Biolinguistics and the Human Language Faculty

Anna Maria Di Sciullo, UQAM and Lyle Jenkins, Biolinguistic Institute

> *'The study of the biological basis for human language capacities may prove to be one of the most exciting frontiers of science in coming years.'' (Chomsky 1976)*

In recent years linguists have gained new insight into human language capacities on the basis of results from linguistics and biology. The so called 'Biolinguistic Enterprise' aims to fill in the explanatory gap between language and biology, both on theoretical and experimental grounds, hoping to reach a deeper understanding of language as a phenomenon rooted in biology. This research program is taking its first steps and it has already given rise to new insights on the human language capacity, as well as controversies, echoing debates that go back to the earlier days of generative grammar. The present discussion note provides a high-level characterization of Biolinguistics. It highlights the main articulation of this research program and points to recent studies linking language and biology. It also compares the Biolinguistic program, as defined in Chomsky 2005 and Di Sciullo & Boeckx 2011 to Jackendoff's 2002 and Culicover & Jackendoff's 2005 view of the human language faculty. It also identifies some misunderstandings emerging from the discussion in Jackendoff 2011.[*]

1. A high-level characterization of biolinguistics

Biolinguistics is the study of the biology of language. It aims to shed light on the biological nature of human language focusing on foundational questions, such as the following: What are the properties of the language phenotype? How does language ability grow and mature in individuals? How is language put to use? How is language implemented in the brain? What evolutionary processes led to human language, if any? These questions have been on the agenda in generative grammar since its beginnings (Chomsky 1965, 1976, a.o.); the Biolinguistic Program brings them to the forefront.

Core biolinguistic research is centered on the understanding of the properties of the human language faculty: the unique capacity for language in humans. Studies of the architecture and the operations of the language faculty and operations giving rise to the

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discrete infinity of language approach the biology of language from a theoretical linguistics perspective. (Hauser, Chomsky and Fitch 2002; Jenkins 2000, 2004, Di Sciullo et al 2010; Di Sciullo & Boeckx 2011; Berwick et al 2012, Boeckx and Grohmann 2013, a.o.). Biolinguistic research also covers experimental studies aiming to understand what differentiates human language from animal communication (Jarvis 2004; Fitch and Hauser 2004, Friederici 2009,d; Fitch 2010; Berwick et al. 2013, a.o.). Results from neuroscience point to the special properties of the human brain for language (Moro et al. 2001, Embick et al. 2000, Albertini and Moro 2012, Friederici et al. 2011). Studies on genetically based language impairments also fall into the realm of the biology of language (Wexler 2003, Ross and Bever 2004, Bishop et al. 2005, Hancock and Bever 2012, a.o.).

Language variation is another important area of biolinguistic research. While the properties of the language faculty are stable, variation is pervasive cross-linguistically. This is not surprising, given that language is a biological object and variation is a constant in the biological world (Cavalli-Sforza and Feldman 1981; Lewontin 2000). The Principle and Parameter model (Chomsky 1981) gave rise to a systematic approach to language variation and acquisition (Borer 1984; Rizzi 2000, 2009, a.o). According to this model, cross-linguistic variation follows from the setting of a limited set of options left open in Universal Grammar. More recent models of parametric syntax opened new avenues for the understanding of the language phylogeny (Bever 1981; Longobardi et al. 2011). Yet, other works address the question of why parameters emerge and why resetting of parameters occurs, as well as take into account the role of factors external to the language faculty in language variation (Di Sciullo 2011, 2012b, Di Sciullo and Somesfaean 2014; Holmberg et al 2013). Language variation arises from languages in contact as well as from language acquisition. While the poverty of the stimulus (Chomsky 2013) and the critical period (Stromworld 2007, 2008, 2010) point to the biological nature of language, theoretical approaches to language development stemming from works on population genetics (Niyogi 2006, Niyogi and Berwick 2009) opened new horizons for the study of language variation. These studies, as well as related ones, addressing central issues related to deterministic/probabilistic theories of language learning and language variation (Yang 2002, 2008, 2011), also qualify as studies of the biology of language in contact with experience.

The relation between the computational procedure of the language faculty and the principles reducing complexity has been part of the research agenda in the generative enterprise since the 1950's. Framed within biolinguistics, the principles of efficient computation are thought of as natural laws affecting the properties of the operations and the derivations of the (Narrow) Language Faculty (Chomsky 2005, 2011). They apply to syntactic derivations (No Tampering Condition, minimal search, phases), to the externalization of the linguistic expressions at the sensory motor interface (SM) (Pronounce the Minimum, Chomsky 2011), and at the conceptual intentional interface (CI) (Reference Set, Reinhart 2006; Local Economy, Fox 1999). Several questions arise regarding the principles of efficient computation, the so-called 'third factor' in language design in Chomsky (2005). One question is whether these principles relate to classical notions of complexity, including Kolmogorov's 1965 and whether the more articulate notions of Internal and External complexity are needed (Di Sciullo 2012d; 2014). Such fundamental questions on complexity and principles of efficient computation also fall into the domain of the biology of language.

Moreover, the unification between language, biology and the other natural sciences is an important aspect of biolinguistics. The understanding of the world proceeds by solving smaller puzzles and in parallel trying to unify the answers. In this regard, principles relying on symmetry, symmetry breaking and asymmetry may help to unify many areas of the sciences. An example of unification in mathematics is the Erlangen program, initiated by Felix Klein in 1872, which classified geometries using the tools of group theory (Klein 2004). In modern times we have the Langlands program, a body of mathematical conjectures, only a few of which have been proven, which seeks to unify apparently unrelated areas of mathematics (Gowers and Barrow-Green 2008). For example, the theory of elliptic curves (number theory) was shown to be connected to the theory of modular forms, as part of the proof of Fermat's Last Theorem by Wiles and Taylor (Singh 1997). As in the case of the Erlangen program, the Langlands program makes crucial use of the tools of symmetry theory (including representation theory) relying on the basic notions of symmetry and asymmetry. There are many other areas of mathematics in which symmetry plays an important role in understanding and unification. In physics Maxwell's theory of electricity and magnetism, along with the theory of light were unified in his theory of electromagnetism. Quantum mechanics in turn unified atomic physics with chemistry. The last frontier in unification is in biology. Of course, there had already been much unification. For example, it was shown that no vital force is necessary to describe the animate world. It was also shown that the same laws of biochemistry that held for the inanimate world could be extended to the organic world. And, of course, many physical principles carry over to the biological domain (such as conservation of energy) and are studied in the field of biophysics. Thus, principles relying on symmetry, symmetry breaking and asymmetry as well as other kinds of principles may help to unify many areas of biology, including the systems of the brain involved in language (Di Sciullo et al. 2010, Di Sciullo 2011, Jenkins 2013).

In sum, Biolinguistics relies on advances in theoretical linguistics, as well as on results from language acquisition and variation. However, it goes beyond linguistics, to biology, physics and chemistry, and asks the question why linguistic phenomena are the way they are. Conversely, results from biology, physics and chemistry serve as an impetus to the development of biolinguistically-grounded theories of the language faculty. This emergent field of inquiry seeks to close the explanatory gap between language and biology by asking the question of what the connection is between the two. The Biolinguistic program is in its early stages, working at present mostly via drawing inspiration and ideas from what we can learn from biology, physics and chemistry, as well as mathematics, and trying to formulate a linguistic theory along the same lines in hope that synergies will emerge or become more evident. In this way the biological study of language will find its place amongst the natural sciences.

In the following sections we discuss the three core aspects of biolinguistic investigation and point to recent studies linking language and biology. In the last section we compare two approaches to the human language faculty. We contrast the Biolinguistic approach developed in Chomsky 2005 and Di Sciullo & Boeckx 2011 to Jackendoff's 2002 and Culicover & Jackendoff's 2005 view and we identify some misunderstandings emerging from the discussion in Jackenfoff 2011.

