CHAPTER 16

Language and Communication as Universal Requirements for Life

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CONTENTS

16.1 INTRODUCTION AND OBJECTIVES

Nowadays, we know that it is an empirical fact that if cells, tissues, organs, and organisms coordinate their behavior, this needs signals. Biotic signaling serves as a primary tool to coordinate groups of individual living agents such as cells and organisms, that is, the whole process we term communication. Current knowledge indicates communication as a basic interaction within and between organisms in all domains of life. Communicative interactions are necessary within organisms—intraorganismic—to coordinate cell–cell interactions, similar to tissue–tissue and organ–organ coordinations especially in complex bodies. This includes also the interpretation of abiotic environmental indices such as light, temperature, gravity, water, and nutrient availability as sensing, monitoring, and feedback control against stored background memories. We find interorganismic communication in all signal-mediated interactions between same and related species. If species communicate with nonmembers, we term this transorganismic communication. Throughout all kingdoms of life, we do not find any coordination and organization that does not depend on communication. In this chapter, I will shortly summarize these communicative levels in various domains of life.

Additionally, all that protein-based life we investigate in cells, tissues, organs, and organisms throughout all domains of life depends on stored information about structure, processing, development, and regulation. The genetic code has four kinds of nucleic acid components that serve as characters of an alphabet (guanine, adenine, thymine, and cytosine) that continuously is translated into amino acid language with 20 amino acids that form the whole variety of protein bodies and, additionally, an abundance of ribonucleic acids (RNAs) (with one varying character in the alphabet; uracil instead of thymine) that regulate all fine-tuned processes of cell replication, transcription, translation, and repair. The nucleotide sequences of the genetic code are base pairing according to the Chargaff rules (adapted by Watson and Crick in their double helix) in which they build complementary sequence structures and serve as information storage medium. We will look at some agents that are competent to edit the genetic code such as viruses and subviral RNAs.

First of all, let us have a look at the current background knowledge on natural languages/codes and on the basic biological features of communication processes. Because of its empirical significance, we can easily adapt this biocommunication approach to nonhuman organisms as well as the natural genome-editing competences of viruses and subviral agents to the evolution and content order of the genetic code.

16.2 SUMMARY OF CURRENT KNOWLEDGE ABOUT NATURAL LANGUAGES/CODES AND COMMUNICATION

Current knowledge in linguistics and communication theory identified three basic features that are essential characteristics to all natural languages/codes:

1. No natural language speaks itself as no natural code codes itself. In natural languages or codes, *living agents* that are competent to generate sign sequences are the ultimate prerequisite for the existence and occurrence of natural languages and codes.

2. The emergence of natural languages and codes depends on populations of living agents. This means that natural languages/codes in communication processes are primarily *social interactions*. Concrete social interactions are the essential experience for socializing children to learn the connections between linguistic utterances and their meaning. (Utterances are sentences with which we do something: convince someone, explain something, implement something, and similar. We do not think and then formulate sentences: we think in language and sentences. Also, every nonverbal expression is an utterance.)

3. Living agents that use natural languages/codes to initiate social interactions must be competent to follow *three levels of rules* that are obligatory and are inherent in any natural language or code: (a) competence to correctly combine signs to sequences (syntactic rules), (b) competence to correctly initiate communicative interactions according to the context specificity (pragmatic rules), and (c) competence to correctly designate objects by appropriate signs (semantic rules). If one level of rules is missing, one cannot seriously speak about a real natural language or code.

16.2.1 Language Is a Natural Language Only If Living Agents Use It

Language use depends on communities, a historically grown group of members that share these three levels of rules. Language use is a social action and is a priori intersubjective. If the time window of childhood learning and training in language words and sentences in social interactions is disturbed, linguistic and communicative competences can be deformed and even be lifelong. From this perspective, we can avoid monological concepts of language, all of which share an essential problem: how to make the move from a state of private consciousness to a state of mutual agreement and cooperation. Monological concepts include metaphysical, philosophy of mind, or other solipsistic approaches such as sender–receiver or coding–decoding narratives.

16.2.2 Mathematical Theories of Language vs. Pragmatics of Languages

The mathematical theory of language and its derivatives (systems theory, information theory, game theory, bioinformatics, synthetic biology, biolinguistics) tried the other way around: there is a logic of relations within material reality that is inherent also in biological matter. In the case of human evolution, this logic determines finally the architecture of neuronal brain construction. If the brain uses a language that depicts this logic, it must be possible to depict material reality with this language. The only language that is able to depict material reality is a formalizable, algorithm-based language, that is, mathematics. Therefore, the human brain must use formalized mathematical language so that it can scientifically depict and explain material reality.

The crucial deficit in this method is that one cannot explain everyday language with it. Everyday language is the ultimate metalanguage. This means that there cannot be any language that could go beyond everyday language. Since it serves as a primary tool for everyday life communication and socialization of humans, it is the source of the original meaning of words in sentences. Everyday language cannot be formalized: we cannot explain deep grammars and illocutionary acts we use primarily to transport a variety of meanings with identical superficial syntactic structures.

For the benefit of the readers, I would like to explain the terms locutionary, illocutionary, and perlocutionary, which are used in this chapter. Locutionary speech act is represented by the superficial syntax of the sentence. In contrast, illocutionary speech acts transport context-dependent meaning. For example, "I will come tomorrow"; its illocutionary force could be a promise, a threat, a secret code, etc., depending on the circumstances and intentions. With perlocutionary speech acts, someone fulfills a complete action. If someone asks you if you are willing to take XY as your wife and you answer "yes," then the yes is a perlocutionary speech act.

The same holds true for information theory: in a recently published article, Sydney Brenner states that biology is, in his opinion, physics with computation. The fundamental concept that integrates biological *information* with matter and energy is the universal Turing machine and von Neumann's self-reproducing machines. However, no single self-reproducing machine had ever been observed within the last 80 years since they presented their concept. There are good reasons for this, because machines cannot create new programs without algorithms. In contrast to the artificial machines that cannot reproduce themselves, the living cells and organisms can reproduce themselves and additionally generate an abundance of behavioral motifs for which no algorithm can be constructed, such as de novo generation of coherent nucleotide sequences.

16.2.3 How to Generate Correct Scientific Sentences: Results of the Philosophy of Science Debate in the Twentieth Century

To get things methodologically straight, we have to remind ourselves of the discussion between 1920 and 1980 in the history of philosophy of science and the transition of metaphysics to the *linguistic turn* and afterward to the foundation and justification of scientific sentences in the *pragmatic turn*.

