

# Deterministic models and statistical aspects to model growth and division

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# Outline of the deterministic part (Marie!)

- ▶ A little bit on Structured Population Models and our motivation
- ▶ The Direct Problem
- ▶ The asymptotic behaviour
- ▶ The Inverse Problem in a deterministic setting
  - ▶ Case of Mitosis (division into 2 equal cells)
  - ▶ General fragmentation kernel
- ▶ deterministic perspectives

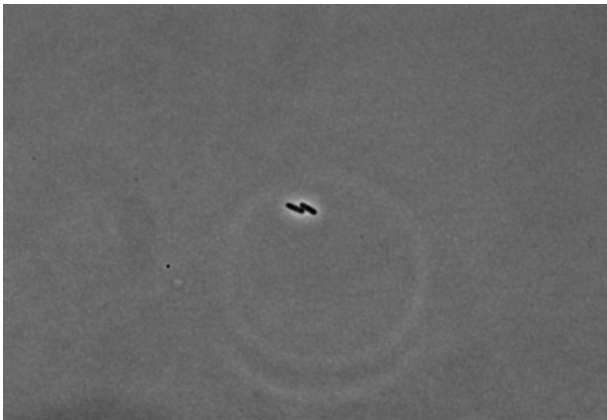


Figure: Evolution of a *E. Coli* population.

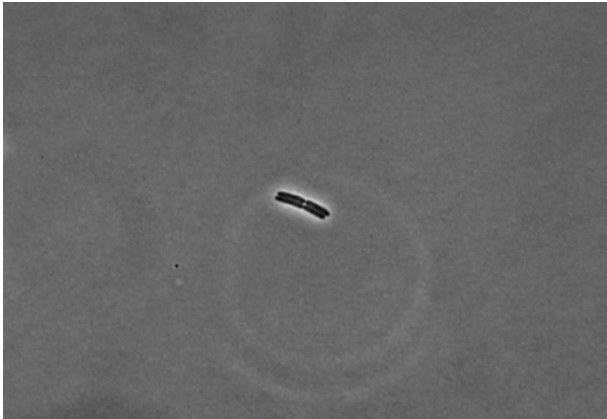


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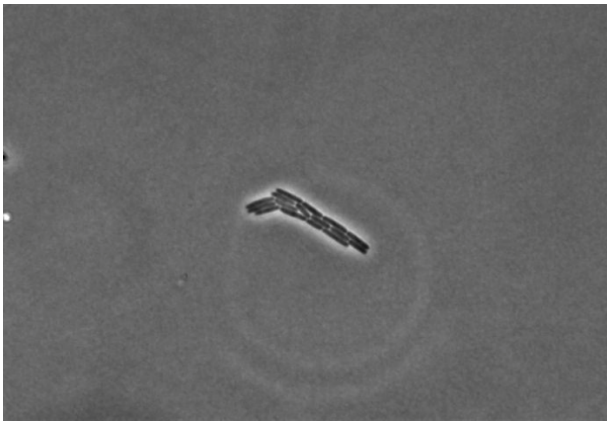


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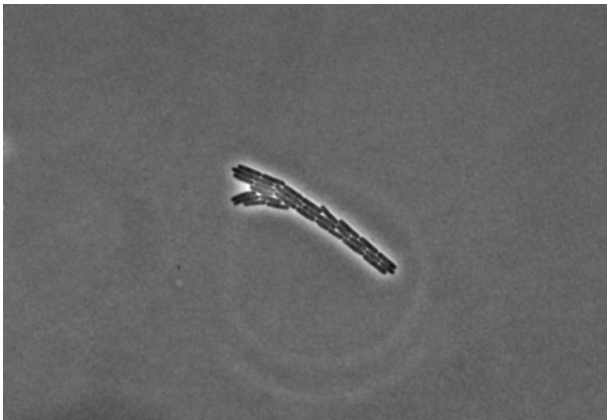


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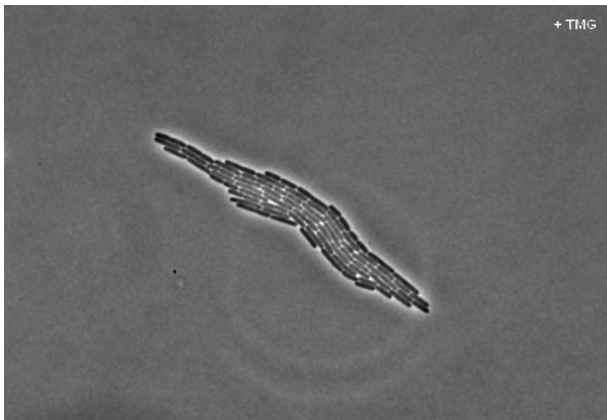


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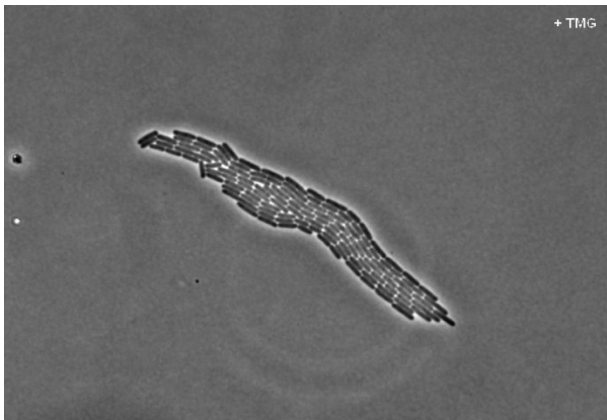