2. Biolinguistic investigations

Biolinguistic investigations aim to reach a better understanding of the human capacity for language. This capacity can be understood in terms of Chomsky's (2005) three factors that contribute to the growth of language in the individual.

(1)　　A. Genetic endowment
　　　　B. Experience
　　　　C. Principles not specific to the faculty of language

The first factor of language growth in the individual narrows down the possible answers to the following question: What is the nature of the human capacity for language? This capacity stems from the human genetic endowment as several studies in genetics indicate. Exactly what genetic configuration is at stake is still to be discovered, however. Several works in theoretical linguistics define models of the language faculty and their architectural properties. A first goal of the biolinguistic program is to define the computational procedure of the human language faculty as stemming from the human genetic endowment.

While there is only one human language faculty, there are many different languages in the world. The second goal of biolinguistic investigations is to reach a better understanding of language variation, as a consequence of the interaction of the language faculty with the environment. Languages vary within the limits imposed by the computational procedure of the language faculty, whose core properties do not change though time. Several works investigate the hypothesis that cross-linguistic variation is an effect of language acquisition and experience triggering binary choices in the feature structure of functional categories.

The computational procedure of the language faculty derives complex expressions and Biolinguistic investigations aim to further our understanding of the factors reducing complexity. As human language is part of the natural world, it is reasonable to expect that these factors interact with the computational procedure of the language faculty. Understanding the effects of these factors, which can be thought of as natural laws affecting other biological organisms, falls naturally within biolinguistic investigation.

Given the cross-disciplinary nature of this field, different methods are used to confirm or refute biolinguistic hypotheses, including standard methods in generative grammar, experimental methods using behavioral and neuro-imaging techniques, as well as computer-based methods. For example, linguists study variation to determine the kinds of permissible variation across languages to separate out the effects of principles of universal grammar from parametric variation (macroparameters and microparameters) (Cinque & Kayne 2005, Cinque and Rizzi 2010). Models of language acquisition can be tested in normals and in children with language disorders, as in the case of the KE family, discussed below (Di Sciullo et al. 2010; Wexler 2004). Statistical models can be applied to the acquisition of parameters in order to develop learning theories for

language (Yang 2004a; Yang 2004b). Finally, some inferences about evolution can be made by comparative studies with other species on both the anatomical level (Sherwood, Broadfield et al. 2003) and the genetic level (Sun and Walsh 2006), and by modeling evolution in dynamical systems theory (Nowak, Komarova et al. 2001).

3. The three factors

Biolinguistic investigations explore the biological basis of language, language development in ontogeny and in phylogeny, the effects of external efficiency principles on linguistic derivations in order to fill the gap between language and biology. The following paragraphs provide further details each one of the three factors in language design.

3.1 Genetic endowment
3.1.1 FOXP2

The human capacity for language is part of the human genetic endowment; however, its genetic underpinning is yet to be discovered. This can be seen in the work on the *FOXP2* gene, and its mutation in the KE family. *FOXP2* was the first gene associated with a language disorder which could be analyzed at the molecular level and is probably the most studied (Marcus and Fisher 2003; Fisher and Marcus 2006http://dx.doi.org/10.1038/nrg1747). However, it is important to point out the usual caveats when discussing genes and language that "the" gene for language does not exist. We now know that most genetic disorders can result from a combination of interactions of many different genes and regulatory elements. The ENCODE Project Consortium (2012) has now published a large database of regulatory elements in non-coding regions of DNA in the human genome to aid in deciphering these gene interactions.

When one has a genetic disorder, it is important to characterize the phenotype for the disorder. In the case of *FOXP2* a speech impairment was noted in a family (called the KE family) in which the patients had problems in a number of areas, including pronunciation, syntax and semantics (Hurst 1990). Additional studies of the phenotype were carried out, including on the difficulties in syntax/morphology (Gopnik et al. 1991) and on the difficulties with articulation. It was found that some of the difficulties in articulation derived from problems with verbal sequencing (Alcock et al. 2000). It was found that the pattern of inheritance of the disorder was autosomal dominant so that only one copy of the gene mutation was necessary to trigger the impairment. The next step was to determine, in parallel with studies of the phenotype, the locus of the gene; i.e., what chromosome the gene was located on. Mapping studies led to the discovery of the gene locus on chromosome 7 (known as 7q31) (Lai et al. 2001). Once the gene was isolated, the DNA sequence of the gene could be determined. Now it was possible to ask whether the same or other mutations were found in other families. Additional mutations, including point mutations and translocations, were discovered (Macdermot et al. 2005). In addition, it was possible to deduce the protein sequence. It was found that the protein contains a particular kind of protein motif and belonged to a known family of proteins containing a forkhead box (FOX) domain, so the protein was named FOXP2. It was

deduced that the function of the protein FOXP2 was that of a "transcription factor," meaning that it was involved in controlling other genes. The next question was what the targets for FOXP2 might be; a number of candidate genes were identified (Konopka et al 2009). In addition, studies were undertaken to determine in what areas of the brain FOXP2 was expressed in (Lai et al. 2003). It is of interest to compare the *FOXP2* gene and protein product in other species; this was done in some non-human primates, in the mouse and in songbirds, among other species (Scharff and Haesler 2005). This allowed one to pose questions such as how strongly the gene was selected for in evolution (Enard et al. 2002). Earlier this year Hilliard et al. (2012) reported that they had "found ~2,000 singing-regulated genes …in area X, the basal ganglia sub-region dedicated to learned vocalizations. These contained known targets of human FOXP2 and potential avian targets."

Another disorder affecting language semantics was recently reported (Briscoe et al. 2012). Eight members of a family over four generations had difficulty with mapping word meanings to concepts; e.g., substituting "tripod" for "stool" or "evolving" for "breeding." Preliminary work indicates that the disorder could be due to a single genetic mutation. The family members reported that they had long had problems in school and at work and were aware that they could not easily follow the plot narration in books or on TV. Reduced grey matter was found in neuroimaging studies in "a brain area known to be involved in the interaction between language and semantic systems" (the posterior inferior portion of the temporal lobe). The researchers consider this case to be "the first example of a heritable, highly specific abnormality affecting semantic cognition in humans." Genetic studies of the kind discussed earlier for *FOXP2* are to be carried out.

Ultimately, of course, we wish to link work on the genetics of language to neural circuits in the brain. As we work bottom-up from the level of the gene, we simultaneously work top-down to understand the brain. From this point of view and for the time being, work in theoretical linguistics can reveal much more to us about the nature of the language faculty than FOXP2 can. In addition, one can learn much from the study of language disorders, including genetic disorders, as we discussed earlier — aphasia, dyslexia, etc. Other perspectives on the organization of brain and language are provided by work on sign language, pidgins and creoles, split brains, bilingual brains, savants, and computational modeling (e.g., parsing). One can combine linguistic studies with other tools, such as imaging (e.g., fMRI, MEG, diffusion tensor imaging, etc. (Shapiro et al. 2006)). Thus one can study language on different levels – the functional, anatomic, cytoarchitectonic and molecular levels (Geschwind & Galaburda 1984; Geschwind & Galaburda 1987; Grodzinsky & Amunts 2006; Hugdahl and Westerhausen 2010). For a review of research at the neural circuit level, with an emphasis on asymmetry, see Concha, Bianco et al. (2012). Note that all the kinds of studies above can be done as part of developmental studies, to answer the question about how language develops (or grows) in the child.