1. The *linguistic turn* was the result of an attempt to delimit the logic of science from philosophy and other *nonscientific* methods. The term *delimit* generally means to define the conditions that must be fulfilled as validity claims of exact sciences. Specifically, the logic of science tried to find a language whose sentences are strictly scientific in contrast to the sentences from poetry, theology, astrology, and other nonscientific fields. Based on good reasons, the linguistic turn states that we do not understand per se objects, relations, structures, intelligence, mind, consciousness, cognition, construction, matter, energy, information, system, and natural laws, but only linguistic sentences in utterances. (Utterances are sentences with which we do something: try to convince someone, explain something to someone, call someone to do something, and similar.) Until linguistic turn, it was assumed in philosophy and sciences in general that sentences somehow depict reality.

   Only protocol propositions of observations that are reproducible in experimental setups are capable of depicting reality on a 1:1 basis, thus a direct correspondence. This is also valid for propositions of a language of theory that would have to be brought into agreement with these protocol propositions. What is required for a language is that it can be formalized, as in logical calculations, algorithms. This language would represent a universal syntax that would be universally valid (a) in the things of the external world, (b) in the physical laws, and (c) in the material reality of the brain of humans speaking in formalizable propositions. But after several unsuccessful attempts, logical empiricism had to abandon its efforts to achieve the ultimate validity claim of a universal scientific language.

2. As a result of this, the *pragmatic turn* refers to the communicative everyday interactions of historically evolved groups and communities that are the basis for learning and training linguistic and communicative competences. Historically grown communicative practice of linguistic communities is the prerequisite for organization and coordination of social interactions, and later of linguistic abstractions, such as scientific languages in communities of specialized disciplines (see Figure 16.1).

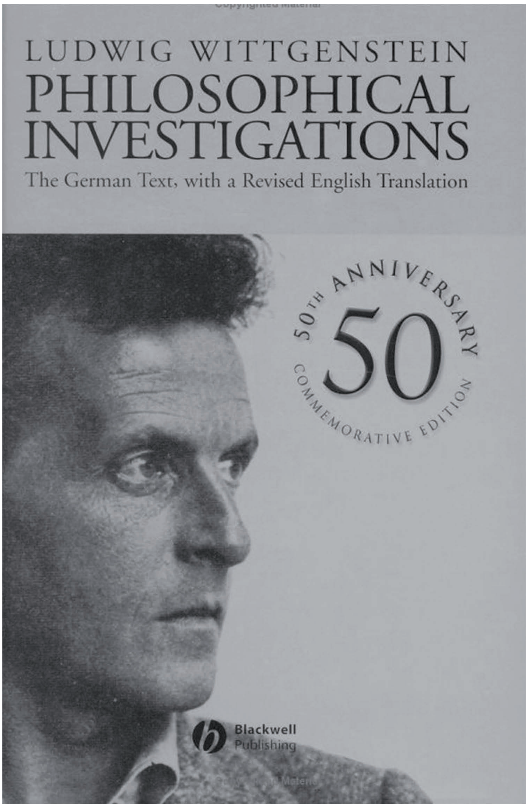

FIGURE 16.1 In his early thinking, which was outlined in the *Tractatus Logico-Philosophicus*, Ludwig Wittgenstein led the foundations for the project *exact scientific language*, that is, formalizable sentences that depict reality in a 1:1 manner. This served as common foundation of the *linguistic turn*. In his late *Philosophical Investigations*, Wittgenstein refuted his early thoughts completely. The basic features of natural languages are the real-life worlds of social groups that use sign systems in everyday use. The context of use determines the meaning of sign sequences. Natural languages serve as an essential tool in social interactions. This was the start of the *pragmatic turn*. (From Wittgenstein, L., *Philosophical Investigations: The German Text with a Revised English Translation*, Blackwell Publishing, Malden, 2001. With permission.)

The pragmatic turn founded and justified the *intersubjective–communicative character of thought, experience, and research.*

Everyday language analysis shows speech acts or *how to do things with words*. As we are both, in parallel, subjects and objects of our utterances, we are in a privileged position to take into account, at the same time, our historically evolved everyday language. We understand utterances as participants in the communicative, representative, imperative, and constitutive speech acts, rather than acting as lonely (*solus ipse*) isolated observers. This enables us to explain central marks of speech acts as there are

- Simultaneous understanding of identical meanings in two interacting partners, as expressed in successfully coordinated activity
- Differentiation between deep and superficial grammar of a statement along with differentiation between locutionary, illocutionary, and perlocutionary speech acts with which the statements are made

The pragmatic turn replaces all *monological* subjects of knowledge by the primacy of linguistic communities. This is the end for a methodological ideal that lasted nearly 2000 years and that maintained as a principle that one subject alone could—monologically—get knowledge and construct a language/code in a process that Thomas McCarthy has described as follows: “The monological approach preordained certain ways of posing the basic problems of thought and action: subject vs. object, reason vs. sense, reason vs. desire, mind vs. body, self vs. other, and so on.”

16.2.4 Meaning of Messages Depends on Contextual Use (Pragmatics), Not Syntax

It is a deep grammar, or as outlined in great detail by John Austin and John Searle, it is the illocutionary act we undertake with what we say. So, besides the locutionary aspect, which is represented by the superficial syntax of the sentence, there is a variety of (hidden) possibilities of what we want to do (intend) with this sentence, namely, the illocutionary act. In extreme cases, we can intend contradictory goals with the same syntactic structure. This is the reality of everyday language that is impossible to capture in the formalized languages that cannot represent both locutionary and illocutionary aspects.

An important consequence of this is that pure language analyses that want to extract deep grammar/illocutionary action out of available syntactic sequences must necessarily fail. This is because the analyses of syntactical rules cannot explain pragmatic interactional contexts that finally determine the meaning of syntactic structures. This has serious consequences:

1. The variety of words combined to form sentences in everyday languages and dialects are not the result of copying errors or damage of preexisting sentences or available sentences. According to Gödel, natural language users are principally capable to produce new sequences that have never been generated before (see Figure 16.2).

