An Evolutionary Perspective on Diachronic Syntax

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Abstract

The paper covers the analogical parallel between biological evolution and language evolution, as it is intended within the biolinguistic perspective, with the aim of accounting for some relevant features of the evolutionary process undergone by grammars. The idea is to systematize hypotheses on the applicability of the evolutionary model outlined in biology to diachronic syntax, favouring the illustration of different perspectives that have been put forward so far. The goal is to provide a scheme in which the parallel can be framed, and to show how the biolinguistic approach on grammatical change plays an essential role in shedding light on the issue. The investigation appears to encourage the idea that biological and syntactic evolution may be modelled following comparable guidelines. Even if some specific factors are shown to be deeply different, it seems reasonable to think that some aspects of the two processes can be studied by means of analogous methods of investigation.

1. *Introduction*

This paper covers an analogical parallel between biological evolution and language evolution, focussing in particular on the diachronic transformation of syntactic systems within the biolinguistic perspective. The comparison is intended neither to force an extensive mapping between the processes in question, nor to outline a full innovative theory of language change. Rather, the idea is to show how some important features of the evolutionary process undergone by languages in general and by grammars in particular can be identified also in light of this type of parallel.

The aim of this work is then to systematize reflections and hypotheses regarding the applicability of the evolutionary model outlined in biology to diachronic syntax. Given the vast scope of the investigation, the discussion favours the theoretical aspects of the question and the illustration of different perspectives that have been put forward so far, even if relevant linguistic data are introduced to clarify the decisive points when needed. The final

goal is to provide a scheme in which the parallel can be effectively framed, highlighting differences and similarities, and to show how the biolinguistic approach on grammatical change plays an essential role in shedding light on the issue.

Before proceeding, it is useful to mention that the term 'evolution' has been used with different meanings in different times and fields (Bowler, 1975; Bowler, 2003: 8) and, although they will become clearer in the course of the discussion, some important distinctions should be immediately made explicit. The Latin word *evolutio* just means 'unrolling', i.e. 'development of a structure from its compact form', and in biology the first mention of 'evolution' referred exactly to the occurrence of this kind of process in embryos. From then on 'evolution' has often been intended as a process of change from simple to complex, from lower to higher states of existence. This description does not apply to the process, to which Darwin[1] and contemporary evolutionary biologists refer to. According to the 'modern synthesis' (see section 2.2), changes that affect organisms and species can determine some kind of improvement of the evolving units, but not necessarily an advance through higher levels of complexity. Of course the term 'evolution' has to be used with an even more neutral meaning in the case of language diachronic development: It is well known that in current literature the term 'linguistic evolution' does not entail any kind of upgrading, but just a process of diachronic change (see section 3.1), and this distinction already reflects a fundamental difference between the biological evolutionary process (as intended in the Darwinian paradigm) and the linguistic one.

The first step towards the achievement of the goal of this work is the introduction of the contemporary perspective on biological evolution, on the one hand illustrating the basic points of Darwin's (1859) original explanation of species diversity, on the other hand highlighting the role played by the integration of genetics within the so-called 'modern synthesis'. This is done in section 2. On this ground, in section 3 a brief overview of the application of evolutionary ideas in the history of linguistics is offered in order to show how the use of biological metaphors in linguistics has led to controversial conclusions in the last two centuries, but also that important insights have been provided in the last decade. The focus on the mechanisms

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[1] Actually, in order to avoid misunderstandings with the embryological theory, Charles Darwin referred to a process of 'descent with modification' in DARWIN (1859) and he used the term 'evolution' just in the closing paragraph of the book. Later 'evolution' became popular thanks to Herbert Spencer and other biologists' works.

of diachronic syntax, which is covered in section 4, allows to provide a more precise account for the issue. The specific modalities of syntactic evolution from the point of view of the biolinguistic approach and, in particular, of the Principles and Parameters Theory are illustrated, underlining the decisive importance of the parametric perspective in the identification of relevant 'evolutionary units' in the study of the transformation process undergone by grammars. The specific characterization of syntactic evolution in comparison with the model of biological evolution is finally reconsidered, framing the discussion within the schema offered by Cavalli-Sforza and Feldman's (1981) quantitative model of cultural evolution, with special regard to the questions of trait transmission and gradualism.

2. *Biological evolution*

Before Darwin (1859) the traditional and most popular belief in Western thought was that species are fixed and do not change into others over time. This view, referred to as 'biblical creationism', was part of the established Christian vision, which essentially followed from the literal interpretation of the Book of Genesis. Given this conceptual background, it is not surprising that, as pointed out by Bowler (2003: 1-3), in the second half of the nineteenth century the 'Darwinian revolution' faced the same resistance that was encountered by the 'Copernican revolution' in the sixteenth century[2]. The following sections are intended to concisely summarize the whole path from Darwin's innovative intuitions to the model proposed within the 'new synthesis' paradigm, focussing on the fundamental ideas that will be recalled later in the discussion.

2.1. *Towards Darwin's synthesis*

Evolutionary thought underwent a rapid and complex development in the decades that preceded Charles Darwin's birth. This was made possible thanks to the interaction between a series of advances in different but related fields of knowledge, especially geology and biological taxonomy.

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[2] The debate between creationists and evolutionists is still going on in our time (its role in contemporary American culture is discussed for instance by WITHAM, 2005), and it originated a number of intermediate positions. A survey of the development of creationist theories can be found in NUMBERS (1987) and WITHAM (2005).

The first widespread theory of evolution (or, more properly, of transformation) of species is Jean-Baptiste Lamarck's, which is known as the 'theory of transmutation of species'. The French naturalist illustrated his model in the *Philosphie Zoologique* (Lamarck, 1809): He hypothesized that each species has his own independent lineage and that lineages can neither branch nor become extinct. Notably Lamarck also thought that species undergo transformations in the course of time, due essentially to two factors. The first one is the 'internal force' of organisms, whose nature remains obscure to scientific inquiry, while the second is the inheritance of acquired characters. This means that according to Lamarck all characters, that an individual acquires in the course of life due to diseases, accidents and, most importantly, the use or disuse of organs, are assumed to be inherited by offspring. In the course of time the inheritance of acquired characters was shown to be completely untenable (e.g. Maynard Smith, 1989: 8-12). Anyway, even if Lamarck's theory got a cold reception after its publication (Ridley, 1993: 9), it remained influential until the second half of the nineteenth century as an alternative to the Darwinian evolutionary theory.

The evolutionary model Charles Darwin came up with was substantially different from Lamarck's, in that it consisted of a tree structure in which all lineages were related and represented by progressively divergent branches derived from a common ancestor. How did the scientist explain the way in which unique species can split into different ones in the course of time? Inspired by Thomas Malthus' *An Essay on the Principle of Population* (1798-1826), Darwin realized that, in the course of the 'struggle for existence' that goes on everywhere, favourable variations in the form are more likely to be preserved than unfavourable ones, which conversely tend to be eliminated. The core of this process, which later took the name of 'natural selection', is the interaction between inheritance of traits, spontaneous variations and adaptation to the environment: If an organism is born in a new form that is better adapted for survival in a specific environment, it has a greater probability to leave offspring and in further generations the frequency of its form will increase in the population. As variations progressively accumulate, the result might be the gradual formation of a new species[3].

Some fundamental objections were (and are still) raised against Dar-

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[3] Apart from other previous incidents, when the naturalist published his theory in *On the Origin of Species* (DARWIN, 1859), a similar idea had already been independently developed by Alfred Russel Wallace.

win's theory. One of them concerned the twin assumptions that changes were supposed to occur gradually and by chance and that they are mainly conserved due to natural selection. In the critics' opinion, there are gaps in the evolutionary history of organisms that cannot be explained assuming a gradual model in which only natural selection acts. What about coadaptations and rudimentary stages in the evolution of organs? Common examples are respectively the development of the giraffe's neck and that of wings, whose early stages did not necessarily represent an advantage for ancestral 'proto-birds'. As for the first case, i.e. complex adaptations, modern evolutionary biologists reply that one can assume that the evolution of many parts of an organ is under common genetic control. The second case can also be explained in the Darwinian paradigm, because on the one hand there are many ways in which also rudimentary development of characters can represent a real advantage (e.g. «proto-winged birds might have glided from cliff tops or between trees - as many animals, such as flying foxes, do now» Ridley, 1993: 328), on the other hand earlier stages could be 'preadaptations' for later stages, which means that an organ that was developed by chance for one use can come to serve a different function with little adjustments. This 'recycling' process is called 'exaptation' after the definition of Gould and Vrba (1982) and essentially entails the shift of function of specific organs or traits. Cases that are traditionally accounted for invoking exaptation are, for instance, the evolution of feathers, whose initial function was related to heath regulation and that were later re-adapted to be used in flight by birds, and more generally the evolution of tetrapods from lobe-finned fishes, as it is described for instance in Ridley (1993: 329). As pointed out is section 3.3, in linguistics the term 'exaptation' is also used with a purely analogical value, among others, by Lass (1990; 1997).

Another objection concerned the model of heredity assumed by Darwin (Ridley, 1993: 32-36). The naturalist chose to adopt the model of blending inheritance, according to which the traits of offspring are a blended mixture of the traits of parents, which, for the reasons summarized for instance in Ridley (1993: 32-36), entails that one generation after the other even favourable mutations would be expected to progressively decrease in the population instead of increasing. The lack of an adequate model of inheritance represented a big problem: The theory could not work without it. The solution came only in the beginning of the twentieth century, when Mendelian genetics was integrated with the evolutionary theory originating the so-called 'modern synthesis' or neo-Darwinism.

2.2. *Towards the 'modern synthesis'*

The most important innovation of the Mendelian theory of genetics is that it allows the description of organisms in terms of discrete traits, whose combination determines the apparent continuous variation of morphological traits observed in populations by biometricians. The shift of focus from continuous to discrete characters represented a major achievement for theoretical and empirical research aimed at reconstructing genealogical relationships between *taxa* in evolutionary biology.

The theoretical synthesis between the Darwinian idea of natural selection and the Mendelian theory of heredity is called 'modern synthesis' after the publication of Huxley (1942). From then on the interest in empirical genetic research progressively increased. Detailed explanations can be found in any introductory book on the subject (e.g. Weaver and Hedrick, 1997): This section is intended to provide a brief overview of some concepts that are used in the following parts of the work.

The heredity material has the form of a molecule of DNA, which is the acronym of deoxyribonucleic acid. A molecule of DNA is a sequence of units, called nucleotides (adenine, cytosine, guanine and thymine). The total length of a DNA molecule can be divided into regions: Some of them are spacer regions, others are called genes. Roughly, one can imagine that each gene encodes a specific protein and that proteins are at the base of the formation of organisms, in that each part of a body is built from a different kind of protein. Therefore genes are the fundamental units of information for designing organisms.

The DNA is also organized into a set of structures, called chromosomes, whose number varies across species. While zygotes, from which adult individuals develop, have these two parallel sets of chromosomes, gametes (e.g. eggs and sperm) have only one (they are haploid): The consequence of reproduction is that the zygote has one set of chromosomes that derives from the female gamete and the other that comes from the male one. Thus, since the new organism that grows from the zygote owns two parallel sets of chromosomes, it also owns two parallel sets of corresponding genes, which are not necessarily identical. The genetic *locus* is the place in which a gene lies in a chromosome: As a consequence, an organism has two genes at each genetic *locus* and the description of the pair of genes for each *locus* is called 'genotype'. These two genes may be identical or slightly different: The variants

of genes that are found in a specific *locus* are called alleles[4]. A population in which more alleles of a single gene exist is called 'polymorphic' for that gene and its condition is called 'polymorphism'. How do organisms with different genotypes appear? Which are the 'phenotypes', i.e. the observable forms, that derive from the genotype? This point is fundamental, because it is at the core of the Mendelian theory of inheritance. In synthesis, there can be a one-to-one correspondence between genotypes and phenotypes or not, if one gene is dominant and the other recessive. The key concept is that, even if phenotypes can appear to be blended, genes remain separated and each one is transmitted unaltered to offspring (unless it is affected by spontaneous mutation). Thus the Mendelian theory of inheritance can complete Darwin's evolutionary theory because it allows to predict how accidental variations of genes are preserved through generations, instead of being blended and reabsorbed in the course of time. On this premise, natural selection can work favouring the more fitting phenotypes.

2.3. *Evolutionary factors and individual transmission*

According to the 'modern synthesis', there are four main factors that intervene in evolutionary processes and determine the diffusion of genes in populations, as summarized for instance by Cavalli-Sforza (2001: 74-81): Mutation, natural selection, migration and genetic drift. Inheritance instead is a basic premise of the model and is taken into account at the end of this section.

Mutations are accidental changes that affect the genetic material: They are relatively rare and mostly harmful, because organisms are complex machines in which slight variations can easily have lethal effects. Deleterious mutations are likely to be eliminated by natural selection and only few mutations are preserved: The favourable ones and the neutral ones, i.e. those which do not have negative effects on phenotype. Mutations arise by chance and cannot be driven by individuals, neither consciously nor unconsciously: In other words, there is nothing similar to Lamarck's 'internal force'. They can be caused either by external factors (e.g. radiations, viruses or mutagenic chemicals) or by internal processes (e.g. transpositions or errors that occur

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[4] The concept of allele in molecular biology recalls that of allophones and allomorphs in linguistics: As alleles are concrete variants of abstract genetic *loci*, in a similar way allophones and allomorphs are respectively context-dependent instantiations of abstract phonemes and morphemes.

during meiosis and replication), and they are assumed to gradually accumulate until the resulting population becomes significantly different from the original one. Some models have been proposed against gradualism. Apart from theories that move from geological catastrophism, which was already contrasted by Lyell's uniformitarian principle in the first half of the eighteenth century, one can remember the so-called 'saltationism': According to this view, derived from the ideas proposed by the biologist Richard Goldschmidt in the '40s, the process of speciation is produced by rapid macromutations, rather than by progressive accumulation of little genotypic variations. This theory remains purely hypothetical for the moment. Another debate is taking place inside the gradualist perspective and regards the rate of accumulation. The fossil records show that on the one hand species show up rapidly, exist for a period and then become extinct, on the other hand there is often little evidence of transition between the ancestor species and their descendent ones. Is this entirely due to the incompleteness of fossil records? If the answer were 'yes', one could assume an evolutionary model, in which the rate of change is constant both during and between speciation events. Eldredge and Gould (1972; 1988) call this view 'phyletic gradualism' but they do not accept it. They propose the 'punctuated equilibrium' model (Maynard Smith, 1989: 282-284; Ridley, 1993: 511-531), according to which species tend to remain in a 'static' state for the most part of their history, a state the scholars refer to as *stasis* and in which no visible changes are supposed to occur. Following Eldredge and Gould's model, relevant mutation events are then assumed to occur rarely and rapidly, breaking the *stasis* and generating sharp branching events in species lineages called *cladogenesis*, actual splits of the original singular species into distinct ones. Thus the scholars think that there are long periods of equilibrium punctuated by rapid episodes of variation. As explained in note 27, a 'punctuated equilibrium model' is also used in historical linguistics to describe the diachronic development of languages, but with a substantially different meaning.

The idea of natural selection is essentially the same anticipated in section 2.1. Superficially one may assume that this process acts on phenotypes, so that in a specific environment the individuals that have a more advantageous phenotype also have more chances to survive and to reproduce, i.e. they have an higher 'fitness'. Apart from features of the territory (e.g. climate), the environment includes also ecological relationships that link conspecifics and individuals that belong to different species. Thus natural selection is the process that begins with adaptation to a specific en-

vironment: If there is no evidence for adaptation, one cannot assume that natural selection had a role in the evolution of a certain lineage. Moreover, similar phenotypic traits are likely to be selected by similar environments, thus they can provide misleading evidence if they are compared in reconstructing genealogical patterns.

Migration is also important in population genetics, since it determines the transfer of genetic material between different populations. That is why it is referred to also as 'genetic flow': When individuals of population *A* migrate in the area occupied by population *B*, they introduce their own alleles in that area. Of course, this process acts only if the populations can interbreed, i.e. they belong to the same biological species. While mutations increase the difference between separated groups and can cause significant genotypic divergence over generations, migrations have the opposite effect, because they make different populations converge. Therefore mutation and migration are opposite factors in models aimed at studying the genetic similarity of populations as pertains to the geographic distance that separates them: The more two groups are distant, the more they are likely to diverge, while if they are closer, they can be more easily involved in migration processes and increase their genetic similarity. One of these models, conceived by Malécot (1959) and then developed by Kimura and Weiss (1964), is the 'stepping-stone-model': The name derives from the fact that human groups are represented as a series of steps that go across a pool. Incidentally, it is worth recalling that Cavalli-Sforza and Wang (1986) apply the same model to analyze the diffusion of linguistic traits across some linguistic communities living in a chain of Micronesian islands.

