

Evolution and Language: Overview

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Keywords: agent-based modeling, cognate, cultural evolution, essentialism, ethology, evolution of language, evolution, historical linguistics, human population history, language, language change, language contact, lineage, meme, phylogeny reconstruction, phylogeny, population thinking, replicator, social cognition, sociolinguistics, species, speech community

Abstract

The close relationship between biological evolution and language was noted by Darwin himself in an oft-quoted passage from *The Descent of Man*: ‘the formation of different languages and of different species, and the proofs that both have been developed through a gradual process, are curiously parallel’ (Darwin 1882). In fact, the development of evolutionary theory in biology was inspired in part by the advances in historical linguistics in the early 19th century. In the 20th century, evolutionary theory did not have much influence on linguistics, in part due to the advent of structuralism and the focus on synchronic linguistic analysis. In the past two decades, there has been a considerable increase in interest in the relationship between language and evolution. The interest has

been manifested in three areas of recent research. The first is the evolutionary origin of the human language capacity, a topic that was actively avoided in linguistics for a century. The second is the employment of techniques of phylogeny reconstruction from biology in the analysis of genetic families of languages. Finally, there is the application of theories of evolutionary processes to language change, based on the hypothesis that, as Darwin wrote, the two are strikingly parallel.

1 The evolutionary origin of language

The evolutionary origin of language is not technically an example of parallelism between biological evolution and language. It simply is an instance of biological evolution, specifically the evolution of a behavioral capacity in one particular species. This topic was avoided in linguistics for over a century because of the absence of empirical evidence about any stage of language prior to modern human language.

All modern human languages are general-purpose communication systems of a similar order of complexity; there is no reason to believe that any contemporary human languages represent an earlier stage in the evolutionary development of the language capacity. Written records of language are very recent—no more than five thousand years old—and they make clear that languages of that age are no different from contemporary human languages (see *Writing, Evolution of*). Languages otherwise do not leave material evidence, so the archaeological record leaves no direct record of the evolution of the language capacity.

Evidence from hominin skeletal remains suggests that there have been anatomical changes that indicate the increased ability of our ancestors to produce a wide range of

vocalizations, and to control our breathing in such a way to produce linguistic sounds. It is generally assumed that the ability to produce a rich variety of vocalizations implies the existence of language at the time of these anatomical changes. However, it could be that such vocalizations had other functions than a general-purpose communication system, such as music and ceremony, or that the sort of language that such vocalizations were used for was quite different in its structure and communicative range than modern human language. Likewise, the great expansion of brain capacity in the development of humankind is an indicator of the emergence of the cognitive capacity for modern human language. But lacking more specific details of neural structure in hominins, this change cannot tell us more about the evolutionary origin of the human language capacity.

The taboo against studying the evolutionary origin of the language capacity has now fallen. A number of different approaches have been taken to tackling the question. All of them are necessarily indirect. Two of the commonest approaches are computer-based models simulating a society of interacting agents, to explore under what circumstances language structures might emerge (e.g. Kirby 1999); and comparative ethology, comparing the communicative, symbolic and interactional capacities of our nearest relatives, the primates, and other species that possess vocal communicative systems, such as various species of birds and cetaceans (e.g. Tomasello 2008). Child language acquisition is also used as a reference point for language origins (Tomasello 2008). Comparison to child language acquisition must be treated with caution because children learn language by being exposed to a modern human language, which will influence their course of development. Also, children largely already have the cognitive and social capacities of modern humans, so they do not represent the sort of hominins in which the

modern human language capacity evolved. More recently, experiments using artificial language learning have come to be used in the search for language origins (see *Evolution and Language: Cultural Transmission*). Again, the subjects of artificial language learning experiments already have the cognitive and social capacities of modern human beings, and they also have knowledge of a modern human language at the point that they engage in the experiments. This latter point also applies to proposals about the origins of language based on more naturalistic examples of language “creation”, such as pidgins, creoles and certain sign languages.

Many earlier studies focused on the structure of the linguistic signal. In comparative ethology, the question was whether or not certain structures of human language utterances were unique, or could be found in the communication systems of other species. For example, it was claimed that vervet monkey alarm calls were symbolic, in that they distinguish three different kinds of predators, and that bee dances and some bird songs involve a combinatoric syntax not unlike that of human languages. In the modeling approaches, the agents would produce strings of units and through simple rules of interpretation and feedback from such interactions, stable meanings of the units (i.e. symbols) and regular syntactic combinations were shown to emerge over several generations of interactions.

