

**Integral and integro-differential equations  
with measure-valued solutions describing  
the evolution of structured populations**

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ACADEMIC DISSERTATION

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# Abstract

In this thesis we analyse the solutions of two different types of integral and integro-differential equations modelling structured populations. More precisely, we study a linear renewal equation that models the dynamics of physiologically structured populations, as well as an extension of the Smoluchowski coagulation equation: the coagulation equation with a constant flux of particles from the origin. The focus is on measure-valued solutions, i.e., solutions that, evaluated in time, are measures. Two different assumptions on the kernel characterizing the linear renewal equation are proven to guarantee asynchronous exponential growth/decline or convergence to a stable distribution for the unique solution of the renewal equation. If the kernel is factorizable, then the proof is based on Feller's classical Renewal Theorem. If, instead the kernel is regularizing the proof is based on the theory of positive operators and on Laplace transform methods. The third main result of this thesis is related with the asymptotic behaviour of the coagulation equation with source. Indeed, the existence of self-similar solutions for the coagulation equation with a constant flux of particles from the origin is proven under the assumption that the kernel satisfies a polynomial bound that also prevents gelation. These self-similar solutions are expected to describe the long term behaviour of the solutions of the coagulation equation with source.



## Articles included in the thesis:

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*I am the first author of the papers [I, II] as I had a leading role in writing all the sections of the papers. I am corresponding author of the paper [III] as I had a leading role in writing all the parts of the paper, but the order of the authors is alphabetic. The scientific articles have not been used in previous dissertations.*





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# 1 An introduction to structured population models

A population is a collection of individuals embedded in an environment. The word individuals can be interpreted in a very broad sense, indeed, we can speak about populations of cells [7], animals [45], humans [76], atmospheric aerosols [84], proteins [17] and many other, see for instance [65, 70].

The number of individuals in a population, as well as their features, changes in time due to individual level mechanisms, including inter-individual interactions, and due to the influence of the environment.

How does the population evolve in time? The aim of structured population models is to answer this question on the basis of the evolution of individual structuring variables, i.e., features that characterize the individual dynamics.

## 1.1 Individual level dynamics

When we want to analyse the evolution of a population, the first step is to determine the individual level mechanisms driving the dynamics and the individual features, called *i-states*, that are suitable to structure the population. The *i-states* at a certain time, together with the environmental conditions, have to fully determine the rates at which the individual level mechanisms take place, hence the future individual states.

One of the simplest examples of structuring variable is age. A population with this type of structure was considered in 1911, when Sharpe and Lotka formulated and analysed an equation describing the evolution in time of a population of individuals undergoing aging, death and giving birth, [76].

In 1917 Smoluchowski formulated the coagulation equation, describing the evolution in time of a population of particles undergoing merging events, [80]. By doing that he introduced another example of structuring variable: size. This structuring variable has also been considered later by Anderson and Bell [7] in their analysis of a model of cell growth and fission.

Since the second half of 1900 the mathematical theory of structured populations has been blooming and the present literature is rich of examples of structured populations, see for instance [65, 70] for examples of models, as well as different techniques to analyse them, and [3] for an historical point of view.

Real world populations are always embedded in an environment which may influence the evolution of the population in different ways. For example, if we consider a population of cells growing and dividing we might assume that the

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growth rate of the cells depends on the amount of nutrient resources, that can, therefore, be interpreted as an environment.

In this case it is reasonable to assume that, in turn, the population evolution affects the dynamics of the environment, as nutrient resources are consumed by cells during growth. This leads to a feedback-loop between the environment and the population. See [26, 27] for examples of this type of environment.

When we model a population of particles interacting with each other we might have to consider a completely different example of environment: a source of particles. The source affects the population dynamics, but the changes in the population do not influence the source, which can be assumed to be constant in time. See for instance [36] and Section 4.2 for more details.

The focus of the thesis is on two classes of models, characterized by different  $i$ -level mechanisms driving the population dynamics. The main difference between the two types of models we consider is that in the models presented in Section 3, the individuals do not interact with each other, while in the models presented in Section 4, the individual level dynamics is driven by the inter-individual interaction. In the examples presented in Section 3 we do not model the environment and assume that the population dynamics is completely determined by the  $i$ -level mechanisms, while in Section 4.2 we consider a source of individuals as an environment.

We now present more details on the type of  $i$ -level mechanisms characterizing the first class of models. The motivation to study this type of mechanisms comes from physiologically structured populations.

Indeed, the population distribution along a structuring physiological feature often evolves in time due to the two following  $i$ -level mechanisms

- smooth deterministic development of the  $i$ -states;
- jump from an  $i$ -state to another  $i$ -state, or alternatively, birth/death of individuals with a certain state. We model jumps in the state space as birth/death events: we assume that the individual with the state before the jump dies and that an individual is born with the new state.

An important assumption is that individuals do not interact between each other, hence jumps/births are not promoted by the interaction between the individuals. They are events that happen at random times with a certain state dependent rate  $\Lambda$ .

Examples of physiologically structured population models characterized by the  $i$ -level mechanisms described above are the model of cell growth and fission introduced by Anderson and Bell in [7] and the model of waning and boosting of the immunity level introduced and analysed in [25] and later in [72]. We provide more details on these examples in Section 3.3.

The second class of models we study in this thesis is a class of coagulation models. In these models the population distribution along the structuring variable,

which is size, changes in time only due to one mechanism: two individuals coagulate instantaneously upon collision. The crucial assumption we make is that the coagulation rate of two individuals depends only on the sizes of the two coalescing individuals. The coagulation rate, therefore, summarises all the underlying individual level mechanisms driving the coagulation. We will provide more details on this in Section 4.

To make the connection between coagulation models and the class of models presented above we might interpret coagulation as a birth/death event: two individuals die and an individual with size equal to the sum of the sizes of the coagulating individuals appears in the population.

In this thesis we aim at studying an extension of the coagulation model. Indeed, we embed the population of coalescing particles into a constant environment, that influences the population evolution. More precisely, we assume that the population is not isolated, by introducing a constant source of individuals of small sizes. We provide more details on the coagulation models with a source in Section 4.2.

## 1.2 From individuals to populations

Multiple approaches can be undertaken to rise from the  $i$ -level mechanisms to the population level ( $p$ -level) dynamics. When the number of individuals is small, the population can be described by a stochastic process  $X^{[N(t)]}(t) = (x_1(t), \dots, x_{N(t)}(t))$ . The  $x_i$  are stochastic processes representing the individual evolution. See [9, 72] for details on the stochastic approach, respectively for individuals evolving piecewise deterministically and for coagulation processes.

When, instead, the size of the population is very large, it is customary to derive, from the interpretation, deterministic equations for the average quantities of interest, neglecting the  $i$ -level stochasticity. This procedure is, in some cases, only justified by a formal law of large number argument. In other cases, it has been proven that, as the size of the population  $N$  tends to infinity, the empirical measure corresponding to the stochastic process  $X^{[N]}(t)$ , converges to a deterministic measure, that satisfies the equation derived via the deterministic approach. See for instance [2, 9] where the coagulation equation has been derived. In this thesis we focus on the deterministic approach and consider equations derived formally from the individual level mechanisms or derived in other works from stochastic models. We now present the equations formalising the model examples presented in Section 1.1.

Consider the first class of models presented in Section 1.1. Let  $b(t, x)$  be the population birth rate, i.e., the rate at which individuals are born at time  $t$  and with state  $x$ . The population birth rate at a certain time  $t$  depends on the population birth rate in the past in the following way

$$b(t, x) = \int_0^t \int_{\Omega_0} K(a, y, x) b(t-a, y) dy da + b_0(t, x). \quad (1.2.1)$$

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Here  $\Omega_0$  is the set of the states at birth and  $b_0$  is the contribution to the population birth rate of the individuals that were born before time 0. The kernel  $K(a, y, x)$  is the rate at which an individual, which had  $i$ -state  $y$  at birth, is expected to give birth to offspring with state at birth  $x$ , when it is of age  $a$ . Thanks to this interpretation we readily see that  $K(a, y, x)b(t - a, y)$  is the contribution to the population birth rate, of newborns with state at birth  $x$ , due to an individual that was born  $a$  time ago with state at birth  $y$ . Summing over all the possible ages  $a$  and states at birth  $y$  we obtain the total contribution to the population birth rate of the individuals that were born after time 0. Studying the qualitative behaviour of the solution of equation (1.2.1) can give important information on the evolution of the population and on its distribution along the structuring variable.

Let us consider now the model of coagulation. As explained above the evolution of the population distribution is, in this case, only a consequence of coagulation. Neglecting the correlations between coagulation events, we can write down Smoluchowski's coagulation equation:

$$\partial_t f(t, x) = (\mathbb{K}f)(t, x), \quad (1.2.2)$$

where the operator  $\mathbb{K}$  is defined as

$$(\mathbb{K}f)(t, x) = \int_0^x k(y, x - y)f(t, y)f(t, x - y)dy - \frac{1}{2} \int_0^\infty k(y, x)f(t, y)dyf(t, x). \quad (1.2.3)$$

The kernel  $k(x, y)$  in (1.2.3) is the rate at which an individual of size  $x$  coagulates with an individual of size  $y$ . Since coagulation is a symmetric event we have that  $k(x, y) = k(y, x)$ .

Smoluchowski's coagulation equation can be seen as a birth/death equation. The birth term, due to the coagulation of an individual of size  $x - y$  with an individual of size  $y$ , is equal to

$$\int_0^x k(y, x - y)f(t, y)f(t, x - y)dy.$$

While the death term, due to the coagulation of an individual of size equal to  $x$  with any other individual, is equal to

$$\frac{1}{2} \int_0^\infty k(y, x)f(t, y)dyf(t, x),$$

where the factor  $\frac{1}{2}$  in the death term guarantees that mass remains constant during coagulation.