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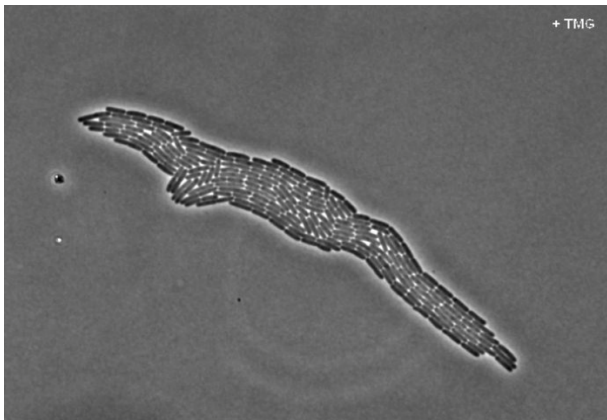


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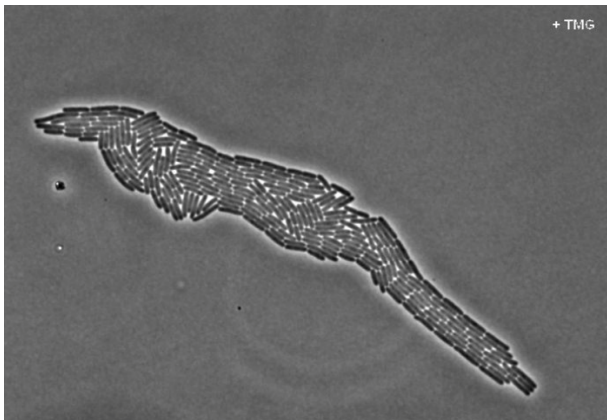


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# To model this: PDMP ? Yes...

## And also Structured Populations...

Population density:  $n(t, x)$

can also be viewed as the law of the empirical measure of a PDMP: ask Nathalie Krell...

$x$  is the "structuring variable", e.g. it may be

- ▶ for unicellular organisms: the mass / volume of the cell
- ▶ for polymers: the number of monomers inside
- ▶ the DNA content of the cell
- ▶ the cell age (age-structured populations)
- ▶ a protein content: cyclin, cyclin-dependent kinases etc
- ▶ a fluorescent label like CFSE
- ▶ a parasite growing inside the individuals
- ▶ for stem cells: the maturity

Recent reference: B. Perthame, *Transport Equations in Biology*, 2007.

## Some examples of structured populations

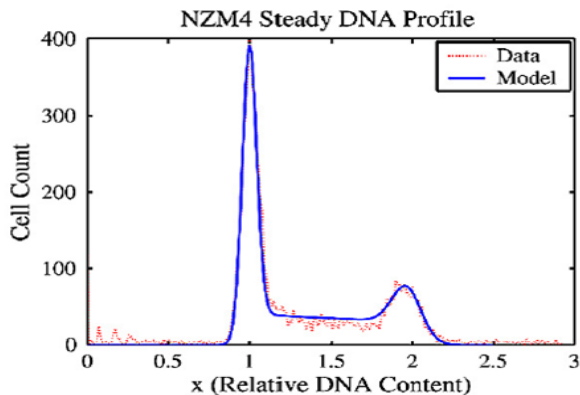
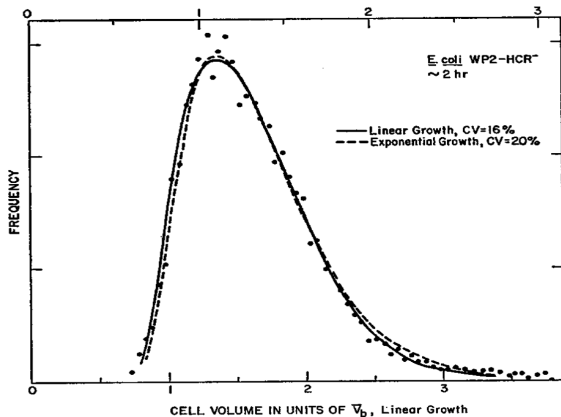


Figure: From B. Basse et al, Modeling the flow of cytometric data obtained from unperturbed human tumor cell lines: parameter fitting and comparison. of Math. Bio., 2005

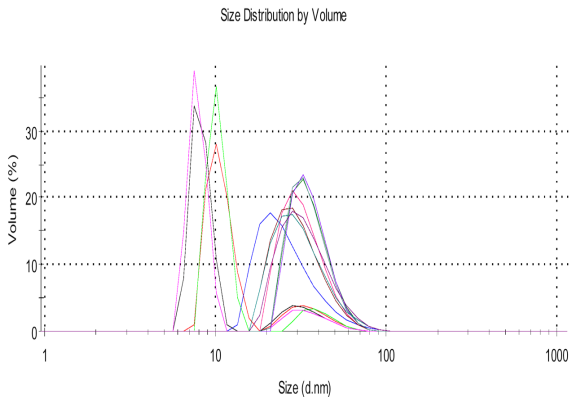
## Some examples of structured populations



**Figure:** Cell volumes distribution for *E. Coli* THU in a glucose minimal medium at a doubling time of 2 hrs. H.E. Kubitschek, Biophysical J. 9:792-809 (1969)



# Some examples of structured populations



**Figure:** Size distribution kinetic of PrP polymerization in physico-chemical condition leading to the formation of amyloid fibrils monitored by MWSLS technique (taken from ANR TOPPAZ, INRA/BPCP data courtesy of H. Rezaei).