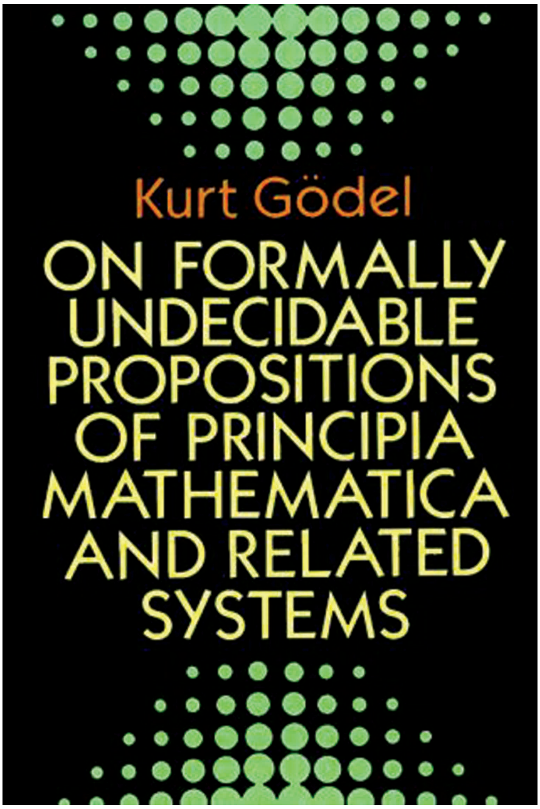

FIGURE 16.2 Gödel discovered the crucial deficit of the linguistic turn: in his investigation, he convincingly proved the fact that in open systems, there is the possibility to create new sentences that have never been created before and cannot be predicted out of preexisting ones in principle. This was the end of Hilbert's program of a self-consistent axiomatic system (Hilbert space) as the ultimate foundation and justification of mathematics. (From Gödel, K., *On Formally Undecidable Propositions of Principia Mathematica and Related Systems*, Dover Publications, New York, 1992. With permission.)

It is an inherent feature of all natural languages that living agents that use them can produce new ones. They may be unpredictable and thus incalculable. As such, they cannot be deduced out of former ones or available ones.

2. In natural languages/codes, there is no syntax based on a universal grammar that transports identical meanings (e.g., with a unique position in a formalizable sequence space as suggested by Manfred Eigen).

3. To learn a natural language means to communicate basic everyday needs with community members. This is how we learn what a word means ("The meaning of a word is its use"—Ludwig Wittgenstein). We can understand words and their sequences, because we have learned a practice of interaction, which includes learning from the community which words are combined with which interactional patterns; we then memorize those.

16.3 KEY LEVELS OF BIOCOMMUNICATION IN PROKARYOTES AND EUKARYOTES

Communication processes within and between organisms are rather complex sign-mediated interactions that significantly differ in prokaryotes (unicellular organisms without a true nucleus) and eukaryotes (uni- and multicellular organisms with true nucleus). Prokaryotes represent a success story in evolution and exist since nearly 3.8 billion years. However, the transition to eukaryotes was a real revolution because it incorporates a variety of former free-living prokaryotes within a double-layered cell and its information-bearing nucleus. The latter was most probably derived from a large double-stranded DNA virus. This means that the basic components of eukaryotic cells are both cellular and viral symbionts that are genetically conserved into a social organism.

16.3.1 Prokaryotes

The bacterial world is a social and communicative one. The production and the exchange of messenger molecules enable unicellular organisms to coordinate their behavior like a multicellular organism. The biocommunication in bacteria communities is not restricted to species-specific levels but represents a clear multilevel communication that enables hundreds of different bacteria groups to co-occupy one and the same ecological niche.

It has been proven that bacteria groups use quorum sensing to determine their strength and to react by coordinating their behavior such as in biofilm formation.

> Studies of quorum sensing systems demonstrate that bacteria have evolved multiple languages for communicating within and between species. Intra- and interspecies cell–cell communication allows bacteria to coordinate various biological activities in order to behave like multicellular organisms.
>
> SCHAUDER AND BASSLER (2001)

Figure 16.3 demonstrates this as a snapshot from a video in which a group of bacteria sense available nutrients and coordinate redirected group movements in the correct direction. Recently, all key levels of biocommunication of soil bacteria have been categorized.

16.3.2 Eukaryotes

16.3.2.1 Fungi

Fungi also communicate and therefore are able to organize and coordinate their behavior. Coordination and organization processes in fungi are seen at the intraorganismic level, for example, during the formation of fruiting bodies, between species of the same kind (interorganismic), and between fungal and nonfungal organisms (transorganismic).

The semiochemicals (from the Greek word *semeion*, meaning sign) used are of biotic origin, in contrast to abiotic indicators that trigger the fungal organism to react in a specific manner. The roles of some of these signaling molecules are as follows: (1) Mitogen-activated protein kinase signaling (MAPK) is involved in cell integrity, cell wall construction,

