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Coordinated aggregation in complex systems:

an interdisciplinary approach

V. Basios[1,2,a], S.C. Nicolis[1,3], and J.L. Deneubourg[1,3]

[1] Université Libre de Bruxelles, (CeNoLi-ULB) Interdisciplinary Center for Nonlinear Phenomena and Complex Systems, Bruxelles, Belgium
[2] Service de Physique des Systèmes Complexes et Mécanique Statistique, Bruxelles, Belgium
[3] Service de Biologie des Organismes, Unité d' Ecologie Sociale (USE), Bruxelles, Belgium

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Abstract. The study of the topic of guided aggregation in biology brings together decision making, collective motion and the dynamical interplay between individuals and groups. At the same time it meets statistical mechanics and the physics of complex systems in a new paradigmatic thinking. We propose a research platform for implementation and for undertaking systematic studies of coordinated aggregation, in a truly multi- and inter-disciplinary fashion.

1 Introduction

Aggregation is one of the most ubiquitous phenomena encountered in many areas of sciences, from statistical mechanics and physical chemistry [1,2] to biology [3]. It can be defined as a higher temporal and spatial density of individuals in some part of space as compared to the surrounding area [3].

In complex systems, aggregation phenomena are more often the result of nonlinearities in their dynamics and are associated to pattern formation and self-organization. One of the challenges is therefore to establish the rules and/or the laws at the basis of such phenomena by understanding their dynamical substratum. During the lasts decades the idea that common rules may be at the origin of a large class of phenomena emerged and opened new ways to tackle research in different fields. In fact, without denying their specificities, physics and biology share many common features [1].

In biology, aggregation of, for example, ants, may be seen as the result of a series of kinetic processes where the encounters of individuals lead to metastable dimers, trimers, etc. having a finite lifetime until one or several stable n-mers emerge under appropriate conditions [4]. The similarities of this biological example with phenomena described in physics in connection for example with crystallization, especially in complex matter [2,5,6], are not to overshadow that the complexity at the individual –be it an ant or a human– level is different from the one at a particle level. Still, under some well-controlled conditions, universal laws can be established, favoring the use

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[a] e-mail: `vbasios@ulb.ac.be`

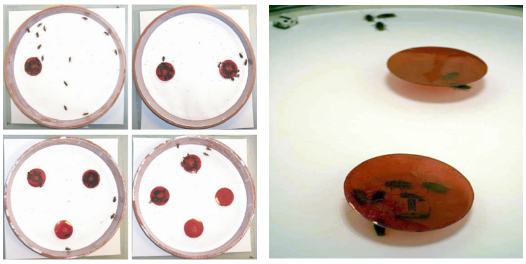

Fig. 1. Shelters and a surrounding arena equipped with data-collection modules. The experiment can accommodate multiple species, even robotic ones. Photo of robot-cockroaches coexistence sharing shelters from our lab at USE in ULB.

of interdisciplinary tools [1,3]. In this context a promising framework that has been successfully followed over the three last decades is the study of collective motion in vertebrates [8,9] (for a recent review see Chap. 19 by Bountis and co-workers in [7]) or collective decision-making in social insects [3].

We describe in this paper a paradigmatic case of aggregation in biology where individuals belonging to two sub-groups and attracted to each other have two different options to choose. Again, this example is reminiscent of phase transitions in multicomponent systems studied in physics (but still with only a few attempts for the non-equilibrium case, [5,6]). Here we develop a mathematical model based on previous experiments [10] and extend it to the case where the two sub-group have two distinct preferences. We also comment on insights from physics of complex systems for further progress in this area. In particular the new-paradigm of non-standard nucleation and self-assembly (here the term "non-standard" means an aggregation process that is not driven by just by density concentration but it is also influenced by structural factors, geometrical effects and other non-density depended variables [1,11–13]) and the revised concept of competitive particle growth [14] bear important relevance and instructive similarities.