Finally, the genetic drift[5] (e.g. Maynard Smith, 1989: 24-27; Ridley, 1996: 126-127; Cavalli-Sforza, 2001: 74-78) is driven exclusively by chance, thus it does not favour genotypes with respect to qualitative criteria like, for instance, natural selection. Essentially it determines a non-predictable fluctuation of the genotype frequencies in the passage from one generation to the next and it acts faster in smaller populations, because in these cases genotype frequencies are more likely to deviate from theoretical expectations. Therefore, if no alternative genotype for a specific *locus* is favoured by natural selection and no genetic flow from external populations occurs, due to the genetic drift one genotype will arrive to prevail on the others in the course of

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[5] Notice the term 'drift' in population genetics has a different meaning respect to that used in linguistics by SAPIR (1921). See section 3.3 for further comments on this terminological overlap.

time. The final result of this process, if other factors do not intervene, is the convergence of the population to any genotype.

In higher plants and animals the inheritance of genetic material occurs from parents to offspring thanks to the mechanism presented in section 2.2. In epidemiological terms, this kind of transmission may be called 'vertical', and a path of vertical transmission corresponds to a proper genealogical path. In nature there are also cases of horizontal transmission, in which an organism receives genetic material from another one even in absence of a parent-offspring relationship. This kind of transmission is known as 'lateral gene transfer' and it has been studied only in the last decades (among others Syvanen, 1985; Syvanen, 1994; Howe *et al.*, 2001). It plays an interesting role in the evolution of unicellular organisms, but its relevance in the evolution of multicellular ones is debated and it may be considered rather marginal here. The terms 'vertical transmission' and 'horizontal transmission' are also adopted by Cavalli-Sforza and Feldman (1981) to indicate different types of transmission of cultural traits between individuals, as explained in section 5.1, and they are also used to describe two important types of evolutionary paths of language development, whose definition is taken into account in section 3.3. Nothing more needs to be said here for the moment, but it is useful to anticipate that using these terms with more than a simple descriptive value in linguistics may give rise to conceptual problems. Actually the same observation is valid for many other ideas that linguistics has borrowed from evolutionary biology, and the following discussion is exactly aimed to show the danger of strict parallels between biological evolution and language evolution.

3. *Evolutionary ideas in historical linguistics*

Many attempts have been made to apply evolutionary ideas to theories of language change so far. This section provides an overview of them with a twofold aim: It is intended on the one hand to anticipate some important points that are taken into account in section 5.3, on the other hand to show why close parallels between biological and linguistic evolution may pose serious difficulties. It is important to point out a fundamental premise before proceeding: The focus here is on the evolutionary approaches adopted to analyze the diachronic development of languages, not on the studies regarding

the evolution of the language faculty, which is a completely different topic. The need to distinguish these two issues should be clear, in that they entail the study of different processes, which involve different periods of time (centuries the former and probably geological ages the latter), different levels of analysis (cultural and natural) and different fields of study[6].

Croft (2000: 10-13) effectively points out that current evolutionary approaches to the study of language change may be divided into three categories: Literal, 'generalizing' and analogical approaches. According to Croft's definition, the premise of literal views is that «language is a genetic capacity, and hence obeys certain principles of biology», thus «[a] literal approach to language diversity would amount to claiming that the differences among languages reflect genetic differences among their speakers», which is «patently false» (Croft, 2000: 10). The last claim is indisputably supported by well-known empirical evidence and there can be no doubt that language change is culturally and not biologically driven, therefore literal approaches (if there are any nowadays) do not require more attention here. However the author misleadingly claims that the literal approach «is associated with Chomskian linguistics, because Chomsky argues for the biological basis of quite specific linguistic properties (e.g. certain syntactic structures and constraints)» (Croft, 2000: 10). Actually there is nothing in the biolinguistic program that is even remotely intended to support a genetically-based interpretation of language change and development: The core idea of the Chomskian framework is rather that there is a set of biologically-determined grammatical features that are shared by all members of our species and that are consequently universal (i.e. the innate language faculty, or Universal Grammar, whose origin can then be studied from a biological-evolutionary perspective as that of any other organ, see section 4.1), while language change has to be analyzed as a cultural and historical process.

The supporters of the 'generalizing' approaches, instead, claim that there is a general theory of evolutionary processes, «which applies to the evolution of species and their traits in biology, to language change in linguistics, and to other domains as well» (Croft, 2000: 11). Croft's (1996; 2000) theory is probably the most complete and extensive example of this category. Finally, analogical approaches are those for which «there are analogies between cer-

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[6] Notice that the same distinction is underlined by Longobardi (2003a: 2-4), when he outlines the extension of Chomsky's (1964) original levels of adequacy adding the level of actual historical adequacy and that of evolutionary adequacy.

tain biological processes as described by evolutionary theory and certain processes of language change that call for description» (Croft, 2000: 11). The following discussion starts from a brief outline of the role that evolutionary concepts have played in the history of comparative linguistics and then it focuses on some of the most recent and significant proposals, i.e. precisely Croft's 'generalizing' view and some important analogical perspectives.

3.1. *Historical overview*

McMahon (1994: 314-340) provides an accurate overview of the application of evolutionary ideas in the history of linguistics. The scholar points out that a creationist view also existed for languages, as it did for species (McMahon, 1994: 316). The idea that languages, like species in the biblical perspective, were created by God and are consequently fixed is suggested by the myth of the Tower of Babel described in the Book of Genesis. Nonetheless, McMahon points out that while the suppression of creationist positions represented a great challenge for evolutionary theories in biology, the idea that languages are subject to transformations was easily accepted. The main reason for this is that language change acts much faster than population diversification and speciation, so that sometimes its effects can be observed even by uneducated speakers in the course of their lifetime, while the same evidence can be less effortlessly provided in support of biological evolution. From this point of view linguistics had an advantage over evolutionary biology in the beginning: A transformational approach was already implicitly assumed by Sir William Jones (1799) arguing in favour of the hypothesis of a common ancestry of languages spoken from India to Europe, and only after two decades Lamarck published his theory of transmutation of species.

Thus the idea of language change was common since the origin of comparative linguistics and one could claim that it has always represented its core premise. Nevertheless the process of change described by nineteenth-century linguists was substantially different from the Darwinian one and more similar to the 'evolutionary process' hypothesized by early embryologists and naturalists. Indeed it was usually assumed that languages are subject either to advances or to decay, depending on each scholar's perspective, i.e. that the evolution of languages always entails some kind of improvement or decline: In particular, the approaches supporting the idea that languages undergo advancement in the course of time can be said to be in line with the 'Growth Principle' using Harris and Campbell's (1995: 17) terminol-

ogy. Such a perspective was common since Friedrich Schlegel's thought, and it was shared, among others, by August Wilhelm Schlegel, Wilhelm von Humboldt and August Friedrich Pott, remaining popular until the beginning of the XX century, when Otto Jespersen was still convinced that the progress of languages is directed from complex to simple, i.e. from synthetic to analytic forms, which are more efficient (Jespersen, 1922: 324).

The same idea of evolution was rooted also in August Schleicher's *Stammbaumtheorie* (Schleicher, 1853), even if the scholar is often mentioned as the first linguist most directly influenced by Darwin's theory. He also adopted the idea that languages are subject to change and he widely used biological terms in his works, so that he explicitly equated «language families with genera, languages with species, dialects with races, and idiolects with individual organisms» (McMahon, 1994: 319), but his first classification attempts were neither formalized as genealogical trees, they were rather taxonomic tables of Linnaeus's kind. Furthermore, in typological terms, according to Schleicher's hierarchy synthetic languages represent an improvement respect to analytic languages. This view encountered the opposition of the Neogrammarians: In particular, Osthoff and Brugmann (1878) were convinced that «the same types of language change apply to all phases of linguistic history» (Harris and Campbell, 1995: 18) and laid the foundations of the current principle of 'uniformitarism', so that it is well known that, agreeing with the Neogrammarian hypothesis, nowadays historical linguists do not interpret language development as a processes entailing advancement or decay, but just 'transformation'.

McMahon (1994: 334-341) observes that the first significant attempts of parallelism between evolutionary ideas and historical linguistics in modern theories go back to the '50s and the '60s. Some biological metaphors begun appearing in creole studies also in the '70s, but, according to Briscoe (2002: 2), only from the '80s interest in the study of languages as evolving systems increased, in his instance taking advantage of the progresses both of the 'modern synthesis' and of the quantitative algorithmic studies of dynamical systems (e.g. Lindblom, 1986; Hurford, 1987; Keller, 1994). However, the most important insights have been provided in the last decade, «perhaps partly because work has only recently begun to address questions seen as central to (generative) linguistic theory» (Briscoe, 2002: 2).

In the next sections some of these recent proposals are taken into account, starting from Croft's 'generalizing' approach and then taking into consideration some of the most interesting analogical views. Again, the fol-

lowing review is intended to show that, while some ideas developed within the biological theory of evolution can be usefully adopted to highlight some important features of language change, the differences between biological and language evolution do not allow going much beyond analogical borrowings of terms between the two disciplines.

3.2. *A 'generalizing' approach*

Croft's (1996; 2000) Theory of Utterance Selection probably represents the most broad-based 'generalizing' approach aimed at explaining language change. The scholar's starting point is Hull's (1988) 'generalized theory of selection', which deals with a fundamental question of evolutionary biology: Which are the 'units of selection'?

Maynard Smith (1987) observes that the only units that can benefit from adaptation, and therefore may be considered direct units of selection, are those that show inheritability. Anyway, not only inheritability is relevant: In order the effect of adaptation to be measurable, a unit of selection should also be permanent enough, so that its frequency can be effectively altered and measured in the course of time. Williams (1966) and Dawkins (1976) argue that only genes are both able to replicate themselves and are designed so that each replication is likely to generate an identical copy of the same unit. On this basis Dawkins (1976) claims that genes may be referred as 'replicators', while their phenotypic projections, i.e. organisms, should be regarded as 'vehicles', whose adaptation to the environment determines either their survival or their disappearance. An extensive account of the question may be found among others in Ridley (1993: 303-322). What is relevant here is that on this basis Hull (1988) develops his generalized theory of selection, in which the following components play a role:

1. Replicator – an entity that passes its structure largely intact in successive replications
2. Interactor – an entity that interacts as a cohesive whole with its environment in such a way that this interaction causes replication to be differential (Dawkin's 'vehicle', editor's note)
3. Selection – a process in which the differential extinction and proliferation of interactors causes the differential perpetuation of the relevant replicators
4. Lineage – an entity that persists indefinitely through time either in the same or an altered state as a result of replication (Hull, 1988: 408-409; quoted in Croft, 2000: 22)

Hull (1988) claims that this model of evolution is general, i.e. it can be recalled in any case in which one needs to describe the evolution of a system, and Croft (2000) applies it precisely to the description of the mechanisms of language change, framing it within a 'usage-based theory of language' and designing his Theory of Utterance Selection, referring with 'utterance' to any kind of humanly possible linguistic expression[7]. In the scholar's opinion, only utterances can be considered 'basic tokens', i.e. specific and concrete entities, whose historical development can be traced (in this sense, a language, say English, would not be a token[8], because it is an abstract entity removed from a specific historical context), and while a language should be intended as «the population of utterances in a speech community», a grammar could be defined as «the cognitive structure in a speaker's mind that contains her knowledge about her language, and is the structure that is used in producing and comprehending utterances» (Croft, 2000: 26). Moreover, the particular 'linguistic structure' embodied in an utterance (e.g. a phoneme, a morpheme or a 'syntactic construction') is called 'lingueme' by Croft[9].

On the basis of these definitions, Croft assigns to each component of Hull's model a linguistic counterpart. According to the Theory of Utterance Selection, while a gene is the paradigm instantiation of the replicator in biological evolution, the same role is played by a lingueme in language evolution. Thus linguemes are assumed to be structured into utterances as genes are organized in the DNA. Normal replication would then correspond to regular utterance production and altered replication to innovative utterance production, which are respectively paralleled to normal reproduction and mutation of the biological model. Croft assigns the role of interactor to the speaker, who notably includes the grammar. Moreover, in the scholar's view the selection process is driven by convention, i.e. the set of the arbitrary (non-functionally and non-biologically determined) grammatical rules shared by a speech community, in any social-communicative context. Finally, for Croft differential replication corresponds to propagation of linguistic change: In

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[7] According to the scholar's specific definition, «[a]n utterance is a particular, actual occurrence of the product of human behavior in communicative interaction (i.e. a string of sounds), as it is pronounced, grammatically structured, and semantically and pragmatically interpreted in its context» (CROFT, 2000: 26).

[8] This point of the model becomes less clear when Croft claims that «[f]rom these basic tokens (i.e. utterances, editor's note), we can describe more complex tokens, such as a specific language or a speech community» (CROFT, 2000: 2).

[9] This term is intended to parallel Dawkins' 'meme', which is 'a unit of cultural inheritance' (CROFT, 2000: 239).

his opinion, while the mechanisms that determine the innovation (the altered replication) is functionally based, i.e. it «involves the form-function mapping», the propagation «is a selection mechanism, in the evolutionary sense, and it is social» (Croft, 2000: 8).

The Theory of Utterance selection does not need to be covered in greater detail here. What is important to highlight is that Croft (2000) makes use of at least two useful and important distinctions. The first one is that between inherent change, a process of change that acts on a single object that changes over time, and replication, which entails the creation of new entities. In particular, notice that in the scholar's view only replications are relevant in language evolution, because what actually evolves for him are utterances: If languages were assumed to develop as 'organisms', as in some nineteenth century views, their diachronic transformation should be more properly called 'inherent change' instead, because only this characterization of the process could account for the continuum of states observed in the genealogical development of specific languages. The second distinction separates altered and differential replication. As for the latter, Croft provides a useful observation saying that altered replication is functionally (but maybe one could more generally say 'internally') driven while differential replication depends on social selection. The fact that the propagation of an innovation has to be studied from the sociolinguistic point of view is undoubted, as the importance of studying the innovation as an internal linguistic process. Finally, one may also agree with Croft's idea that altered and differential replications are respectively synchronic and diachronic phenomena, because the former occurs «in a speaker action in a given point in time» and the latter «over a very long period of time, even centuries» (Croft, 2000: 5). However, the need to distinguish between synchronic innovation and diachronic diffusion is well-known in sociolinguistic studies at least since Labov (1966) and Weinreich *et al.* (1968).

Croft's view is debatable in other respects. His usage-based theory of language, which assigns a central role to utterances, is completely incompatible with the theoretical framework adopted here, i.e. the biolinguistic framework developed since Chomsky (1965), and one could object that it leads to bizarre conclusions. A first observation regards the fact that, according to Croft's line of reasoning, since linguemes should be replicators and speakers, together with their grammar, interactors, utterances result to be associated with genetic material and grammar with phenotypic appearance.

This parallelism appears to be misleading: It does not take into account the fact that there is also a causal relation between the genotype and the phenotype in biology, according to which the phenotype is (partially) determined by the genotype, while the common belief in the biolinguistic paradigm is that grammar generates utterances (or better, sentences), not the other way around. In other words, looking at the instantiation of the evolutionary process in biology, one should expect not only that the replicator replicates itself and the interactor interacts with the environment, but also that the replicator projects itself onto the interactor: If one assumed that the interactor is the grammar and the replicators are the linguemes, the grammar would be a result of a projection of the linguistic usage. Croft is aware of this objection and claims that it is not an issue, because «the generalized theory of selection does not apply only to the levels of the gene and the organism in biology» and «[i]t is independent of the levels of organization of biological entities» (Croft, 2000: 40). In other words, the replicator and the interactor are assumed to be very specialized roles, which abstract away from the concrete relationship that exists between their instantiations. But then to what extent could one benefit of a model of language evolution, in which the application of the categories of replicator and interactor is so abstract?

Another possible objection to the Theory of Utterance selection regards the exact generalization of the process of selection, which is claimed to be the same process instantiated in different ways in biological evolution and language evolution. Actually natural selection and social selection are substantially different processes: Putting it in Croft's terms, while the former is driven by the environment and the interactors have a passive role, the latter is actively (and often consciously) determined by the interactors. Again, convention (which notably the scholar considers to play a more decisive role in language change than functional and formal features of language) as a mechanism of selection may probably be claimed to be too abstract to account for the actual social process of propagation, unless one considers 'convention' as a transcendent internal force of the speech community. Thus one might wonder whether Croft's need to insert an extensive mapping between biological evolution and language evolution leads him to neglect some fundamental aspects of language change, in favour of debatable conceptual generalizations.

3.3. *Analogical approaches*

Analogical approaches are those, in which linguists make subsidiary use of biological terms and concepts to describe or to shed light on specific facts regarding the process of language change. The use of biological metaphors in linguistics has led to controversial conclusions in the last two centuries, because this practice has often entailed an «overenthusiastic appropriation (of biological concepts, editor's note) with insufficient sense of subtlety or precise applicability of the originals» (Lass, 1990: 79; quoted in McMahon, 1994: 314). Nonetheless, many scholars have adopted cautious analogical approaches in recent times, being aware that such attempts require a careful reflection on the consequences of their comparison: Due to this prudence, in some cases the analogies do not go much beyond the terminological borrowing.

