Sergey Vakulenko

Complexity and Evolution of Dissipative Systems

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Complexity and Evolution of Dissipative Systems

An Analytical Approach

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Preface

This book is focused on mathematical methods for dissipative system dynamics and mathematical biology. We consider the problem of the *emergence of complexity* in dissipative systems and chaos, stability and evolution for genetic networks.

We investigate important classes of dynamical systems generating complicated patterns and strange (chaotic) attractors. This question is inspired by the famous paper by D. Ruelle and F. Takens [235], where the notion of the *strange, or chaotic, attractor* is introduced. We analytically prove the existence of strange attractors of *arbitrarily high dimension* for many fundamental models, such as Hopfield neural networks, genetic circuits, and basic systems of phase transition theory.

We also prove the existence of chaotic dynamics for large classes of reaction-diffusion systems, coupled oscillator and population dynamics systems. A general method is proposed that allows us to study the chaotic behavior of *unbounded complexity*, i. e. dimension of corresponding attractors can go to infinity when we vary some system parameters. This approach is constructive and yields *attractor control algorithms*.

The second problem is *increasing complexity in biological evolution*. Charles Darwin formulated the following question of critical importance for evolution theory: How can a gradual evolution produce complex special organs functioning in a correct manner? ([57, Ch. VI]).

This question has provoked a great discussion between creationists and scientists believing Darwin's theory [26, 60, 91, 109, 175–177, 227, 231, 238]. Is Darwin evolution sufficiently fast enough to create complex structures? Is evolution is really feasible? Or, maybe, biological structures are actually not so complex?

In this book, we also develop a mathematical approach in order to explain increasing complexity. Using the viability theory [13–16], ideas proposed by M. Gromov and A. Carbone [97], the attractor theory, the Kolmogorov complexity and new methods for hard combinatorial problems (for example, [1, 184]), we consider some mathematically rigorous approaches for viability, pattern complexity, evolution rate and feasibility. We find a connection between the attractor complexity problem and the viability of biological systems.

Let us outline results on the attractor complexity in more detail. It is well known that, under fairly general conditions, dissipative infinite dimensional dynamical systems can have finite dimensional attractors and finite dimensional invariant (or inertial) manifolds. However, excluding some narrow classes of systems (monotone and gradient systems, see [111–114, 256]), only upper estimates of attractor dimensions and dimensions of the invariant (inertial) manifolds can be obtained [18, 50, 61, 77, 78, 101, 108, 129, 155, 168, 170]. Many problems on complexity of attractors and large time behavior are left open. In particular, an analytical proof of the existence of the chaotic dynamics for fundamental physical systems such as Navier–Stokes equations or reaction-diffusion systems is unknown. Chapter I presents a brief review on dynamical

system theory. In particular, we describe classes of systems having relatively simple large time behavior (monotone and gradient semiflows). These systems can have important biological applications.

In Chapters 2 and 3, our goal is to investigate some important classes of systems with complicated behavior. Chapter 2 considers coupled oscillator systems, neural and genetic networks. In Chapter 3, we extend this approach to systems of partial differential equations. We describe a special method that allows us to find semiflows with a complicated large time behavior. These semiflows can produce all possible finite dimensional structurally stable dynamics when we vary some system parameters. Semiflows with this property are the *maximally complicated family of semiflows*, or, briefly, MC semiflows. The corresponding parameters can be called *control parameters*. The class of MC systems includes such fundamental models as Hopfield networks, genetical circuits and some systems of phase transition theory connected with the scalar Ginzburg–Landau equation. We also describe new classes of spatially localized chemical waves. Although these waves move in an inhomogeneous medium, the propagation speed of these waves is a complicated time function and the front form can vary in a periodical or even chaotical manner.

In many important reaction-diffusion systems, some reagents diffuse much faster than others. We can observe such situations in numerous biological systems, where large molecules (for example, proteins) are much less mobile than small ones (substrats, microRNA). In such systems, parameters are diffusion and degradation coefficients. Moreover, these systems involve some additive spatially inhomogeneous external fluxes which do not depend on unknown reagent densities.

Beginning with the seminal paper [272], where the Turing instability was invented, this class of systems has received great attention [103, 138, 178, 179, 193, 196]. In Chapter 3, we consider such reaction-diffusion systems, where we take as attractor control parameters, diffusion and degradation coefficients and external fluxes. Then, we show that there exists an alternative: either this reaction-diffusion system induces a strongly monotone semiflow (therefore, we can observe no chaotic local attractors here), or this system induces a family of maximally dynamically complex semiflows (and thus can generate all structurally stable attractors which can be chaotic). A criterion that guarantees maximal dynamical complexity admits a transparent chemical interpretation: there is a reagent, which is neither an activator nor an inhibitor. The complexity depends on the parameter $r = D/d$, where D, d are diffusion rates. In order to obtain attractors of larger dimensions, we must take larger r.

This result on reaction-diffusion systems has interesting biological and physical interpretation. Biological systems convert a space information contained in DNA sequences to a complex behavior in time (and in space). This shows that a physicochemical basis of such a transformation is as follows: (i) coexistence of mobile and slow reagents (components); (ii) a sufficient reagent interaction complexity: either we have reagents, which are neither activators nor inhibitors, or we have a number of inhibitors and activators (this case of genetic networks is considered in Chapter 2). Such

systems with complicate dynamics can transform a complicated spatial information (contained in spatially inhomogeneous terms) into a complex time behavior.

From the physical point of view, this result can be interpreted as follows. Monotone and gradient systems describe, in a sense, an "ordered" dynamics. For example, for gradient systems, there exists a Lyapunov function decreasing along the trajectories. Physically, it corresponds to the case of systems having an entropy that is automatically time monotone due to system functioning laws. Our result means that if such an ordering is absent (no entropy or another thermodynamic function), then we can create any prescribed hyperbolic chaos in this system by a variation of external fluxes, diffusion and degradation coefficients.

Although our constructions use some sophisticated mathematical methods (mainly, realization of vector fields proposed by P. Poláčik, see [212–214]), the basic idea beyond this mathematics is simple and admits a transparent physical interpretation. We use the so-called slaving principle [100]: if system dynamics can be decomposed in fast and slow modes, then for large times, the whole system dynamics is captured by the slow modes. To this well-known idea (that can be justified by the invariant manifold theory), we add a new one: one can control the system dynamics by adjusting parameters that define an interaction between slow and fast modes.

In Chapter 2, we show how these two ideas work for neural and genetical networks. We exploit a special topology of a weighted graph that defines node interaction in the network (nodes are genes or neurons). This topology can be named "centralized topology," or "empire structure." In the centralized networks, highly connected hubs play the role of organizing centers. The hubs receive and dispatch interactions. Each center interacts with many weakly connected nodes (satellites). We assume that satellites do not interact, but only obtain orders from center (ancient roman principle *divide et impera*, an ideal for some empires).

