

Statistical inference in transport-fragmentation models

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Statistical
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TEMPORAL
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THE SIZE
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ESTIMATING
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Context (1/4)

- We consider (simple) **branching processes** with **deterministic evolution** between jump times.
- Such models appear as toy models for population growth in cellular biology.
- We wish to **statistically estimate** the parameters of the model, in order to ultimately **discriminate** between different hypotheses related to the mechanisms that trigger cell division.

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Context (2/4)

- We structure the model by state variables for each individual like **size**, **age**, growth rate, DNA content and so on.
- The evolution of the particle system is described by a common mechanism:
 - 1 Each particle grows by “ingesting a common nutrient” = **deterministic evolution**.
 - 2 After some time, depending on a structure variable, each particle gives rise to $k = 2$ offsprings by cell division = **branching event**.
- Our goal in this talk: estimate the **branching rate** as a function of age or size (or both).

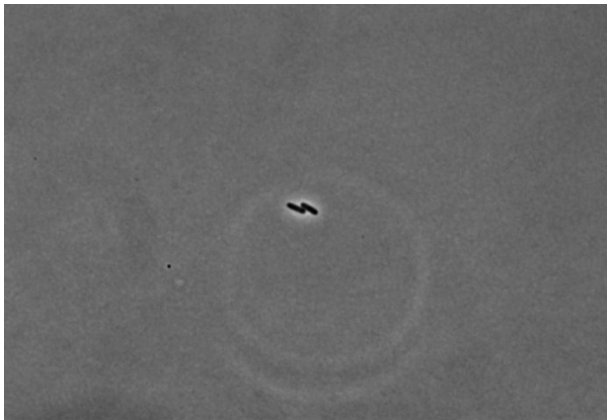


Figure : Evolution of a *E. Coli* population.

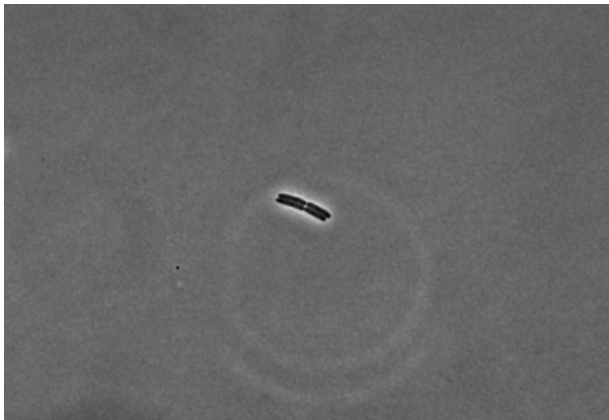


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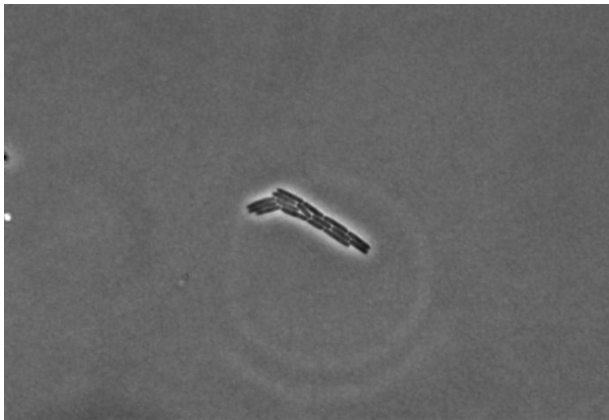


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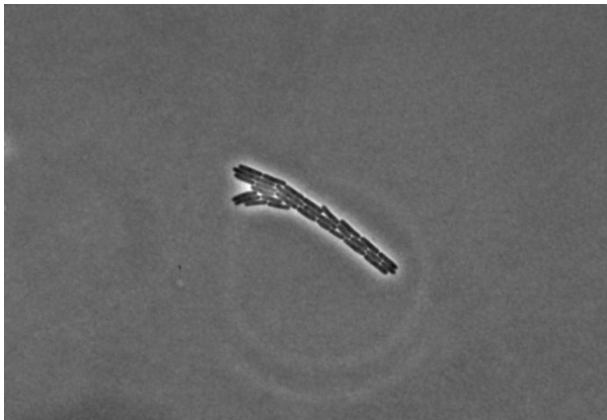


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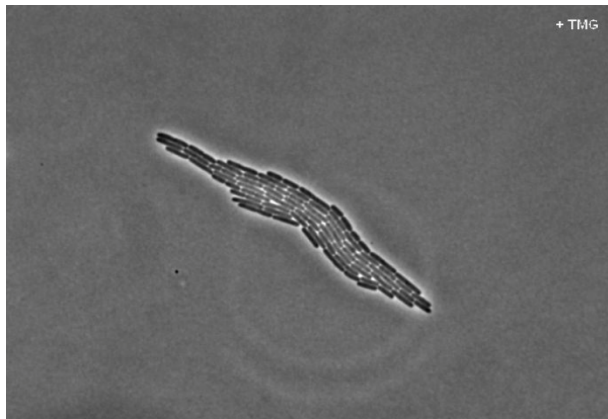