More recent studies have taken a broader perspective on the evolution of the human language capacity. Language structure does not evolve for its own sake, but only as part of a larger system of social interaction among human beings. Even the function of communication, often taken to be the *raison d'être* for language, actually serves the ultimate goal of achieving some joint action between persons. These joint actions form

the basis of human culture and society. In other words, the evolution of language is part of the evolution of human social interaction and human culture (Tomasello 2008).

This broader perspective implies, for example, that the computational modeling of the emergence of language will have limited success with disembodied agents simply reacting to whether a string of units refers to some object or not. In one modeling project from this perspective, the agents are robots that have perceptual and motor abilities, and the modeling includes visual processing and the establishment of joint attention on the part of the robots towards a potential referent for any utterance that is produced (Steels 2011). Of course, this type of modeling is very ambitious, and requires solving problems in visual and auditory processing, motor activity and social interaction as well as language structure processing and cognitive categorization and combination. In other words, one must model human beings in their full perceptual, motor, cognitive and social abilities in order to model the emergence of language.

In the case of comparative ethological approaches, the broader perspective implies looking at the social behavioral capacities of primates and other species, including joint attention, reasoning about other individual's beliefs ("theory of mind"), coordination of actions, and the ability to engage in cooperative activity, as well as cognitive abilities of categorization, causal reasoning, and representing knowledge of displaced experience (i.e. not the "here and now") that have been traditionally associated with the evolution of the language capacity. All of these social behaviors are preconditions for the evolution of modern human languages. Comparative studies suggest that many other species have the simple cognitive capacities listed above, but few if any have the social cognitive capacities required for language, and not to the degree that modern humans do.

Language embedded in its social interactional context is part of a very complex suite of human behavioral capacities. It is highly unlikely that this complex suite evolved suddenly. Thus, the transition to modern human language in the hominid lineage was probably a gradual one, with a number of intermediate stages of “pre-language”. Unfortunately, there is still a great gap between animal communication systems known to us and modern human language, so just what those intermediate stages are is largely a matter of speculation. One common proposal is that there was a stage in which utterances consisted of only one symbolic unit (a “one-word” stage). Some argue that a multiword stage developed by combining these single units in a single utterance, while others argue that a multiword stage developed by reanalyzing the single symbolic unit (a complex vocalization) into meaningful parts. Other proposals are based on the functions of the linguistic units. An earlier stage may involve gestures that are indexical, establishing joint attention in order to coordinate joint actions; names for individuals and symbolic gestures that denote things or actions emerge in a later stage. Or an earlier stage may involve more direct interactions such as commands or questions; utterances whose sole purpose is to share information, especially about displaced experience, develop in a later stage. Such intermediate stages of pre-language only make sense in the context of plausible intermediate stages of social interaction between what is observed in other primates (or other species) and what occurs between human beings in contemporary societies.

2 The use of biological methods for language classification (phylogenies)

The most obvious respect in which biological evolution and language are parallel is that languages form lineages in much the same way as species do (see *Evolution and*

Language: Phylogenetic Analyses). Languages have parents and daughters, and form trees of ancestors and descendants; these trees are called phylogenies in biology (see *Comparative Method in Evolutionary Studies*). In both domains, the ancestors are no longer present, because they have either become extinct or the ancestral species or language has split up into the contemporary species or languages. In only a few cases is there a material record of ancestral forms—fossil individuals of ancient species and written records of ancient languages. As a consequence, evidence for the phylogeny of both species and languages is indirect, namely, the traits of the currently existing species or languages. Comparative work among languages uncovers genetic trees, just as comparative work among species uncovers biological taxa. In some cases, historical linguists have arrived at conclusions about the nature of comparative historical analysis before biologists have. For example, an important principle of comparative historical linguistics is that a trait that is an innovation among daughter languages is more important evidence that the daughter languages form a subgroup than retention of a shared trait from an ancestral language. This principle was later independently adopted in the cladistic approach to constructing phylogenies (Hull 1988).

Thus, both the basic fact—branching lineages—and the basic method—comparison of present-day members—are the same for biology and language. For this reason, recent work has increased in the application of phylogeny reconstruction methods from biology to language data (see *Evolution and Language: Phylogenetic Analyses*). For the most part, it has been biologists using these methods on language data, rather than linguists adopting these methods for historical linguistics. The basic reason for this fact is that the

biological methods are essentially quantitative (and increasingly complex), while the methods of traditional historical linguists are essentially qualitative.