Thus, *FOXP2* was believed by some to be a 'language gene', until homologous genes were found in other species. However, the fact that the human species is the only one that developed natural language, suggests that there are genetic properties, or combinations of properties, yet to be discovered, which are specific to human language. Moreover, given our knowledge of the initial stages of human embryogenesis, it is reasonable to think that the language ability grows and matures in individuals as a biological organ. The fact that the critical period for language growth in the individual is

anchored in time, around puberty (Stromswold 2007, 2008, 2010), also indicates that the language faculty is a biological organ, with a determined time span for full development, under normal conditions. Finally the poverty of the stimulus to which the child is exposed and the fact that (s)he typically does not make ''mistakes'' that violate core structure dependency principles (Chomsky 2013) also point to the human biological predisposition for language growth.

3.1.2 Merge

The human capacity for language, as part of genetic endowment, has been studied in linguistics in terms of models of Universal Grammar in early generative syntax, and in terms of the language faculty in the Minimalist Program. Results stemming from linguistics are an important part of biolinguistic investigations.

The investigation of the properties of the language faculty -- Merge and its computational properties, such as binarity, recursion and (a)symmetry -- reveal properties that must be accounted for by some physical mechanisms, which may be (partially) related to analogous mechanisms in other domains of biology, or may possibly not yet have been discovered.

While there is a general consensus on the existence of the language faculty, there are lively debates on the specific articulation of its components, their connections and the properties of the operations and the computational procedure generating linguistic expressions. We will consider the hypotheses formulated in the Minimalist Program (Chomsky 1995 and related works). This research program focuses on the properties of the narrow language faculty, the purely syntactic component enabling humans to relate sound and meanings. The architecture of the language faculty in this research program is represented in (2), where narrow syntax (NS) relate sounds, legible at the sensorimotor interface (SM), and meaning, legible at the conceptual-intentional interface (CI), in order to express complex thoughts.

(2)

    NS
    /\
  CI   SM
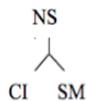
The Minimalist Program aims to provide a model of the language faculty applying the methodological principle of parsimony. That is, a model of the language faculty, where narrow syntax consists of a very limited set of operations and internal interface conditions. The Minimalist model of the language faculty is likely to have qualitative advantages over more complex models, such as the Government and Binding model (Chomsky 1981) on methodological grounds. The principle of parsimony prevails in this research program, as it does in the other sciences. It is also preferable to other models on evolutionary grounds. If language emerged from a small biological change leading to a rewiring of the brain, this might suggest that the architecture of the language faculty was reduced to a minimum required to relate sound and meaning and the operations of the language faculty must be very limited in number. Ideally, they would be reduced to only one simple operation. Merge is the basic combinatorial operation capable of deriving the discrete infinity of language. It is necessarily a part of the computational procedure

of the language faculty. Merge is a binary operator that takes two syntactic objects *a* and *b* and derives another syntactic object consisting of the two objects that have been merged. A binary operation is preferable to an n-ary operation on both theoretical and empirical grounds. It restricts the choices of combinations between syntactic objects to a minimum, as well as derives constituents that are motivated by syntactic and prosodic properties. This is not the case for operations deriving n-ary structures. In (3), Merge (M) derives the set {a,b} whose elements a and b are unordered, in (4), Merge derives an ordered set <a,b>, where a precedes b. Set-Merge introduces arguments and Pair-Merge introduces adjuncts in Chomsky (2000). Whether Merge is free or subject to constraints is under investigation (Chomsky 1995, 2011, Frampton and Gutmann 2002, Di Sciullo and Isac 2008, Boeckx 2010, Kayne 2011, a.o.). Whether free or not, Merge is a binary operation. This basic combinatorial operation applies to objects that have not been merged in a previous step of a derivation. Call this instance of Merge, External Merge, (5). Merge may also apply to objects that were already merged in previous stages of a derivation in order to remerge a given object. Call this instance of Merge Internal Merge, (6).[1]

(3) M(a,b) : {a,b}
(4) M(a,b) : <a,b>

(5) ∧
　　 c ∧
　　　 a b

(6) ∧
　　 c ∧
　　　 d ∧
　　　　 e̶ ∧
　　　　　 a b

Merge has been proposed to derive morphological structures in Distributed Morphology (Hale and Marantz 1973, a.o.), and I-Morphology (Di Sciullo 2005, 2014, a.o.). In these theories the basic combinatorial operation, Merge, may also combine already derived trees. Thus the generative capacity of Merge, initially proposed for syntactic merger, extends to morphological merger in specific ways.

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[1] The formal simplicity of the central operation of the language faculty can be appreciated by contrast with the rules proposed in earlier models in generative grammar. In Chomsky (1955, 1957) a set of phrase structure rules derived kernel sentences. Transformational rules, such as passive and affix hopping, were applied to kernel sentences and the former were combined using generalized transformations. The Aspect Model (Chomsky 1965), the 'Standard Theory', developed into the 'Extended Standard Theory' (Chomsky (1970) and still included several sorts of syntactic rules (see Emonds' 1976 typology of transformations). In the Government and Binding Model (Chomsky 1981), phrase structure rules were subsumed under the two meta-rules of X-bar theory, and the transformations were subsumed under move NP and Move WH, and unified further into 'move α' where α is a category. With the Minimalist Program, X-bar theory and the Move α modules, along with the other modules of the grammar, were subsumed under Merge.

Merge derives hierachical structures recursively. The human capacity for language must rely on a recursive procedure able to derive the discrete infinity of language. Recursion, as defined in (7), is a property of Merge, which may reapply to its own output, as the derivation in (8) illustrates for External Merge. Internal Merge implies the displacement of categories that will be properly included in the resulting binary branching hierarchical structure. This is illustrated in (9) from Di Sciullo and Isac (2008) with the displacement of the DP subject in the specifier of vP to the specifer of TP. In (9), the proper inclusion relation also holds between the set of features of the items undergoing Merge. Thus, in the merger of Num with NP, the set of features of Num is the superset and the set of features of NP is the proper subset, and so on for the other steps of the derivation. The proper inclusion relation is an asymmetrical relation, as if *a* is the proper subset of *b*, *b* is not the proper subset of *a*. That structural and feature asymmetry is part of syntactic derivations and is expected if properties of relations, including asymmetry are core properties of the computational procedure of the language faculty.

(7) Recursion: the property of a rule to reapply to its own output

(8) Merge (a,b) : {a,b}
    Merge (c, {a,b}) : {c, {a,b}}
    Merge (d {c, {a,b}}) : {d {c, {a,b}}}

(9)
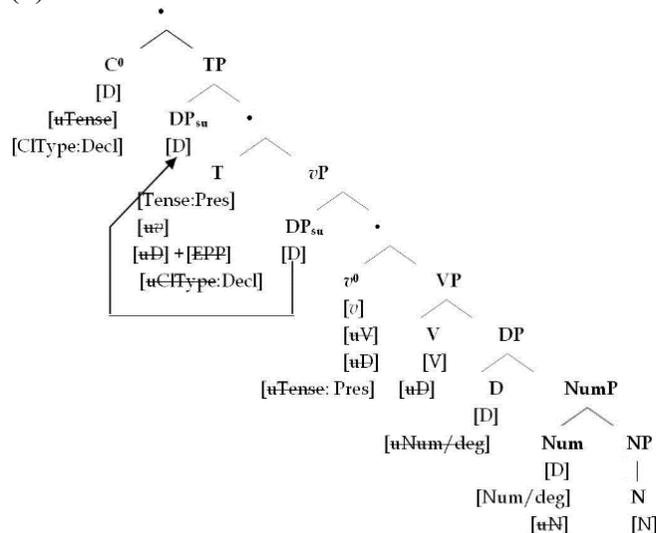
Merge is especially important for the study of the biology of language, as the human language phenotype can be thought of as being the hierarchical structures derived by Merge. This is a biolinguistic reason for why it is important to understand its properties.