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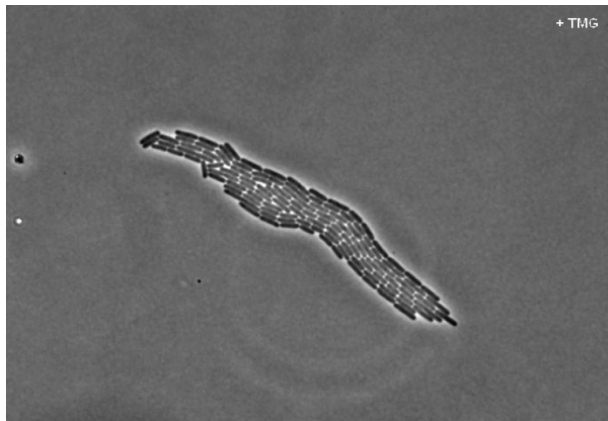


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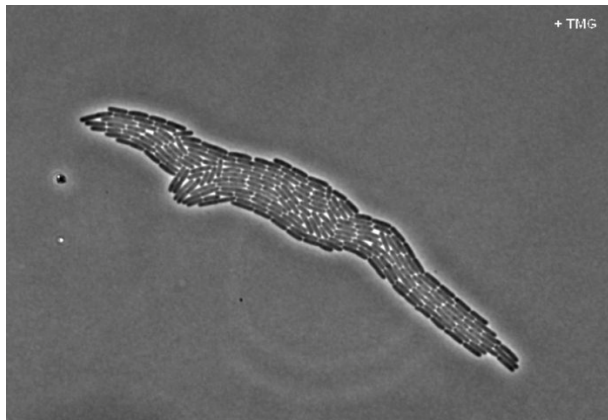


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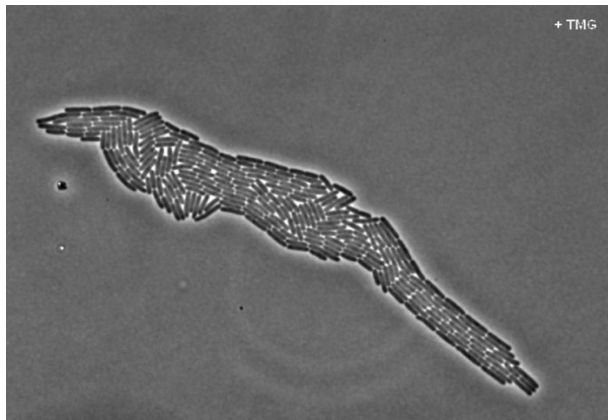


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- Deterministically the density of structured state variables evolves according to a so-called **fragmentation-transport PDEs**
- Stochastically, the particles evolve according to a **piecewise deterministic Markov process** that evolves along a branching tree.
- We study **nonparametric inference of the division rate**, with the concern of matching deterministic and stochastic approaches.

Context (4/4)

- I will follow a “pedestrian route” by reviewing some of the results we progressively obtained by “trial-and-error”.
- In particular, the results are **highly sensitive** to the choice of the observation schemes (genealogical versus temporal).
- Our control experiments are data sets extracted from the observation of 88 microcolonies of *E. Coli* bacteria cultures (a colony is followed from a single ancestor up to a few hundreds descendants).

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Genealogical representation

- In the talk we focus on structuring variables that are either **age** or **size**.
- The population evolution is associated with an **infinite marked binary tree**

$$\mathcal{U} = \bigcup_{n=0}^{\infty} \{0, 1\}^n \quad \text{with } \{0, 1\}^0 := \emptyset.$$

- To each cell or node $u \in \mathcal{U}$, we associate a cell with **size at birth** given by ξ_u and **lifetime** ζ_u .
- To each $u \in \mathcal{U}$, we associate a **birth time** b_u and a **time of death** d_u so that $\zeta_u = d_u - b_u$.

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Observation scheme I: temporal data

- Fix a (large) $T > 0$. Define

$$\mathcal{U}_T = \{u \in \mathcal{U}, b_u \leq T\}.$$

- We have $\mathcal{U}_T = \mathring{\mathcal{U}}_T \cup \partial\mathcal{U}_T$, with

$$\mathring{\mathcal{U}}_T = \{u, d_u \leq T\} \quad \text{and} \quad \partial\mathcal{U}_T = \{u, b_u \leq T < d_u\}$$

- We observe

$$\{\zeta_u^T \text{ and/or } \xi_u^T, u \in \mathcal{U}_T\}$$

where $\zeta_u^T = \min\{d_u, T\} - b_u$, and $\xi_u^T = \xi_u$ if $d_u \leq T$ and the “size of u at time T ” otherwise.

Observation scheme II: genealogical data

- $|u| = n$ if $u = (u_1, \dots, u_n) \in \mathcal{U}$,
 $uv = (u_1, \dots, u_n, v_1, \dots, v_m)$ if $v = (v_1, \dots, v_m) \in \mathcal{U}$.
- **Sparse tree case** Given $u^{(n)} \in \mathcal{U}$, with $|u^{(n)}| = n$, let

$$\mathcal{U}_{u^{(n)}} = \{u \in \mathcal{U}, uw = u^{(n)} \text{ for some } w \in \mathcal{U}\}.$$