We study complex behavior and bifurcations in the networks where the node interaction has the empire structure. We show that the corresponding dissipative semiflows are maximally dynamically complex. This means that depending on the network parameters (thresholds, synaptic weights and the neuron number), these semiflows can realize all structurally stable dynamics. These semiflows are capable of generating (up to an orbital topological equivalency) all structurally stable dynamics including chaotic, periodic etc., for example, all Anosov flows and Smale axiom A systems, Smale horseshoes and all hyperbolic dynamics. There is an explicit algorithm to construct a network with a prescribed dynamics. The algorithm is based on the well-known theorem of neural network theory that multilayered perceptrons can serve as universal approximators. The attractor control parameters are coefficients that define interaction between satellites and centers.

For centralized genetical networks, we also present a mathematical realization of the famous Wolpert's idea: positional information form multicellular organisms [325]. We show that it is sufficient to have three morphogen gradients and a sufficient number of genes to create different complicated dynamics in different cells of an "organ-

ism." Then, there arises a natural question as to how such a complicated dynamics in such a multicellular structure can be synchronized? We can answer this key question by using a combination of our methods with Kuramoto's ideas [152]. These results are presented in Chapter 4.

In Chapter 2, we also show that the dynamics of large classes of coupled oscillator systems with quadratic interactions is maximally complex. These classes, in particular, include the celebrated Lotka–Volterra model.

In Chapter 4, we consider viability of systems investigated in Chapters 2 and 3 under random fluctuations. This helps us to shed light on the problem of complexity increasing in evolution. We can outline key ideas here as follows.

One of the main characteristics of biological systems is that these systems support their own life functions. In particular, a biological system tries to keep the values of the main characteristics of each cell – such as temperature, pressure, pH (acidity measure), concentrations of different reagents – within a certain range of values that makes the biological processes possible. These domains of values are called *viability domains*, and the process of supporting the life functions – by keeping the values inside viability domains – is called *homeostasis*. The concept of homeostasis was first developed by a French physiologist Claude Bernard; it is now one of the main concepts of biology; see, e. g. [42].

The homeostasis process is notoriously difficult to describe in precise mathematical terms. At first glance, homeostasis is similar to the well-known and well-studied notion of stability: in both cases, once a system deviates from the desirable domain, it is pushed back. However, a more detailed analysis shows that these notions are actually different:

- the usual mathematical descriptions of stability mean that a system will indefinitely remain in the desired state, for time $t \to \infty$, while
- a biological cell (and the whole living being) eventually dies.

This difference has been emphasized by M. Gromov and A. Carbone: "Homeostasis of an individual cell cannot be stable for a long time as it would be destroyed by random fluctuations within and off cell ([97, p. 40])."

One might argue that while individuals die, their children survive and thus, species remain. However, it turns out that the biological species are unstable too. This conclusion was confirmed, e. g. by L. Van Valen based on his analysis of empirical data; see, e. g. [227, 301]. Moreover, he concluded that the species extinction rate is approximately constant for all species.

Species extinction does not necessarily mean complete extinction, it usually means that a species evolves and a new mutated better-fit species replaces the original one. From this viewpoint, the evolution is "stable," in the sense that it keeps life on Earth effectively functioning. However, as M. Gromov and A. Carbone mention, it is very difficult to describe this "stability" in precise terms: "There is no adequate mathematical formalism to express the intuitively clear idea of replicative stability of dynamical systems ([97], p. 40)."

Specifically, we need to formalize two ideas:

- First, the biological systems are unstable (in particular, under random perturbations).
- Second, that these systems can be stabilized by replication (evolution).

A progress in solving both aspects of the viability problem can be achieved if we use the notion of Kolmogorov complexity. In our formalizations, we will use the basic concepts and ideas proposed by M. Gromov and A. Carbone [97], L. Van Valen [301], and L. Valiant [303, 304].

We introduce classes of random dynamical systems modeling biological systems under *large fluctuations*. For them, we mathematically formalize the homeostasis concept using the viability theory mainly developed by P. Aubin with colleagues [13–16]. For these systems, we prove the first part of the Gromov–Carbone hypothesis: a "generic" system of our class is capable of supporting homeostasis only within a bounded time interval. We obtain a result that, nonformally speaking, states that: *reaction-diffusion systems are unviable under two generic multiplicative noises*.

Some explicit estimates of the viability times and probabilities can be found for genetic networks. We can express the viability probability via the genetical network parameters. These estimates show that this approach is consistent with key experimental data [133, 134]. Namely, the interaction graph should contain strongly connected nodes: centrality correlates with lethality. Moreover, this result is in a good accordance with the fact that species emerge in periods of ecological catastrophe [143] and L. Van Valen's law on species evolution [301].

The next step is connected with the Kolmogorov complexity theory starting with seminal papers [145, 259] developed in many works [64, 71, 315], see [159, 187] for a overview. This theory is important for such applications such as information compression and others [157, 333, 334].

We know that biological systems are coded by a discrete genetic code. Therefore, we can introduce the Kolmogorov complexity $K(C)$ of such codes C. To estimate the DNA sequence, complexity is important for applications and evolution comprehension, and the problems on gene complexity, organism complexity and complexity increasing in evolution have received a great deal of attention in many fundamental works, for example, [3, 33, 34, 44, 58, 106, 147, 160, 180, 181, 185, 222, 230, 231, 238, 302, 318, 319]. Mathematically, a precise computation of the Kolmogorov complexity is nondecidable problem, i. e. it is impossible to invent a universal algorithm that is capable of computing the complexity for all DNAs, however, we can find upper estimates of the DNA complexity.

The next result states that the survival time $T_{\text{surv}}(C)$ of a system coded by C and the Kolmogorov complexity C are connected. Roughly speaking, we have the following assertion: if $K(C)$ is bounded by a constant K_0, the survival time is bounded as well. This result shows (for a precise mathematical formulation, see Theorem 4.24 of Chapter 4) that the code complexity is a time function which has a tendency to increase, i. e. this

function cannot be a priori bounded. (We say that a function $K(t)$, where $t \in (0, +\infty)$, has a tendency to grow if for each number a, there is a time moment $t(a)$ such that $K(t(a)) > a$.) The proof of this fact is based on results from the Gromov–Carbone problem and nonviability of "generic" systems under extremal fluctuations. To be viable under extremal events (strong fluctuations of environment), the gene code of biological systems should have *large Kolmogorov complexity*, and this complexity has a tendency to grow in evolution. Notice that a connection between complexity of gene code and organism complexity is not direct. Under some conditions, one can show that the attractor complexity also has a tendency to increase during evolution.

Notice that the relation between organism complexity and the corresponding code complexity can be, in principle, arbitrary. Our assertion can be considered as a mathematical formulation of the arrow-of-complexity hypothesis [24]:

> The hypothesis of the arrow of complexity asserts that the complex functional organization of the most complex products of open-ended evolutionary systems has a general tendency to increase with time.

So, it is shown that organisms have tendency to a complexification, but the next fundamental question is about the evolution rate. What does the "slow" evolution rate and "fast" evolution rate mean? From a mathematical point of view, this question needs a formalization. Let us consider an example: how we can distinguish a mountain and a hill?

Fortunately, since we can consider the genetic code as a discrete one, for evolution, we can overcome this difficulty without fuzzy procedures. These ideas are inspired by a remarkable paper by L. Valiant [303].