In comparative historical linguistics, the traits used to classify languages into genetic families (i.e. phylogenies) are words, that is, combinations of form and meaning. Words are particularly good traits to use for phylogenies. Words generally evolve independently of each other, so a large number of words represents a large set of independent pieces of evidence for a phylogeny. (In some cases, words are derivationally related, such as *long* and *length*, and so are not entirely independent.) The pairing of form and meaning is largely arbitrary, so other factors are unlikely to lead to convergence across languages. (There are cases of onomatopoeia, such as *meow*, but they are few and are avoided by historical linguists.) For this reason, historical linguists avoid schematic grammatical traits, such as subject-verb-object word order and the presence of grammatical gender. These traits are limited in their possibilities (much more so than the possible pairings of forms and meanings), and their presence is often due to universals of grammatical structure, of the sort studied in linguistic typology, rather than common ancestry of the languages that contain them. In biological terms, words are weakly filtered by selection but schematic grammatical patterns are not. Individual words form lineages themselves, but these word lineages bundle together, especially in basic vocabulary. This is what allows us to say that a language is the daughter of another language: most of its linguistic material comes from a single source. Of course, some words come from a language other than its parent; these are borrowings. Borrowings are more common in nonbasic vocabulary, though they occur in basic vocabulary as well. To the extent that borrowings

can be identified and excluded from analysis, then the phylogeny of languages is tree-like: a single parent and multiple daughters.

Most applications of biological methods in phylogeny reconstruction to language data begin with a set of words that are assumed to be cognate, that is, inherited from a common ancestor language (called a protolanguage). That is, for a set of languages, the data consists of whether or not some or all of the languages share a cognate for that meaning, for all the meanings in the wordlist. The phylogeny reconstruction algorithms use computational statistical methods to construct a phylogeny for the languages in question, given the distribution of cognate forms across the languages. These methods have increased in sophistication in recent years, aided by increases in computational power (e.g. Bouckaert et al. 2012; see *Comparative Method, in Evolutionary Studies; Evolution and Language: Phylogenetic Analyses*).

The phylogeny reconstruction methods provide a more precisely quantifiable judgement weighing the evidence from the complex distribution of a large number of cognates. They have been applied to universally-accepted, chronologically relatively shallow families such as Austronesian (in Oceania) and Bantu (in Africa) in order to clarify the subgroupings of those language families and provide support for hypotheses about the prehistoric migrations of the speakers of those languages. Such methods have their limits, however. For even a relatively small number of languages, the number of possible trees that can be constructed is far larger than the number that can be tested using current computing power. Hence, the phylogeny reconstruction algorithm can only test a small subset of the possible trees against the data provided by the list of cognate forms. (Much of the recent effort in refining phylogeny reconstruction algorithms is in how to explore

the search space of possible trees.) One consequence of this fact is that a phylogeny reconstruction algorithm does not produce a single “best” family tree; it produces a probability distribution of greater or less likely trees for the data.

Against this concern is the fact that even crude methods can find the major subgroups for the language families to which they are applied, such as the major subgroups of Indo-European. That is, the phylogenetic signal is very strong. But that signal is strong enough that visual inspection of cognate lists reveals those aspects of the phylogeny, and employment of quantitative methods is unnecessary. When it comes to resolving phylogenetic questions which are still a matter of debate among historical linguists, then the ability to find the most likely trees becomes an important issue in applying quantitative methods to historical linguistic problems.

Any list of cognates for a set of languages is going to give conflicting information about the phylogeny of those languages. Languages lose cognate forms; the original cognate changes meaning, or is lost entirely, and its form is replaced by another, unrelated form. Hence a missing cognate is not necessarily evidence that the language does not belong to the family in question. Deciding whether a set of cognate forms is a common innovation, justifying placing those languages into a subgroup, or a common retention, whose survival or loss is an accident, is not an automatic process. It requires balancing evidence from other cognate distributions to decide which cognates define a subgroup and which ones do not. The phylogeny reconstruction algorithms encode a particular way to make these decisions, based on their utility in biological evolution. The algorithm may or may not have the same utility in language change (this factor has not been discussed in the relevant literature).