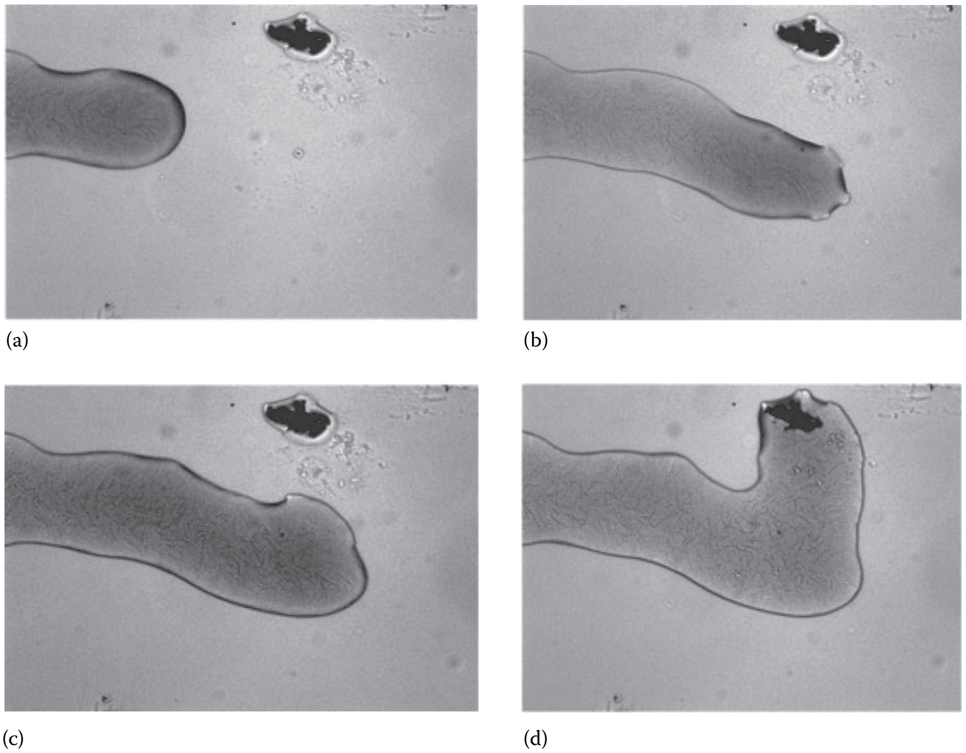

FIGURE 16.3 Swarming intelligence in bacteria: some extracellular food was positioned near a bacteria colony (a). After sensing of the food (b), the colony swarm moved toward the resource (c and d). Intra- and intercellular signaling is necessary to sense, interpret, and coordinate common motile behavior. (From Ben-Jacob, E., *Ann. N.Y. Acad. Sci.*, 1178, 78, 2009. With permission.)

pheromones/mating, and osmoregulation; (2) the cyclic adenosine monophosphate/protein kinase A (cAMP/PKA) system is involved in fungal development and virulence; (3) the RAS (protein family members that belong to a class of small GTPase) protein is involved in the cross talk between signaling cascades; (4) calcium, calmodulin, and calcineurin are involved in cell survival under oxidative stress, high temperature, and membrane/cell wall perturbation; (5) rapamycin is involved in the control of cell growth and proliferation; (6) aromatic alcohols tryptophol and phenylethylalcohol are used as quorum-sensing molecules; and also (7) a variety of volatile (alcohols, esters, ketones, acids, lipids) and nonvolatile inhibitory compounds (farnesol, H_2O_2).

To date, 400 different secondary metabolites have been documented. Development and growth of fungal organisms depend upon successful communication processes within, and between, cells of fungal organisms.

In order to generate an appropriate behavioral response, fungal organisms additionally must be able to sense, interpret, and memorize important indices from the abiotic environment and adapt to them appropriately (see Figure 16.4). Interestingly, certain rules of fungal communication are very similar to those of animals, while others more closely resemble those of plants.

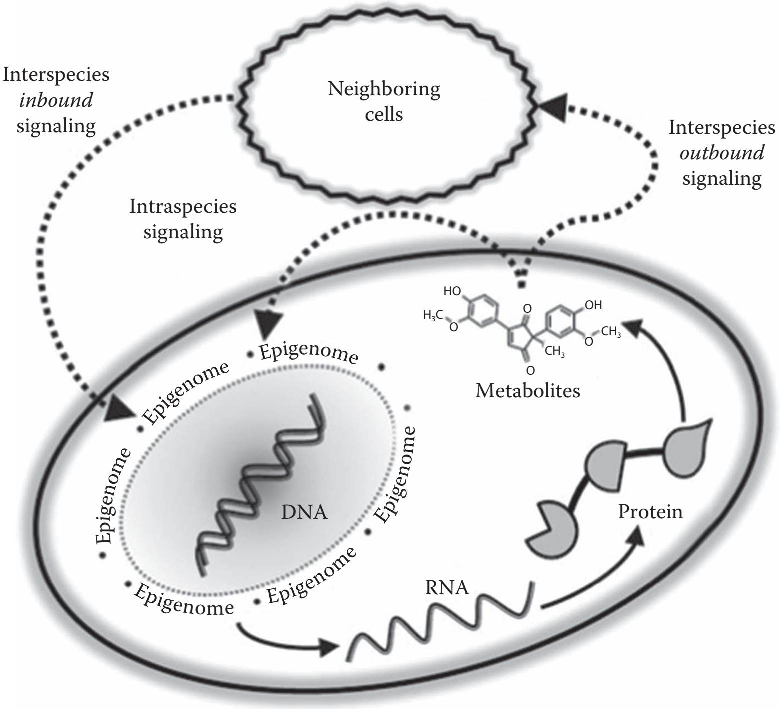

FIGURE 16.4 Depending on the real-life context of fungal organisms, epigenetic regulation can suppress or amplify incoming or transmitted secondary metabolites, an important signal resource of fungal organisms. Therefore, not for every message, a novel sequence has to be produced (multiple meanings of identical syntax structures). (From Cichewicz, R., *Epigenetic Regulation of Secondary Metabolite Biosynthetic Genes in Fungi*, Springer Science+Business Media, Dordrecht, the Netherlands, 2012. With permission.)

16.3.2.2 Animals

Animals also depend primarily on volatile substances such as pheromones to identify group identity of self and nonself. However, in addition, they depend on a variety of signs that convey meaning via vocal sounds and visual gestures. This opens up a variety of combinatorial possibilities and broadens the communicative competencies. Such complexity increases exponentially in comparison to biocommunication of bacteria, fungi, and plants. The signaling molecules, vocal and tactile signs, gestures, and their combinations differ throughout all species according to their evolutionary origins and variety of adaptation processes. However, certain levels of biocommunication can be found in all animal species:

1. Abiotic environmental indices such as temperature, light, water, and gravity that affect the local ecosphere of an organism are sensed and interpreted (against stored background memory). Then they are being used for organization of behavioral response to adapt accordingly (taking into account also optimal energy cost).
2. Trans-specific communication with nonrelated organisms as found in attack, defense, and symbiotic (even endosymbiotic) sign-mediated interactions.

3. Interorganismic communication between same or related species.
4. Intraorganismic communication, that is, sign-mediated coordination within the body of the organism. This means two sublevels, such as cell–cell communication and intracellular signaling between cellular parts.

16.3.2.3 Plants

Plants are sessile organisms that actively compete for environmental resources both above and below the ground. They assess their surroundings, estimate how much energy they need for particular goals, and then realize the optimum variant. They take measures to control certain environmental resources. They perceive themselves and can distinguish between *self* and *nonself*. They process and evaluate information and then modify their behavior accordingly (see Figure 16.5). Plant communication centers are the stem and the rhizosphere (the entire area of interactions within the root zone). The rhizosphere of plants is a realm of overlapping communicative interactions and a dynamic environment featuring dense microbiological life, high growth rates and metabolic activities, as well as rapidly changing physical conditions. The communication processes between tissues and cells in plants are incredibly complex and encompass nucleic acids, oligonucleotides, proteins and peptides, minerals, oxidative signals, gases, mechanical signals, electrical signals, fatty acids, and oligosaccharides, growth factors, several amino acids, various secondary metabolite products, and simple sugars.

