The Design of Natural and Artificial Adaptive Systems

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I. Introduction

The design of adaptive systems will be among the key research problems of the 21st century. This new field is emerging from several distinct lines of work.

- Modern immunology is based on the theory of clonal selection and adaptive immunity. The remarkable recognition abilities of the vertebrate immune system depend on the programmed mechanisms of antibody variation and selection that occur within each individual.
- The design of intelligent computer systems and robots depends on a balance between adaptive improvement by exploration and efficient exploitation of known solutions. Many of the current computer implementations use evolutionary algorithms to achieve adaptation to novel or changing environments.
- The adaptive response of genetic systems to environmental challenge depends strongly on the tempo and mode of sex and recombination. Sexual systems vary widely in nature. Which processes have shaped this variation is a major puzzle in evolutionary biology.
- Wiring a brain during development and using that brain to learn are great problems of information management. Recent studies in neuroscience suggest that programmed mechanisms of stochastic variation and controlled selection guide neural development and learning. If true, then nature has solved these informational problems by using somatic adaptive systems that are programmed to work in the same way as natural selection.

What do these different fields have in common? Will there be a new science of adaptation shared by biology and engineering? Can a unified theory guide the study of so many different phenomena? What will be the central tenets of such a theory?

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These are difficult questions. To make a start, I survey the range of adaptive systems as they are currently understood: adaptive immunity, learning, development, culture and symbiosis, the origin and evolution of genetic systems, and artificial adaptive systems in engineering. The facts that I present in my survey, fascinating in their own right, provide the database from which more general insights must be built.

II. Challenges to Adaptive Systems

Before starting on the survey, it is useful to have a conceptual framework. I begin with a rough definition. An "adaptive system" is a population of entities that satisfy the three conditions of natural selection: the entities vary, they have continuity (heritability), and they differ in their success. The entities in the population can be genes, competing computer programs, or anything else that satisfies the three conditions.

A. *Types of challenge*

In this section I propose a classification of the challenges that have shaped adaptive systems and the ways in which adaptive systems have responded to these challenges. A surprisingly small number of challenges and responses cover the main features of adaptive systems ranging from genetics to robotics. I illustrate the concepts with brief examples that will be discussed in more detail during the survey.

Information decay is one kind of challenge. For example, genetic systems suffer information decay when random mutations occur. If mutations accumulate too rapidly then adaptive improvement by natural selection is impossible. The population suffers an "error catastrophe" (Eigen, 1992) or "mutational meltdown" (Lynch et al., 1993).

Predictable complexity is another type of challenge. For example, the information required to specify the point-to-point neural connections of a human brain greatly exceeds the amount of information encoded by the genome. Thus the genetic system must cope with the problem of creating a complex pattern during development from a relatively limited set of instructions.

Unpredictable challenges are the third type of problem faced by adaptive systems. For example, parasites vary unpredictably over space and time. To give an engineering example, a robot engaged in war cannot have prewired responses for all possible attack strategies that the enemies may use. A successful robot must adjust to unpredictable events.

I will argue during my survey that this small list—information decay, complexity, and unpredictability—describes the main challenges faced by adaptive systems (Table 1). The next step is to consider how adaptive systems respond to these challenges (Table 2).

TABLE 1
Challenges to Adaptive Systems

Challenge	Comments
Information Decay	A ubiquitous "tax" on information storage and transmission.
Predictable complexity	Challenge is to learn predictable pattern or achieve predictable form, but complexity of pattern greatly exceeds the available information storage.
Unpredictable challenge	(a) Environmental—abiotic challenges and biotic interactions without feedback. (b) Coevolutionary—biotic interactions with feedback between systems.

B. *Responses of adaptive systems*

Enhancing *transmission fidelity* is one way to overcome the problem of information decay. For example, Bernstein et al. (1988) suggest that sex is the genetic system's way of enhancing transmission fidelity in response to the information decay imposed by mutation. In their theory sex brings together two different copies of the genetic material, which allows a damaged copy to be corrected by the undamaged copy.

The problem of balancing *exploration versus exploitation* recurs in all adaptive systems (Holland, 1975). Exploration of new ways to solve problems often carries a cost because competitors may devote more energy to the efficient exploitation of known solutions. For example, sex increases genetic variability among offspring compared with asexual reproduction. Greater variability improves the chances that some of the offspring will have genotypes that match an unpredictable environment. Thus sexual systems may be a form of exploration, but this exploration is costly because asexuality is usually a more efficient mode of reproduction. There is much controversy among evolutionary biologists about whether sexual systems have evolved as a method of exploration in response to unpredictable challenge or as a method to enhance transmission fidelity in response to the to challenge of information decay.

TABLE 2
Responses to Challenge

Response	Comments
Transmission fidelity	Mechanisms to reduce errors in the storage and transmission of encoded solutions.
Exploration versus exploitation	The balance between costly exploration for improved efficiency and the cheap exploitation of known solutions.
Generative rules	Simple rules to generate complex phenotypes. Genotypes do not specify explicit blueprints for structure.
Instructional subsystem	Mechanism to store information obtained directly from the environment.
Adaptive subsystem	A system of variation and selection "spawned" by an evolving system to solve a particular problem.
Symbiosis	Cooperation between separate evolving entities to achieve greater group efficiency. Conflicts among group members often arise.

The transmissible information (genotype) of an adaptive system often contains *generative rules* for the design of phenotypic structure (Thompson, 1961; Lindenmayer, 1971). In organisms each detail of morphology and behavior is not coded by an explicit DNA sequence; there is no blueprint for design. Fingerprints are generated by the biochemical rules of morphogenesis contained in the genome. Those rules may be fairly simple, but the outcome is complex and partly influenced by chance.

Simple environmental patterns may directly influence the internal information store through an *instructional subsystem.* For example, repeated stimulation of some neurons causes an increase in the stimulus required to evoke a response. The instructional subsystem takes a direct measure of environmental pattern.

Adaptive systems may spawn *adaptive subsystems* to handle difficult challenges (Gell-Mann, 1994). For example, the immune system of vertebrates has a specialized set of mechanisms to generate variability among recognition molecules and a second set of mechanisms to select and amplify recognition molecules that react with invading parasites. These controls of the adaptive immune system are specified by the underlying genetic system, or, put another way, the genetic system has spawned an adaptive subsystem to handle the unpredictable challenges of parasitic attack. In later sections I will discuss certain aspects of development and learning as adaptive subsystems spawned by the genetic system.

Symbiosis is the living together of two or more dissimilar organisms. An interesting theory about the origin of life illustrates the importance of symbiosis (Eigen, 1992). Information decay was a severe problem for the first replicating molecules because of high mutation rates. The mutation rate sets an "error threshold" that determines the upper limit on the size of informational molecules and thus the storage capacity of genetic systems. The early replicators were limited to very small genome sizes because of the error threshold. This creates a paradox: small genomes do not have sufficient information to code for an error-correcting replication machinery; without error correction larger genomes cannot evolve.

Symbiosis appears to be the solution. A set of small replicators, each below the error threshold, may have cooperated to produce error-correcting enzymes. This symbiotic group, with a reduced rate of transmission errors, could then increase in size and complexity.

Cooperation among early replicators was the first successful symbiosis. The most recent example of symbiosis in adaptive systems comes from research on robot design. Teamwork among robots boosts efficiency for tasks that require division of labor and specialization, such as automated manufacturing, search and rescue, or surveillance (Parker, 1993). Both biological symbiosis and robot teamwork must resolve the tension between the autonomy of components and the control of the symbiotic group. I will discuss this problem for both genomes and robots in later sections.

C. Outline of survey

I turn next to my survey of adaptive systems. I start with the transformation of genotype into phenotype. The first of these sections describes vertebrate immunity, an adaptive subsystem of variation and selection that occurs within each

individual's body. The following section considers the problems of neural development and learning. I raise the possibility that adaptive subsystems play a role in these complex informational processes. The final section of this group focuses on morphology. I contrast simple generative rules for development with more complex processes of developmental variation and selection.

After the genotype-phenotype transformations, I turn to the evolution of genetic systems. There is a natural tendency to view a genetic system as a stable, well-defined core of hereditary information. But each apparent system is actually a complex symbiosis of partly conflicting and partly cooperating hereditary systems. Each has its own pattern of continuity (transmission) and its own generative rules for the production of phenotype. Sex and recombination define one widespread pattern of hereditary mixture and symbiosis. I consider how sex fits into the recurring challenges and responses of adaptive systems outlined in Tables 1 and 2.

The final section places some new aspects of human engineering in the framework of adaptive systems. At one level these new methods are simply the use of variation and selection as an engineering tool for problems such as robotics. The effective use of selection follows in many ways the design of natural adaptive systems. At another level the new forms of "artificial life," with their new symbioses and their higher-order adaptive subsystems spawned by humans, are simply the next historical stage in the evolution of adaptive systems.

III. Adaptive Immunity in Vertebrates

How does a host recognize foreign molecules that signal a parasitic invasion? How does an individual distinguish self from nonself to avoid attacking its own tissues? A vertebrate host solves these problems with an adaptive system that causes evolutionary change among the populations of cells within its body. These evolutionary changes within the body—somatic evolution—are controlled by a complex set of mechanisms that are encoded within the genome. In my language of environmental challenge and adaptive response, the genetic system spawned an adaptive subsystem to handle the unpredictable challenges of parasitic invasion.

In this section I summarize many details about vertebrate immunity. The details are fascinating and provide the basis on which theories of adaptive systems must be built. But in a general survey of adaptive systems the details can also be overwhelming. So in this introduction I provide a link between the abstract discussion about challenges and responses in the previous section and the details of adaptive immunity that follow.

The response of an adaptive subsystem depends on two levels of evolutionary change. At the somatic level of vertebrate immunity, cellular clones undergo programmed genetic recombination and enhanced mutation during particular periods. These mechanisms create variation in the ability to recognize and bind foreign molecules. Variants that bind invaders are amplified by programmed controls that enhance the replication rate of some cellular clones while reducing the replication of other clones. The mechanisms that control somatic recombination, mutation, and selection (amplification) are coded at the genetic level. Thus evolutionary modifications at the genetic level ultimately control the responses of the somatic system.

This two-level system provides special opportunities to study the forces that

shape adaptive systems. The challenge—parasitic invasion—is clearly defined. The response requires recognition of invaders. Adaptive immunity uses a number of techniques to adjust exploration for better recognition of invaders versus exploitation of existing recognition tools. This dynamic balancing between exploration and exploitation occurs on short time scales. Although studying immunology is not easy, we will see that other adaptive systems rarely provide such clear challenge-response couples.

The vertebrate immune system is actually a complex mixture of adaptive subsystems and traits that are encoded directly by the genome. For example, several important aspects of recognition depend on subsystems of random variation and selective amplification, but at least one key aspect of recognition is controlled directly by a genetically encoded set of alleles (MHC). This mix of somatic exploration and the exploitation of fixed recognition presents several interesting and unsolved problems in this two-level adaptive system. I will discuss these problems later in the section, but first some biological background is needed to set the stage.

A. Positive Selection and Clonal Expansion

I will describe a measles infection to introduce some of the details of adaptive immunity. Measles viruses invade the upper respiratory tract. Toward the end of the 10- to 12-day incubation period, the first symptoms of headache, fever, and sore throat appear. At this time the viral population within the host is large and rising rapidly. Viral particles enter the blood and spread, forming secondary infections in the skin that lead to the characteristic measles rash (Davis et al., 1990).

The body maintains a vast array of nonself detectors—the antibodies. Each antibody recognizes a particular molecular pattern. When a measles virus invades the body, only a few antibodies can recognize the surface molecules of the viral coat. Recognition stimulates division of the B cells that produce matching antibody. This process, called clonal expansion, generates a large population of antibody-producing cells that are specific for the measles virus. (I present a simplified description of the immune system. Good introductions are given by Mims, 1987; Golub and Green, 1991; Mims et al., 1993.)

Antibody can bind and neutralize free virus particles. However, the host has few antibodies that can react with the measles virus on first encounter, thus the virus enters cells and begins rapid multiplication. Meanwhile, the antibodies that react with the virus stimulate clonal expansion of B cells. After several days the antibody titer is high. At this stage antibodies alone cannot clear the infection, perhaps because many infected cells harbor the virus internally.

A second defense, the killer T cells, destroys host cells that harbor viruses. T cells have dynamics similar to the B cells. The large population of T cells can recognize many different kinds of foreign molecules, but only very few T cells recognize a measles virus on first infection. Those T cells that recognize the virus stimulate clonal expansion. Members of this expanded clone, specific for measles, can clear the infection.

Upon reinfection with measles, the host can mount a rapid antibody and T cell response that clears the virus. This immunological memory lasts throughout

life. There are several controversial theories about how immunological memory is maintained but, at present, there is not enough evidence to end the debate.

Evolution by natural selection occurs when there is variation, selection, and transmission. The clonal expansion of B and T cells, leading to infection clearance and immunological memory, satisfies the requirements for adaptive evolution caused by natural selection. Cell lines (clones) vary in their recognition properties; reproductive rate varies according to these recognition properties; and offspring cells resemble their parents. This adaptive system causes evolutionary change among the populations of cells within the body. The idea that adaptive immunity is based on natural selection was first proposed by Jerne (1955; see also Burnet, 1959).

B. Diversity: Somatic Recombination and Mutation

Clonal expansion of specific B and T cells in response to challenge by foreign molecules is easy enough to imagine. But how does the body generate sufficient variation so that each new invader can be recognized?

The remarkable mechanisms that generate clonal diversity of B and T cells have been worked out over the past two decades (Golub and Green, 1991; Janeway, 1993; Nossal, 1993). The process differs slightly for B and T cells. I describe the generation of B cell (antibody) diversity (see Fig. 1).

Each antibody molecule has two kinds of amino acid chains, the heavy chains and the light chains. A heavy chain has three regions that affect recognition: variable (V), diversity (D), and joining (J). A light chain has only the V and J regions. There are 100 different V genes, 12 D genes, and 4 J genes.

Each progenitor of a B cell clone undergoes a special type of DNA recombination that brings together a V–D–J combination to form a heavy chain coding region. There are 100 x 12 x 4 = 4800 V–D–J combinations. A separate recombination event creates a V–J combination for the light chain, of which there are 100 x 4=400 combinations. The independent formation of heavy and light chains creates the potential for 4800 x 400=1,920,000 different antibodies. In addition, randomly chosen DNA bases are added between the segments that are brought together by recombination, greatly increasing the total number of antibody types.

The mechanism for generating the diversity on which selection acts switches from recombination to mutation during the course of an infection (Fig. 2). Recombination creates a large number of very different antibodies. Initially, each of these antibodies is rare. Upon infection one of these rare types may match, stimulating selective amplification of the B cell clone. The matching B cells increase their mutation rate, creating many slightly different antibodies that vary in their affinity to the invader. Those mutant cells that bind more tightly are stimulated to divide more rapidly. This evolutionary fine-tuning of the B cell population is called affinity maturation (Golub and Green, 1991).

C. Negative Selection and Self versus Nonself Discrimination

If recognition sequences are generated randomly, then how does the host discriminate self from nonself? Another selective mechanism solves this problem.