According to Chomsky, Hauser and Fitch (2002) unbounded recursion is unique to human language. There is no limit on the number of words in a sentence. This view has been challenged in several works, including Jackendoff (2011). It has been claimed, for example, that recursion is also part of other human cognitive faculties, and that recursion is also found in communication systems in non-human primates for example. However, the definition in (7) would not apply to other human cognitive faculties or to

other natural systems if there is no other object like language in the natural world. The kind of recursion found in language would not be found elsewhere in the biological world.

It is useful here to distinguish recursion from iteration in order to appreciate the hypothesis that recursion is a unique property of the language faculty. Chomsky's (1956) Hierarchy of formal grammars provides a ranking of the expressive power of grammars according to a scale of increasing complexity (Type 0 (Turing equivalent (context-sensitive (context-free (finite-state))))). The languages described by these grammars are classified according to a subset relation, and each language has a corresponding class of machine that recognizes it (Turing machine (linear bound automaton (pushdown automaton (finite state machine)))). Tail recursion can be simulated by iteration in Finite State grammars; however, this is not the case for center embedded recursion.

A finite state grammar may generate sentences in a linear word-by-word sequence. And the finite state automaton is a machine that generates a string of words linearly ordered by the actions of the automaton from an initial state to a final state passing through intermediate states. This is illustrated in (9), where the finite-state automaton derives the string *Pat's happy Leslie's happy Lee's happy*.

(10)
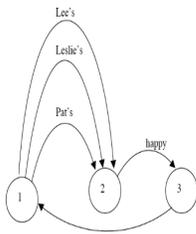
Lasnik (2011: 361) points out that n-ary branching structure may underlie structures including stacked adjectives, e.g., an *old old old … document*, that can be derived by finite-state grammars. He also references work by Morris Halle on word internal recursion, e.g., *anti missile missile, anti anti missile missile missile, …* , requiring the generative capacity of context-free grammar. Several works going back to the 60s (Bar-Hillel and Shamir 1960, Carden 1983, Langendoen 1981, Shieber 1985) discuss recursion in word structure, which also requires the power of a context-free grammar for their generation. Given that context-free grammar properly includes finite state grammars in Chomsky's Hierarchy, finite state iteration can be derived by context-free recursion. However, this is not the case the other way around.

There are major differences between finite-state and context-free grammars. In contrast to finite-state grammars, context-free grammars apply to elements projecting categories, they derive constituents and hierarchical structures, and they keep track of the number of constituents of a certain category that have been generated.

Finite state grammars are more limited than phrase structure grammars with respect to recursion. A finite state grammar may simulate recursion by iteration if a recursive node occurs at the right or at the left edge of a phrase structure grammar, but not if a terminal node is located on both sides. In other words, tail recursion (rightward or leftward recursion), can be simulated by iteration with finite state grammars. However, finite state grammars do not have the descriptive power to generate center

embedded recursion, which is found in human languages, but in no other biological systems. The results of the experiments conducted by Fitch and Hauser (2004) with cotton top tamarins indicate that non-human primates are able to learn finite state grammars, deriving linear sequences, but not phrase structure grammars, deriving hierarchical structure. The fact that unbounded center-embeddings can be generated in syntactic derivations makes the language faculty a unique biological object. Friederici (2009) points to specific areas in the human brain for processing language (BA$_{44}$, BA$_{45}$B) that are also present in the macaque brain (Petrides and Pandya 1994), albeit with more limited size and granularity.

> *'[...] the human ability to process hierarchical structures may depend on the brain region which is not fully developed in monkeys but is fully developed in humans, and that this phylogenetically younger piece of cortex may be fundamentally relevant for the learning of the PSG.'* *(Friederici 2009: 185)*

Assuming that the results of these experiments are robust, while iteration would not be a uniquely human property of the Language Faculty, recursion would be.

Neuroimaging experiments (Embick et al. 2000, Moro et al. 2001, a.o.) investigate whether recursive syntactic (hierarchical) computations activate a dedicated network in the human brain. Results from recent experiments reported in Chesi and Moro (2012) indicate that "the theoretical distinction between recursive vs. non-recursive rules is reflected in brain activity. More specifically, the activity of (a deep component of) Broca's area within a more complex network including subcortical elements such as the left nucleus caudatus appears to be sensitive to this distinction as the BOLD signal is increased in this area only when the subjects increase their performance in manipulating recursive rules.''

While there is no other object like human language, the investigations of language as a biological object may lead to the discovery of unique properties of language. For example, recursive processes are observed in biology, including cell duplication and morphogenesis, see figure 1.
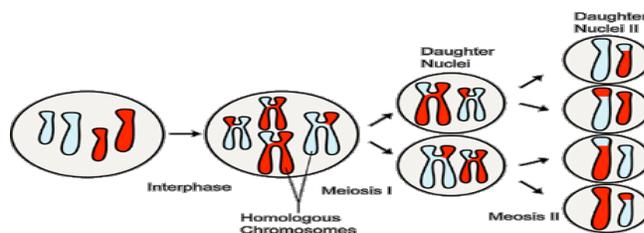
Figure 1: Cells duplicate by dividing in half, with both halves containing all the necessary DNA information of the organism. Thus, 1 cell becomes 2, then they divide and become 4, they divide to make 8, then 16, 32, 64, 128, 256, etc.

The recursive merger of two linguistic objects deriving a more complex object differs from cell duplication and morphogenesis, where a single cell separates into two cells. Furthermore, it is unclear whether the different sorts of recursion in language, including

tail and center embedded recursion have correlates in biology. Tail recursion and center embedded recursion are observed in human language. Tail recursion is the recursion of a constituent to the right or to the left of another constituent (rightward or leftward recursion). Center-embedded recursion is the recursion of a constituent within another constituent, e.g. *[cp the bug [cp the programmer found] is not fixed]*. In addition to the recursion of Merge, recursion is also thought of as a procedure of replication of the same. Considering sentential embedding, three phenomena have been taken as instantiating recursion: the embedding of adverbial clauses in other adverbial clauses, nonfinite complementation in causative constructions, and long-distance wh-movement. Phrasal recursion includes PP modification, relative clauses, phrasal conjunction and disjunction. Here again, correlates with biology are yet to be identified. It might be the case that recursion in language is mediated by a (covert) functional category, as discussed in Di Sciullo 2005, 2010, 2013. Languages vary with respect to the pronunciation of this functional category. For example, in Brazilian Portuguese, a prepositional element must be pronounced in deverbal compounds such as *controle de passaporte, ponto de controle de passaporte*, whereas the functional element is silent in other languages, such as Italian *controllo passaporto, punto controllo passaporto* and English *passport control*, *passport control point*. Likewise for complex numerals, a conjunction or another functional item, a prepositional element or case is overt in certain languages, for example, in Romanian additive and multiplicative numerals, (11), or in Arabic, where morphological case is pronounced, (11). These and other facts suggest that in natural languages recursion of constituents of the same categorical nature would be mediated by a functional projection, (12). In the case of complex numerals, the functional head in (12), whether it is a conjunction, (11a), a prepositional element (11b) or morphological case, (12), is the locus of unvalued NUM features, to be valued in the course of the derivation, as well as interpretable ADD and MULT features, (13), as argued in Di Sciullo (2012c).