In this thesis we study an extension of this equation: the coagulation equation with a source

$$\partial_t f(t, x) = (\mathbb{K}f)(t, x) + \eta(x). \quad (1.2.4)$$

The term  $\eta$  in (1.2.4) represents a source of individuals, which is assumed to be constant in time and to be concentrated in the region of small sizes. In this

thesis we will focus on the limiting case in which the source is concentrated at size 0, see Section 4.2.

Due to their interpretation, the qualitative behaviour of the solutions of equations (1.2.1) and (1.2.4) is interesting for the applications as, when the model parameters are known, it allows to make predictions. On the other hand, when a parameter is not known, comparing the expected long-time behaviour with the available data allows to set an inverse problem that aims at deducing the value of the unknown parameter. See for instance [28, 77].

The aim of this thesis is to study different problems related to the analysis of the above equations, (1.2.1) and (1.2.4). These include analysing the long time behaviour of the solutions of equation (1.2.1) and to prove the existence of self-similar solutions for equation (1.2.4) when the source is concentrated at the origin.

The solutions of equations (1.2.1) and (1.2.4) exhibit non trivial dynamics. In the case of equation (1.2.1) we often deal with two competing mechanisms. This is the case of the cell growth and fission model and of the waning and boosting model. It is, therefore, interesting to understand under which conditions on the model parameters (i.e., the rates at which the processes take place) the two processes balance and to understand what the asymptotic behaviour will be.

In the model of coagulation with source both processes drive the individual sizes towards larger sizes. Still, the solutions of the coagulation equation with source exhibit rich dynamics: there might exist non-equilibrium stationary solutions and self-similar solutions. Understanding the domain of attraction of these two types of solutions is a very difficult problem, partly due to the non-linearity of the coagulation operator  $\mathbb{K}$  and partly due to the uncertainty related to the uniqueness of the solutions of equation (1.2.4), see for instance [68] and [32].

Equations (1.2.4) and (1.2.1) are very different equations and their properties need to be analysed separately, but in both cases we are interested in measure-valued solutions, in other words, we look for solutions that are functions in the time variable and measures in the state variable.

This motivates the following organization of the remaining part of the introduction. In Section 2 we introduce the main concepts that we need to work with measure valued solutions of equations (1.2.1) and (1.2.4). In Section 3 we discuss equation (1.2.1) and in Section 4 we discuss equation (1.2.4).





## 2 A short excursion on equations with measure-valued solutions

In the last years, dynamical systems with measure-valued solutions modelling structured populations have gained much interest, as shown by the increasing number of publications on this subject, see for instance [31] for an overview. In Section 2.1 we motivate the choice of working with measure-valued solutions, in Section 2.2 we describe the spaces of measures that we consider in this thesis. Finally in Section 2.3 we introduce the type of solutions we work with.

### 2.1 Motivations

There are multiple reasons for considering dynamical systems with measure-valued solutions when modelling structured populations. Some motivations come from the interpretation of the dynamical system and are therefore closely connected with the applications. Other motivations are mathematical.

Consider the evolution in time of a population of cells, undergoing fission and growth, originated by a unique cell. In this case the initial distribution has to be modelled via a Dirac measure and, as a consequence, the evolution of the population is, in principle, a measure-valued function of time. See [64] for other examples of Dirac initial data in biological applications.

Additionally, dynamical systems with measure-valued solutions allow to study, in a unified way, the case in which the set of the  $i$ -states is discrete and the case in which we have a continuum of  $i$ -states. This is not only an advantage by itself, but it also provides a useful framework to compare a function-valued solution and its discretization.

The above observation is relevant to understand numerical simulations. For example, working with measure-valued solutions has been crucial to prove the convergence of the Excalator Boxcar Train (EBT), which is a numerical method introduced in 1988 by de Roos [23] to study structured population models. We refer to [13] for the proof of the convergence.

In the mathematical literature of structured population models, we find examples of dynamical systems whose solutions converge, in finite or infinite time, to Dirac measures, see [1, 17, 19, 83] for examples. This suggests that the natural framework to study these systems is the one of measure-valued solutions.

Finally, results from probability theory and stochastic analysis can be applied to study the long term behaviour of the measure-valued solutions of some of the equations we are interested in. When the solution evaluated in time is a

probability measure, we say that the equation is conservative and we can apply these results directly. When, instead, the equation is non-conservative these techniques have to be adapted. For successful examples of the application of results from probability theory to non-conservative equations we refer to the application of Harris' theorem and of the Feynman-Kac representation formula to study the non-conservative growth fragmentation equation [10, 20].

## 2.2 Spaces of measures

We now define the spaces of measures that we are going to consider in this thesis. Let  $A$  be a Borel subset of  $(0, \infty)$ . We endow the set  $A$  with the classical Euclidean norm  $|\cdot|$ . Let  $\mathcal{M}_b(A)$  be the set of the Radon measures with sign on the set  $A$  that are finite, that is the measures  $\mu$  that satisfy  $|\mu(A)| < \infty$ .

The space  $\mathcal{M}_b(A)$  can be endowed with different topologies having different properties. Here we compare two of them: the topology induced by the total variation norm and the weak- $*$  topology.

The total variation norm of a measure  $\mu \in \mathcal{M}_b(A)$  is defined by

$$\|\mu\|_{TV} = \sup_{\Pi} \sum_{i=1}^n |\mu(A^i)|,$$

where the supremum is taken over all the finite measurable partitions  $\Pi := \{A^1, \dots, A^n\}$  of the set  $A$ . A first drawback of the total variation norm is that it does not take into account the underlying Euclidean metric on the set  $A$ . Indeed,

$$\|\delta_x - \delta_y\|_{TV} = 2 \tag{2.2.1}$$

for every  $x, y \in A$  with  $x \neq y$ .

This means that if the Dirac measures  $\delta_x$  and  $\delta_y$  represent two cohorts of cells, one localized at size  $x$  and one at size  $y$ , the distance between the two cohorts is constant and does not depend on the relative distance between the localization of the cohorts in the set  $A$ . This is not suitable from the interpretation point of view as, intuitively, the distance between two cohorts should be proportional to the effort necessary to move one cohort on the other, hence should depend on  $|x - y|$ .

Equality (2.2.1) also implies that the space  $(\mathcal{M}_b(A), \|\cdot\|_{TV})$  is not separable if  $A$  is uncountable. We will see later, in Section 3, that this might bring some complications. Moreover, it is not easy to prove that a subset of  $(\mathcal{M}_b(A), \|\cdot\|_{TV})$  is compact, see for instance [82]. This might be a problem as compactness arguments are very useful to study the long term behaviour of the solution of equation (1.2.1), but also to prove the existence of special type of solutions, for instance self-similar or stationary solutions, of equation (1.2.4).

Despite these shortcomings, the total variation norm often appears in the literature as the space  $(\mathcal{M}_b(A), \|\cdot\|_{TV})$  is a Banach space, but there are alternatives. For instance, if we endow  $\mathcal{M}_b(A)$  with the weak- $*$  topology we can

apply Banach-Alaoglu theorem to prove that a given set is compact. Moreover the space  $\mathcal{M}_b(A)$  endowed with the weak- $*$  topology is separable, [12].

Although also the weak- $*$  topology has at least a drawback: it is not metrizable. But, luckily, subsets of the topology might be metrizable, as we will see soon.

When dealing with structured population models we usually aim at studying the dynamics of quantities that are positive. For instance we are interested in the population birth rate or in the density of individuals in a certain state.

As a result, we can restrict our attention to the cone of the positive measures  $\mathcal{M}_{+,b}(A) \subset \mathcal{M}_b(A)$ . The advantage is that the restriction of the weak- $*$  topology on  $\mathcal{M}_b(A)$  to the set of the positive measures is metrizable (see [12]). The corresponding norm is the flat norm, that we are going to define below.

Before introducing the definition, we fix the notation. Let  $BL(A)$  be the space of the real valued bounded Lipschitz functions. We endow  $BL(A)$  with the norm

$$\|f\|_{BL} := \sup_{x \in A} |f(x)| + L(f)$$

where

$$L(f) := \sup_{x \neq y} \frac{|f(x) - f(y)|}{|x - y|}. \quad (2.2.2)$$

The flat norm of a measure  $\mu \in \mathcal{M}_b(A)$  is defined by

$$\|\mu\|_b = \sup \left\{ \left| \int_A f d\mu \right| : f \in BL(A) \text{ such that } \|f\|_{BL} \leq 1 \right\}.$$

By its definition we can see that, in contrast with the total variation norm, the flat norm takes into account the Euclidean topological structure that we have on the set  $A$ . Indeed, for every  $x, y \in A$  it holds that

$$\|\delta_x - \delta_y\|_b \leq |x - y|.$$

It is interesting to mention, as done in [31], that the flat norm is a generalization of the Wasserstein metric to  $\mathcal{M}_b(A)$ . Indeed, the Wasserstein metric is defined on the space of probability measures  $\mathcal{P}(A)$  as

$$W^1(\mu, \nu) = \sup \left\{ \left| \int_A f d(\mu - \nu) \right| : f : A \rightarrow \mathbb{R} \text{ Lipschitz cont. with } L(f) \leq 1 \right\},$$

where  $L(f)$  is the Lipschitz constant (2.2.2), and it is not well defined if  $\mu(A) \neq \nu(A)$  as, in that case,  $W^1(\mu, \nu) = \infty$ .

