Macroscopic and microscopic polymers-monomers dynamics

with Amandine Véber and François Robin
at MAP5

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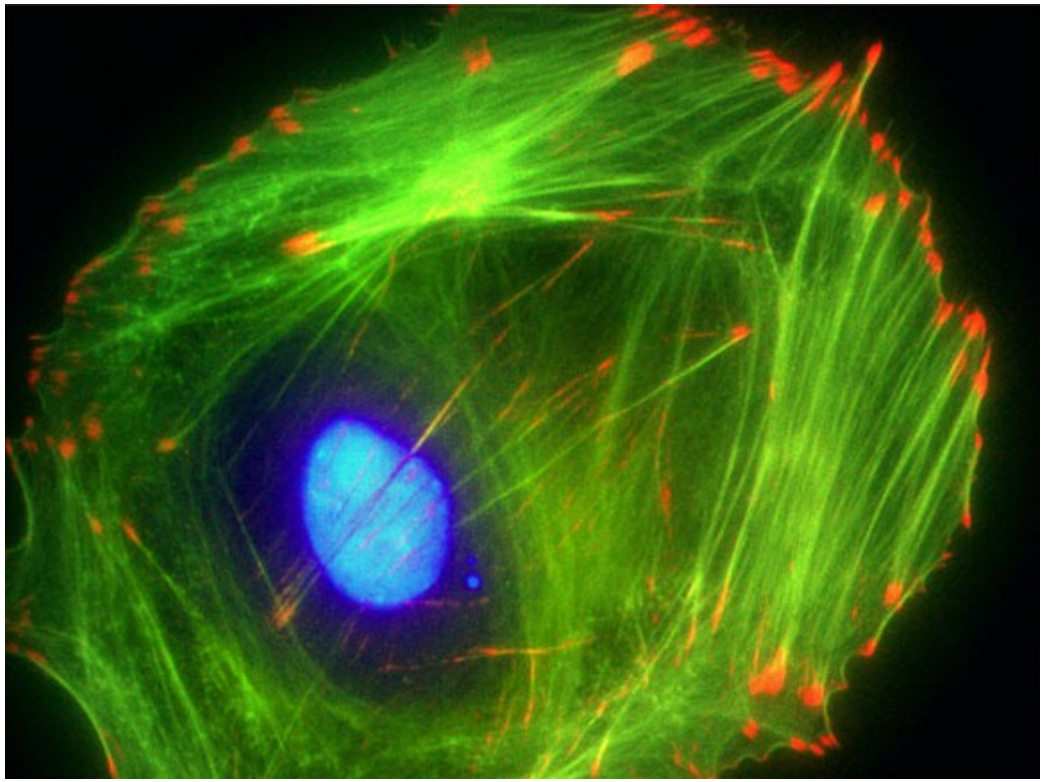
Biological problem