(11)   a. douăzeci   şi unu (Ro) (Di Sciullo 2012c)
              twenty   and one
              'twenty one'
        b. două sute   de mii   de cărti
              two hundred-PL DE thousand-PL DE books
              'two hundred thousands books'

(12) a. arba –**u**   aalaaf- –**in**   rajul-**in** (AR) (Zabbal 2005)
          four-NOM thousand-GEN men-GEN
          '4000 men'
     b. arba –at-**u** aalaaf-   –**in**   wa- xams-u   mi at   -in rajul-in rajul-**in**
          four-NOM thousands-GEN   and   five-NOM hundred-GEN men-GEN
          '4500 men'

 (13)

```
      NumP                      NumP
      /  \                      /  \
 Twenty   FP                  two    FP
 [Num]   /  \                [Num]  /  \
       F     two                  F      hundred
    [ADD]   [Num]              [MULT]   [Num]
    [uNum]                     [uNum]
    [uNum]                     [uNum]
```
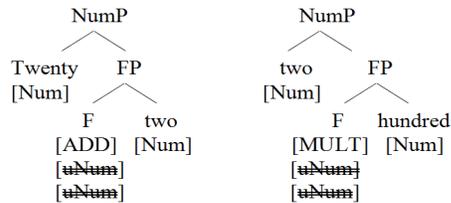
It is unclear however what the biological correlate of the functional projection bringing about the typical asymmetrical hierarchical structure of linguistic expressions would be. However, specific properties of recursion are expected in language. We agree with Jackendoff's 2011 statement that recursion is not unique to language. Indeed, it is not, but recursion in language has specific properties that may or may not be found elsewhere in the mind/brain or nature. Further work on asymmetry in language and biology may reveal elements that would bridge the gap here as well. For example, the asymmetrical recursion observed in human language could be related to the properties of cell division and morphogenesis. According to Montell 2008, the asymmetry responsible for how cells move and divide. Montell (2008) notes that asymmetry explains morphogenetic dynamics:

" It is probably generally the case that signalling pathways [...] function to localize mechanical forces asymmetrically within cells. By definition, an asymmetry in force will cause dynamics.'' (ibid. 1505).

 Such parallels should be taken with caution, however, as the asymmetry that brings about cell movement and division cannot be readily equated with the asymmetry of phrasal projection and displacements. Asymmetric relations are central in language and in biology in ways still to be detailed.

Thus, binarity, recursion and asymmetry are at the very core of language and biology. There is no one to one mapping between binarity, asymmetry and recursion in language and biology. However, further understanding of these properties may contribute to fill the explanatory gap between language and biology.

3.2 Experience

Language growth and maturation in the individual requires experience. This gives rise to the following questions. Did the human capacity for language evolve? Was it the result of an evolutionary leap? While there is a consensus on the role of experience in language growth, there are different views on these questions, as well as extensive debates on the "origin of language''. The following paragraphs single out the main claims of the gradualist and the emergent views on the topic.

According to the gradualist view (see Bickerton 1990, 1998, and the Continuity Paradox), language evolved from proto-language, which is an intermediate step in the historical development of language, which is often represented in terms of linear precedence in historical stages: pre-syntactic stage > proto-syntax stage > modern syntax. While there is no direct evidence for these historical stages, there are several hypotheses on the properties of each one of these stages aside from the simplistic view
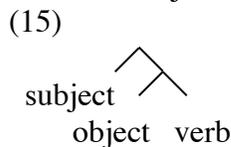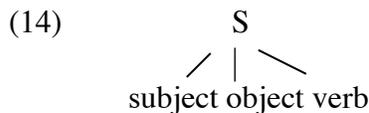
that the pre-syntactic stage consists of one-word expressions and the proto-syntactic stage consists of two-word expressions. Theories of proto-language differ. According to Bickerton (1990), in proto-language, although words may have been uttered in short sequences, there were no rules defining well-formedness of strings, and therefore words in proto-language could not be said to belong to separate syntactic classes, such as Noun or Verb. Some theories of proto-language relate to the development of subject-predicate relations, (Gil 2011). Other theories take proto-language to be limited to concatenation of predicates only. According to Hurford (2001) proto-thought had something like predicate calculus, but had no quantifier or logical name. Jackendoff (1999, 2002) proposed that the relatively flat (non-hierarchical) structure of adjuncts, as well as the raw concatenation of compounds, still retain a bit of proto-linguistic flavor. Progovac (2010) proposed that English V-N compounds such as *dare-devil* should be analyzed as syntactic 'fossils' of a previous stage of syntax, now co-existing with more complex syntactic constructions (see also Bickerton 1990, 1998, for the notion of linguistic 'fossil'). For Jackendoff (1999, 2002), minimal syntactic specification, and extensive involvement of pragmatics are the hallmarks of what have been proposed to be syntactic fossils. Proto-language involves flat structure derived by concatenation or adjunction but not binary branching hierarchical structure. Basically, proto-language is a kind of communication system with no syntax.

According to the emergent view of language development (Chomsky 2008, 2011, Berwick and Chomsky 2011, Di Sciullo 2013, Hauser et al. 2014, a.o.), language did not evolve from previous, simpler forms, or ''proto'' languages, but emerged in its entirety. The emergence of language in humans would probably be due to a minimal change in the human brain. There is no proto-language, nor a preceding pre-syntactic (one word) stage in language evolution. The language faculty emerged late in historical development, and its main operator is Merge. Merge is a binary operator deriving expressions that can be represented in terms of hierarchical binary branching structures. According to this view, language did not start from something simpler, and it did not evolve from simpler stages to more complex stages. In a recent review article, Hauser et al. (2014) argue that language evolution is still a mystery, notwithstanding the 40 years of research on the origin of language and the processes that led to change. The authors discuss four approaches to the evolution of language: comparative animal behavior, paleontology and archeology, molecular biology and mathematical modeling, and point out that the so -called "progress" in these areas is not supported by strong evidence and offers no explanation of why and how the human capacities for language evolved.

The two views of the origin and the development of language make different predictions for the properties of first language acquisition, as well as for language historical development. The gradualist view predicts that languages become more complex as they evolve in time (Hurford c). This is not the prediction made by the emergent view of language, according to which the language faculty is stable, and does not change through time. On the contrary, given the effect of the third factors reducing complexity, there is a reduction of the computational load, which may lead to the minimization of the length of derivations and the pronunciation of certain constituents (Di Sciullo 2011, and related works). These two predictions are under scrutiny, and preliminary results discussed in section 3.3 suggest that the second view is to be preferred to the first on empirical grounds.

Similarly for language acquisition, the first hypothesis predicts that the child's

knowledge of language develops mainly on the basis of exposure to data. The second hypothesis predicts that the child is genetically determined to learn any natural language (s)he is exposed to without formal instruction. The computational procedure of the language faculty is not occurrence or string-dependent and the second hypothesis predicts that the child typically will not make errors that contravene structure-dependent constraints. Such predictions are outside of the realm of the first hypothesis. Further support for the second hypothesis comes also from experimental results on the perception of functional elements by infants, including determiners and demonstratives, indicating that infants have the ability to perceive functional structure notwithstanding the fact they do not produce functional categories in their speech (Shi, Werker and Cutler 2006, Shi 2007, Shi and Lepage 2008). In the emergent view of language, the lack of overt functional elements in infants' speech, as well as the absence of overt functional structure in certain ancient languages and in creoles do not lead to the conclusion that functional structure evolves from a state where functional structure was lacking. Covert functional structure is already in place to begin with and it is necessary to account for the properties that so-called "proto'' languages share with modern languages. For example, languages with apparent free word order at the clause level, such as Warlpiri, a central Australian aboriginal language, were thought of as being non-configurational languages, with a flat phrasal structure, (14), instead of the hierarchical structure, (15).