2 Shelter selection and guided aggregation

In many cases aggregation is the result of environmental heterogeneities but in the case of homogeneous environment composed by identical patches, it is solely the result of interaction between individuals. The design of controlled experiments highlighted the mechanisms at the basis of decision-making in different species and opened a pathway to rigorous mathematical modelling able to predict yet untested situations. For example, it has been shown that a population of cockroaches (see Fig. 1a) facing the choice between identical shelters is able to reach a consensus (all individuals share one shelter) even though no central intelligence – or leader exists. This consensus simply emerges from a set of quantitative laws: after having explored the environment, an individual choose randomly a shelter and has a probability to leave it that is decreasing nonlinearly with the number of individuals already on this shelter.

In the vast majority of the studies, aggregation is considered within a single species [15]. In fact, aggregation is also observed at the heterospecific level (be it between strains, casts or species) and generate non trivial patterns [10]. In this paper, we study aggregation in heterospecific condition, when two sub-groups having different preferences are offered two patches in an homogeneous environment. To this end, we adopt an interdisciplinary approach, combining tools from physics and biology in order to predict different patterns of aggregation that occur according to two main parameters.

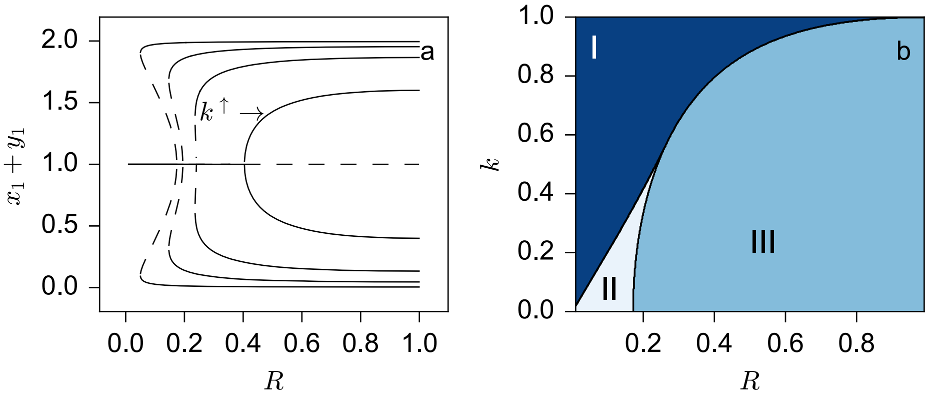

Fig. 2. Bifurcation diagrams of the steady state solutions $x_1 + y_1$ of model 1 as a function of R $(\theta_1/\theta 2)$ for 4 values of k $(k = 0.1, 0.3, 0.5, 0.8)$ (a) and state diagram as a function of R and k (b).

3 A minimal model for aggregation and segregation during shelter selection

Let us consider individuals of two sub-groups X and Y of equal size (i.e. $N_x = N_y = N$; $N_x + N_y = 2N$) having to choose between different patches $i (i = 1, m)$. The evolution in time of the fraction of individuals spending time on each patch can be written as

$$\frac{dx_i}{dt} = \frac{1}{m-1} \sum_{j=1, j \neq i}^{m} \left[-\frac{\theta_i x_i}{k^n + (x_i + \beta_{xy} y_i)^n} + \frac{\theta_j x_j}{k^n + (x_i + \beta_{xy} y_i)^n} \right]$$

$$\frac{dy_i}{dt} = \frac{1}{m-1} \sum_{j=1, j \neq i}^{m} \left[-\frac{\theta_j y_i}{k^n + (\beta_{yx} x_i + y_i)^n} + \frac{\theta_i y_j}{k^n + (\beta_{yx} x_i + y_i)^n} \right]$$

$$i, j = 1, m, i \neq i \qquad (1)$$

the negative and additive terms being respectively the rates of leaving and joining shelters i, j. Here, θ_i is the maximal speed for joining/leaving the shelter i, k and n are parameters related to how individuals respond to each others and β_{xy} (or β_{yx}) correspond to how x (or y) individuals are attracted to y (or x) individuals. We fix the number of shelters equal to two with the Hill-like parameter $n = 2$. Furthermore, in the sequel, we will accept the hypothesis that x and y are indifferently attracted to each other (i.e. $\beta_{xy} = \beta_{yx} = 1$) and that individuals from sub-group X have a preference for shelter 2 and that individuals from sub-group Y prefer the shelter 1 (i.e., $\theta_2 > \theta_1$). Solving at the steady-state we are left with an equation of degree 5 with two parameters: k, which can be viewed as proportional of the inverse of the total population and $R = \theta_1/\theta_2$, a new order parameter which describes the relative propensities of the population preferences for the two shelters.