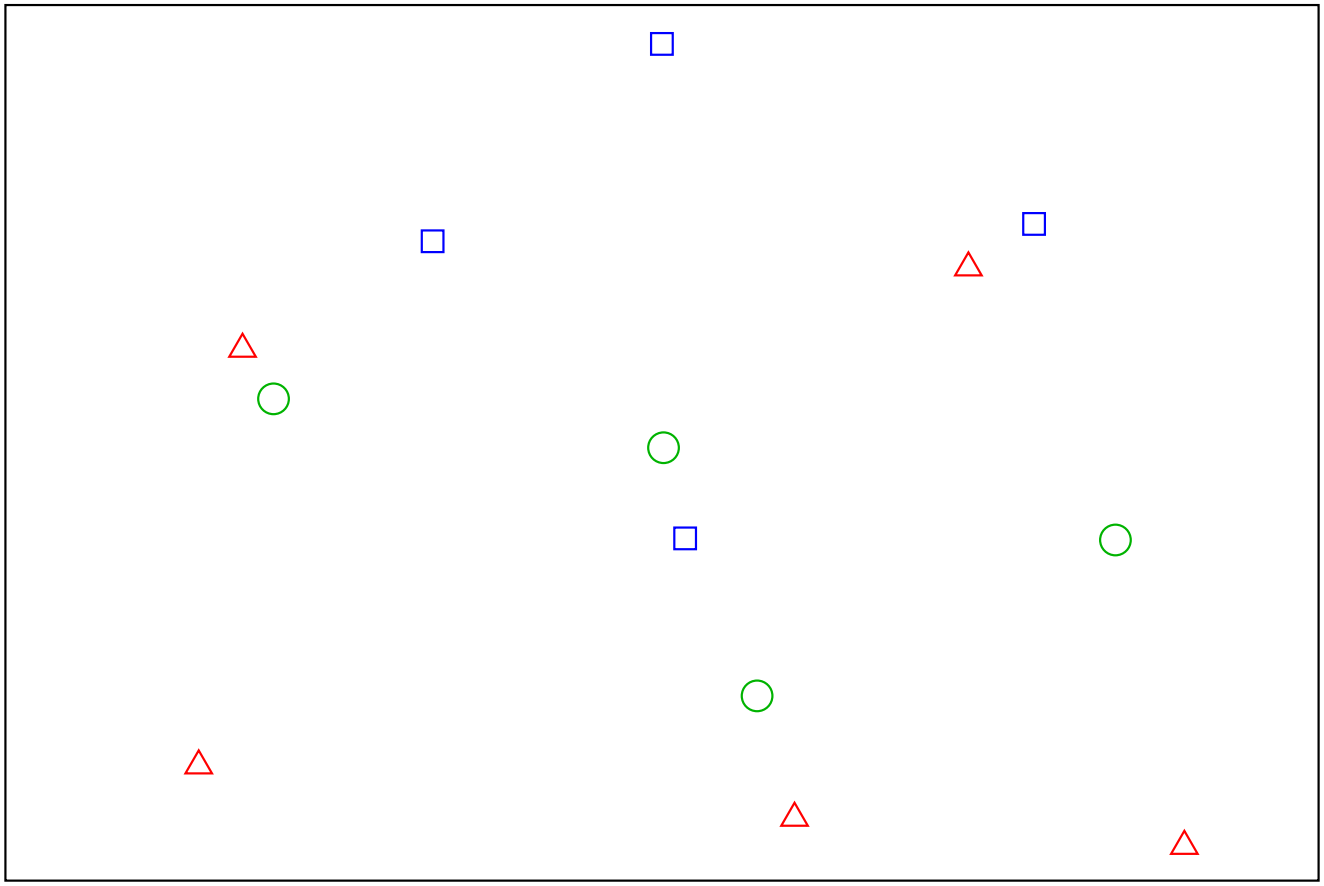
Actin polymers in the cell, shown in green.

Mathematical framework

- A geographical space $E \subseteq \mathbb{R}^d$.
- Chemical species $\{A_1, \ldots, A_n\}$ evolving in E,
- each associated with a diffusion factor $D_i \geq 0$.
- A set of reactions, for example

$$A_1 + 2A_2 \mapsto A_3,$$
$$A_3 \mapsto \emptyset.$$

- Every reaction r has a rate $\lambda_r > 0$, and can be localized at a certain point $y_r \in E$, or non-localized.
- A reaction kernel $\Gamma : \mathbb{R}^d \to \mathbb{R}_+$, positive, with support in a ball of some radius $\varepsilon > 0$ (the reaction radius).