We conclude this section by stressing that, as explained above, there is not a univocal way to decide with which topology to endow the space  $\mathcal{M}_b(A)$ . Indeed, this choice depends on the aim. For instance, when we aim at studying the convergence of a sequence of measures, it is convenient to use the flat norm. Instead, if we need to apply theorems that hold only for complete spaces, such as, for instance, Banach fixed point theorem, it is convenient to work with the total variation norm.

## 2.3 Definitions of solutions

Now that we have introduced the setting in which we are going to work, we define the solutions of the dynamical systems we aim at studying. Equation (1.2.1) can be easily adapted to the context of measure-valued solutions since it is an integral equation. Let us see how.

Assume that the *forcing function*  $B_0$  is a measure-valued function of time and that the kernel  $K(a, x, \omega)$  is the rate at which an individual, born  $a$  time ago with state-at-birth  $x$ , produces an individual with state in the set  $\omega \in \mathcal{B}(\Omega_0)$ , where  $\Omega_0$  is a Borel subset of  $(0, \infty)$  and where  $\mathcal{B}(\Omega_0) := \{\omega \cap \Omega_0 : \omega \text{ is a Borel subset of } \mathbb{R}\}$ .

Equation (1.2.1) can be rewritten as

$$B(t, \omega) = \int_0^t \int_{\Omega_0} K(a, y, \omega) B(t-a, dy) da + B_0(t, \omega) \quad (2.3.1)$$

where  $B : [0, \infty) \times \mathcal{B}(\Omega_0) \rightarrow [0, \infty)$  is the unknown.

We assume that  $B_0$  and  $K$  satisfy some natural boundedness and measurability assumptions. These assumptions are precisely stated in [I] and guarantee the existence of a solution  $B$  that is locally bounded in time and that satisfies some minimal measurability assumption that guarantee the integral in equation (2.3.1) to be well defined.

The set of the possible solutions is

$$\mathcal{X} := \left\{ \begin{array}{l} f : [0, \infty) \times \mathcal{B}(\Omega_0) \rightarrow [0, \infty) \text{ s.t. } \forall a \in [0, \infty), f(a, \cdot) \in \mathcal{M}_{+,b}(\Omega_0), \\ \forall \omega \in \mathcal{B}(\Omega_0) \text{ the function } a \mapsto f(a, \omega) \text{ is measurable} \\ \text{and } f(\cdot, \Omega_0) \text{ is locally integrable} \end{array} \right\} \quad (2.3.2)$$

A characterization of the space  $\mathcal{X}$  as a closed subset of a Banach space and of a possible topological structure on it is still missing. More details on this open problem can be found in the Appendix of [I].

A similar straightforward adaptation to measure-valued solutions is, in general, not possible for PDEs and in particular it is not possible for the coagulation equation with source (1.2.4). The simplest option to define measure-valued solutions of equation (1.2.4) is to consider the dual equation. Indeed the Riesz–Markov–Kakutani theorem ensures that  $\mathcal{M}_b((0, \infty)) \cong C_0((0, \infty))^* = C_c((0, \infty))^*$  and, even better we can associate univocally a positive Radon measure to every positive linear functional on  $C_c((0, \infty))$ .

As a consequence, we say that  $f \in C^1([0, \infty), \mathcal{M}_b((0, \infty)))$ , where we endow  $\mathcal{M}_b((0, \infty))$  with the total variation norm to ensure that  $C^1([0, \infty), \mathcal{M}_b((0, \infty)))$  is a Banach space, is a solution of equation (1.2.4), if it satisfies

$$\frac{d}{dt} f(t, \cdot) = (\mathcal{G}f)(t, \cdot)$$

where  $\frac{d}{dt} f(t, \cdot)$  is the derivative of the map  $t \mapsto f(t, \cdot)$  and is identified with a linear operator from  $C_c([0, \infty))$  to  $\mathbb{R}$ .

Similarly,  $\mathcal{G}$  is the linear operator  $\mathcal{G}f(t, \cdot) : C_c((0, \infty)) \rightarrow \mathbb{R}$  defined by

$$\langle (\mathcal{G}f)(t, \cdot), \varphi \rangle := \frac{1}{2} \int_0^\infty \int_0^\infty [\varphi(x+y) - \varphi(x) - \varphi(y)] k(x, y) f(t, dx) f(t, dy). \quad (2.3.3)$$

More precisely, we say that  $f \in C^1([0, \infty), \mathcal{M}_b((0, \infty)))$  is a *strong solution* of (1.2.4) with initial condition  $f(0, \cdot) = f_0$  if the operator  $\mathcal{G}$  is well defined, namely if the integral at the right hand side of (2.3.3) is finite for every  $\varphi$ , and if it satisfies

$$\begin{aligned} \int_0^\infty \varphi(x) \frac{d}{dt} f(t, dx) &= \frac{1}{2} \int_0^\infty \int_0^\infty [\varphi(x+y) - \varphi(x) - \varphi(y)] k(x, y) f(t, dx) f(t, dy) \\ &+ \int_0^\infty \varphi(x) \eta(dx) \end{aligned} \quad (2.3.4)$$

for every test function  $\varphi \in C_c((0, \infty))$  and every time  $t > 0$ .

When we do not want to restrict our attention to solutions  $f$  that are differentiable in time we define the *weak solution* in the sense of measures. We say that  $f \in C((0, \infty), \mathcal{M}_b((0, \infty)))$  is a weak solution of (1.2.4), with initial condition  $f(0, \cdot) = f_0(\cdot)$ , if it satisfies

$$\begin{aligned} \int_0^\infty \varphi(t, x) f(t, dx) &= \int_0^\infty \varphi(0, x) f_0(dx) + \int_0^t \int_0^\infty \partial_s \varphi(s, x) f(s, dx) ds \\ &+ \frac{1}{2} \int_0^t \int_0^\infty \int_0^\infty [\varphi(s, x+y) - \varphi(s, x) - \varphi(s, y)] k(x, y) f(s, dx) f(s, dy) ds \\ &+ \int_0^t \int_0^\infty \varphi(s, x) \eta(dx) ds, \end{aligned}$$

for every  $t > 0$  and every  $\varphi \in C^1([0, \infty), C_c((0, \infty)))$ .



## 3 Linear renewal equation modelling structured populations

In this section we discuss the linear renewal equation (2.3.1) that formalizes the first class of models introduced in Section 1.1. We recall that this class of models is characterized via the following  $i$ -level mechanisms: smooth deterministic development of the  $i$ -state and instantaneous stochastic change of the  $i$ -state, modelled via a birth/death event.

### 3.1 Linear renewal equations: existence of a unique solution and its asymptotic behaviour

The proof of the existence of a unique measure-valued solution for linear renewal equations of the form (1.2.1) is a simple adaptation of the proof of the existence of a unique scalar solution for the classical renewal equation

$$b(t) = \int_0^t b(a)K(t-a)da + b_0(t).$$

The reason is that the proof of the existence of a unique solution of a linear renewal equation relies on algebraic considerations that can be easily adapted to the context of measure-valued solutions. We briefly explain this algebraic approach due to Gripenberg, see [44] for more details.

Equation (2.3.1) can be written as

$$B = \mathcal{L}_K B + B_0 \tag{3.1.1}$$

where  $B_0$ , the forcing function, is a given datum and  $\mathcal{L}_K$  is given by

$$(\mathcal{L}_K \mu)(t, \omega) := \int_0^t \int_{\Omega_0} K(a, x, \omega) \mu(t-a, dx) da$$

where  $\Omega_0$  is a Borel subset of  $(0, \infty)$ .

We denote with  $*$  the following generalization of the classical convolution product between kernels, defined by

$$(K_2 * K_1)(t, x, \omega) := \int_0^t \int_{\Omega_0} K_2(t-s, \xi, \omega) K_1(s, x, d\xi) ds.$$

### 3 Linear renewal equation modelling structured populations

We denote by  $\mathcal{A}$  the family of admissible kernels  $K$  and by  $\mathcal{F}$  the family of admissible forcing functions. We refer to [1] for a rigorous definition of the term "admissible" in the context of measure-valued solutions.

The existence and uniqueness of a solution of equation (3.1.1), belonging to  $\mathcal{F}$ , is guaranteed if  $(\mathcal{A}, *)$  is an associative algebra,  $\mathcal{F}$  is a left-module over  $\mathcal{A}$  and if the kernel  $K$  has a *resolvent*  $R$  that belongs to  $\mathcal{A}$ . That is, if the operator  $R$  defined by  $R := \sum_{n=1}^{\infty} K^{*n}$  with  $K^{*1} = K$  and  $K^{*n} = K^{*(n-1)} * K$  for every  $n \geq 2$  belongs to  $\mathcal{A}$ . Moreover, the solution  $B$  of equation (3.1.1) has the following form

$$B = \mathcal{L}_R B_0 + B_0.$$

We refer to [44, pp. 233-234] for the details of the proofs.

Once the existence and uniqueness of a solution is established, we aim at studying its asymptotic behaviour. Results on the asymptotic behaviour of the measure-valued solutions of renewal equations on the basis of assumptions on the kernel  $K$  can be found in [82], but are lacking for the model examples studied in this section.

In the abstract setting important results on the long term behaviour of the solutions of renewal equations have been proven by Gripenberg in [43]. To understand and apply these results we have to rewrite equation (1.2.1) in the following abstract form:

$$B(t) = \int_0^t \mathbf{K}(a)B(t-a)da + B_0(t). \quad (3.1.2)$$

where  $\mathbf{K} : [0, \infty) \rightarrow \mathcal{L}(X)$  where  $\mathcal{L}(X)$  is the space of the linear and bounded operators from the Banach space  $X$  to itself and  $B_0 : [0, \infty) \rightarrow X$ . To keep the notation lighter, we are denoting with  $B$  both the function from  $[0, \infty) \times \Omega_0$  to  $[0, \infty)$  introduced in Section 2.3 and the function  $t \mapsto B(t, \cdot)$ .