Before going through some relevant cases of analogy, consider that the occurrence of overlaps between terms used in biology and in linguistics is not necessarily due to intentional borrowing. Take for instance the use of the term 'drift', mentioned in section 2.3. The first systematic introduction of the concept of 'drift of a language' can be found in Sapir (1921), who defines it as «constituted by the unconscious selection on the part of its speakers of those individual variations that are cumulative in some special direction» (Sapir, 1921: 166). In essence Sapir's idea of drift is deeply bound with the role that the individual psychology plays in determining the general direction of language change. The relevance of this historical concept is investigated into deeper detail for instance in Marotta (1986). What is relevant here is that the scholar distinguishes between short-term and long-term drift: Both these processes are intended by the scholar as differentiating processes, i.e. processes of change that determine language divergence. Conversely, as explained in section 2.3, in population genetics the genetic drift has a homogenizing effect on a population, which entails an entirely different perspective on the process.

As for proper terminological borrowing, Croft (2000: 11) asserts that some recent perspectives in creole studies may be considered analogical. In particular, one may think about Whinnom (1971), who attempts to make use of the biological concept of hybridization to explain some dynamics of language contact, and Mufwene (2000), who declares that there are some informative similarities between the concepts of language and species. Actually, the scholar's perspective has become more 'generalizing' in later works

(e.g. Mufwene, 2002; 2008), whose review is not covered here. A recent analogical proposal made in historical linguistics is for instance Lass' (1990; 1997) adoption of the biological concept of exaptation (see section 4.2) to refer to a diachronic process of reanalysis alternative to grammaticalization. However, the scholar points out that «while claiming that the notion of exaptation seems useful in establishing a name and a descriptive framework for a class of historical events», he remains «fully aware (even insistent) that languages are not biological systems in any deep sense» (Lass, 1990: 96). As anticipated, even the term 'transmission', which is borrowed from epidemiological studies, has been used with a peculiar meaning in recent literature. For instance, Wang and Minett's (2005) work is dedicated to the quantitative analysis of the role of vertical and horizontal transmission in language evolution: Nevertheless with 'vertical transmission' the scholars refer to the kind of language evolution that is due exclusively to the accumulation of innovations independently arisen in the history of a language, i.e. independently of contact situations, while with 'horizontal transmission' they mean the evolutionary paths in which contact-induced changes occurred. In other words, Wang and Minett's intention is to distinguish between pure genealogical evolution and evolution due to areal convergence. This use of 'transmission' is equivalent neither to that made in evolutionary biology nor to Cavalli-Sforza and Feldman's (1981) one, which is covered in section 5.1: If it were, it would entail Wang and Minett's analysis to concern how individual transmission occurs in languages assuming that languages are like organisms, which undergo inherent change and processes somehow similar to biological lateral gene transfer. Actually this is not the case and Wang and Minett (2005) do not even mention such problematic aspect of their terminological choice. Rather, the purely descriptive use of terms like 'vertical transmission' and 'horizontal transmission' appears to be particularly useful to classify two important types of evolutionary paths of language evolution. For the aims of the present work, provided that 'vertical transmission' and 'horizontal transmission' do not entail any conceptual parallelism between languages and organisms and that they have a high descriptive value, from now on these terms are used to indicate respectively pure genealogical evolution and areal convergence, while the passage of traits (being them genetic, cultural or linguistic) between individuals is referred to with 'individual transmission' or, alternatively, with 'transmission' alone.

Another group of analogical approaches includes all evolutionary-oriented works grounded on computational simulation of formal models of

language evolution. A collection of representative papers based on this kind of perspective is that introduced by Briscoe (2002). Among them, the most interesting from the point of view of this paper are those dedicated to the simulation of the evolution of parametric systems, i.e. Niyogi (2002) and Turkel (2002). These models and in particular the development of Niyogi's framework are not introduced in this section, but what is relevant here is just to incidentally mention that Niyogi's (2002) starting point is Cavalli-Sforza and Feldman's (1981) model of cultural change (see section 5.1).

Analogical approaches are also more or less implicitly adopted in quantitative studies of language evolution, which may be referred to as 'linguistic studies in quantitative phylogenetics'. The term 'quantitative phylogenetics' refers to the research field, whose aim is to automatically infer genealogical (or, more generally, historical) relations between sets of *taxa* by means of algorithmic procedures applied to comparative datasets. The adjective 'quantitative' refers to a basic property of the techniques used in this field, i.e. the fact that the reconstruction process is (almost) completely independent of the nature of the analyzed data and relies only (or mostly) on the numerical aspects of the comparison. Thus the same procedures can be (cautiously) exported through disparate disciplines, even if the basic concepts of the current quantitative phylogenetic paradigm were originally conceived in molecular biology in the '50s. The implicit analogy adopted by the quantitative studies in linguistics regards the comparative data, which actually varies a lot depending on each scholar's view. As illustrated in Rigon (2009: 122-128), many experiments are exclusively conducted on lexical and morpho-phonological datasets (e.g. Cavalli-Sforza and Wang, 1986; McMahon and McMahon, 2003; Nakhleh *et al.*, 2005; Gray *et al.*, 2009), while only a minority of them are focused on syntactic comparison (e.g. Dunn *et al.*, 2005; Gray, 2005; Spruit, 2005; 2008). However, all of these works assume that the quantitative analysis of linguistic characters can be equated to that of genetic characters: In other words, linguistic traits, for example lexical encodings of meanings or syntactic features, are considered comparatively equivalent to genetic traits, i.e. genes, for the aims of the quantitative reconstruction. Of course this correspondence is not straightforward and depends on the peculiarities of the evolutionary process undergone by the specific linguistic traits that one is considering. In section 5.2 something more is said about the equivalence between genetic markers and the specific grammatical traits that represent the focus of the present investigation. Before then, these traits have to be introduced within the general framework of diachronic syntax.

4. *Syntactic evolution*

This part of the work is intended to cover the extension of the biolinguistic perspective developed within generative grammar to the study of diachronic syntax, with the goal of grounding the analogical parallel provided in section 5 and of showing how syntactic evolution may be effectively interpreted within a 'parameter-based' model of grammatical variation. To this end the following discussion is firstly concerned with the illustration of the fundamental points of the 'Principles and Parameters' approach, with particular reference to parameter forms and interaction. The focus is then shifted to syntactic variation, thus an overview of the issues related to the description and the explanation of grammatical change and 'borrowing'[10] are taken into account. Finally, both these types of variation are reconsidered within the parametric explanatory account in section 4.3.

4.1. *The parametric framework*

In the biolinguistic program developed at least since Chomsky (1965) it is recognized that there must be a system responsible for language acquisition, which guides the process providing a specific set of constraints that «have historically been termed 'innate disposition', with those underlying language referred to as 'universal grammar'» (Hauser *et al.*, 2002: 1577)[11]. Universal Grammar has to be interpreted as an actual cognitive object, that is present in the speakers' mind since they are born as 'language faculty' and that consists of a set of formal linguistic universals[12]. Typological investigations such as those already suggested in Chomsky (1965) have revealed that some syntactic traits, called 'principles of the Universal Grammar', seem to be invariant across languages and to «constraint the application of every grammatical operation in every language» (Radford, 2002: 11). Then associated with principles «there may be certain limited options which remain

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[10] Here the terms 'borrowing' is used referring to any kind of possible non-genealogical influence between languages. See the definition provided in section 4.2.

[11] Intending the language faculty in the narrow sense as «the abstract computational system alone, independent of other systems with which it interacts and interfaces» (Hauser *et al.*, 2002: 1571), i.e. as the 'narrow syntax', recent research suggests that this faculty is not only innate and common to all humans, but also species-specific (Hauser *et al.*, 2002).

[12] Even if the present discussion is exclusively focussed on syntax, in principle Universal Grammar is also supposed to include relevant rules regarding phonology, morphology and semantics (e.g. Roberts, 2007: 12).

open, to be 'filled in', as it were, by experience» (Roberts, 2007: 21): These options, that are usually thought to entail a choice between two distinct opposite values, are referred to as 'parameters' and may be intended to represent proper *loci* of linguistic variation (as genes are *loci* of genetic variation), since ideally they are expected to define the exact dimensions of syntactic variation across languages (Baker, 2008: 352). In the first place the Principles and Parameters Theory (Chomsky, 1981) permits clearly characterizing the process of language acquisition as a procedure in which the values of parameters are set one after the other (Chomsky, 1986: 25). The parametric approach also represents a starting point for the explanation of non-random variation of syntax, i.e. of the patterns of variation as those described for instance since by Greenberg (1963), because parameters are thought to represent deep generalizations regarding syntactic properties of languages. Finally, «parameters can tell us which aspects of syntax are subject to change in the diachronic dimension» (Roberts, 2007: 24). The application of the parametric perspective to the explanation of diachronic syntactic variation is the point of section 4.3 but, in order to appreciate it, it is necessary to go through the illustration of parameter forms.

The general format for describing parameters proposed by Roberts and Roussou (2003) and Roberts (2007) follows from specific hypotheses regarding the interpretation of functional categories[13], i.e. words that have no descriptive content, but just serve a grammatical function, and from the notion of 'markedness'. Roberts and Roussou (2003) assume that the same set of functional features (intended as features that mark grammatical properties like person, number, tense and so on) is present in all languages, thus it is universally mapped onto the Logical Form (LF)[14], but each language may or may not provide specific functional features with a phonetic representation. Furthermore, according to the scholars there are two operations by means of which functional features may be mapped onto the Phonetic Form (PF) and become phonetically interpretable (*F), either Merge or Move, which are the basic operations of grammatical composition assumed within the Minimal-

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[13]   Assuming that the lexical items that are subject to parameterization are those belonging to functional categories, see for instance CHOMSKY (1995: 6, 55).

[14]   «There is, however, another possible alternative that the authors do not discuss: it is conceivable that some interpretable features may be lacking completely from LF in (certain constructions of) certain languages (e.g. definiteness in Latin and perhaps Russian DPs), not just from PF» (LONGOBARDI and RIGON, 2008: 429).

ist Program (Chomsky, 1995)[15]. In Roberts and Roussou's (2003) perspective a minimal system of parametric variation should be formulated in terms of two binary choices then:

a. F*? Yes/No
b. if F*, is it satisfied by Move or Merge? (Roberts and Roussou, 2003: 30)

From this line of reasoning the authors determine a markedness hierarchy, whose simplified formulation is the following ('>' means 'is more marked than'):

$F^*_{Move} > F^*_{Merge} > F$ (adapted from Roberts and Roussou, 2003: 210)

A closely similar set of abstract formats for parameters is proposed by Longobardi (2005): The scholar calls them 'parameter schemata'. These formats derive from the cross-linguistic empirical study of the DP-internal structure that allowed the collection of the parametric data used in a series of quantitative investigations of language taxonomies (among others Longobardi, 2003a; Guardiano and Longobardi, 2005; Gianollo *et al*., 2008; Longobardi and Guardiano, 2009; Rigon, 2009). In particular, Longobardi (2005) claims that the vast majority of the parameters included in this dataset falls into one of the following four schemata:

a. Is F, a functional feature, grammaticalized?
b. Is F, F a grammaticalized feature, checked by X, X a lexical category?
c. Is F, F a grammaticalized feature, spread on Y, Y a lexical category?
d. Is F, F a grammaticalized feature checked by X, strong (i.e. overtly attracts X)?
   (Longobardi, 2005: 410)

Roberts and Roussou's (2003) and Longobardi's (2005) model appear to be very close. Essentially a grammaticalized feature in Longobardi (2005) corresponds to a feature that has a phonological representation in Roberts and Roussou's (2003) basic formalism, even if while in Roberts and Rous-

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[15]   The operation Merge «takes a pair of given syntactic objects (S_i, S_j) and creates a single syntactic object out of them, namely a labeled set $(S (S_i, S_j))$, where the label S is either S_i or S_j. The operation Move in effect is Merge of A and K, where A and K are (contained in) a syntactic object already formed, and A raises to target K. The operation Move then creates two copies of the same element, A. A chain is the ordered pair consisting of A in derived position, and of its copy, technically its trace t_A, in the original position» (MANZINI, 1995: 324).

sou's (2003) model the actual realization of a feature may occur by means of Merge or Move, Longobardi (2005) distinguishes between the three possibilities (*b-d*). In both models then the actual parameters derivable from the abstract formats are related one to the other and, more specifically, hierarchically ordered. This structural characterization of the parametric space is immediately understandable if one considers that in Roberts and Roussou (2003) parameters governing the phonological realization of features condition the application of parameters that determine their instantiation, while in Longobardi's (2005) approach the setting of an *a*-schema parameter allows or forbids *b*- and *d*-schema parameters to be relevant in a language, and parameters of type *d* are assumed to depend on *b*-schema ones. Among others, Baker (2001) argues in favour of this point when he introduces the concept of 'ranking' (Baker, 2001: 163). The scholar develops his approach providing a concrete example of ordered parameters, a real 'Parameter Hierarchy', i.e. PH (Baker, 2001: 183; Baker, 2003: 352; see for instance the reviews provided in Newmeyer, 2005: 85-87; Roberts and Holmberg, 2005; Boeckx, 2008: 4).

A further development of this line of inquiry is related to the distinction between micro and macro-parameters, which may be brought back to the distinction between micro and macrocomparison in historical linguistics. It is problematical to give a formal account for these notions, but in general «microcomparative syntax can be thought of as comparative syntax work done on a set of very closely related languages or dialects» (Kayne, 2005: 6), which thus largely shows identical syntactic patterns and just small points of variation, while conversely macrocomparison should be aimed at identifying large-scale clusters of divergent properties between languages that belong to different groups or families. The separation of these two domains of study is ultimately challenging as that between language and dialect, but it can be of some use when, as a first approximation, it is projected onto the parametric framework. In particular, Kayne (2005: 8) claims that «apparently microparametric differences might all turn out to dissolve into arrays of microparametric ones (i.e. into differences produced by the additive effects of some number of microparameters)». Following this view, Baker (2008: 354-355) sketches a parallel with biological evolution, claiming that the accumulation of microparametric differences between closely related languages resembles the process of gradual divergence between populations assumed in the standard paradigm of the modern synthesis, while abrupt events of macroparametric deviation may be regarded as analogous to the

process described by Eldredge and Gould's (1972; 1988) punctuated equilibrium model. It should be clear that such analogy can only be considered useful on a purely descriptive level of analysis, lacking any deep explanatory pretension with respect to the actual dynamics of syntactic evolution. Also Roberts (2008) adopts the micro/macroparametric distinction in relation to the implicational ordering of parameters and he shows that the more parameters rank higher in parameters networks[16], the more they should be considered 'macro'.

Having outlined some of the main current hypotheses regarding both the format and the interaction between parameters, from the next section on it is possible to show how the synchronically-based parametric perspective may be applied to highlight the dynamics of diachronic variation. This is done starting from the overview of syntactic change and variation.

4.2. *Syntactic variation*

On first approximation, the term 'syntactic change' may be intended to indicate any event of diachronic variation occurring in the history of a language and an early fundamental criterion to classify the possible types of change can be separating those derived from contact phenomena from those occurred independently of areal convergence, e.g. purely genealogically. This distinction fits together with that between horizontal and vertical transmission outlined by Wang and Minett (2005). However, such a binary classification is designed with exclusive reference to a specific characterization of the causes of changes, i.e. asking whether these are to be regarded as lineage-internal or external. To understand the actual dynamics of diachronic syntax would necessitate providing a finer account for the different processes that may intervene. But is it possible to design a typology of syntactic variation in light of the description of a limited set of fundamental mechanisms? This is an open question: Currently there is no agreement and just little explicit debate about the typology of syntactic change, while even the possibility that some kind of areal transmission of traits may occur is under discussion. Indeed in the tradition of study of historical syntax the debate concerning syntactic change has been mainly focused on the nature of single diachronic processes and on hypothesises related to their nature and theoretical status,

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[16] Actually the structures ROBERTS (2007: 277-282; 2008) refers to as 'networks', e.g. BAKER's (2001) PH, are tree-graphs.

while «there are few cases in which historical-comparative generalizations have risen in syntax [...]» (Longobardi, 2003b: 165, translation by GR).

Among the recent synthesis on diachronic phenomena concerning grammar, the descriptive typology of syntactic change adopted by Roberts (2007: 121-205) provides a particularly useful account for the issue. The author outlines his classification, which includes processes of grammaticalization, word-order change, argument-structure change and complementation change, with no explicit claim of being descriptively exhaustive, but just to show how apparently different cases of diachronic variation involve reanalysis, the process «which changes the underlying structure of a syntactic pattern and which does not involve any modification of its surface manifestation» (Harris and Campbell, 1995: 50).

Take for instance grammaticalization. In the last decades the idea that it should be regarded as a sub-type of change with respect to reanalysis is shared by diverse scholars. For instance, Hopper and Traugott (1993) are convinced that «reanalysis and analogy are the major mechanisms in language change» and «[t]hey do not define grammaticalization, nor are they coextensive with it, but grammaticalization does not occur without them» (Hopper and Traugott, 1993: 61). This assumption is in line with Campbell's (2001) view, according to which grammaticalization theory has no explanatory value in itself, essentially because it cannot provide explanations without referring back to other types of change (Campbell, 2001: 151). Therefore, grammaticalization may be regarded as a useful term, as it describes a specific instantiation of other basic mechanisms, but only once it has been established that it has no independent status with respect to them (Newmeyer, 2001: 202-203). Some of the most important problems in the generalization of grammaticalization processes concern the empirical support to their directionality. On the one hand, it seems like it is not true that the same lexical categories create the same grammatical elements in all languages, so that «[...] grammaticalization fails to evince the most important distinguishing feature of a distinct process – the unfolding of its component parts in a determinate sequence in which one step of the sequence inevitably engenders the following one» (Newmeyer, 2001: 195). On the other hand, the validity of the unidirectional characterization of grammaticalization is questioned: If, for instance, Haspelmath (2004: 21-23) regards counter-examples as misleading, as recalled by Narrog (2007: 2) in the last years 'degrammaticalization' has become the topic of many investigations (e.g.