$t = t_0$

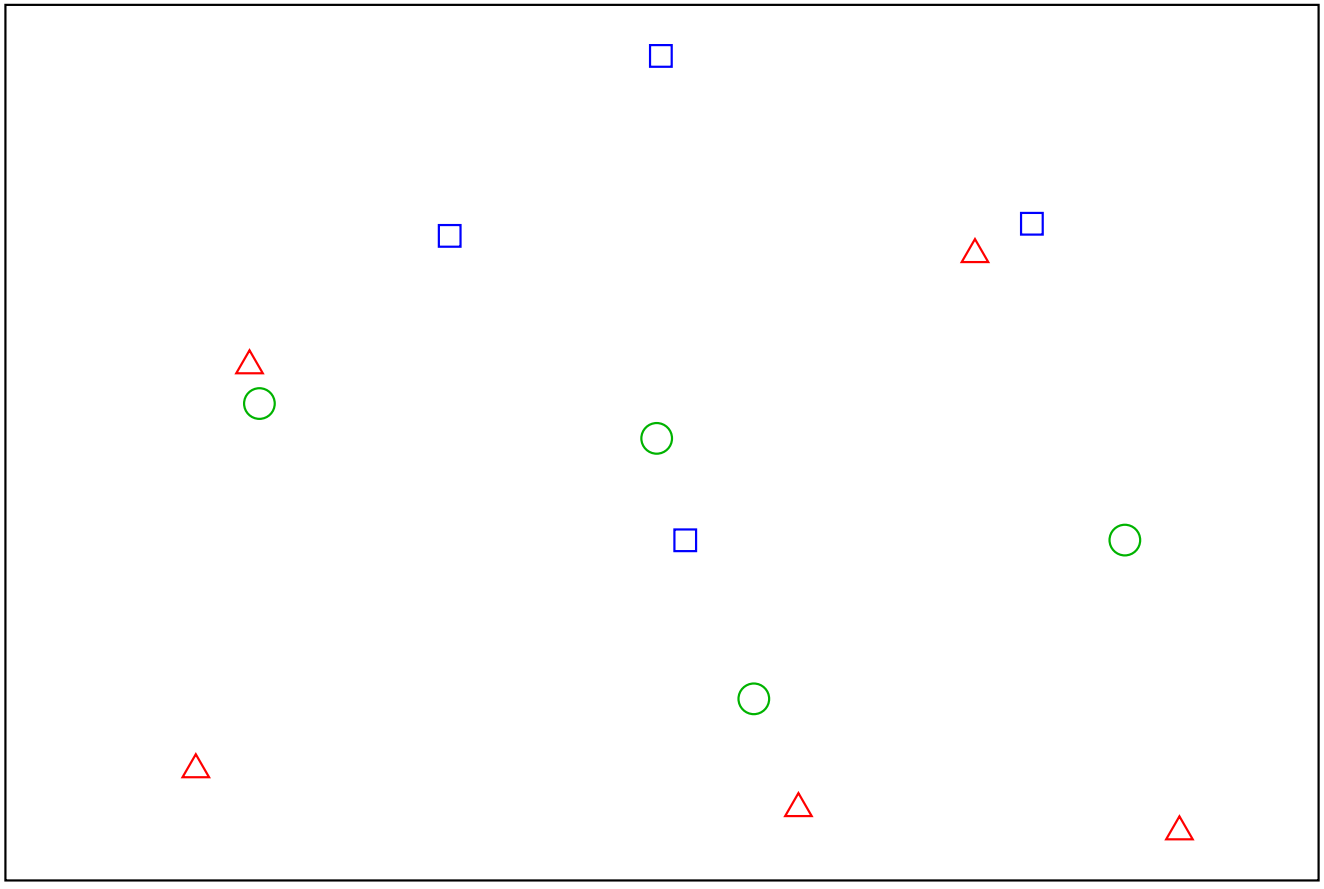
E

A_1

A_2

A_3

$A_1 + A_2 \mapsto A_3$



$t = t_0 + 0.1$

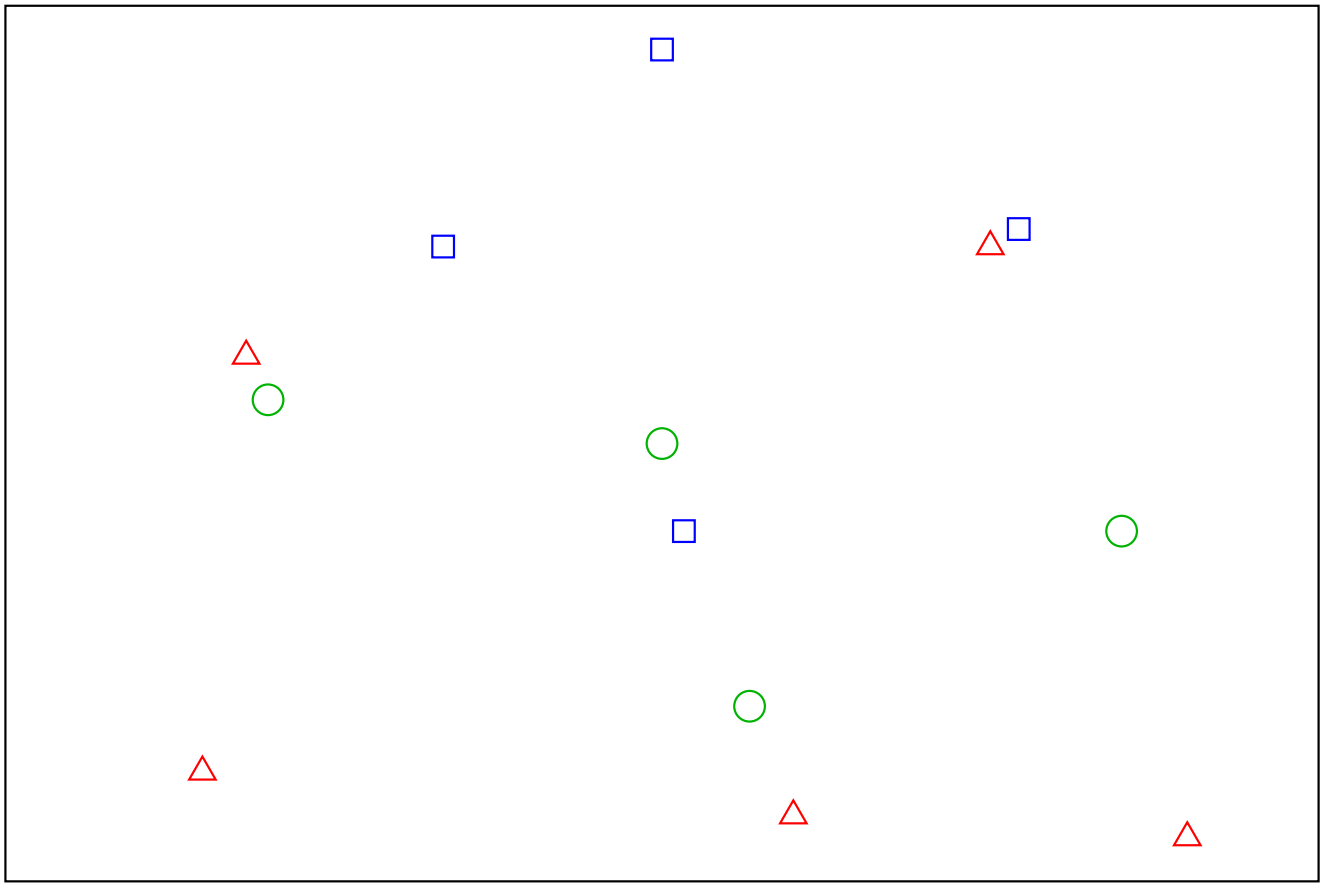
E

A_1

A_2

A_3