Assume we are looking for a code X of size $|X|$, which satisfies a number M of constraints necessary for the organism viability. If the numbers N, M are both large, we obtain a typical hard combinatorial problem. Important examples of such hard problems are given by the $K - SAT$ (K-satisfiability) problem (it is considered to be one of the most famous due to the seminal work [51]), integer and Boolean linear programming, the problem regarding the search of a Hamiltonian cycle in a graph, and many others [52]. A list of such problems contains thousands of examples and many of them are important for bioinformatics [83]. They have received great attention during the last decades [2, 49, 52, 56, 63, 80, 183, 184, 245].

For such problems as Boolean and integer programming, and $K - SAT$, we introduce a parameter $\beta = M/N$ playing a crucial role: (relation between restriction number and a free variable number, N is usually proportional to $|X|$). In general, to resolve a hard combinatorial problem, we need exponentially large resources (if we use a bounded memory, the algorithm running time is more than $O(\exp(bN))$ with $b > 0$, if the running time is bounded, then we should use an exponentially large memory). In some cases, however, we are capable of resolving the problem by $\mathrm{Poly}(N)$ elementary steps, where Poly denotes a polynomial of N.

Since $\exp(bN)/\mathrm{Poly}(N) \to \infty$ as $N \to \infty$, we can describe about two classes of problems: easy ones where the running time is polynomial in the problem size, and

hard, where this time is more than any polynomial (usually here, the time is exponentially large). Using these ideas, we can say that an evolution algorithm is *fast* if this algorithm finds a correct genetic code (that makes a viable organism) within a running time polynomial in N, and *slow* if the algorithm works, say, during an exponential running time.

Then, the key question can be reformulated as follows: is there a fast "evolution" algorithm capable of resolving complicated evolution problems? Regarding the precise notion of the "evolution" algorithm, we can consider gradient or greedy algorithms, random search etc., or combinations of gradient algorithms with random search (simulated annealing).

To answer this question, we apply new ideas proposed recently for hard combinatorial problems by mathematicians and physicians [1, 2, 49, 80, 183, 184]. Namely, in many hard combinatorial problems, we observe a phase transition. If the parameter β is less than some critical level, $\beta < \beta_c$, there exists natural gradient algorithms that resolve the problem within $\mathrm{Poly}(N)$ running time. For large β, we have no solutions. Thus, we observe a phase transition in these hard combinatorial problems. This allows us to demonstrate that an evolution of Darwin's type can, in a gradual manner, create a complicated multicellular organism.

Here, we have two parameters playing a decisive role. The first parameter β is, roughly speaking, the number of ecological constraints divided by the number of genes. The second one, K, can be interpreted as gene redundancy. If $\beta < A(K)2^K$, where $A(K)$ is a slowly growing function, i. e. we have a sufficient genetic freedom ("Freedom Principle," proposed by Prof. A. Kondrashov), evolution goes, or otherwise it stops. Numerical experiments confirm this assertion and thus "mutations plus natural selection have led to the marvels found in Nature."

In Chapter 4, we also discuss robustness of centralized networks whose dynamical properties have been investigated in Chapter 2. Here, we discuss connections between viability, robustness and functioning rate. We show that centralized networks can be robust (viable) and flexible, i. e. have a number of local attractors. They can thus support a great multistationarity. However, we show that there is a slow-down effect: if a center controls a number of satellites, the network rate must be bounded and can be estimated via network parameters. This effect restricts possibilities of centralized networks controlled by the center. There are also other possible functioning regimes when satellites control the center or satellites interact. These results are applied to estimate viability of an "empire structure." We compare here, for a simple illustration, the contemporary Russian Federation and the "Stalin" empire.

Furthermore, we consider the so-called Standard model introduced in ecology to study the famous plankton paradox [124]. The plankton paradox is connected with the known ecology principle that a number of species cannot share the single resource. Actually, however, we sometimes observe that numerous species use the same resource. To resolve this paradox, the Standard model was introduced [124]. We study this model in a more general case than in previous works and consider a number of

species under random fluctuations. We find an asymptotic formula for the number of coexisting species that connects the viability, the species number and some other parameters. We also address that when random perturbations are absent, the Standard model can be reduced to the Lotka–Volterra model with n resources (studied in Chapter 2) and, therefore, it also exhibits all kinds of dynamical chaos.

Finally, Chapter 4 can be summarized as follows. We connect concepts of structural stability and genericity with the Kolmogorov complexity theory in order to explain main properties of biological evolution. To describe mathematically biological systems, we consider classical main models of mathematical biology (circuits, reaction-diffusion equations). Recall that R. Thom [268] proposed the concept of structural stability to describe complex structures observed in biology and other applications (so-called "stability dogma," as it was named by J. Guckenheimer and P. Holmes, [99]).

These stability ideas have been successfully applied by many authors (*catastrophe theory*). However, this fundamental concept also meets some serious difficulties (see an interesting discussion in [254]).

Quite opposite ideas were proposed in [301] and [97]. Based on some experimental data, L. Van Valen concluded that biological species are unstable, but evolution can stabilize them. This assertion (the so-called Red Queen hypothesis) drew upon the apparent constant probability of extinction in families of related organisms.

In Chapter 4, we have proposed a mathematical basis for the Van-Valen–Gromov–Carbone instability ideas. Under large random perturbations, an organism with fixed complicated structure is viable only within some bounded time intervals; there is a relation between organism genetic code complexity and viability.

Although organisms of fixed structure are unviable, it is possible that populations of evolving organisms are viable eternally with nonzero probability. This evolution may be gradual and, nonetheless, in a sense, fast.

Briefly, organisms are fragile and they are not eternal, but organism evolution may go eternally.

Many results of Chapter 4 are conjoint with D. Yu. Grigoriev. Results on the Lotka–Volterra systems are conjoint with V. A. Kozlov, and results on centralized genetic networks have been obtained together with O. Radulescu.

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Contents

1 Introduction

This chapter contains prerequisite material, in particular, some basic concepts and definitions of dynamical system theory that play a central role in the book. Details can be found in [12, 101, 108, 129, 135, 204, 205, 207, 208, 211, 228, 232, 254] and other monographs and reviews. In this chapter, we only consider the results and definitions essential in what follows. We state here definitions of attractors, hyperbolic sets and invariant manifolds. We formulate some important results of theory of monotone and gradient dynamical systems.

1.1 Flows and semiflows

The simplest class of finite dimensional *dynamical systems* with continuous time is defined by systems of ordinary differential equations

$$x_t = F(x) \tag{1.1}$$

where F is a sufficiently smooth vector field on a smooth finite dimensional compact manifold $\mathcal{M}$, $x \in \mathcal{M}$. Typical examples of such manifolds are the n-dimensional torus T^n and the sphere S^n.

Let us consider the Cauchy problem for (1.1) with the initial condition $x(0) = y$. Since F is a smooth field, this Cauchy problem has a unique solution for all $t \in (-\infty, +\infty)$, and we obtain a trajectory $t \to x(t, y)$ such that $x(0, y) = y$. We can then define a family of maps $S^t : X \to X$, where X is a phase space by the relation $S^t y = x(t, y)$.