(14)   S
                      ╱ │ ╲
              subject object verb
(15)
               ╱╲
     subject ╱ ╲
          ╱╲
      object   verb

Several works showed, however, that Warlpiri's clause internal relations between anaphors and their antecedent are subject to the same configurational restrictions observed in other languages, including English (Hale 1983, Simpson 1991, Legate, 2002, a.o.). For example, non-finite complementizers supplete according to the grammatical function of the controller of their PRO subject, as discussed in Hale (1983, 1995). Furthermore, both Binding and Control, defined on the basis of the asymmetrical c-command relation, as in Chomsky (1981, 1995, a.o.), indicate that Warlpiri's syntax is not different from any other language with respect to configurationality.

Merge recursively derives binary branching hierarchical structures. It is simpler on formal grounds than operations deriving n-ary structures. It correctly derives the asymmetrical relations between the constituents of linguistic expressions. It is also motivated from an evolutionary developmental perspective. According to the emergent view of language, the language faculty emerged a few thousands years ago, as a consequence of a minimal change in the wiring of the brain. It emerged at a point in time where other cognitive structures were already in place. From this perspective, Merge could not have proto-Merge, a concatenating operation, as its predecessor. The concatenation operation is formally distinct from Merge. Furthermore, if the language faculty is human specific and non-human primates can learn to produce expressions

equivalent to proto-language, viz., flat structures generated by finite state grammars, then proto-language is not the predecessor of language. Proto-language is not conceivable in an emergent view of the language faculty.[2] In contrast, Merge elegantly expresses the combinatorial capacity of the language faculty, as represented by hierarchical structures. Experience, while a necessary factor in language growth in the individual and development in time, does not affect the core properties of the central operations of the language faculty, which do not change through time.

3.3 Factors external to the language faculty

Chomsky suggested a few candidates for the so-called ''third factor''; viz. "principles of data analysis that might be used in language acquisition and other domains, principles of structural architecture and developmental constraints that enter into canalization, organic form, and action over a wide range, including principles of efficient computation." Since language is a computational system, Chomsky suggests that principles of efficient computation might "be of particular significance."

Several works in mathematics and in computer sciences provide methods to measure the complexity of expressions, including strings of characters (Kolmogorov 1965). Linguistic expressions are not strings of characters, and their complexity goes beyond the number of characters, lexical items or phrases they include. The question arises whether standard complexity metrics are of any relevance for measuring the complexity of the expressions derived for the operations of the language faculty. Chomsky's 1956 hierarchy of formal grammars provides a basic tool to evaluate the complexity of languages on the basis of generative capacity. Several works on human animal studies use this hierarchy as a baseline. Earlier works in psycholinguistics (Fodor, Bever and Garrett 1974) focus on the computational load associated with the application of the operations of the grammar. The recursive operations of the language faculty bring about complexity that can be tractable by the human brain up to a certain limit imposed by other sub-systems of the brain, including memory (Miller and Chomsky 1963, Chomsky and Miller 1986, Bever 1970, Kimball 1973, a.o.). The investigation of complexity in language and in other biological systems falls in the domain of biolinguistics. Current research (Chomsky 2011) suggests that principles of efficient computation may very well be reduced to natural laws, operative in other natural systems.

We would like to suggest symmetry breaking as another third factor candidate. Symmetry breaking is not specific to language or to any other cognitive domain for that matter. It is ubiquitous throughout the natural sciences.

---

[2] There is an alternative view of proto-language mentioned by an anonymous reviewer. According to this view, the modern language faculty developed (not gradually) but in three semi-discrete leaps forward—for example, External Merge of a predicate and its arguments, then clausal embedding, then movement/Internal Merge. That could, according to the reviewer, be still more like an emergent picture than a gradualist picture, but it would yield a well-defined sense of proto-language: the language that resulted after the first one or two leaps forward would be proto-language. The alternative the reviewer suggests is a more articulated notion of protolanguage that has already been proposed by linguists. However, it does not seem plausible either on simplicity grounds. Restricting Merge to External Merge in previous historical stages of language evolution, is a complication, an unnecessary stipulation.

In addition to applications in physics and biology, symmetry breaking has applications in language; moreover, it also contributes to bridge the explanatory gap between language and biology.

In theoretical linguistics, Moro (2000) proposed that points of symmetry can be derived in syntax; for example, in the case of direct and inverse copular constructions, where displacement of one or the other constituent of the small clause in the domain of the copula must be displaced in order to break the symmetry. Di Sciullo (2005) showed that points of symmetry never arise in morphology, as morphological operations combine objects whose internal structure is already asymmetrical. Word-structure is asymmetrical in the sense that its parts cannot be reordered without destroying the integrity of the structure. This might be possible, however, in syntax, where the ordering of the constituents with respect to a head could be integrity preserving. Chomsky (2012) relies on symmetry breaking in order to derive the effect of the EPP, according to which the subject generated within the verbal projection vP must raise to the specifier of TP.

Symmetry breaking is part of the factors reducing the complexity that arises in language diachronic variation under the influence of language acquisition, languages in contact as well as pragmatic factors. The Directional Asymmetry Principle, (16) is part of the principles reducing complexity, and has been proposed on the basis of the historical development of possessive pronouns in Greek and in Italian. The DAP, having correlates in evolutionary developmental biology, reduces the complexity that arises in the development of functional elements in the extended nominal projection,[3] alongside other principles of efficient computation. These principles include Minimal link: Limit the search space. (Chomsky 1995), Pronounce the Minimum: Limit the externalization. (Chomsky 2012), Minimize length of derivations: Limit the computation. (Di Sciullo 2012d) and Minimize symmetry: Limit the choice points. (Moro 2000, Di Sciullo 2005).

(16)   *Directional Asymmetry Principle* (DAP) (Di Sciullo 2011)
        Language development is symmetry breaking.

The predictions of the DAP have also been validated on the basis of the historical development of the definite determiner from Old to Modern Romanian (Di Sciullo and Somesfalean 2013, 2014), as well as on the basis of the historical development of prepositions in Indo-European languages (Di Sciullo and Nicolis 2012). For example in both the development of English and Italian, fluctuation in the pre and post position of the pronominal complement of the preposition is observed in earlier stages of these languages, whereas only the prepositional variant remains in Modern English and Italian. While both orders (17a) and (17b) are attested in Old English, this is no longer the case in Middle English as well as in Modern English, where a pronoun may only follow a prepositional head.

(17) a. Þa his gebroþru **to him** comon (O.E.)
         when his brethren to him came

---

[3] The DAP is not reducible to a processing constraint, such as the Maximize On-line Processing (MaOP), proposed in Hawkins 2004 given that the variation in word order is observed with adjacent constituents.

'When his brethren came to him'
  (cocathom1,ÆCHom_I,_21:346.24.412)
  b. ...oððæt se halga gast **him to** com
      until   the holy spirit him to came
      '... until the holy spirit came to him'
      (cocathom1,ÆCHom_I,_21:346.24.412(7))

Likewise, the analysis of Boccaccio's Decameron and of a 13th century Old Florentine corpus *TLIO* reveals that P uniformly precedes its complement except in the case of the preposition *con*, where monosyllabic personal pronouns are cliticized onto the preposition (*meco*, *teco*, *seco*), (18), (19). Instances where *con* precedes a monosyllabic personal pronoun are also attested, (20). In this diachronic phase (13th 14th c) *meco, teco, seco* appear more often without *con* than with *con,* (21). Modern Italian attests exclusive pronominal use of *con*, e.g. *con me, con te, con se*.