$A_1 + A_2 \mapsto A_3$



$t = t_0 + 0.2^-$

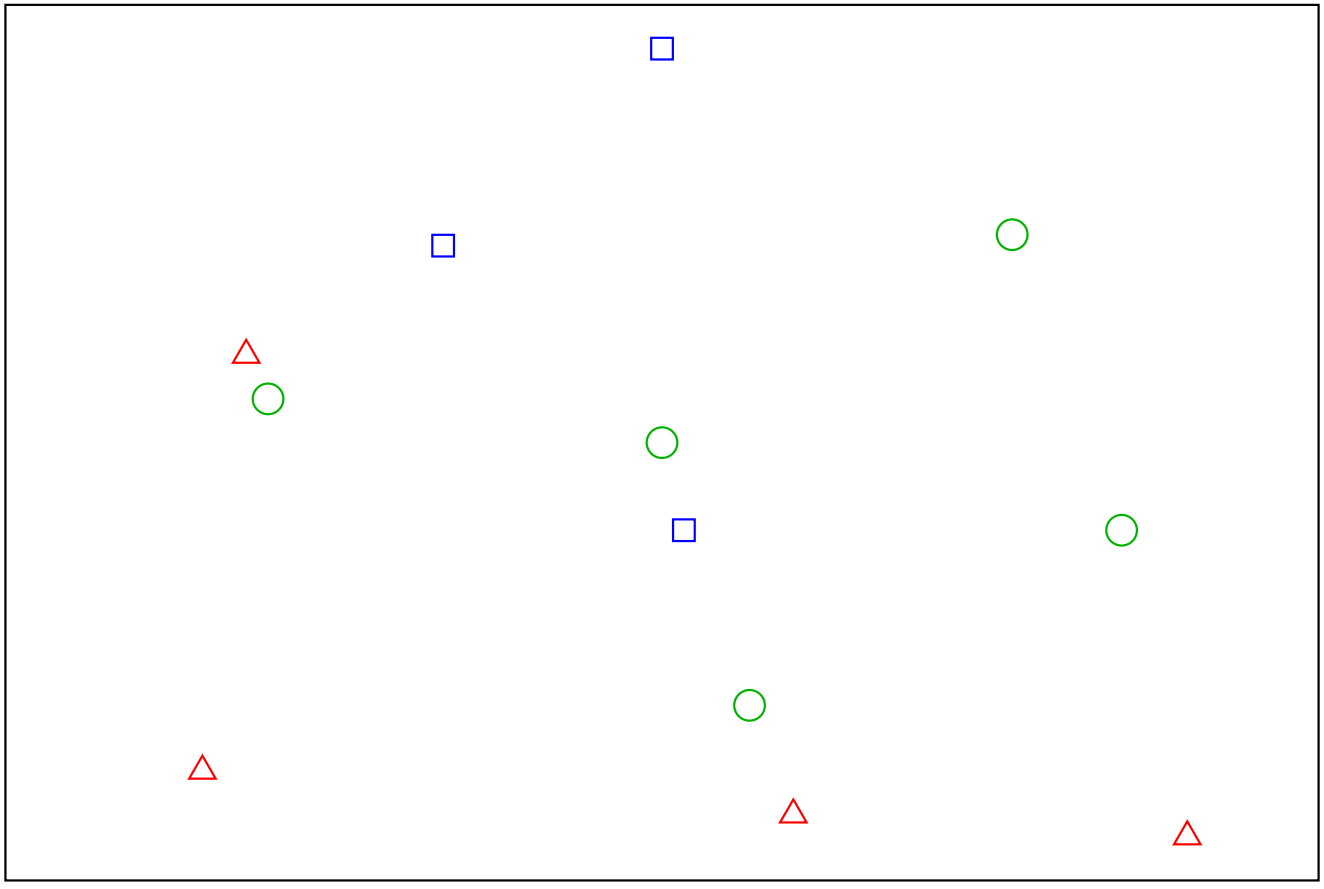
E

A_1

A_2

A_3

$A_1 + A_2 \mapsto A_3$



$t = t_0 + 0.2$

E

A_1

A_2

A_3

$A_1 + A_2 \mapsto A_3$

Mathematical framework

A state of the system at a given time is represented by a point measure on the phase space $\mathcal{P} = E \times \{A_1, \ldots, A_n\}$.