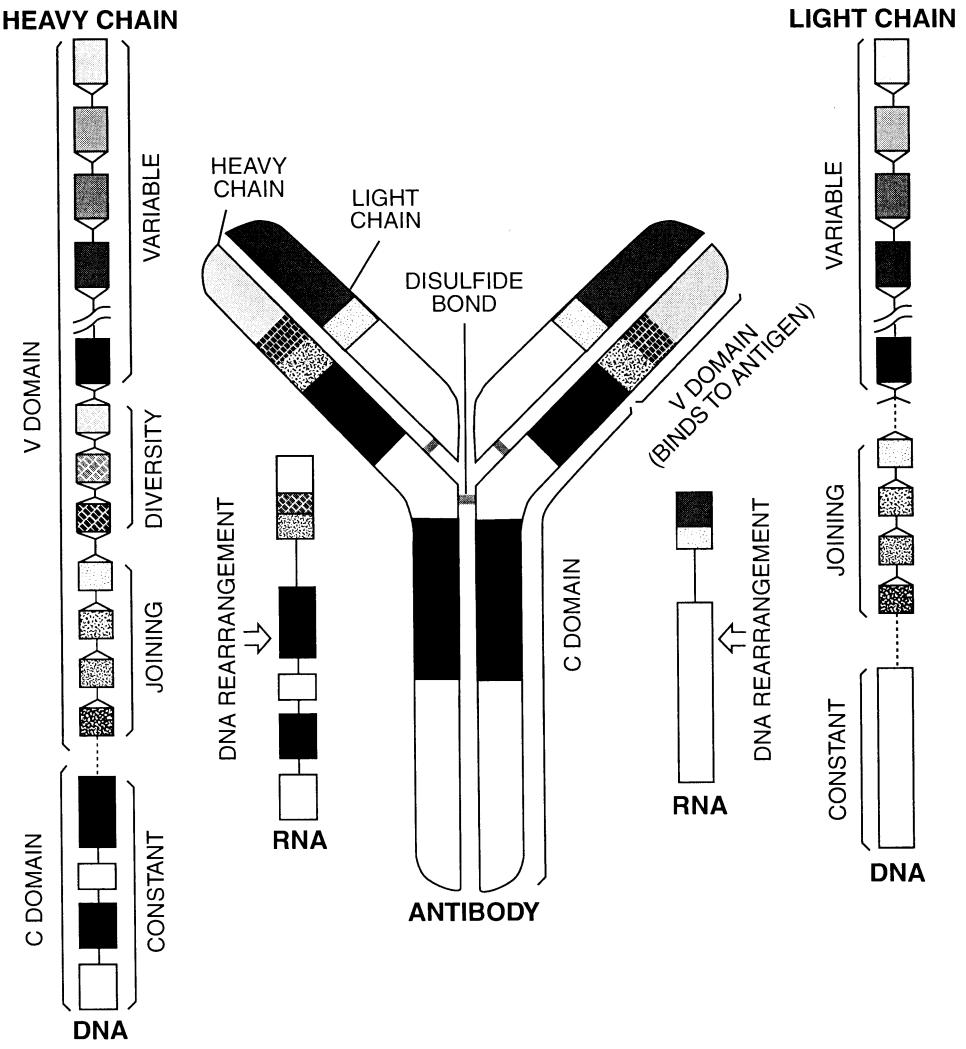


Figure 1 The coding and assembly of antibody molecules. Randomly chosen alternatives are used from different DNA modules to construct a "recombined" RNA transcript, which is then translated into a protein chain. Two heavy and two light chains are assembled into an antibody molecule. Redrawn from Janeway (1993).

The T cells mature in the (T)hymus. The randomly generated recognition type of each maturing T cell is tested against the molecules of the body before the cell is released. The cell dies if it recognizes self molecules. Thus random generation of variation followed by selective death creates circulating T cells that react only with nonself molecules. The processes by which B cells are prevented from reacting with self molecules are not fully understood. It may be that the absence of self-

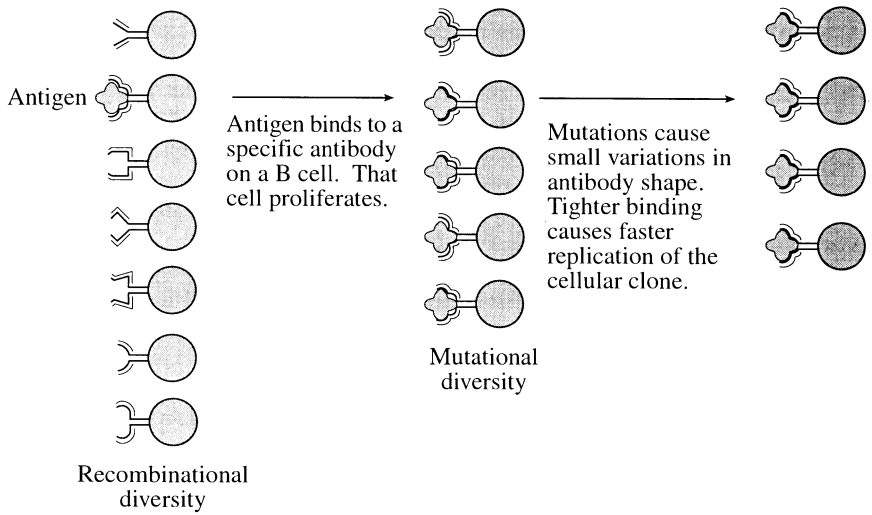


Figure 2 Clonal selection of B cells to produce antibody that matches an invading antigen. Recombinational mechanisms produce a wide variety of different antibody molecules (Fig. 1). All B cells of a particular clone are derived from a single ancestral cell that underwent antibody recombination. Members of a clone express only a single antibody type. Cells are stimulated to divide rapidly when an antigen matches the antibody receptor. This creates a large population of B cells that can bind the antigen. These cells undergo increased mutation in their antibody gene during cell division, producing a set of antibodies that vary slightly in their binding properties. Tighter binding causes more rapid cellular reproduction. Thus this second stage of selection (affinity maturation) enhances the antibody-antigen fit. Modified from Golub and Green (1991).

reactive T cells is sufficient to prevent clonal expansion of self-reactive B cells.

The use of a selection mechanism to create the self versus nonself distinction is costly because many of the newly formed T cells react with self and never mature. However, it is difficult to imagine how the vast array of recognition sequences could be generated without random combinatorial mechanisms. Janeway (1993) notes that the total antibody diversity is particularly impressive because a human has approximately 100,000 genes, but, at any one time, the 10 trillion B cells in an individual can make more than 100 million distinct antibody proteins. Thus random variation and selection appear to be a very good solution to the problems of information storage and response to unpredictable challenges.

Thus far I have described adaptive immunity caused by selection of cell clones within an individual. The adaptive immune system is itself a product of genetical evolution by natural selection. The evolutionary analysis of adaptive immunity therefore requires attention to two levels of selective processes, genetical and cellular.

D. Genetical Evolution of Adaptive Immunity

The adaptive immune system has a complex set of control mechanisms that generate variation, destroy T cells that react with self (negative selection), amplify cellular clones that react with invaders (positive selection), and maintain the ability to react quickly to reinfection by past invaders (memory). These controls of adaptive immunity are inherited (innate) traits produced by genetical evolution.

The immune system has, in addition to the controls of adaptive immunity, many other traits that are innate. Perhaps the best understood is the major histocompatibility complex (MHC), which I now describe.

T cells destroy an infected host cell if they can recognize the infection. In order to signal the T cells, host cells continually cut up intracellular proteins and present these fragments on the cell surface. The circulating T cells distinguish between presented fragments that are self or nonself and respond accordingly.

The molecules that bind intracellular protein fragments and bring them to the surface are coded by genes that reside within the MHC region. Each antigen-presenting molecule from the MHC has a groove that accommodates a peptide of 9 amino acids. Each particular MHC molecule can recognize and present on the cell surface only a subset of protein fragments (peptides). An individual has several different MHC types that, taken together, determine the set of peptides that can be recognized and carried to the cell surface for presentation. (Nine amino acids may seem, at first glance, to be too few for a discriminating recognition system. But there are 20 amino acids and 20^9=512,000,000,000 different peptides with 9 amino acids.)

There are both costs and benefits to having a large number of MHC types (Fig. 3; Nowak et al., 1992; Mitchison, 1993). The MHC molecules, which are found on cell surfaces typically bound to self peptides, define tissues as self. As T cells mature they are tested against the innate repertoire of MHC-self peptide complexes. A developing T cell dies if it would destroy a cell with self MHC. Thus the greater the MHC repertoire, the larger the number of T cells that are destroyed during development. If the MHC repertoire is too broad, then too few T cells would be able to develop.

On the other hand, if too few MHC types were present, then the host would not be able to recognize and present the protein fragments from many pathogens. The optimal number of MHC types must strike a balance between the costs of too broad a definition of self, causing a narrow T cell repertoire, and the benefits of recognizing a wide array of invaders. This type of optimality argument can help to define the forces that have influenced the genetical evolution of innate components in the immune system. There are, of course, many other factors that may have influenced the evolution of the MHC loci, such as the processes of gene duplication by which these loci have multiplied from a single ancestral locus.

The MHC loci are highly polymorphic, with between 10 and 80 different alleles known for each locus. Two lines of evidence suggest that resistance to particular diseases can strongly affect the frequency of MHC alleles. First, most of the variation among alleles occurs in the groove that binds protein fragments—the specific recognition area. Second, a few cases are known in which there is a strong spatial correlation between endemic diseases and MHC alleles that are associated with resistance to those diseases. For example, the allele HLA–B53 is associated

with resistance to a severe strain of malaria that occurs in children in The Gambia. HLA–B53 occurs at a frequency of 25% in this west African nation; by contrast, the frequency of this allele in Europe is 1% (McMichael, 1993). Other MHC alleles are implicated in resistance to HIV, the cause of AIDS, and to Epstein–Barr virus, the cause of various cancers. Disease correlations with MHC alleles suggest that selective pressures continue to influence the genetical evolution of the immune system (Thomson, 1991; Mitchison, 1993).

I close this section by summarizing four cases in which genetical evolution influences adaptive immunity.

(1) Genetical evolution of MHC loci affects the control of adaptive immunity. The number of MHC loci and the level of polymorphism at each locus determine the balance between negative selection of T cell clones and the ability to present foreign protein fragments on the cell surface.

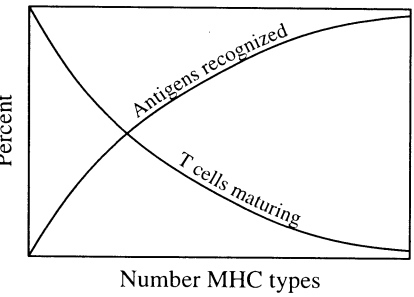
(2) The immune system uses adaptive mechanisms for some types of recognition (B and T cells) and direct (genetically encoded MHC) recognition for the presentation of protein fragments. This raises some interesting questions. From the point of view of an optimally designed immune system, is this particular mix of adaptive and innate recognition ideal? Or, would genetical evolution favor a shift toward adaptive recognition of protein fragments if suitable genetic variation existed?

(3) Regulation of the immune response is another form of innate control over adaptive immunity. Deployment of defenses is often costly in terms of energy spent on the production of new cells and toxic substances. In addition, the battle against invaders may lead to inflammation or local swelling because the methods used to clear infection can also damage the host tissues. Thus regulation of the components of the immune system and the setpoint for triggering a response are under strong selective pressures. These regulatory aspects of the vertebrate immune system are not well understood at present.

Induction of defense is a complex subject. It may be useful to look at much simpler forms of inducible defense to understand the problems involved. Harvell (1990a, b) has written excellent reviews of the inducible defenses that occur in a wide variety of organisms. The selective pressures on the setpoint for induction have been studied in two recent papers (Clark and Harvell, 1992; Frank, 1993). A phylogenetic perspective of the evolution of immune responses is presented by Klein (1986).

(4) The process of affinity maturation, discussed above, is another example of innate control. Affinity maturation occurs when the mutation rate of a B cell clone increases in response to a match between the clone's antibody and a foreign molecule. Those mutant cells that bind more tightly are stimulated to divide more rapidly. A quantitative trait such as enhanced mutation rate is very likely to be influenced by the processes of genetic variation and natural selection—put another way, the quantitative controls of affinity maturation are the product of adaptive processes at the genetic (innate) level.

Affinity maturation dynamically balances exploration versus exploitation in adaptive immunity. Initially the system explores widely by recombination to meet unpredictable challenges. After a close match is found the system exploits the match by reducing the information decay that further recombination would cause while simultaneously exploring for small improvements by mutation.



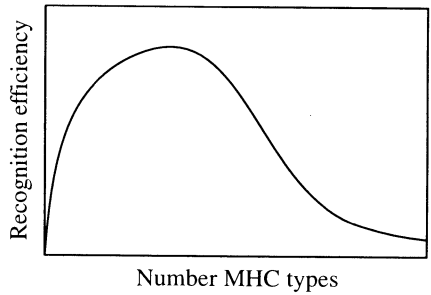


Figure 3 Optimal number of MHC types to recognize foreign antigen. The left panel shows two opposing forces. On the one hand, increasing numbers of MHC types enhance the probability that a foreign antigen will be recognized by the array of MHC specificities. On the other hand, more MHC types reduce the number of T cells that mature because self-reactive T cells are destroyed. The right panel shows that, by combining these two effects, there is an intermediate optimum that maximizes the recognition efficiency per T cell produced. There are not enough data to estimate accurately the magnitude of the two processes and the actual number of MHC types expressed (Nowak et al., 1992). The best estimate from current data is that 1-7% of T cells are removed by negative selection per MHC type. Each MHC type can bind a set of nine amino acid peptides with varying affinities. Thus each MHC type probably binds a fraction between 10^{-8} and 10^{-10} of the 5.12×10^{11} possible antigens. The number of MHC types expressed is estimated between 8-40 for humans. The actual number expressed in many different cell types is probably closer to the low end of the range.

The questions I have discussed about the immune system can be phrased more generally to apply to any two-level adaptive system. What is the optimal mix of innate (closed) and adaptive (open) mechanisms for particular problems in pattern recognition? What is an efficient mode of selection in order to achieve rapid learning and accurate memory? How is this selective mode achieved by the genetical evolution of innate controls of the adaptive process? What forces influence the setpoint that triggers a response to a recognized pattern? How are the problems of information storage and transmission solved?

I will show in the following sections that these questions, introduced with the immune system, apply to a variety of other adaptive systems.

IV. Learning

A newborn organism, faced with the world for the first time, begins to receive signals about the environment. Simple organisms often detect light, temperature, and chemical gradients. A baby mammal, endowed with a rich array of feature detectors, receives a tremendous amount of information. At first, sensory input has only the limited meaning encoded in the genome that guides the preliminary wiring of the nervous system—the primary repertoire. As the organism interacts with its environment during early development the neural connections undergo rapid changes, leading to an altered neural wiring pattern—the secondary repertoire.

All aspects of perception, meaning, and even consciousness must derive from the organism's physiological and neural interactions with the environment. Thus

the problem is to understand how genes shape the primary repertoire, how interactions between the primary repertoire and the environment lead to the secondary repertoire, and how learning is embodied in neural-environment interactions.

Consider an analogy with the immune system. The problem in immunity is to recognize all molecules within the body and categorize those molecules as self or nonself. The nonself molecules must further be categorized according to the appropriate type of defensive response that should be induced. Finally, the immune system remembers its categorizations over long time periods.

The number of molecules to be recognized and placed into different categories greatly exceeds the informational capacity of the genome. Thus there are only two ways for the body to obtain the information to recognize the diversity of molecules encountered: instruction or selection.

The instructional idea, popular in immunology in the 1930s and 1940s, suggests that new antibody (recognition) is achieved by shaping the antibody to the foreign template (see Golub and Green, 1991, pp. 8-12). Instruction directly from the environment is possible in principle, but is not known to occur. Under direct instruction, the body must be able to build its informational molecules to match a template—this requires a sufficiently malleable informational structure that can handle whatever external template is posed. In addition, the external information, now encoded in a similar internal molecule, must be transmitted successfully within the body. This seems to require that internal communication encodes information in a way that matches unpredictable forms of external information. As discussed in the previous section, the immune system uses selection rather than instruction to recognize and categorize the world.

Recognition and categorization, central to immunity, are also the fundamental problems of perception. The external world contains too much information and poses too many problems for all information and solutions to be coded directly into the genome. Once again, the alternatives for acquiring information are instruction or selection.