In order to generalize this example, let us consider a family of maps $S^t : X \to X$, depending on $t \in (-\infty, +\infty)$, and where X is a Banach space. Assume this family has the following properties, that is,

$$\text{(i)} \qquad S^0 = I, \tag{1.2}$$

$$\text{(ii)} \qquad S^{t+\tau} = S^t S^\tau, \quad \text{for all } t, \tau \in \mathbf{R}, \tag{1.3}$$

$$\text{(iii)} \qquad S^t \in C^0(X, X) \quad \text{for each fixed } t, \tag{1.4}$$

$$\text{(iv)} \qquad \text{the map } (t, x) \to S^t x \text{ is continuous in } (t, x) \in (-\infty, \infty) \times X, \tag{1.5}$$

where $I : X \to X$ is the identity operator.

A family S^t satisfying (i)–(iv) is said to be a *flow* in X. For (1.1), we take $X = \mathcal{M}$. A flow can be defined as well on a manifold $\mathcal{M}$ with a boundary $\partial\mathcal{M}$ if the vector field is tangent to the boundary.

Dynamical systems with discrete time $t \in \mathbf{Z}$ can be defined by diffeomorphisms $x \to F(x)$ such that $F\mathcal{M} \subset \mathcal{M}$. In some cases, we can obtain such a system from a flow S^t by the so-called Poincaré map [232]. The Poincaré maps are useful when we

are dealing with nonautonomous equations (1.1), where $f = f(t, x)$ is a T periodical function of t [208].

To investigate models defined by partial differential equations or systems of coupled oscillators, we extend this approach, admitting that x lies in an infinite dimensional Banach space B (which serves as a *phase space*). In this case, we consider differential equations of the following form, namely,

$$u_t = Au + F(u) \tag{1.6}$$

where F is a sufficiently smooth (for example, C^r-smooth, $r \geq 1$) map, $F \in C^r(B, B)$, A is a linear operator $A : \operatorname{Dom} A \to B$. For bounded operators A, equations (1.6) were investigated first by the pioneering work of Peter Bohl [32]. The theory of the evolution equations (1.6) with bounded operators A can be found, for example, in [54].

To study systems of partial differential equations, we should investigate (1.6) with *unbounded* linear operators A. Let us consider, for example, parabolic equations

$$u_t = \Delta u + f(x, u, \nabla u) \tag{1.7}$$

with initial and boundary conditions

$$u(x, 0) = \phi(x), \tag{1.8}$$

$$u(x, t) = 0, \quad x \in \partial\Omega \tag{1.9}$$

where $u(x, t)$ is an unknown function defined for $x \in \Omega$, Ω is a connected domain with a smooth boundary $\partial\Omega$. Here, one can apply the following standard approach [108, 167].

Let $B = L_p(\Omega)$, where $p \in (1, \infty)$, be the Banach spaces of measurable functions u such that

$$\|u\|_p = \left(\int_\Omega |u(x)|^p dx \right)^{1/p} < \infty,$$

where $\| \ \|_p$ the norm in these spaces. Then, the operator $Au = \Delta u$ with a domain $\operatorname{Dom} A \subset L_p(\Omega)$ is sectorial in $C(R)$ [108, 167]. If $p = 2$, we deal with the Hilbert space $H = L_2(\Omega)$, and then our operator is self-adjoint and negatively defined in H. We can then introduce the fractional spaces, associated with B, by $B^\alpha = \operatorname{Dom} A_1^\alpha$. These spaces are equipped by the norms

$$\|u\|_{p,\alpha} = \|A_1^\alpha u\|_p,$$

where $\alpha \geq 0$, $A_1 = A - aI$, $a > 0$ and I is the identity operator. The theory of the fractional spaces is well-developed, see [108, 167, 260].

The operator A defines a semigroup $\exp(At)$ by the linear evolution equation

$$u_t = Au, \quad u(0) = v, \tag{1.10}$$

where $\exp(At)v = u(t)$. This allows us to rewrite (1.7) as an abstract evolution equation (1.6). Here, F is a map associated with the nonlinear term f in (1.7), i. e. $F(u) : u \to f(x, u, \nabla u)$. The local in time existence of solutions of (1.6) can be obtained, for example, if, for some $\alpha \in (0, 1)$, F is a C^1-map from some bounded subdomain $U \subset B^\alpha$ to B. To check this property, one applies the Sobolev embeddings [260]. Rewriting (1.6) as an integral equation

$$u(t) = \exp(At)u_0 + \int_0^t \exp(A(t-s))F(u(s))ds, \tag{1.11}$$

we can establish the existence of solutions on a bounded time interval by the standard contracting map principle in B^α [108]. In this case, (1.6) defines a *local semiflow* S^t defined for $t \in [0, T)$. To obtain existence of solutions to (1.6) for all $t > 0$, we need an *a priori estimate* that guarantees that our solutions are bounded in a weak norm. There are different methods that allow us to obtain such estimates (see, for example, [167, 258, 311]). However, it is necessary to note, that, in general, f should satisfy some conditions, otherwise the norms of solutions of (1.6) may increase to $+\infty$ within a finite time interval (the blow-up effect). The blow-up effects are well-studied. For most systems considered in this book, blow-up effects are forbidden by a priori estimates that can be checked in a quite straightforward way.

If we have found an a priori estimate, then solutions of (1.6) exist for all times t, and then our evolution equation defines *a global semiflow (semigroup)* in an appropriate Banach space B having the properties

$$\text{(i)} \qquad S^0 = I \tag{1.12}$$

$$\text{(ii)} \qquad S^{t+\tau} = S^t S^\tau, \quad \text{for all } t, \tau \in \mathbf{R}^+, \tag{1.13}$$

$$\text{(iii)} \qquad S^t \in C^0(B, B) \quad \text{for each fixed } t > 0 \tag{1.14}$$

and

$$\text{(iv)} \qquad \text{the map } (t, x) \to S^t x \text{ is continuous in } (t, x) \in (0, \infty) \times X. \tag{1.15}$$

Ordinary differential equations (1.1) generate global semiflows under the following assumptions. Let us consider an open connected domain $D \subset \mathbb{R}^n$ with a smooth boundary ∂D (for example, a ball B_R^n in $\mathbb{R}^n$ of radius R centered at 0). Then, in order to obtain a global semiflow, we can suppose that the vector field F is directed strictly inward at the boundary ∂D:

$$n(x) \cdot F(x) < 0, \quad \text{for each } x \in \partial D, \tag{1.16}$$

where $n(x)$ is the outward normal vector to ∂D at the point x.

In the following sections, we review some basic notions of dynamical system theory.

1.2 Dissipative semiflows. Attractors

Many physical, chemical and biological effects, such as fluid viscosity, diffusion and protein degradation, lead to an energy dissipation. The concept of a *dissipative system* is a mathematical formalization of phenomena that we observe in systems with dissipation.

In dissipative systems, we often observe a typical picture of global semiflow trajectories in the phase space B, when a "small" set attracts all trajectories of the semiflow. To formulate it in more precise mathematical words, we introduce different concepts of "attraction." Let us consider a global semiflow S^t on X. A trajectory $x(t)$ of x is the map $t : [0, +\infty) \to X$ defined by $x(t) = S^t x$, and a trajectory of a set B is the map defined by $S^t B$, where $S^t B$ denotes the image of B under action of the semiflow at the time moment t. The positive orbit of the set B is the union of all $S^t B$ with $t > 0$, and the orbit of B is the union of $S^t B$ over all $t \in \mathbb{R}$.