Notation

$\mathcal{M}(\mathcal{P})$ is the space of all finite measures on $\mathcal{P}$.
$\mathcal{M}_p(\mathcal{P})$ is the space of all finite *point* measures on $\mathcal{P}$, that is, sum of Dirac masses.

Denote by $(\mu_t)_{t\geq 0}$ the (random) process evolving over time.
μ is a random variable taking values in the space of càdlàg paths in $\mathcal{M}_p(\mathcal{P})$.

A model

Two species M (monomers) and P (polymers), evolving in the circle $\mathbb{T} := \mathbb{R}/\mathbb{Z}$. Monomers move as standard Brownian motion. Polymers are very long so that they are never depleted, and are fixed at zero.
Polymerisation :

$$P + M \mapsto P.$$

Depolymerisation :

$$P \mapsto P + M$$

With respective rates $\lambda^-, \lambda^+ > 0$, both localized at $0 \in \mathbb{T}$.

Cleaner version of the model

One species M (monomers), evolving in the circle $\mathbb{T} := \mathbb{R}/\mathbb{Z}$, moving with standard Brownian motion.
Polymerisation :

$$M \mapsto \emptyset.$$

Depolymerisation :

$$\emptyset \mapsto M$$

With respective rates $\lambda^-, \lambda^+ > 0$, both localized at $0 \in \mathbb{T}$.

Macroscopic limit

Set $\lambda^- = N$ and $\lambda^+ = 1$. The expected number or monomers (at any given time $t > 0$) is of order N.

Definition

Define $(\mu_t^N)_{t\geq 0}$ the process contructed starting with $\mu_0^N = 0$ and $\lambda^- = N, \lambda^+ = 1$.
Define its normalization $\widetilde{\mu}^N = \frac{1}{N}\mu^N$.

Theorem (Large population limit)

As $N \to \infty$, $\widetilde{\mu}^N$ converges in law to a deterministic process $\nu : \mathbb{R}_+ \to \mathcal{M}(\mathcal{P})$, which is the solution to the PDE

$$\partial_t \nu_t = \frac{1}{2}\Delta v_t + \delta_0 - \Gamma \nu_t,$$

and initial condition $\nu_0 = 0$.

Microscopic results

Definition

Let B be standard Brownian motion, $\mathcal{E}$ be an exponential variable independant of B, and

$$\tau_\Gamma := \inf\left\{t > 0 : \int_0^t \Gamma(B_s)ds > \mathcal{E}\right\}.$$

τ_Γ is the survival time of a particle emitted at 0, absorbed at rate Γ.

Theorem

For any $t > 0$,

$$\mathbb{P}(\tau_\Gamma \leq t) = \int_{\mathbb{T}} \Gamma \, d\nu_t.$$

Microscopic results

Assume $\Gamma = \frac{1}{2\varepsilon}\mathbb{1}_{[-\varepsilon,\varepsilon]}$.

Theorem

The number of particles in $[-\varepsilon, \varepsilon]$ at time t is Poisson-distributed with mean

$$2\varepsilon N \mathbb{P}(\tau_{\Gamma_\varepsilon} \leq t).$$

This model is quite peculiar because particles can be considered to be independent.

