Dynamics of Evolutionary Processes

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Starting with a brief historical introduction, we review recent results in the theory of evolutionary dynamics, emphasizing new mathematical and simulation methods that promise to provide experimental access to evolutionary phenomena. One impetus for these developments comes from a fresh look at evolutionary population dynamics from the computer science perspectives of stochastic search and adaptive computation. These applications of evolutionary processes are complemented by new theoretical approaches to Wright's concept of *adaptive landscapes*—analyses that borrow heavily from the theories of phase transitions, critical phenomena, and self-organization in statistical physics and of bifurcations, pattern formation, and chaos in dynamical systems theory. We also discuss extensions of basic neo-Darwinian dynamics that include, for example, morphological and functional aspects of phenotypes, as well as cooperative interactions between individuals and between species. We argue that understanding the behavioral and structural richness these extensions engender requires new levels of mathematical and theoretical inventiveness that are appropriate for the massive amounts of data soon to be produced by automated experimental evolutionary systems.

Evolutionary Dynamics — Exploring the
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1 INTRODUCTION

Evolution unfolds over a stunningly wide range of temporal and spatial scales—from seconds and nanometers at the molecular level to geologic epochs and continents at the macro-evolutionary level. The mathematical theory of *evolutionary dynamics* attempts to articulate a consistent conceptual description of these processes—what is similar and what is different across these scales. It even asks if such consistency is at all possible. It focuses especially on how the component mechanisms of selection, genetic variation, population dynamics, the spontaneous emergence of structure, morphological constraints, environmental variation, and so on interact to produce the huge diversity of biological structure, function, and behavior that we observe. Since analysis always has limitations, in its attempt to understand the interplay of these components evolutionary dynamics integrates modern analytical methods from statistics and nonlinear physics and mathematics with current software engineering techniques and simulation methods.

This book presents an up-to-date, but selected, overview of results in the theory and practice of evolutionary dynamics. Starting with a brief historical introduction, here we set the context for the collection by reviewing new developments that promise to provide experimental access to evolutionary phenomena. One impetus for these developments comes from a fresh look at evolutionary population dynamics from the perspective of computer science: stochastic search and adaptive computation. These applications of evolutionary processes are complemented by new theoretical approaches to Wright's concept of *adaptive landscapes*—analyses that borrow heavily from the theories of phase transitions, critical phenomena, and self-organization in statistical physics and of bifurcations, pattern formation, and chaos in dynamical systems theory. These new investigations depend heavily on simulation; partly, to test analytical results, but also to push into regimes where analysis fails or cannot yet be employed. When viewed as a whole, the new developments promise to provide deeper insights into the mechanisms of Darwinian optimization through variation and selection and into the roles of stochasticity and nonadaptive evolution—processes beyond the optimization metaphor. The new methods are particularly important in teasing out how evolutionary mechanisms interact nonlinearly to produce such a wide range of biological organization and dynamical behavior.

There are important extensions of basic neo-Darwinian dynamics that include morphological and functional aspects of phenotypes, as well as cooperative interactions between individuals and between species. Cooperative interactions, for example, are now believed to play a predominant role in the major evolutionary transitions. Understanding the behavior and structural richness these extensions engender will require, we believe, new levels of mathematical and theoretical inventiveness that address the coming deluge of data produced by automated experimental evolutionary systems. The contributions in this volume on evolutionary dynamics are dedicated to stimulating a balanced synthesis of creativity, theoretical analysis, and experimental exploration.

2 A BRIEF HISTORY OF EVOLUTIONARY DYNAMICS

For decades after Darwin laid down its basic principles evolution was the domain of biologists and paleontologists. When the synthetic theory brought the successful union of Darwinian principles with Mendelian genetics [64, 81] at the turn of the 19^{th} century most biologists were confident that they had a solid conceptual basis for biology. The mathematical theory of evolution was dominated by population genetics, which was commonly thought to provide a sufficiently deep theoretical framework for analyzing the constituent mechanisms driving evolutionary processes. The synthetic theory—*neo-Darwinian evolution*—came to be viewed as a universal paradigm for biology.

By the mid-20^{th} century, however, the successes of the molecular life sciences [47] introduced new perspectives into evolutionary biology. First, a great number of empirical facts and time-worn rules—such as, the Mendelian laws of inheritance, the structure of cellular metabolism, and the mechanisms underlying mutation—found straightforward and satisfactory explanations at the molecular scale. Second, the concepts and methods of chemistry and physics slowly began to make their way into biological thought. The result today is that molecular reasoning has become an indispensable part of biology. Chemical kinetics, as one example, was successfully integrated with population genetics [23, 24], resulting in a single framework for analyzing prokaryotic and, in particular, viral evolution [22]. Finally, and perhaps predictably, the successes of molecular biology have revealed that the fundamental concept of the *gene*—in many ways is responsible for this progress—is now in need of an overhaul [52].