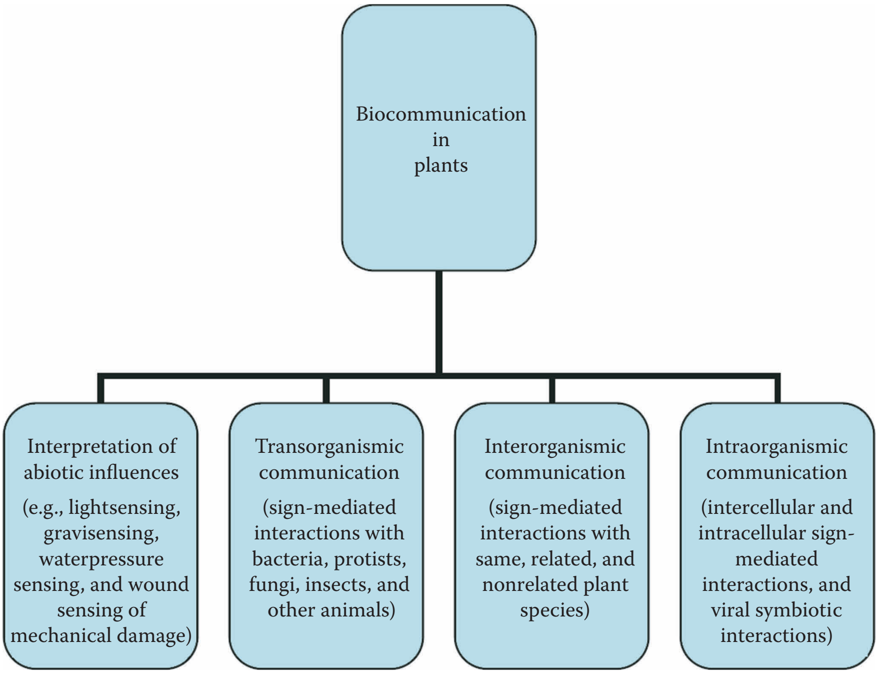

FIGURE 16.5 Key levels of biocommunication in plants. (From Witzany, G., *Key Levels of Biocommunication in Plants*, Springer-Verlag, Berlin, Germany, 2012. With permission.)

As in every biocommunication process of real lifeworld (pragmatic) situations, context determines semantic meaning of signals. Auxin, for example, is an ancient signaling molecule in plants. It functions in different hormonal, morphogen, and transmitter signaling pathways. Thus, it is very difficult to decipher the actual semantics of auxin, since it depends on whether it is used as hormonal or morphogen or transmitter signal. The same signal can take on different meanings and trigger different effects, depending on whether it reaches the whole plant, a tissue, or a cell. Because of this, the respective developmental status of the organism serves as a memory for each individual plant.

16.4 NUCLEIC ACID LANGUAGE AS NATURAL CODE

Concepts such as *genetic code*, *nucleic acid language*, *recognition sequences*, *translation process*, *amino acid language*, *immune responses*, and *cell–cell communication* represent irreplaceable core concepts in molecular biology. These concepts were not introduced into biochemistry and molecular biology by linguists, communication experts, or language philosophers. Rather, they were independently coined by molecular biologists to explain observed phenomena and were clearly invoked due to the strong analogy to processes of human communication. Francis Crick termed the genetic code a *code without commas*. However, Manfred Eigen investigated the genetic code as real language and not just as a metaphor, as revealed by the following citations: “The relative arrangement of the individual genes, the gene map, as well as the syntax and semantics of this molecular language are (…) largely known today” (Eigen and Winkler, 1983, p. 207). “All the words of the molecular language are combined to a meaningful text, which can be broken down into sentences” (p. 305). “At any rate one can say that the prerequisite for both great evolutionary processes of nature—the origin of all forms of life and the evolution of the mind—was the existence of a language” (p. 314).

As we know today, Eigen followed the opinion of his time, that language follows the structure of a *universal* and *context-free grammar* (Noam Chomsky) that underlies strict natural laws as it represents the logic of the material reality. The core functions of languages are limited, formalizable, predicable, and computable. The only real language that depicts material reality is mathematics. Therefore, the molecular genetic code can be investigated and described sufficiently by physics and chemistry. Eigen adapted the opinion of the linguistic turn as described earlier.

Several other derivatives of the linguistic turn and its mathematical theories of language, such as systems theory, cybernetic information theory, synthetic biology, and even biolinguistics, all share this deficit. None of them take the full range of levels of rules into their theoretical assumptions but let these levels of rules be restricted to syntax and semantics. But the demission of the primary role, pragmatics, to the investigations of natural languages has a fatal consequence. It installs a permanent deficit into these theoretical realms that determines their failure to explain sufficiently natural languages.

Because natural language/code tools are limited, the information-bearing sequences denote several independent and even contradictory contexts. One nucleotide word, such as a pseudoknot (a type of the nucleic acid secondary structure), may have several different meanings. Because living agents cannot invent new signs for every new situation or designation (energy costs), this evidently makes sense. Similar or equal combinations of signs, characters, and words that result in sentences can be used as informational tools to transport different meanings about a whole genome. Examples include overlapping epigenetic marking (the genetic sequence is marked through environmental influences that determine the context-relevant meaning/expression pattern) and silencing of transposons (DNA sequences that move), which induce repression of maternal cytotype (having different chromosomal factors) in animals, among others.

From human communication, we know that different gestures or spelling may indicate different meanings of the same words. Without contextual explanation, the phrase *the shooting of the hunters* cannot be understood unequivocably. The identical sequence may transport contradicting messages (see Figure 16.6). The marking of syntactic sequences by marking tools is common use in natural languages/codes and determines semantic content according to the needs of the pragmatic interacting agents.

To investigate syntactic sequences without knowing something about the real-life context of code using agents is senseless because syntactic structures do not represent unequivocable semantic meaning. Quantifiable analyses of signs, words, or sequences cannot extract context-dependent meaning. In a restricted sense, this is possible through sequence comparison, for example, if we know which sequences determine certain functions. But all these features are absent in nonanimate nature. If water freezes to ice, no living agents nor semiotic rules or signs are necessary.