The application of biological phylogeny reconstruction algorithms to language classification is actually a hybrid method. The data to which the algorithm is applied is already processed by a linguist: a linguist has decided which words are cognates and which ones are not. One of the chief problems in determining cognates is whether words that are similar in form and meaning across languages are borrowings or not. Some putative cognates may turn out to be borrowings. Some phylogeny reconstruction programs produce networks rather than trees. In most if not all cases in language history, ancestry vs. contact are clearly distinct; for example, English is a Germanic language albeit with many words borrowed via contact with French. Historical linguists look for patterns in the distribution of similar forms in order to differentiate common ancestry from borrowing. For example, similar forms across the bulk of basic vocabulary is indicative of common ancestry, whereas similar forms concentrated in particular semantic domains of nonbasic vocabulary (e.g. animal husbandry, religious ceremony) is indicative of contact; and a high degree of similarity of forms to the forms in just one language suggest that the latter language is the source of borrowing. Judgements based on differentiating types of vocabulary, or patterns of distribution across sets of languages, are not yet incorporated into phylogeny reconstruction algorithms.

What is of most interest to linguists (and nonlinguists) is the establishment of chronologically deeper language families than those widely accepted among linguists today. The comparative historical linguistic method starts from languages that are accepted to form a group; phylogeny reconstruction algorithms do the same, by starting with cognates for accepted families. Deeper language families have been proposed, but are controversial among linguists. In principle it is possible to create algorithms that

would identify form-meaning similarities among a complete set of words across a large set of languages not accepted to be related; look for correspondences between the sounds occurring in equivalent positions in the words, which is strong evidence for cognacy; use distributional patterns of form-meaning similarities to differentiate likely cognates from likely borrowings; and use all of this information to postulate likely family trees. It is only very recently that the first efforts to devise such algorithms are being made.

Biologists interested in prehistoric human population history have compared phylogenies reconstructed from biological data to language family trees, and have observed parallels between biological phylogenies of humans (and the migration patterns they imply) and language family trees. The combination of biological and linguistic phylogenies has been used to clarify the prehistoric movements of Austronesian and Bantu peoples, where the language families are widely accepted; and the migration of Native Americans into the New World, where the language families that resemble the biological phylogenies remain controversial (Reich et al. 2012). The parallels between biological and language phylogenies do not necessarily match in all details, because human populations may give up their heritage language and shift to another language. Nevertheless, considering both biological and language families together gives us a more refined picture of human prehistory.

3 The parallel between biological and linguistic evolution

The fact that both languages and species form lineages, and numerous other parallels between biological evolution and language change, has led many linguists to discuss analogies between the two domains. Although observing analogies may provide

inspiration for theories of language change in linguistics, they do not provide a principled basis for constructing an evolutionary theory of language change. In particular, when one finds a disanalogy between biological evolution and language change, it is unclear whether the disanalogy is due to simply a difference between the two empirical domains, or the disanalogy points to profound differences between biological evolution and language change. In fact, domain-general theories of evolutionary units and processes have been proposed. These theories are intended to subsume both biological evolution and some form of cultural evolution (see *Cultural Evolution: Overview*). There is major debate over the appropriateness of these theories; the following sections will briefly summarize the major issues.

Most biologists consider the fundamental principles of Darwin's evolutionary theory (Darwin 1859) to continue to hold (see *Darwinism*). These principles are descent with modification and selection. Descent with modification leads to lineages, and occurs through a process that is now generally called replication. Indeed, evolution can be thought of as a model of change by replication, as opposed to a model of inherent change. Replication also occurs in cultural transmission, including language change (Mesoudi et al. 2004). In both biological and cultural evolution, there is debate over what is the replicator, that is, what it is that replicates. In neo-Darwinian evolutionary theory, the paradigm case of the replicator is the gene, and we will use this example for initial illustration.

The fundamental properties of the replication process, most of which are explicated by Darwin, can be grouped into two categories (Dawkins 1976). The first category has to do with how replicators form lineages. A replicated unit can itself be replicated; the

replication process can proceed indefinitely. And some replicators must survive long enough to be replicated (these properties are also called longevity and fecundity). The second category has to do with inheritance, namely what makes the replication process nonrandom. Replicated units possess much of the structure of the original unit. The replication process is mostly faithful. But replication can produce heritable variation: that is, the replication process introduces variation, and that variation is cumulative over generations of replicators.