A. Instruction versus Selection

Consider an instructional model of learning (Fig. 4). The genotype codes for generative rules that specify how to build a neural network. The network has four inputs that react differently to features of the environment. Environment A stimulates (1, 2, 4). Environment C stimulates (1, 3, 4). Learning rules change synaptic connections between nodes (neurons) according to correlations in activation. Eventually the network learns to categorize features (1, 2, 4) as A and (1, 3, 4) as C by stimulating an internal node representing the environmental state. These internal nodes stimulate, in turn, other nodes that trigger appropriate action for each environment.

The network has learned by acquiring information about correlated features of the environment. However, the network architecture, the learning rules, and the interpretation of A and C must be strictly specified by the genotype for this learned information to be useful. Simple types of associative learning may be achieved in this way, with a specific module built to obtain information (instruction) directly from the environment.

The internal nodes A and C may be part of a larger network. Environmental categorization could then occur at a deeper level, without the need to specify directly the interpretation and action at such a fine scale. But this simply pushes the problem back without solving it. At some internal level, meaning and interpretation with respect to fitness consequences must be encoded by the genotype. There is no way for a network to self-organize toward an unspecified goal such as reproduction.

The instructional model in Fig. 4 seems to require too much of the genotype in terms of specifying the architecture, learning rules and meanings for each instructional module of a complex brain. Selection may be the only way to build a complex and meaningful information system from simple rules. The vertebrate immune system is an excellent example.

How could there be a selective, adaptive subsystem in the brain built by simple rules encoded in the genotype? The answer differs in only a few details from the instructional model of Fig. 4. Figure 5 shows a typical neural network fantasy that has the key elements of a selective system: random variation, continuity, and differential success.

The top row of nodes (1, 2, 3) are stimulated by three detectors of environmental state. For example, if the environment has states (1, 3), then the (1, 3) nodes will be stimulated in each of the three neuronal groups. In this case the group on the left will pass on the strongest stimulus to the next layer, which in turn stimulates the coordinating center A. Note that A is simply a richly connected region where neuronal groups tend to converge; there is no intrinsic meaning to the A region.

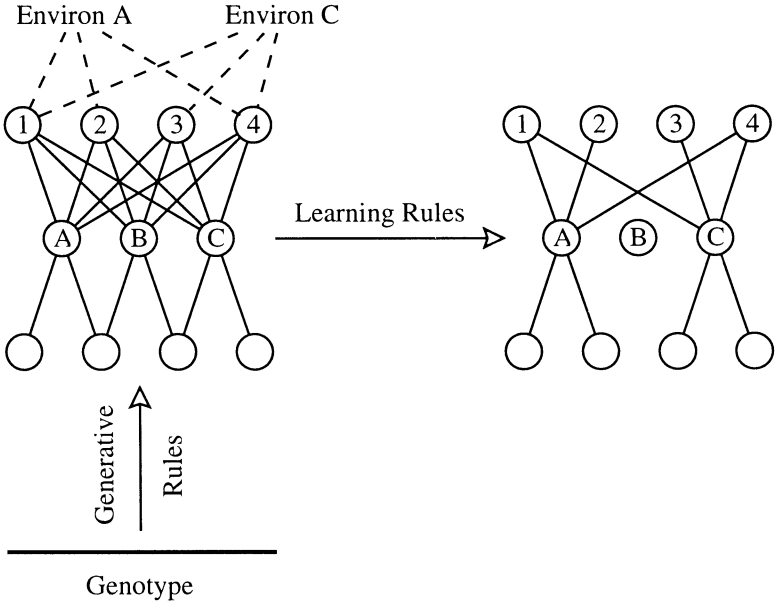


Figure 4 An instructional model of learning. This is a simple neural network example. See Hertz et al. (1991) for an introduction to the literature on neural processing of information and simple learning models.

When A is stimulated then connections are activated to two complex centers, which are treated here as "black boxes." The Move Forward center triggers simple motions that, in this case, result in detection of water. The Thirst center is a genetically coded region that returns positive stimulus when water is detected or acquired.

We can now trace the events that follow detection of environmental state (1, 3) along the bold connections. Starting at the top, the neuronal group at the left responds most strongly to the stimulus and passes a relatively stronger signal to the connection center at A. This switching point has connections to both the motion and thirst centers. In this case behaviors are triggered that cause water detection, sending a positive signal to the thirst center. The thirst center initiates a return pathway of stimulus, following the lines of the most strongly active connections. Internal rules of synaptic change cause the bold pathway to be strengthened—a form of credit allocation or fitness assignment for relative success with respect to the internal goal of satisfying thirst.

This is a simple neural network with basic learning rules. But it differs from the instructional model in three important ways. First, the system begins with a population of neuronal groups that respond differently to the same input. Second, the initial structure of each neuronal group is uncorrelated (random) with respect to environmental challenge and "meaning." Third, categorization of environments arises spontaneously as a result of the differential success of neuronal groups. The categorizations and success are subordinate to innate (genetically encoded) goals.

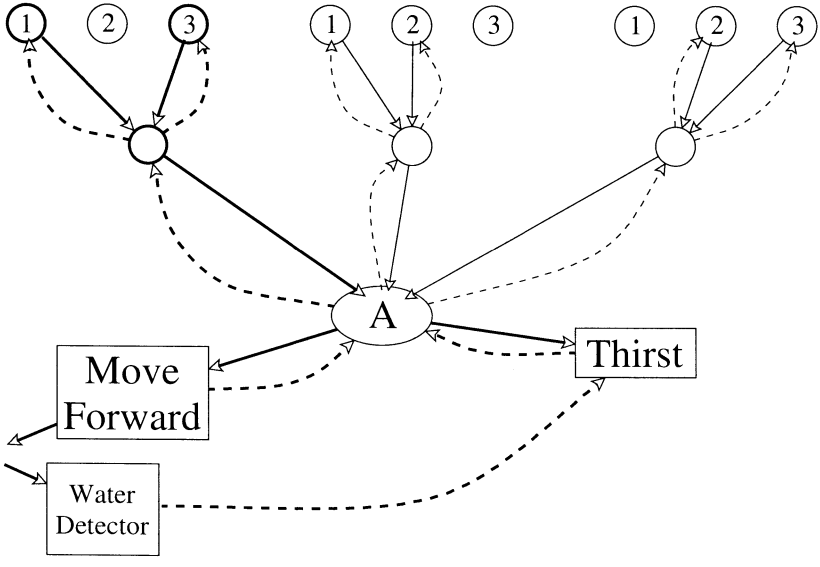


Figure 5 A selection model of learning. Note at the top that the system begins with a population of neuronal groups, where each group responds in a different way to the environmental features labeled (1, 2, 3).

B. Neural Darwinism

I now turn to a summary of the selective theory of brain development and learning recently proposed by Edelman (1987, 1988, 1989, 1992; see Edelman, 1987, pp. 14-22 for a review of earlier, related ideas by J. Z. Young, J.-P. Changeux and others). This theory of "neural darwinism" shares many features with neural network models (Rumelhart et al., 1986; McClelland et al., 1986; Hertz et al., 1991) and ideas from other areas of neurosciences. But Edelman's work differs in its explicit emphasis on selective ideas and a strong effort to tie every detail of the theory directly to biological observations of neural development and structure.

The basic components of neural darwinism are:

1. *Genes plus stochastic variation plus developmental selection create the primary repertoire.* The morphology (wiring) of the vertebrate nervous system at birth is an immensely complex structure. The information in the wiring pattern far exceeds the amount of information contained in the genome. Yet even the most helpless organism at birth has considerable sensory and motor abilities. Edelman (1992, p. 64) suggests that the wiring at birth—the primary repertoire—forms by a process of developmental selection:

> Imagine now this epigenetic drama in which sheets of nerve cells in the developing brain form a neighborhood. Neighbors in that neighborhood exchange signals as they are linked... They send processes out in a profuse fashion, sometimes bunched together in bundles called fascicles. When they reach other neighborhoods and sheets they stimulate target cells. These in turn release diffusible substances or signals which, if the ingrowing processes have correlated signals, allow them to branch and make attachments. Those that do not either pass on or retract. Indeed, if they do not meet their targets, their parent cells may die. Finally, as growth and selection operate, a mapped neural structure with a function may form. The number of cells being made, dying, and becoming incorporated is huge. The entire situation is a dynamic one, depending on signals, genes, proteins, cell movement, division, and death, all interacting at many levels.

Chance plays a large role in the actual neural connections formed. Even identical twins are predicted to have different neural maps at a fine scale. Indeed, this variability is inevitable given the fact that the information in the primary repertoire greatly exceeds the information in the genome.

The variability in the primary repertoire provides the basis for neuronal group selection to form the secondary repertoire.

2. *Selection of neuronal groups leads to perceptual categorization, memory, and learning.* A neuronal group is, roughly speaking, a set of neurons activated together in response to a particular stimulus. The selective processes act on populations of neuronal groups in the manner illustrated previously in Fig. 5.

For this selective process of learning to work effectively, the primary repertoire must contain many partly coupled groups whose connection strengths can subsequently be altered by rules of synaptic change. The initial synaptic diversity and subsequent change correspond to variation and selection in

Edelman's theory.

Two points about neuronal group selection must be stressed. First, the theory focuses on neuronal groups as the appropriate unit of analysis. This makes sense because individual neurons or synapses have too little information to provide a basis for selective differentiation of their performance. Second, selection of neuronal groups leads to altered synaptic strengths of connection rather than differential reproduction. "Group selection proceeds through synaptic modifications induced by the correlated activation of cells within a group" (Edelman, 1987, p. 169; see also Merzenich et al., 1988).

Group competition plays a central role in the theory. Roughly speaking, groups compete for members and for feedback connections from other groups: those groups poised to receive frequent correlated stimulus among all members will be constantly strengthened relative to other groups that less frequently receive correlated stimulus. Groups do not have clear boundaries because they are defined simply by correlated firing of local neurons; thus individual neurons may be in several groups and their associations necessarily change as a result of neuronal group selection.

3. *All learning and memory are embodied in the interaction between the environment and neural physiology as modulated by the innate value systems.* Categorization occurs by correlations of firing among neuronal groups in response to external stimuli. The types of category formed by this process depend on the sensitivity of the feature detectors and any biases in the primary repertoire. Thus even the simplest process of category formation has a strong innate (genetic) component that is subject to evolutionary modification by natural selection. However, this simple form of categorization is not sufficient to explain the types of goal-directed learning and behavior observed.

Edelman suggests that there are internal value systems or hedonic centers that are themselves embodied in neuronal groups, for example, thirst in Fig. 5. Other hedonic centers include hunger, sex drive, and curiosity. These centers are linked extensively throughout the brain to other neuronal groups by feedback connections. These control centers establish the basis for assigning "fitness" in competition among neuronal groups. These controls are directly influenced by the genotype and are subject to evolutionary modification.

Selective ideas about the brain are exciting, not because they are clearly true—it is too early to say yet—but because they could form a relatively complete theory of the nervous system and of behavior. Edelman has made a serious attempt to account for observed details of development and plasticity in neural maps, the causation of behavior, and the evolutionary modification of internal value systems (Plotkin, 1987). The idea that classification and behavior are controlled by synaptic modification of neural maps is not new. The novelty is an emphasis on selective systems and a consistent vision that explains many aspects of neurobiology and behavior—a global brain theory.

The special aspects of selective systems for neurobiology are sometimes difficult to keep clear. Therefore I close this section by emphasizing the distinction between selective and instructive theories. These theories are not strict alternatives about brain development and function. Any complex nervous system is likely to use both systems. The empirical issue is the relative importance of the two systems for the traits we wish to understand.

A selective (adaptive) system acquires information by selecting from *variation*

in a *population* of individual architectures generated *independently* of the environmental challenge. An instructional systems acquires information by *varying* a *single* architecture in a manner *correlated* with environmental challenge. The distinction leads to different predictions about neural development and learning. For example, selective systems require stochastic variation during development to provide the necessary variation for selection. Instructional systems will generally perform more poorly as stochastic variation increases in the development of the initial architecture.

C. Genetical Evolution of Learning

There are many ways in which genetic information interacts with the environment to affect behavior and learning (e.g., Drickamer, 1992; Alcock, 1993). For example, the external sensors (vision, olfaction, etc.) are mainly innate, imposing particular channels of communication between the organism and its environment. There are closed behavioral programs that follow a fixed pattern once invoked by environmental cues—these closed programs are also mainly innate. There are open behavioral programs subject to modification and learning through interaction with the environment. Learning is inevitably guided by internal value systems (McFarland and Bösser, 1993).

Interesting questions about the role of genetical evolution in learning include: What sorts of environments favor a closed program in which all information is stored in the genome? How does the genetic system discover closed programs? What environments favor an open program that causes behaviors, with initial biases fixed by the genome, to change with experience? What forces shape the innate biases and genetic controls of learning?

These evolutionary questions about the control of learning parallel those questions that I raised about the controls of immunity. Some controls of the immune response are innate, such as the specific set of MHC types (closed program). By contrast, other parts of the immune system are built by the genetic specification of controls on the adaptive subsystem, such as the negative selection against self recognition and the positive selection of clones with antibody that matches foreign molecules (open program).

I summarize two key issues for an evolutionary analysis of learning.

1. Learning Accelerates Genetical Evolution—the Baldwin Effect

How can a complex behavioral sequence be favored by natural selection if each isolated part of the sequence is of little value? A genetic mutation that caused the whole sequence is unlikely to occur all at once, and each genetic variant for part of the sequence will not be favored in isolation.

Baldwin (1896) suggested that learning can help to overcome natural selection's limited ability to discover complex behavioral traits, thereby accelerating the rate of evolutionary change. The idea that phenotypic modifications such as learning can feed back to inherited changes suggests a lamarckian mechanism of evolution that has essentially been disproved. The association between Baldwin's ideas and the discredited lamarckian mechanism confined acceptance of these ideas to a minority of evolutionary biologists.

However, recent work has shown that learning can indeed greatly accelerate evolutionary change without appeal to lamarckian inheritance (Hinton and Nowlan, 1987; Maynard Smith, 1987; Ackley and Littman, 1992; Fontanari and Meir, 1990; French and Messinger, 1994; Anderson, 1995).

Learning provides information about how close the genotype is to a good solution (Fig. 6). Imagine that a complex behavioral sequence (phenotype) has a high fitness but that slightly altered sequences are no better than random behaviors. If there is no learning then a genotype has to encode exactly the right sequence to gain any fitness advantage; nearly correct genotypes are no better than random. The chance of the favored genotype arising from a background of random behaviors is vanishingly small.

Now suppose that some learning occurs. Learning can be thought of as an exploration of behavioral sequences similar to the genetically encoded sequence, where sequences with improved performance are adopted by the animal. An animal's chance of finding the correct behavioral sequence depends on how near it is to the correct sequence initially. Fitness therefore drops off gradually from a peak at which the genotype encodes the optimal behavioral sequence, the height dropping with the number of behavioral changes that must be discovered to find the optimum. Natural selection is very good at pushing genotypic composition

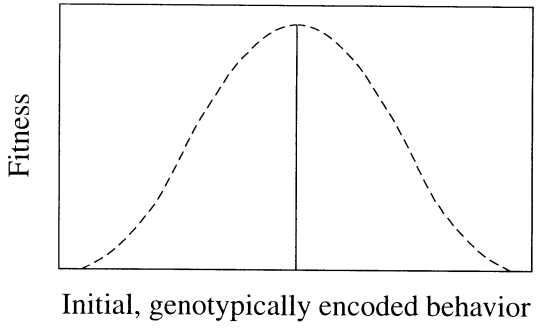


Figure 6 The Baldwin effect. Without learning, each organism expresses its genetically encoded behavior. Only a particular, complex behavioral sequence has high fitness, all other behavioral sequences have equally low fitness. This is shown by the solid line for a narrow fitness peak among possible genotypes. An exceptionally rare mutation is required to improve fitness. All other variations are equally bad with respect to the optimum. Thus natural selection will not move the population closer to the optimal behavioral sequence. Now suppose that learning occurs, with initial behavior determined by genotype. Those genotypes near the peak have a high probability of finding and learning the optimal sequence in a reasonable period of time. Genotypes more distant from the peak have a lower probability of learning the optimal sequence. Thus fitness increases smoothly with decreasing genetic distance from the optimum, allowing natural selection to cause steady improvement over time (dashed curve).

steadily up a slope of improving fitness. Thus learning, by providing clues about the distance to the favored behavioral sequence, greatly accelerates the rate of evolutionary change.