We observe

$$\{\zeta_u \text{ and/or } \xi_u, u \in \mathcal{U}_{u^{(n)}}\}.$$

- **Full tree case** For $n = 2^{k_n}$, define

$$\mathcal{U}_{[n]} = \{u \in \mathcal{U}, |u| \leq k_n\}.$$

We observe

$$\{\xi_u \text{ and/or } \zeta_u, u \in \mathcal{U}_{[n]}\}.$$

Temporal data

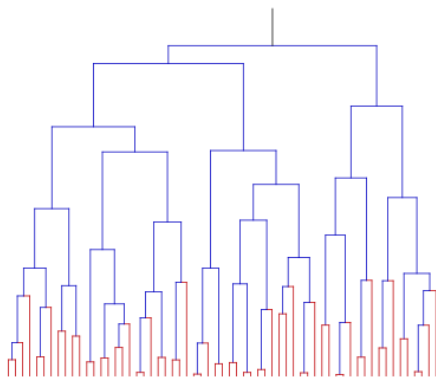


Figure : Genealogical tree observed up to $T = 7$ for a time-dependent division rate $B(a) = a^2$ (60 cells). In blue: $\dot{\mathcal{U}}_T$. In red: $\partial\mathcal{U}_T$.

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Genealogical data

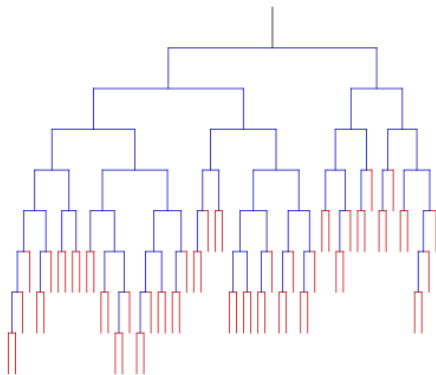


Figure : *The same outcome organised at a genealogical level.*

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Size dependent division rate (1/2)

- Perthame, *Transport equations in biology*, Birkäuser, 2006.
- $n(t, x)$: density of cells of size x .
- Parameter of interest: **Division rate $B(x)$** .
- 1 cell of size x gives birth to 2 cells of size $x/2$.
- The growth of the cell size by nutrient uptake is given by a **growth rate $g(x) = \tau x$ in this talk**: it follows the deterministic evolution

$$\frac{dX(t)}{dt} = g(X(t))dt$$

Size dependent division rate (2/2)

- The deterministic model: **transport-fragmentation** equation

$$\partial_t n(t, x) + \partial_x (\tau x n(t, x)) + B(x) n(t, x) = 4B(2x) n(t, 2x)$$

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

- obtained by mass conservation law:
 - LHS: density evolution + growth by nutrient + division of cells of size x .
 - RHS: division of cells of size $2x$.

Nonparametric estimation of B : First approach

- Represent the solution of the transport-fragmentation equation in a stationary regime.
- Obtain a reconstruction formula for $B(x)$ via this representation in terms of the steady-state or stationary density of the model.
- Postulate a proxy model where one observes exactly a drawn from the stationary density.
- Transfer standard nonparametric estimation techniques in this setting.

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Solution by stable distribution

- Start with the transport-fragmentation equation

$$\partial_t n(t, x) + \partial_x (\tau x n(t, x)) + B(x) n(t, x) = 4B(2x) n(t, 2x)$$

- Ansatz** $n(t, x) = e^{\lambda t} N(x)$.

$$\partial_x (\tau x N(x)) + (\lambda + B(x)) N(x) = 4B(2x) N(2x)$$

- $N(0) = 0$, $N(x) > 0$ for $x > 0$ and $\int_{[0, \infty)} N(x) dx = 1$.
- Perthame *et al.* (2005) prove $n(t, x) \approx e^{\lambda t} N(x)$ with explicit (fast) rates of convergence (steady-state) under fairly general conditions.

A proxy statistical model (1/4)

- Yields a strategy for the nonparametric estimation of B .
- At time T , the data **approximately behave like drawn** from $N(x)dx$.
- Recover B through the representation

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

with

$$\begin{aligned}L(f, \lambda)(x) &= \partial_x(\tau x f(x)) + \lambda f(x), \\ \mathfrak{L}(f)(x) &= 4f(2x) - f(x).\end{aligned}$$

- The operator $L(\cdot, \lambda)$ has ill-posedness degree of order 1.

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A proxy statistical model (2/4)

- We postulate the observation of outcomes of cell size X_1, \dots, X_n in a **stationary regime** and that are **independent**:

$$\mathbb{P}(X_1 \in dx_1, \dots, X_n \in dx_n) := \prod_{i=1}^n N(x_i) dx_i.$$

- We can take advantage of **kernel methods in nonparametric estimation**.
- τ and λ assumed to be known (or λ_n proxy of λ given within sufficient accuracy).

A proxy statistical model (3/4)

■ Reconstruction method:

- 1 Construct an estimator $\widehat{L}_n(x)$ of the action

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

- 2 Build an **approximate inverse** \mathfrak{L}_k^{-1} of the inverse of $\mathfrak{L}(f)(x) = 4f(2x) - f(x)$.
- 3 Use representation

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

and take as final estimator

$$\widehat{B}_n(x) := \frac{\mathfrak{L}_{k_n}^{-1}(\widehat{L}_n(x))}{\widehat{N}_n(x)}$$

where $\widehat{N}_n(x) = n^{-1} \sum_{i=1}^n h_n^{-1} K(h_n^{-1}(x - X_i))$ kernel estimator of $N(x)$ for an appropriate bandwidth $h_n > 0$.

