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Self-organized populations interacting under pursuit-evasion dynamics

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h i g h l i g h t s

We introduce a hierarchy of models for interacting preys-predators populations.

- We discuss on numerical grounds the formation of remarkable patterns.
- We analyze a model of the hierarchy and prove global existence of solutions.

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1. Introduction

The formation of space–time heterogeneous patterns is a universal feature of living organisms. Many attempts can be found to model the behavioral mechanisms that lead to the observed self-organization of interacting populations. We refer the reader to [\[1\]](#page--1-0) for a detailed introduction to such phenomena, in the specific case of fish schools, and to the review in [\[2\]](#page--1-1). The question can be rephrased as to describe the information exchanges between self-propelled individuals: the individuals can use the information contained in a certain subdomain of their environment, so that, according to a set of basic rules, the motion of the whole population

organizes with a remarkable pattern. This phenomenon is referred to as ''flocking'' or ''swarming''. The mathematical modeling of these natural behaviors has motivated an intense research activity, after the seminal works of Vicsek et al. [\[3\]](#page--1-2). Flocking can be represented by hydrodynamical models [\[4\]](#page--1-3) as well as many particles systems, where the interaction between individuals is embodied into some potential [\[5,](#page--1-4)[6\]](#page--1-5). This potential encodes how the motion of an individual adapts to the others, e.g. by adjusting the relative velocities. The advantage of hydrodynamical models is to describe the dynamic through a reduced set of macroscopic quantities, like the concentration and bulk velocity. Individual-based and continuum models, stochastic or not, have led to original problems for mathematical analysis and fascinating numerical simulations that reproduce certain features of natural phenomena [\[7–11\]](#page--1-6). Hierarchies of models, à la BBGKY, have been derived, which offer a complete picture, ranging from *N*-particles systems to hydrodynamic models, through kinetic equations where individuals are described according to the principles of statistical physics, see $[12-15]$. Roughly speaking, in these models,

A B S T R A C T

We discuss the modeling of interacting populations through pursuit-evasion – or attraction–repulsion – principles : preys try to escape chasers, chasers are attracted by the presence of preys. We construct a hierarchy of models, ranging from ODEs systems with finite numbers of individuals of each population, to hydrodynamic systems. First-order macroscopic models look like generalized ''two-species Keller–Segel equations''. But, due to cross-interactions, we can show that the system does not exhibit any blow up phenomena in finite time. We also obtain second-order models, that have the form of systems of balance laws, derived from kinetic models. We bring out a few remarkable features of the models based either on mathematical analysis or numerical simulations.

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the motion of the individuals is driven by the combination of self-propulsion, friction and an attractive/repulsive potential. The latter has the general shape of the Morse potential, describing the tendency to pack individuals together, up to a certain critical distance where a repelling effect dominates. Interestingly, these models lead to a large variety of possible behaviors, with complex selection mechanisms driven by certain thresholds on the parameters of the equations.

Here, we are considering a different situation since we deal with *two* populations and we address the question of constructing a mathematical model that produces such self-organized patterns through pursuit-evasion – or attraction–repulsion – simple principles.We shall discuss ''toy-models'', certainly (and intentionally) too rough to capture quantitative features; nevertheless, the interactions of the idealized populations we are dealing with are sufficient to bring out relevant behaviors. We neglect direct interactions between individuals of the same species, the motion is only determined by the potential created by the other population. The dynamic can be seen as the interaction between preys and chasers, described by their respective concentrations: preys are repelled by the chasers while chasers are attracted by the presence of preys. The model can equally be interpreted as a simple ''cops and robbers game'' (we warn the reader not to confuse with a more complex problem referred to with this name in computer science and graph theory). We refer the reader to $[16,17]$ $[16,17]$ for similar attempts, and more recently to $[18,9,19]$ $[18,9,19]$ $[18,9,19]$, but with a different definition of the attraction–repulsion mechanisms. Our work is rather complementary to $[10,11]$ $[10,11]$ where the interested reader will find further details on the modeling issues and very impressive simulations. The modeling also echoes to certain applications in robotics. In this work, the potential is obtained through convolution formulae with the densities. A possible model for designing the interaction potential can be obtained by mimicking the repulsive/attractive effects used when dealing with charged or gravitational particles respectively. The latter principle has been adapted from astrophysics, see [\[20\]](#page--1-15), to population dynamics and it leads to remarkable aggregation phenomena, typical of the behavior of certain populations of bacteria, see [\[21\]](#page--1-16). At first sight, (one of) our hydrodynamic models share(s) the structure of the Keller–Segel system. This system has motivated a huge amount of mathematical works because it exhibits interesting singularity formations: we refer the reader for instance to [\[22–24\]](#page--1-17) for the analysis of such phenomena. In the classical Keller–Segel model the individuals (cells, bacteria) move according to the gradient of the concentration of a substance they emit themselves: the higher the concentration of individuals, the higher the production of the attracting chemical signal. This principle is the basis of chemotaxis. This aggregation process is counter-balanced by spacial diffusion: the two effects compete to determine whether or not the solution blows up in finite time. Thresholds on the initial mass can be discussed accordingly. At least in dimension 2, the situation is quite well understood now. The Keller–Segel system can be obtained through hydrodynamic regimes from a kinetic model for chemotaxis, based on run and tumbling responses to the chemoattractant: this approach is proposed and analyzed in [\[25\]](#page--1-18) and [\[26,](#page--1-19) Section 5.7]. Several modifications of the model have been introduced in order to prevent the overcrowding: concentration-dependent chemotactic sensitivity and diffusion coefficient, reaction terms, cross-diffusion effects, etc. [\[27,](#page--1-20)[28\]](#page--1-21) We refer the reader to the overviews on chemotaxis models in [\[29–31\]](#page--1-22) and [\[26,](#page--1-19) Chap. 5] for further details and results. It is also worth mentioning that similar ideas are also at the basis of PDEs systems proposed to model criminal behavior [\[32\]](#page--1-23): these models are intended to reproduce the formation of ''hotspots'' of criminal activity.

