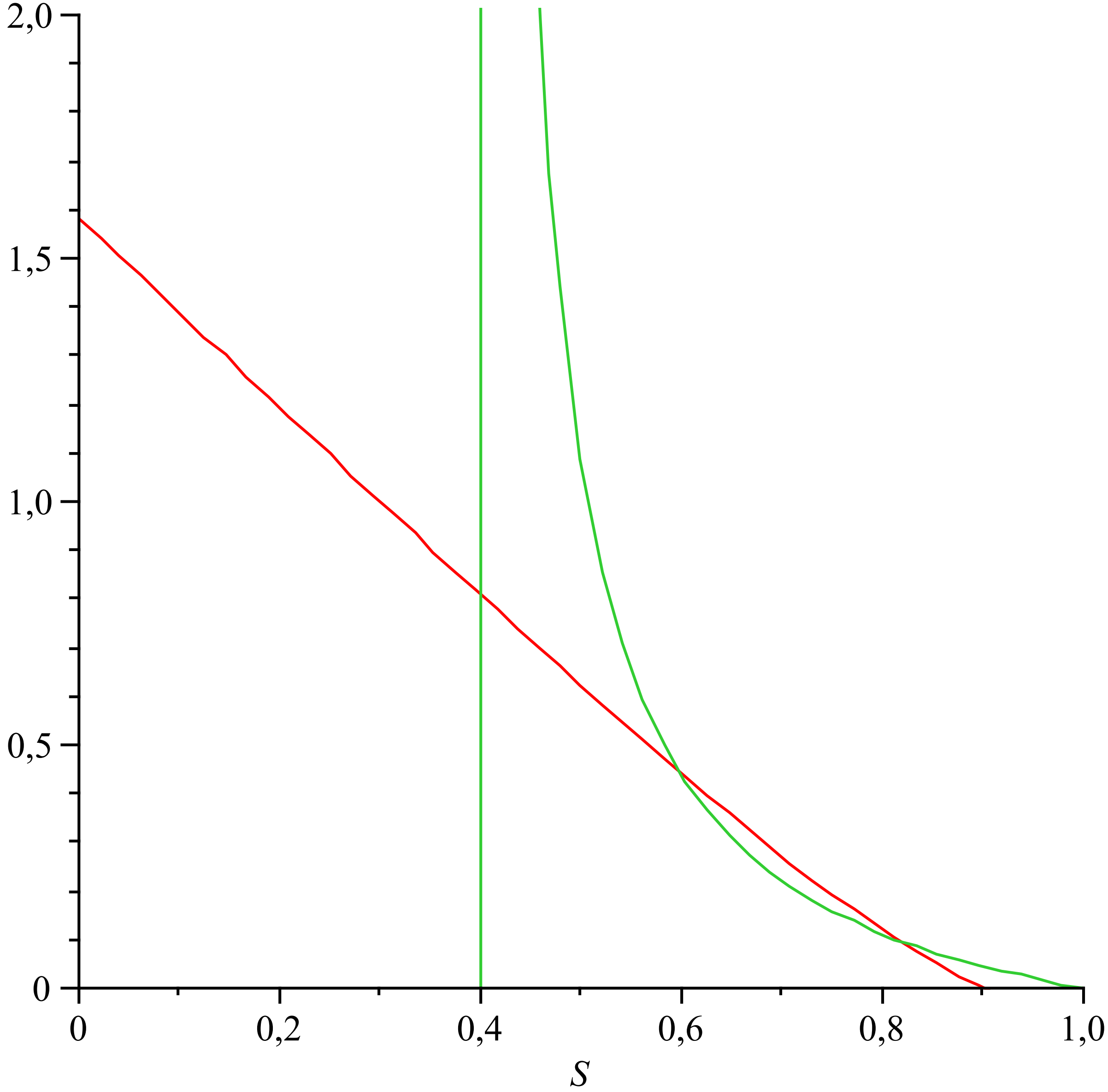
Les équilibres

- Si $\lambda_L > \lambda_A$ la fonction F est décroissante.
- Si $\lambda_L < S_{in}$, alors il y a au moins un équilibre positif. Il peut y avoir un nombre impaire. Ils sont alternativement stables et instables.
- Si $\lambda_L > S_{in}$, alors il peut y avoir 0 ou un nombre paire d'équilibres positifs. Ils sont alternativement stables et instables.
- La présence de biomasse agrégée peut empêcher le lessivage car l'attachement des flocs ($D_A \leq D_L$) vient compenser la croissance moins forte ($\mu_A(S) \leq \mu_L(S)$).