As a result, evolution has come to be modeled as an intrinsically stochastic and (nonlinear) dynamical system in which a population of structured individuals, monitored as a set of genotypes, diffuses through the space of all possible genotypes. The diffusion is far from random, but instead is driven by genetic variation and environmental fluctuations and guided by constraints imposed by developmental processes and selection according to phenotypic fitness, for example. Genotype space is now formulated as a sequence space of genes [97], proteins [62] or, most appropriately, polynucleotides [23].

This blueprint is incomplete, however. For example, the discovery of gene sequence variation having no apparent effect on fitness led to the idea of nonadaptive, or *neutral*, evolution [53]. The result of the many-to-one nature of the mappings from genotype to phenotype and phenotype to fitness, neutrality radically modifies the effective architecture of genotype space and so, too, the resulting evolutionary dynamics. At the macroscopic scale, phenotypes appear unchanged for long periods of time; while at the microscopic scale genotypes constantly change as they diffuse across large, selectively neutral networks in genotype space. In this view, selection acts mainly to eliminate deleterious mutations. The result is that the majority of mutants reaching fixation in a population consists of individuals with selectively neutral genotypes. The flip side is that advantageous mutants are rare and can have little influence on the genetic sequences recorded in phylogenetic trees [53].

Certainly of equal significance, the theory of evolutionary dynamics must confront the difficult questions of how developmental processes interact with, constrain, and drive the evolution of biological complexity [39]. Considering even the simplest class of model one runs into daunting technical problems. Populating an evolutionary system with pattern-forming individuals leads to a process that operates on two basic time scales. The first is evolutionary and relatively long; the second developmental and markedly faster. In addition to the complications of analyzing this type of two-scale stochastic dynamical system, one must first analyze the nonlinear pattern formation that occurs during development and then identify which of the emergent features become evolutionarily relevant so that selection can act on them. To top all of this off, a predictive developmental evolutionary theory will need a quantitative measure of these features' structure and function.

These observations only serve to emphasize the magnitude of the task of building a theory of evolutionary dynamics that naturally integrates selection, accident, neutrality, structure, and function. Fortunately, biology is not alone in facing many of the attendant theoretical problems. Over the same period, starting in the mid- to late-19th century, that witnessed the flourishing of evolutionary science, new concepts and methods were developed in mathematics and the physical sciences that now promise to remove several of the roadblocks to an integrative theory of evolutionary dynamics.

3 ORIGINS OF NOVELTY AND STRUCTURE

In parallel with the rise of evolutionary science, phenomena were investigated in physics, chemistry, and other areas of science outside biology that turned out to be intimately related to biological evolution. From the mid-19th to the mid-20th centuries a number of mechanisms underlying the emergence of randomness and structure in nature were discovered and mathematically analyzed. Today, we now appreciate that phase transitions and critical phenomena, pattern formation, bifurcations, and deterministic chaos occur in both inanimate and animate nature and are implicated in fundamental ways with evolutionary population dynamics and self-organization in biological development. Perhaps somewhat surprisingly, even optimization through variation and selection turned out not to be restricted to biological systems. By way of elucidating several parallels and possible future tools for evolutionary dynamics theory, let's consider these phenomena in turn.

One of the most widely applicable lessons from other disciplines is that when systems consist of competing elementary forces the tensions that arise create structural complexity. Some of the earliest examples of the spontaneous formation of order are found in the equilibrium statistical mechanics of interacting spins on a lattice. At low temperatures the energy of spin interactions dominates and, in a ferromagnet for example, the neighboring spins align, creating a global order of all "up" spins. At high temperatures, though, thermal fluctuations overcome the local ordering force of spin alignment and configurations consist of an array of randomly oriented spins. There must be an intermediate temperature, it was argued [77], at which the tendencies to order and to disorder balance, producing a new kind of structured *critical state* with long-range correlations and aligned-spin clusters of all sizes. In other words, at these *phase transitions* the forces leading to order and disorder compete, resulting in states more complex than those away from the transition. Analogous tensions are well known in evolution: the selection-mutation balance, the balance between replication fidelity and mutation (the *error threshold*), and the interaction between gene stability, which is required for survival, and genetic diversity, which is necessary for species adaptability, are only three examples. The emergence of complexity, an apparently common phenomenon, and the parallels between the architecture of physical and biological phenomena hint at the beginnings of a necessary synthesis. There is, however, a much broader constellation of ideas that can brought to bear on the difficult conceptual problems of evolutionary dynamics.