# The Size-Structured Population equation (or transport-fragmentation equation)

We consider a populations of "individuals" such that

- ▶ each particle of size  $x$  grows with a growth rate  $g(x)$ ,
- ▶ a particle of size  $y$  may divide with a division rate  $B(y)$

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- ▶ for a given dividing particle of size  $y$ , the probability to give rise to two offsprings of respective size  $x$  and  $y - x$  is given by a probability law  $k(x, y) = k(y - x, y)$ , so that

$$\int_0^y k(x, y) dx = 1 \text{ and due to symetry } \int_0^y x k(x, y) dx = \frac{y}{2}$$

First and probably most studied case: "equal mitosis" :

$$k(x, y) = \delta_{x=\frac{y}{2}}.$$

# The Size-Structured Population equation (or transport-fragmentation equation)

The deterministic model is obtained by a **mass conservation law**:

$$\frac{\partial}{\partial t} n(t, x) + \frac{\partial}{\partial x} (g(x)n(t, x)) = -B(x)n(t, x) + 2 \int_x^{\infty} B(y)k(x, y)n(t, y)dy$$

with  $g(x=0)n(t, x=0) = 0$ ,  $t > 0$  and  $n(0, x) = n^{(0)}(x)$ ,  $x \geq 0$ .

- ▶ LHS: density evolution + growth (e.g. by nutrient uptake).
- ▶ RHS: exchanges by division:  
loss by the division of cells of size  $x$ , income by the division of cells of size  $y > x$  according the division law  $k(x, y)$ .

For  $k = \delta_{x=\frac{y}{2}}$  :  $2 \int_x^{\infty} B(y)k(x, y)n(t, y)dy = 4B(2x)$ .

# The Size-Structured Population equation

## 2 major relations, Direct vs Inverse Problem

The number of individuals only evolves by fragmentation:

$$\frac{d}{dt} \int n(t, x) dx = \int B(x) n(t, x) dx.$$

The total mass only evolves by growth:

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**Our Inverse Problem:** we suppose  $k$  known,  $g = cg_0$  with  $g_0$  a known function,

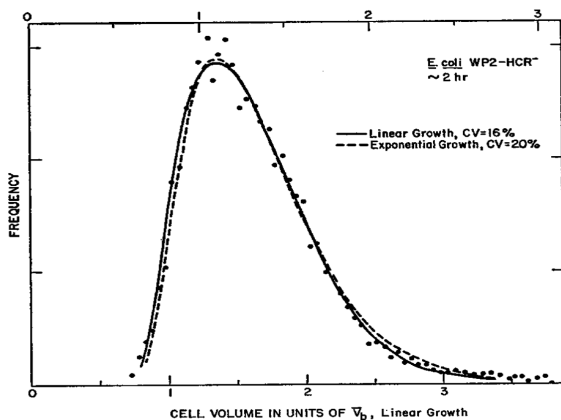
$c > 0$  a constant and  $B$  are to be estimated.



# The Size-Structured Population equation

## Direct vs Inverse Problem

What is really observed ? Remember:



We do not observe  $n(t, x)$  but rather a DOUBLING TIME and a STEADY DISTRIBUTION.

# The Size-Structured Population equation

## Long-time asymptotics

This motivated the method proposed by Perthame & Zubelli (*Inverse Problems*, 2007): **Use the asymptotic behaviour.**

2 Seminal references on the asymptotics obtained *via* the *General Relative Entropy* (GRE) principle:

- ▶ for the mitotic case: Perthame, Ryzhik, *J. Diff. Equ.*, 2004
- ▶ for GRE in general: Michel, Mischler, Perthame, *JMPA*, 2004,

If we look at a solution under the form  $n(t, x) = e^{\lambda t} N(x)$ ,  $x \geq 0$  :

$$\left\{ \begin{array}{l} \frac{\partial}{\partial x}(g(x)N(x)) + \lambda N(x) = -B(x)N(x) + 2 \int_x^\infty B(y)k(x, y)N(y)dy, \\ gN(x=0) = 0, \quad N(x) \geq 0, \quad \int_0^\infty N(x)dx = 1, \\ -g(x)\frac{\partial}{\partial x}(\phi(x)) + \lambda\phi(x) = B(x)(-\phi(x) + 2 \int_0^x k(y, x)\phi(y)dy), \\ \phi(x) \geq 0, \quad \int_0^\infty \phi(x)N(x)dx = 1. \end{array} \right. \quad (1)$$

# The Size-Structured Population equation

## Long-time asymptotics

Theorem (MD, P. Gabriel, M3AS, 2010)

*Under some technical assumptions on  $g$ ,  $B$  and  $k$ , there exists a unique triplet  $(\lambda, N, \phi)$  with  $\lambda > 0$ , solution of the eigenproblem (1)*

and then we have, by the GRE principle (ref. above)

$$\int_{\mathbb{R}_+} |n(t, x)e^{-\lambda t} - \langle n^{(0)}, \phi \rangle N(x)| \phi(x) dx \rightarrow 0 \text{ as } t \rightarrow \infty$$

(generalizes previous results by Michel, M3AS, 2004. Under some extra assumptions, the convergence is exponential: last work M.J. Càceres, J.A. Cañizo, S. Mischler, JMPA, 2011)

# The Direct Problem

The direct mapping is  $\Gamma : (c, B) \rightarrow (\lambda, N)$ .