FIGURE 16.6 *The shooting of the hunters*: in natural languages/codes, the meaning of syntactical identical sequences depends on the real-life world context in which competent sign users are interwoven. The use of identical syntax structures to transport different (and even contradictory) meanings saves energy costs. Algorithm-based machines (computers) that must extract the meaning of given syntax structures cannot decide between superficial grammar and deep grammar (illocutionary acts) intended by sign users. (Reprinted by permission from Macmillan Publishers Ltd. *EMBO Reports*, Witzany, G. and Baluška, F., Life's code script does not code itself. The machine metaphor for living organisms is outdated, 13, 1054–1056, Copyright 2012. Graphics by Uta Mackensen.)

16.5 AGENTS OF NATURAL GENOME EDITING

Within the last decade, views on natural genetic engineering and natural genome editing have changed dramatically. In particular, research in virology has opened perspectives on early evolution of life, as well as on viruses as essential agents within the roots and stem of the tree of life. From the early RNA world perspective, the whole diversity of processes within and between evolutionarily later-derived cellular life depends on various RNAs. The precellular RNA world must have been dominated by quasi-species consortia-based evolution, as are current RNA viruses.

Viruses can parasitize almost any replication system—even prebiotic ones. RNA viruses store crucial and dynamic information. Based on this and the results of phylogenetic analyses and comparative genomics, it is possible to establish viral lines of ancestral origin. These lines of origin can also be nonlinear because different parts of viruses contain different evolutionary histories. Since viruses with RNA genomes are the only living beings that use RNA as a storage medium, they are considered to be witnesses of an earlier RNA world. Current negatively stranded RNA viruses have genome structures and replication patterns that are dissimilar to all known cell types.

No similarity between RNA-viral replicases and those of any known cell types has been identified. DNA viruses, too, do not give any reference to a cellular origin. DNA-repair proteins of DNA viruses do not have any counterparts in cells. One milliliter of seawater contains one million bacteria and 10 times more viral sequences. 10^{31} bacteriophages infect 10^{24} bacteria each second. The enormous viral genetic diversity in the ocean has established pathways for the integration of complete and complex genetic data sets into host genomes, for example, acquisition of complex new phenotypes. A prophage can provide the acquisition of >100 new genes in a single genome-editing event. Today, it is assumed that the gene word order in bacterial genomes is determined by viral settlers of bacterial host genomes. Not only bacterial life is determined by nonlytic viral settlements, but also the evolution of eukaryotes has strongly depended on viral properties. In contrast to the mitochondria and other eukaryotic parts of bacterial descent, the eukaryotic nucleus was formerly a large double-stranded DNA virus. All properties of the eukaryotic nucleus are lacking in bacterial life forms but are typical features of DNA viruses. Even lethally irradiated viruses can often repair themselves. They are competent to recombine combinations of defective viral genomes in order to assemble intact viruses. Therefore, viruses are the only living agents capable of meaningfully recombining text fragments of a damaged genome into a fully functional viral genome that is capable of self-replication.

Lytic diseases that are caused by viral infections are the exception in viral life strategies, although they might have epidemic and pandemic and therefore catastrophic consequences for infected populations. The most dominant viral life strategy is the nonlytic but persistent viral settlement of cytoplasm of cellular hosts and even more of cellular host genomes. Addiction modules are the result of integration of former competing viral infections. As symbiotic neutralization and counterpart regulation, they represent new host phenotypic features. One feature is regulated exactly by the antagonist according to developmental stages in the cell cycle, replication, and tissue growth. Should this suppressor function become unbalanced, then the normally downregulated part might become lytic again. We can identify virus-derived addiction

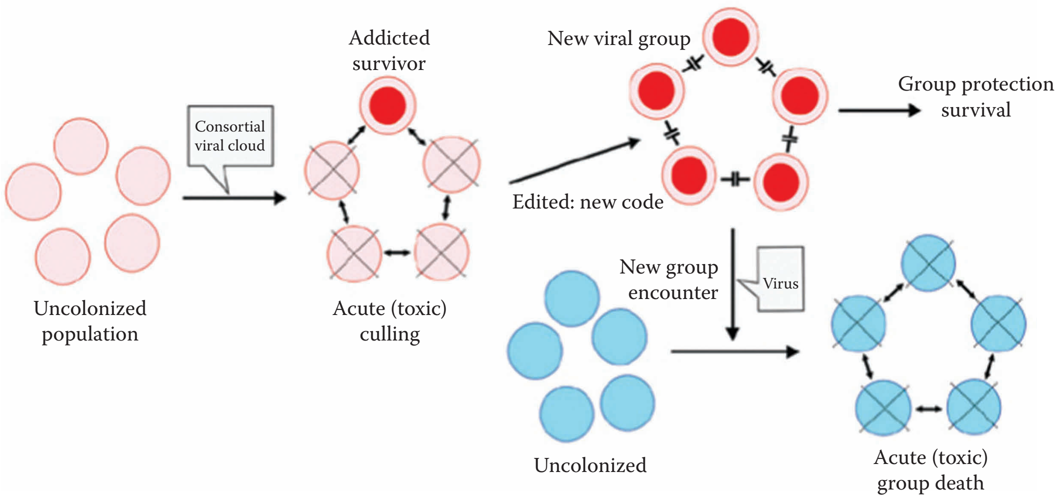

FIGURE 16.7 Basic interactional motif of infection-derived group identities: the addiction module as a result of counterbalanced, infection-derived, and persistent genetic parasites that initiate evolutionary inventions by natural genetic engineering of host genetic identities, some we can find as toxin/antitoxin, restriction/modification, or insertion/deletion modules. (From Villarreal, L.P. Viruses and host evolution: Virus-mediated self identity. In López-Larrea, C. (ed.), *Self and Nonself*, Springer Science+Business Media, Austin, LandesBioscience, New York, pp. 185–217, 2012b. With permission.)

modules in every toxin/antitoxin, restriction/modification, or insertion/deletion modules in which former competing viral clouds are now immunologically balanced (Figure 16.7). If a balanced status is reached, this means a changed genetic identity of the host organism and, in consequence, a changing genetic identity of the viral settler. Current knowledge indicates that most evolutionarily novel derived species are the result of changed and expanded genomic identities caused by persistent viral colonization. Research results in virology have led to the assumption that, besides communicative competences of cellular organisms, which are involved in coordinating behavior, there are *linguistic* competences of viruses and virus-derived viral parts (e.g., env, gag, pol), which not only regulate all cellular processes but edit the genetic content of living organisms. This viral genetic text-editing competence depends on living organisms that are different from each other, and it therefore needs a biotic matrix to expand this competence. Without living and interacting organisms and cells, genomic creativity would only be a possibility that is restricted to mere RNA combinatorial events (in an early precellular RNA world), which has no relevance to the generation of a biosphere.