The integral on the right hand side of equation (3.1.2) is a Bochner integral, i.e., the analogue of the Lebesgue integral for functions between Banach spaces. We refer to [78] for the definition of Bochner integral and of Bochner measurability. When we consider measure-valued solutions the integral at the right-hand side of (3.1.2) is well defined if we endow the space  $\mathcal{M}_b(\Omega_0)$  with a norm which makes it a Banach space: the total variation norm.

Additionally, we have to provide measurability assumptions on  $B_0$  and  $\mathbf{K}$  that guarantee that the integral is well defined. The minimal assumptions are that  $a \mapsto \mathbf{K}(a)f$  is Bochner measurable, for every  $f \in \mathcal{M}_b(\Omega_0)$  and that  $a \mapsto B_0(a)$  is Bochner measurable. Finally, we have to ask boundedness conditions on  $\mathbf{K}$  and  $B_0$  that guarantee that the integral is finite.

As a consequence of these assumptions we deduce that there exists a unique solution  $B$  of equation (3.1.2) such that  $B : [0, \infty) \rightarrow \mathcal{M}_b(\Omega_0)$  is Bochner measurable, satisfies the same boundedness condition of  $B_0$ , and can be expressed as a function of the forcing function  $B_0$  and of the resolvent  $\mathbf{R}$  corresponding



### 3.1 Linear renewal equations: existence of a unique solution and its asymptotic behaviour

to the kernel  $\mathbf{K}$ . More importantly, we can apply the results presented in the paper to analyse the asymptotic behaviour of the solution.

The main result of [43] is indeed a theorem that discusses the behaviour of the resolvent. Namely, Theorem 2 in [43] reads as follows. Let  $X$  be a Banach space.

1. If  $a \mapsto \mathbf{K}(a)$  is measurable with respect to the topology induced by the operator norm on  $\mathcal{L}(X)$ ,
2. and if there exists a  $\rho \in \mathbb{R}$  such that the kernel  $\mathbf{K}$  is controlled by an exponential, in the sense that  $\int_0^\infty e^{-\rho a} \|\mathbf{K}(a)\|_X da < \infty$ , and such that

$$I - \int_0^\infty e^{-\lambda a} \mathbf{K}(a) da \quad (3.1.3)$$

is invertible for every  $\lambda \in \mathbb{C}$  with  $\Re \lambda > \rho$ ,

then

$$\int_0^\infty e^{-\rho a} \|\mathbf{R}(a)\|_X da < \infty. \quad (3.1.4)$$

Thanks to the expression of  $B$  as a function of the initial datum and of the resolvent  $\mathbf{R}$ , the asymptotic behaviour of  $B$  can be deduced using (3.1.4). To this end it would be necessary to adapt the reasoning used in [44, Section 7] and in [II, Section 4.6] to the context of measure-valued solutions.

The assumptions of Theorem 2 in [43] are, in practise, difficult to verify, when we deal with measure-valued solutions. First of all, we are forced to work with  $(\mathcal{M}_b(\Omega_0), \|\cdot\|_{TV})$  which is not separable, see Section 2.2. As a result, we cannot prove that the map  $a \mapsto \mathbf{K}(a)f$  is Bochner measurable only by proving that it is weakly measurable as it is possible to do, thanks to Pettis measurability theorem, [78], in the case of a separable Banach spaces.

Moreover, to be able to apply Theorem 2 in [43] we need to have that the map  $a \mapsto \mathbf{K}(a)$  is measurable with respect to the topology induced by the operator norm on  $\mathcal{L}(\mathcal{M}_b(\Omega_0))$ . This is a stronger property than pointwise Bochner measurability and requires stronger assumptions on the model parameters.

To study the invertibility of (3.1.3) we need to study the spectrum of the operator  $\int_0^\infty e^{-\lambda a} \mathbf{K}(a) da$  for every  $\lambda \in \mathbb{C}$  for which the Laplace transform of  $\mathbf{K}$  is finite. To this end, working with a compact operator would be extremely helpful, but as explained in Section 2.2 the compactness of an operator is very difficult to prove when working with the total variation norm.

For all these reasons in the papers [I] and [II] we do not follow the approach designed by Gripenberg. Instead, we provide assumptions on the kernel  $K$  that allow to deduce the asymptotic behaviour of the solution of (2.3.1). Moreover, we illustrate how to check the assumptions via some examples.

We conclude this section by explaining the most common, asymptotic behaviour of the solution of equation (1.2.1). If we exclude pathological cases, that sometimes take place, see for instance Section 3.3.1, the expected behaviour is asynchronous exponential growth, decline or convergence to a stable distribution.

In other words, the typical behaviour is  $B(t, \omega) \sim e^{rt} \Psi_r(\omega)$  as time tends to infinity where  $r$  is called Malthusian parameter and  $\Psi_r$  stable distribution.

We speak about asynchronous behaviour because the possible synchronization of the initial data, for instance in the case of Dirac measures initial data, is lost for large times. This loss of information does not necessarily imply the convergence of the population to a steady state, but is rather the consequence of a reorganization of the states distribution towards the stable distribution  $\Psi_r$  while the population keeps growing or declining deterministically in time. We refer to [47] for a nice explanation of this process.

## 3.2 Comparison with partial differential equations

The models considered in this section can be formalized also via PDEs. The PDE typically consists of three terms. A transport term, representing the deterministic development, and birth/death terms due to birth/death events or jumps in the  $i$ -states. The connection between the two formulations, via PDEs and REs, is drawn in [6, 15] when  $\Omega_0 = \{x_0\}$ .

Both approaches are valuable methods to study physiologically structured population models. The focus of this thesis is, for the class of models presented in this section, on the first approach and in this section we briefly explain the motivations behind this choice.

When considering PDEs of transport type with measure-valued solutions it is in general not possible to prove constructively the existence and uniqueness of a solution. The reason is that the definition of strong solutions for the PDEs has to be adapted to the context of measure-valued solutions. Depending on the techniques applied to study the asymptotic behaviour the solution can be defined in different ways, see for instance [18, 24]. The simplest way is to define strong solutions in a dual sense, as was done for the coagulation equation in Section 2.3.

To be able to speak about strong solutions for PDEs we need to ask for the differentiability of the solutions in the time variable. In some cases, see for instance [II], the solutions are not differentiable in the time variable. Hence weak solutions, in the sense of measures, have to be considered.

As explained in Section 2.3, the definition of function-valued solutions of renewal equations can be adapted to the case of measure-valued solutions. Moreover, we have a constructive proof of existence and uniqueness of solutions that does not require any additional regularity assumption on the solution. In this sense working with REs allows to remain closer to the interpretation and avoids working with dual equations and weak solutions.

Despite these observations, the theory of PDEs is more developed than the theory available for REs when the aim is to study the asymptotic behaviour. The intent of the papers [I, II] is to contribute towards filling this gap, so that RE could be more applicable in practise.

### 3.3 Model examples

In this subsection we discuss two examples of models that can be studied in the framework of the papers [I] and [II]: the growth and fission model and the waning and boosting model.

#### 3.3.1 Growth and fission

Consider a population of cells growing at a size dependent rate  $g$ , dividing at a size dependent rate  $\Lambda$  and dying at a size dependent rate  $\mu$ . Does the population decline or grow exponentially in time? How does the distribution of the population along the structuring variable evolve in time?

We focus here on the case of a population of mammal cells as done in [7]. Therefore, we assume that the  $i$ -state is size, i.e., mass. Although we have in mind this type of population, we stress that the model of growth and fission can be adapted to also describe plasmid reproduction (growth) and segregation (fission) [81], one single species reproducing by fission [79], prion lengthening and depolymerization, [16, 39] and many other processes.

This type of models is characterized by two competing processes: growth and fission. The total mass of the population increases in time due to the individual growth and due to the fact that fission conserves the mass. Also the number of individuals is, in general, not constant in time.

This model fits into the class of models described in Section 1.1. In [I] and [II] we prove, under different assumptions on the model parameters, asynchronous exponential growth for the population birth rate, that in this case is the rate at which cells appear in the system due to the fission of their mother. In [II], we prove asynchronous exponential growth also for the population distribution.

In [I] we assume that cells divide only after having reached a certain size, called renewal point. This assumption is removed in [II] where we only ask that, due to a combination of growth and fission, a regularizing effect takes place.

We prove asynchronous exponential growth for the population birth rate under conditions on the growth rate and on the fission rate that guarantee that shattering (i.e., escape of mass towards zero) and gelation (i.e. escape of mass towards infinity) do not take place. We refer to [I] and [II] for precise assumptions. We study the asymptotic behaviour of the population birth rate both for the case of fission into unequal pieces and for the case of fission into equal pieces. The latter case requires non-degeneracy assumptions on the growth rate  $g$  that avoid synchronization. We refer to [8, 63] for an example of synchronization when it is assumed that  $g$  does not satisfy the non-degeneracy assumptions.

As anticipated, we study this problem by analysing the renewal equation. But there are other techniques for analysing the corresponding PDE formalisation of the model. Among these methods we find relative entropy [24], Feynman-Kac formula [10], Harris' theorem [5].

### 3.3.2 Waning and boosting of the immunity level

Imagine a population of individuals (human or animals) susceptible to infection from a pathogen. Each individual is born with a certain immunity level against the pathogen. It is known, [25], that the immunity level does not remain constant in time. Instead, it wains and it boosts upon encounters with the pathogen.