The space of interest is  $L^2(\mathbb{R}_+)$ : general framework for inverse problems

(see Engl, Hanke, Neubauer, *Regularization of Inverse Problems*, 1995)

In (Perthame, Zubelli, 2007):

results for mitotic division and  $0 < B_m \leq B \leq B_M < +\infty$ .

Extension to the general case:

**Theorem (MD, L.M. Tine, submitted, 2011)**

*Under the previous T.A. (and one other), if  $B \in L^2(\mathbb{R}_+)$ , the map  $\Gamma$  is injective and Lipschitz-continuous (and even Fréchet derivable) from a proper definition domain to  $\mathbb{R}_+^* \times L^2$ , under the strong topology of  $L^2$ .*

Moreover, for  $g$  and  $k$  regular enough, **if  $B \in H^s$ , then  $N \in H^{s+1}$ .**

# The Inverse Problem

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- ▶ We postulate  $k(x, y)$  and some  $g_0(x)$  with  $g = cg_0$ .
- ▶ We measure  $N$  and  $\lambda$  with an error term modeled by

$$\|N_\varepsilon - N\|_{L^2} \leq \varepsilon \quad \text{and} \quad |\lambda_\varepsilon - \lambda| \leq \varepsilon.$$

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- ▶ We seek  $c$  and  $B$  such that

$$c \frac{\partial}{\partial x} (g_0(x)N(x)) + \lambda N(x) = -B(x)N(x) + 2 \int_x^\infty B(y)k(x, y)N(y)dy$$

Estimate  $B$  through

$$L(N, \lambda) = \mathfrak{L}(BN),$$

with

$$L(N, \lambda)(x) = c \partial_x (g(x)N(x)) + \lambda N(x),$$

$$\mathfrak{L}(f)(x) = 2 \int_x^\infty f(y)k(x, y)dy - f(x).$$

If we forget about  $c$  and  $\lambda$  : the problem  $N \rightarrow H = BN$  is linear. 



# The Inverse Problem

## The deterministic approach

$$c \int g_0(x) N(x) dx = \lambda \int x N(x) dx,$$

so the following definition (or slight variants) gives good results:

$$c_\varepsilon := \lambda_\varepsilon \frac{\int x N_\varepsilon(x) dx}{\int g_0(x) N_\varepsilon(x) dx}.$$

# The Inverse Problem

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Our problem is reduced to a linear one (+ some work) which writes: find  $B$  solution of

$$L(N, \lambda) = \mathfrak{L}(BN),$$

with

$$L(N, \lambda)(x) = c\partial_x(g(x)N(x)) + \lambda N(x),$$
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1. solve the dilation problem: for  $L$  in a proper space, find  $H$  such that

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and  $H$  in a proper space - ideally, the "proper space" is  $L^2$ .  
For mitosis, the equation becomes:

$$4H(2x) - H(x) = L(x).$$

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2. solve the derivative inverse problem: estimate  $L(N, \lambda) = c_\varepsilon \partial_x (g_0(x)N(x)) + \lambda N(x)$  from a measure  $N_\varepsilon \in L^2$ . Classical inverse problem of *degree of ill-posedness* 1 for a  $L^2$ -noise: use your favorite regularization method to treat the derivative & gain 1 degree of regularity.

# The Inverse Problem

## the Dilation Equation: Equal Mitosis

Proposition (MD, B. Perthame, J.P. Zubelli, 2009)

Let  $L \in L^2(\mathbb{R}_+, x^p dx)$ , with  $p \neq 3$ , then there exists a unique solution  $H \in L^2(\mathbb{R}_+, x^p dx)$  to

$$4H(2x) - H(x) = L(x).$$

For  $p < 3$ , this solution is given explicitly by  $H^{(1)}$  below, and for  $p > 3$ , by  $H^{(2)}$  :

$$H^{(1)}(x) = \sum_{n=1}^{+\infty} 2^{-2n} L(2^{-n}x), \quad H^{(2)}(x) = - \sum_{n=0}^{+\infty} 2^{2n} L(2^n x).$$

The solutions with  $L = 0$  in  $\mathcal{D}'(0, \infty)$  have the form  $\frac{f(\log(x))}{x^2}$  with  $f \in \mathcal{D}'(\mathbb{R})$  a  $\log(2)$ -periodic distribution.