The paper is organized as follows. We start by introducing first-order models: the concentrations of preys and chasers obey transport equations, the velocities of which are gradients of potentials satisfying Poisson equations. The right hand side of the Poisson equation is proportional to the concentration of the opposite population, the sign depending whether the effect is attractive or repulsive. Coming back to a single species, we obtain a diffusionless Keller–Segel equation, as analyzed in [\[33](#page--1-24)[,34\]](#page--1-25), but we shall see that in the present context the crossed effects between preys and chasers prevent the formation of blow up. We discuss *N*-particles versions of the model. Within this interpretation, it turns out that it might be relevant to replace the Poisson kernel by convolution kernels that take into account further distance effects. Next, we turn to second-order models where the presence of preys and chasers is interpreted as creating attractive and repulsive forces. Hence, we obtain individual-based models that have the form of non-linear ODEs systems derived from the standard principles of classical mechanics. We propose a kinetic version of such models. Finally, based on asymptotic arguments we set up a hierarchy of hydrodynamic-like systems for the interacting populations, see e.g. $[12-14,35,33,36]$ $[12-14,35,33,36]$ $[12-14,35,33,36]$ $[12-14,35,33,36]$ for similar arguments in different contexts. Section [3](#page--1-28) is concerned with numerical simulations. We investigate the behavior of individualbased and continuum models in 1D and 2D, discussing the role of the parameters entering into the models. The simulations exhibit an interesting variety of behaviors, that could be valuable sources for further mathematical analysis. Eventually, Section [4](#page--1-29) is devoted to the analysis of the first-order continuum model. In contrast with the single species problem analyzed in [\[33,](#page--1-24)[37](#page--1-30)[,34\]](#page--1-25), concentration in finite time cannot occur as far as initial data are bounded functions. Therefore, we establish the existence and uniqueness of bounded weak solutions, for a wide variety of interaction kernels.

2. A hierarchy of models for pursuit-evasion dynamics

In what follows we will discuss models based either on ODEs or PDEs. The two viewpoints are intimately connected, as a consequence of the following basic remark about the transport equation

$$
\partial_t \rho + \nabla_x \cdot (\rho u) = 0. \tag{1}
$$

We start by assuming that $u : \mathbb{R} \times \mathbb{R}^N \to \mathbb{R}^N$ is smooth enough, so that characteristics curves are well defined by the ODE

$$
\frac{d}{dt}X(t; s, x) = u(t, X(t; s, x)), \quad X(s; s, x) = x.
$$

Namely $X(t; s, x)$ is the position at time t of a particle driven by the velocity field *u*, knowing that it starts from position *x* at time *s*. Our discussion will use the following claim (for the sake of selfcontainedness the proof is detailed in [Appendix A,](#page--1-31) see also [\[38\]](#page--1-32)).

Proposition 2.1. (i) *The measure* $\sum_{i=1}^{I} \delta(x) = X(t; 0, x_{0,i})$ *is a solution of* [\(1\)](#page-1-0) *associated to the initial datum* $\sum_{i=1}^{l} \delta(x = x_{0,i})$ *.*

(ii) *For* $\rho_{\text{init}} \in L^p(\mathbb{R}^N)$, $1 \leq p \leq \infty$, the unique solution of [\(1\)](#page-1-0) having ρinit *as initial datum is given by*

$$
\rho(t, x) = \rho_{init}(X(0; t, x))
$$

$$
\times \exp\left(-\int_0^t (\nabla_x \cdot u)(s, X(s; t, x)) ds\right).
$$

The solution lies in $C^0([0,\infty); L^p(\mathbb{R}^N))$ when p is finite, or in $C^0([0,\infty); L^\infty(\mathbb{R}^N) - \text{weak} - \star)$ otherwise.

We shall deal with nonlinear models where, roughly speaking, the velocity *u* depends on the concentration ρ through non-local definitions. It leads to mathematical difficulties since the regularity necessary to define properly the characteristic curves is not directly guaranteed in this context (see for instance [\[37,](#page--1-30)[33](#page--1-24)[,34\]](#page--1-25) for the analysis of a similar problem). Nevertheless it is worth bearing in mind [Proposition 2.1](#page-1-1) to make connection, at least formally, between individual-based modeling and PDEs description.

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