Microscopic results

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Theorem

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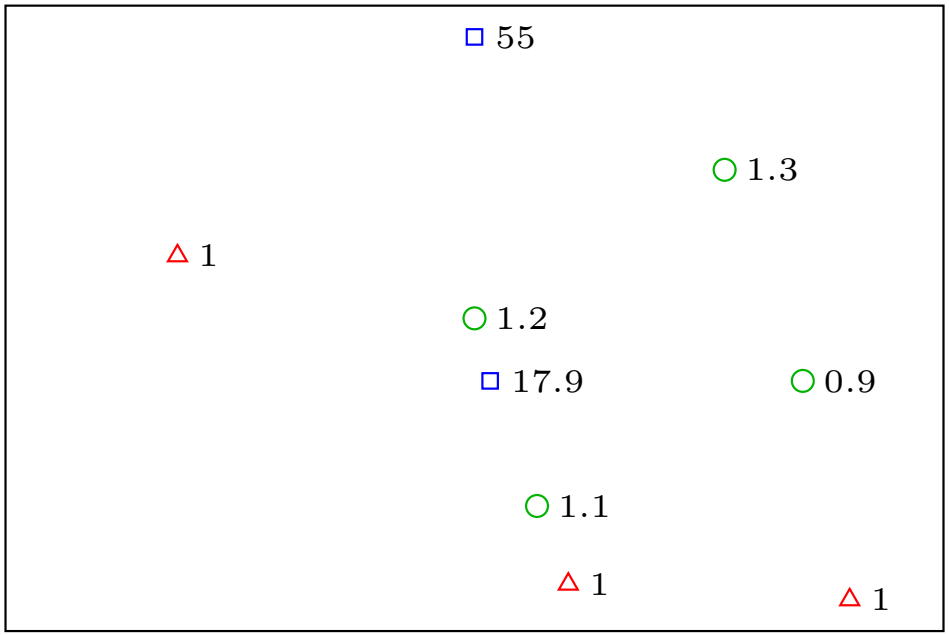
Conjecture

In more complex models, with $\Gamma = \frac{1}{2\varepsilon}\mathbb{1}_{[-\varepsilon,\varepsilon]}$, the expected number of particles in $[-\varepsilon, \varepsilon]$ is of order εN.

Length model : Adding traits

Let us go back to the general model and complexify it a bit.
Every particule can have a size (or length) $l \in \mathbb{R}_+$.
The process μ now belongs to $\mathbb{R}_+ \to \mathcal{M}_p(\mathcal{P} \times \mathbb{R}_+)$.



Length model

Two species :

- Monomers M, diffuse with diffusion factor $D > 0$ on $\mathbb{T} = \mathbb{R}/\mathbb{Z}$, all have the same size $\delta > 0$;
- Polymers P, fixed at zero, have a length $l \in \delta\mathbb{N}$.

Reactions :

$$\begin{aligned} (P, 0, l) + (M, y, \delta) &\to (P, 0, l + \delta) && l \geq \delta \\ (P, 0, l) &\to (P, 0, l - \delta) + (M, 0, \delta) && l \geq \delta \end{aligned}$$

with respective rates λ^-, λ^+, both localized at $0 \in \mathbb{T}$.

Length model : Macroscopic limit

Definition

Define $(\mu_t^N)_{t\geq 0}$ the process contructed with $\lambda^- = N, \lambda^+ = 1, \delta = \delta_N$. Define its normalization

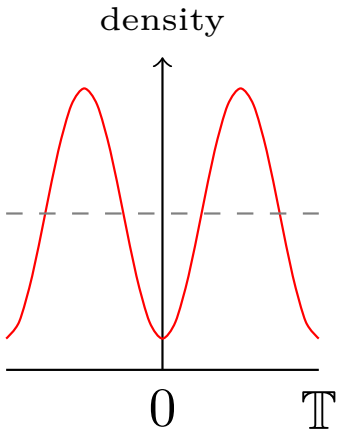
$$\widetilde{\mu}^{N,M} = \frac{1}{N}\mu^{N,M}, \qquad \widetilde{\mu}^{N,P} = \frac{1}{N\delta_N}\mu^{N,P}.$$

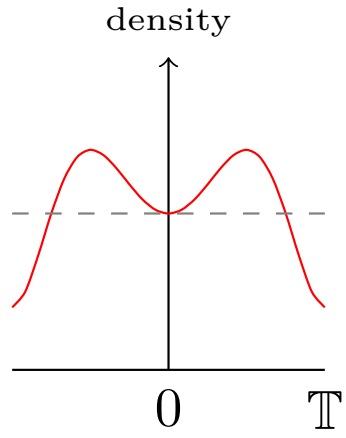
Assume that $N\delta_N \to \infty$ and $\delta_N \to 0$ as $N \to \infty$.