## The general case: nonlocal fragmentation kernel

$$H(x) - 2 \int_x^\infty H(y)k(x, y)dy = F, \quad (2)$$

Proposition (MD, L.M. Tine, submitted)

Let  $k$  a fragmentation kernel and  $p \in \mathbb{R}$  satisfying:

$$C_p = \sup_x \int_x^\infty \frac{x^p}{y^p} k(x, y)dy < \frac{1}{4}. \quad (3)$$

$\forall F \in L^2(\mathbb{R}_+, x^p dx)$ ,  $\exists!$   $u \in L^2(x^p dx)$  to (2), and

$$\|H\|_{L^2(x^p dx)} \leq \frac{1}{1 - 2\sqrt{C_p}} \|F\|_{L^2(x^p dx)}.$$

## 2nd step: Regularizing the derivative term

### 1st method: Quasi-Reversibility

(in Perthame, Zubelli, 2006) Add a small derivative for  $BN$  : we obtain the following **well-posed** problem:

$$\begin{cases} \alpha \frac{\partial}{\partial y} (B_{\varepsilon, \alpha} N_{\varepsilon})(y) + 4B_{\varepsilon, \alpha}(y)N_{\varepsilon}(y) - B_{\varepsilon, \alpha}\left(\frac{y}{2}\right)N_{\varepsilon}\left(\frac{y}{2}\right) = \\ \quad + \lambda_{\varepsilon, \alpha} N_{\varepsilon}\left(\frac{y}{2}\right) + 2 \frac{\partial}{\partial y} \left( N_{\varepsilon}\left(\frac{y}{2}\right) \right), & y > 0, \\ (B_{\varepsilon, \alpha} N_{\varepsilon})(0) = 0. \end{cases}$$

### Theorem (Perthame, Zubelli, 2006)

We have the error estimate, optimal for  $\alpha = O(\sqrt{\varepsilon})$  :

$$\|B_{\varepsilon, \alpha} N_{\varepsilon, \alpha} - B N\|_{L^2(dx)}^2 \leq C \left(1 + \frac{1}{\alpha^2}\right) \|N_{\varepsilon} - N\|_{L^2(dx)}^2 + C \alpha^2 \|N\|_{H^2(\mathbb{R}_+)}^2,$$



# Regularization step

## 2nd method: Filtering

(in MD, B. Perthame, J.P. Zubelli, Inv. Prob., 2009)

Filter the derivative with a mollifier kernel  $\rho_\alpha$ ,  $\alpha > 0$  :

$$\begin{cases} 4B_{\varepsilon,\alpha}(y)N_\varepsilon(y) - B_{\varepsilon,\alpha}\left(\frac{y}{2}\right)N_\varepsilon\left(\frac{y}{2}\right) = \rho_\alpha * \left( \lambda_{\varepsilon,\alpha}N_\varepsilon\left(\frac{y}{2}\right) + 2\frac{\partial}{\partial y}\left(N_\varepsilon\left(\frac{y}{2}\right)\right) \right), \\ (B_{\varepsilon,\alpha}N_\varepsilon)(0) = 0, \end{cases}$$

with

$$\rho_\alpha(x) = \frac{1}{\alpha}\rho\left(\frac{x}{\alpha}\right), \quad \rho \in C_c^\infty(\mathbb{R}), \quad \int_0^\infty \rho(x) dx = 1, \quad \rho \geq 0.$$

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# Numerical Scheme

## Mitotic Case

General requirements:

- ▶ avoid instability
- ▶ conserve main properties of the continuous model: laws for the increase
  - ▶ of biomass
  - ▶ of number of cells, e.g. for the quasi-reversibility method:

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1 question (possible only for the mitotic case): in

$$4H(2x) - H(x) = L(x),$$

shall we begin from the left, deducing  $B(2x)$  from  $B(x)$  or from the right, deducing  $B(x)$  from  $B(2x)$  ?

# Numerical Scheme

## Mitotic Case

Recall the identity:

$$H^{(1)}(x) = \sum_{n=1}^{+\infty} 2^{-2n} L(2^{-n}x), \quad H^{(2)}(x) = - \sum_{n=0}^{+\infty} 2^{2n} L(2^n x).$$

Departing from large  $x$  : choose  $H^{(2)}$

Departing from 0 : choose  $H^{(1)}$

$H^{(1)}$  is "more regular" (in  $L^p$  for  $1 \leq p \leq \infty$  if  $L$  is in  $L^p$ )

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**BEST CHOICE: departing from 0.**

# Numerical Scheme

## Mitotic Case (with B. Perthame, J.P. Zubelli)

- ▶ departs from zero (mimics  $H^{(1)}$ )
- ▶ mass and number of cells balance laws preserved:
- ▶ stability:  $4H(2x)$  is approximated by  $4H_{2i}$

$$4H_i^f = H_{\frac{i}{2}}^f + L_{\frac{i}{2}}^f, \quad \forall 0 \leq i \leq I,$$

and we need to define the quantities  $G_{\frac{i}{2}}$ . We choose

$$G_{\frac{i}{2}} = \begin{cases} G_{\frac{i}{2}} & \text{when } i \text{ is even,} \\ \frac{1}{2}(G_{\frac{i-1}{2}} + G_{\frac{i+1}{2}}) & \text{when } i \text{ is odd.} \end{cases}$$

# Numerical schemes: steps

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- ▶ solve the direct problem for a given  $B(x)$  Method: use of the exponential convergence of  $n(t,x)$  to  $N(x)$ : Finite volume scheme to solve the time-dependent problem.