2. What environmental challenges favor learning?

Learning provides a genotype with a method of phenotypic exploration. The Baldwin effect shows that exploration can ultimately cause the transfer of learned behaviors into an innate genetic program. Innate (closed) genetic solutions have an advantage over learned (open) solutions in a fixed environment because no energy is wasted on failed explorations. If the Baldwin effect were the only force operating, all unchanging problems would be solved by closed programs that exploit known solutions rather than open programs that explore opportunities for improvement. Learning would disappear.

What types of environmental challenge favor learning? There is no coherent body of theory on this important question (see preliminary efforts in Holland, 1975; Boyd and Richerson, 1985, chapter 4; Todd and Wilson, 1993).

Questions about learning can be stated in a more general way when learning is viewed as an emergent adaptive system that has evolved by natural selection of genetic variants: What types of challenge favor an adaptive system (genetics) to spawn a subsystem of variation and selection (learning)? In what ways will adaptive subsystems such as learning differ when they have been shaped by different kinds of challenge?

These questions can be addressed only when cognitive mechanisms are viewed both as controls of adaptive learning systems and as evolved adaptations of the underlying genetic system. This dual view of learning has a long history (Richards, 1987), but has only recently gained attention in evolutionary biology (Real, 1992, 1993), psychology (Barkow et al., 1992) and computer science (Meyer et al., 1993).

Computer models of learning are perhaps the greatest spur to conceptual work. Computers can be used to test which learning programs and types of cognition perform best under different kinds of environmental challenge.

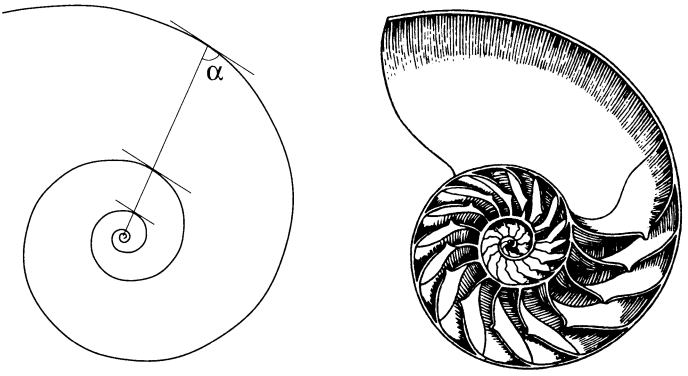


Figure 7 The logarithmic spiral. The *Nautilus* shell on right is copied from Thompson (1961, p. 173).

Advances in robotics and engineering control also depend on a clear understanding of how different types of learning and cognition influence performance. Although many recent papers have focused on these topics (Meyer et al., 1993; Brooks and Maes, 1994; Cliff et al., 1994), there are no general conclusions yet.

The problem once again focuses attention on the specific kinds of challenge that shape adaptive systems. Referring to Table 1, each of the three main challenges can favor learning. Information decay in the genome can be corrected phenotypically by an adaptive subsystem that learns. Predictable complexity may be an important challenge when the motor controls and input-output connections for a behavioral sequence contain too much information to store within the limited genome. Young animals sometimes use trial-and-error learning periods to develop behaviors that eventually converge to a fairly routine, species-typical sequence. This type of "developmental" learning may be a response to the challenge of information storage for complex behaviors. Finally, unpredictable challenges can be met with an adaptive subsystem that learns by using processes of variation and selection.

V. Development

Parasitic attack or unpredictable abiotic environments require flexibility. Many animals produce phenotypic solutions with adaptive subsystems, such as immunity and learning. Immunity and learning are two aspects of development—the creation of a phenotype from the information encoded in the genotype. Morphology is another, more traditional, domain of developmental study. The problem is how the one-dimensional information in the genotype is transformed into the three-dimensional structure.

A. Morphology

Mollusc shells develop according to simple generative rules (Thompson, 1961; Meinhardt, 1995). The left panel of Fig. 7 shows a logarithmic spiral, which is a nearly perfect match for the coiling pattern of the *Nautilus* shell shown on the right. A logarithmic spiral is produced by drawing a line from the center to the current tip of the spiral, and then adding to the spiral such that the angle between the radial line and direction of growth is constant. Shells can grow only by adding new material to the leading edge. New growth typically follows a constant angle relative to the radius, causing a logarithmic coiling pattern.

Variation in the angle of growth explains variation in coiling patterns in the radial direction, as shown in the top row of Fig. 8. Shells also vary in the tightness of coiling with respect to height, which can be explained by the relative rate of growth down from the radial direction (bottom row of Fig. 8).

B. Developmental Selection

The full range of physicochemical processes involved in shell growth are complex. Yet there is a certain determinism in the rules of growth when compared with

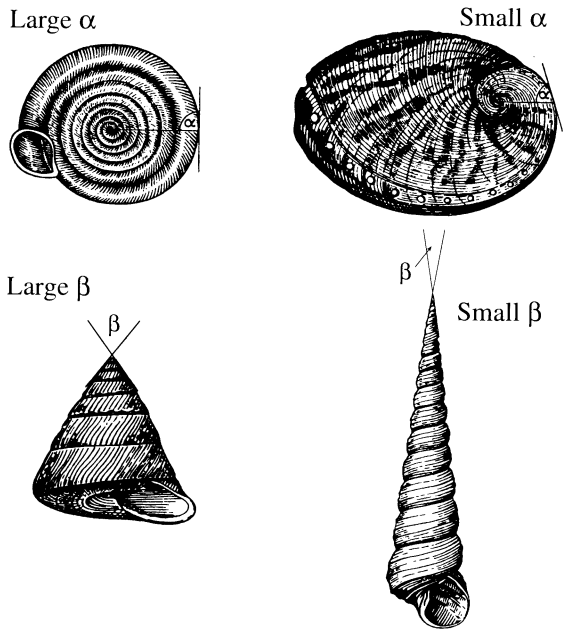


Figure 8 Logarithmic coiling patterns of shells. The angle α controls coiling in the radial direction, and the angle β controls coiling in the vertical direction. From Thompson (1961, p. 192).

immunity and learning. Figure 9 shows the contrast between these direct rules of morphology and the indirect route by which immunity and learning affect the phenotype.

The shell example suggests that morphological pattern formation follows direct generative rules specified by the genotype. However, there is considerable controversy about the details of those rules (Hall, 1992; Goodwin et al., 1993). Several authors have proposed, as an alternative to direct rules of growth, that pattern formation is best viewed as the outcome of developmental selection. This theory emphasizes stochastic variation among a population of growth trajectories coupled with selection of particular trajectories that meet critical design criteria. (Recent suggestions of this theory include Edelman, 1988; Sachs, 1988; Wagner and Misof, 1993.)

Developmental selection determines the innate wiring pattern of brains in Edelman's theory of neural darwinism. The process depends on stochastic fluctuations in the movement and proliferation of cells to generate variability in structure. Two selective systems act on the variability generated by stochastic fluctuations. Positive selective controls stimulate cell division and the formation of particular neural connections. Negative selective controls cause rapid cell death

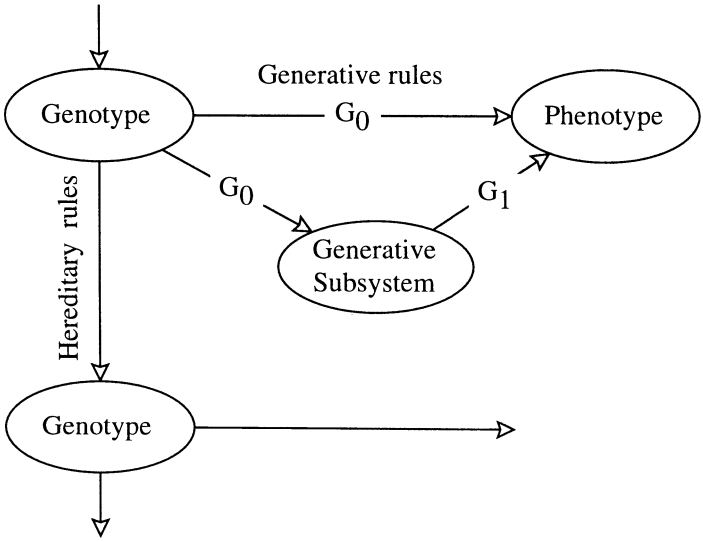


Figure 9 Generative rules for the development of the phenotype. The genotype is passed from generation to generation according to the hereditary rules for transmission, as in traditional models of biological populations. The success of each genotype depends on its phenotype. The genotype specifies properties of the phenotype through generative rules for development. The genotype directly encodes the generative rules G_0. These rules may lead directly to the phenotype, such as specific genes for metabolic enzymes or laws of growth for morphological development. Alternatively, G_0 may produce a generative subsystem, which in turn specifies a second set of generative rules, G_1. The vertebrate immune system is an adaptive subsystem that specifies generative rules for variation and selection. Simple learning rules are generative rules that change the phenotype in response to the environment; adaptive learning rules produce phenotypic change by variation and selection. A language module may be a generative subsystem that influences the basic grammatical rules used to generate sentences. The grammatical rules, and all aspects of phenotype, are also influenced by the environment (not shown).

among those neurons that fail to make selectively favored movements and connections. The primary repertoire created by developmental selection is highly variable at the level of particular cell-cell connections. This variability forms the substrate on which neuronal group selection shapes the secondary repertoire of the learning organism.

Developmental selection is a reasonable hypothesis for neuronal development. But the nervous system is so complex that it is difficult to compare selective theories with other ideas. Two simpler developmental problems provide a clearer view of the conceptual issues.

Distribution of stomata on leaf surfaces.—Plants exchange gases with the air through small openings (stomata) on the leaf surface (Fig. 10). The distribution of stomata on the leaf surface is a classic example of spatial patterning in development (Sachs, 1991). Pairs of stomata rarely develop adjacent to each other, and the distances between neighboring stomata are larger than if locations were determined randomly. But the developmental program is not a deterministic

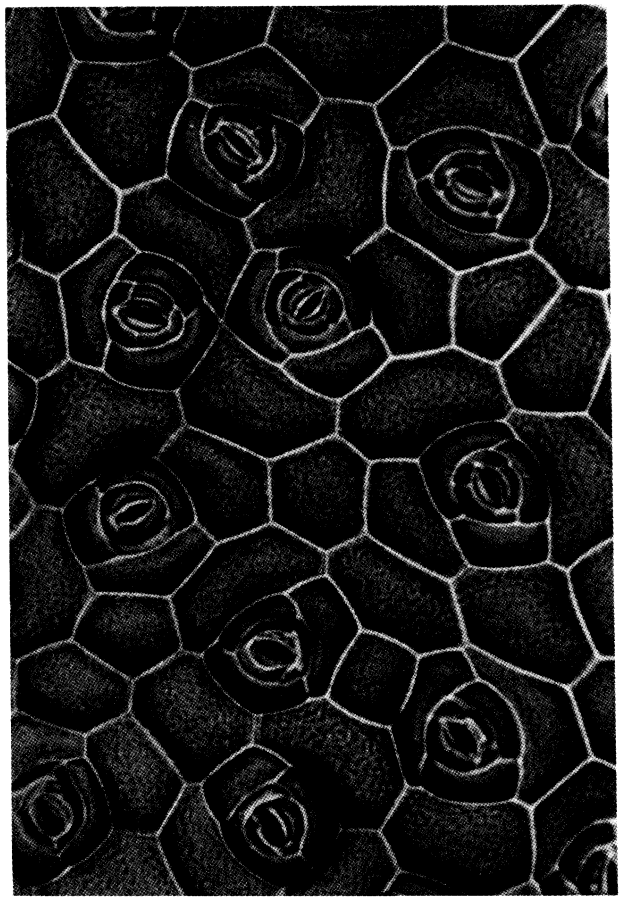


Figure 10 Stomata on the surface of a *Begonia* leaf. The stomata are opened and closed by the changing shape of the small guard cells that surround the pore. The spatial distribution is regulated developmentally to prevent neighboring cells from differentiating into stomata. But the particular cell lineages that differentiate into stomata and the distances between neighboring stomata appear to be strongly influenced by chance events. From Sachs (1991, p 7), copyright © 1991. Reprinted with the permission of Cambridge University Press.

unfolding of pattern—the fate of particular cellular lineages and the ultimate location of stomata depend on many chance events.

Kagan et al. (1992) have proposed a model of developmental selection to explain stomatal patterns. In the model each cellular lineage is an *individual* growth trajectory. Pattern is determined by variation and selection among the *population* of cellular lineages that contribute to the leaf surface.

Each stoma typically develops from differentiation of a single cellular lineage. Differentiation begins with an unequal cellular division. The smaller product may divide a second time, more or less unequally. The process continues until an equal division forms the two guard cells of the stoma (Fig. 10).

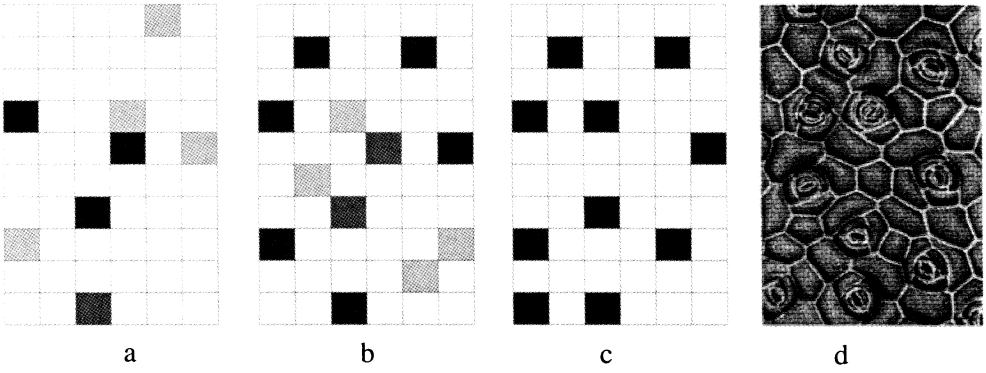


Figure 11 A model of variation and selection that develops a spatial pattern similar to the stomata on a *Begonia* leaf. Each square represents a cellular lineage. All lineages begin as normal epidermal cells (white). In each time step a normal lineage switches to a growth trajectory leading to stomatal development with probability 0.05. The early stage is coded by the lightest gray and assigned a value of one. A second stage of differentiation is dark gray, with a value of two. A late stage is black, with a value of three. In each time step, a sum of values is calculated for the eight neighbors of each cell, discounting the four corners by one-half. (The edges are connected in a torrus so that all cells have eight neighbors.) A sum of less than one allows an intermediate stage to progress to the next stage. A sum between one and three causes reversion to the previous stage. A sum greater than three resets the lineage to the normal state. (Reversion may often be caused by death of a lineage and filling in by neighbors.) The panels a, b, and c show the state of a sample run after 5, 15, and 30 time steps. At the final step in panel c all intermediate stages revert to normal cells, leaving only normal and final, stomatal stages. This type of model is known as a cellular automata, popularized in the *Game of Life* and found on many computer screen savers.

The development of a single stoma depends on programs internal to the cell lineage. But observations suggest that variation and selection among lineages play an important role in final pattern (Kagan et al., 1992). The initial unequal divisions appear to arise spontaneously among lineages without any particular pattern. When neighboring lineages begin differentiation, one or both revert to a typical developmental program that leads to normal epidermal cells. Figure 11 shows how a simple model of variation and selection can produce a spatial pattern typical of stomata.

A model with random variation and local selection seems so simple that it hardly needs justification. Indeed, the classic reaction-diffusion model for spatial pattern depends on similar principles (Murray, 1989). In each location chemical reactions cause the increase or decrease of a particular substance. Diffusion of the reactants causes spatial interactions between neighboring sites. Simple models produce patterns that match zebra stripes, leopard spots, and coloring on sea shells (Murray, 1989; Meinhardt, 1995).