Novel, and rather straightforward, interpretations of common phenomena initiated the development of more general theories of self-organization as it occurs in *nonequilibrium* systems. (The latter are, by the way, often more appropriate models for biological processes, which are sustained by fluxes of energy and resources, than equilibrium systems.) One example is the spontaneous formation of spatial patterns in systems *far from equilibrium*. Interestingly, this phenomenon had been predicted and developed as a model of embryological morphogenesis in the 1950s by Alan Turing, one of the founders of theoretical computer science [87]. Twenty years later these ideas were turned into a comprehensive model of pattern formation in biological development [65]. It was only about ten years ago, though, that Turing's predictions were verified in an experimental chemical reaction-diffusion system [15]. There have been even more direct arguments—for example, [41, 69]—that biological evolution itself is an example of far-from-equilibrium self-organization.

Another, complementary approach to the evolution of biological complexity originates from the observation that rich dynamical behavior and intricate structures emerge when a few simple rules are applied over and over again. This is the domain of *dynamical systems theory* [48, 74, 86, 94] which classifies temporal behavior into four categories: (i) equilibrium or *fixed point* behavior, (ii) oscillations or *limit cycle* behavior, (iii) *deterministic chaos*, and (iv) *transients* (that relax onto stable behaviors (i), (ii), or (iii)). *Bifurcation theory*, a branch of dynamical systems, analyzes and classifies the structural changes that can occur when one kind of behavior makes a transition to another, as a system control parameter is varied. A result that typifies the kind of general principle available from dynamical systems theory is that the dominant signature of a system undergoing a bifurcation is that its transient behavior is enhanced. That is, the system takes longer and longer to settle down as a transition nears.

A hybrid approach to complex systems, combining ideas from equilibrium and nonequilibrium statistical mechanics and dynamical systems, is found in the study of *cellular automata*, a class of spatial system consisting of a lattice of locally coupled finite-state machines. Although invented in the 1940s by John von Neumann in part to formally investigate the minimal requirements of self-reproduction [92], the study of their spatio-temporal behavior was rekindled in the early 1980s with the introduction of a classification scheme that mimics the four dynamical categories above [96]. For example, in addition to periodic and "chaotic" behavior, those cellular automata expressing the richest kinds of self-organization, those in "class IV", are associated with transient behavior. It was suggested that their behavior is a product of a dynamical interplay between regularity and disorder [57, 75].

One of the most popular examples of self-organization in cellular automata is John Conway's two-dimensional cellular automaton, the *Game of Life*. The Game of Life produces a wide diversity of intricate static and propagating structures, despite the fact that its behavior is entirely specified by a simple rule that operates on local neighborhoods of "live" or "dead" cells. One notable indication of its behavioral richness is that a universal Turing machine, the most powerful kind of discrete computational device, can be embedded in the Game of Life by carefully programming the initial configuration of live and dead cells [8, 78].

Conway's Game of Life was introduced and popularized in the early 1970s, but it was not until the mid-1980s that a more systematic investigation of the dynamics and structures generated by cellular automata was begun using the methods of dynamical systems, information and computation theories, and statistical mechanics. The general goal in this was to develop an thorough appreciation of the possible behaviors and structures that systems with demonstrably simple architectures could generate. Implicit in this agenda was the belief that if one could not develop a consistent vocabulary and set of analytical tools for cellular automata, then systems with more complicated architectures, such as those found in biological processes, would remain forever inaccessible. Exhaustive surveys of cellular automata in one and two spatial dimensions were carried out [96]. The surveys suggested that universal computing could also be performed by even by one-dimensional cellular automata and constructive proofs of particularly simple examples were then produced [60].

At the time, it was believed that these results suggested an alternative and novel view of the evolution of biological complexity [28, 56]: By varying dynamical properties it appeared possible that qualitatively different levels of computational structure could emerge in pattern-forming systems and that these levels could become a substrate for novel forms of biological structure and information processing [17,20,49,57]. The emergence of this kind of structural complexity was investigated in an evolutionary setting to test if evolution could find cellular automata with increased computational power [18, 68, 75] or find formal logic systems with increased organization [30, 50, 80].

At about the same time a new mechanism for self-organization was discovered through simulation studies of critical phenomena in nonequilibrium systems; specifically, simple models of sand-pile avalanching. It turned out that the size distribution of avalanches exhibits a *power-law* scaling indicating that there were no characteristic temporal or spatial scales. In fact, there was structure at all scales. More notably, for systems expressing this *self-organized criticality* it was proposed that they systems naturally tend to these complex states and that, in turn, these states are stable [6]. An analog of this kind of self-regulating, stable complexity could be important for the evolutionary maintenance of biological structure and function.