Among theorists of cultural evolution, three sorts of entities have been proposed as replicators: artifacts, behaviors and concepts, that is, mental entities. An issue with all of these replicator types is that their replication must be indirect. Artifacts and behaviors are reproduced by human agents, who use their cultural knowledge (i.e. mental conceptual structures) to replicate them. For concepts to be replicated from one person to another (“learning”), they must be publicly displayed in terms of human actions (behavior) or products (artifacts). In addition, concepts are not directly observable and there is evidence that the neural structures and patterns of activation for the same concept may differ from person to person.

In language change, the debate has been traditionally framed in terms of whether language change takes place through imperfect learning by children, or via language use. In evolutionary terms, this is a debate over whether the replicator is a grammar (that is, a speaker’s knowledge about their language) or linguistic structures in utterances (such structures are replicated every time we speak). Both theories have been debated since the emergence of historical linguistics in the nineteenth century, and the debate continues.

There is considerable empirical evidence that imperfect learning by children cannot be the source of language change (Croft 2000). Children's errors in acquisition (that is, their linguistic innovations) do not match the processes observed in language change. Children are very good at learning the language spoken around them even though they are not provided with direct negative evidence about the structure of their language. (Specialists in child language acquisition call this the "no negative evidence problem".) Finally, children's language is not emulated by other social groups in language change; instead, children expend their effort in emulating other social groups, in particular their older peers when they become adolescents.

By contrast, the sort of variation that is found in the phonetic realization of sounds, and in the verbalization of experience into words and constructions, does match observed language changes (Croft 2010). An important element of the usage-based model of language change is that knowledge of language includes knowledge of language variation, and that language variation is pervasive in language. Hence language change is actually a process by which change occurs in the distribution of linguistic variants across phonetic space (for sounds) or conceptual space (for words or constructions). While adults are not as flexible as children in changing their patterns of language use, there is some flexibility, which is greater for some linguistic units (e.g. new words) and less for others (accent); and adults vary in their receptiveness to novel linguistic variants.

Cultural replicators have been called memes (Dawkins 1976). However, memetics has combined the basic properties of replicators and replication with a "selfish gene/selfish meme" theory of selection. Selection represents the other fundamental principle of Darwinian evolutionary theory. Selection is a process by which some replicators are

successfully propagated in a population while other replicators go extinct (in the extreme case). Selection is a separate process from replication. Most evolutionary biologists recognize that evolution is a two-step process: the generation of variation via replication, and selection of some variants over others (also called differential replication).

In the “selfish gene/meme” approach, the replicator (gene or meme) functions as both the locus of replication and of selection. In biology, the organism is merely a vehicle to facilitate the gene’s successful replication, and by analogy, in cultural change, a human agent is merely a means for concepts to differentially replicate themselves. This approach has been controversial in both biology and theories of cultural evolution including language change (but see Ritt 2004).

Most biologists consider the selfish gene theory to miss the important roles that entities other than the gene play in biological evolution. Analogously, the selfish meme theory misses the important roles that entities other than the meme, in particular human agents, play in cultural evolution. Another generalized theory of evolution, the General Analysis of Selection, provides a richer, though still highly abstract, theory of evolutionary processes (Hull 1988). The General Analysis of Selection includes the replication process, but analyzes selection as a process of environmental interaction that causes differential replication to take place. Environmental interaction defines two more roles, the environment and the interactor. In the neo-Darwinian theory of biological evolution, the canonical interactor is the organism: an organism interacts with its environment, and natural selection brings about the differential replication of its genes depending on the survival and reproductive success or failure of the organism.

The General Analysis of Selection can also be applied to language (Croft 2000). The interactor is the human agent, namely the speaker. The speaker's environment includes the experience being communicated, the speakers with whom she converses, and the social structures that bind those speakers together in a speech community. In that context of language use, speakers make choices as to which linguistic variants to replicate. The variants that get replicated more frequently are propagated through a speech community, and in the end a historical linguist observes that a language change has taken place.

The General Analysis of Selection provides a framework for an evolutionary model of the processes that have been observed in sociolinguistics. Sociolinguistics observes variation in language use in a speech community. (Sociolinguists generally do not consider the origins of that variation; it has been argued to result from language production, as discussed above.) In particular, some of the variation in language use is socially structured: that is, it correlates with social parameters such as gender, age and socioeconomic status. The association of variants with particular social parameters appears to drive the propagation of certain variants in the speech community, that is, selection of those variants by the speakers in the community.