A proxy statistical model (4/4)

- In Doumic, H, Rivoirard and Reynaud-Bouret (2011), we construct an **approximate inverse** \mathfrak{L}_k^{-1} such that

$$\|\mathfrak{L}_k^{-1}(\varphi) - \mathfrak{L}^{-1}(\varphi)\|_{L^2(\mathcal{D})} \lesssim k^{-1/2} \|\varphi\|_{H^1}$$

and reconstruct $L(N, \lambda)(x)$ by kernel methods. We obtain an estimator \widehat{B}_n s.t.

$$\left(\mathbb{E} \left[\|\widehat{B}_n - B\|_{L^2(\mathcal{D})}^2 \right] \right)^{1/2} \lesssim n^{-s/(2s+3)}$$

uniformly in B over Sobolev balls (over the compact $\mathcal{D} \subset (0, \infty)$).

- The result is compatible with previous deterministic results by Perthame and collaborators.

Limitations of the deterministic based approach

- We implicitly assume a **stationary regime** (the steady-state approximation).
- We do not take advantage of **richer available observation schemes**. In particular, if we have access of the finer structure of the tree, can we beat the ill-posedness imposed by our approach?
- And more: constant growth rate, assuming two (sibling) offsprings are of the same size at birth, etc.

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The stochastic (cell level) approach (1/3)

- We start with a **singe cell of size x_0** . The cell grows exponentially according to a **constant rate τ** .
- The mother cell gives rize to **two offsprings**, at a **rate $B(x)$** that depend on its size x .
- The two offsprings have **initial size $x_1/2$** , where x_1 is the size of the mother at division.
- The two offsprings **start independent growth** according to the rate τ and divide according to the rate $B(x)$.

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The stochastic (cell level) approach (2/3)

- To each node $u \in \mathcal{U}$, we associate a cell with **size at birth** given by ξ_u and **lifetime** ζ_u .
- u^- denotes **the parent** of u . Thus

$$2\xi_u = \xi_{u^-} \exp(\tau\zeta_{u^-}).$$

- $X(t) = (X_1(t), X_2(t), \dots)$ process of the sizes of the population at time t .

The stochastic approach (3/3)

- $X(t) \leftrightarrow$ finite point measure valued process $\sum_{i=1}^{\#X(t)} \delta_{X_i(t)}$
- Identity between point measures

$$\sum_{i=1}^{\infty} \mathbf{1}_{\{X_i(t) > 0\}} \delta_{X_i(t)} = \sum_{u \in \mathcal{U}} \delta_{\xi_u} e^{\tau(t-b_u)} \mathbf{1}_{\{b_u \leq t < b_u + \zeta_u\}}.$$

- In particular, observing $(X(t), t \in [0, T])$ is equivalent to observing $\{\xi_u^T, \zeta_u^T, u \in \mathcal{U}_T\}$.

Matching det. and stoch. approaches (1/3)

- We can relate $X(t)$ and $n(t, x)$ via so-called **many-to-one formulae**.
- Classical technique for fragmentation and branching processes (see *e.g.* Bansaye *et al.* 2009, Bertoin, 2006, Cloez 2011): Pick a cell **at random at each division** and follow its size $\chi(t)$ through time. For $\xi_\emptyset = x$

$$\chi(t) = x \frac{e^{\tau t}}{2^{N_t}}$$

where N_t is the **number of divisions** of the tagged fragment up to time t .

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Matching det. and stoch. approaches (2/3)

- **Step 1** for every (regular compactly supported) f :

$$\mathbb{E} \left[\sum_{i=1}^{\infty} f(X_i(t)) \right] = \mathbb{E} \left[\sum_{u \in \mathcal{U}} f(\xi_t^u) \right]$$

- **Step 2** : many-to-one formula

$$\mathbb{E} \left[f(\chi(t)) \right] = \mathbb{E} \left[\sum_{u \in \mathcal{U}} \xi_t^u \frac{e^{-\tau t}}{x} f(\xi_t^u) \right]$$

- **Step 3** Finally

$$\mathbb{E} \left[\frac{f(\chi(t))}{\chi(t)} x e^{\tau t} \right] = \mathbb{E} \left[\sum_{i=1}^{\infty} f(X_i(t)) \right].$$

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Transport-fragmentation equation

- Set, for (regular compactly supported) f

$$\langle n(t, \cdot), f \rangle := \mathbb{E} \left[\sum_{i=1}^{\infty} f(X_i(t)) \right].$$

We have (in a weak sense)

$$\partial_t n(t, x) + \partial_x (\tau x n(t, x)) + B(x)n(t, x) = 4B(2x)n(t, 2x).$$

- Therefore the **mean empirical distribution** of $X(t)$ satisfies the **deterministic** transport-fragmentation equation.

Statistical estimation of $B(x)$

- **Observation scheme:** genealogical data from two possible schemes:

- **Sparse tree:** we observe, for some $u^{(n)}$ with $|u^{(n)}| = n$,

$$\{\xi_u, uw = u^{(n)} \text{ for some } w \in \mathcal{U}\}$$

- **Full tree:** we observe, for $n = 2^{k_n}$,

$$\{\xi_u, |u| \leq k_n\}$$

- **Asymptotics:** $n \rightarrow \infty$.