Note that all of these investigations—some theoretical, many simulation-based—turn on the idea that between the extremes of pure order and utter disorder lie behavioral regimes that produce structural complexity. Moreover, it appears that processes, evolutionary or not, can naturally move to structured states. Very recently, similar ideas have reinvigorated the analysis of networks dynamics. It has been suggested that highly structured networks, such as those found in a wide range of natural and artificial systems, lie between regular and purely random topologies [93]. Despite a sometimes checkered history, the notion that complexity arises at the order-disorder border has highlighted an important interplay between dynamics, structure, information processing, and computation in pattern formation and in evolutionary processes.

This brief history of the origins of novelty and structure emphasizes, despite its idiosyncrasies, that one of the overriding problems in all fields concerned with self-organization—whether with its phenomenology, analysis, application, or function—is the issue of complexity. How does one detect that a system has become organized? For that matter, what does one mean by "organization" in the first place? Where is the "self" in self-organization? These questions have stimulated a substantial, though disparate, body of research that addresses how to define and quantify structural complexity [16]. It seems fair to say, though, that as things stand today the implications for evolutionary dynamics have yet to be fully exploited. This observation leads us to think more broadly about the future.

4 EVOLUTION OF STRUCTURE AND FUNCTION?

Self-organization of the general kinds mentioned here sets the stage for evolution at two levels. First, self-organization guides the processes that produce the structured entities on which variation and selection operate [39, 50]. Second, self-organization emerges spontaneously in evolutionary dynamics itself, as complex temporal population dynamics or as spatially structured populations. Of course, these two levels interact and this interaction greatly complicates mathematical modeling and analysis, and controlled experimentation.

What lessons for evolutionary dynamics should one take away from the parallel developments outside biology? First and foremost, they force one to recognize the essential tension between the roles of selection, accident, organization, and neutrality in evolutionary processes. One also comes to appreciate the shear complication that can result from this interplay and that will certainly outstrip that found in simply chaotic dynamical systems and cellular automata. Second and more concretely, they provide a hopeful new set of conceptual and analytical tools with which to begin modeling complex evolutionary and developmental processes. An abiding question, however, presents itself, How do we integrate these results and tools into a comprehensive whole? We believe many key pieces (such as the few mentioned above) are now in place. We also believe that their integration has only just begun. What would be the goal, beyond success in this integration? Perhaps the most important would be that the resulting synthesis lead to *predictive* theories that bear directly on experimental observations. It would appear that there needs to be a new balance between evolutionary theory and experiment that bridges the gulf that now exists.

In addition to the constant need to revisit and reformulate the mathematical foundations of evolutionary dynamics, as we just argued, we believe that a new conceptual framework is a pragmatic priority. It is clear, even passé today, that the exploration of molecular genetics proceeds at a breathtaking pace and has led to a rapidly growing number of fully sequenced genomes. Together with an impressive array of other molecular data and new laboratory-scale biological evolutionary systems, the available information represents a vast and untapped wealth that waits to be exploited by theorists with new concepts and analytical methods.

To put some flesh on these bones, in the following two sections we discuss recent experimental and theoretical approaches to evolutionary behavior. The choice of subjects was guided by a desire to highlight a few stepping stones that may play a role in articulating an integrative and experimentally relevant theory of evolutionary dynamics. The final section briefly introduces the contributions to this volume within this setting. The chapters are intended as a collection of recent ideas in evolutionary dynamics. We will consider the collection a success if it brings some of the current conceptual challenges to the attention of a wide range of theorists and, in this way, is sufficiently provocative to stimulate novel synthetic approaches. We also hope that experimentalists and engineers will find the reviews and the diversity of topics and results a stimulus to new experimental directions.

5 EXPERIMENT AND DESIGN

5.1 BIOLOGICAL AND MOLECULAR MODEL SYSTEMS

Research on biological evolution suffers from the fact that until recently no direct experimental studies have been possible on the dynamics of evolutionary adaptation. The time scales of many evolutionary processes are simply not compatible with experimentalists' lifetimes. Hence, one has to extract information from, for example, the fossil record or from comparisons of genetic sequence data of (almost exclusively) contemporary organisms [14, 59]. Moreover, running control experiments in these cases is out of the question; a situation reminiscent of that found in astrophysics and cosmology.