Reaction-diffusion models differ from population models of variation and selection in several ways. Reaction-diffusion is a continuous chemical process that leads to a highly ordered final state. Population models have discrete births and deaths of cellular lineages. The final pattern is ordered but the growth trajectories and details of final state are unpredictable. In population models, form depends on the range of variant growth trajectories that are generated, and the control

processes that select among alternative trajectories.

Competition among shoots for root resources.—A particular shoot on a plant typically obtains resources from a corresponding subset of roots. The association between roots and shoots can change over time by modification of vascular contacts among neighboring shoots.

Sachs et al. (1993) suggested that a plant contains a population of competing shoots. Those shoots in the best condition outcompete their neighbors and obtain additional root support by modification of vascular connections.

The individual shoot "modules" compete for resources based on variable growth rates. The developmental program, which evolved by genetical selection, controls the flow of resources among members of the shoot population. Thus simple, local generative rules can develop an efficient, large-scale phenotype by imposing selection on uncontrollable aspects of cellular and modular variation. Indeed, developmental selection works only if there is significant variation among alternative, competing developmental trajectories.

C. Summary

This section concludes my summary of adaptive subsystems and generative rules. These processes transform hereditary information (genotype) into mechanisms that can interact with the environment (phenotype).

I have assumed that the genotype varies in its coding for particular generative rules, such as the generation of antibody variants or the number of MHC types. But I have not considered the processes that influence the kinds of hereditary information that are bound together to form a genotype. How is such a complex unit of information formed by evolutionary processes? Why is information regularly mixed between units by sex in order to produce subsequent generations? Why do different evolving populations—adaptive systems—often mix to form higher-order groups that cooperate and compete? In the next two section I turn to these questions on the evolution of hereditary information.

VI. Symbiosis

Adaptive systems are highly social. That may seem a strange statement. But the fact is that adaptive systems often compete with one another and often join forces in cooperative communities. This social structure is perhaps the most important and difficult problem in understanding the natural history of adaptive systems.

In later sections I will discuss some of the consequences of interactions among adaptive systems. In this section I briefly describe the natural history of symbiosis. My goal here is to discuss the main concepts and to provide an introduction to the literature. I begin with an analogy between culture and bacterial gut symbionts. This surprising analogy emphasizes that the boundaries between separate evolving systems blur in real life. This is a fact that must be faced squarely by historical descriptions of adaptive systems and by any theory that attempts to explain the main properties of such systems.

A. Culture

Culture is the ideas, facts, attitudes, and beliefs that are *transmitted* from one member of the society to another. Dawkins (1976a) coined the term "memes" to refer to individual units of culturally transmitted information. A word of a language is an example of a meme. Darwin and many others have noted that languages evolve by differential success of words and rules of composition.

Memes are analogous to genes because both have (1) temporal continuity transcending their containers (bodies or brains), (2) particular patterns of transmission, (3) imperfect transmission that generates variability (mutation), and (4) differential rates of transmission (reproduction). Thus cultural units—memes—form an evolutionary population that has its component frequencies determined mainly by a system of variation and selection (Dennett, 1995).

Cultural selection is different from the somatic selective systems of immunity and learning discussed earlier. The somatic selective systems are simply phenotypic mechanisms by which an organism meets environmental challenge, just as regulation of body temperature is a phenotypic mechanism that can enhance survival and reproduction. Because the somatic systems are governed by innate (genetic) controls, the apparent goal-directed nature of these somatic systems is wholly subordinate to the goal-directed nature of the underlying genetic system (Plotkin and Odling-Smee, 1981).

Memes, by contrast, have a continuity that transcends a single body and a transmission system that differs from genes. In short, culture has a life of its own.

Genetic systems are familiar, but memes may seem a bit strange at first. Memes live in bodies but can be passed from parent to offspring, from teacher to student, among friends, among enemies, or from child to grandparent. Memes are transmitted like the symbiotic flora and fauna that live in digestive tracts. Gut bacteria, and memes, face two opposing selective pressures. Bacteria or memes that enhance host survival also enhance their own survival—the cooperative side of the relationship. By contrast, a trait that enhances transmission of a bacteria or meme from host to host, but also harms the host, could increase in frequency.

The potentially harmful effects of gut symbionts are illustrated by gut bacteria that cause diarrhea. Natural selection favors an increase in the virulence of the bacterial flora when diarrhea can increase host-to-host bacterial transmission at a rate sufficient to offset the reduced survival of the bacteria caused by harm to the host. Natural selection favors a decline in virulence when diarrhea does not increase transmission sufficiently to offset reduced survival (Anderson and May, 1982; Ewald, 1994; Frank, 1996).

A simple meme example is less easy to find. Dawkins (1976a, p. 198) discusses the meme for human celibacy as a case in which a meme maintains itself in spite of reducing the genetic success of the host. A truly celibate priest does not reproduce, yet his celibacy meme has managed to transmit itself to enough young men to maintain its numbers over many hundreds of years. Although celibacy may have alternative explanations, a meme that did increase its host-to-host transmission at the expense of host survival is a virulent meme in the same way that diarrhea is caused by virulent symbionts increasing their host-to-host transmission. Both memes and bacteria can be helpful symbionts or harmful parasites.

Memes, like bacteria, create their own apparent goal-directedness because they form a selective system with replicators whose permanence transcends individual bodies. But a meme's ability to be transmitted—literally, to infect a mind—depends on the structure of minds. Minds, in turn, have some innate (genetic) controls, so the genes of the host and the symbiotic memes cannot be wholly independent. People disagree about the extent that genes, by shaping the structure of minds, can constrain the types of memes (cultures) that can succeed (Boyd and Richerson, 1985; Barkow et al., 1992). I briefly mention some of the issues.

The tension between the direction of evolution favored by genes versus memes has two components (Cavalli-Sforza and Feldman, 1981; Boyd and Richerson, 1985). The first concerns the extent to which these directions will differ. The second concerns how tensions are resolved when selection of genes versus memes favors different traits. I examine each of these components in turn.

If a meme is transmitted only from parent to offspring, then the inheritance patterns of genes and memes are symmetric (Boyd and Richerson, 1985). In this case any trait that enhances meme transmission also enhances gene transmission and vice versa. All members of the symbiotic community favor the same direction of evolutionary change. One can therefore analyze which traits are favored by selection from either a purely genetic or a purely memetic point of view. The conclusion from either analysis is that selection favors traits that increase relative reproductive success. (See Feldman and Zhivotovsky, 1992, for a more sophisticated theory of symmetric transmission.)

Memes frequently have a pattern of transmission that differs from genetic transmission. Genes and memes may favor different directions of evolutionary change with asymmetric inheritance. The diarrhea and celibacy examples show that a tension arises when symbionts (memes or bacteria) enhance their host-to-host transmission at the expense of host survival and reproduction.

Who wins when there is a conflict between host and symbiont? One line of thought suggests that the host has the upper hand. The idea can once again be described by a parallel with gut symbionts.

Ruminants have an additional niche for symbionts in their second stomach chamber. The additional chamber was probably favored by natural selection of genetic variants because the symbionts enhance genetic transmission of the host, or at least they did at some time in the past. Put another way, the structure and physiology of the additional stomach probably evolved to use symbionts in a way that enhances host fitness.

Minds, to the extent that they contain and transmit memes, are a niche for memetic symbionts. The structure of minds evolved, and continues to evolve, by selection of genetic variants that favor enhanced genetic transmission. Thus genes, by controlling the structure of the mind, may be able to constrain the types of memes that can succeed. If so, then joint selection of gene-culture interactions should favor traits that enhance the relative reproductive success of genes.

On the other hand, some people argue that once a niche for cultural transmission evolves in minds, cultural evolution can proceed unconstrained. Thus culture can be understood without reference to the historical reasons for the evolution of the cultural niche. In terms of the ruminant, once the second stomach exists, bacterial evolution is unconstrained by reproductive consequences for the host.

The truth is undoubtedly between the extremes of wholly unconstrained cultural evolution and cultural change purely subordinate to genetical evolution. The point I wish to emphasize here is that the symbiosis between bodies and culture is influenced by the same evolutionary processes as the symbiosis between bodies and gut flora. A body contains a large community of many different evolving systems. These systems share common interests only to the extent that their transmission patterns overlap. Memes are simply one type of inhabitant in this complex community.

B. Symbiosis in the Genome

The genome itself is also a community that contains both common and conflicting interests. The factors that influence conflict and cooperation among parts of the genome have been discussed extensively (Hurst, this volume). I present one brief example to illustrate the problem.

Most organisms inherit mitochondrial DNA from their mother, with no input from their father. By contrast, most other genetic material is obtained equally from the mother and father. For most traits these different modes of transmission, matrilineal versus biparental, have no consequences for the direction of evolutionary change favored by selection. For example, efficient respiration increases both matrilineal and biparental transmission.

The allocation of resources to sons and daughters affects matrilineal and biparental transmission differently. Traits that enhance the production of daughters at the expense of sons always increase the transmission of matrilineally inherited genes. For example, in some hermaphroditic plants the mitochondrial genes may inhibit pollen development and simultaneously enhance the production of seeds (Edwardson, 1970; Hanson, 1991). Selection of genetic variants in the mitochondria would favor complete loss of pollen production in exchange for a small increase in seed production because the mitochondrial genes are transmitted only through seeds (Lewis, 1941). Such reallocation of reproduction would greatly reduce the transmission of biparental genes because biparental transmission depends on the sum of the success through seeds and pollen. Thus there is a conflict of interest between the mitochondrial and nuclear genes over the allocation of resources to male (pollen) and female (ovules) reproduction (Gouyon and Couvet, 1985; Frank, 1989).

This conflict within the genome is similar in structure to the tension between genes and memes. Conflict occurs whenever a trait can cause differences in the rate of transmission of subgroups within the organism (Dawkins, 1982). Different traits partition the organism in different ways. In the example given here, respiration unifies the whole community, whereas resource allocation to sons and daughters splits the community among subgroups that are inherited matrilineally, patrilineally and biparentally (Fig. 12).

There are many similar types of conflict that occur within genomes (Hurst, this volume). Leigh (1977) has referred to this aggregate of common and competing interests as the "parliament of the genes." I discussed the mitochondrial example because it also illustrates my theme of symbiosis. At one time in evolutionary history cells existed but none had mitochondria. Several hundred million years ago a cell formed a successful symbiosis with an

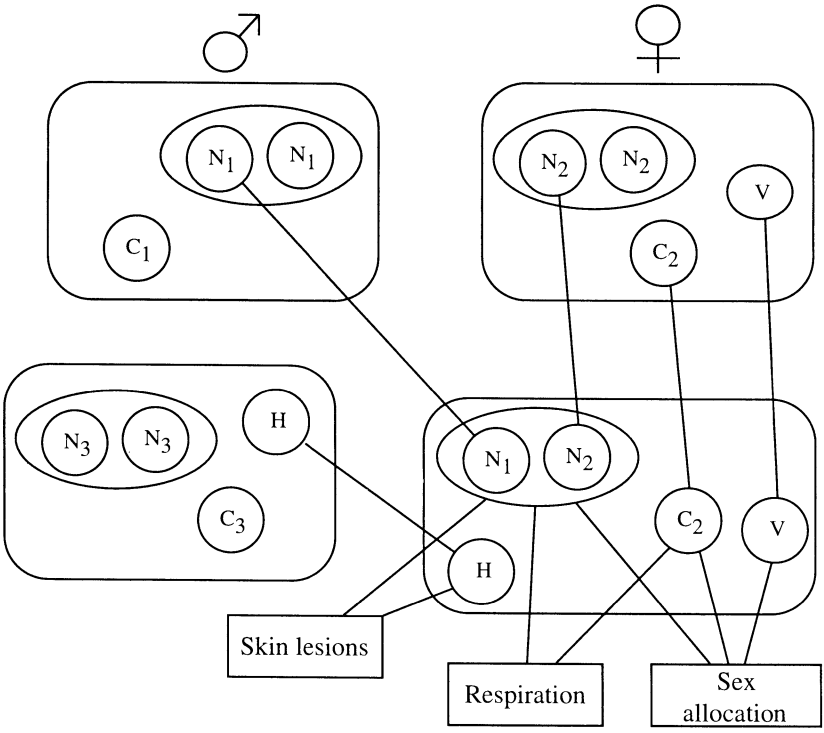


Figure 12 The mosaic nature of hereditary transmission, symbiosis, and the generation of phenotype. The top male and female individuals, which are really communities of symbionts, produce the offspring on the lower right by sexual reproduction. One-half of the nuclear (N) genes come from each parent. The cytoplasmic (C) elements, including the mitochondria, come only from the mother. Vertically (V) transmitted symbionts, which are typically viruses and bacteria, also follow the matriline. The individual on the lower left carries a horizontally (H) transmitted parasite, which infects the new offspring. This offspring expresses several traits, three of which are shown. Each trait is influenced by different hereditary subsets of the community. For example, the horizontal parasite produces skin lesions that enhance its rate of transmission, and the nuclear genes produce traits that attempt to clear the infection and heal the lesions. All components of the community, (N, C, V), are in conflict with the horizontal parasite (H) over the lesions because only the parasite is transmitted through lesions. The C and N components directly affect respiration. All components favor efficient respiration because all gain longer life and greater transmission from this trait. The matrilineally transmitted C and V components favor production of daughters. The biparentally transmitted N components favor equal production of sons and daughters. The transmission of H is unaffected by sex allocation.

intracellular bacteria. The bacteria probably had a metabolic pathway absent in its host (Margulis, 1981; see Khakhina, 1992, and Cavalier-Smith, 1993, for history of this research).

C. The Organism as a Community

An organism is a complex community. Conflicts occur within the genome; tissues house a vast array of bacteria, viruses, and other symbionts; and in some organisms the brain provides a home to memes. If the genome is a parliament, then the "organism" is a loose federation of states. Each particular challenge defines how interests overlap or conflict.

Although an organism is a complex symbiosis, the simpler, traditional view of organisms as unitary is adequate for many questions. For example, a trait such as efficient respiration unites the community with a common goal. In addition, most genes are transmitted in the usual biparental way. These genes often dominate the community because they can influence the substrate (tissues and brain) for all other symbionts.

It is a simple fact that adaptive systems tend to form symbioses. In the next section I examine the role symbiosis plays in genetic systems.

VII. The Origin and Evolution of Genetic Systems

Oparin (1924) and Haldane (1929) asked: How did life begin? Of course they were not the first to ask that question, but their ideas formed the first plausible theories for how replicating molecules arose from the prebiotic environment. The tradition established by Oparin and Haldane has led to many interesting studies on the chemistry of early life (Deamer and Fleischaker, 1994). Three questions dominate this work. Which organic molecules arose spontaneously in the prebiotic environment? What are the properties of these molecules in terms of stability, capacity for information storage, and a tendency to replicate? Which are the precursors of life?

The chemical research assumed that natural selection sorted among early competitors and refined the replication process. However, chemical problems dominated the research and few thought explicitly about the origin of life as the evolution of an adaptive system. Eigen (1971) initiated a new era by examining the balance between information decay in replication (mutation) and improvement by natural selection. Although this tension between mutation and selection had been widely studied in population genetics, application to the origin of life identified special problems about early evolution that stimulated a new wave of research.

Meanwhile, books by Williams (1975) and Maynard Smith (1978) on the evolution of sex focused attention on the other end of the problem. This work starts at the present, with the great diversity of genetic systems that exists in nature, and asks about the evolutionary forces in the past that have shaped this diversity. The well-developed theories from this work have recently been applied to problems near the origin of life, leading to many new insights about the evolution of genetic systems.