16.5.1 Biocommunication in the RNA World: RNA Sociology

The ancient RNA world hypothesis is currently updated with RNA world facts and increasing knowledge about the abundance of different but compatible RNAs. In this world of life processes actively dominated by RNA, DNA is increasingly cast in the role of the *habitat* of genetic information storage, whereas the interacting RNAs seem to be the *inhabitants*

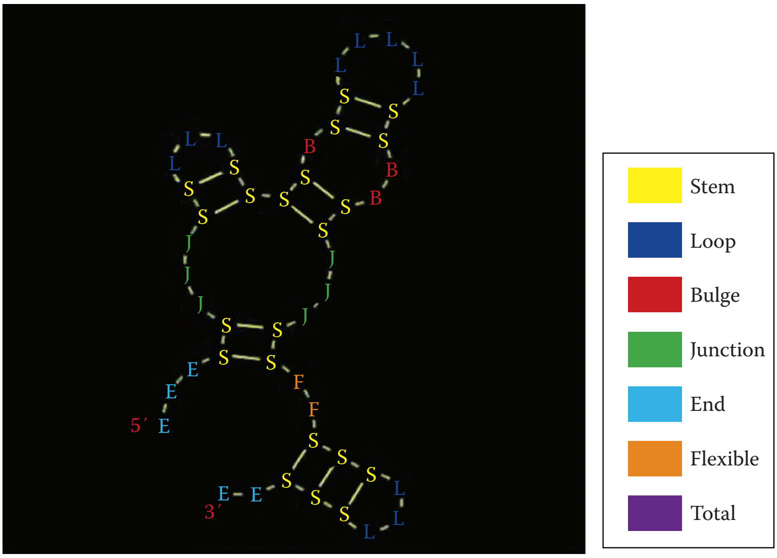

FIGURE 16.8 The RNA stem loops have several distinct parts/subunits: stems consisting of base-paired nucleic acids and loops/bulges/junctions consisting of unpaired regions limited by stems. Important: any RNA is part of such stem loops. (From Smit, S. et al., *RNA*, 12, 1, 2006.)

within this habitat. If we look at these network-like cooperating inhabitants, we can see a secondary structure that is shared by all these RNA nucleic acid sequences: it is the stem-loop structure or, in the case of more complex agents such as tRNA or ribosomal subunits, the ligated consortia of such stem loops (see Figure 16.8).

The rather astonishing result of investigations is that randomly associated RNAs that have no evolutionary history show the same structure-dependent compositional bias as natural derived (ribosomal) RNAs. This means that the differences do not depend on selection processes but on the overall composition of the RNA consortium.

16.5.2 Biocommunication at the Level of the RNA Group Membership

RNA group membership can never be completely specified, since it can always be further parasitized by as yet to be encountered members or parasites. This essential and most important feature renders the ability to absolutely specify membership (absolute immunity) as basically indefinable. Thus, an RNA group can never be fully secure from as yet undefined parasite agents. But a crucial consequence from this *insecurity* is that it provides the inherent capacity for novelty, that is, the precondition for evolutionary innovation such as greater complexity.

To introduce sociological terms, we now have to ask: How do agents emerge from chemicals to form identity and then form groups that learn membership? Single RNA stem-loop generation occurs by physical chemical properties solely as demonstrated by natural and randomized RNA experiments. If stem-loop consortia build complex consortia, they initiate social interactions not present in a pure chemical world, that is, biological selection emerges. This designates the crucial step from inanimate world to life.

Now we have molecular structures coherent with physical laws that store genetic information. In contrast to inanimate nature, they actively generate behavioral motifs and patterns of interaction, that is, coordinate common behavior according to rules that lead to consortia of self and nonself groups. This resembles some kinds of social group behavior with shared features:

- De novo initiation of behavior that cannot be deduced from former behavioral patterns
- Highly adaptive processes
- Lacking central or fittest type control
- Retaining a contextual history
- Smart (optimal energy costs)
- Solves problems beyond the capacity of its individual members
- Fast-changing reactions against nonmembers

Together these features are clearly and exclusively at the foundation of all living nature. If we were to eliminate these complementary competences out of the life processes, would there remain a living organism, or would it now simply be a chemical state? It seems not; thus, social RNAgents are essential.

16.5.3 Cooperation Outcompetes Selfishness

If we look at some interactional motifs of RNAgents to form consortial biotic structures that follow biological selection processes and not mere physical chemical reaction patterns, we must look at the group building of RNA stem-loop structures.

Recently, it has been found that single stem loops interact in a pure physical chemical mode without selective forces, independently whether they are derived randomly or are constructed under in vitro conditions. In contrast to this, if these single RNA stem loops build groups, they transcend pure physical chemical interaction pattern and emerge biological selection forces, biological identities of self/nonself identification and preclusion, immune functions, and dynamically changing (adapting) membership roles. A single alteration in a base-pairing RNA stem that leads to a new bulge may dynamically alter not solely this single stem loop but may change the whole group identity of which this stem loop is part of.

Simple self-ligating RNA stem loops can build much larger groups of RNA stem loops that serve for increase in complexity (Figure 16.9).

Significantly, RNA fragments that self-ligate into self-replicating ribozymes spontaneously form cooperative networks. For example, three-membered networks showed highly cooperative growth dynamics. When such cooperative networks compete directly against selfish autocatalytic cycles, the former grow faster, indicating competence of RNA populations to evolve greater complexity through cooperation. In this respect, cooperation clearly outcompetes selfishness.