A set I is positively invariant if $S^t I = I$ [102] for all $t \geq 0$. A set I is invariant if $S^t I = I$ for all t (of course, then S^t is a flow or I trajectories of S^t can be defined for all $t < 0$).

Definition 1.1. A set $A \subset X$ *attracts* a set B if

$$\lim_{t \to +\infty} \operatorname*{dist}_X(S^t B, A) = 0, \tag{1.17}$$

where the $\operatorname{dist}(B, A)$ denotes the distance between sets B, A in the norm of X:

$$\operatorname*{dist}_X(B, A) = \sup_{x \in B} \inf_{y \in A} \|x - y\|_X.$$

A set A attracts a point x if (1.17) holds with $B = \{x\}$.

Definition 1.2. We say that the global semiflow S^t is *point dissipative* if there is a bounded set D that attracts each point of X.

Definition 1.3. We say that the global semiflow S^t is *dissipative* if there is a bounded *absorbing* set A attracting each bounded subset of X.

The following fundamental concept is that of the *attractor*. There is a large variation in attractor definitions. We shall use the following definition which is popular in mathematical physics [102] (see also [18, 101, 155]).

Definition 1.4. We say that the set $\mathcal{A}$ is a compact global attractor of the semiflow S^t if this set is compact, invariant under S^t and attracts each bounded subset of X.

Remark. Other main definition variants are as follows. We can require that an attractor attracts each point of X. Such an attractor is, in general, a subset of the global attractor. For example, in the gradient systems, the global attractor contains not only all

stable stationary solutions (equilibria), saddle solutions, but even repellers, and stable and unstable manifolds connecting different equilibria. Physically, the unstable connecting manifolds can be interpreted as transient regimes. The attractor, which attracts all points, does not contain unstable manifolds. An interesting definition is given by J. Milnor [186]. Let us assume that the phase space X is enabled by a measure μ. Then, the Milnor attractor is a set A such that the basin of attraction $B(A)$, consisting of all points whose orbits converge towards A, has a strictly positive measure. Moreover, for any closed proper subset $A' \subset A$, the set difference $B(A) - B(A')$ also has a strictly positive measure.

The Milnor attractor does not contain saddle invariant sets, repellers and unstable manifolds. The *statistical* attractor was suggested by Yu. Ilyashenko [130].

The existence of global attractors can be established for large classes of dynamical systems. The following result is essentially due to V. Pliss [208], see also [102]:

Theorem 1.5. *If S^t is a point dissipative global semiflow on locally compact metric space X, then S^t has a compact global attractor $\mathcal{A}$.*

During 1970–1980, it was understood that many parabolic partial differential equations (PDE), hyperbolic PDEs with dissipative terms and systems of PDEs generate semiflows with global attractors. Often, these attractors are not only compact, but also have finite Hausdorff and fractal dimensions [101, 102, 129, 155, 265]. The main physical reason beyond attractor existence is that many dissipative semiflows, defined by PDEs, are determined by a few *main modes*. The first work, where this fundamental concept was realized by a rigorous mathematical method for the Navier–Stokes equations, is [77]. We state these ideas in the following section.

1.3 Invariant manifolds and slaving principle

The following principle plays a central role in the investigation of many dissipative systems. Following H. Haken [100], we call it the *slaving principle*: under some natural conditions, dynamics of fast modes is captured completely by dynamics of slow modes. The mathematical formalization of this nonrigorous assertion is connected with concepts of the *invariant manifold*, *center manifold* and *slow manifold* [50, 72, 108, 135, 208, 228, 232, 265].

To illustrate these ideas, let us consider a system where all variables u can be decomposed in a finite number of slow modes q and fast modes w. The fast mode can contain an infinite number of components, i. e. lies in a Banach or Hilbert space. The following system can be considered as a simple example:

$$q_t = \epsilon Q(q, w) \tag{1.18}$$

$$w_t = Aw + F(q), \tag{1.19}$$

where $q \in \mathbf{R}^n$, Q and F are sufficiently smooth maps, A is a self-adjoint operator, $w \in B$, where B is a Banach phase space and ϵ is a small positive parameter. Let us assume that A is negatively defined, i. e. the spectrum of the operator A lies in the negative half plane and is separated by a barrier away from the imaginary axe:

$$\text{Re Spec}\, A < -b_0. \tag{1.20}$$

We suppose that this barrier $b_0 > 0$ is independent of the small parameter ϵ. This barrier property leads to the following estimate

$$\|\exp(At)w\| \leq C\exp(-b_0 t)\|w\|, \quad C > 0. \tag{1.21}$$

We can then present solutions of (1.19) as follows:

$$w(t) = \exp(At)w(0) + \int_0^t \exp(A(t-s))F(q(s))ds. \tag{1.22}$$

To explain the main idea, let us assume, temporarily, that $q(s)$ in F in the right-hand side of (1.19) does not depend on s. Then, in (1.22), $F(q(s)) = F(q)$ is a constant, the integral in (1.22) can be computed and we obtain

$$w(t) = \exp(-At)(w(0) + A^{-1}F(q)) - A^{-1}F(q). \tag{1.23}$$

We see that for large times $t >> b_0^{-1}$ and small ϵ, the fast component w is a function of the slow mode q:

$$w_{as}(t) = W(q) = -A^{-1}F(q(\epsilon t)). \tag{1.24}$$

For small ϵ, this relation gives a good approximation for w that works for large times. One can expect that the precision of this formula is $O(\epsilon)$. The function w_{as} depends on t via $q(\epsilon t)$ and it is a slow time function.

Let us give some formal definitions. We say that a global semiflow S^t in a Banach space B has a finite dimensional positively invariant manifold $\mathcal{M}$ if $\mathcal{M}$ is a manifold and it is a positively invariant set, i. e. $S^t\mathcal{M} = \mathcal{M}$ for each $t \geq 0$. This means that the invariant manifold consists of semiorbits. We will consider invariant manifolds embedded in B by maps, i. e. they are graphs of sufficiently smooth maps:

$$\mathcal{M} = \{u = (q, w) : w = W(q), q \in U \subset \mathbb{R}^n\},$$

where $W \in C^r(U, B)$ is a C^r smooth map from U to B, and U is an open connected domain in $\mathbb{R}^n$ with a smooth boundary. Sometimes, it is difficult to obtain an invariant manifold, however, we can construct a locally invariant one.

We say that a global semiflow S^t in a Banach space B has a finite dimensional locally invariant manifold $\mathcal{M}$ if $\mathcal{M}$ is a finite dimensional manifold and if $u_0 \in \mathcal{M}$, and then for some $\tau_0 > 0$, $u(t, u_0) = S^t u_0 \in \mathcal{M}$ for $t \in [0, \tau_0)$, i. e. a part of the orbit of u_0 lies in $\mathcal{M}$.