Statistical estimation: identifying $B(x)$

- We have

$$\mathbb{P}(\zeta_u \in [t, t + dt] | \zeta_u \geq t, \xi_u = x) = B(xe^{\tau t})dt$$

from which we obtain the **density of the lifetime** ζ_{u-} conditional on $\xi_{u-} = x$:

$$t \rightsquigarrow B(xe^{\tau t}) \exp\left(-\int_0^t B(xe^{\tau s})ds\right).$$

Toward a Markov kernel

- Using $2\xi_u = \xi_{u-} \exp(\tau\zeta_{u-})$, we further infer

$$\begin{aligned} & \mathbb{P}(\xi_u \in dx' | \xi_{u-} = x) \\ &= \frac{B(2x')}{\tau x'} \mathbf{1}_{\{x' \geq x/2\}} \exp\left(-\int_{x/2}^{x'} \frac{B(2s)}{\tau s} ds\right) dx'. \end{aligned}$$

- We thus obtain a simple an explicit representation for the transition kernel $\mathcal{P}_B(x, dx') = \mathcal{P}_B(x, x') dx'$:

$$\mathcal{P}_B(x, x') = \frac{B(2x')}{\tau x'} \mathbf{1}_{\{x' \geq x/2\}} \exp\left(-\int_{x/2}^{x'} \frac{B(2s)}{\tau s} ds\right).$$

Assumptions on B

- Under appropriate conditions on B , the Markov chain on $(0, \infty)$ is geometrically ergodic: there exists a unique invariant probability $\nu_B(dx) = \nu_B(x)dx$ on $[0, \infty)$ such that

$$\nu_B \mathcal{P}_B = \nu_B.$$

(the chain is however not reversible.)

- More precisely, we have the contraction property

$$\sup_{|g| \leq V} |\mathcal{P}_B^k g(x) - \int_S g(z) \nu_B(z) dz| \leq RV(x) \gamma^k$$

for an appropriate Lyapunov function V and some (explicitly computable) $\gamma < 1$.

Identifying $B(x)$ through the invariant measure

- Expand the equation $\nu_B \mathcal{P}_B = \nu_B$:

$$\begin{aligned}\nu_B(y) &= \int_0^\infty \nu_B(x) \mathcal{P}_B(x, y) dx \\ &= \frac{B(2y)}{\tau y} \int_0^{2y} \nu_B(x) \exp\left(-\int_{x/2}^y \frac{B(2s)}{\tau s} ds\right) dx \\ &= \frac{B(2y)}{\tau y} \int_0^\infty \int_0^\infty \mathbf{1}_{\{x \leq 2y, s \geq y\}} \nu_B(x) \mathcal{P}_B(x, s) ds dx.\end{aligned}$$

- This yields the **key representation**

$$\nu_B(y) = \frac{B(2y)}{\tau y} \mathbb{P}_{\nu_B}(\xi_{u^-} \leq 2y, \xi_u \geq y).$$

Key representation

- We conclude

$$B(y) = \frac{\tau y}{2} \frac{\nu_B(y/2)}{\mathbb{P}_{\nu_B}(\xi_u^- \leq y, \xi_u \geq y/2)}.$$

- This yields the estimator

$$\hat{B}_n(y) = \frac{\tau y}{2} \frac{n^{-1} \sum_{u \in \mathcal{U}_{[n]}} K_{h_n}(\xi_u - y/2)}{n^{-1} \sum_{u \in \mathcal{U}_{[n]}} \mathbf{1}_{\{\xi_u^- \leq y, \xi_u \geq y/2\}} \sqrt{\varpi_n}},$$

where the kernel $K_{h_n}(y) = h^{-1}K(h^{-1}y)$ is specified with an appropriate bandwidth (and technical threshold ϖ_n).

- Under the previous assumptions (+ the additional condition $\gamma < \frac{1}{2}$ for the geometric ergodicity decay in the full tree case), we have

$$\mathbb{E}_\mu [\|\widehat{B}_n - B\|_{L^2(\mathcal{D})}^2]^{1/2} \lesssim (\log n)^{1/2} n^{-s/(2s+1)}$$

uniformly in B over s -smooth Hölder balls intersected with “nice geometrically ergodic classes”.

- Here, μ is any initial condition so that V^2 is μ -integrable.

Remarks and extensions

- **Smoothness adaptation** (by means of appropriate concentration inequalities on trees)
- The rate are **minimax** (which is of course no surprise).
- (Possible extension: variability in the growth rate: extension to a cell-dependent $\tau = \tau_u$ drawn via a Markov kernel $\kappa(\tau_{u-}, d\tau)$.)
- (Possible extension: the cell mother divides into offsprings of different sizes.)