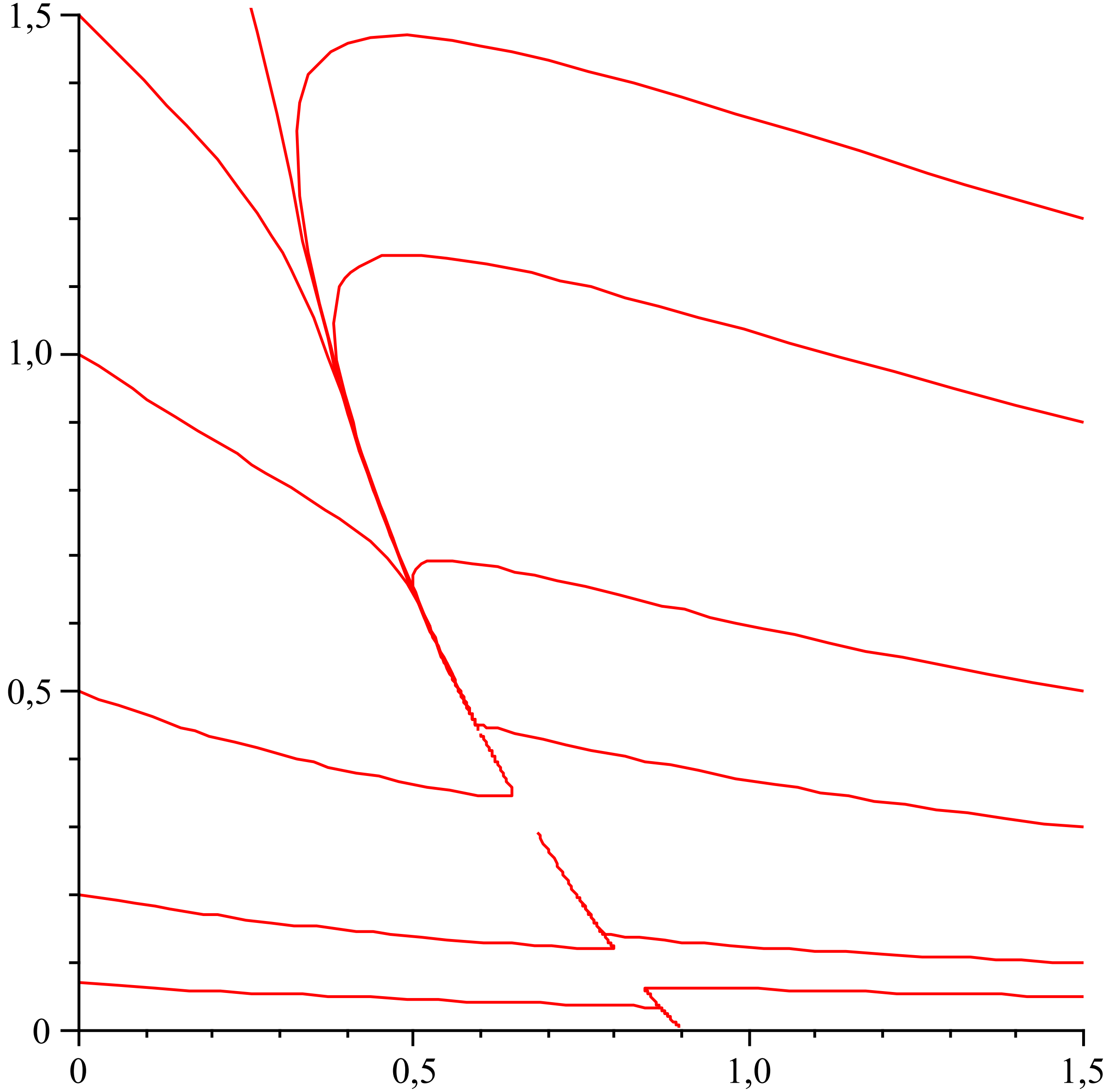
Simulations numériques



Simulations numériques



Simulations numériques



La compétition dans le chemostat

$$\left\{\begin{array}{rcl} S' & = & D(S_{in} - S) - \mu_1(S)X_1 - \mu_2(S)X_2 \\ X_1' & = & (\mu_1(S) - D)X_1 \\ X_2' & = & (\mu_2(S) - D)X_2 \end{array}\right.$$