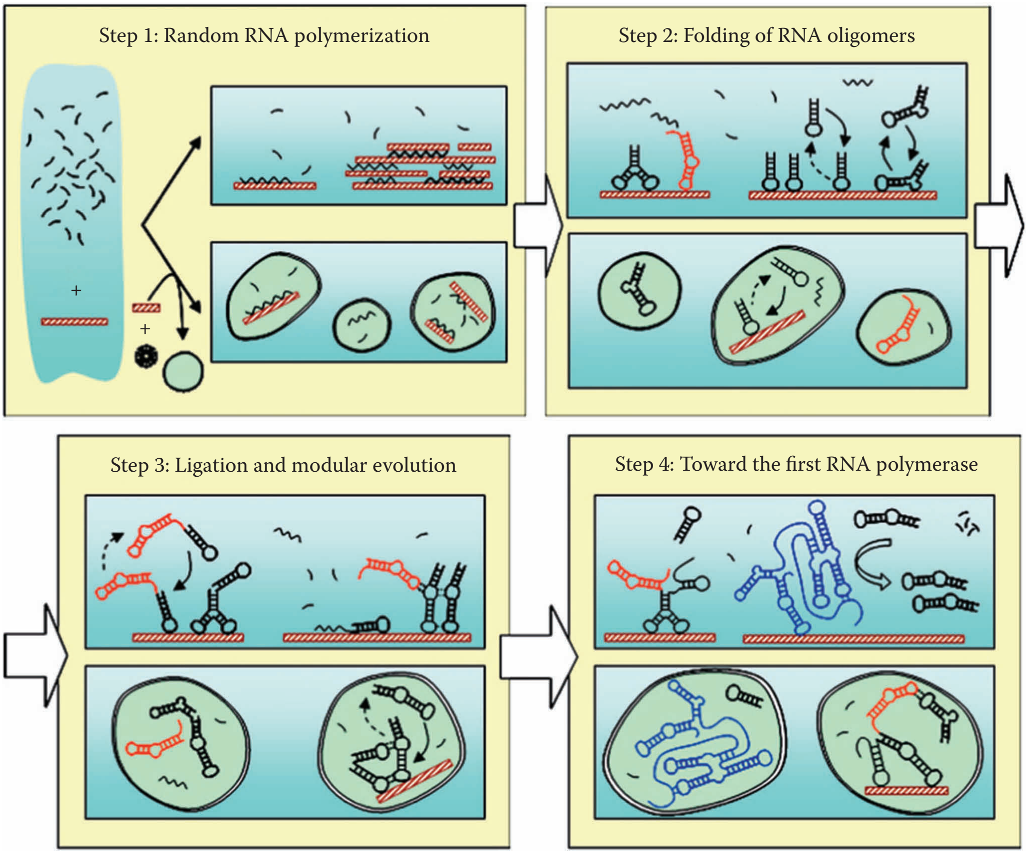

FIGURE 16.9 Schematic representation of the stepwise process toward a template-dependent RNA polymerase. In every step, we depict two possible and compatible scenarios: evolution on mineral surfaces (shown as brown rectangles) in bulk solution and evolution inside vesicles that could also encapsulate mineral particles. Functional hairpin structures (with ligase activity) are shown in red. Solid and dotted arrows stand for the surface-bound to in-solution equilibria. The RNA polymerase emerging from this process is depicted in blue. (From Briones, C. et al., *RNA*, 15, 743, 2009.)

16.6 CONCLUSION

What is the benefit of this concept of language and communication as universal requirements of life in contrast to mechanistic, holistic, objectivistic, mathematically derived formalizable concepts such as system theoretical, bioinformatics, or synthetic biology approaches in molecular biology, genetics, epigenetics, and microbiology? The biocommunication and natural genome-editing approach on processual reality of living agents brings some advantages to traditional scholarly conviction:

- Clear distinction between life and nonlife.
- Empirical nonmechanistic and nonreductionistic description method of biotic interactional patterns throughout all organismic kingdoms.

- Any observed coordination within and between organisms can be deciphered by research that identifies signaling molecules and syntactic, pragmatic, and semantic rules underlying the mode of signal use.

- Biological research must not concentrate any longer on experimental setups and theoretical approaches that want to elucidate language and communication in nonhuman living nature by mathematical (algorithm-based) modeling.

GLOSSARY

Biochemically related terms: Please consult the following recommended readings.

Biofilm: Bacterial group building by signaling interactions.

Communication: Interactions via signals between living organisms according to syntactic, pragmatic, and semantic rules.

Evolutionary biology: Genotype/phenotype novelty as a result of variation (mutation = replication error) and selection.

Language: Any repertoire of signs that is used according to syntactic, pragmatic, and semantic rules.

Linguistic turn: We do not understand the outer and the inner world, but sentences about it.

Natural genome editing: Evolutionarily relevant variation results out of de novo sequence generation and recombination by competent RNA consortia, not of replication error.

Noncoding RNAs: RNAs that shortly after transcription out of DNA are not translated into proteins but serve as gene regulatory tools, increasing the main part of genetic information in eukaryotes.

Pragmatics: Level of rules that determine how to correctly combine words/sentences with real-life context.

Pragmatic turn: Language use is a kind of social interaction, that is, needs user groups.

Semantics: Level of rules that determine the correct designation of objects with words/sentences, that is, meaning.

Syntax: Level of rules that determine how parts of an alphabet can be correctly combined.

REVIEW QUESTIONS

1. If we would find extraterrestrial life, how do you think we would identify communication within it? Suggest how the material on language and communication you have learned from this chapter may or may not be helpful for answering this question.

2. Write a short essay on one way of biocommunication in life, such as bacteria and fungi, based on the material in this chapter. Research further a subtopic that you like, for example, the way plants communicate.

3. Why is context dependency crucial for identifying *meaning* of words and sentences? Try to formulate examples in which illocutionary acts determine the meaning of syntax of sentences (e.g., *the shooting of the hunters*).

4. Who was John Searle and how is his philosophy of language relevant to sufficiently explain communication? Explore this topic; exemplify the difference of locutionary, illocutionary, and perlocutionary speech acts; and write a short essay to present to the class.
5. What are the basic differences of natural languages/codes and mathematical concepts of languages?
6. What are the essential differences between single RNA stem loops and (self-)ligated groups of RNAs? Is there any evolutionary important divergence?
7. What is meant by *RNA sociology*? Nominate the differences to a strict physical/chemical vocabulary.
8. For decades, it was assumed that errors in replication (mutations) are key for evolution, that is, variations that then are subject to biological selection. Now it is recognized that genetic novelty is better explained by natural genetic engineering and natural genome editing initiated by competent RNA agents. Why do you think was the error-based narrative insufficient to explain genetic novelty?

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