A. The Error Threshold and the Origin of Life

The first replicating molecules were copied without the aid of error-reducing replication enzymes. This undoubtedly led to high mutation rates. Evolutionary improvements are difficult with high mutation rates because replication errors erode any gains in reproductive efficiency caused by natural selection. Roughly, if more than one mutation occurred in a molecular sequence in each round of replication, then the population would eventually consist of random sequences. If the mutation rate were less than one per molecule, sequences with a reproductive advantage would spread in the population (Eigen, 1971; Eigen and Schuster, 1977; see reviews in Maynard Smith, 1979; Eigen, 1992).

The mutation rate sets a limit on the size of evolving molecules. If the error rate per site in a molecular sequence is μ, then molecules of length greater than $1/\mu$ will have more than one error per round of replication. Only molecules smaller than this "error threshold" can be improved by natural selection.

Eigen and Schuster (1977, 1978a,b) estimate that an RNA molecule of between 10 and 100 base pairs is above the error threshold if there are no replication enzymes to enhance accuracy. Information to produce a replicase probably requires between 1000 and 10,000 base pairs. This size range is above the error threshold, thus a replicase cannot evolve by natural selection. The error threshold presents a barrier to the evolution of large genomes with efficient replication. As Maynard Smith (1983) said, "No large genomes without enzymes, and no enzymes without a large genome."

Eigen and Schuster (1977, 1978a,b; Eigen, 1992) suggested the hypercycle model to explain how replication enzymes evolved in spite of the constraint imposed by the error threshold. Maynard Smith (1979), in his elegant example of the hypercycle, describes replication of the message GOD SAVE THE QUEEN. Suppose that each letter is coded by five bits in a sequence of 0's and 1's. (A string of five 0's and 1's is needed to code for the 26 letters of the alphabet because $2^4=16$ and $2^5=32$.) The 15 letters require 75 bits. If the mutation rate is 1/50, then the processes of mutation, replication, and selection of the strings closest to the target message would lead to random strings because the error rate overpowers the rate of selective improvement. The message is too long.

Now suppose that each word is encoded on a separate molecule. The largest word needs only 25 bits, which is less than the error threshold of 50. Mutational decay is no longer a problem. But separation of words causes a different problem: the replication rates of the words are likely to differ. Because the molecules for each word compete for substrates, the population would ultimately consist of only the fastest replicating word and the mutants derived from that word. The whole message cannot succeed by independent evolution of the individual words.

The hypercycle solves the problem of coordinating a symbiotic group that is composed of competing subunits. Suppose an increase in the number of GODs increases the rate of replication of the SAVEs, an increase in the SAVEs aids the replication of the THEs, the THEs enhance the QUEENs, and the QUEENs complete the cycle by enhancing the replication rate of the GODs, yielding: GOD $\rightarrow$ SAVE $\rightarrow$ THE $\rightarrow$ QUEEN $\rightarrow$ GOD $\rightarrow$...

The hypercycle is stabilized by the coupling of replication rates among words. A member of a cycle can outcompete any isolated word, and an efficiently coupled

cycle can outcompete less efficient cycles. The cycles act as individuals that compete against other cycles. Each word in a cycle is like a gene in an individual.

The components of a cycle could cooperate in producing a replication enzyme that decreased the error rate in copying molecules. The replicase would then reduce the mutation rate, making large genomes possible. Compartmentalization into protocells is the next evolutionary step. Compartmental cycles with increasing genome size lead to the cellular (or viral) forms of life that exist today and that appear in the earliest fossils.

This view emphasizes the role of symbiosis in the evolution of adaptive systems. The very strength of the hypercycle theory, the power of symbiosis among small replicators to produce complex function, also turns out to be its greatest weakness.

B. Symbiosis and Early Evolution

Conflict frequently destroys symbiotic relationships even when there is great potential for mutual benefit and an overall increase in the efficiency of the system. The major evolutionary increases in complexity have occurred on those few occasions when the conflicting interests of symbionts were partly subjugated to the overall benefit of the association (Maynard Smith, 1988; Maynard Smith and Szathmáry, 1995). Examples include populations of replicating molecules that cooperate in protocells, symbiosis among prokaryotic cells to form the modern eukaryotic cell, cooperation of cells to form multicellular organisms, cooperation of individuals to form social groups, and gene-culture symbiosis.

Hypercycles provide an excellent introduction to the conceptual problems of symbiosis. Maynard Smith (1979) showed that the basic hypercycle can be invaded by parasitic components that destroy the overall efficiency of the system (see also Bresch et al., 1980).

In the GOD SAVE THE QUEEN example, each word has two important functions. The enzymatic replicase enhances the reproductive rate of the next word. The target function affects a molecule's ability to use the replicase of the previous word.

Mutations that enhance target efficiency spread because they increase self-replication. Mutations that increase replicase efficiency are neutral in a randomly mixing population. For example, suppose a mutant GOB produces a better replicase for SAVE than does GOD. The better replicase enhances the reproduction of SAVE, which enhances THE, which enhances QUEEN. More QUEEN means more replicase for the GOD/GOB species. But the GOD and GOB subspecies benefit equally from the additional replicase, so the more efficient producer, GOB, does not increase relative to GOD. A similar argument shows that GOB will also be neutral if it produces a poorer replicase than GOD. Thus hypercycles cannot develop in a mixed population because the replicase is a neutral trait.

An established hypercycle also has a problem. Suppose that GOB produces no replicase for SAVE and has an enhanced target affinity for the replicase from QUEEN. The lack of replicase is a neutral trait, but the greater target affinity will cause GOB to outcompete GOD. The cycle will collapse because of parasitism. The basic hypercycle fails.

What can explain the origin and maintenance of symbiotic replicators in the first protocells? Perhaps the order of events must be switched. Eigen's hypercycle theory suggests that successful symbioses (hypercycles) are followed by compartmentalization into protocells. But compartments of replicating molecules may have come first, followed by cooperation among replicators (Maynard Smith, 1979; Bresch et al., 1980).

If the replicators of a developing cycle share a compartment, then the success of each replicator depends on two levels of selection. A parasite can spread within its compartment, but that parasite's success may be low because its compartment will be outcompeted in the population. For example, if a parasite takes over its own compartment it will have increased in frequency locally. But the compartment's rate of division may drop to zero because the parasite disrupts the orderly functioning of the protocell. The parasite, by damaging its container, dooms itself to extinction.

The higher, compartment level of selection can potentially screen off the lower level of competition within the compartment (Brandon, 1984). This is a form of group selection. The effective formation of an evolutionary unit at the compartment level requires that compartments differ significantly in their rate of division. Roughly speaking, the rate at which selection increases the frequency of parasite-free compartments must be greater than the rate at which parasites can take over their own compartmental lineage (Szathmáry and Demeter, 1987; Szathmáry, 1989a,b).

Maynard Smith and Szathmáry (1993) extend these ideas to show that the evolutionary origin of chromosomes depends on a similar sort of group selection and formation of a new evolutionary level. A chromosome is a set of physically linked replicators (genes). The problem is how genes that were initially separate became linked.

In Maynard Smith and Szathmáry's model, linked pairs of genes suffer a disadvantage within cells because large chromosomes replicate more slowly than single genes. Thus the frequency of chromosomes declines within a single lineage. This disadvantage for linkage may be offset by the positive synergistic effect of pairs of genes. If a cell lacking one of the two genes functioned poorly, then the chromosomes would have the advantage that they never end up in cells lacking one of the genes. Whether chromosomes succeed depends on the rate at which unlinked genes can take over their own compartmental lineage compared with the frequency and reproductive disadvantage of cells that lack one of the synergistic pair of genes.

These models for the evolution of cooperation within genomes assume that the transmission of the symbionts is purely vertical, confined entirely within a lineage of dividing compartments. However, compartments are bound by simple membranes and the symbionts may be transmitted horizontally between lineages. For example, different compartments may occasionally fuse, mixing the symbionts from two groups, or individual replicators may occasionally be freed from compartments and picked up by another compartment.

Horizontal transmission of symbionts between compartments changes the evolutionary dynamics. A parasite can succeed if its rate of horizontal transmission is large enough to offset the reduced efficiency that it imposes on its host compartment. This is the problem of the evolution of virulence that I discussed previously in the context of culture and gut flora.

It seems inevitable that horizontal transmission and parasitism were key features in the origin and evolution of genetic systems (Bremermann, 1983; Frank, 1996). For example, a replicator might contribute nothing to the functioning and reproduction of the cell, but instead use all of its coding information for two parasitic functions. The first is rapid replication within cells and the ability to outcompete the other replicators for limited substrates. The second is enhanced horizontal transmission by either release into the environment and absorption into other cells or by increasing the rate at which the host cell fuses with other cells. Cellular fusion causes mixing of genomes and a primitive form of sex (Hickey and Rose, 1988).

Ideas about hypercycles, chromosomes, and parasites raise many interesting questions. What role did the mutation rate and the error threshold play at various stages in the origin and evolution of genetic systems? How did the tensions between levels of selection shape genetics? Were genomic parasites and horizontal transmission common? Was defense against parasitic invasion an important challenge? Unfortunately there is no way to study directly the early evolution of genetic systems.

C. Artificial Life

Ray (1992) suggested that artificial life in computer models may provide clues about the evolution of genetic systems. Ray's creatures live in the memory of a computer. The location in memory can be thought of as a compartmentalized cell. Each creature is a set of instructions that influences survival, reproduction, and interaction with other creatures. Replication produces a daughter copy next to the parent. Mutations may occur during replication.

These artificial creatures evolve as replicating algorithms that compete for CPU time and memory space. The algorithms are coded in the Tierran language, which has only 32 different instructions. This is approximately the size of the alphabet used to build proteins: there are 64 DNA triplets that are translated into 20 amino acids. The language is composed mostly of typical machine instructions for a computer: flipping bits, copying bit strings, tracking locations in a sequence, and so on.

The mode of addressing is a special feature of the language. A computer system associates a numeric address with a physical location. Tierran addressing is based on a biological analogy. Molecules diffuse and interactions occur when two molecules have complementary physical structures. Thus Tierran finds addresses by template matching; an instruction to jump to an address causes a search for a template match among physically close creatures. This allows for simple types of recognition.

Ray's model is not designed to study the origin of life but rather early evolution once replicating molecules exist. Thus he had to seed his system with a self-replicating program. In most runs he used a seed (ancestor) that is 80 instructions long and has only the minimal capacity of self-replication. No specific evolutionary potential was designed into this ancestor, it simply replicates itself indefinitely when there is no mutation.

The system proceeds by the following cycle. Each individual (algorithm) is allowed in turn to execute some of its instructions. Lifespan is determined by a

queue. Newborns enter the bottom, and death is imposed at the top to keep empty a specified fraction of the environment (memory). Individuals move up the queue as additional births are added at the bottom. Errors in executing code can accelerate movement toward the reaper at the top. Mutation occurs by a low rate of bit-flipping in all organisms, and an additional error rate during replication. Size mutations also occur during the replication process. Thus genome length can evolve.

A run starts with the ancestor sequence and follows the life cycle. The system quickly diversifies and forms complex communities. These communities can be difficult to analyze in detail because the algorithms, composed of bit flips and memory jumps, are not easy to read. Ray, in his preliminary work, has identified several ecological types.

Parasites with short genomes cannot self-replicate but use the code of other creatures to specify how to reproduce. Hyper-parasites attack parasites. A hyper-parasite gets its own address into the copy pointer of the parasite, so a parasite replicates the hyper-parasite's genome rather than its own.

Social hyper-parasites can only replicate in aggregations. Each individual needs the code of a genetically similar neighbor to reproduce. The fact that an offspring is placed close to its parent may cause spatial aggregation of closely related creatures that aids the evolution of cooperation. Spatial aggregation has the same effect as compartmentalization and can lead to higher-level evolutionary units as discussed for the hypercycle and related models. Those earlier models suggested that higher evolutionary units are prone to internal parasites. As expected, Ray found cheaters that he calls hyper-hyper-parasites. These cheaters position themselves between social hyper-parasites and gain the benefits of neighbor-aided replication without reciprocating.

Ray briefly mentioned host immunity and parasite countermeasures to avoid detection. Recognition among cooperating and competing symbionts probably plays an important role in the coevolutionary dynamics of the system.

Ray made only a brief comment on the role of mutation (information decay). In a few runs the community became dominated by creatures with 700 to 1400 instructions per genome. These communities died because creatures in this size range exceed the error threshold that sets an upper limit on genome size (see Maynard Smith, 1992). It would be interesting to test whether larger and more complex symbiotic genomes could evolve in Ray's system if some form of expanded compartmentalization were introduced. This type of analysis would allow one to study jointly information decay (mutation) and symbiosis, the two main forces that influenced the early evolution of genetic systems.

D. The Evolution of Sex

I have described how symbiosis and information decay influenced the early evolution of genetic systems. In this section I add a new theme to the discussion, the role of exploration versus exploitation.

The biological problem is sex. In eukaryotes (nonbacteria), sex typically causes the orderly mixing of genes from two parents to form an offspring. How did complex systems of genetic mixing arise? What kinds of challenge to adaptive systems maintain sex relative to nonmixing, asexual systems? There are many

theories about the origin and maintenance of sex (Maynard Smith, 1978; Michod and Levin, 1988; Kondrashov, 1993). I will briefly summarize the most prominent theories as they relate to my themes about the evolution of adaptive systems.

Theories for the origin of sex focus on prokaryotes (bacteria). The prokaryotes have simple forms of genetic mixing that, presumably, are similar to the types of mixing that occurred during early evolution.

One theory focuses on the challenge of information decay (Bernstein et al., 1988; Michod, 1993). In this theory genetic mixing brings together two copies of homologous DNA by fusion of haploid cells. The paired DNA allows one strand to correct damage to the other strand, greatly reducing the rate of deleterious mutation.

A competing theory for the origin of sex focuses on symbiosis. As discussed above, genomic parasites can spread if their rate of horizontal transfer overcomes their reduced vertical transmission within the host's lineage. Hickey and Rose (1988) have suggested that horizontal transfer by parasites led to the mixing of whole genomes, the first step in the sexual cycle. This idea cannot be tested directly because the origin of mixis occurred in the past. In support of the theory, mixis in modern prokaryotes is caused by horizontally transmitted subgenomic plasmids (Hurst, 1991).

Bell (1993) has extended the parasite theory for the origin of sex. Eukaryotes have two distinct phases in their life cycle: a vegetative phase of growth and reproduction and a sexual phase of genetic mixing followed by genetic segregation. Bell argued that the characteristic features of the eukaryote genome arose from the entrainment of parasitic genetic elements into the life cycle. In Bell's theory, mixis originated by the Hickey-Rose model of parasitic transmission. Bell also argues that mating type genes and centromeres, part of the machinery of orderly segregation and meiosis, had a parasitic origin. See Hurst (this volume) for more on genomic parasites and the evolution of genetic systems.

The maintenance of sex poses a different kind of problem. Asexual reproduction is a more efficient mode of reproduction than sex, so why are most systems sexual? Sex requires the time-consuming processes of mating, mixing of genetic material in diploid offspring, and the orderly reduction of chromosomes to form haploid gametes. Sex also breaks up coadapted gene complexes.

The most spectacular puzzle concerns the "twofold cost" of sex (Williams, 1975; Maynard Smith, 1978). Multicellular species typically have large gametes (females) and small gametes (males). The small gametes contribute only genes to the offspring but no resources—in effect, small gametes are parasitic on the reproductive effort of the large gametes. Because sexual females invest all of the resources but only one-half of the genes in offspring, their rate of genetic propagation is one-half that of an asexually reproducing individual that transmits all of its genes to offspring.

TABLE 3

Classification of Theories to Explain the Maintenance of Sex

	Decay	Explore vs exploit
Species	Muller's ratchet	Adaptive radiation
Gene	Mutation clearance	Variable environment

Many theories attempt to explain why sex is maintained in spite of a twofold disadvantage (Maynard Smith, 1978; Kondrashov, 1993). I summarize the four leading theories. These theories can be classified in two ways. One division splits the models by the challenge to the adaptive system, either exploration versus exploitation or information decay (mutation). The second division splits according to the level of selection, either long-term effects and species selection or short-term effects and genic selection. Table 3 shows this classification.