Figure 2a describes the bifurcation diagram of the variable $x_1 + y_1$ (i.e., the total population on shelter 1) against R for different values of k. As seen, for low values of of R and k, the system possesses up to three stable states in coexistence reflecting either an aggregation state (lower and upper branches) or a mixed segregation state (middle branch). The region of coexistence becomes smaller and smaller as k increases until it disappears for large values of k. In terms of bifurcations, we observe for sufficiently low values of ka central sub-critical pitchfork bifurcation flanked by two saddle-node bifurcations which disappear gradually as k increases leaving only the central pitchfork bifurcation.

A more thorough view is provided by Fig. 2b which describes all the states available to our system of Eq. (1) according to the order parameters k and R. As seen, decreasing k and increasing R, we switch from a regime of mixed segregation (region I) to a coexistence regime where one can observe either aggregation or mixed segregation (region II) to a regime of aggregation (region III).

4 Conclusions and a research programme

In understanding the collective dynamics and motion of aggregating self-propelled particles (organisms, hybrid animal-robot societies, macromolecules, "smart" granular materials, ...) the prevailing methodology is to consider more and more sophisticated "agent-based" programming and emulate "gedanken" experiments in-silico. The other methodology is purely mathematical modelling. Yet for a practical appeal to experimentation one has to navigate between an abstract yet useful approximation and a simple yet realistic implementation avoiding ex-post prediction or hidden assumptions to sneak in the setting. Our model system is such a candidate as it ensures, and straight-forwardly so, proper and optimal controlled conditions for observations by changing a wide array of parameters.

This kind of minimal, yet powerfully descriptive classes of models, provide an opportunity to develop interdisciplinary methods from controlled experiments to a common mathematical language. For example the multi-step nucleation/self-assembly mechanism via intermediates shares essential characteristics with food management via trophalaxis in ants [16,17]. The model developed here predicts many non standard behaviors, e.g. different levels of agregation, segregation and even mixed regimes even if it doesn't consider explicitly the spatial dimension. Still, incorporating such dependences (e.g., cross diffusion) would lead to a more refined picture of the patterns described in this paper and would bear strong similarities with the competitive/cooperative particle growth extended to multi-component systems. Moreover, recently, collective behaviours for biological nanosized macromolecules for self propelled particles [18] and bacteria have started to gain some more attention. The development of ideas for implementing a "lab-on-a-chip" platform for the to study of such systems under guided aggregation [19] inspires research towards automated experimentation not only with bacteria or nanoparticles but also other communities of as it has been achieved by the robotic reactors for gene expression. Given the successful synergy of mathematical, agent-based simulations and biological experiments in a common research platform a useful extension is to augment the setting shown in Fig. 1 with feedback mechanisms which can control the experimental constrains and launch trials according to the outcome of an in-situ monitoring model. Via a combination of simulation, bifurcation analysis and appropriate feedback control from the robotic component and/or sensor network that would coexist in the arena with the aggregating organisms a plethora of investigations can be launched. In particular the possibility of controlling the overall patterns via the guiding influence of few members from the overall population -either of the same or different species or even robotic ones- is another added asset of such an approach. In view of recent developments in data collecting & processing technology and the important advances in coarse-graining methods (especially in relation to autonomous agents as in [20], see also Kevrekidis' contribution in this volume) the above seems a quite realistic step for the near future.

Emphasis on immediate future research can be placed on the role of the group's size, the relation between the complexity of the units or their propensities and the differentiation of the systems, the trends for forming sub-groups, clustering & cliques due to environmental constrains to mention a few. By its nature such a "research platform" can only be truly interdisciplinary and fully integrated as a complex-system lab or network of such.

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