- Break-even concentrations : $\lambda_i = \mu_i^{-1}(D)$
- $E_0 = (S = S_{in}, X_1 = 0, x_2 = 0)$
- $E_1 = (S = \lambda_1, X_1 = S_{in} - \lambda_1, X_2 = 0)$
- $E_2 = (S = \lambda_2, X_1 = 0, X_2 = S_{in} - \lambda_2)$
- If $\lambda_1 < \lambda_2$ then E_1 is stable and E_0 and E_2 are unstable

The Competitive Exclusion Principle

- If $\lambda_1 < \lambda_2$ then $E_1 = (\lambda_1, S_{in} - \lambda_1, 0)$ is a globally asymptotically stable (GAS) equilibrium.
- The solutions with positive initial conditions converge to

$$S = \lambda_1, \qquad X_1 = S_{in} - \lambda_1, \qquad X_2 = 0$$

- At equilibrium E_1 the species X_2 is excluded
- the CEP is in contradiction with the observations
- The mathematical model is not good : find mechanisms that explain the coexistence

Flocculation of two species

- Each species is present in two forms: isolated bacteria, of density X_{Li}, and bacteria in flocks, of density X_{Ai}, for $i = 1, 2$.
- Isolated bacteria can stick with isolated bacteria with flocks to form new flocks, with rate $\alpha_i(\cdot)X_{Li}$.
- Flocks can split and liberate isolated bacteria with rate $\beta_i(\cdot)X_{Ai}$.

$$X_{L1} \xrightarrow{\alpha_1(\cdot)X_{L1}} X_{A1}, \qquad X_{L1} \xleftarrow{\beta_1(\cdot)X_{A1}} X_{A1},$$

$$X_{L2} \xrightarrow{\alpha_2(\cdot)X_{L2}} X_{A2}, \qquad X_{L2} \xleftarrow{\beta_2(\cdot)X_{A2}} X_{A2}.$$

Flocculation of two species

$$\left\{\begin{array}{lcl} \dot{S} & = & D(S_{in}-S)-\mu_{L1}(S)X_{L1}-\mu_{A1}(S)X_{A1} \\ & & \qquad -\mu_{L2}(S)X_{L2}-\mu_{A2}(S)X_{A2} \\ \dot{X}_{L1} & = & (\mu_{L1}(S)-D)X_{L1}-\alpha_1(\cdot)X_{L1}+\beta_1(\cdot)X_{A1} \\ \dot{X}_{L2} & = & (\mu_{L2}(S)-D)X_{L2}-\alpha_2(\cdot)X_{L2}+\beta_2(\cdot)X_{A2} \\ \dot{X}_{A1} & = & (\mu_{A1}(S)-D_1)X_{A1}+\alpha_1(\cdot)X_{L1}-\beta_1(\cdot)X_{A1} \\ \dot{X}_{A2} & = & (\mu_{A2}(S)-D_2)X_{A2}+\alpha_2(\cdot)X_{L2}-\beta_2(\cdot)X_{A2} \end{array}\right.$$

$$\alpha_i(\cdot)=\frac{a_{i1}X_1+a_{i2}X_2}{\varepsilon}, \qquad \beta_i(\cdot)=\frac{b_i}{\varepsilon},$$

where a_{ij} and b_i are positive constants and $X_i = X_{Li}+X_{Ai}$, $i=1,2$.

Modèle réduit

$$\dot{S} = D(S_{in} - S) - \mu_1(S, X_1, X_2)X_1 - \mu_2(S, X_1, X_2)X_2$$
$$\dot{X}_1 = \left[\mu_1(S, X_1, X_2) - D_1(X_1, X_2)\right] X_1$$
$$\dot{X}_2 = \left[\mu_2(S, X_1, X_2) - D_2(X_1, X_2)\right] X_2$$

Avec

$$\mu_i(S, X_1, X_2) = \mu_{Li}(S)g_i(X_1, X_2) + \mu_{Ai}(S)(1 - g_i(X_1, X_2))$$

$$D_i(X_1, X_2) = Dg_i(X_1, X_2) + D_i(1 - g_i(X_1, X_2))$$

et

$$g_i(X_1, X_2) = \frac{b_i}{b_i + a_{i1}X_1 + a_{i2}X_2}$$

References

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