Giacalone Ramat, 1998; van der Auwera, 2002; Norde, 2002). Incidentally, at this point it is worth recalling that exaptation, as defined by Lass (1990; 1997), is another descriptive type of syntactic change closely associated with grammaticalization. The term 'exaptation' has already been mentioned in section 2.1 in connection with the use that this term has in evolutionary biology, where it was originally conceived (Gould and Vrba, 1982). Lass (1990; 1997) intends it as a process that has the same goals of grammaticalization, i.e. the formation of new grammatical material, but while the latter performs it starting from lexical elements, exaptation is assumed to recycle former grammatical elements that have become functionally unclear and to give them a new role. In general exaptation appears to be rare and specific, i.e. not to be cross-linguistically replicated (however see the attempt to find a cross-linguistic account for grammaticalization in Narrog, 2007), but due to its characterization this process requires to be descriptively distinguished from grammaticalization (see the general review provided by Traugott, 2005).

An example of how in Roberts and Roussou's (2003) paradigm a case of grammaticalization may be reduced to reanalysis and parameter resetting is illustrated in the following section. For the moment consider that currently it is broadly accepted that reanalysis plays a central role in the understanding of syntactic evolution dynamics (Langacker, 1977: 57). What is important to underline here is that the reduction of many sub-types of syntactic change (i.e. types defined on more descriptive grounds) to reanalysis appears to represent an important generalization on the way to find the extensive explanatory account provided within the parametric framework.

What about change derived from contact between different grammars? First of all, consider that there is no agreement on the typology of contact situations, which appear to be potentially very complex (e.g. Thomason and Kaufmann, 1988; Ross, 1999; 2001; Kroch, 2000: 176; Roberts, 2007: 391), and its exhaustive discussion is not relevant here. Therefore, taking inspiration from Thomason's (2001: 3) notion of general contact-induced change, borrowing is intended here as any kind of linguistic change that is less likely to have occurred outside a specific contact situation. This designation is broad enough to include any kind of at least suspected non-genealogical events of contact-induced change, regardless of the specific socio-linguistic processes that they entail. For what concerns contacts that may affect grammatical systems in particular, it has already been pointed out that the very

possibility and the degree of syntactic borrowing is questioned, thus the main aim of the following discussion is to offer evidence in favour of the possibility of this phenomenon.

The debate regarding the possibility of grammatical interference leads back to the first decades of the twentieth century, when contradictory views started appearing in the literature (e.g. Meillet, 1921: 82; Sapir, 1921: 217; Schuchardt, 1928: 125). Weinreich (1979) observes that those clashing perspectives could essentially be brought back to «the lack of agreement between them on fundamental terms and concepts» (Weinreich, 1979: 29), and he supports the idea that «morphemes and grammatical relations belonging to one language can occur in the speech of another language as 'borrowings'» (Weinreich, 1979: 30). More recently the same opposite views regarding syntactic borrowing have been discussed in the literature about language contact (Sankoff, 2001: 13): Some scholars hypothesise that morphosyntactic elements and rules can be subject to genuine and direct borrowing as any other linguistic element (e.g. Thomason and Kaufmann, 1988; Campbell, 1993; Thomason, 2001), others believe that this kind of transfer is almost impossible, and they account for internal syntactic change only as a consequence of lexical or pragmatic inter-influence (e.g. Lefebvre, 1985; Prince, 1988; King, 2000; Nakhleh *et al.*, 2005). In particular, according to Thomason (2001) «[...] no absolute constraint against direct rule[17] transfer can be maintained» and «[...] the continuing popularity of the no-rule-borrowing position results in part from a pervasive tendency to underestimate speakers' ability to manipulate their languages' structures deliberately» (Thomason, 2001: 2). Nakhleh *et al.*'s (2005) position instead is in line with the most restrictive model and relies on the evidence provided by recent research on language contact, in which it is demonstrated that the inter-linguistic transfer of 'closed-class' items occurs via processes different from those of typical lexical borrowing (e.g. Rayfield, 1970: 103-107; Prince and Pintzuk, 2000). Within historical syntax «for a long time syntactic interference was considered either impossible or marginal» (Bowern, 2008: 199), even if in some lines of research it has been believed that any kind of change is a type or a result of language contact (e.g. Poussa, 1982; Mufwene, 2001). Harris and Campbell (1995) include borrowing among the basic mechanisms that would allow to explain syntactic change and they define

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[17] 'Rule' is intended as any kind of grammatical generalization, including morphosyntactic and word-order patterns.

it as «a change in which a foreign syntactic pattern [...] is incorporated into the borrowing language through the influence of a donor pattern found in a contact language» (Harris and Campbell, 1995: 122).

Evidence in favour of the possibility of grammatical contact-induced change may be found for example in Thomason (2001), where the scholar reports many cases of hypothesized rule borrowing, mainly regarding morphological patterns, but including also examples of syntactic-features transfer. Among the best documented ones she considers, there is the situation of Kupwar (systematically studied by Gumperz and Wilson, 1971), an Indian village that lies on the border between the Indic and the Dravidian speaking areas: Four linguistic communities are settled there, two of them are Indic and two Dravidian. A massive syntactic borrowing has occurred among these varieties without any mediation of lexical transfer, since no shared morphemes are concerned in the relevant constructions. The data provided by Gumperz and Wilson (1971) seems to support Ross' (1999; 2001) idea of metatypy too. Perhaps Ross' most famous account for this process is based on the study of the adoption of semantic-syntactic patterns from the Papuan language Waskia into the Oceanic language Takia, which appears to have occurred without any lexical or phonological diffusion of any kind: In the scenario drawn by the scholar, the semantic shift and the syntactic restructuring are part of the same underlying process. Other attested cases of significant syntactic borrowing regard, for instance, inter-influence among the Tamangic languages (Noonan, 2008), that regarding the Indian (Emeneau, 1964) and the Balkan *Sprachbund* (Joseph, 1983), as well as the transfers described from Finnish into Russian (Thomason and Kaufman, 1988), from north-western Afro-asiatic into Insular Celtic (Gensler, 1993) and from Cushitic into Ethiopian Semitic (Weninger, 2001). Moreover, a particularly appealing hypothesis is that regarding the supposed contact-induced diffusion of definite articles throughout the European area (Heine and Kuteva, 2006: 97-139), while another relevant case mentioned by Roberts (2007) concerns the borrowing of Preposition Stranding from English to Prince Edward Island French. The latter case is reconsidered more in detail in the next section, where some ideas regarding the possible interpretation of syntactic borrowing within the parametric perspective are presented.

4.3. *The parametric explanation*

The idea that the explanation of language change in general has to be connected with language acquisition, i.e. that language change takes place in the course of language acquisition, is common since the early generative approaches to historical linguistics (e.g. Klima, 1964; Traugott, 1965; King, 1969; Lakoff, 1968). However, one may take Lightfoot (1979) as the first extensive account for diachronic syntax within the generative perspective. In this work the scholar outlines some proposals regarding the application of the Extended Standard Theory (Chomsky, 1973) to syntactic change, putting forward two main questioned hypotheses. The first one is that syntactic change is independent of any connection with semantic relations, pragmatic considerations and discourse function, while, according to the second, the author assumes that grammatical changes largely occur as catastrophic restructuring events that follow from the gradual accumulation of small 'environmental' changes ('Transparency Principle'). Even if modified, the core of the latter idea is maintained in Lightfoot's thought until the '90s and its discussion may be better framed within that concerning the issue of 'gradualism', which is considered again in section 5.3. In Lightfoot (1991) the scholar reinterprets his hypotheses regarding diachronic syntax within the Principles and Parameters Theory. Essentially, according to his proposal the main mechanism underlying syntactic change is the change of the value of parameters from one generation to the other, i.e. parameter resetting, and this idea is in line with the thought that syntactic change occurs through reanalysis during language acquisition.

But given that in the biolinguistic perspective it is expected that the grammar acquired by a child matches the grammar that generated the corpus, to which the child has been exposed to, how is it possible that changes occur from one generation to the following one, i.e. that one or more parameters may be set differently in the two generations? (Clark and Roberts, 1994: 12). The explanation of this apparent paradox is a crucial milestone on the way to defining a coherent theory of parametric change. A possible solution to the logical problem is to relax the deterministic thesis regarding language acquisition and to suppose that in the course of the process «all parameter values must be fixed, but there is no requirement for convergence with the adult grammar (although this happens most of the times)» (Roberts and Roussou, 2003: 13). In this sense, the aim of language acquisition should primarily be to approximate adult grammar, not of replicating

it, even if the latter is largely the most frequent case (Roberts, 2007: 231). What about the cases of divergence? One may think that, even if generally children's grammar perfectly overlaps with the parental one, «[s]ometimes [...] minor changes in the relevant childhood experience cross a threshold and have consequences for the grammars that emerge» (Lightfoot, 1999: 78-79). More specifically, these critical minor changes may be thought to be those that affect the relevant triggering experience, i.e. the parameter triggers (Roberts and Roussou, 2003: 12-13). This view significantly relies on Keenan (1994; 2002) and Longobardi's (2001) Inertial Theory. According to it, syntax is assumed to be inert in diachrony, that is to be entirely unaffected by spontaneous internal change. In general terms, in syntax it is expected that «[t]hing stay as they are unless acted on by an outside force or decay» (Keenan, 2002: 2). On the one hand, to regard syntactic change as an indirect consequence of extra-syntactic changes permits solving the logical problem of language change that is raised within the acquisitional approach: Indeed, no paradox becomes evident if one considers that the adult grammar and the learner's are not directly connected, but are related by means of the primary linguistic data, and nothing prevents this data to be subject to, say, morphological erosion, semantic shift and so on. On the other hand, the idea that a syntactic change may recursively derive from another one is coherent with the hypotheses that (many) parameters interact one with the other.

How can the theory of parametric change, as outlined so far, be applied to concrete linguistic cases? Which is the link between the abstract parameter formats and actual syntactic variation? In the rest of this section some relevant studies are taken into account in order to show how empirical cases can be interpreted in light of the theoretical biolinguistic framework. These analyses will cover both an example of what we can refer to as proper genealogical change, and the examination of a clear instance of syntactic borrowing.

A relevant premise that should be pointed out before introducing the former case is that Roberts and Roussou (2003) apply the parameter formats and the markedness hierarchy mentioned in section 4.1 to parametric change arguing that whenever the trigger of a certain parameter has become ambiguous and obscure, «the learner will opt for the default option as part of the built-in preference of the learning device for simpler representations» (Roberts and Roussou, 2003: 17). This proposal seems to be corroborated by a number of cross-linguistic examples of grammaticalization and in the following discussion one of the scholars' examples is illustrated in order to

clarify their approach: The development of the Romance definite article.

It is well-known that Romance definite articles (e.g. Italian *il*, Spanish *el*, French *le* and so on) mostly developed out of the Latin demonstrative *ille*[18] (e.g. Tagliavini, 1999: 257-259). Latin had no definite articles, but it is documented that in Vulgar Latin (say around the V century) *ille* started occurring with nominals as definite article. One of the hypotheses that Roberts and Roussou (2003) take into account and aim to reinterpret within their framework is Giusti's (2001) one, whose premise is that definite articles are directly merged in D, while demonstratives are generated lower in the structure and then move to merge to SpecD. Thus, considering the reanalysis undergone by *ille* from Latin to Vulgar Latin, one should account for the fact that there was a passage from the structure given in Figure 1a to that presented in Figure 1b.
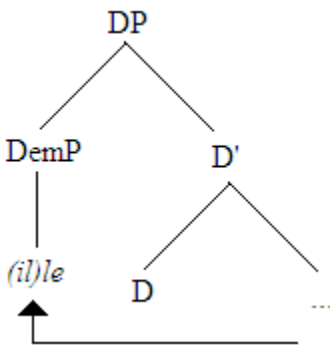

Figure 1a. *Position of the demonstrative*   Figure 1b. *The reanalysis of* ille *in Vulgar*
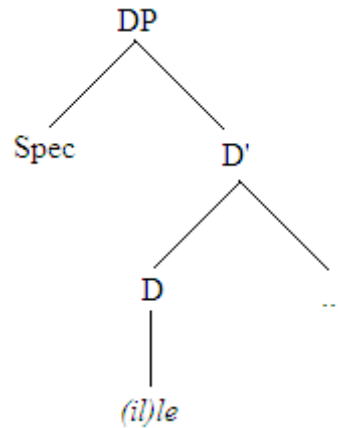   ille *in Latin (Giusti, 2001)*   *Latin (Giusti, 2001)*

According to the approach adopted by Roberts and Roussou (2003), «[t]he trigger for the reanalysis was the phonological weakening of *ille* coupled with the loss of case morphology» (Roberts and Roussou, 2003: 135). The background idea is that in nominal phrases that lack a definite article the nominal head (N) is obligatorily subject to N-to-D movement,

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[18]   And from *ipse* in varieties that are not considered here, like Sardinian and, partially, Catalan and Gascon.

which is assumed to be aimed at checking the Case features that are found in D. The rich case morphology of Latin allowed N-to-D movement to be not entirely expressed at PF, i.e. to optionally occur after the spell-out, because the N-to-D chain would have been visible anyway (Giusti, 2001: 168). Since the inflectional endings in general and case morphology in particular were deteriorating starting from Vulgar Latin, in Romance languages the insertion of a definite article in D could have represented a solution to make the N-to-D chain visible and, therefore, to allow case checking. Summing up, Giusti (2001) and Roberts and Roussou (2003: 131-136) are convinced that *ille* came to play this role because on the one hand, as former demonstrative, it was already independently +definite and on the other hand its phonological weakening facilitated its reanalysis as functional element. In this case of grammaticalization Roberts and Roussou's (2003) markedness hierarchy seems to fit, in that their analysis entails a structural simplification of the nominal phrase. In particular, an instantiation of Move is lost (i.e. the movement of *ille* to the D area) and the demonstrative is reanalyzed as an element that is directly merged in D.

Nonetheless, we can observe here that the structural simplification does not necessarily correspond to the resetting of a parameter to an unmarked/ default value, but rather in this example the parameter resetting appears to proceed in the opposite direction: Indeed, this case of grammaticalization seems to be reducible to the resetting of an *a*-scheme parameter, in Longobardi's (2005) terms, from the value 'not grammaticalized' to 'grammaticalized'. Putting it differently, if it is true that Longobardi's (2005) *a*-scheme corresponds to a feature that has a phonological representation in Roberts and Roussou's (2003) basic formalism, then the grammaticalization of definiteness from Latin to Romance languages could be regarded as the resetting of the relevant parameter to the marked value. Therefore, one cannot make the general prediction that, since changes tend to trigger the less complex options, all languages should tend to have all the same unmarked parametric values: As claimed by Roberts and Roussou (2003), «the simplifications effected by changes are always local, and may increase the complexity elsewhere in the system» (Roberts and Roussou, 2003: 17).

As for syntactic borrowing, within the already mentioned Longobardi's (2001) Inertial Theory paradigm this phenomenon is not excluded from the process of diachronic development, but it is claimed that its theoretical *status* has to be distinguished from that of proper change (Longobardi, 2001:

278). Furthermore, Roberts (2007: 383-406) largely investigates the role of language contact in diachronic syntax, claiming that indisputably the intervention of an alien grammatical system can significantly contaminate the primary corpus on which a new generation acquires a target language, thus causing a shift in the fixation of the parametric values.

As already pointed out, among the clearest cases of syntactic borrowing, one may consider the direct contact between English and Prince Edward Island French (Roberts, 2007: 238-242), which resulted in borrowing of Preposition Stranding (PS), along with some English prepositions, into the insular Romance variety. PS indicates the rule, which allows the complement of a prepositional phrase to raise to a higher position leaving the prepositional head behind, i.e. 'stranded' in its original position. The example in (1) shows how PS applies to English.

> English (Roberts, 2007: 238)
>
> (1)   [*Who*]$_i$ *did you speak to* t$_i$?

In standard modern French PS is not valid, in that it generates the ungrammatical sentences in (2), but, as known at least since King and Roberge (1990) and illustrated in (3), PS is applicable in Prince Edward Island French instead.

> Standard French (Roberts, 2007: 238)
>
> (2)   *[Qui]i as-tu parlé à ti?
>   Who have-you speak to
>
> Prince Edward Island French (King, 2000: 136)
>
> (3)   [Où]i ce-qu'elle vient de ti?
>   Where that-she come from?