(18) …. e per li compagnoni che **teco** fuggiro , per li dei... (Brunetto, Rettorica)
(19) neiente de lo mondo ; **con te** le tue, parole voria conte avere...
                                        (Rinuccino, Sonetti)
(20) E perciò ch' io so bene ch' assai val meglio che tu parli **con teco**, che né
      io né altri , sì fo io fine alla mia diceria. (Brunetto, ProLigario)
(21) Non ti dar malinconia, figliuola, no, che egli si fa bene anche qua;
      Neerbale ne servira bene **con esso teco** Domenedio.
                                        (Boccaccio, The Decameron)

The DAP is not a global principle of the directionality of diachronic variation. It is a local principle applying to micro feature structures, for example the micro-structure consisting of a functional head and its complement. Once an asymmetrical stage is attained, i.e., a stage where a choice point arises in the derivation of a given micro-structure, DAP predicts that this point of symmetry will gradually be eliminated. For example, while there is fluctuation in the position of the pronominal complement with respect to its commitative prepositional head in Old Italian (18-21), only the prepositional structure survives in Modern Italian, as discussed in Di Sciullo et al. (2014) and summarized here as follows. We assume that the language faculty is stable, that languages vary given contact with the environment and that linguistic variation in word order is the consequence of a change in the properties of grammatical features, triggering or not the displacement of a constituent. Thus, PPs are universally head-initial (Kayne 1997, 2005); all object DPs move to F to check [uD] on F, where [uD] is plausibly Case. Further movement of DP is attested in post-positional languages, as the following P shells illustrate.

(20)

18
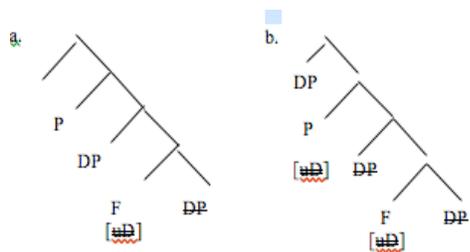
One has the dynamics of historical variation on the one hand, parametric pressure enforced by the principle of preservation, and on the other hand, principles reducing complexity. Thus two P heads, *con me* and *meco* are part of the P-Shell, (21a.,b.). Both P heads are pronounced in a given linguistic expression at a given point of the historical development of Italian, *con meco*, (21c); this derivation is too costly because it goes against the economy principle "pronounce the minimum"; as a consequence, *con meco* is eliminated. Finally, *meco* is eliminated because of the economy principle of preservation; Modern Italian will thus only display one option: P DP, *con me*. This follows ultimately from the DAP, a biologically grounded, third factor principle, in the sense of Chomsky 2005, 2011, which drives evolution from a Fluctuating Asymmetry phase R(a,b) & R(b,a) to a Directional Asymmetry phase R(a,b), R an H-C relation in this case.

(21)a.   b.   c.   d.
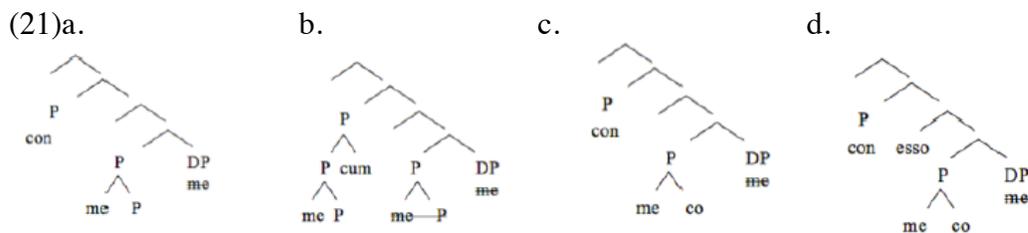
While the computational procedure of the narrow language faculty is stable and is reduced to the minimum required by conceptual necessity, complexity may arise from experience (language acquisition, language contact, etc.) giving rise to choice points (symmetry) in functional feature structure, as illustrated in (22) where a set of features of a functional element include both a valued and an unvalued feature variant of feature F, having the consequence of enlarging the set of possible derivations. Economy principles, falling into the third factor, will eliminate the complexity by breaking the symmetry brought about by experience.

(22)   a.   F : { [F], [uF]}

     b.   F
           / \
       [F]   [uF]

Complexity-reducing principles, such as the DAP will manifest themselves overtly whenever grammatical principles stop mandating certain operations. Whenever the choice between two competing structures is not mandated by formal grammar principles, third factor principles will exert their pressure, re-shaping the system to reduce choice points (e.g. points of symmetry).

DAP contrasts with Greenberg's (1966) absolute and implicational universals, such as the ones for prepositions, as well as more recent proposals, including Biberauer, Holmberg and Roberts' (2010) proposal on head-directionality and complementation in extended projections and Kayne's (2011) proposal on head-directionality and Probe-goal search. The DAP is a Developmental Universal which provides a new approach to language variation.

In the emergent view of the origin of language, the language faculty did not evolve from previous simpler stages, such as a purely symmetrical stage, where asymmetry would be lacking. There is evidence however coming from the historical evolution of constituents in Indo-European languages as well as in non Indo-European languages, such as Hungarian and Chinese, that fluctuating asymmetry is observed in the position of functional categories with respect to their complement, and that this fluctuation is no longer available in later stages of the languages. For example, Homeric Greek (1000-800 BC) was predominantly prepositional, in later stages of the language pre- and post-positions were equally possible. Modern Greek, however, is fully prepositional. Fluctuating asymmetry in the position of prepositions with respect to their nominal complement is also observed in the historical development of non Indo-European languages, including Chinese and Hungarian. Assuming Biberauer and Richards' (2006) implementation of language internal optionality, the development of prepositions from postpositions reduces the complexity of the derivations. The derivation of prepositional structures, where the preposition precedes its complement requires less derivational steps than the derivation of postpositions, where the preposition follows its complement. Di Sciullo (2012b) proposed that evolutionary developmental universals, such as the Head Initial/Final Constraint, account for micro-variation in diachrony. According to this constraint the choice between the initial and the final position for a functional head in the same extended projection is eliminated in the evolution of languages.

There is an interesting parallel in the dynamics of variance in the form of bipartite organisms and in the form of functional projections, suggesting that the language faculty is subject to external evolutionary developmental laws that may affect the external shape of the objects it generates. For example, Palmer (1996, 2004, 2007, 2012) identifies phylogenetic patterns of variance in the evolution of bilateral asymmetric species. Three stages in evolution and change are identified: The symmetric stage - there is no left or right difference in the organism. The following antisymmetric stage presents random prominence of the right or the left side of organisms. In the last stage, the asymmetric stage, the prominence is observed only to the right or only to the left of the organism. Figure 3 illustrates the evolution and development in male fiddler crab claw asymmetry. In evolutionary developmental biology, Random asymmetry or Antisymmetry, is the stage where right- and left-handed is equally frequent in a species; whereas Fixed asymmetry or Directional asymmetry is the following stage where there are only right- or only left-handed forms in a species. Further work on the genetics and the evolution of floral morphology also indicate the development of asymmetries from a primary symmetry-breaking step. See Figure 4.
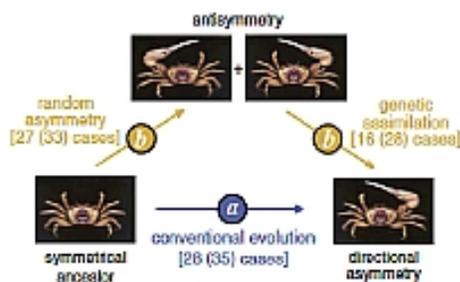
Figure 3: Symmetry breaking and the evolution of development
in male fiddler crab asymmetry
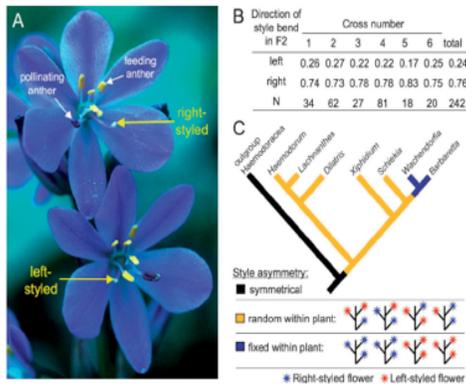(from R. A Palmer *Science* (2004: 306:828-833.)