How does the population immunity evolve in time? This question is very important to predict outbreaks and to plan vaccination campaigns. To answer this question, a structured population model has been introduced in [25].

One of the main assumptions of the model is that boosting is instantaneous, takes place at a constant rate and it is not a consequence of inter-individuals interactions. The individual level mechanisms that drive the dynamics are deterministic development, waning of the immunity level, and jumps from one immunity level to another one due to boosting.

The dynamics of this model is similar to the one of the growth and fission model, but the main difference is that, in this case the population number remains constant in time. Since we have to do with two competing mechanisms: waning and boosting, the question is, what assumptions do we need on the model parameters to see convergence to a stable distribution?

In [I] and [II] we discuss different assumptions on the boosting function, on the boosting rate and on the waning rate that guarantee convergence to a steady state. Namely in [I] we assume that the boosting function and the boosting rate have a very special shape that ensures that the kernel  $K$  is factorizable.

Instead, in [II] we consider constant boosting rate and a boosting function which is piecewise monotone. Additionally, we assume a condition on the growth rate and on the boosting function that guarantees that the kernel is regularizing.

## 4 Coagulation models

This section is devoted to the coagulation equation with source, equation (1.2.4), considered in [III]. Since equation (1.2.4) is an extension of the classical coagulation equation we start this section presenting some of the main properties of the solutions of the coagulation equation. This is done in Section 4.1. In the following section, Section 4.2, we translate the concepts introduced in Section 4.1 to the coagulation equation with source. In Section 4.3 we introduce the class of kernels on which we focus and we present some results on the coagulation equation with source with respect to this class of kernels.

### 4.1 Smoluchowski's coagulation equation

The literature on coagulation equations is vast and we do not aim at covering all the known results here. Instead, we give an overview useful to introduce the coagulation equations with source.

The first question is: can we model with a deterministic equation a population evolving due to coagulation, hence evolving according to a stochastic coagulation process? For the solvable kernels  $k(x, y) = 1$ ,  $k(x, y) = x + y$  and  $k(x, y) = xy$  it has been proven that the empirical measure corresponding to the stochastic process modelling the population evolution converges, as the size of the population tends to infinity, to a deterministic measure. Additionally, it has been proven that this measure satisfies the Smoluchowski's coagulation equation. See for instance [9] for an overview on these results. Similar results have been proven by Norris in [68] for kernels satisfying

$$k(x, y) \leq \varphi(x)\varphi(y) \text{ and } \varphi^{-1}(x)\varphi^{-1}(y)k(x, y) \rightarrow 0 \text{ as } x \rightarrow \infty, y \rightarrow \infty \quad (4.1.1)$$

for some continuous sublinear function  $\varphi$ . A rigorous derivation is still an open problem for other classes of kernels, but there are empirical arguments in this direction, see for instance [38].

Since during coagulation mass is conserved and the sum of the sizes of the coalescing particles is equal to the size of the newborn particle, it seems very natural to expect that the total mass of the system is constant in time. Surprisingly, this is not always the case and mass conservation is a property that depend on the shape of the coagulation kernel.

We explain the loss of mass conservation following the reasoning presented by Dubovskii in [29]. Considering, formally, the test function  $x \mapsto x\chi_{[0,z]}(x)$  in

#### 4 Coagulation models

equation (2.3.4) we deduce that

$$\frac{d}{dt} \int_0^z x f(t, x) dx = -J_{f(t, \cdot)}(z) \quad (4.1.2)$$

where  $J_{f(t, \cdot)}$  is the flux of mass from sizes smaller than  $z$  to sizes larger than  $z$ , and is defined by

$$J_\phi(z) := \int_0^z \int_{z-x}^\infty x k(x, y) \phi(x) \phi(y) dy dx.$$

Since  $J_\phi$  is positive, passing to the limit as  $z \rightarrow \infty$  in equality (4.1.2) we easily see that

$$\frac{d}{dt} \int_0^\infty x f(t, x) dx \leq 0.$$

More precisely, if

$$\int_0^\infty \int_0^\infty x k(x, y) f(t, x) dx f(t, y) dy < \infty,$$

then  $\frac{d}{dt} \int_0^\infty x f(t, x) dx = 0$  and the total mass remains constant in time.

In contrast, if

$$\int_0^\infty \int_0^\infty x k(x, y) f(t, x) dx f(t, y) dy dx = \infty$$

there might exist a  $\bar{t} > 0$  such that  $\frac{d}{dt} \int_0^\infty x f(t, x) dx|_{\bar{t}} < 0$ , in other words the total mass in the system might decrease in time. A simple example for which this happens is the product coagulation kernel:  $k(x, y) = xy$ , see for instance [2]. Heuristically, we can say that the total mass of the system decreases in time as mass escapes towards infinity and a particle of infinite size is formed in finite time. This phenomenon is called *gelation* and in some contexts it has been interpreted as a phase transition [2].

Another important question is the existence and uniqueness of (time dependent) solutions. Explicit solutions of the coagulation equation have been obtained, via Laplace transform methods, for initial conditions concentrated in the region of small sizes, for the solvable kernels (constant  $k = 1$ ,  $k(x, y) = x + y$  and  $k(x, y) = xy$  see respectively [74], [42] and [61]). These results have been extended in [62] where the existence of a unique solution for the solvable kernels has been proven for more general initial conditions.

Existence of time dependent solutions has been proven also for more general types of kernels. Some of the main results in this direction are the ones presented in [68], where the existence of a time dependent solution of the coagulation equation is proven for a class of kernels satisfying (4.1.1). The importance of the paper [68] lies not only in the results presented, but also in the strategy adopted to prove the existence of a solution: approximating the solution of equation (1.2.2) with a sequence of solutions of a corresponding sequence of truncated equations.

#### 4.1 Smoluchowski's coagulation equation

Except for the solvable kernels, proving that the coagulation equation has a unique solution or not is a very challenging, and still open, problem. This is not only due to lack of techniques, but also due to the fact there are examples of non-uniqueness for special classes of kernels, see [68] for an example.

An important class of coagulation kernels is the class of *homogeneous kernels*, namely kernels that satisfy

$$k(ax, ay) = a^\gamma k(x, y) \quad x, y, a > 0, \quad (4.1.3)$$

for a parameter  $\gamma$ , called *homogeneity* of the kernel. In this thesis we always assume that  $\gamma < 1$ . This condition is a necessary condition to guarantee that the kernel  $k$  does not give rise to gelation, [22].

Homogenous kernels are important because a dimensional analysis, together with numerical evidence, [38], suggests that self-similar solutions of the form

$$f(t, x) = s(t)^\alpha \Phi(y) \quad y = \frac{x}{s(t)}, \quad (4.1.4)$$

for suitable functions  $s$  and  $\Phi$  and  $\alpha \in \mathbb{R}$ , exist when the kernel is homogeneous. In this thesis we look for self-similar solutions of constant finite mass, hence we are interested in the case in which  $\alpha = 2$ :

$$f(t, x) = \frac{1}{s(t)^2} \Phi(y) \quad y = \frac{x}{s(t)}. \quad (4.1.5)$$

The reason why  $\alpha = 2$  is that this condition guarantees that the mass remains constant

$$\int_0^\infty x f(t, x) dx = \int_0^\infty \frac{x}{s(t)^2} \Phi\left(\frac{x}{s(t)}\right) dx = \int_0^\infty y \Phi(y) dy.$$

Substituting the ansatz (4.1.5) in (1.2.2) we deduce that  $s(t)$  behaves as  $t^{\frac{1}{1-\gamma}}$  while  $\Phi$  is the solution of

$$c_1 \Phi(x) + c_2 x \partial_x \Phi(x) = \mathbb{K}[\Phi](x) \quad (4.1.6)$$

for suitable constants  $c_1, c_2 > 0$ . Proving the existence of self-similar solutions, is therefore equivalent to prove that there exists a solution of equation (4.1.6). The function  $\Phi$  in (4.1.4) is called *self-similar profile* and its shape determines the shape of the self-similar solution.

It is, in general, very difficult to prove that self-similar solutions are attractive even if, in some cases, there is numerical and experimental evidence of that. See [22, 38] for an example. A complete description of the domain of attraction of self-similar solutions has been proven in [62] for the solvable kernels, but it is an open problem for other kernels.

## 4.2 Coagulation equation with source

In this section we present some known results regarding an extension of the coagulation equation: the coagulation equation with a time independent source of finite mass. This equation is analysed in [III].

The motivation to consider this equation comes from atmospheric science applications, where it is common to deal with a population of particles of primary type (originated by a source) or secondary type (originated from the interaction of particles), see for instance [52].

One of the main differences between the coagulation equation and the coagulation equation with source is that in the latter case we do not expect the solutions to have constant mass due to the influx of particles in the system. Yet we can speak about gelation as we will show below.

Repeating the reasoning presented above for the coagulation equation we integrate against the test function  $x\chi_{[0,z]}(x)$  equation (1.2.4) and deduce that

$$\frac{d}{dt} \int_0^z xf(t,x)dx = -J_{f(t,\cdot)}(z) + \int_0^z x\eta(dx). \quad (4.2.1)$$

Since the source has finite mass  $\int_0^\infty x\eta(dx) < \infty$  we can pass to the limit as  $z \rightarrow \infty$  in equality (4.1.2) and see that

$$\frac{d}{dt} \int_0^\infty xf(t,x)dx \leq \int_0^\infty x\eta(dx).$$

As a consequence, in the non gelation regime, i.e., when

$$\int_0^\infty \int_0^\infty xk(x,y)f(t,x)f(t,y)dxdy < \infty,$$

we have that

$$\frac{d}{dt} \int_0^\infty xf(t,x)dx = \int_0^\infty x\eta(dx)$$

and the total mass grows linearly in time. In contrast, in the gelation regime, the mass grows less than linearly in time as mass is lost at infinity.