Notice that Prince Edward Island French borrowed many prepositions from English, e.g. *off* and *about*, so the first hypothesis that can be made is that PS has been regularly imported in the Romance language together with prepositions. This would be confirmed also by other cases, in which there has been large borrowing of prepositions from English to North American French varieties, which now allow PS, e.g. Monctoc French (Roy, 1979) and Nova Scotia Acadian varieties (Flikeid, 1989). Where the lexical borrowing has been more limited, e.g. in Newfoundland varieties of Acadian (King, 2000: 144), the rule has not been transmitted. None-

theless the new syntactic patterns of Prince Edward Island French are not identical with English patterns: Rather, it seem like the rule of PS has been generalized by the Romance speakers, so that it can apply also to cases in which in English it would generate (almost) ungrammatical sentences. So, the examples in (4) show the contrast between English (4a) and Prince Edward Island French (4b).

English (King, 2000: 146)

(4)   a. *[Who]i did Pugsley give a book yesterday to ti?

Prince Edward Island French (King, 2000: 146)
b. [Quoi]i ce-que tu as parlé hier à Jean de ti?
    What that-that you have speak yesterday to Jean about

Whatever the exact explanation of this syntactic borrowing, being it indirect or direct, i.e. mediated or not by lexical borrowing, it is clear that the change occurred in Prince Edward Island French can be significantly brought back to a contact situation and it may be considered an actual instance of 'syntactic borrowing'. The contact between English and the Romance variety can be accounted for in general terms within the parametric perspective claiming that at a certain point English expressions that incorporated PS (and therefore prepositions) must have been included in the primary linguistic data of the insular French acquirers. As a consequence, in that way the value of the relevant parameter that governs PS was changed respective of standard French. Roberts (2007) does not indicate which parameter should be responsible of PS, but a proposal that deserves to be mentioned is that of Snyder (2001) and Sugisaki and Snyder (2002), who consider PS (and, following Stowell, 1981; 1982, other relevant constructions, e.g. V + particle constructions) as a rule determined by the setting of a specific noun-compounding parameter. This idea is based on the observations that languages that have endocentric compounds allow PS and that during the acquisition of English children start applying PS only after they have learned how to produce noun compounds. If true, this hypothesis would entail the identification of the exact parameter that underwent resetting in the history of Prince Edward Island French, but, as shown by Gebhardt (2005), it is not: Indeed English speakers productively use noun-compounding, but speakers of both French and Prince Edward Island French use endocentric compounds at similar minimal rates. Even if this seems not to be the right parametric model and the case in question

remains open, what is relevant to underline again is that syntactic borrowing, as an instance of syntactic change, can be regularly interpreted within the biolinguistic approach.

5. *An analogical parallel*

It has already been claimed in the introduction that providing a detailed evolutionary model for diachronic syntax is not the goal of the present work. Thus in this section an analogical approach is adopted assuming that some ideas developed within the biological theory of evolution can be usefully adopted to reinterpret some important features of grammatical change, even if the differences between biological and language evolution prevent drawing a strict parallel between these two processes. The intent is to start from the presentation of a quantitative model of cultural evolution, which is done in section 5.1. Then in the course of the discussion presented in section 5.2 some points of convergence between the dynamics of biological evolution, cultural evolution and syntactic evolution are pointed out, as well as the essential features that differentiate them. The analogical parallel is framed within the biolinguistic perspective outlined in the preceding sections and it is mainly focused on syntax, but the evolutionary mechanisms pertaining other levels of linguistic analysis (e.g. phonology and lexical semantics) are also taken into consideration with the aim of clarifying some relevant aspects of the discussion. Finally, section 5.3 covers two fundamental issue regarding grammatical evolution: Individual transmission and gradualness.

5.1. *Cultural evolution*

Before outlining the comparison between the factors that intervene in biological evolution and those that are relevant in grammatical evolution, it is useful to look at the 'cultural' aspect of language change and to illustrate how the evolution of 'cultural' traits can be modelled. Abstracting away from detailed sociological and anthropological descriptions, one may assume the broadest possible definition of 'culture', meaning «what is learned from others, in opposition to what is learned by oneself, in isolation» (Cavalli-Sforza, 2001: 249, translation by GR). Consequently, a cultural system may be viewed as the set of cultural traits that are typically ascribed to a human

group[19] and that may concern, for instance, religious or political belief, family structure, diet and moral attitude, i.e. all those features that affect individuals' habits and social interactions, as well as, of course, language. Indeed, according to the biolinguistic approach while language faculty is genetically inherited, knowledge of a specific language, I-language in Chomsky's (1986) terms, is culturally transmitted, because a specific language is fundamentally learned by others.

Everyone can observe that, as biological and linguistic features, also cultural traits change over time. The first models aimed at shedding light on the dynamics of cultural change in an evolutionary perspective appeared in the '80s. Among them, probably the most famous and extensive is Cavalli-Sforza and Feldman's (1981). The scholars design a quantitative analysis of cultural change taking advantage of the main concepts developed in population genetics and with particular reference to the mechanisms of individual transmission of cultural traits. The premise of the model is that a cultural trait (or cultural unit) can be considered comparable to a genetic trait (a gene). According to this view, what do biological and cultural evolution have in common?

To answer this question, mutation is the first evolutionary factor that has to be taken into account. The fact that, as genetic mutations, cultural innovations have a gradual diversification effect on cultures is indisputable. However, while genetic mutations occur by chance due to chemical changes or errors in the copy of the original genetic material and they are frequently damaging for organisms, Cavalli-Sforza and Feldman affirm that in the cultural process the change is more frequently likely to be directed non-random innovation, having a purpose and a specific direction (Cavalli-Sforza and Feldman, 1981: 66). In other words, in principle any individual can consciously evaluate the possibility of adopting cultural change (e.g. her religious belief) with respect to personal preferences, values, advantages and so on. Thus the main difference between genetic mutation and cultural change seems to regard the fact that while the former is random, the latter is mostly directed and intentional. This does not mean that cultural changes are always advantageous for individuals or groups. As natural selection influences the frequency of alleles in a population and leads to the disappearance of those, that are originated from harmful mutations, in the same way it can

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[19] However notice that «culture is important for animals too. The parents' teaching, above all that provided by the mother for mammals and birds, is essential for most species» (Cavalli-Sforza, 2001: 250, translation by GR).

determine the deletion of cultural traits that are injurious to the existence of an individual or a group (e.g. smoking). However, any innovative cultural trait has to be accepted before undergoing natural selection: In particular, it has to be approved by single individuals in order to increase its frequency in the social group. Thus one may think that there are two levels of selection for cultural changes: The first one is social and the second one is natural.

Also migration plays an important role in cultural evolution. The passage of knowledge, techniques and habits between different human groups is widespread. Notice that, while in biology migration has effect only if the contact occurs between interbreeding populations, i.e. populations that belong to the same species, in principle there are no barriers against the flow of cultural units, at most there is (often temporary) resistance. Moreover, Cavalli-Sforza and Feldman point out that, unlike in the biological evolutionary model, migration can take two different forms: There can be migration of people, which carry their own cultural traits, and migration of ideas on their own. These migrations are respectively referred to as 'demic' and 'cultural' (Cavalli-Sforza and Feldman, 1981: 68): Conversely, it s clear that gene flow can be only demic. Finally, the process of drift that intervenes in biological models (the genetic drift) perfectly applies to cultural evolution as well. This because the drift just determines a random fluctuation of the frequency of any type of traits in a population and from this point of view it acts purely quantitatively, i.e. independently of the intrinsic meaning of the traits. Also in cultural evolution the drift is expected to have an homogenizing effect on the population and to act faster in smaller groups of individuals.

The modalities of cultural transmission between individuals are rather different instead. While the individual transmission of genes that occurs during reproduction is vertical (apart from the marginal cases of lateral gene transfer mentioned in the end of section 2.3), Cavalli-Sforza and Feldman (1981) argue that the situation is more complex in cultural evolution. In particular, they identify four types of individual transmission. The first one may be assumed to be regularly (from the biological point of view) vertical, in that it occurs from one generation to the next between persons that have either a biological or a strong and lasting social relationship, e.g. from parents to children. Then the scholars recognize the possibility of individual horizontal transmission between two persons that do not have either a biological or a strong and lasting social relationship (e.g. friends): In particular, they call this transmission 'oblique' if the transmitter belongs to an older generation respect to the recipient. The other two types of individual trans-

mission introduced by the scholars are one-to-many, from one transmitter to many recipients (e.g. from a teacher to her students), and many-to-one, from many transmitters to one recipient (e.g. from a whole family to a new member). What about inheritance? The Mendelian model adopted in evolutionary biology only marginally applies to cultural evolution. On the one hand cultural units are often neither discrete nor 'atomic', thus nothing prevents them from being blended (e.g. a child brought up by parents used to different diets may decide to mix them). On the other hand, cultural units are also subject to change and may be acquired at any moment in the course of an individual's life (apart from few cases in which a 'critical period' for the acquisition is assumed, see Cavalli-Sforza, 2001: 281-285), and what is effectively transmitted is the state of these units as they appear in the specific period in which the transmission occurs. In this sense, cultural transmission is more similar to a Lamarckian than a Mendelian process, because in practice it always entails inheritance of acquired characters.

5.2. *The evolutionary factors in diachronic syntax*

As for language evolution in general, it is important to point out an important premise regarding the above mentioned four evolutionary factors, i.e. that only one of them refers to the individual and specific occurrence of innovations, i.e. mutation, while the others, namely selection, genetic drift and migration, are relevant to describe the diffusion of changes. In Croft's (2000) terms, mutation corresponds to altered replication, whereas selection, genetic drift and migration regard the mechanisms of differential replication, or propagation.

Keeping this observation in mind, the first question that one should face concerns the parallel between the evolutionary units that are relevant in biology and syntax. In particular, why should syntactic parameters represent an adequate counterpart of genes? Are there reasons to think that they would fit the parallel with genes better than other linguistic traits? In order to clarify this point, it is useful to mention the basic principles put forward at least since Longobardi (2003a), according to which the shift of focus to parameters as *loci* of syntactic variation may allow solving the problem of the choice of the *comparanda* in historical syntax[20]. The idea, supported also by

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[20] The perspective summarized here represents the core of the so-called 'Parametric comparison method', which has been conceived and developed at least since LONGOBARDI (2003a).

Roberts (1998), is that parameters appear to be perfectly suitable for comparing languages, because they are a universal finite list of discrete biological options (Longobardi, 2003a: 106). Thus this set of *comparanda* is applicable to any group of possible human languages, in that parameters (or, better, parametric values) are assumed to be incorporated into any individual's knowledge of language. Moreover, since these cognitive objects correspond to precise discrete grammatical choices, on the one hand there is no doubt that one is always comparing 'like with like', on the other hand ambiguous parameter settings are thought to be impossible, in the sense that each language has to be provided with a clear and exhaustive list of parametric values, each of them corresponding precisely to one of the two possible options entailed by each parameter. Finally, parameters are assumed constitute a set that is finite, as, consequently, the number of grammars that they can generate is finite, and also limited, at least relatively to the number of surface syntactic features that they control. To sum up, parameters as comparative characters are intended to share fundamental properties with genetic markers, i.e. universality, discreteness, non-ambiguity and finiteness.

Having clarified how parameters can be assimilated to genes and considering now the role of evolutionary factors in diachronic syntax, the mechanisms by means of which syntactic changes arise can be taken into account. As argued in section 4.3, here it is assumed that the ultimate cause of them is the resetting of specific parameter values from one generation to the following one, which is hypothesized to occur during single individuals' attainment of the 'steady state'. This entails that, as it is more or less implicitly known since Schmidt (1872) and as it is expected for all kinds of linguistic innovations, syntactic changes are not assumed to abstractly originate in E-language, using again Chomsky's (1986) terminology, but rather to show up in I-language and then to spread in the speech community in the course of time. Notice that the distinction between innovation and diffusion would be lost, if one considered languages as organisms, and language change could be described only as 'inherent change'. Given this framework, are grammatical innovations more similar to genetic or cultural innovations? In the last section it has been shown in which sense genetic mutation is random and often harmful while cultural innovation is directed and intentional. Syntactic changes cannot be described in terms of 'harmfulness' in any sense, as explained later discussing the role of natural selection, but they can be widely characterized as unintentional, i.e. not consciously directed by the

speaker, differently from changes that may affect, for instance, peripheral lexicon (among others see the introduction to the concept of 'etymological motivation' in Benedetti, 2003: 215-216).

Something more can be said about randomness, and this topic may be better understood considering the general dynamics of linguistic innovations, i.e. abstracting away from the specific case of grammatical ones. Thus even if language changes in general remain unpredictable[21], it is often observed that they do not occur randomly, but that in some sense they are rather 'structurally driven', i.e. somehow influenced by 'structural' properties of the linguistic system (in the sense meant, for instance, by Kiparsky, 2008). This is simply another presentation of a fundamental issue investigated by diachronic linguistics: The identification of universals and paths of change. Indeed «one of the most peculiar aspects of language change is the frequent occurrence – already known by Neogrammarians – of a certain degree of symmetry» (Lazzeroni, 2006: 975, translation by GR), which, according to Lazzeroni (2006), represents the outcome of diachronic directed processes. To identify directions of change appears to be hard for lexical-semantic changes, since they are particularly subject to apparent arbitrariness (due to the arbitrariness of the relationship between *signifiant* and *signifié*) and they are sensible to factors external to language, e.g. specific social and historical contexts of use[22]. However, significant generalizations about paths of semantic change, e.g. the irreversibility of shifts from concrete to abstract, have been clarified (see among others the summary provided by Lazzeroni, 1996: 24-30; Traugott and Dasher, 2002; Giacalone Ramat and Mauri, 2008). In phonology different types of 'structure-dependent' changes have been investigated at least since the '20s (e.g. Kiparsky, 1995: 3).

Some paths of change and constraints appear to be related to the inventory of phonemes of specific languages. For instance, having studied the inventories of phonemes on a wide sample of languages, Maddieson

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[21] As claimed by CROFT (2000), there are two positions regarding the possibility of constructing a predictive model of language change. According to the optimistic one, if linguists knew in enough detail all relevant linguistic facts, they would be able to exactly predict the occurrence of changes. Oppositely, for the pessimistic view «we would never be able to predict the change because there is at least some element of randomness in the process, as is the case with the randomness of mutation in biological reproduction and the random factors for survival of individual organisms» (CROFT, 2000: 3). However, the existence of a large set of structurally driven changes might suggest that, provided a full understanding of the 'relevant linguistic facts', in principle it could be possible to predict them at least in probabilistic terms.

[22] Among the strangest cases, see for instance the etymological derivation of Italian *cotillon* ('gift that is offered at the end of a ball'), which is a borrowing from French *cotillon* ('skirt').

(1984) affirms that «[t]he total number of consonants in an inventory varies between 6 and 95 with a mean of 22.8» and «[t]he total number of vowels varies between 3 and 46 with a mean of 8.7» (Maddieson, 1984: 9): Looking at these typological data, one may hypothesize that there are upper and lower limits to the number (and type) of phonemes that can be included in a specific inventory, thus the phonetic changes that lead to create or merge phonemes (namely, splits and mergers) might tend to be somehow constrained. On this respect in the '40s Jakobson (1941) pointed out that «[a]n *a* emerges as the first vowel, and generally a labial as the first consonant, in child language. The first consonantal opposition is that of nasal or oral stop (e.g. *mama-papa*), which is followed by the opposition of labials and dentals (e.g. *papa-tata* and *mama-nana*). These two oppositions form the minimal consonantal system of the languages of the world» (Jakobson, 1941: 47-48). Moreover, the scholar proposed a hierarchy of implicational rules ('laws of solidarity') based on evidence provided by the study of child-language acquisition and synchronic typology: For instance, according to the first of these rules «[t]he acquisition of fricatives presupposes the acquisition of stops in child language; and in the linguistic systems of the world the former cannot exist unless the latter exist as well» (Jakobson, 1941: 51). As for specific constraints that affect phonological change, one can think about 'mergers' instead, which are well known to be irreversible processes, since the original phonemes are usually not restored by successive transformations. Other paths of phonological change concern articulatory constraints on segmental contiguity, which are also well-studied within natural phonology (Dressler, 1985). For example, the consonantal cluster /tl/ appears to be marked in some languages, e.g. Italian, as it is shown by the following paradigmatic development: Latin *vetulus* ('old') > *vetlus* > *veclus* > Italian *vecchio*. This fact is also related to the specific distribution of coronals[23] that is observed in Latin as well as in other languages (Marotta, 1993). As for morphology, one of the most famous collection of works about universal paths of change is probably Greenberg *et al.* (1978). However, as pointed out by Giannini (2003: 94), morphological change cannot be easily characterized on its own, because the boarder between morphology and other levels of linguistic analysis, namely phonology and syntax, often appears 'mobile' in diachrony.

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[23] Among others, see KIPARSKY (1985) for the unmarkedness of coronal place of articulation ('coronal syndrome').