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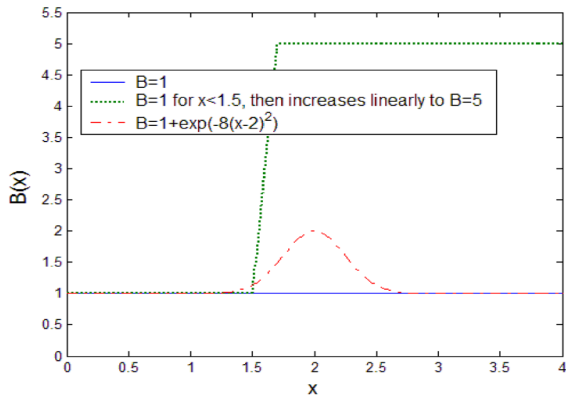
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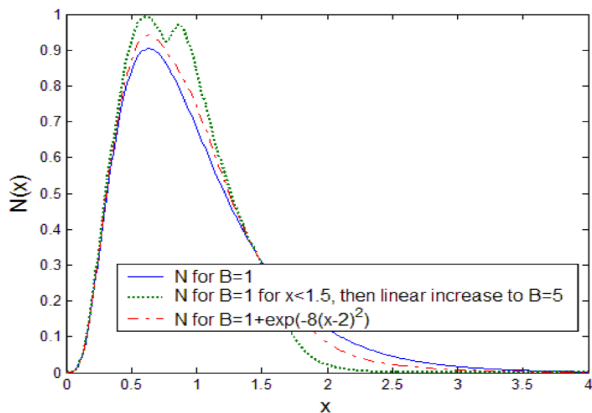
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- ▶ Then renormalization at each time-step to reach the asymptotic distribution
- ▶ add an artificial noise to  $N(x)$  to get a noisy data  $N_\varepsilon(x)$
- ▶ Run the numerical scheme for the inverse problem to get a birth rate  $B_{\varepsilon,\alpha}(x)N_\varepsilon(x)$  and compare it with the initial data  $B(x)$  - look for the best  $\alpha$  for a given error  $\varepsilon$ .

# Numerical Results - Mitosis



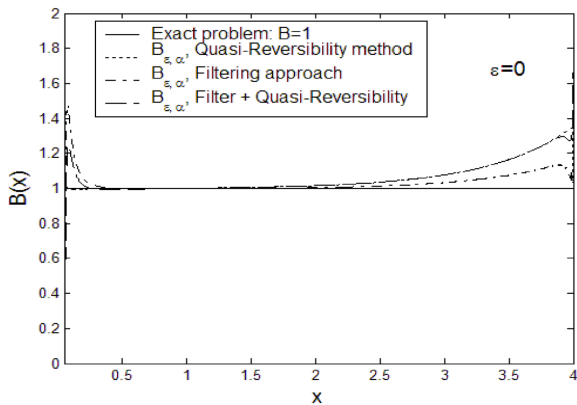
Three tested division rates  $B$

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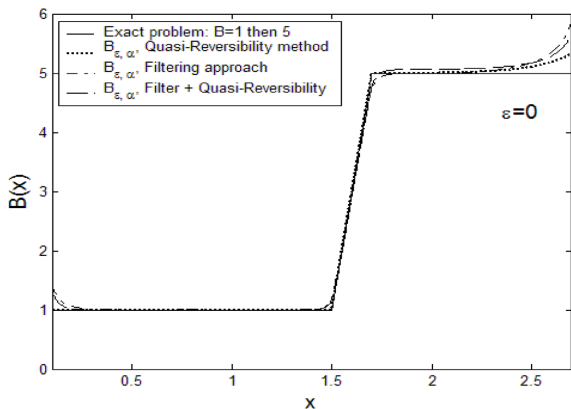
Three related asymptotic distributions  $N$

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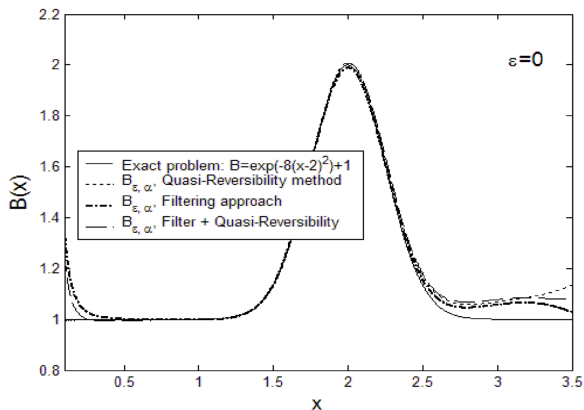
Results with no noise - constant  $B$