Muller's ratchet causes deleterious mutations to accumulate in small, asexual populations (Muller, 1964; Maynard Smith, 1978). The effects on population fitness can be understood by following the rise in the number of deleterious mutations carried by the best chromosomes in the population. Label each chromosome in the population by the number of deleterious mutations that it carries. Suppose initially that some chromosomes have zero mutations. Occasionally, by chance, all of the surviving replicates of a zero chromosome will have one or more mutations, transferring this chromosome lineage to the class with one mutation. In a small population the rate at which chromosome lineages increase the number of mutations carried outpaces the rate at which selection favors chromosomes with fewer mutations. Eventually all chromosomes with zero mutations will be lost and the best class will have one mutation—the ratchet has turned. The process continues over time, with population fitness steadily declining.

Sex and genetic recombination can prevent the ratchet. Two chromosomes, each with a different mutation, can recombine to form progeny with zero mutations. The rate of chromosomal improvement by recombination is usually sufficient to prevent the decline of population fitness. Thus sexual populations can outcompete asexual populations over long periods of time. The problem with this theory is that an asexual individual within a sexual population has a twofold reproductive advantage because it avoids the cost of sex.

Muller's ratchet is a sufficient explanation for sex only if the rate at which asexual populations suffer "mutational meltdown" (Lynch et al., 1993) is sufficient to overcome asexuality's short-term advantage within populations. This is, once again, the problem of two competing levels of selection, similar to the origin of compartmentalized protocells struggling against the lower level of genomic parasites.

The adaptive radiation theory is another species-level model. In this case sexual species have an advantage because they generate a wider diversity of genotypes and can adapt more quickly to new habitats than asexual species (Fisher, 1958). Thus asexual genotypes, which have a short-term advantage, lose when new environmental challenges arise. In this model sexual species gain because they are better at exploring and discovering new solutions to new problems. Asexual species gain because they are better at exploiting a fixed environment.

The two gene-level theories assume that species-level advantages for sex are not sufficient. They explain how sex can have a short-term advantage over asexuality in spite of the twofold cost of sex. The mutation clearance model focuses on information decay; the variable environment model examines exploration versus exploitation in rapidly changing environments. Both models can be explained by an elegant theory that is hidden in the appendix of Haldane's (1932) classic book *The Causes of Evolution.* Haldane's model examines intense

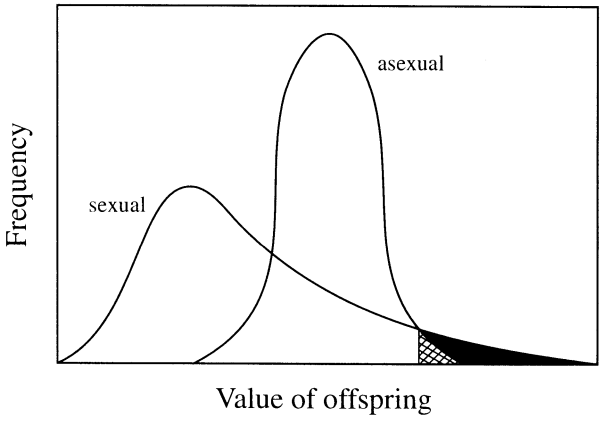


Figure 13 The effect of variation in offspring value on the evolution of sex. Each curve is the distribution of offspring value in a family from a parent's point of view. Asexual families have a relatively higher mean because a parent transmits twice as many genes per offspring compared with sexual progeny. Sexual distributions have greater phenotypic variability because genetic information is mixed randomly between parents. Here, only the offspring above a cutoff survive—the hatched area among asexuals and the hatched plus shaded areas among sexuals. In this case the sexual strategy transmits more genes to future generations than the asexual strategy in spite of the twofold advantage of asexuality. In general, "intense competition favors variable response to the environment rather than high average response. Were this not so, I expect that the world would be much duller than is actually the case" (Haldane, 1932, pp. 177-178).

selection in which only the best individuals survive. In that case selection favors genotypes that produce highly variable traits rather than a high average value. If only the best individuals are picked, then a wide distribution with a relatively low mean has an advantage over a narrow distribution with a high mean (Fig. 13).

In the mutation clearance model each individual carries many deleterious alleles (Kondrashov, 1988). Asexual individuals have a narrow range of offspring quality because each offspring has approximately the same number of mutations as its parent. The stochastic processes of segregation and recombination in sexual genotypes produce a wide range in the number of mutants per offspring. The average value of offspring for a sexual genotype is reduced by the cost of sex, but sex can beat asexual genotypes because of the higher variance in quality. This requires sufficiently frequent mutations to produce a wide distribution of offspring quality, and strong selection that picks only the best offspring.

In a variable environment model the favored genotypes change from generation to generation. Sex increases the probability that a parent will have some offspring close to the favored genotype because sex increases the diversity of genotypes produced. Sex's ability to produce diversity and increase its chance to match a changing environment can outweigh the reproductive efficiency of asexuality. Sex is better at exploration of a changing environment, asexuality is better at exploitation of a fixed environment. (The way in which environments change can have an important effect. See Charlesworth, 1993.)

What could cause the environment to change sufficiently to favor sexual exploration at a twofold cost in efficiency? Several authors favor coevolving parasites (Levin, 1975; Jaenike, 1978; Hamilton, 1980). Parasite traits that avoid

host immunity require counteradaptations by the host. Host-parasite interactions are a form of biotic challenge with coevolutionary feedback. In this view sex is a method to mix cooperative symbionts (genes) in search of good combinations against antagonistic symbionts (parasites): "Sex also creates true species in an otherwise straggling mess of clones: if the idea about parasites is right, species may be seen in essence as guilds of genotypes committed to free fair exchange of biochemical technology for parasite exclusion" (Hamilton, 1982, p. 271).

Opinions differ about the processes that favor sex. My purpose here was not to solve this puzzle, on which there is little agreement, but to show that certain types of argument recur in the evolution of adaptive systems. For the origin of sex, information decay and symbiosis dominate the arguments. The conflict between genomic parasites at the genic level of selection and survival of lineages at the cellular level also plays an important role. For the maintenance of sex, information decay and exploration versus exploitation divide the main theories in one dimension. Genic versus species level selection divide the theories in a second dimension. The genic level theory for exploration versus exploitation implicates antagonistic coevolution as a major challenge to the evolution of genetic systems.

VIII. Adaptive Systems as an Engineering Tool

Engineering faces many of the same challenges found in biological systems: information storage, complexity, and unpredictability. In recent years scientists have exploited adaptive systems to solve engineering problems. I present a few examples to show that engineering shares many challenges and solutions with genetics, learning, and development.

A. The Design of Biochemical Catalysts by Chemical Engineers

Three methods have been used to design catalysts (Benner, 1993). The first designs molecules based on the catalytic properties of functional groups and the predicted folding pattern of the components. The second method uses the adaptive properties of the vertebrate immune system to create catalytic antibodies (Lerner et al., 1991). The immune system can create an antibody that binds the rate-determining transition state of a reaction. Stabilizing the transition state lowers the activation energy and speeds the reaction.

A new adaptive method of variation and selection has recently been used to design RNA catalysts (ribozymes). Bartel and Szostak's (1993) goal was to create a ribozyme that catalyzed RNA replication. The discovery of self-catalyzing RNA would support the view that the origin and early evolution of life was based on a purely RNA system. In this theory RNA would be both the genotype encoding information and the phenotype controlling replication (Cech, 1993).

Although Bartel and Szostak's goal was basic understanding of the origin of life, their problem was one of engineering. They wished to find an efficient ribozyme that could enhance replication. They focused on ligation, the joining of separate RNA sequences into a single long sequence. They began their search with 10^{15} randomly generated RNA sequences. They then screened this large pool for those RNAs that extended themselves. The specific reaction was the attachment of

a test sequence onto the end of the putative catalyst RNA. Those RNAs that attached to the test sequence under experimental conditions were selected for replication. The replication was conducted by a standard biochemical method, the polymerase chain reaction (PCR). The PCR process was intentionally modified to introduce mutations during replication, providing additional variability for the next round of selection. The methods of variation and selection were applied for 10 generations.

The final sequences enhanced the reaction rate by seven orders of magnitude relative to the random sequences at the start of the evolutionary process. This performance is not impressive if one uses natural systems as a benchmark. Natural ribozymes typically enhance reaction rates by three or four orders of magnitude more than Bartel and Szostak's selected ribozymes. Protein catalysts do even better, outperforming ribozymes by three to six orders of magnitude. On the other hand, the laboratory-evolved ribozymes beat the typical performance of both human-designed and antibody-selected enzymes, which typically cause reaction-rate enhancements of two to six orders of magnitude. The success of the ribozyme selection scheme is remarkable because both the designed and antibody-selected enzymes are composed of the 20 different amino acids, which provide a much wider range of biochemical properties for enzymes than the four nucleosides that compose RNA sequences (Benner, 1993).

Molecular design by natural selection is in its infancy. Although these methods will not displace all other approaches, adaptive design may play an important role in the future of biochemistry.

Adaptive systems are a tool used for discovery in molecular design. Once the exploration has finished and an efficient catalyst has been found, other more efficient techniques can be used to exploit that discovery. In this regard molecular design shares two general properties with other adaptive systems.

First, adaptive design is a process of discovery that follows cycles of broad exploration and efficient exploitation. The previous sections showed that exploration versus exploitation is a common theme in adaptive systems.

Second, I argued earlier that learning and vertebrate immunity are adaptive subsystems spawned by the genetic system to handle environmental challenge. Both learning and immunity have their processes of variation and their selective systems (goals) set by genetical evolution. From this point of view adaptive molecular design is a subsystem of variation and selection spawned by learning humans to handle an environmental challenge. This may seem an unnecessarily complicated way to describe a simple method. But in the sweep of evolutionary history, adaptive systems have occasionally discovered the use of subsystems of variation and selection to solve their problems. These subsystems greatly altered subsequent evolution.

It remains to be seen whether adaptive subsystems created by humans will be important. Adaptive design of catalysts and the following examples illustrate recent applications.

B. Genetic Algorithms and Protein Folding

A protein sequence is a string of amino acids. Biochemical tools can be used to read a protein sequence or to change particular amino acids within the string.

However, the ability to read and manipulate sequences has practical limitations because the structural and catalytic properties are determined by three-dimensional conformation. It has not been possible to predict conformation from the sequence.

A protein folds according to the energies of covalent bonds among the individual amino acids. The problem is to predict how particular bonds cause a linear sequence to fold into a three-dimensional shape. At each step in the folding process there are a large number of possible conformations. In principle, a computer program could search each of the possible conformations at each step and predict the folding pathway. However, this search process suffers from a common problem in computer optimization known as combinatorial explosion. The number of possible pathways is too large to search by any computer available now or in the future.

There are many computer techniques to search for solutions to large problems. The genetic algorithm is a popular method based on an analogy with natural selection (Holland, 1975; Forrest, 1993). Each potential solution is coded in a linear sequence of information (a chromosome). In the protein example, the goal is to find a minimum-energy conformation. For this case each "chromosome" represents a particular conformation.

The genetic algorithm is natural selection applied to a population of chromosomes. The initial population can be created randomly. Then in each generation selection, variation, and transmission occur. Selection chooses chromosomes for reproduction according to their fitness—in this case lower energy states have higher fitness. Selected chromosomes mutate with a probability set by the program. Chromosomes may also pair to mate and recombine. Recombination follows the biological process of swapping pieces of the chromosome. Enough progeny are produced for the next generation to form a new population. The cycle is repeated. The quality of the best solutions in the population usually improves for many generations and then levels off. The best solution (chromosome) during a run is the optimum discovered by the search process.

An interesting series of papers on genetic algorithms and protein folding illustrates the power and potential problems with adaptive search techniques (Judson et al., 1992, 1993; McGarrah and Judson, 1993; Tufféry et al., 1993). Unger and Moult (1993) compared the ability of a genetic algorithm and a "Monte Carlo" search method to find a minimum-energy conformation for a protein that folds in two dimensions. The Monte Carlo method has four components. (1) Start with a random conformation. (2) Make a single random change in the conformation. (3) Accept the change if the new conformation has lower energy. Otherwise accept the change with a probability that decreases as the energy of the new conformation rises. (4) Continue to test changes until some stopping criteria is met. The Monte Carlo method was the best search technique available in 1991 (Unger and Moult, 1993).

Unger and Moult's (1993) genetic algorithm encoded different protein conformations in the chromosomes of the evolving population. Conformations with lower energy states have higher fitness. Each mutation follows steps (2) and (3) of the Monte Carlo method. Recombination breaks two protein sequences at the same amino acid positions and swaps the fragments. The conformation of the fragments is maintained while swapping.

The genetic algorithm found lower energy conformations in shorter periods of time than the Monte Carlo method. Unger and Moult (1993) argue that the genetic algorithm succeeds because it naturally follows folding pathways (Judson, 1992). Real proteins are believed to fold in steps. Local regions of the chain fold first; a higher order structure forms by combination of these local conformations.

The genetic algorithm succeeds for problems in which subsets of the instructions can work well together in creating high fitness (Holland, 1975). In the case of protein conformation, the calculation of fitness (energy state) implicitly evaluates the quality in the population of every locally folded fragment with two amino acids, with three amino acids, with four amino acids, and so on. Fragments with low energy conformations increase the relative fitnesses of the conformations in which they reside; thus low energy fragments will increase in frequency in each generation.

The selection process causes the parents chosen for reproduction to have a higher than average fitness, and thus a set of relatively low energy fragments. Recombination of conformations is done by building offspring from fragments of the two parents. Thus recombination creates new conformations from good fragments.

The great power of the method is that the fitness calculation simultaneously evaluates the quality of fragments of all sizes. Initially, small fragments will contribute the most to fitness differences among conformations. As the better of the small fragments spread by selection and recombination, and most conformations contain them, fitness differences depend primarily on good combinations of small fragments and differences among the slightly larger size classes of fragments. Thus selection emphasizes conformations of increasingly larger fragments.

A simple genetic algorithm often performs reasonably well for a wide range of problems. However, for any specific case, specially tailored algorithms can often outperform a basic genetic algorithm. The tradeoffs are the familiar ones of general exploration versus exploitation of specific information (Newell, 1969; Davis, 1991).

For protein folding, McGarrah and Judson (1993) showed the superiority of a hybrid method that combines the genetic algorithm with a local search. The genetic algorithm is often good at broadly searching the space of possible conformations. However, because genetics includes the stochastic processes of mutation and recombination, the algorithm is inefficient at fine-tuning a conformation that is close to a local minimum. McGarrah and Judson used an alternating cycle of the genetic algorithm and an efficient local search (gradient descent).

The genetic algorithm provides a good spread of candidate conformations. The gradient descent uses these candidates as starting points and efficiently obtains the best local conformation. The fitness is assigned to each chromosome based on its conformation after gradient descent. Thus local optimization can be thought of as a period of learning during the phenotypic phase of the cycle. One can optionally use the phenotype after the learning period as the genotype for reproduction, providing a component of Lamarckian inheritance to the search process (Judson et al., 1992).

The work on protein folding follows a common pattern of growth in optimization studies. When a new problem is encountered, the first efforts use a

general purpose method such as a basic genetic algorithm. Experience with the problem often shows that better performance can be obtained by enhancing the simple algorithm, that is, encoding problem-specific knowledge into the genetic program. The incorporation of problem-specific knowledge is similar to the Baldwin effect discussed earlier (see section on *Learning*).

At present, such problem-specific knowledge is usually inserted into the genetic algorithm by human intervention. One goal for optimization research is to mimic the Baldwin effect more closely, causing techniques learned by the evolving population to be incorporated into the search algorithm without intervention. This would allow general-purpose methods to evolve into problem-specific techniques by dynamically balancing further exploration versus exploitation of discovered knowledge.

C. Genetic Algorithms and Neural Nets

A brain is a network of neurons. Each individual processor (neuron) in a brain is relatively slow by engineering standards, with a response time measured in milliseconds. Yet an animal's neural network is capable of many tasks far beyond the success of the most powerful computers available today. Examples include vision and complex pattern recognition.