Most relevantly considering the aims of the present work, structurally-dependent change is particularly clear in syntax, especially from the point of view of the generative analysis. Indeed a central principle of Universal Grammar is precisely the 'Structure dependence principle', according to which «[a]ll grammatical operations are structural dependent» (Radford, 2002: 12): Putting it simply, the core idea implied by this principle is that syntactic operations can apply to syntactic objects with exclusive reference to the position and the role that these objects play within the syntactic structure they belong to. No other criterion, for instance based on the linear order of words in sentences, is relevant for syntactic operations. Therefore «syntactic rules cannot refer either to the number of words in a sentence or to the position of a word in a word-string» (Moro, 2006: 197, translation by GR). Such a principle alone largely restricts the possibility of syntactic variation, given that the description of structure and of the mechanisms of its derivation are assumed to be universally valid. The fact that syntactic change appears to be structurally dependent is even clearer if one considers it within the parametric perspective, in that, as illustrated in section 4.1, it is hypothesized that the parameter space corresponds to a finite set of biologically-determined options. Moreover, it has been claimed that recent investigations are providing support to the idea that these options not only are discrete, entailing a choice between two distinct opposite values, but may also be reduced to a limited number of formats. Finally, Roberts and Roussou (2003) and Roberts' (2007) markedness hierarchy, according to which there should be a tendency towards the resetting of parameters to less marked values when the trigger experience becomes ambiguous or obscure for the learner, appears to represent a further step on the way to understand the structural dependent characterization of syntactic innovations.

The structural dependency of linguistic change may be interpreted as some kind of 'structural pre-selection' in evolutionary terms, in the sense that, even before occurring, some changes are favoured over others, i.e. they have a higher probability of occurrence than others. Notice that similar mechanisms intervene also in biological evolution and, for instance, they regard the occurrence of specific types of nucleotides substitutions in mutation. Indeed two distinct types of DNA substitutions are recognized: When either a purine is replaced by another purine nucleotide (A ↔ G) or a pyramidine by another pyramidine nucleotide (C ↔ T) the mutation is called transition, while when a purine changes to a pyramidine nucleotide or the other way around, a transversion occurs. Transitions are much more com-

mon than transversions. Thus nucleotides have a direct influence on the occurrence of the substitutions and, even if they do not prevent the genetic system to be altered in one way or another, their distribution makes some paths of mutation more or less probable than others[24].

It appears straightforward that proper natural selection does not intervene in language evolution instead, since there is no evidence for environmental adaptation of linguistic traits. One may not claim, for instance, that a specific climate influenced the diffusion of a specific syntactic innovation, say the shift from OV to VO word order in early Middle English. For the same reason, grammatical innovations cannot be regarded as harmful or advantageous for a language: There is no environmental advantage in using a specific word order instead of another or in having definiteness grammaticalized. At most, similar hypotheses could have been taken in consideration until Jespersen (1922) (see section 3.1), but not in modern linguistics. What about cases like, for instance, the progressive loss of free word order from Latin to Romance languages? One may assume that, hypothesizing that this change was triggered by the loss of case marking, the more fixed word order might have come to represent an advantageous feature, helping decoding grammatical relations when cases started disappearing[25]. Nonetheless, calling such a change 'advantageous', as if it entailed an adaptation of the language system, would be misleading in this context. Indeed when we are talking about adaptation in evolutionary biology we are referring to the pressure of environmental factors that are external to the 'biological system' that undergoes changes and, ultimately, natural selection. On the other hand, following the line of reasoning developed so far, we are assuming that the factors that trigger syntactic changes are internal to the 'linguistic system', having to do only with its general equilibrium. In synthesis, *a priori* there is no reason to discard the hypothesis that from the diachronic perspec-

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[24] As for cultural evolution, generalizations and predictions on patters and possibilities of cultural evolution can probably be provided only tentatively. Nonetheless, if one looks at the interaction between two specific cultural subsystems, e.g. the religious and the moral one, some reasonable predictions can be made. For instance, it is likely that a community, in which the vast majority of people profess Catholicism, would be less prone to accept an innovation regarding the moral acceptability of, say, euthanasia. In this sense religious belief could modify the probability of change of a specific moral trait and one might claim that the process of (pre-)selection is internally driven.

[25] The generalization according to which languages with more extensive case-marking tend to allow less strict word order is popular since the dawn of historical linguistics. Among others, see for instance SAPIR (1921: 66).

tive the loss of case marking might be compensated by the loss of free word order, but this does not mean that we are talking about the same 'adaptation' mechanism that selects genes. Rather we are just confirming that the structural dependency of linguistic change, intended precisely as the set of system-internal constraints that condition the occurrence and the direction of grammatical innovations, cannot be neglected.

On the other hand it is realistic to assume that the same 'immunity' to natural selection applies to all levels of language development (in particular morphology and phonology), even if it is opportune to underline that lexical-semantics makes an exception in this sense, since it is known to conserve traces of the territory inhabited by a speech community. This observation is particularly relevant for archaeological-linguistic studies aimed at reconstructing the geographic location of proto-languages (e.g. Gimbutas, 1970). Social selection, instead, applies to language evolution in general and to syntactic development in particular (even if differently from what happens in cultural systems it is not followed by natural selection): The effect of social factors on diffusion of linguistic innovations is studied since the dawn of sociolinguistics (Weinreich *et al.*, 1968; Labov, 1966; 1977), and there is no need to go deeper into this question here.

The process of drift applies to grammatical evolution as well, for the reasons outlined in section 5.1 discussing about cultural evolution: Essentially, because the drift is a purely quantitative process. The role of migration in language evolution, instead, is inextricably bounded to the issues of language contact and syntactic borrowing. There is no doubt that the contact between neighbouring languages may lead them to share some innovations, i.e. to converge with respect to some linguistic traits, even if there is not a close genealogical relationship between them. Thus the effect of language contact is perfectly comparable with that of migration in population genetics: Trivially, while innovations tend to differentiate similar languages, contact tends to homogenize different ones. Of course the same observation is valid for the specific case of grammatical evolution given that, for the reasons explained in sections 4.2 and 4.3, there is no reason to exclude the possibility of contact-induced syntactic change and this type of change may be coherently interpreted within the parametric framework. Furthermore, it appears also plausible to assume that the contact may occur from both in the 'demic' and in the 'cultural' form, in the sense of Cavalli-Sforza and Feldman (1981: 68), and actually the distinction between these two types seems to be quite rough in comparison with the already mentioned proposals regarding the typology of contact events.

5.3. *Individual transmission and gradualness*

Two questions deserve to be considered separately: The mechanisms responsible for the individual transmission of syntactic traits and the issue of gradualness, which is closely connected to that of the diffusion of syntactic change.

'Individual transmission' is intended here in the sense meant in evolutionary biology and Cavalli-Sforza and Feldman (1981), i.e. as the passage of traits between individuals, and, for what concerns grammatical evolution, the passage of knowledge that occurs in the course of language acquisition and determines the formation of the relevant set of parametric settings that characterizes a specific I-language. Ultimately, considering the question within a wide diachronic perspective, this is the process the determines the instantiation of a proper 'σ relation' between two I-languages in Longobardi's (2003b: 173) terms, i.e. a relation according to which the children's knowledge of a certain language may be said to 'immediately derive' from the parent's one. Thus how similar is this process to the biological one? A first statement about individual transmission of syntactic traits within the parametric perspective might be that it does not entail a Mendelian-like process of inheritance: The process appears to be memoryless, in the sense that, unlike genetic transmission, previous parameter states are not preserved and they neither surface nor do they influence successive stages of diachronic development of I-language (see for instance Longobardi, 2003b: 180-182). Nonetheless, the mechanism of inheritance does not even appear to be Lamarckian in general, because it is assumed that no significant modifications should affect (at least) narrow components of linguistic knowledge in Chomsky's (1986: 25) sense after the attainment of the 'steady state', which entails that there is no generalized inheritance of grammatical traits that are acquired in the course of the entire life, but only of those that are acquired during the 'critical period'.

Therefore there is a substantial difference between individual transmission of grammar and individual biological transmission, since the former is assumed to be spread during the whole critical period while the latter is a punctuated event: However, this difference does not contrast with the fact that once the process is completed (after the critical period for grammar and after reproduction for genetic material), in both cases the relevant traits (narrow components of I-language, i.e. more specifically parameter settings, and genes) do not undergo further modifications in the course of an individual's

life[26], so that they cannot be inherited in Lamarckian sense. This framework appears to be plausibly applicable to other 'narrow' aspects of the linguistic competence concerning for instance phonology and morphology, but it seems plain that the situation is rather different for non-narrow components of I-language. Indeed lexical acquisition and change, especially in the case of non-basic vocabulary items as intended for instance by Swadesh (1952), commonly overcome the limits of the critical period, so that the transmission of these items would properly entail inheritance of acquired (in Lamarckian sense) characters. This means that no clear and general mapping between the inheritance mechanisms that act in biology and those that are found in 'language transmission' in general can be provided. As for the different modalities of individual cultural transmission outlined by Cavalli-Sforza and Feldman (1981) (vertical, horizontal, one-to-many and many-to-one), they could probably be of some use in the classification of the modalities of individual language transmission, in that they reflect possible instantiations of the process, but the discussion of this issue is not relevant here.

What about gradualness? The debate regarding this question closely resembles the discussion that has developed in evolutionary biology since Eldredge and Gould's (1972) 'punctuated equilibrium' model[27] and it is mainly based on the empirical evaluation of historical data provided by different scholars. As recalled by Kroch (2001), the idea that syntactic change occurs gradually was not under discussion before the emergence of generative grammar. In particular «[s]yntactic change, once actuated, was conceived primarily as a slow drift in usage frequencies, which occasionally led to the loss of some linguistic forms» (Kroch, 2001: 719). This hypothesis is still shared by a number of scholars and, among them, Croft (2000) also claims that it is common that «different linguistic features shift at different times, and the different variants coexist, sometimes in the same text» (Croft,

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[26] Apart from cases of traumatic neurological and physiological alterations, which are not related to the language faculty, but to biological acquired modifications that, according to the Mendelian model, are not passed to successive generations.

[27] Notice that ELDREDGE and GOULD's (1972) 'punctuated equilibrium' model is substantially different from DIXON's (1997), which instead concerns the identification of the different contribution of vertical and horizontal transmission in diachronic variation. The scholar argues that genealogical development of languages is the exception, being the result of just momentary 'punctuation' events (such as the introduction of agriculture or other relevant technologies), while the norm should be an 'equilibrium' situation, in which languages coexist and repeatedly interfere with one another. In other words, in Dixon's 'punctuated equilibrium model' the weight of the horizontal transmission is expected to be much greater than that of the vertical one in determining linguistic diversification.

2000: 49). There are many examples that support gradualness: One of them may be, for instance, the fact that, studying early middle English texts, Allen (2000) does not find evidence «of an abrupt shift from OV to VO word order in that period; in fact, the coexistence of both orders must be accommodated» (Croft, 2000: 51). Within the generative perspective, Lightfoot (1979; 1991; 1999) provides a radical perspective on the issue, arguing that changes are to be regarded as 'catastrophic events' that abruptly occur in the history of languages. Thus according to the scholar's idea «there must be points in history when grammars differed in terms of some structural parameter setting» and «[i]n that case, changes are abrupt and catastrophic, with many surface effects» (Lightfoot, 1999: 88). At first sight one may say that this view necessarily follows from any child-based approach to syntactic evolution, because if one assumes that changes take place in language acquisition, then changes should be regarded as individual and punctual innovations, which primarily cause the knowledge of language of a single acquirer to diverge from that owned by the adult generation. Moreover, adopting a parameter-resetting model to explain language evolution, the abrupt characterization of syntactic change naturally arises, in that parameters represent discrete (binary) options, thus there should be nothing similar to a 'partial' resetting of the values: Either a parameter is fixed to a certain value or to the other, no continuity or gradualness is expected between the two choices.

However this interpretation of Lightfoot's hypothesis is wrong, in that it is biased by the neglect of a fundamental distinction, that should be explicated speaking about 'gradualness' both in language and in biological evolution: The distinction between facts that concern the synchronic occurrence of innovations and those that regard their diachronic diffusion. In biology mutations are sudden changes that affect the discrete units (i.e. genes) owned by individual organisms, but what is assumed to be gradual is their accumulation in populations and the consequent process of speciation. In the same way, parametric changes have to be thought of as innovations that arise punctually in single speakers' I-language and then spread in the linguistic community in the course of time, determining the diachronic variation between E-languages. Thus the parametric approach to syntactic change leads to expect that syntactic evolution could be only locally, that is, at I-language level, abrupt. Nonetheless, consider that even this hypothesis oversimplifies the matter, because it does not account for the possibility that different settings of the same parameter may coexist in individual speakers' competence. Indeed mentioning the attempts to investigate parameter reset-

ting in diachrony by means of simulation studies, Kroch (2001) also takes into account Niyogi and Berwick's (1997) investigation, which according to the author is fundamentally biased by the fact of considering only competing parameter settings at population level, not including the possibility of variants within individual I-languages. According to Kroch (2001) instead «texts from the same time period generally seem more similar than different in their frequencies of the competing variants» and «it is necessary to allow for syntactic diglossia within individual authors as the normal situation during a period of change» (Kroch, 2001: 722). These observations should clarify why the parametric approach to syntactic change *per se* does not directly support Lightfoot's (1991) idea that also at E-language level grammatical changes should be expected to occur rapidly as a consequence of a large-scale parameter resetting. Essentially, it seems clear that a parametric approach to syntactic evolution entails an «abruptness of grammar change in individuals of different generations», but «there is nothing in this cognitive model which requires the spread about which Lightfoot speaks of a new parameter setting throughout a speech community to be rapid or S-shaped (see below, editor's note)» (Harris and Campbell, 1995: 41).

Of course dealing with the dynamics of diffusion of parametric change within speech communities would entail a digression into the sociolinguistic aspects of syntactic variation, which may be found, among others, in the review provided in Roberts (2007: 315-340). Being this work more focussed on the biolinguistic implications of the question, it suffices to observe that among the recent attempts to face the problem within a biolinguistic paradigm one may recall the line of research initiated at least from Kroch (1989), in which it is argued in favour of a rough 'S-shaped' curve of change (about the S-curved trajectory of linguistic change see also Osgood and Sebeok, 1954: 155; Weinreich *et al.*, 1968: 113; Denison, 1999) and of the so-called 'Constant Rate Effect': According to this hypothesis, that is supported by a number of case studies (e.g. Fontana, 1993, Pintzuk, 1995; Taylor, 1994), it is assumed that «the rate of change in different surface contexts reflecting a single underlying parameter change is the same» (Kroch, 2001: 720). Such an idea is quite unusual especially outside the generative framework, as it is more commonly assumed a variable context-sensitive rate of change (e.g. Bailey, 1973; Croft, 2000: 49). Nonetheless, it is worth pointing out that the empirical-based estimates of the rate of parametric change provided in the quantitative analyses introduced in Rigon (2009) seem to encourage a constant-rate hypothesis. The work is focused on the experimentation of

quantitative algorithmic procedures for the study of language evolution by means of the application of quantitative methods originally designed within molecular biology to the parametric comparative dataset that has already been mentioned in section 4.1 (Longobardi, 2003a; Longobardi, 2003b; Guardiano and Longobardi, 2005; Gianollo *et al.*, 2008; Longobardi and Guardiano, 2009): The analyses that are provided (Rigon, 2009: 147-190) do not reveal anything about the specific trajectory of changes, i.e. if they are linear or S-shaped, but they show that in the sample of languages and parameters in question there are not remarkable differences between the rates of change in different lineages (for instance, those including Latin and modern Romance varieties), which appears to be a reasonable assumption to be further tested in future investigations.

In synthesis, the issue of gradualness has recently come to represent a relevant focus of investigations in diachronic syntax, and, even if the debate about this problem is still open and decisive conclusions have not been achieved so far, for the aims of the present work it is important to underline that the increasing interest in the topic represents another fundamental point that the inquiries aimed to shed light on the mechanisms of grammatical evolution share with the agenda of evolutionary biology.

6. *Conclusion*

This paper has covered an overview of the basic factors and mechanisms that are assumed to intervene in the evolution of biological entities, in order to elucidate whether and to what extent they may be thought to play a role also in grammatical evolution, as it is interpreted within the biolinguistic framework.

The points that have been put forward in this paper are summarized in Table 1, in which also the characterization of Cavalli-Sforza and Feldman's (1981) model of cultural evolution is taken into account. As illustrated in the Table, it has been assumed that the units that are relevant in biological and in grammatical evolution are respectively genes and parameters: In both cases these units are thought to constitute a finite list of biologically pre-designed discrete traits. The difference is that while genes are entirely biologically-determined, syntactic parameters, even though they are designed as innate cognitive objects in the form of open options in all members of our species, are 'closed' in response of the linguistic environment in which the

process of acquisition takes place, i.e. in response of purely cultural stimuli. Nonetheless parameters are rather different from Cavalli-Sforza and Feldman's (1981) 'cultural units', which lack a unified formal characterization, but are not typically biologically pre-designed features.

Following the notes reported in Table 1 under 'factors', it seems clear that genetic mutations and syntactic innovations require to be modelled slightly differently instead. On the one hand it is assumed that in both domains changes share a number of characteristics that sharply differentiate them from those affecting cultural features, because they represent unintentional, un-directed, memoryless and, what is more, rather clearly abrupt events at individual (organism and I-language) level, whose trajectory of diffusion at population level is debated. It has then been stated that migration and drift play a similar role in the diffusion of biological, syntactic and, in this case, cultural innovations too, therefore these factors can be included within all models of evolution in question unproblematically. In particular syntactic borrowing represents an actual possibility of areal interference between syntactic systems and, trivially, it has the effect of making these systems more similar, just as it happens with gene flow in population genetics.