The existence and uniqueness of time dependent solutions of equation (1.2.4) has been proven by Dubovskii in [29] for the constant kernel. On the other hand, the existence of a time dependent solution for equation (1.2.4) has been proven in [32] for kernels of the form  $k(x,y) = x^ay^b + x^by^a$  with  $a, b \in [-1, 1]$ ,  $0 \leq a + b < 1$  and  $a > b - 1$ .

An important feature that distinguishes equation (1.2.4) from equation (1.2.2) is the existence of stationary solutions. Indeed, thanks to the presence of the source, we can expect equation (1.2.4) to have stationary solutions. These solutions are non-equilibrium stationary solutions because they do not correspond to an equilibrium state of the system as there is a constant flux of mass from small sizes toward large sizes.



The existence of a unique and attractive stationary solution has been proven in [29] for the constant kernel and has been studied in [22] for more general classes of kernels via a combination of numerics, heuristic and analytic methods, but a complete picture of the dynamics is available only for the constant coagulation kernel.

Another difference between equation (1.2.2) and equation (1.2.4) is that for the latter we do not expect self-similar solutions to exist due to the presence of the source. We can indeed easily see that it is not possible to obtain a time independent equation for the self-similar profile  $\Phi$  by substituting the self-similar ansatz (4.1.4) in (1.2.4).

The only case in which it is possible to expect the existence of self-similar solutions is the limiting case in which the source is concentrated at the origin. In this case equation (1.2.4) can be formally written as

$$\partial_t x f(t, x) = x \mathbb{K}[f](t, x) + \delta_0(x), \quad (4.2.2)$$

where the term  $\delta_0$  has to be interpreted in the proper manner, we refer to [III] for that.

Even if we do not expect self-similar solutions for equation (1.2.4) when the support of the source has positive measure, there is numerical and experimental evidence, see for instance [22], that the solution of (1.2.4) behave, for large times, as the self-similar solutions of equation (4.2.2). Therefore, proving the existence of a self-similar solution for equation (4.2.2) and analysing its behaviour is crucial to gain information on the asymptotic behaviour of equation (1.2.4).

Now we introduce the class of kernels on which we are interested in this work.

### 4.3 Coagulation of atmospheric aerosols

Atmospheric aerosols are suspension of particles in the atmosphere. They directly affect climate since they scatter and reflect sunlight. Moreover, aerosols are one of the main factors to determine the air quality and therefore influence human health, [84].

The effect of atmospheric aerosols on climate and on human health depends on their sizes and on their composition. In this thesis we focus only on the size of the aerosols and assume that they are composed of a unique chemical element. We refer to [35, 54] for mathematical models of multicomponent coagulation.

The size distribution of atmospheric aerosols evolves due to various complex mechanisms among which we find coagulation, fission, particle injection via a source and deposition, see [38] for an exhaustive explanation. In this thesis we focus on coagulation and on injection.

As already mentioned, the kernel summarizes the underlying mechanisms behind coagulation. The most important atmospheric coagulation kernels, that will be introduced below, satisfy the following assumption

$$c_1 \left( x^{\gamma+\lambda} y^{-\lambda} + y^{\gamma+\lambda} x^{-\lambda} \right) \leq k(x, y) \leq c_2 \left( x^{\gamma+\lambda} y^{-\lambda} + y^{\gamma+\lambda} x^{-\lambda} \right) \quad (4.3.1)$$

## 4 Coagulation models

for  $c_1, c_2 > 0$  and are homogenous of homogeneity  $\gamma < 1$ .

As anticipated above aerosols are atmospheric suspensions of particles in air. From a modelling point of view then we deal with a population of coalescing particles embedded in a background of non-coalescing air particles.

We now list the main assumptions on the microscopical model behind coagulation of atmospheric aerosols:

- coalescing particles are spheres and move in a 3-dimensional isotropic space;
- $n$ -particle collisions happen with probability equal to zero when  $n > 2$ ;
- collisions between air and coalescing particles are more frequent than collisions between coalescing particles;
- coalescing particles elastically collide with air particles.

Considering the above assumptions on the interactions between coalescing particles and air particles two kernels have been empirically derived from kinetic theory, [38]: the Brownian and the ballistic (aka. free molecular) kernels. The Brownian kernel is

$$k(x, y) = \left(x^{-1/3} + y^{-1/3}\right) \left(x^{1/3} + y^{1/3}\right),$$

while the ballistic kernel is equal to

$$k(x, y) = \left(x^{1/3} + y^{1/3}\right)^2 \left(x^{-1} + y^{-1}\right)^{1/2}.$$

These kernels correspond to two different regimes that depend on the *mean free path*, i.e., the average distance covered by a particle before colliding with an air particle. When the mean free path is smaller than the average size of the coalescing particles, the regime is Brownian. The word Brownian here refers to the type of resulting dynamic: the coalescing particles in this regime move according to Brownian motion.

If, instead, the mean free path is larger than the average size of the coalescing particles, then we are in the free molecular regime (or ballistic regime). The resulting type of dynamic of the coalescing particles is free molecular motion.

The coagulation regimes are not intrinsic properties of the population of aerosol that we consider. Indeed, the relation between the mean free path and the average size of the particles in a system changes in time due to coagulation. Although, the derivation of an interpolating kernel, covering both the ballistic, the Brownian and the transition regimes is still an open problem.

Both the Brownian and the free molecular kernels satisfy the bounds (4.3.1). In particular, the ballistic kernel satisfies (4.3.1) with  $\gamma = 1/6$  and  $\lambda = 1/2$ , while the Brownian kernel satisfies (4.3.1) with  $\gamma = 0$  and  $\lambda = 1/3$  and both

### 4.3 Coagulation of atmospheric aerosols

the kernels are homogeneous with homogeneity parameter  $\gamma = 1/6$  and  $\gamma = 0$  respectively.

We now give insights on the interpretation of  $\gamma + 2\lambda$  and  $\gamma$ . We already know that  $\gamma$  is the homogeneity, hence

$$k(x, x) = x^\gamma k(1, 1).$$

In other words,  $\gamma$  measures the strength of the interaction of particles of similar sizes. On the contrary,

$$c_1 \left( x^{\gamma+2\lambda} + x^{-(\gamma+2\lambda)} \right) \leq k \left( x, \frac{1}{x} \right) \leq \left( x^{\gamma+2\lambda} + x^{-(\gamma+2\lambda)} \right)$$

hence  $\gamma + 2\lambda$  measures the interaction between particles of very different sizes. It has been proven in [36] that if  $|\gamma + 2\lambda| < 1$  a steady state of (1.2.4) exists, while a stationary solution does not exist when  $|\gamma + 2\lambda| \geq 1$ . It is easy to see that the Brownian kernel belongs to the first class of kernels while the ballistic kernel belongs to the second class.

The crucial observation that leads to the existence of a stationary solution  $f$ , if  $|\gamma+2\lambda| < 1$ , is that the contribution to the flux  $J_f$  due to the interaction between particles of very different sizes is negligible compared to the contribution to  $J_f$  due to the interaction of particles of comparable sizes. This turns out to be false if  $|\gamma + 2\lambda| \geq 1$ , hence we expect that the reason why stationary solutions do not exist is that, in this case, the kernel strongly promotes the interaction of particles of very different sizes.

In [III] we focus on a class of kernels  $k$  satisfying (4.3.1) for parameters  $\gamma$  and  $\lambda$  satisfying  $|\gamma + 2\lambda| < 1$  and  $\gamma < 1$ . The condition  $\gamma < 1$  guarantees that the kernel is non-gelling, while the assumption  $|\gamma + 2\lambda| < 1$  guarantees the existence of a steady state for equation (1.2.4).



## 5 Conclusions and open problems

The common aim of the three papers [I, II, III] is to analyse the asymptotic behaviour of the solutions of equations arising from different types of structured population models. We prove asynchronous exponential growth for the solution of the linear renewal equations considered in Section 3, while we prove the existence of special class of solutions of equation (4.2.2) that are only expected to describe the asymptotic behaviour of the solutions of (1.2.4).

In [I, II], we analyse equation (2.3.1) under different assumptions on the kernel  $K$ . As already anticipated in Section 2.3, the renewal formulation is very natural when dealing with measure-valued solutions, but applicable results to analyse the asymptotic behaviour of the two models are lacking. The aim of these two papers is to contribute filling this gap, by providing applicable techniques to study the asymptotic behaviour of (2.3.1) under different assumptions on the kernel.

A natural extension of the models studied in [I, II] is to consider a population embedded into an environment. As explained in Section 1.1, this leads to a feedback loop interaction between the environment and the population: as the population changes the environment changes and, as the environment changes, the population changes. Coupling equation (2.3.1) with an equation for the environment we obtain a system of the form

$$B(t, \omega) = \int_0^\infty \int_{\Omega_0} B(t-a, d\xi) K(a, \xi, E_t, E(t), \omega) da \quad (5.0.1)$$

$$\frac{d}{dt} E(t) = f(E(t)) - \int_0^\infty \int_{\Omega_0} B(t-a, d\xi) c(a, \xi, E_t, E(t)) da \quad (5.0.2)$$

where the kernel  $K$  now depends also on the history of the environment (i.e. it depends on all the values of  $E$  before time  $t$ ), where  $\frac{dE(t)}{dt} = f(E(t))$  is the evolution of the environment in the absence of the population, while  $c(a, \xi, E_t, E(t))$  measures the influence on the environment of an individual born with state  $\xi$ , that at time  $t$  has age  $a$ . Notice that equation (5.0.1) is the translational invariant reformulation of equation (2.3.1) and we assume that the population birth rate  $B(t, \cdot)$  for negative times  $t$  is a known data. Even though this system of equations is non-linear we expect the factorization assumption and the regularization assumption on  $K$ , presented in [I, II], to drastically simplify the study of the asymptotic behaviour of  $B$  and of  $E$ .