Statistical
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GENEALOGICAL
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TEMPORAL
DATA

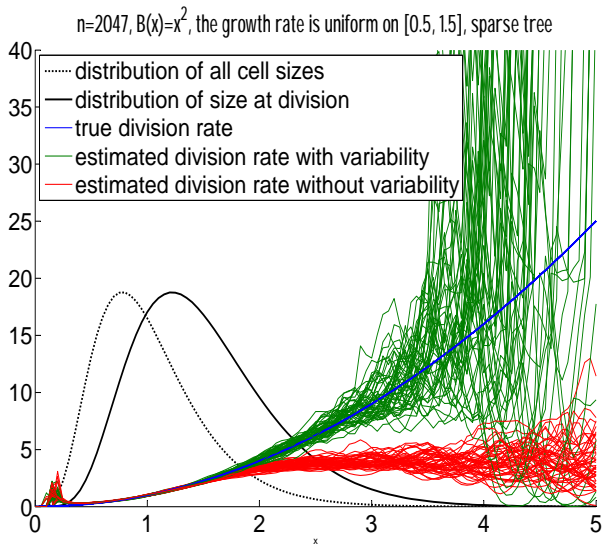
THE SIZE
DEPENDENT
DIVISION RATE
MODEL

Estimation at a
(large) fixed
time in a proxy
model

Estimation
through
genealogical
data

ESTIMATING
THE AGE
DEPENDENT
DIVISION RATE

Effect of variability (sparse tree case)



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GENEALOGICAL VERSUS TEMPORAL DATA

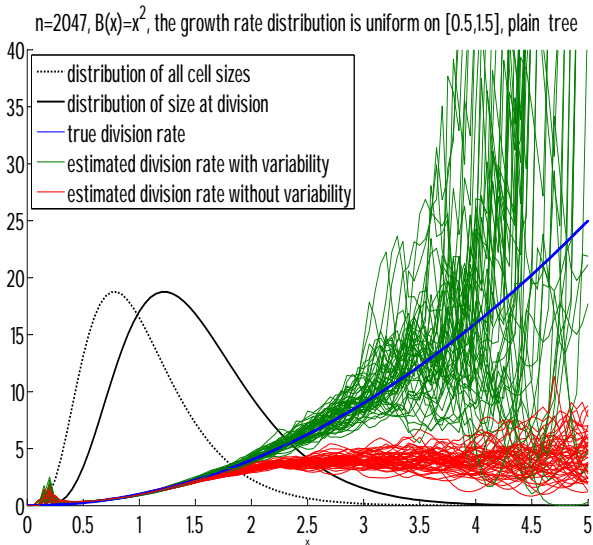
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Une légère surprise (1/3)

- Revisit the representation formula

$$B(y) = \frac{\tau y}{2} \frac{\nu_B(y/2)}{\mathbb{P}_{\nu_B}(\xi_{u^-} \leq y, \xi_u \geq y/2)}.$$

- We always have $\{\xi_{u^-} \geq y\} \subset \{\xi_u \geq y/2\}$, hence

$$\begin{aligned} \mathbb{P}_{\nu_B}(\xi_{u^-} \leq y, \xi_u \geq y/2) &= \mathbb{P}_{\nu_B}(\xi_u \geq y/2) - \mathbb{P}_{\nu_B}(\xi_{u^-} \geq y) \\ &= \int_{y/2}^{\infty} - \int_y^{\infty} \\ &= \int_{y/2}^y \nu_B(x) dx \quad (!). \end{aligned}$$

Une légère surprise (2/3)

- Finally (for constant growth rate) we have

$$B(y) = \frac{\tau y}{2} \frac{\nu_B(y/2)}{\int_{y/2}^y \nu_B(x) dx}$$

- We have a “gain”: rate $n^{-s/(2s+1)}$ versus $n^{-s/(2s+3)}$ in the proxy model based on the transport-fragmentation equation...
- But it only comes from the fact that we estimate the invariant measure “at division”, versus the invariant measure “at fixed time” in the proxy model.

Une légère surprise (3/3)

- There seems to be more “nonparametric statistical information” in data extracted from \dot{U}_T rather than ∂U_T
- However $|\dot{U}_T| \approx |\partial U_T|$ (supercritical branching processes).
- Can we make that argument more precise (up to changing the model)?

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- 1 GENEALOGICAL VERSUS TEMPORAL DATA
- 2 THE SIZE DEPENDENT DIVISION RATE MODEL
 - Estimation at a (large) fixed time in a proxy model
 - Estimation through genealogical data
- 3 ESTIMATING THE AGE DEPENDENT DIVISION RATE

Age dependent division rate $B(a)$

- $n(t, a)$ is now solution to

$$\partial_t n(t, a) + \partial_a (an(t, a)) + B(a)n(t, a) = 0,$$

$$n(t, a = 0) = 2 \int_0^\infty B(a)n(t, a)da \quad n(t = 0, a) = n^{(0)}(a).$$

- This translates into the stochastic model as

$$\mathbb{P}(\zeta_u \in [a, a + da] \mid \zeta_u \geq a) = B(a)da.$$

- Here, the ζ_u are i.i.d. We have nothing but a renewal process on a tree.

- The ζ_u are i.i.d.: the case of genealogical data is readily embedded into standard density estimation.
- **Temporal data:** we observe, for some (large) $T > 0$

$$\{\zeta_u^T, u \in \mathcal{U}_T\}$$

which can be split into two data sets

$$\{\zeta_u, u \in \mathring{\mathcal{U}}_T\} \cup \{T - b_u, u \in \partial\mathcal{U}_T\}.$$

Estimation of $B(a)$ from $\dot{\mathcal{U}}_T$ (1/4)

- Analogue of what we did for the size dependent $B(x)$ in the sense that we have (empirical) access to **the time at division**.
- Additional difficulty: **bias selection** (small lifetimes are observed more often than large lifetimes).
- Strategy: **many-to-one formulae** (Bansaye *et al.*, 2009, Cloez, 2012)

Estimation of $B(a)$ from $\dot{\mathcal{U}}_T$ (2/4)

- Many-to-one formula (Cloeze, 2012): we have, for a nice test function g :

$$\mathbb{E} \left[\sum_{u \in \dot{\mathcal{U}}_T} g(\zeta_u) \right] = \int_0^T e^{\lambda_B s} \mathbb{E} [g(\chi(s)) H_B(\chi(s))] ds.$$

where $\chi(t)$ is a tagged branch picked at random on the tree, and $H_B(a)$ an explicit function.