On the other hand it has been illustrated that changes are triggered differently in biology, syntax and cultural systems, and that they carry different effects. Indeed the most evident difference between biological evolution and syntactic evolution regards the modalities of selection. While in the former case the core device of the transformation process undergone by organisms is natural selection, in diachronic syntax there is nothing similar to this filter and there is no evidence of environmental adaptation driven by system-external factors, but rather a 'structural pre-selection' may be clearly defined in light of the limits of parametric variation and, of course, sociolinguistic variables are expected to intervene to socially select changes. Cultural traits are typically socially selected instead, which, differently from what happens both in genetic and grammatical evolution, again entails a conscious and intentional intervention of individuals and populations in the definition and the acceptance of innovations.

Finally, the dynamics of individual transmission appear to be relevantly similar between the biological and the syntactic domain. As argued in the last section, there is a substantial difference between individual transmission of parameter settings and genetic characteristics: The former occurs during the whole critical period of language acquisition, while the latter is a punctuated event. Nonetheless, once the process is completed, ideally in both cases

the relevant traits are not further modified in the course of individuals' lifetime. This cannot be said for what concerns the transmission of generic cultural features, which can be passed on and modified in the whole course of an individual's lifetime. Furthermore, even if genetic transmission can occur only vertically while that of grammatical and cultural traits can follow different directions (vertical, horizontal, one-to-many or many to one), both in biology and syntax clear inheritance mechanisms can be defined (i.e. respectively the Mendelian and the acquisitional one), whose definition can hardly be generalized in Cavalli-Sforza and Feldman's (1981) model.

On the whole, the analogical parallel illustrated in this work seems to encourage the idea that biological and syntactic evolution may be effectively modelled following similar, even if not identical, guidelines, so that it is reasonable to think that some aspects of the two processes can be studied by means of analogous methods of investigation. This is particularly relevant for the quantitative aspects of the analyses that can be designed, and actually it already represents a more or less implicit premise of the projects developed within the biolinguistic framework that in the last years have been studying the history of syntactic systems by means of empirical investigations (e.g. Longobardi and Guardiano, 2009; Rigon, 2009) and of algorithmic simulations (e.g. Niyogi and Berwick, 1997; Niyogi, 2002).

Biological evolution		
Relevant units		• Genes.
Factors	Mutation	• Often harmful for organisms; • Random; • Punctual/abrupt at organism level; • Gradual accumulation, the actual trajectory followed by this accumulation at population-level is debated; • Memoryless; • Diversification effect between populations.
	Selection	• Mainly natural selection, related to adaptation.
	Migration	• Relevant only between populations, i.e. interbreeding groups; • Only demic; • Homogenizing effect between populations.
	Genetic drift	• Random; • Homogenizing effect within a population.
Individual transmission		• Vertical (in higher animals and plants); • Mendelian inheritance model.
Cultural evolution		
Relevant units		• 'Cultural traits/units'.
Factors	Cultural change	• Often directed and intentional; • Gradual accumulation; • Diversification effect between cultural systems.
	Selection	• Social selection, related to individual/social acceptance; • Social selection is often followed by natural selection.
	Migration	• Always relevant, i.e. there are no 'interbreeding barriers'; • Demic or cultural; • Homogenizing effect between different cultural systems.
	Genetic drift	• Random; • Homogenizing effect within a population.
Individual transmission		• Vertical, horizontal (oblique), one-to-many or many-to-one; • No general inheritance model.
Syntactic evolution		
Relevant units		• Syntactic parameters.
Factors	Syntactic change	• Determined by diachronic parameter resetting; • Parameter resetting is an indirect consequence of syntax-external changes (either morpho-phonological or semantic) or of other syntactic changes (Inertial Theory); • Neither harmful nor advantageous; • Punctual/abrupt at I-language level; • Gradual accumulation at E-language level, the actual trajectory followed by this accumulation at population-level is debated; • Memoryless; • Diversification effect between I- and, ultimately, E-languages.
	Selection	• Structural pre-selection due to the limits of parametric variation; • Social selection.
	Syntactic borrowing	• Always possible; • Homogenizing effect between different syntactic systems.
	Genetic drift	• Random; • Homogenizing effect within a language.
Individual transmission		• Vertical, horizontal (oblique), one-to-many or many-to-one; • Acquisition-driven.

Table 1. *Overview of the relevant features of biological evolution, cultural evolution and language evolution*

References

ALLEN, C. (2000), *Obsolescence and sudden death in syntax: the decline of verb-final order in early Middle English*, in BERMÚDEZ-OTERO, R., DENISON, D., HOGG, R. M. and MCCULLY, C. B. (2000, eds.), *Generative theory and corpus studies: a dialogue from 10 Icehl*, Mouton de Gruyter, Berlin, pp. 3-25.

BAKER, M. (2001), *The Atoms of Language: The Mind's Hidden Rules of Grammar*, Oxford University Press, Oxford.

BAKER, M. (2008), *The macroparameter in a microparametric world*, in BIBERAUER, T. (2008, ed.), *The Limits of Syntactic Variation*, John Benjamins, Amsterdam, pp. 351-373.

BAILEY, C.-J. (1973), *Variation and linguistic theory*, Center for Applied Linguistics, Arlington, VA.

BENEDETTI, M. (2003), *L'etimologia fra tipologia e storia*, in MANCINI, M. (2003, ed.), *Il cambiamento linguistico*, Carocci, Roma, pp. 209-262.

BOECKX, C. (2008), *Approaching Parameters from Below*, Manuscript, Harvard University.

BORER, H. (1984), *Parametric Syntax*, Foris, Dordrecht.

BOWERN, C. (2008), *Syntactic Change and Syntactic Borrowing in Generative Grammar*, in FERARRESI, G. and GOLDBACH, M. (2008, eds.), *Principles of Syntactic Reconstruction*, John Benjamins, Amsterdam, pp. 187-216.

BOWLER, P. J. (1975), *The Changing Meaning of 'Evolution'*, in «Journal of the History of Ideas», 36, 1, pp. 95-114.

BOWLER, P. J. (2003), *Evolution. The History of an Idea*, University of California Press, Berkley-Los Angeles-London.

BRISCOE, T. (2002), *Introduction*, in BRISCOE, T. (2002, ed.), *Linguistic evolution through language acquisition*, Cambridge University Press, Cambridge, pp. 1-21.

CAMPBELL, L. (1993), *On proposed universals of grammatical borrowing*, in AERTSEN, H. and JEFFERS, R. J. (1993, eds.), *Historical Linguistics 1989: Papers from the 9th International Conference on Historical Linguistics, Rutgers University, 14-18 August 1989*, John Benjamins, Amsterdam, pp. 91-109.

CAMPBELL, L. (2001), *What's wrong with grammaticalization?*, in «Language Sciences», 23, pp. 113-162.

CAVALLI-SFORZA, L. L. (2001), *Geni, popoli e lingue*, Adelphi, Milano.

CAVALLI-SFORZA, L. L. and FELDMAN, M. (1981), *Cultural Transmission and Evolution. A Quantitative Approach*, Princeton University Press, Princeton.

Cavalli-Sforza, L. L. and Wang. S.-Y. (1986), *Spatial distance and lexical replacement*, in «Language», 62, pp. 38-55.

Chomsky, N. (1964), *Current issues in linguistic theory*, Mouton, The Hague.

Chomsky, N. (1965), *Aspects of the theory of syntax*, MIT Press, Cambridge, MA.

Chomsky, N. (1973), *Conditions on transformations*, in Anderson, S. R. and Kiparsky, P. (1973, eds.), *A festschrift for Morris Halle*, Holt, Rinehart and Winston, New York, pp. 232-286.

Chomsky, N. (1981), *Lectures on Government and Binding*, Foris, Dordrecht.

Chomsky, N. (1986), *Knowledge of language*, Praeger, New York.

Chomsky, N. (1995), *The Minimalist Program*, MIT Press, Cambridge, MA.

Clark, R. and Roberts, I. (1994), *On Complexity as the Engine of Variation*, Manuscript, University of Pennsylvania and Bangor.

Croft, W. (1996), *Linguistic selection: an utterance-based evolutionary theory of language change*, in «Nordic Journal of Linguistics», 19, pp. 99-139.

Croft, W. (2000), *Explaining Language Change. An evolutionary Approach*, Longman, Harlow, Essex.

Darwin, C. (1859), *On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life*, John Murray, London.

Dawkins, R. (1976), *The Selfish Gene*, Oxford University Press, Oxford.

Denison, D. (1999), *Slow, Slow, Quick, Quick, Slow: the Dance of Language Change?*, in Bringas López, A. M., González Alvarez, D., Pérez Guerra, J., Rama Martínez, E. and Varela Bravo, E. (1999, eds.), *'Woodenrous Ænglissce': SELIM Studies in Medieval English Language*, Universidad de Vigo (Servicio de Publicacións), Vigo, pp. 51-64.

Dixon, R. M. W. (1997), *The rise and fall of languages*, Cambridge University Press, Cambridge.

Dressler, W. U. (1985), *Morphonology*, Karoma Press, Ann Arbor.

Dunn, M., Terrill, A., Reesink, G., Foley, R. A. and Levinson, S. C. (2005), *Structural Phylogenetics and the Reconstruction of Ancient Language History*, in «Science», 309, 5743, pp. 2072-2075.

Eldredge, N. and Gould, S. J. (1972), *Punctuated equilibria: an alternative to phyletic gradualism*, in Schopf, T. J. M. (1972, ed.), *Models in Paleobiology*, Freeman and Cooper, San Francisco, pp. 82-115.

Eldredge, N. and Gould, S. J. (1988), *Punctuated equilibrium prevails*, in «Nature», 332, pp. 211-212.

EMENEAU, M. B. (1964), *India as a linguistic area*, in HYMES, D. (1964, ed.), *Language in culture and society*, Harper and Row, New York, pp. 650-653.

FLIKEID, K. (1989), *'Moitié Français, moitié anglais?' Emprunts and alternances de langues dans les communautés acadiennes de la Nouvelle-Ecosse*, in «Revue Québécoise de Linguistique Théorique et Appliquée», 8, pp. 277-228.

FONTANA, J. M. (1993), *Phrase structure and the syntax of clitics in the history of Spanish*, Ph.D. dissertation, University of Pennsylvania.

GEBHARDT, L. (2005), *Preposition stranding and the noun compounding parameter*, presented at the «NWAV34, October 20th-23rd 2008, New York University».

GENSLER, O. D. (1993), *A typological evaluation of Celtic/Hamito-Semitic syntactic parallels*, Ph.D. dissertation, University of California, Berkley.

GIACALONE RAMAT, A. (1998), *Testing the boundaries of grammaticalization*, in GIACALONE RAMAT, A. and HOPPER, P. J. (1998, eds.), *The Limits of Grammaticalization*, John Benjamins, Amsterdam, pp. 107-127.

GIACALONE RAMAT, A. and MAURI, C. (2008), *From cause to contrast: A study in semantic change*, in VERHOEVEN, E., SKOPETEAS, S., SHIN, Y.-M., NISHINA, Y. and HELMBRECHT, J. (2008, eds.), *Studies on Grammaticalization*, Mouton de Gruyter, Berlin-New York, pp. 303-320.

GIANNINI, S. (2003), *Il mutamento morfologico*, in MANCINI, M. (2003, ed.), *Il cambiamento linguistico*, Carocci, Roma, pp. 89-163.

GIANOLLO, C., GUARDIANO, C. and LONGOBARDI, G. (2008), *Three fundamental issues in parametric linguistics*, in BIBERAUER, T. (2008, ed.), *The Limits of Syntactic Variation*, John Benjamins, Amsterdam, pp. 109-142.

GIMBUTAS, M. (1970), *Proto-Indo-European culture: The Kurgan culture during the fifth to the third millennia B.C.*, in CADORNA, G. C., HÖNIGSWALD, H. M. and SENN, A. (1970, eds.), *Indo-European and Indo-Europeans*, University of Philadelphia Press, Philadelphia, pp. 155-198.

GIUSTI, G. (2001), *The birth of a functional category: from Latin ILLE to the Romance article and personal pronoun*, in CINQUE, G. and SALVI, G. (2001, eds.), *Current Studies in Italian Syntax: Essays Offered to Lorenzo Renzi*, North Holland, Amsterdam, pp. 157-171.

GOULD, S. J. and VBRA, E. S. (1982), *Exaptation – a missing term in the science of form*, in «Paleobiology», 8, pp. 4-15.

GRAY, R. D. (2005), *Pushing the Time Barrier in the Quest for Language Roots*, in «Science», 309, 5743, pp. 2007-2008.

Gray, R. D., Drummond, A. J. and Greenhill, S. J. (2009), *Language Phylogenies Reveal Expansion Pulses and Pauses in Pacific Settlement*, in «Science», 323, 5913, pp. 479-483.

Greenberg, J. (1963), *Some universals of grammar with particular reference to the order of meaningful elements*, in Greenberg, J. (1963, ed.), *Universals of Grammar*, MIT Press, Cambridge, MA, pp. 73-113.

Greenberg, J., Ferguson, C. A. and Moravcsik, E. A. (1978, eds.), *Universals of human Language*. **Vol. 3:** *Word Structure*, Stanford University Press, Stanford.

Guardiano, C. and Longobardi, G. (2005), *Parametric Comparison and Language Taxonomy*, in Batllori, M., Hernanz, M. L., Picallo, C. and Roca, F. (2005, eds.), *Grammaticalization and Parametric Variation*, Oxford University Press, Oxford, pp. 149-174.

Gumperz, J. J. and Wilson, R. (1971), *Convergence and Creolization: a case from the Indo-Aryan /Dravidian border*, in Hymes, D. (1971, ed.), *Pigdization and creolization of languages*, Cambridge University Press, Cambridge, pp. 151-167.

Harris, A. C. and Campbell, L. (1995), *Historical Syntax in cross-linguistic Perspective*, Cambridge University Press, Cambridge.

Haspelmath, M. (2004), *On directionality in language change with particular reference to grammaticalization*, in Fischer, O., Norde, M. and Peridon, H. (2004, eds.), *Up and down the cline: The nature of grammaticalization*, John Benjamins, Amsterdam, pp. 17-44.

Hauser, M. D., Chomsky, N. and Fitch, W. T. (2002), *The Faculty of Language: What Is It, Who Has It, and How Did It Evolve?*, in «Science», 298, pp. 1569-1579.

Heine, B. and Kuteva, T. (2006), *The changing Languages of Europe*, Oxford University Press, Oxford.

Hopper, P. J. and Traugott, E. C. (1993), *Grammaticalization*, Cambridge University Press, Cambridge.

Howe, C. J., Barbrook, A. C., Spencer, M., Robinson, P., Bordalejo, B. and Mooney, L. R. (2001), *Manuscript evolution*, in «Trends in Genetics», 17, pp. 147-152.

Hull, D. L. (1988), *Science as a progress: an evolutionary account of the social and conceptual development of science*, University of Chicago Press, Chicago.

Hurford, J. (1987), *Language and Number*, Blackwell, Oxford.

Huxley, J. (1942), *Evolution: The Modern Synthesis*, Allen & Unwin, London.

JAKOBSON, R. (1941), *Child Language, Aphasia, and Phonological Universals*, Mouton de Gruyter, The Hague.

JESPERSEN, O. (1922), *Language: its Nature, Development and Origin*, Allen & Unwin, London.

JONES, W. (1799), *The third anniversary discourse, on the Hindus, delivered 2d February 1786*, in JONES, W. (1799, ed.), *The works of Sir William Jones*, Robinson and Evans, London, pp. 19-34.

JOSEPH, B. D. (1983), *The Synchrony and Diachrony of Balkan Infinitive: A Study in Areal, General and Historical Linguistics*, Cambridge University Press, Cambridge.

KAYNE, R. (2005), *Some notes on comparative syntax, with special reference to English and French*, in CINQUE, G. and KAYNE, R. (2005, eds.), *The Oxford Handbook of Comparative Syntax*, Oxford University Press, New York, pp. 3-69.

KEENAN, E. (1994), *Creating anaphors. An historical study of the English reflexive pronouns*, Manuscript, UCLA.

KEENAN, E. (2002), *Explaining the Creation of Reflexive Pronouns in English*, in MINKOVA, D. and STOCKWELL, R. (2002, eds.), *Studies in the history of English: A millennia Perspective*, Mouton de Gruyter, Berlin, pp. 325-355.

KELLER, R. (1994), *On Language Change: The Invisible Hand in Language*, Routledge, London.

KIMURA, M. and WEISS, G. H. (1964), *The stepping-stone model of population structure and the decrease of genetic correlation with distance*, in «Genetics», 49, pp. 561-576.

KING, R. D. (1969), *Historical linguistics and generative grammar*, Prentice Hall, Englewood Cliffs, NJ.

KING, R. (2000), *The Lexical Basis of Grammatical Borrowing: A Prince Edward Island French Case Study*, John Benjamins, Amsterdam-Philadelphia.

KING, R. and ROBERGE, Y. (1990), *Preposition stranding in Prince Edward Island French*, in «Probus», 2, 3, pp. 351-369.