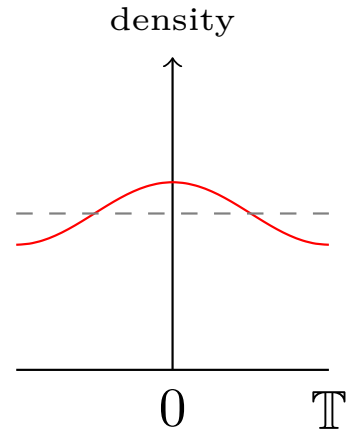
Conjecture

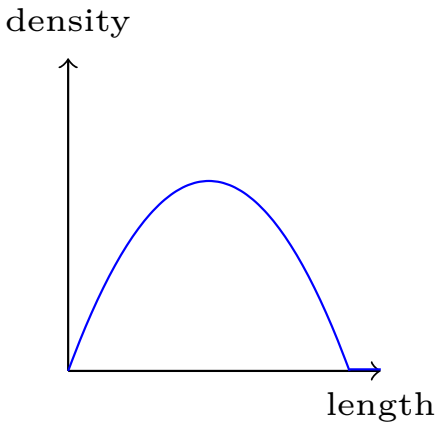
Under mild assumptions, $\widetilde{\mu}^N$ converges to a deterministic process $\nu : \mathbb{R}_+ \to \mathcal{M}(\mathcal{P})$, which is the solution to the PDE

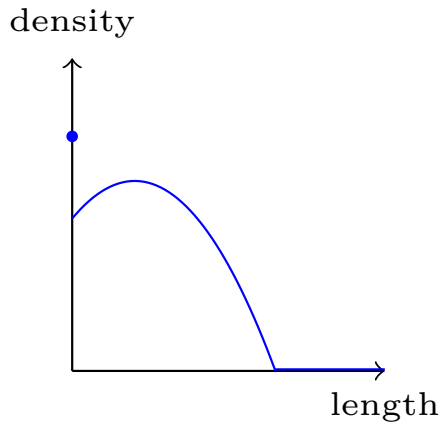
$$\begin{cases} \partial_t \nu_t^M = D\Delta\nu_t^M - \left(\lambda^+ \Gamma_\varepsilon \nu_t^M - \lambda^- \delta_0\right)\langle \nu_t^S, \mathbb{1}_{l>0}\rangle, \\ \partial_t \langle \nu_t^S, f^S\rangle = \left(\lambda^+ \langle \nu_t^M, \Gamma_\varepsilon\rangle - \lambda^-\right)\langle \nu_t^S, \mathbb{1}_{l>0}\partial_l f^S\rangle. \end{cases}$$

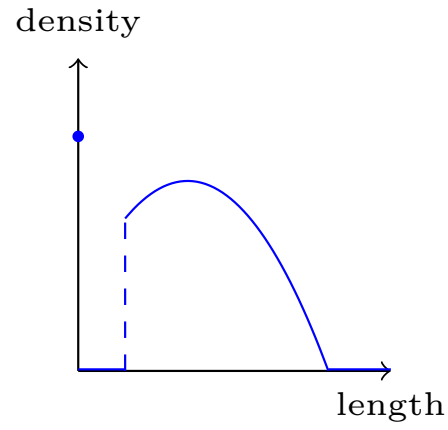












at $t = t_0$

at $t = t_1 > t_0$

at $t = t_2 > t_1$