- Also $\mathbb{E}[|\dot{\mathcal{U}}_T|] \sim \kappa_B e^{\lambda_B T}$.
- All the ingredients needed for a law of large numbers.

Estimation of $B(a)$ from $\dot{\mathcal{U}}_T$ (3/4)

- Let $f_B(a) = B(a) \exp(-\int_0^\infty B(s) ds)$.
- We have

$$\frac{1}{|\dot{\mathcal{U}}_T|} \sum_{u \in \dot{\mathcal{U}}_T} g(\zeta_u) \xrightarrow{\mathbb{P}} 2 \int_0^\infty g(a) e^{\lambda_B a} f_B(a) da.$$

- We even obtain a rate of convergence (in probability)

$$(\exp(\lambda_B T))^{1/2}$$

with some uniformity in $B \in \mathcal{B}$ (in a “neighbourhood” of constant functions B).

- Proof: rates of convergence in the many-to-one formula for $g(\zeta_u, \zeta_v)$ for $u, v \in \dot{\mathcal{U}}_T$ + geometric ergodicity.

Estimation of $B(a)$ from $\dot{\mathcal{U}}_T$ (4/4)

- We derive **kernel estimators** that achieve the rate

$$\left(\exp(\lambda_B T)\right)^{s/(2s+1)}$$

uniformly over $\mathcal{B} \cap \mathcal{H}(s, M)$.

- The rate is **nearly minimax** (use likelihood expansions established by Löcherbach in the early 2000's).

What if data are taken from $\partial\mathcal{U}_T$ solely?

- We now have (using Cloez's many-to-one formulae), for a test function g

$$\begin{aligned} |\partial\mathcal{U}_T|^{-1} \sum_{u \in \partial\mathcal{U}_T} g(\zeta_u) &\xrightarrow{\mathbb{P}} 2\lambda_B \int_0^\infty g(a) e^{\lambda_B a} \frac{f_B(a)}{B(a)} da \\ &= 2\lambda_B \int_0^\infty g(a) e^{\lambda_B a} e^{-\int_0^a B(s) ds} da. \end{aligned}$$

- We have a rate of convergence (in probability) $(\exp(\lambda_B T))^{1/2}$ uniformly in $B \in \mathcal{B}$.
- We retrieve an **ill-posed problem of order 1**, leading to convergence rate $(\exp(\lambda_B T))^{s/(2s+3)}$.

The age dependent model, simulated data

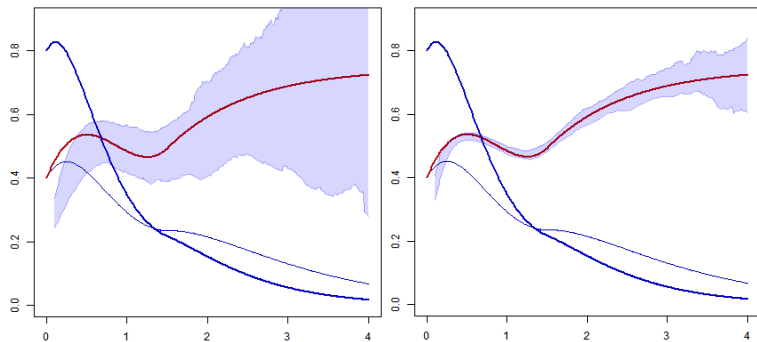


Figure : Reconstruction of B over $\mathcal{D} = [0.1, 4]$ with 95%-level confidence bands constructed over $M = 100$ Monte-Carlo trees. In bold red line: $x \rightsquigarrow B(x)$; in bold blue line: f_{H_B} ; in blue line: f_B . Left: $T = 15$. Right: $T = 23$.

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Conclusion/Overall picture

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data	Size model	Age model
proxy model	$n^{-s/(2s+3)}$ + adaptation	irrelevant
$\partial \mathcal{U}_T$?	$(e^{\lambda_B T})^{-s/(2s+3)}$
genealogical	$n^{-s/(2s+1)}$ + adaptation	irrelevant
$\dot{\mathcal{U}}_T$?	$(e^{\lambda_B T})^{-s/(2s+1)}$

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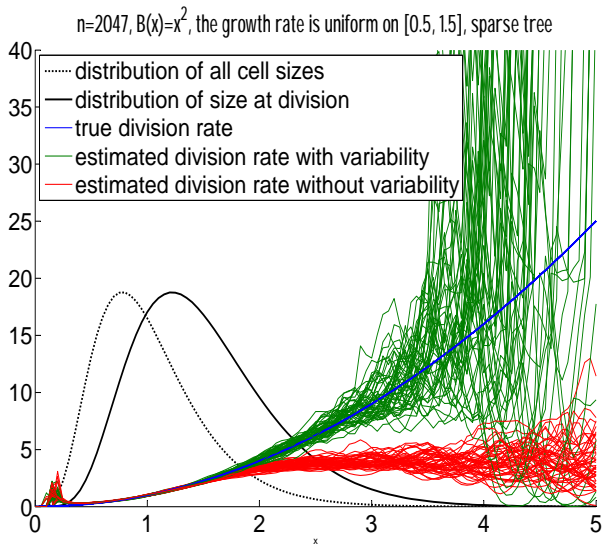
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THANK YOU FOR YOUR ATTENTION!