The manifold is locally attractive if there is an open neighborhood U of this manifold such that the manifold attracts all bounded sets $B_0 \subset U$ (Definition 1.1). Sometimes, one can prove the existence of so-called an inertial manifold which attracts all bounded sets [50, 170, 265]. The existence of a smooth finite dimensional inertial manifold means that the global semiflow can be completely reduced to a semiflow defined by a finite dimensional system of differential equations. If system (1.18), (1.19) has an inertial manifold $\mathcal{M}_I$ with equation $w = W(q)$, this means that for large times, dynamics of this system can be described by a finite dimensional system of differential equations

$$q_t = \epsilon Q(q, W(q)) = \epsilon \bar{Q}(q). \tag{1.25}$$

This reduction can be considered as a mathematical formalization of the intuitive slaving principle. In this case, the global attractor exists, has a finite dimension $d \leq \dim\ q = n$), and all attractors of semiflow (1.18), (1.19) lie on $\mathcal{M}_I$. However, conditions that guarantee an inertial manifold existence are restrictive [50, 170, 265]. We can, however, find inertial manifolds with delay [61] that exist under essentially less restrictive conditions. Here, the reduced dynamics is defined by differential equations with a delay.

There are two main methods that allow us to prove invariant manifold existence: the Hadamard graph transform method and the Lyapunov–Perron method [108]. Both methods are based on the contracting map principle. In Section 3.5, one can find examples of theorems on invariant manifold existence.

1.4 Relatively simple behavior: gradient systems

Let us consider the initial boundary value problem (IBVP) defined by (1.7), (1.8) and (1.9). Our goal is to study the large time behavior of the trajectories. However, it is a difficult problem, especially for a more general situation, where u is a vector valued function and we are dealing with a system of quasilinear parabolic PDEs of the second order.

In the next two sections, we consider some cases where one can obtain qualitative information on the large time behavior of a semiflow. Consider reaction-diffusion equations

$$u_t = \epsilon^2 \Delta u + f(x, u), \tag{1.26}$$

initial and boundary conditions are (1.8), (1.9). These equations have a number of applications, for example, in population dynamics, chemistry, liquid crystals, phase transitions and others [100, 108, 193, 196]. Let us assume that $f \in C^1$ satisfies a sign condition, for example, $f(x, u)u < 0$ for sufficiently large $|u|$. Then, solutions of (1.26) are a priori bounded due to the maximum principle [258] and we conclude that IBVP (1.26),(1.8) and (1.9) define a global semiflow S^t on $B = L_p(\Omega)$ with $p > d$, $d = \dim\ \Omega$ [108].

This system belongs to the class of gradient systems. Indeed, let us define a functional $V[u]$

$$V = \int_\Omega \left(\frac{\epsilon^2 (\nabla u)^2}{2} + \Phi(x,u) \right) dx, \tag{1.27}$$

where $\Phi_u = f(x,u)$ is an antiderivative of f with respect to u. Equation (1.26) implies

$$\frac{dV}{dt} = -\frac{1}{2} \int_\Omega u_t^2 dx \le 0 \tag{1.28}$$

along the trajectories $u(x,t)$ of the semiflow S^t. Therefore, the Lyapunov functional $V[u(t)]$ decreases along trajectories of S^t, which are not equilibria. Since V is continuous on B^α and the orbits are relatively compact sets, V is a constant function on ω-limit sets. The ω-limit set is invariant, and therefore it can only contain equilibrium solutions [211]. We denote by E_f the set of all equilibria. There are two main possible cases when all trajectories are convergent to equilibria. Let us formulate the remarkable theorem of Simon [252].

Theorem 1.6. *Assume $f : \bar{\Omega} \times \mathbb{R} \to \mathbb{R}$ is continuous and real analytic in u. Then, any bounded solution of IBVP* (1.9),(1.26) *converges to an equilibrium of* (1.9),(1.26).

The proof uses the Lojasiewicz inequality for analytic functions (for an outline of this proof, see [211]).

An important case is when all equilibria are hyperbolic. This means the following. Assume $u_{eq}(x) = U$ is an equilibrium, i. e. a stationary solution of (1.26), (1.9). Let us introduce a linearized evolution equation

$$v_t = \epsilon^2 \Delta v + f_u(x,U)v = L_U v. \tag{1.29}$$

Assume that the spectrum of L_U has no intersections with the imaginary axis, i. e. the exponential dichotomy property [54] holds. Then, we say that U is a hyperbolic equilibrium (for more details about hyperbolic equilibria and sets, see Section 1.6.2 and [135, 197, 228]). Results on invariant manifolds show then that with each hyperbolic equilibrium, we can associate two smooth manifolds, namely, the unstable manifold $M^u(U)$ and the stable manifold $M^s(U)$. Locally, they are close to the corresponding linear subspaces $\mathcal{L}^u$ and $\mathcal{L}^u$.

It is difficult to check this hyperbolicity property, in particular, for multidimensional problems $\operatorname{Dim}\Omega > 1$. However, if the nonlinear term f is not analytic, we can obtain the important result (Brunovský–Polácik [41]), which shows that, in a sense, almost all reaction-diffusion equations generate a "simple" behavior. Before formulation, let us remember the notion of the *Morse–Smale* system. Finite dimensional Morse–Smale systems play an important role in dynamical system theory as an example of systems with a simple behavior [128, 135, 197, 228, 232, 254]. Systems with a "complicated" behavior can be obtained as perturbations of Morse–Smale systems [128]. This strategy will be used in this book.

We say that a dynamical system is *Morse–Smale* if

(i) there are only a finite number of equilibria, each is hyperbolic with smooth stable and unstable manifolds,
(ii) there are only a finite number of periodical orbits, each is hyperbolic with smooth stable and unstable manifolds,
(iii) stable and unstable manifolds of equilibria and periodical orbits intersect transversely;
(iv) the union of equilibria and periodical orbits coincides with the nonwandering set $NW(S^t)$.

Let us remember that the nonwandering set is defined as a set NW of points $x \in B$ such that for each neighborhood V of x, and for each t_0, there exists a $t > t_0$ such that $S^t V \cap V$ is not empty.

The Brunovský–Polácik theorem can be formulated as follows.

Theorem 1.7. *There is a residual set $\mathcal{R} \subset C^\infty(\Omega \times \mathcal{U}, \mathbb{R})$ of functions f such that, for every f, system* (1.26) *is Morse–Smale, that is, each element of the equilibrium set E_f is hyperbolic and the corresponding stable and unstable manifolds intersect transversally.*

Recall that the residual set in a topological space X is the complement of a set, which is a countable union of nowhere dense sets.

In the one-dimensional case when $x \in [0, \pi]$, we can apply arguments of Sturm–Liouville type that allows us to verify hyperbolicity.