KIPARSKY, P. (1985), *Some consequences of Lexical Phonology*, in «Phonology Yearbook», 2, 82-138.

KIPARSKY, P. (1995), *The Phonological Basis of Sound Change*, in GOLDSMITH, J. (1995, ed.), *Handbook of Phonological Theory*, Blackwell, Oxford, pp. 640-670.

KIPARSKY, P. (2008), *Universals constrain change; change results in typological generalizations*, in GOOD, J. (2008, ed.), *Linguistic Universals and Language Change*, Oxford University Press, Oxford, pp. 23-53.

Klima, E. S. (1964), *Relatedness between grammatical systems*, in «Language», 40, pp. 1-20.

Kroch, A. (1989), *Function and grammar in the history of English: Periphrastic 'do'*, in Fasold, R. (1989, ed.), *Language change and variation*, John Benjamins, Amsterdam, pp. 133-172.

Kroch, A. (2000), *Verb-complement order in Middle English*, in Pintzuk, S., Tsoulas, G. and Warner, A. (2000, eds.), *Diachronic Syntax: Models and Mechanisms*, Oxford University Press, Oxford, pp. 132-163.

Kroch, A. (2001), *Syntactic change*, in Baltin, M. R. and Collins, C. (2001, eds.), *Handbook of Contemporary Syntactic Theory*, Blackwell Publishers, Oxford, pp. 699-729.

Labov, W. (1966), *The Social Stratification of English in New York City*, Center for Applied Linguistics, Washington, DC.

Labov, W. (1977), *Il continuo e il discreto nel linguaggio*, Il Mulino, Bologna.

Lakoff, R. (1968), *Abstract syntax and Latin complementation*, MIT Press, Cambridge, MA.

Lamarck, J.-B. (1809), *Philosophie zoologique ou exposition des considérations relatives à l'histoire naturelle des animaux*, Dentu, Paris.

Langacker, R. W. (1977), *Syntactic Reanalysis*, in Li, C. N. (1977, ed.), *Mechanisms of Syntactic Change*, University of Texas Press, Austin, pp. 59-139.

Lass, R. (1990), *How to Do Things with Junk: Exaptation in Language Evolution*, in «Journal of Linguistics», 26, pp. 79-102.

Lass, R. (1997), *Historical linguistics and language change*, Cambridge University Press, Cambridge.

Lazzeroni, R. (1996), *Il mutamento linguistico*, in Lazzeroni, R. (1996, ed.), *Linguistica storica*, La Nuova Italia Scientifica, Roma, pp. 13-54.

Lazzeroni, R. (2006), *I percorsi del mutamento linguistico. Un'ipotesi*, in Bombi, R., Cifoletti, G., Fusco, F., Innocente, L. and Orioles, V. (2006, eds.), *Studi linguistici in onore di Roberto Gusmani*, Edizioni dell'Orso, Alessandria, pp. 975-983.

Lefebvre, C. (1985), *Grammaires en contact: définition et perspectives de recherche*, in «Revue québécoise de Linguistique», 14, pp. 11-47.

Lightfoot, D. (1979), *Principles of Diachronic Syntax*, Cambridge University Press, Cambridge.

LIGHTFOOT, D. (1991), *How to Set Parameters: Arguments for Language Change*, MIT Press, Cambridge, MA.

LIGHTFOOT, D. (1999), *The Development of Language: Acquisition, Change, and Evolution*, Blackwell Publishing, Oxford.

LINDBLOM, B. (1986), *Phonetic universals in vowel systems*, in OHALA, J. and JÄGER, J. J. (1986, eds.), *Experimental Phonology*, Academic Press, Orlando, FL, pp. 13-44.

LONGOBARDI, G. (2001), *Formal Syntax, Diachronic Minimalism, and Etymology: The History of French Chez*, in «Linguistic Inquiry», 32, 2, pp. 275-302.

LONGOBARDI, G. (2003a), *Methods in Parametric Linguistics and Cognitive History*, in «Linguistic Variation Yearbook», 3, pp. 101-138.

LONGOBARDI, G. (2003b), *La sintassi storica*, in MANCINI, M. (2003, ed.), *Il cambiamento linguistico*, Carocci, Roma, pp. 165-207.

LONGOBARDI, G. (2005), *A Minimalist Program for Parametric Linguistics?*, in BROEKHUIS, H., CORVER, N., EVERAERT, M. and KOSTER, J. (2005, eds.), *Organising Grammar: A Festschrift for Henk van Riemsdijk*, Mouton de Gruyter, Berlin, pp. 407-414.

LONGOBARDI, G. and GUARDIANO, C. (2009), *Evidence for Syntax as a Signal of Historical Relatedness*, in «Lingua», 119, 11, pp. 1679-1706.

LONGOBARDI, G. and RIGON, G. (2008), Review of ROBERTS, I. and ROUSSOU, A. (2003), *Syntactic change. A minimalist approach to grammaticalization*, Cambridge University Press, Cambridge, in «Language», 84, 2, pp. 428-433.

MADDIESON, I. (1984), *Patterns of sound*, Cambridge University Press, Cambridge.

MALÉCOT, G. (1959), *Quelques schemas probabilistes sur la variabilité des populations naturelles*, in «Annales de l'Université de Lyon Sciences, Section A», 13, pp. 37-60.

MANZINI, M.-R. (1995), *From Merge and Move to Form Dependency*, in «UCL Working Papers in Linguistics», 7, pp. 323-345.

MANZINI, M.-R. and WEXLER, K. (1987), *Parameters, Binding theory and Learnability*, in «Linguistic Inquiry», 18, pp. 413-444.

MAROTTA, G. (1986), *Sulla nozione di 'deriva' in Sapir*, in «Quaderni dell'Istituto di Linguistica dell'Università di Urbino», 4, pp. 59-91.

MAROTTA, G. (1993), *Dental stops in Latin: A special class*, in «Rivista di linguistica», 2, 5, pp. 55-101.

MAYNARD SMITH, J. (1987), *How to model evolution*, in DUPRÉ, J. (1987, ed.), *The Latest on the Best*, MIT Press, Cambridge, MA, pp. 119-131.

MAYNARD SMITH, J. (1989), *Evolutionary genetics*, Oxford University Press, New York.

MCMAHON, A. (1994), *Understanding Language Change*, Cambridge University Press, Cambridge-New York.

MCMAHON, A. and MCMAHON, R. (2003), *Finding families: Quantitative methods in language classification*, in «Transactions of the Philological Society», 101, 1, pp. 7-55.

MEILLET, A. (1921), *Linguistique historique et linguistique générale*, É. Champion, Paris.

MORO, A. (2006), *I confine di Babele*, Longanesi, Milano.

MUFWENE, S. S. (2000), *Language contact, evolution, and death: how ecology rolls the dice*, in KINDELL, G. and LEWIS, M. P. (2000, eds.), *Assessing ethnolinguistic vitality: theory and practice; selected papers from the Third International Language assessment Conference*, SIL International, Dallas, pp. 39-64.

MUFWENE, S. S. (2001), *The Ecology of Language Evolution*, Cambridge University Press, Cambridge.

MUFWENE, S. S. (2002), *Competition and selection in language evolution*, in «Selection», 3, 1, pp. 45-56.

MUFWENE, S. S. (2008), *Language evolution: Contact, Competition and Change*, Continuum Press, New York.

NAKHLEH, L., RINGE, D. and WARNOW, T. (2005), *Perfect Phylogenetic Networks: A New Methodology for Reconstructing the Evolutionary History of Natural Languages*, in «Language», 81, 2, pp. 382-420.

NARROG, H. (2007), *Exaptation, Grammaticalization and Reanalysis*, in «California Linguistics Notes», 32, 1, pp. 1-27.

NEWMEYER, F. (2001), *Deconstructing grammaticalization*, in «Language Sciences», 23, pp. 187-230.

NEWMEYER, F. (2005), *Possible and Probable Languages: A Generative Perspective on Linguistic Typology*, Oxford University Press, Oxford.

NIYOGI, P. (2002), *Theories of cultural evolution and their application to language evolution*, in BRISCOE, T. (2002, ed.), *Linguistic Evolution through Language Acquisition: Formal and Computational Models*, Cambridge University Press, Cambridge, pp. 205-234.

NIYOGI, P. and BERWICK, R. C. (1997), *Evolutionary Consequences of Language Learning*, in «Linguistics and Philosophy», 20, 6, pp. 697-719.

NOONAN, M. (2008), *Contact-induced change in the Himalayas: the case of the Tamangic languages*, in SIEMUND, P. and KINTANA, N. (2008, eds.), *Language contact and contact languages*, John Benjamins, Amsterdam, pp. 81-106.

NORDE, M. (2002), *The final stages of grammaticalization: Affixhood and beyond*, in WISCHER, I. and DIEWALD, G. (2002, eds.), *New reflections on grammaticalization*, John Benjamins, Amsterdam, pp. 45-65.

NUMBERS, R. L. (1987), *Creationists*, in «Zygon», 22, 2, pp. 133-164.

OSGOOD, C. and SEBEOK, T. (1954), *Psycholinguistic: A survey of theory and research problems*, in «Journal of Abnormal and Social Psychology», 49, 4, pp. 1-203.

OSTHOFF, H. and BRUGMANN, K. (1878), *Morphologische Untersuchungen auf dem Gebiete der indogermanischen Sprachen*, S. Hirzel, Leipzig.

PINTZUK, S. (1995), *Phrase structure variation in Old English*, in «Language Variation and Change», 7, pp. 152-167.

POUSSA, P. (1982), *The Evolution of Early Standard English: The Creolization Hypothesis*, in «Studia Anglica Posnaniesia», 14, pp. 69-85.

PRINCE, E. F. (1988), *On pragmatic change: the borrowing of discourse functions*, in «Journal of Pragmatics», 12, pp. 505-518.

PRINCE, E. F., and PINTZUK, S. (2000), *Bilingual code-switching and the open/closed class distinction*, in «University of Pennsylvania Working Papers in Linguistics», 6, 3, pp. 237-257.

RADFORD, A. (2002), *Syntax. A minimalist introduction*, Cambridge University Press, Cambridge.

RAYFIELD, J. R. (1970), *The Languages of a bilingual Community*, Mouton, The Hague.

RIDLEY, M. (1993), *Evolution*, Blackwell Scientific Publications, Boston.

RIGON, G. (2009), *A quantitative approach to the study of syntactic evolution*, Ph.D. dissertation, Università di Pisa.

ROBERTS, I. (1998), Review of HARRIS, A. C. and CAMPBELL, L. (1995), *Historical Syntax in cross-linguistic Perspective*, Cambridge University Press, Cambridge, in «Romance Philology», 51, pp. 363-370.

ROBERTS, I. (2007), *Diachronic Syntax*, Oxford University Press, Oxford.

ROBERTS, I. (2008), *Macroparameters, Markedness and Typological Drift*, presented at «Levels of Analysis in the History of Indo-European Languages, May 22nd-24th 2008, University of Trieste».

ROBERTS, I. and HOLMBERG, A. (2005), *On the Role of Parameters in Universal Grammar: A reply to Newmeyer*, in BROEKHUIS, H., CORVER, N., EVERAERT, M. and KOSTER, J. (2005, eds.), *Organising Grammar: A Festschrift for Henk van Riemsdijk*, Mouton de Gruyter, Berlin, pp. 538-553.

ROBERTS, I. and ROUSSOU, A. (2003), *Syntactic change. A minimalist approach to grammaticalization*, Cambridge University Press, Cambridge.

ROSS, M. (1999), *Exploring metatypy: how does contact-induced typological change come about?*, Manuscript, Australian National University.

ROSS, M. (2001), *Contact-induced change in Oceanic Languages in north-west Melanesia*, in DIXON, R. M. W. and AIKHENVALD, A. Y. (2001, eds.), *Areal diffusion and genetic inheritance*, Oxford University Press, Oxford, pp. 134-166.

ROY, M.-M. (1979), *Les conjonctions anglaises "but" et "so" dans le français de Moncton*, M.A. dissertation, Université du Québec à Montréal.

SANKOFF, G. (2001), *Linguistic Outcomes of Language Contact*, in TRUDGILL, P., CHAMBERS, J. and SCHILLING-ESTES, N. (2001, eds.), *Handbook of Sociolinguistics*, Basil Blackwell, Oxford, pp. 638-668.

SAPIR, E. (1921), *Language. An introduction to the study of speech*, Harcourt, Brace and company, New York.

SCHLEICHER, A. (1853), *Die ersten Spaltungen des indogermanischen Urvolkes*, in «Allgemeine Zeitung für Wissenschaft und Literatur», August 1853.

SCHMIDT, J. (1872), *Die Verwandtschaftsverhältnisse der Indogermanischen Sprachen*, H. Böhlau, Weimar.

SCHUCHARDT, H. (1928), *Hugo Schuchardt-Brevier: Ein Vademecum der allgemeinen Sprachwissenschaft*, Niemeyer, Halle/Saale.

SNYDER, W. (2001), *On the nature of syntactic variation: evidence from complex predicates and complex word-formation*, in «Language», 77, pp. 324-342.

SPRUIT, M. R. (2005), *Classifying Dutch dialects using a syntactic measure*, in «Linguistics in the Netherlands 2005», pp. 166-179.

SPRUIT, M. R. (2008), *Quantitative perspectives on syntactic variation in Dutch dialects*, LOT, Utrecht.

STOWELL, T. (1981), *Origins of phrase structure*, Ph.D. dissertation, MIT.

STOWELL, T. (1982), *Conditions on reanalysis*, in «MIT Working Papers in Linguistics», 4, pp. 245-269.

SYVANEN, M. (1985), *Cross-species gene transfer: Implications for a New Theory of Evolution*, in «Journal of theoretical Biology», 112, pp. 333-343.

Syvanen, M. (1994), *Horizontal Gene Transfer: Evidence and Possible Consequences*, in «Annual Review of Genetics», 28, pp. 237-261.

Sugisaki, K. and Snyder, W. (2002), *Preposition stranding and the compounding parameter: a developmental perspective*, in Skarabela, B., Fish, S. and Do, A. H.-J. (2002, eds.), *Proceedings of the 26th Annual Boston University Conference on Language Development*, Cascadilla Press, Somerville.

Swadesh, M. (1952), *Lexico-Statistic Dating of Prehistoric Ethnic Contact*, in «Proceedings of the American Philosophical Society», 96, pp. 453-463.

Tagliavini, C. (1999), *Le origini delle lingue neolatine*, Pàtron Editore, Bologna.

Taylor, A. (1994), *The change from SOV to SVO in Ancient Greek*, in «Language Variation and Change», 6, pp. 1-37.

Thomason, S. and Kaufman, T. (1988), *Language Contact, Creolization, and Genetic Linguistics*, University of California Press, Berkeley.

Thomason, S. (2001), *Can rules be borrowed?*, Manuscript, University of Michigan.

Traugott, E. C. (1965), *Diachronic syntax and generative grammar*, in «Language», 41, pp. 402-415.

Traugott, E. C. (2005), *Exaptation and grammaticalization*, in Akimoto, M. (2005, ed.), *Linguistic Studies Based on Corpora*, Hituzi Syobo Publishing Co., Tokyo, pp. 133-156.

Traugott, E. and Dasher, R. (2002), *Regularity in semantic change*, Oxford University Press, Oxford.

Turkel, W. J. (2002), *The learning guided evolution of natural language*, in Briscoe, T. (2002, ed.), *Linguistic Evolution through Language Acquisition: Formal and Computational Models*, Cambridge University Press, Cambridge, pp. 235-254.

van der Auwera, J. (2002), *More thoughts on degrammaticalization*, in Wischer, I. and Diewald, G. (2002, eds.), *New reflections on grammaticalization*, John Benjamins, Amsterdam, pp. 19-29.

Wang, W. S.-Y. and Minett, J. W. (2005), *Vertical and horizontal transmission in language evolution*, in «Transactions of the Philological Society», 103, 2, pp. 121-146.

Weaver, R. and Hendrick, P. (1997), *Genetics*, William C. Brown Publishing, Dubuque, IA.

Weninger, S. (2001), *Vom Altätiopischen zu den neuäthiopischen Sprachen*, in Haspelmath, M., König, H., Oesterreicher, W. and Raible, W. (2001, eds.), *Language typology and language universals*, Vol. 2, de Gruyter, Berlin, pp. 1762-1774.

Weinreich, U. (1979), *Languages in Contact. Findings and Problems*, Mouton, The Hauge.

Weinreich, U., Labov, W. and Herzog, M. I. (1968), *Empirical foundations for a theory of langue change*, in Lehmann, W. and Malkiel, Y. (1968, eds.), *Directions for historical linguistics*, University of Texas Press, Austin, pp. 97-195.

Whinnom, K. (1971), *Linguistic hybridization and the 'special case' of pidgins and creoles*, in Humes, D. (1971, ed.), *Pigdization and creolization of languages*, Cambridge University Press, Cambridge, pp. 91-115.

Williams, G. C. (1966), *Adaptation and Natural Selection*, Princeton University Press, Princeton.

Witham, L. A. (2005), *Where Darwin Meets the Bible. Creationists and Evolutionists in America*, Oxford University Press, Oxford.

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