Fortunately, new biological and molecular model systems have begun to break down the barriers of time and control. Experiments with rapidly multiplying bacteria and molecules replicating *in vitro* have recently led to a marked reduction in generation times to less than one hour. At this time scale evolutionary phenomena become observable within days, weeks, and years. To date, populations of the eubacterium *Escherichia coli* have been studied for thousands of generations under precisely controlled conditions [25, 58, 76]. Two findings from these experiments are of particular interest for evolutionary dynamics. First, the optimization of bacterial phenotypes, monitored through recording cell size (a more or less direct correlate of fitness) does not show a gradual adaptation towards an optimum. Rather, innovations in fitness occur in jumps interrupted by rather long quasistationary epochs [25]. Second, genetic evolution recorded in terms of DNA sequences does not stop during the epochs of phenotypic stasis, but proceeds at least at the same pace, if not faster than, during the adaptive innovations [76]. Punctuation in bacterial evolution thus occurs without external triggers, and there is clear evidence for neutral evolution which manifests itself in genetic changes despite observationally constant phenotypes. Although occurring at the level of single-cell organisms, this intermittent dynamics reminds one, of course, of the punctuated equilibria proposed to explain the long periods of morphological constancy found in the fossil record [40].

The first attempts to study the evolution of molecules in the test tube date back to the 1960s [84]. In RNA evolution, to take one example, the rate of RNA synthesis is the proxy for the mean fitness of a population of RNA molecules. In RNA evolution experiments this fitness was optimized in serial transfer experiments. Later on *in vitro* evolution of RNA was investigated and analyzed in great detail [10] and the mechanism of optimization through mutation and selection is now fully understood at the level of chemical reaction kinetics [9]. One take-home lesson of *in vitro* molecular evolution concerns the entities that can be subjected to evolutionary optimization. That is, evolution is not restricted to cells or higher-level organisms: The operation of a Darwinian mechanism can be observed with free molecules in solution, provided that they are capable of replication and that the reaction medium sustains it.

5.2 EVOLUTIONARY ENGINEERING

The engineering applications of *in vitro* molecular evolution to the production of molecules with predefined properties—called *applied molecular evolution* or *evolutionary biotechnology*—generated additional key insights on the mechanisms underlying optimization through variation and selection [95]. In these applications, the desired molecular properties often do not use high replication efficiency as a proxy for fitness. One illustration of this is found in *molecule breeding*, which plays off the analogy between an evolutionary "producer" of molecules and an animal breeder or gardener in a plant nursery. In contrast to natural selection, in *artificial selection* the experimentalist interrupts the process of optimizing fitness by picking out suitable candidates from the molecular progeny, discarding the remaining variants irrespective of their potential reproductive success. In other words, the molecular breeder defines a modified fitness through this kind of intervention.

Most molecular breeding experiments to date have been performed with RNA or DNA molecules, since they are readily amplified through replication without requiring other molecules as intermediates. (Protein evolution, in contrast, depends on DNA or RNA genes and so requires translation and its attendant complex molecular machinery.) Genetic diversity of molecular populations can be controlled in a more or less straightforward way either by replication with properly adjusted mutation rates or by random chemical synthesis of oligonucleotides. Selection, though, requires ingenious chemical or physical devices. Unfortunately, it would take us too far afield to discuss these here. Instead, we mention two successes in molecular breeding. In the first, RNA or DNA molecules—*aptamers*, which bind specifically to predefined targets—were produced for almost all classes of known (bio)molecules. Binding constants were then optimized through mutation and selection [12, 61]. In the second example, catalysts based on RNA or DNA, known as *(deoxy)ribozymes*, were evolved for a wide variety of natural reactions, as well as for some chemical processes. Interestingly, some of these processes have no counterpart in biochemistry or molecular biology [13, 45].

Molecular breeding illustrates an important feature of evolution in general: The evolutionary process creates or produces "solutions" to "problems" without (intentionally) designing them, as an engineer would attempt to do. In order to produce molecules with desired properties or functions by means of variation and selection one need not know the exact molecular structure that solves the task or that expresses a function. Biochemical engineers performing rational design, in contrast, start by constructing a structure that they expect to serve a predefined purpose. Then, they try to find biopolymer sequences that hopefully form the structure in question. In the production step the sequence is synthesized and transformed into the structure with the desired property. Clearly, the rational engineering approach is a different kind of process from evolution.