In [III] we prove the existence of a self-similar solution for a coagulation equation with a constant influx of particles from the origin, namely for equation (4.2.2), and with homogeneous kernels satisfying (4.3.1) with  $\gamma < 1$  and  $|\gamma + 2\lambda| < 1$ .

## 5 Conclusions and open problems

Additionally, we prove that the self-similar profile  $\Phi$  is estimated from above and below by  $x^{-\frac{(\gamma+3)}{2}}$  as  $x \rightarrow 0$ , while it decays at least exponentially as  $x \rightarrow \infty$ . These regularity results agree with the numerical simulations performed in [22]. The reason why this result is interesting is that it is numerically observed in [22] that these self-similar solutions describe the long time behaviour of the solutions of equation (1.2.4). Hence the result we deduce supports the study presented in [22] and opens the question whether the self-similar solutions are attractive or not and how to characterize the domain of attraction.

In [III, Section 2.3] we present a formal argument which shows that, if equation (4.2.2) has a unique solution, then for certain initial conditions, the solutions of equation (1.2.4) approach the self-similar solution of equation (4.2.2) as time goes to infinity. Proving the uniqueness of the solution of equation (4.2.2) is a very difficult open problem and there are no available results in this direction for the class of kernels we are interested in. On the other hand, there are results on the uniqueness of the self-similar solutions of the coagulation equation for special classes of kernels. See [67] for results on the uniqueness of the self-similar solution when the kernel  $k$  is a perturbation of the constant kernels and [56] for results on kernels satisfying (4.3.1) with  $c_1 = c_2 = 1$  and with  $\gamma + 2\lambda = 0$ . It would be interesting to investigate if these uniqueness results for the self-similar solutions could be adapted to the case of the coagulation equation with source. Finally, as a continuation of [III], it would be interesting to study the existence of self-similar solutions of equation (4.2.2) under the parameter assumption  $|\gamma + 2\lambda| \geq 1$  and the non-gelling condition  $\gamma < 1$ ,  $\gamma + \lambda < 1$  and  $-\lambda$ . Notice that the ballistic kernel, relevant for the atmospheric science applications, belongs to the regime  $\gamma < 1$ ,  $\gamma + \lambda < 1$  and  $|\gamma + 2\lambda| \geq 1$ . The assumption  $|\gamma + 2\lambda| \geq 1$  is the complementary condition to the one considered in [III]. Since we know from [36] that under these conditions a stationary solution does not exist, investigating the existence of a self-similar solutions and its properties might give insights on the asymptotic behaviour of the solution of equation (4.2.2).

## 6 Summary of the research articles

### 6.1 Article [I]

We start with a warning: to make the notation of the introduction uniform we change the notation used in [I]. In particular, here  $B$  is the solution of equation (2.3.1) (and corresponds to  $b$  in the notation used in [I]) and  $B_r$  is the cumulative crossing number defined by (6.1.3) (it corresponds to  $B$  in the notation adopted in [I]) the kernel is denoted by  $K$  while in [I] is denoted by  $k$ .

In [I] we prove asynchronous exponential growth for the solution of equation (2.3.1) under a factorization assumption on the kernel  $K$ . Namely, we assume that the kernel  $K$  satisfies

$$K(a, \xi, \omega) = \int_{[0, a]} \mu_L(d\sigma, \xi) M(a - \sigma, \omega). \quad (6.1.1)$$

where  $M$  and  $L$  are suitable functions and  $\mu_L(\cdot, \xi)$  is the Lebesgue-Stieltjes measure corresponding to  $L(\cdot, \xi)$ .

If we assume that there exists a state, called *renewal point*, that each individual must pass before it can possibly produce a new individual, then the kernel satisfies (6.1.1). The probability of an individual, born with size  $\xi$ , passing the renewal state before it has reached age  $\sigma$  is  $L(\sigma, \xi)$ , while the rate at which an individual, who passed the renewal state  $\tau$  time units ago, produces offspring in the set  $\omega$  is  $M(\tau, \omega)$ .

In the biological examples we are interested in, the function  $L(\cdot, \xi)$  is typically equal to 0 if  $\sigma < h(\xi)$ , where  $h(\xi)$  is the time that it takes for an individual with state at birth  $\xi$  to reach the renewal point. Hence

$$L(\sigma, \xi) := f(\xi)H(\sigma - h(\xi)) \quad (6.1.2)$$

where  $f$  and  $h$  are suitable functions with  $0 \leq f \leq 1$  and  $H$  is the Heaviside function. Formula (6.1.2) clarifies the reason for our characterisation of  $L$  as a cumulative quantity: its derivative is often a measure with a discrete component and hence we repress it with  $\mu_L(\cdot, \xi)$  in the factorization assumption (6.1.1).

Substituting the kernel (6.1.1) in the renewal equation (2.3.1), we deduce that the scalar function  $B_r$  defined by

$$\begin{aligned} B_r(t) &:= \int_0^t \int_{\Omega_0} B(t - \sigma, d\xi) L(\sigma, \xi) d\sigma, \quad t > 0, \\ B_r(0) &:= 0, \end{aligned} \quad (6.1.3)$$

is the unique solution of the one dimensional renewal equation

$$B_r(t) = \int_0^t \mu_{B_r}(d\tau) K_1(t - \tau) + z(t) \quad t > 0. \quad (6.1.4)$$

Also in this case  $\mu_{B_r}$  is the Lebesgue-Stieltjes measure corresponding to  $B_r$  and  $K_1, z$  are functions that depend on the forcing function  $B_0$  and on the kernel components  $L$  and  $M$ .

We study the asymptotic behaviour of the solution  $B_r$  of equation (6.1.4) by applying the classical Feller's Renewal Theorem for scalar renewal equations. This theorem can be applied only if the kernel  $K_1$  is non-arithmetic and non-decreasing. This leads to additional non-degeneracy assumptions on the kernel components  $M$  and  $L$ .

From the asymptotic behaviour of  $B_r$  we deduce the long term behaviour of  $B$  using its expression as a function of  $B_r$ , obtained via integral manipulations of (1.2.1),

$$B(t, \omega) = \int_0^t \mu_{B_r}(d\sigma) M(t - \sigma, \omega) + f_0(t, \omega), \quad t > 0, \quad \omega \in \mathcal{B}(\Omega_0) \quad (6.1.5)$$

where  $f_0$  is a function of  $B_0$  and of the kernel components.

The main statement of the paper can be formally rewritten as follows. Assume the kernel  $K$  to be factorizable and assume the kernel components  $L$  and  $M$  be such that  $K_1$  is non-arithmetic and non-decreasing. Then there exists a constant  $r \in \mathbb{R}$  and a constant  $C_r > 0$  such that

$$\lim_{t \rightarrow \infty} \|e^{-rt} B(t, \cdot) - rC_r \int_0^\infty e^{-ra} M(a, \cdot) da\| = 0.$$

with  $\|\cdot\| = \|\cdot\|_{TV} = \|\cdot\|_b$ .

In the paper we present examples of kernels that appear in various applications and that satisfy the factorization assumption with respect to kernel components satisfying the non-degeneracy conditions necessary to study equation (6.1.4) with Feller's Renewal Theorem.

## 6.2 Article [III]

The aim of this paper is to prove asynchronous exponential growth for the solution of equation (2.3.1) under a regularization assumption on the kernel  $K$ . First of all, we assume that there exists a constant  $c > 0$  and a constant  $z_0 < 0$  such that

$$\sup_{x \in \Omega_0} K(t, x, \Omega_0) \leq ce^{z_0 t}.$$

Moreover, we assume that the kernel  $K$  has two regularizing properties:

1.  $(K * K)(t, x, \cdot)$  is absolutely continuous with respect to the Lebesgue measure, where  $*$  is the convolution product introduced in Section 3,



2. the measure

$$\omega \mapsto \int_{\Omega} K(t, x, \omega) f(x) dx \quad (6.2.1)$$

is absolutely continuous with respect to the Lebesgue measure.

The first regularizing property of  $K$  implies that the singular component of the measure  $B$  tends exponentially to zero as time tends to infinity if we assume that  $B_0(t, \Omega_0) \leq ce^{z_0 t}$ . Indeed,

$$B^s = (\mathcal{L}_R B_0)^s + B_0^s = (\mathcal{L}_K B_0 + \mathcal{L}_{\sum_{n=2}^{\infty} K^{*n} B_0})^s + B_0^s = (\mathcal{L}_K B_0)^s + B_0^s$$

where  $R$  is the resolvent of  $K$  and where  $(\mathcal{L}_{\sum_{n=2}^{\infty} K^{*n} B_0})^s = 0$  thanks to the first regularization condition and the definition of the convolution product  $*$ . Hence the asymptotic behaviour of  $B$  is determined by the asymptotic behaviour of  $B^{AC}(t, \cdot)$ , the absolutely continuous component, with respect to the Lebesgue measure, of the measure  $B(t, \cdot)$ .

Thanks to (6.2.1), to the linearity of  $\mathcal{L}_K$  and to the fact that  $B = B^{AC} + B^s$  satisfies equation (1.2.1), we deduce that  $B^{AC}$  satisfies the following renewal equation

$$B^{AC} = (\mathcal{L}_K B)^{AC} + B_0^{AC} = \mathcal{L}_K B^{AC} + B_0^{AC} + (\mathcal{L}_K B^s)^{AC}$$

where  $(\mathcal{L}_K B^s)^{AC} + B_0^{AC}$  is the forcing function.