# Numerical Results - Mitosis



Results with no noise - step  $B$

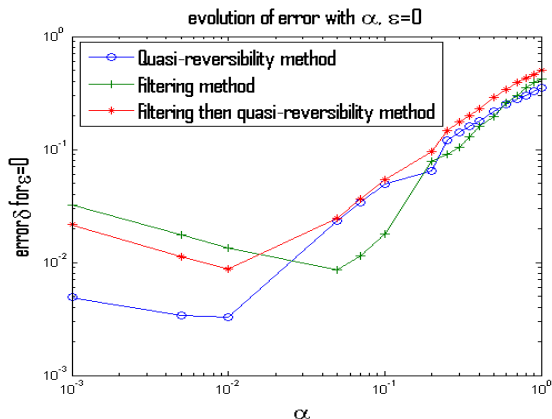
## Numerical Results - Mitosis



Results with no noise - varying  $B$

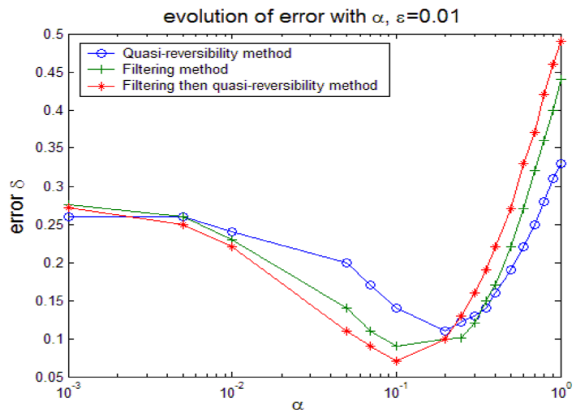


# Numerical Results - Mitosis



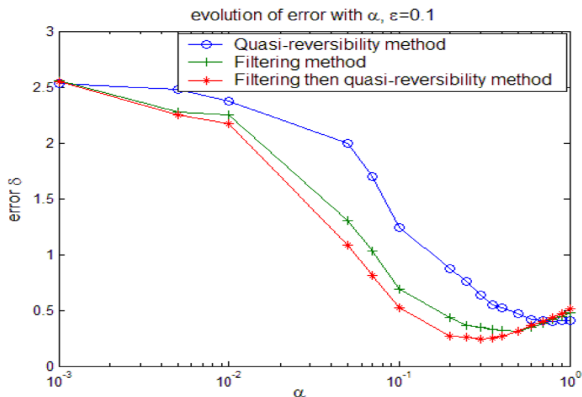
Results with no noise - Error with respect to the regularization parameter  $\alpha$

# Numerical Results - Mitosis



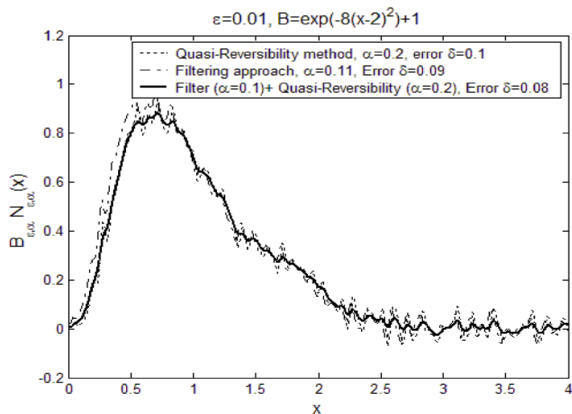
Results with noise  $\varepsilon = 0.01$  - Error with respect to the regularization parameter  $\alpha$

# Numerical Results - Mitosis



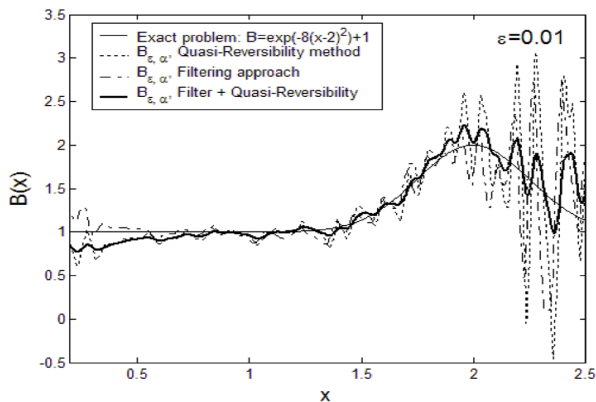
Results with noise  $\varepsilon = 0.1$  - Error with respect to the regularization parameter  $\alpha$

# Numerical Results - Mitosis



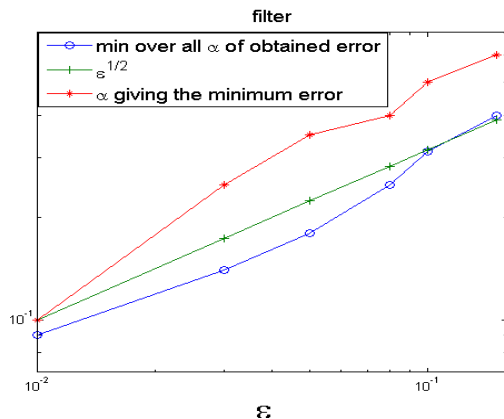
Results with noise  $\varepsilon = 0.01$  -  $BN$

# Numerical Results - Mitosis



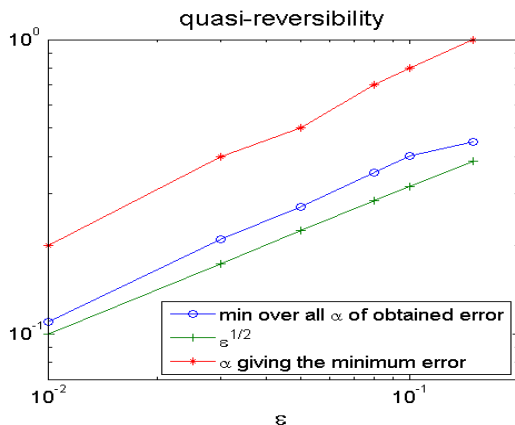
Results with noise  $\varepsilon = 0.01$  -  $B$