As an example, let us consider the following Chaffee–Infante problem:

$$u_t = u_{xx} + af(u), \quad x \in [0, \pi] \tag{1.30}$$

$$u(0, t) = u(\pi, t) = 0, \tag{1.31}$$

where $a > 0$ is a parameter, $f \in C^2$ is a nonlinear function satisfying some conditions (that hold for the important cases $f = u - u^3$, $f = \sin u$). Such a problem appears in many applications, in particular, in nematic liquid crystals, morphogenesis theory, and Euler's rod problem. In nematic liquid crystals, this problem describes the so-called *Frederiks transition*. Under some natural conditions to f problem (1.30), (1.31) defines an infinite dimensional *Morse–Smale* system. The semiflow, defined by problem (1.30), (1.31), has no periodic orbits since this semiflow has a Lyapunov function. The global attractor is a union of equilibria and some manifolds. Only a single equilibrium U_0 is stable. For $a < a_c$, where a_c is a critical value, this stationary solution is trivial: $U_0 \equiv 0$. For $a > a_c$, it is a nontrivial solution without zero in $(0, \pi)$ (this bifurcation at $a = a_c$ corresponds to the Frederiks transition in nematic crystals).

Unstable equilibria $u^{(n)}(x)$ have zeroes inside $(0, \pi)$ and describe oscillating in x periodical patterns. The number of zeroes gives us the dimension of the corresponding unstable manifold $\mathcal{M}^u(u^{(n)}) = W^n$. The global attractor is defined by the formula $\mathcal{A} = \Cup_n W^n$, i. e. the attractor is a union of unstable manifolds of all the equilibria.

In a similar way, we also investigate the Neumann case, where $u_x(x,t)|_{x=0,\pi} = 0$. Here, stable equilibria are constants C such that $f(C) = 0$ and $f'(C) < 0$, and these solutions have no zeroes.

For (1.30), (1.31), the stationary solutions (patterns) can be described analytically in two cases: $a \approx a_c$ and $a = \epsilon^{-2} >> 1$, where ϵ is a small parameter.

This example shows that the attractor complexity increases in a (or, that is, equivalent, in ϵ^{-1}). Indeed, the number of equilibria grows as a function of the parameter a and the dimension $N(\epsilon)$ of the invariant manifolds also goes to ∞ as $\epsilon \to 0$.

Let us consider an important system of coupled oscillators which can also generate a gradient semiflow with a Lyapunov function. This system has the form

$$\frac{dq_i}{dt} = \sum_{j=1}^{m} K_{ij}\sigma(q_j) - bq_i + \theta_i, \quad i = 1, \dots m \tag{1.32}$$

where $q = (q_1, q_2, \dots, q_m) \in \mathbf{R}^m$, $m > 0$ is the number of oscillators (neurons), $\mathbf{K}$ is a matrix that determines neuron interaction (synaptic matrix), the terms $-bq_i$ with a parameter $b > 0$ define a dissipative force, and $\theta_i \in C^0$ are constant external forces (thresholds). Function $\sigma(z) \in C^1(\mathbb{R})$ satisfies $\lim_{z\to+\infty} \sigma(z) = 1, \lim_{z\to-\infty} \sigma(z) = 0$. System (1.32) defines the famous Hopfield model [118], basic for the theory of attractor neural networks. If $b > 0$, equations (1.32) generate a global dissipative semiflow.

If $\sigma'(z) > 0$ and $\mathbf{K}$ is symmetric, then dynamics (1.32) is gradient. In this case, existence of an "energy" (Lyapunov function) can be applied for neural computations [118]. For nonsymmetric $\mathbf{K}$, we can observe some nontrivial dynamical effects (Chapter 1).

1.5 Monotone systems

For general quasilinear parabolic IBVP (1.7)–(1.9), the Lyapunov function does not exist. However, the corresponding semiflows have a remarkable property: they are monotone. This property restricts the trajectory behavior and gives us information about the large time dynamics. An abstract theory of monotone flows started with the seminal works of M. Hirsch [111, 112], and now it is the well-developed [113, 114, 256, 266]. Here, we outline this theory following [211]. Monotone systems exhibit, in a sense, a relatively simple behavior.

Assume (1.7),(1.9) defines a semiflow in an appropriate Banach space B. The monotonicity of this semiflow is a consequence of the well-known comparison principle [258].

Lemma 1.8 (Comparison principle). *Assume for initial data $\phi, \phi \in B^\alpha$ the following inequality is fulfilled:*

$$\phi(x) \le \phi^+(x) \quad x \in \Omega.$$

Then, the corresponding solutions of (1.7), (1.9) *satisfy the same inequality for all* $t > 0$*:*

$$u(x,t,\phi) \le u(x,t,\phi^+) \quad x \in \Omega,\ t > 0.$$

To formulate an analogue of this principle for abstract semiflows in a Banach space Y, we use the notion of *an ordered cone*. A cone Y^+ is an ordered cone if it is a closed convex cone with nonempty interior $\operatorname{int} Y^+$ such that the intersection of Y^+ and $-Y^+$ is the singleton $\{0\}$. Then, we can introduce the following relations between elements of Y:

$$\begin{aligned} x \le y \quad & \text{if } y - x \in Y^+, \\ x < y \quad & \text{if } x \le y \text{ and } y \ne x, \\ x \ll y \quad & \text{if } y - x \in \operatorname{int} Y^+. \end{aligned}$$

A mapping $F : D(F) \subset Y \to Y$, where Y is an ordered Banach space, is said to be *monotone* if $x, y \in D(F)$ and $x \le y$ imply $F(x) \le F(y)$. It is called *strongly monotone* if $x, y \in D(F)$ and $x < y$ imply $F(x) << F(y)$. A semiflow S^t is monotone if $F = S^t$ is a monotone mapping for each $t > 0$ (similarly, it is strongly monotone if S^t is strongly monotone for each $t > 0$).

We say that a point $x \in B$ is *quasiconvergent* relative to a semiflow if the corresponding orbit is relatively compact and the ω -limit set of this orbit consists of equilibria. Let us formulate the fundamental theorem by M. W. Hirsch [112].

Theorem 1.9. *Let* S *be a compact strongly monotone semiflow on* Y*. Let* D *be an open set such that the corresponding orbit*

$$O(S^\delta D) = \{S^t D : t \ge \delta\}$$

is bounded. Then, the set of quasiconvergent points contains an open and dense subset of D*.*

So, we can expect that, in a sense, almost all trajectories converge to equilibria.

For quasilinear problems (1.7)–(1.9) in the one-dimensional case $x \in \Omega = [a, b] \subset \mathbb{R}$, we have the following theorem first established by T. Zelenyak [329] (see an overview in [211]). Here, $Y = B = L_p(\Omega)$ with an appropriate p.

Theorem 1.10. *Assume that* f *satisfies the following conditions:*
(N1) *For some integer* $m \ge 0$, $f : (x, u, \nabla u) \to f(x, u, \nabla u)$ *is continuous in* $x, u, \xi = \nabla u$ *with all partial derivatives with respect to* (u, ξ) *up to order* m*;*
(N2) *If* $m = 0$, f *is locally Lipschitz continuous in* (x, ξ)*;*

Let $u(t, \phi(\cdot))$ *be any solution of* (1.7), (1.9) *that is globally defined and bounded in* B^α*. Then, there is an equilibrium solution* $v(x)$ *of* (1.7), (1.9) *such that*

$$\|u(t, \phi(\cdot)) - v\| \to 0 \quad \text{as } t \to \infty.$$

This means that dynamics in one space dimension are always relatively simple: each trajectory is convergent.

In the multidimensional case $\dim \Omega > 1$, this theorem is invalid. For the plane case $\dim \Omega = 2$, one can construct an example of chaotic dynamics, but the dynamics can be realized on unstable invariant manifolds [55, 212–214]. However, this chaos is unstable and numerically nonrealizable.