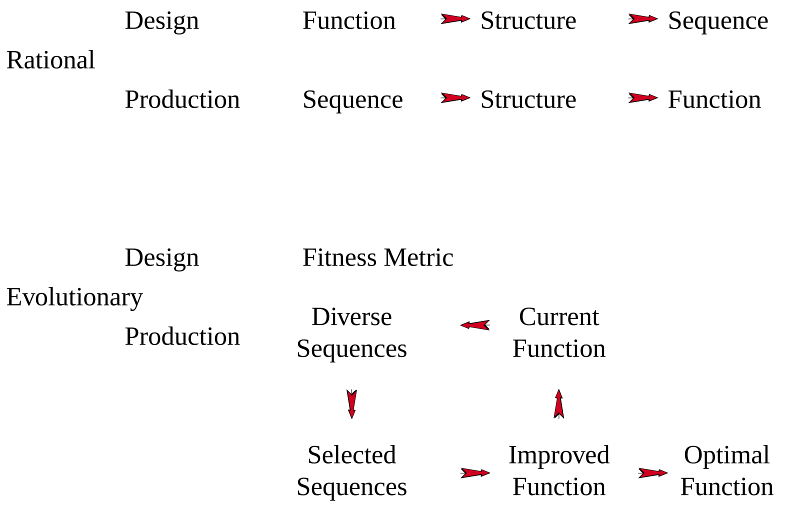

FIGURE 1 Engineering paradigms: Comparing rational and evolutionary design and production methodologies.

To draw out this difference and so emphasize the role of dynamics in evolutionary processes, Fig. 1 compares these two strategies for engineering biomolecules with predefined functions. What the figure illustrates is the dynamical nature of the evolutionary approach: The inclusion of the feedback loop in an evolutionary process is crucial. It introduces an implicit temporal component (dynamics). Most importantly, feedback allows for rapid convergence—even exponentially fast near an optimum.

With the current state of the art, rational design often encounters great difficulties because the contemporary knowledge of the relationships between the sequence, structure, and function of biomolecules is simply not adequate for the requirements of top-down design. Given this, it is an advantage in evolutionary production that prior knowledge of structure is not necessary. In fact, one can even forego a focus on reaching a unique optimum. Often two or more structures serving a purpose equally well have been found by selection dynamics. In some ways this multiplicity is not so unexpected. Different solutions for the same task are frequently observed in macroscopic biology, since only function and efficiency count in the selection-mediated evaluation of fitness.

5.3 EVOLUTIONARY COMPUTATION

Over the last two decades the theory of evolution and, in particular, population genetics have found application to general combinatorial optimization problems as various kinds of population-based stochastic search algorithm. In these, a population consists of candidate solutions that compete via a fitness based on how well they solve the problem. Those (partial) solutions with the best performances are selected as parents of the next generation's population; the members of which are formed from the parents by replication with genetic modification. Variations on this basic theme go by different names: *genetic algorithms* [38, 66], *genetic programming* [54], *evolutionary strategies* [4], and *evolutionary computation* [46], among others. These search methods differ in their preference for one or another type of problem encoding—such as, binary strings or function trees—or in their emphasis on one or another mechanism for genetic variation, recombination, and selection. Evolutionary search methods have found a wide range of application; see, for example, [7, 21, 27, 34]. In fact, the interest in adapting evolutionary ideas to problems in computer science—such as, artificial intelligence—has a long history [29, 43]. One can view the design of adaptive and evolutionary algorithms as examples of engineering's attempt to take advantage of Nature's strategies for problem solving [5, 44].

6 CONCEPTS, MODELS, AND METHODS

6.1 "LANDSCAPES"

The concept of *adaptive landscapes* was introduced by Sewall Wright in the 1930s, initially as a metaphor to visualize evolution as a hill-climbing (local optimization) process [79, 97]. Much later, his geographic analogy was revived with the development of formal methods to handle optimization problems in complex physical systems [35]—such as, finding configurations with minimum free energy in spin glasses. In simple evolutionary dynamics models, one makes an analogy between a physical system minimizing energy as its state moves down an *energy surface* and an evolving population maximizing fitness as it climbs a "landscape" to an adaptive peak. The *fitness landscape* (or, more properly, *fitness function* is defined by assigning a reproduction rate to every point in genotype space.

Though specified by simple interaction rules, it turns out that the spin-configuration energy functions of spin glasses are interesting models for a class of evolutionary dynamics in which there are many adaptive peaks. Their main feature is that, as fitness functions, they have a large number of local energy minima [11]. In slightly modified form spin-glass-like fitness functions are used in the popular NK model of "rugged" fitness landscapes [51], which have been used as simple models of gene-to-gene coupling in genetic networks.

The central question to be answered before one uses the geographic metaphor of landscapes as a starting point for modeling evolutionary dynamics is whether or not a direct analog of an energy function exists. As has been appreciated for some time in mathematical population genetics, this is typically not the case. Except in fairly restricted settings, there is no energy function whose gradient determines the dynamics of evolutionary processes. One generally must employ the theory of dynamical systems [86] or, when the fluctuations due to finite-population sampling are dominant, stochastic extensions of this theory.