- Doumic, M., H. M., Reynaud-Bouret, P. and Rivoirard, V. (2012) *Nonparametric estimation of the division rate of a size-structured population*. SIAM Journal on Numerical Analysis. **50**, 25pp.
- Doumic, M., H., M., Krell, N. and Robert, L. (2013) *Statistical estimation of a growth-fragmentation model observed on a genealogical tree*. *Bernoulli*, in press.
- L Robert, M.H., N. Krell, S. Aymerich, J. Robert and M. Doumic. (2014) *Division control in Escherichia coli is based on a size-sensing rather than a timing mechanism*. BMC Biology, 02/2014 10pp.
- M.H., Olivier, A. (2014) *Nonparametric estimation of the division rate of an age dependent branching process*. arXiv:1412.5936. 32pp.

Effect of variability (sparse tree case)



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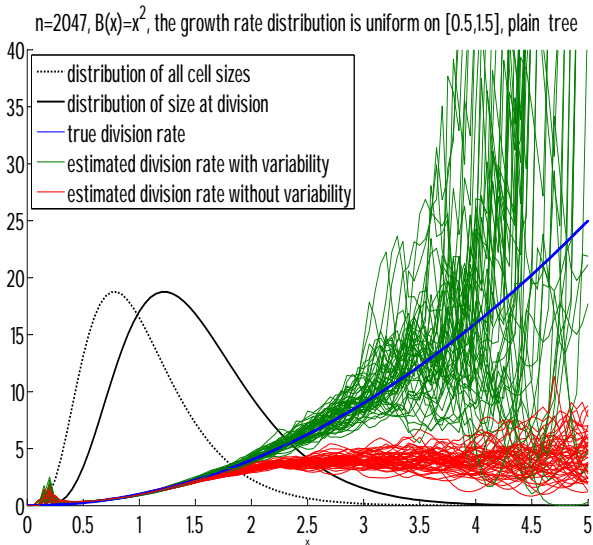
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Exploration on real data (*E. Coli*, sparse and dense tree case)

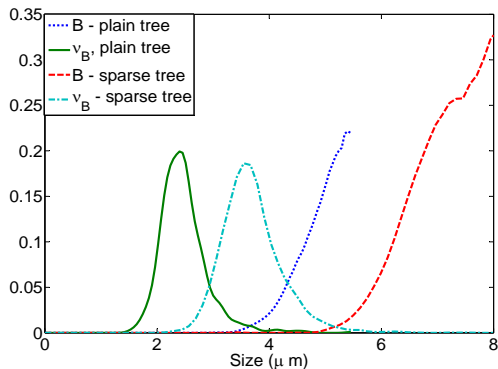


Figure : Implementation on real data

Statistical inference in transport-fragmentation models

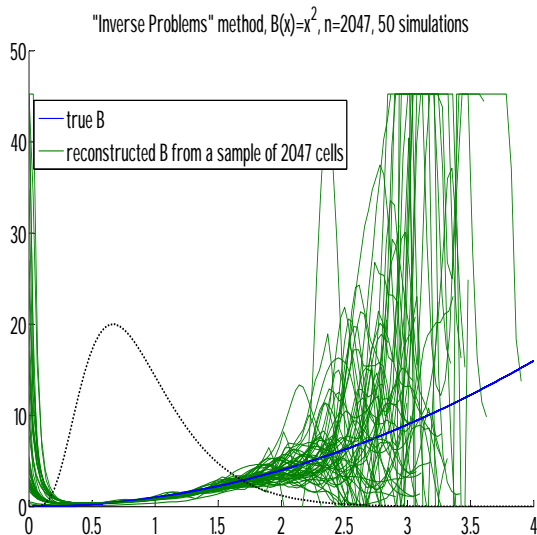
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Comparison with the inverse problem approach



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Numerical implementation

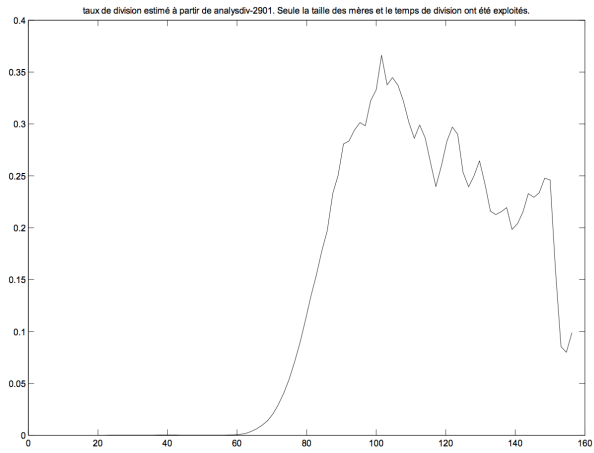


Figure : Exploration on real-data. Sparse tree, $n \approx 3000$.

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