Examples of monotone dynamics can be given by so-called competitive and cooperative systems which are important for biological and ecological applications. System

$$\frac{dX_i}{dt} = F_i(X)$$

is said to be *cooperative* [112, 114] if

$$\frac{\partial F_i}{\partial x_j} \geq 0 \quad \text{for all } j \neq i. \tag{1.33}$$

For more information regarding competitive systems, see Subsection 3.4.4. Under some mild restrictions, almost all trajectories of cooperative systems are convergent (if they are bounded) [112, 114]. For example, the dynamics of the Hopfield system is cooperative if $K_{ij} > 0$ for $i \neq j$. Many results for reaction-diffusion equations can be extended to monotone systems of reaction-diffusion equations [310, 311, 313].

1.6 Complicated large time behavior

1.6.1 General facts and ideas

Naturally, we would like to have a description of large time behavior for semiflows generated by fundamental PDEs and systems of PDEs. Theorems 1.7 and 1.10 show that the large time behavior of semiflows induced by reaction-diffusion equations and quasilinear parabolic equations of the second order are relatively simple. We have here an analogue of the Poincaré–Bendixon theory, which shows that for flows defined by systems of two ordinary differential equations on a compact smooth manifold, the ω-limit sets consist of equilibria and limit cycles.

In many applications for physics, biology, ecology and chemistry, we are dealing with a system of reaction-diffusion equations of the form

$$\frac{\partial u_i}{\partial t} = d_i \Delta u_i + f_i(x, u), \tag{1.34}$$

under the following boundary and initial conditions

$$\nabla u_i(x, t) \cdot n = 0, \quad (x \in \partial\Omega), \tag{1.35}$$

$$u_i(x, 0) = u_i^0(x), \tag{1.36}$$

where $u = (u_1, \dots, u_m)$, $x \in \Omega$ and $f_i \in C^1(\Omega \times \mathbf{R})$, $n(x)$ is an outward normal vector to the boundary $\partial\Omega$ at x. Semiflows, defined by IBVP (1.34), (1.35), (1.36), in general, are not monotone or gradient. For such systems, we can use a general theory of attractors of infinite dimensional dissipative systems developed by many works [18, 50, 101, 108, 128, 155, 265]. Under some conditions, initial boundary value problems (1.34), (1.35) and (1.36) generate a global semiflow possessing a compact global attractor of finite Hausdorff dimension. However, for applications, it would be interesting to understand the attractor structure. These general results only show that if we fix the norm of f ($|f|_{C^1} < C$), then upper estimates of the attractor dimension $\dim_H \mathcal{A} < g(\bar{d})$ are defined by functions increasing in $\bar{d} = \min_i d_i$. Therefore, to obtain a complicated attractor, we should investigate systems where some diffusion coefficients d_i are small, thus presenting a hard problem. In order to explain the strategy of this investigation, we shall review some fundamental concepts of the finite dimensional dynamical system theory.

Let us consider a system of ordinary differential equations

$$\frac{du_i}{dt} = g_i(u), \quad f \in C^1(\mathcal{M}) \tag{1.37}$$

where u lies in the n-dimensional smooth compact manifold $\mathcal{M}$ (say, a torus $\mathcal{M} = T_n$) or in a ball $B^n \subset \mathbb{R}^n$ (in the second case, the field g should be directed inward on the boundary). These equations define a dynamical system (a global flow) for the case of the manifold and a global semiflow for the case B^n (or a compact smooth manifold with a smooth boundary).

The fundamental concept of structural stability was introduced by A. Andronov and L. Pontryagin in 1937. Roughly speaking, this stability means that small perturbations of a structurally stable (robust) dynamical system does not change the topological structure of the system trajectories.

Definition 1.11. We say that a dynamical system S^t on X is equivalent to a dynamical system T^t on Y if there is a homeomorphism $h\colon X \to Y$ which preserves orbits and the sense of direction in time.

Remark. One can use less restrictive definitions when h is a homeomorphism connecting the corresponding attractors or the corresponding nonwandering sets, or neighborhoods of the attractors. We also can restrict h to some invariant sets (definitions and an interesting discussion can be found in [197]).

Definition 1.12. We say that a dynamical system S^t on a compact smooth manifold $\mathcal{M}$ defined by (1.37) is structurally stable if each perturbed field $g + \tilde{g}$ such that

$$\tilde{|}g|_{C^1_{\mathcal{M}}} < \epsilon$$

generates a dynamics that is equivalent to S^t if $\epsilon > 0$ is small enough.

For two-dimensional fields, we have two fundamental theorems of Peixoto [128].

Theorem 1.13. *A vector field on a two-dimensional smooth compact manifold (a surface) is structurally stable if and only if this field is Morse–Smale.*

Theorem 1.14. *For any integer $r \geq 1$, the set of the Morse–Smale fields of class C^r is open and dense in the set of all C^r vector fields.*

So, the case $n = 2$ is relatively simple, however, for $n > 2$, formidable difficulties appear. It is impossible to find a classification, up to homeomorphisms, of finite dimensional dynamical systems. This fact follows from the next theorems due to S. Smale.

Theorem 1.15. *There is a structurally stable system that is not Morse–Smale.*

Theorem 1.16. *The set of structurally stable fields of class C^r is not open and dense in the set of all C^r vector fields if* $\dim \mathcal{M} > 3$.

Therefore, it is impossible to construct a general theory even for the finite dimensional case. In this case, one can use the following strategies. We can study some systems where dynamics are well-understood, for example, systems with hyperbolic dynamics (for a definition and examples of hyperbolic sets, see above, and [135, 197, 228]). Some particular cases such as the Lorenz and Rössler systems, the Smale horseshoe and others are well-studied. We can also investigate small perturbations of the Morse–Smale systems and bifurcations in such systems [128].

For neural, genetical networks and reaction-diffusion systems, we apply the following strategy. The main technical tools are the slaving principle and a special method (realization of vector fields, or, briefly, RVF, see Section 2.1) [55, 211–214]. We find that, under a special choice of these system parameters, the corresponding dynamics can be decomposed in slow and fast variables, and it can be reduced to a finite low dimensional dynamics by the slaving principle. For some fundamental systems, we can show that this reduced low dimensional dynamics take practically any form when we vary some system parameters.

Let us outline here two examples of this strategy. The first example [217] shows that dynamics of some exceptional parabolic equations (1.7) is complicated:

Theorem 1.17. *Let us consider systems* (1.7), (1.9) *in the Sobolev space $W^{1,q}$ for an appropriate $q > \dim \Omega$, where f is a C^1-function. For any given n dimensional ODE* (1.37) *with $g \in C^1(\mathbf{R}^n)$, there is a parabolic equation with a center manifold on which the flow contains the flow of the ODE* (1.37).

Such systems have specific forms since, according to Theorem 1.7, a generic quasilinear parabolic equation (1.7) has “simple” dynamics. Moreover, this realization of (1.37) uses a unstable center manifold, and, therefore, this realization is also unstable: if our initial data lie outside this manifold, the corresponding trajectory is convergent