Neural nets achieve their power by massively parallel information channels. A net can have millions of simultaneously active, parallel connections, whereas most computers use only one or a few serial channels at any instant. Networks also have redundancy and fault tolerance. Cutting a few individual connections usually has very little effect. In serial architectures, loss of a few bits of information often causes total failure.

The admirable properties of computational networks were first studied in the 1940s (McCulloch and Pitts, 1943). This research has grown into a large enterprise focused on neural networks, sometimes called parallel distributed processing (McClelland et al., 1986; Rumelhart et al., 1986). Part of the research emphasizes models of real nervous systems. This is an extension of neurobiology. Another group has exploited the power of networks for engineering applications (Hertz et al., 1991). Examples include recognition of handwritten words, digital signal processing, and control systems in robots.

Constructing a neural net for an engineering application has three phases. First, the basic architecture of the net is chosen. This includes the number of neurons, the initial strength of interconnections, the detectors that pass information from the environment into the net, and the output system that signals the net's action in response to the environment. In the second phase the net is put through a training process. Inputs are provided, and the difference between the net's output and the desired goal are used to adjust the connection strengths among the neurons. Finally, the net is put to use when it can match inputs to desired outputs with sufficient accuracy, for example, if handwritten letters can be recognized within tolerable error limits.

The training method is usually deterministic. Thus a given architecture converges to a particular input-output response pattern. The quality of performance is therefore determined by the initial architecture. Although there are some guidelines about how architecture will affect performance (Hertz et al.,

1991; Kung, 1993), there is often a huge number of plausible structures. Testing the performance of each architecture is not possible. The difficulty is combinatorial explosion, just as in the protein-folding problem.

Genetic algorithms have had some success in the problem of network design (Harp and Samad, 1991; Harvey, 1991; Harvey et al., 1993). A chromosome represents a single architecture. In each generation a chromosome is translated into a net, the net is trained, and then performance is measured. The performance is fitness. The genetic algorithm then follows its usual cycle.

One problem is the developmental translation of linear information in the chromosome into a three-dimensional network (Harp and Samad, 1991; Harvey, 1991; Kitano, 1994). At present, each investigator specifies an *ad hoc* method for developmental translation. These range from direct coding of three-dimensional structure to a variety of clever generative rules that allow compression of structural information. Hemmi et al. (1994) have recently taken the next step, in which the generative rules are themselves encoded in the linear genome, allowing the developmental "language" to evolve along with the particular structural information. This active area of research may provide some interesting insights into generative rules, development and language in natural systems (Batali, 1994; Dellaert and Beer, 1994).

Natural networks may be wired by a program of developmental selection, although this remains an open question (see section on *Development*). If true, then chromosomes contain two types of information. First, there is the program of developmental selection. This information codes the processes of variation and selection that control the development of wiring patterns. Second, there is a set of initial conditions that provide the material for developmental selection. These initial conditions shape the final outcome via developmental selection.

Analogies with natural systems suggest some experiments with genetic algorithms. A chromosome that encoded a developmental selection program and initial conditions has two interesting features. First, each chromosome spawns an adaptive subsystem of developmental selection to create its phenotype. The nature of this subsystem will evolve in the usual cycle of the genetic algorithm. Second, a relatively small chromosome is needed to encode the developmental program and initial conditions when compared with chromosomes that encode the entire architecture.

Whether an experiment of this type is practical for engineering applications remains to be seen. These experiments would, however, provide insight into the power of developmental adaptive subsystems to store complex patterns in small chromosomes.

D. The Evolution of Robots

Robots require environmental detectors, motor controls, and computational machinery to link sensory input with motor output. Robots that perform simple, repetitive tasks are used in many applications. But current robots are not good at handling unpredictable conditions. Thus, several research groups have reasoned as follows: Animals handle unpredictability well. Animals evolved. Perhaps robots should be designed by evolutionary processes.

The Sussex research group has made an interesting start in this direction

(Harvey et al., 1993; Cliff et al., 1993). They believe that evolution can be a very effective design method, but that evolutionary complexity must be built with small steps. Robots cannot sweep the garage before they can avoid crashing into walls. The Sussex group has chosen effective maneuvering in space as a simple but crucial first step in robot evolution.

How to build a robot that avoids bumping into walls? Harvey et al. (1993) argue that the first design phases can be done entirely by computer simulation without the need to build costly prototypes. The problem for the robot is to avoid the walls while moving in a circular room with black walls and white floor and ceiling. The robot has visual sensors, an internal neural network, and two motorized wheels that can be controlled independently. The physics—location in the room, visual input, and motion in response to settings for the wheel motors—are tracked by computer simulation. A linear chromosome is used to encode the structure of the sensory system and the architecture of the neural network. At present both the network's structure and the connection weights are set by the genotype. Each robot could learn by adjusting connection weights as discussed in the previous example.

Evolutionary change follows the cycle of the genetic algorithm. An initial population of chromosomes is formed, each specifying the design of a robot. Each design is tested in the simulated room, the performance is scored and used as fitness. Chromosomes are chosen according to their fitness. Pairing, recombination, and mutation occur to form offspring for the next generation of the cycle.

Performance improves over the generations. Following the plan of incremental evolution, the next step is maneuvering in a cluttered room (Cliff et al., 1993). The technique of simulating the physical environment does not work very well for this problem because it is computationally very intensive. So Cliff et al. (1993) created a cluttered environment and a robot. The robot has visual detectors that it can move to scan its surroundings. The robot can also move itself. Fitness is determined by success at navigating through this environment. A genetically encoded neural network controls sensory scanning and does the computations that connect the sensory input with motor output. The network and the processing occur in software on a remote system, allowing the rapid evaluation of many different genetic programs (chromosomes). No results have been published with this system.

The coupling of sensory scanning and movement is particularly interesting in this system. Edelman (1987, 1992) has stressed the importance of this coupling in his theory of neural darwinism and has presented some simulations of his own with simple robots (see earlier section on *Learning*). Edelman's goal is to understand the functioning of real nervous systems; the Sussex group is trying to design efficient robots. It will be interesting to follow the parallel development of these two research programs.

E. Hierarchical Control and Learning in Robots

The examples of robot maneuvering illustrate one method of design by incremental evolution. Other research groups have taken a different evolutionary approach (Meyer et al., 1993; Cliff et al., 1994; Brooks and Maes, 1994). For

example, Colombetti and Dorigo (1993) have emphasized the ability of an individual robot to learn. Their approach may be thought of as phenotypic evolution given a particular design (genotype), whereas the Sussex group focused on genotypic evolution without any phenotypic evolution.

Colombetti and Dorigo studied a hierarchy of independent behavioral components coordinated by a global integrator. For example, approaching, chasing, escaping, and eating are possible responses to a particular stimulus. The actual behavior depends on a resolution among the tendencies of each component, leading to suppression of one component by another or to an orderly sequence of behaviors. Issues of hierarchy and coordination are central problems of animal behavior (ethology) and were widely discussed in the 1950s and 1960s (e.g., Tinbergen, 1951; Dawkins, 1976b).

Each component behavior in Colombetti and Dorigo's robot learns by an extended genetic algorithm known as a classifier system (Holland et al., 1986). Classifiers are evolving populations of chromosomes in the genetic algorithm cycle, but each chromosome may use a portion of its coding for a series of condition-action rules that can control behavior. The condition part of the rule can be triggered by external sensors or the actions of other chromosomes; the actions can stimulate other chromosomes or activate output controls such as motors. Thus a population of classifiers forms an activation network.

Here is a simple behavioral hierarchy (Colombetti and Dorigo, 1993):

if there is a predator
  then Escape
  else if hungry
    then Feed
    else Chase the moving object

Each behavior, escape, feed, and chase, has its own classifier system that evolves (learns) over time. The robot has sensory detectors that pass a message to each behavioral component. Each component generates a message in response. The response from each component is passed directly to the action controls or to the behavioral integrator, which is itself a classifier system. The integrator may then send a message to the action controls.

The robot learns by reinforcement or punishment, as in psychological conditioning experiments. Reinforcement notifies the classifier systems of success. Each classifier system assigns credit (high fitness) to the chromosomes that participated in the correct decision. The wrong behavioral choice leads to punishment and low fitness to participating chromosomes. These fitnesses are then used in a cycle of the genetic algorithm, with mating, recombination, and mutation to form a new population of chromosomes in each classifier system.

The hierarchical decomposition of this robot is set by the experimenters. It would be interesting to study how hierarchical decomposition evolves. This would require a mixture of the approaches by the Sussex group and Colombetti and Dorigo. The Sussex approach focuses on an evolving population of robots, where the genotype for each robot specifies a particular design. To study behavioral decomposition, the genotype must be able to encode a variety of components that divide environmental challenges in different ways. The phenotypic interactions for each genotype would follow Colombetti and Dorigo's approach: each behavioral component specified by the genotype spawns its own adaptive (classifier) subsystem in order to learn during the phenotypic stage of the life cycle.

F. Robot Symbiosis

Colombetti and Dorigo's (1993) classifier robot uses a distributed model of behavioral control. Each component is simple, mostly autonomous, and computes in parallel with other components. This is an internal symbiosis of cooperating components. Behavioral decomposition is a central tenet of many current research programs in robotics (Meyer et al., 1993; decomposition of complex problems arises in many fields, see Alexander, 1964; Simon, 1981; Minsky, 1985; Dennett, 1991).

Another design method emphasizes teamwork among a group of individual robots. Teams are useful for simple tasks that can be done in parallel, such as clearing a field of rocks. Teamwork can also boost efficiency for tasks that require division of labor and specialization, such as automated manufacturing, search and rescue, or surveillance (Parker, 1993).

Both internal symbiosis and teamwork must resolve the tension between the autonomy of components and control of the symbiotic group (Numaoka and Takeuchi, 1993). This is a difficult problem. A global control mechanism could assign tasks to components based on progress to the ultimate goal. But this global mechanism must be complex, difficult to design because it requires great foresight, and prone to failure. When a global controller fails, then the whole system fails.

On the other hand, each component may blindly pursue its own simple subgoal without regard for the success of the group. Efficient group behavior may emerge from pursuit of the individual subgoals. This is the strategy used by several research programs.

Parker (1993) proposed a model for division of labor and specialization among groups of "selfish" robots. For example, in janitorial service the team must empty the garbage, dust the furniture, and clean the floor. Each robot is controlled by a distributed hierarchy of behavioral controls as in the Colombetti and Dorigo study (see also Brooks, 1986). Several low-level controls deal with tasks such as collision avoidance. These are active at all times. Higher-level controls are grouped according to the garbage, furniture, and floor tasks. Only one of these task-specific groups is active at any one time. Each group is controlled by a motivational unit that receives sensory input, inhibitory feedback from other behaviors, and a variety of other connections.

There are also control units devoted to internal "behaviors" such as the competing factors of impatience and laziness. These set the goals that control the behavior of each robot. For example, two robots may be motivated to empty the same garbage can. One gets there first and begins; laziness in the other robot causes it to give way. However, if the task of emptying the garbage is not completed, the second robot grows increasingly impatient. After a while, it will step in and try to finish the task.

Parker uses the market economy approach to achieve group coordination and efficiency. Each robot desires that all tasks be accomplished; each is motivated to do a task with high supply and low demand.

It will be interesting to follow this "selfish" approach to teamwork. In biological examples of symbiosis, creating higher levels of organization from autonomous components has worked very well in a few cases, but there are also

many inefficiencies caused by internal conflict (e.g., Hölldobler and Wilson, 1990; Hurst, this volume).

IX. Conclusions

The study of adaptive systems is composed of the individual puzzles in biology and engineering that made up my survey. This field is at a special time, when many of the puzzles have been defined, work has started, and the problems are just coming into focus. Much of the excitement is in the details of these puzzles and the ideas that are growing up simultaneously in traditionally separated academic disciplines.

What can be said beyond the listing of individual cases? I have argued throughout the chapter that a small set of challenges and responses have shaped adaptive systems (Tables 1 and 2). Classifications of this type can be problematic. On the positive side, they highlight simple, common features that can be obscured by details. On the negative side, classifications can be a semantic convenience that hides real differences. The balance often turns on matters of personal taste. My classification did bring some order to a diverse range of problems. I look forward to better classifications that will develop with a general theory of adaptive systems.

I turn now to a few speculations. First, I suggest that unpredictable challenge from coevolving systems has played a particularly important role in the history of adaptive systems. This is an old idea. What I find particularly interesting is that robotics provides new opportunities to test this idea.

The early evolution of robots will require much exploration. Adaptive systems influence two levels of design. At the hard-wired or genotypic level, evolutionary computation, such as a genetic algorithm, is used to search for effective architecture. This algorithm, which tests designs from a population of alternatives, shares many properties with genetical evolution. The good designs will proliferate and be modified, the bad designs will disappear.

Most of the early designs will be inefficient. But, for simple tasks such as cleaning office buildings and scraping barnacles from the bottoms of ships, the rate of architectural (genetic) evolution will slow as successful designs are discovered. Which brings up the interesting question: What types of challenge will favor continual evolution of architectures? Antagonistic coevolution seems the most likely answer; to use more common terms—war, combat, law enforcement, games of pursuit. Opponents will evolve to exploit design weaknesses, which require countermeasures to close the gaps. While shoring up defense, the search goes on for weakness in the opponents. And so on. Perhaps it is no surprise that the Office of Naval Research (USA) funded much of the early research on genetic algorithms.

My second comment is about cooperative symbioses that form in response to another kind of war. The battle is between humans and their parasites. In earlier sections I mentioned that host-parasite coevolution influences genetic polymorphism and that parasites are the challenge that shaped adaptive immunity. I also discussed the hypothesis that sex and the exploratory function of genetic mixing is shaped by parasitic challenge. There are two additional adaptive systems that humans use against parasites: learning and culture. As Mims (1987, p. 322) noted:

> Vaccines have been of immense importance in the past and hold great promise for the future. *The evolution of a microorganism can be decisively terminated by the proper application of knowledge.* Smallpox, the most widespread and fatal disease in England in the eighteenth century and a major cause of blindness, has been totally eradicated from the earth. [italics added]

Genetics, adaptive immunity, learning, and culture have all been used in the battle against parasites. In addition, science (learning plus culture) has itself spawned new adaptive subsystems in the form of evolutionary computation.

This battle against parasites, waged by medical research, is an enormous cooperative symbiosis. Like all symbioses composed of autonomous agents, medical research is rife with internal conflict, for example, competition among research groups. The symbiosis is held together by a common external threat—parasites.

My final comment is about a different kind of symbiosis, in which the individual agents are themselves subsystems of a single evolutionary unit. For example, teams of robots may be the most effective way to solve complex problems. Although each robot makes its own behavioral decisions, the whole system is typically designed with a single purpose controlled externally by humans. I discussed some of the difficulties in my survey. First, how should complex tasks be divided into simpler subgoals, each subgoal achievable by single agents (robots)? Second, how can pursuit of subgoals be combined to solve a larger problem?

This work in robotics matches an approach that has recently been developed to study the human mind and the evolution of consciousness (e.g., Minsky, 1985; Dennett, 1991). According to this view, the mind has many nearly autonomous subsystems that handle particular tasks. A major feature of consciousness and focused attention is simply the temporary dominance of a particular subsystem. In some theories, the subsystems compete for control according to the importance of the challenges that they face. This is similar to Sachs et al.'s (1993) developmental selection in which the individual shoots of a single plant compete for root resources, or Parker's (1993) robot example, in which autonomy and controlled competition appear to be the only way to achieve workable complexity.

It will be interesting to follow the development of robotics and cognition. These fields have very different histories, but the recent "cognitive revolution" may break down barriers (Gardner, 1985). On the other hand, many people believe that natural selection, robotics, and "artificial" systems will teach us nothing very profound about the mind (references in Gardner, 1985; Dennett, 1991, 1995). Time will tell.

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