It follows that the density of  $B^{AC}$ ,  $b(t) \in L^1(\Omega_0)$ , is the unique solution of the renewal equation

$$b(t) = \int_0^t \mathbf{K}(a) b(t-a) da + b_0(t). \quad (6.2.2)$$

where the kernel  $\mathbf{K}(a)$ , mapping positive integrable functions to positive integrable functions, depends on the kernel  $K$  and  $b_0$  depends on  $B^s$  and  $B_0$ .

To analyse the long term behaviour of  $b(t)$  we adapt to our context the approach developed by Heijmans in [50]. The outline of the analysis of the asymptotic behaviour of  $b$  is the following. Performing the Laplace transform to all the terms of equation (6.2.2) we obtain a non-linear eigenproblem

$$f = \mathbb{K}_{\lambda} f \quad \Re \lambda > z_0$$

where

$$\mathbb{K}_{\lambda} = \int_0^{\infty} e^{-\lambda a} \mathbf{K}(a) da.$$

If the operator  $\mathbb{K}_{\lambda}$  is compact for every  $\lambda \in \mathbb{C}$  with  $\Re \lambda > z_0$  and non-supporting for every  $\lambda \in \mathbb{R}$  with  $\lambda > z_0$ , then the non-linear eigenproblem has a unique, up to renormalization, real eigensolution  $(r, \psi_r)$ . The second step of the proof consists in proving that this solution is attracting. This part of the proof is based on the existence of a spectral gap, i.e., every  $\lambda \in \mathbb{C}$  with  $r \neq \lambda$ , and with  $\Re \lambda > z_0$  and such that 1 belongs to the spectrum of  $\mathbb{K}_{\lambda}$ , satisfies  $\Re \lambda < r$ . The

existence of a spectral gap is crucial as it enables us to deduce, using tools from complex analysis as the residue theorem, Cauchy theorem and Laplace inversion formulas, that  $b(t) = ce^{rt}\psi_r + Me^{(r-v)t}$  where  $0 < v < r$  and  $c, M > 0$ . From this we can derive the asymptotic behaviour of  $B$ .

The main theorem proven in the paper can be formally written as follows. Assume the kernel  $K$  to be regularizing and assume that the corresponding operator  $\mathbb{K}_\lambda$  is compact for every  $\lambda \in \mathbb{C}$  with  $\Re\lambda > z_0$  and non-supporting for every  $\lambda \in \mathbb{R}$  with  $\lambda > z_0$ . Then there exists a constant  $r \in \mathbb{R}$  and a constant  $C_r > 0$  and a measure  $\Psi_r$  such that

$$\lim_{t \rightarrow \infty} \left\| e^{-rt}B(t, \cdot) - rC_r \int_0^\infty e^{-ra}\Psi_r da \right\| = 0$$

with  $\|\cdot\| = \|\cdot\|_{TV} = \|\cdot\|_b$ .

Also in this case we provide examples of kernels  $K$  arising in various applications that satisfy the regularization assumptions and whose corresponding operator  $\mathbb{K}_\lambda$  is compact and non-supporting. We also draw the connection with the PDE formulation of the analogous models.

### 6.3 Article [III]

In this paper we prove the existence of self-similar solutions of equation (4.2.2), with initial condition  $f_0 = 0$ , when the kernel  $k$  satisfies (4.3.1) for  $\gamma < 1$  and  $|\gamma + 2\lambda| < 1$ . Plugging the self-similar ansatz

$$f_s(t, x) = \frac{1}{t^{\frac{3+\gamma}{1-\gamma}}} \Phi(y) \quad \text{with } y = \frac{x}{t^{\frac{2}{1-\gamma}}} \quad (6.3.1)$$

in equation (4.2.2), we deduce that a self-similar solution exists, if there exists a solution (which will be the self-similar profile) to

$$0 = \frac{3+\gamma}{1-\gamma} \xi \Phi(\xi) + \frac{2}{1-\gamma} \xi^2 \partial_\xi \Phi(\xi) + \xi \mathbb{K}[\Phi](\xi) + \delta_0. \quad (6.3.2)$$

The rigorous way to write this equation, as well as the corresponding time dependent equation (4.2.2), is by integrating it against a test function. Namely, we say that a measure is a self-similar solution if it satisfies

$$\begin{aligned} \int_{(0,\infty)} \varphi(z) J_\Phi(z) dz &= \int_{(0,\infty)} \varphi(z) dz - \int_{(0,\infty)} \varphi(z) \int_0^z x \Phi(dx) dz \\ &\quad + \frac{2}{1-\gamma} \int_{(0,\infty)} \varphi(z) z^2 \Phi(dz) \end{aligned} \quad (6.3.3)$$

for every test function  $\varphi \in C_c((0, \infty))$ .

Nevertheless, equation (6.3.2) gives insights on the techniques that we adopt to prove the existence of a self-similar profile. Indeed, we prove the existence of a

solution of equation (6.3.3) by proving that there exists at least a solution  $\Phi_\varepsilon$  of equation

$$0 = \frac{3 + \gamma}{1 - \gamma} \Phi_\varepsilon(\xi) + \frac{2}{1 - \gamma} \xi \partial_\xi \Phi_\varepsilon(\xi) + \mathbb{K}[\Phi_\varepsilon](\xi) + \eta_\varepsilon, \quad (6.3.4)$$

where  $\xi \eta_\varepsilon(\xi) \rightarrow \delta_0(\xi)$  as  $\varepsilon \rightarrow 0$ , and that  $\Phi_\varepsilon$  approximates the self-similar profile  $\Phi$  as  $\varepsilon \rightarrow 0$ .

To prove that, for every fixed  $\varepsilon > 0$ , equation (6.3.4) has at least a solution we regularize and truncate the corresponding time dependent problem. We apply Banach fixed point theorem to prove the existence of a regularized and truncated time dependent solution and we apply Tychonoff fixed point theorem to prove the existence of a regularized truncated stationary solution  $\Phi_{R,a,\varepsilon}$  where  $a, R$  are the parameters corresponding to the truncation and to the regularization respectively.

To prove that  $\Phi_{R,a,\varepsilon} \rightarrow \Phi_\varepsilon$  in the weak- $*$  topology as  $a \rightarrow \infty$  and  $R \rightarrow \infty$  we use estimates of the type

$$\frac{1}{z} \int_{[b_1 z, z]} \Phi_{R,a,\varepsilon}(dx) \leq C z^{-\frac{3+\gamma}{2}}. \quad (6.3.5)$$

This estimate, which is fundamental to apply Banach-Alaoglu theorem, is proven adapting the argument presented in [36] to prove the analogue inequality for the stationary solutions of equation (1.2.4).

Similarly, to prove that  $\Phi_\varepsilon \rightarrow \Phi$  in the weak- $*$  topology, it is crucial the following estimate derived by (6.3.5)

$$\frac{1}{z} \int_{[b_1 z, z]} \Phi_\varepsilon(dx) \leq C z^{-\frac{3+\gamma}{2}}.$$

The measure  $\Phi$  constructed with this procedure has mass less than or equal to 1 and is bounded, in a suitable sense, by the polynomial  $x^{-\frac{\gamma+3}{2}}$ . Combining these properties with the shape of equation (6.3.3) we deduce that for every  $\mu \in \mathbb{R}$

$$\int_{[1, \infty)} x^\mu \Phi(dx) < \infty.$$

This enables us to adapt the strategy developed in [37] to prove that there exists a positive constant  $L > 0$  such that

$$\int_{[1, \infty)} e^{Lx} \Phi(dx) < \infty. \quad (6.3.6)$$

Using the moment bounds that we have and the shape of equation (6.3.3), we deduce that for every compact set  $\mathcal{K} \subset (0, \infty)$  and for every  $q > 1$

$$\int_{(0, \infty)} f(z) \Phi(dz) \leq C(\gamma, \lambda, \Phi) \|f\|_{L^q(\mathcal{K})} \quad \forall f \in L^q(\mathcal{K})$$

## 6 Summary of the research articles

From this we deduce that the measure  $\Phi$  is absolutely continuous with respect to the Lebesgue measure and that its density  $\phi$  satisfies the following equation

$$J_\phi(z) = 1 - \int_0^z x\phi(x)dx + \frac{2}{1-\gamma}z^2\phi(z) \quad (6.3.7)$$

Additionally, we prove that  $\phi(x) \sim x^{-\frac{\gamma+3}{2}}$  as  $x \rightarrow 0$  and that there exists a  $\rho > 0$  such that  $\phi(x) \leq e^{-\rho x}$  as  $x \rightarrow \infty$ , in agreement with the conjecture presented in [22].

We conclude by proving that if the kernel satisfies some regularity assumptions, then also the self-similar solution satisfies some regularity conditions. To this end we adapt the techniques presented in [53] based on Sobolev inequalities and on the shape of the equation.

The main results of this paper can be summarized as follows.

Assume that the kernel  $k$  satisfies (4.3.1) for  $\gamma < 1$  and  $|\gamma + 2\lambda| < 1$ . Then there exists a self-similar solution  $\Phi$  of equation (4.2.2). The self-similar profile has mass equal to 1 and is absolutely continuous with respect to the Lebesgue measure. Its density is such that  $\phi \sim x^{-\frac{\gamma+3}{2}}$  as  $x \rightarrow 0$  and decays at least exponentially as  $x \rightarrow \infty$ . Finally, if the kernel  $k$  is smooth, then also  $\phi$  is smooth.

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