# Numerical Results - Mitosis



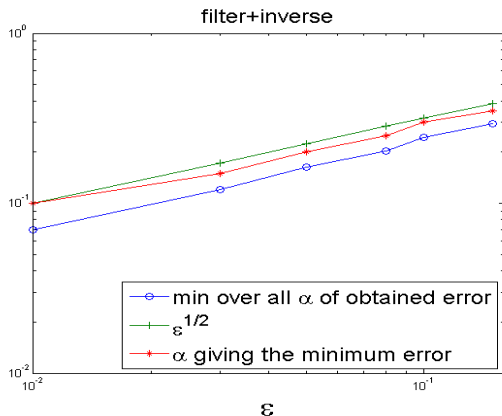
Optimal  $\alpha$  with respect to  $\varepsilon$ , compared to  $\sqrt{\varepsilon}$  and the optimal error

# Numerical Results - Mitosis



Optimal  $\alpha$  with respect to  $\varepsilon$ , compared to  $\sqrt{\varepsilon}$  and the optimal error

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Optimal  $\alpha$  with respect to  $\varepsilon$ , compared to  $\sqrt{\varepsilon}$  and the optimal error



# The Kubitschek data

(with P. Maia, J.P. Zubelli)

- ▶ An **approximate doubling time  $T_\varepsilon$  is observed** (which yields an estimator  $\lambda_\varepsilon$  of  $\lambda_0$  through  $T_0 = \log(2)/\lambda_0$ ).
- ▶ **Measurements of densities of cells of size  $x$  are given** for a given irregular grid  $\{x_i, i = 1, \dots\}$ .
- ▶ By **spline interpolation**, the curve  $N_\varepsilon$  is obtained.
- ▶ The growth rate is postulated to be of the form  $g(x) = \lambda x$

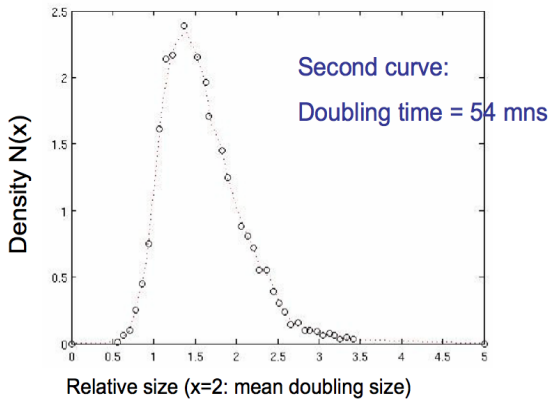


Figure: The construction of  $N_\epsilon$  for a given  $\lambda_\epsilon$

Doubling Time: 54 minutes

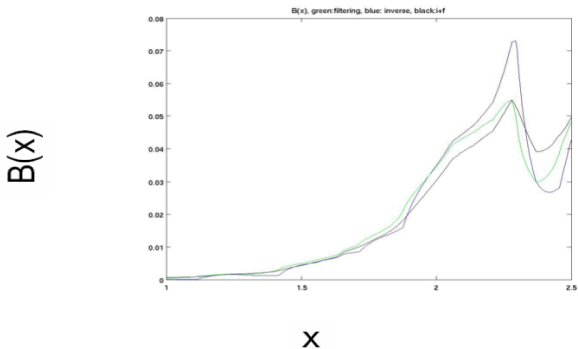


Figure: Estimation of  $B(x)$  for a given  $\lambda_\epsilon$  by numerical regularisation.

# Numerical Scheme: general fragmentation kernel (with L.M. Tine)

Quasi-Reversibility Method:

$$\left\{ \begin{array}{l} -\alpha x_i^{-m} \left( \frac{x_{i+1}^{m+1} H_{i+1} - x_i^{m+1} H_i}{\Delta x} \right) + H_i - 2 \sum_{j=i}^{ka} H_j \kappa_{i,j} \Delta x = L_i \\ \text{with } L_i = -\lambda_0 N_i - c \left( \frac{g_{i+1} N_{i+1} - g_i N_i}{\Delta x} \right), \quad \forall i = 1, \dots, ka \\ H_0 = 0 \text{ and } H_l = 0, \quad \forall l > ka. \end{array} \right.$$

what gives (scheme has to depart from the upper bound):

$$\left\{ \begin{array}{l} H_{ka} = \frac{L_{ka}}{A_{ka,ka}}; \\ H_i = \frac{1}{A_{i,i}} \left( L_i - \sum_{j=i+1}^{ka} A_{i,j} H_j \right); \quad \forall i = ka - 1, \dots, 1 \end{array} \right.$$

Since  $A_{ij} > 0$  for  $j \geq i + 1$ , we choose  $\Delta x$  small enough so that  $A_{ii} = 1 + \alpha i - 2\kappa_{i,i}\Delta x > 0$  for all  $i$ . This guarantees that no oscillations (should) appear.

# Introduction to Patricia's talk: the statistical approach (joint with M. Hoffmann, P. Reynaud-Bouret & V. Rivoirard)

Till now: we have supposed

$$\|N - N_\varepsilon\|_{L^2} \leq \varepsilon$$

But why an  $L^2$  norm ? What about real data ?

Kubitschek: pre-processed data. Our will: **global approach to incorporate a more realistic model for the noise.**

## Perspectives (coming soon...)

- ▶ Further investigation of the solution for the general fragmentation kernel (with T. Bourgeron and M. Escobedo)
- ▶ Construct a **PDMP** that matches with the PDE's approximation and that takes advantage of richer observation schemes (with M. Hoffmann, N. Krell, L. Robert).
- ▶ Extend this framework to a **more realistic biological framework**, that encompasses in particular **variability in cell growth**.
- ▶ What is the real structuring variable, age, size, else ?