Concern over how to best model evolutionary behavior and how to analyze the mechanisms that drive adaptive dynamics has stimulated recent work on a number of different kinds of fitness function that are not "landscapes"—i.e., that do not specify gradient dynamical systems. For example, in the theory of evolutionary computation the *Royal Road* fitness functions, which require specific blocks of "genes" to be correctly set before a unit of fitness is given to a genotype, were invented to test the "building block" hypothesis [43] that genetic algorithms using crossover during replication preferentially assemble functional subsets of genes. The building-block hypothesis turned out not to hold in general [67], but they study led to a detailed mathematical analysis of the finite-population dynamics of the Royal Road genetic algorithm [91] and the discovery of how neutrality leads to epochal evolution [19].

Another interesting example of investigating the behavioral consequences of structured fitness functions, the *holey adaptive landscape*, was developed in population biology [36, 37] to probe the effects of neutrality on evolutionary dynamics. There, a network of genotypes of (almost equally) high fitness percolates sequence space, leaving holes of low fitness. A similar model, with a neutral genotypic plateau above genotypes of low fitness, was shown to spontaneously lead to the emergence of phenotypes with increased resilience to mutational variation—phenotypes that are *mutationally robustness* or, using an older terminology, phenotypes that can sustain a higher *genetic load* [89]. Finally, there have been attempts to investigate evolutionary dynamics produced by molecularly realistic fitness functions based on folding RNA sequences into RNA secondary structures [2, 33]. These studies predicted a high degree of neutrality for properties of RNA molecules [83], which was confirmed recently by an elegant experimental study [82].

A wide class of fitness functions can be compared and studied analytically with respect to the nature of their "ruggedness" using methods based on the algebra of linear operators [85]. They can be compared also in terms of the statistics of adaptive walks or of optimization processes taking place on them.

In many of these studies simulations play an important role, initially giving access to a basic appreciation of the diverse behaviors that can be generated and finally providing confirmation of theoretical predictions. For example, simulation studies of evolutionary dynamics have given direct insights into the mechanisms that promote and inhibit optimization on a spin glass landscape [1], on the Royal Road genetic algorithm [90], and in RNA evolution [31, 32].

Time and again in these mathematical and simulation studies, one is confronted by the shear complication and richness of evolutionary dynamics. The result is that it is difficult to make blanket statements about how evolution "works". For example, population dynamics depends, critically sometimes, on parameters—such as, population size and mutation rate. Varying a parameter, even a small amount, can lead to very different population dynamics. In addition, subtle variations in fitness are simply not seen by selection and so do not control, even local, optimization [73, 88]. One of the overriding lessons is that specifying the fitness function is only one, and sometimes not the dominant, contributor to evolutionary behavior. More generally, the interplay of accident, selection, neutrality, and function is multifaceted. This, of course, points to the challenges and also the opportunities in evolutionary dynamics research.

6.2 COEVOLUTIONARY DYNAMICS AND COOPERATION

Stepping back a bit, note that we have been talking here largely about modeling and analysis *within* the neo-Darwinian framework. One important area of research on evolutionary dynamics that, strictly speaking, lies outside the conventional Darwinian paradigm of variation and selection concerns the coevolution and cooperation within and between species. In symbiosis, for example, competition is suppressed because the long-term benefits of cooperation outweight short-term competitive advantages. Evolution of cooperation that combines competitors into a new functional unit has been invoked as an explanation of the occurrence of major evolutionary transitions [24, 63]. Periods of cooperation, in which Darwinian survival is suppressed, are thought to be implicated in the transition to more complex and hierarchically organized entities. Examples of these include transitions from unicellular to multicellular organisms and from solitary individuals to societies. Notably, cooperation is possible even between molecular species in cell-free assays. Experiments studying the emergence of cooperative molecular assemblies are under way [26]. A mathematical framework to model adaptive dynamics in such non-Darwinian systems has already been developed [42]. Particular attention has also been directed to the evolution of cooperation in animal and human societies [3, 70–72].

7 A SNAPSHOT OF EVOLUTIONARY DYNAMICS

The contributions to this volume were initiated by a conference, **Towards a Comprehensive Dynamics of Evolution—Exploring the Interplay of Selection, Neutrality, Accident, and Function**, held 5-9 October 1998 at the Santa Fe Institute. We have loosely grouped them into a few major headings: macroevolution; epochal evolution; population genetics, dynamics, and optimization; and evolution of cooperation. The chapters should be seen as pointing to an enriched perspective on evolutionary dynamics, one that appreciates the shear diversity of behavior and that acknowledges that this diversity emerges from, and is often not directly determined, by evolution's elementary operations.