Another element of a generalized evolutionary theory that plays a central role in cultural evolution and language change is "population thinking". The term "population thinking" refers to the definition of species that emerged by the neo-Darwinian synthesis in the early twentieth century. The population definition replaces the essentialist definition of species that preceded evolutionary theory. In the essentialist approach to species, a species is defined as an ahistorical type with certain essential properties. The essentialist approach is problematic for actual biological species for several reasons. There is a high

degree of variation among individuals in a single species; “essential” traits may be lacking in many individuals. Conversely, two species may overlap substantially in their traits, so “essential” traits would not distinguish species (and in fact, there are many disputes about how many species there are in particular genera). Finally, the “essential” traits of a species change over time as species evolve.

The population approach avoids all of these problems. In the population approach, a species is defined not by an essential trait of individuals, but an interactional trait among the members, namely interbreeding (in sexual organisms) and its converse, reproductive isolation between populations. This interactional trait is also the way in which populations form lineages: interbreeding leads to reproduction, and lack of interbreeding eventually splits a population. Recently, different definitions of species have been proposed. However, these definitions appear to be the consequence of the fact that populations diverge slowly when interbreeding stops between the populations, and the recent species definitions differ as to what point diverging populations are said to constitute distinct species.

Languages suffer from the same problems with essentialist definitions as biological species. Languages are internally highly variable, so that one cannot provide an “essential” set of words and/or grammatical rules that would define a language. Two languages may share large amounts of lexicon and grammar, and there are disputes in many cases as to whether there are two languages or two dialects of a single language. Finally, languages change, so “essential” features of languages may change.

The general solution is to offer a social definition of a language, since a structural (i.e. essentialist) definition is unsatisfactory. More precisely, a population definition of a

speech community will avoid the problems of defining a language, since a language is produced by members of the speech community (Croft 2000; Mufwene 2001). A population definition of a speech community is a set of speakers that converse with each other. Since what the members of the speech community produce in conversation is the language of that community, it accommodates variation in the language. When a speech community splits, the languages they speak gradually diverge as the speakers of the two communities stop interacting. At first, the languages are structurally quite similar, but over time they will come to differ; linguists may disagree about the point at which they would say there are now two distinct languages.

Language populations, that is, speech communities, are never completely communicatively isolated from their neighbors. The result is language contact. Although this is sometimes held up as a disanalogy between language change and biological evolution, there is in fact much hybridization in the biological world outside of animals, and many instances of introgression that leads to the transfer of genes from one population to another through incomplete reproductive isolation. Language contact leads to sometimes large-scale transfer of linguistic structures or features from one speech community to another, particularly in the creation of new speech communities through the immigration of multiple populations in colonial situations (new-dialect formation and creole formation; Mufwene 2001, 2008). As in the case of the selection of certain linguistic variants in a single speech community, selection of linguistic variants from the members of different speech communities that come together in a colonial situation is influenced by social factors that operate in the circumstances of the colonization (the

dominance of some groups and enslavement of others, the demographic proportions of speakers, and so on).

The employment of an evolutionary framework for understanding language change allows for the development of mathematical models of mechanisms and processes of language change. Such models are agent-based models, in which entities that represent speakers (as human agents) interact with each other and produce linguistic structures, constrained by a range of competing factors. The process of replicating these linguistic structures feeds back into future linguistic behavior of the agents in a cumulative fashion, leading to evolutionary change in the language produced by the agents/speakers. In other words, these mathematical models represent language as a complex adaptive system.

The relationship between evolution and language is sufficiently parallel that both can be subsumed under a generalized model of evolutionary processes, and specific mathematical models can be applied to both. While many linguists, particularly historical linguists, have observed the parallels between evolution and language, a reassessment of the nature of theories and models of language based on an evolutionary perspective is a relatively recent phenomenon in linguistics. The level of impact of evolutionary thinking on linguistic theorizing remains to be seen.

See also: Comparative Method, in Evolutionary Studies; Cultural Evolution: Overview; Darwinism; Evolution and Language: Cultural Transmission; Evolution and Language: Phylogenetic Analyses

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Relevant Websites

- Evolutionary Linguistics: <http://www.evolutionarylinguistics.org>
- Max Planck Institute for Evolutionary Anthropology: <http://www.eva.mpg.de>
- Evolution of Language International Conferences: <http://www.evolang.org>