Macroevolution: Niles Eldridge starts with an up-to-date presentation on external triggers in biological evolution. Next, Gunther Eble describes the interaction between developmental morphology and evolution using a space of parametrized organism shapes. Looking at the fossil record reveals different evolutionary stages of morphological divergence and convergence. Then, Stefan Bornholdt reviews the present state of the art in modeling the dynamics of macroscopic biological systems. Despite an overwhelming amount of new data, a comprehensive model of macroevolution is still out of reach, but individual questions—such as, the origin of punctuated equilibria—can already be addressed successfully, as several of the other contributors relate.

Epochal Evolution: Aviv Bergman and Marcus Feldman review the classical analysis of punctuation and stasis in evolution. They show that the occurrence of epochal or stepwise evolution need not depend on external triggering. It can be intrinsic to the stochastic sampling dynamics of intermittent fixation that is induced by finite populations. Moreover, punctuation happens independently of many details in the governing evolution equations; in particular, it occurs in asexual as well as in Mendelian populations. James Crutchfield reviews Erik van Nimwegen and his analysis of the mechanisms leading to epochal evolution via sudden adaptive innovations. They use the methods of maximum entropy and self-averaging from statistical physics to show how evolutionary innovations arise via a series of phase transitions: a population dynamical system can discover (via genetic variation) and then stabilize (through selection) new levels of structural complexity. Sergey Gavrilets introduces his concept of holey landscapes and analyzes the evolutionary dynamics on them. An impressive number of applications of the concept ranging from molecular evolution to organismic evolution and speciation are discussed. Peter Schuster addresses the evolutionary dynamics of asexual reproduction. He reviews the theory of molecular quasispecies and presents a comprehensive theory of evolution for molecular phenotypes, which leads to new definitions of continuity and discontinuities in evolution.

Population Genetics, Dynamics, and Optimization: Tomoko Ohta presents the most recent developments in the nearly neutral theory of evolution, one of the most important extensions of Motoo Kimura's neutral theory. It explicitly considers weakly selected and slightly deleterious mutations. Peter Stadler then presents a formal and mathematically quite demanding theory of adaptive landscapes. Basic to the idea is the analysis of the spectra of linear operators on "rugged landscapes". The Fourier transform provides a useful tool for a classification of linearly decomposable landscapes according to the hardness of optimization dynamics. Next, Nigel Snoad and Martin Nilsson extend the concept of quasispecies to dynamic fitness functions. They find two thresholds for the copying fidelity: The lower bound is given by the well known error-threshold, which itself sets an upper limit on mutation rate. The upper fidelity limit expresses the fact that a population with exact replication is doomed to die out on a dynamic landscape since it cannot adapt to a changing environment. Lionell Barnett studies evolutionary dynamics in finite populations with recombination. He models the system as a birth-and-death process under the assumptions of the Moran model. Interestingly, he observes bistability: different initial conditions give rise to different stationary populations.

Evolution of Cooperation: Kristian Lindgren and Johan Johansson present results on the evolutionary dynamics of a population of finite-state agents playing the N-person Prisoner's Dilemma—a well known model for competitive game-theoretic interactions. They analyze a difference equation that models the resulting population dynamics in the case of nonoverlapping generations and asexual reproduction. One class of their models exhibits a predominance of cooperation through a dynamics that avoids less cooperative stable fixed points. Guy Sella and Michael Lachmann also study the evolutionary dynamics of a population of agents interacting via the Prisoners' Dilemma. They investigate spatial cooperation with a population of agents on a lattice. The common scenario consists in life cycles of populations that are established by spreading from single cooperators which then die after invasion by agents with parasitic "defect" strategies. A dynamical steady state with persistent cooperation is encountered when the global birth rate of populations founded by dispersed cooperators is balanced by the death rate of populations caused by invading defectors. In the final chapter, James Crutchfield, Raja Das, and Melanie Mitchell analyze the evolutionary emergence of global computation in spatial lattices of finite-state machines (cellular automata). They focus particularly on the interaction between the series of evolutionary innovations (ultimately producing high computational performance) and the structural aspects of spatial cooperation that convey high fitness to the best cellular automata.

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Resources

A number of resources for evolutionary dynamics are available at the workshop's website: http://www.santafe.edu/∼jpc/evdyn.html. We also recommend the book *Evolution as Computation* [55] as a companion to this one.

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