Figure 4. A: Genetics and evolution of floral bending of the style.
(from Levin and Richard 2007)

Symmetry breaking may also contribute to reduce complexity in language acquisition. Language develops in the child because of the unique properties of the language faculty, enabling humans to naturally develop the grammar of the language(s) they are exposed to, notwithstanding the scarcity of the stimulus (Chomsky 1986, 2011, Berwick et al 2011). The study of the relations between language development in the child and the historical development of languages has been a topic of research since the beginning of generative grammar (Lightfoot 1986, 1991). The idea is that by looking at historical change, it is possible to reconstruct what children at different times must have gone through. Lenneberg (1956) observed that irrespective of the language the child is exposed to, (s)he will develop that language going through the same biologically determined steps that coincide with the development of motion. The relations between ontogeny (individual development) and phylogeny (evolution of species and lineages) in biology may further our understanding of the development of language in the child and language historical development. However, as discussed in Gould (1985), among other works, the view that ontogeny recapitulates phylogeny has been challenged. It might be the case instead that innovation is a central aspect of variation. This view may offer support to theories of language acquisition that account for the fact that the child's language is not identical to the languages (s)he is exposed to. Assuming that the elements of linguistic variation are those that determine the growth of language in the individual (Chomsky 2005, 2007), antisymmetric stages are also part of language development. For example, new compounds can be coined in any language. Children produce these forms quite early, around age two or three (Clark and Barron 1998, Hiramatsu et al. 1999, Micoladis 2007), sometimes with meanings that they are unlikely to have heard before, and always without any formal instruction. Around three, children consistently produce compounds of the type V-N instead of N-V-er, and they go through an intermediate V-N-er stage, e.g., *bounce-ball, bounce-baller, ball-bouncer*. Data from language development show that these stages in the acquisition of compounds could also be understood as undergoing a familiar biologically based symmetry breaking sequence.

Thus, while there is nothing like language, language remains an object of the natural world, and thus, it is subject to natural laws, including symmetry breaking, which are external to the language faculty. The evolutionary developmental approach to language historical variation may contribute to the understanding of language as an object of the natural world, which is exposed to natural laws, as well as may lead to the discovery of new sorts of universals accounting for the residue that binary parameters do not cover. It may also contribute to our understanding of why parameters emerge and why they can be reset over time, and thus contribute to biolinguistics.

4. Two Views of the Language Faculty

It might be instructive to compare slightly different approaches from the biolinguistics perspective. We will compare a biolinguistics program incorporating the Minimalist program with the proposal outlined in Jackendoff (2011). We would argue these two approaches are research variants within the biolinguistics framework.

Biolinguistics is the study of the biology of language. The main research areas of the field are knowledge of language, language acquisition, and evolution of language. This is true for any approach within the biolinguistics framework. Even when we look into more specific assumptions, we find that Jackendoff shares many assumptions in common with researchers working within the Minimalist Program (and other approaches); e.g., that there is a faculty of language, that there are systems of syntax, semantics, lexicon and phonology and mappings between them, that there is a Universal Grammar of some kind, and that a useful distinction is that between "Broad Language Faculty" and "Narrow Language Faculty" defined in Hauser, Chomsky and Fitch 2002.

However, there are common misconceptions of biolinguistics that are worth mentioning. One of them is that the psychological/functional and neural levels is not the only way biolinguists make connections between language and biology. We would insist that work on formal linguistics, including all the work that Jackendoff has done in this area, from the Extended Standard Theory on, is doing biology. For example, he provides an analysis of sentences like "every acorn grew into an oak" and other syntactic structures to construct arguments for notions like Universal Grammar, structure-dependence and poverty of stimulus (which he calls the Paradox of Language Acquisition). He thus demonstrates himself that one can quite reasonably give arguments for innate structure (genetic endowment) based on linguistic structures, without needing to bring in further speculations about FOXP2 or neural circuits, if they don't add anything to the argument. In doing so, biolinguists are outlining properties that the language faculty must have (in the narrow or broad sense), and are "doing biology." This activity is analogous to Mendel showing what the internal properties of plants (and other organisms) must be to account for their inheritance patterns.

Thus, both the Minimalist program and other frameworks in generative grammar assume that core research areas are knowledge of language, acquisition and evolution and presuppose a (narrow/broad) faculty of language, systems of syntax, semantics, lexicon and phonology, some variant of Universal Grammar, genetic endowment, Paradox of Language Acquisition (aka poverty of stimulus). These frameworks differ however on the architecture of the language faculty. Another misunderstanding of the biolinguistic framework is that it polarizes the discussion on whether the architecture of

the language faculty is parallel or not. It is useful to underline that different proposals are available on the architecture of the language faculty/Universal Grammar in generative grammar, starting with Syntactic Structure, the Standard theory, the Extended standard theory, Government and Binding and the Minimalist program. Different architectures have been proposed with Minimalism, including a linear model (Bobaljik 2012), a workspace model (Di Sciullo 2014), a clash model Uriagereka (2012), Furthermore, different implementations in a parallel architecture are available, including Jackendoff 2002, Culicover and Jackendoff 2005, as well in LFG, Autolexical Syntax and Role and Reference Grammar. Thus, the architecture of the language faculty is part of the research agenda since its beginnings.

Jackendoff argues for the superiority of his parallel model (phonology, syntax, semantics) on the basis of a discussion of the following points: the necessity of redundancy in the lexicon and the rule system, the ubiquity of recursion in cognition, the derivational vs. constraint-based formalisms, the relation between lexical items and grammatical rules, the roles of phonology and semantics in the grammar, the combinatorial character of thought in humans and nonhumans, the interfaces between language, thought, and vision, and the possible course of evolution of the language faculty. It seems to us that the following clarifications are needed.

The Minimalist Program has put forth extensive proposals in the literature on the computations required to account for syntactic phenomena, such as syntactic constraints, structure dependencies locality involving the architecture of the faculty of language, principles of efficient computation, etc. The goal is to reduce the technical machinery of the grammar to the minimum required by conceptual necessity. Other approaches, on the other hand, have adopted constraint-driven unification in his framework, incorporating the computational operation of Unification (Shieber 1985): "The brain's characteristic combinatorial operation is Unification rather than Merge." (Jackendoff 2011). Although we can't compare step-by-step derivations in the space here, we note that there are many studies that have pointed out that the Unification operation is too powerful and less restrictive in various ways (see, Berwick and Weinberg 1984, Johnson 1988, Kobele 2006, a.o.) Jackendoff also disputes the role of recursion in language, arguing that "recursion is not the defining characteristic of language; it is found everywhere in higher cognition." However, the claim that there are recursive mechanisms in other cognitive modules, e.g., vision, but see Ullman (1979, 1996, 2006) for a different view, is not incompatible with the Minimalist Program. But evidence is required to show that the recursive mechanisms are the same across different cognitive domains. Pinker and Jackendoff (2005) have also noted the claims that a particular language might not employ recursion (e.g., Everett 2004, 2005). But see Nervins, Pesetsky and Rodrigues (2009) for convincing counterarguments. Most work in the Minimalist Program proposes that recursive mechanisms be available in UG, part of the genetic endowment

Jackendoff also argues for the need of redundancy in the grammar and contrasts this to other works in the Minimalist Program. However, his arguments apply primarily to the lexicon, while the Minimalist work he is criticizing pertains to syntactic derivations, where it has been argued that in many cases what appeared to be a syntactic redundancy disappeared upon closer examination with a simpler reformulation of the syntactic computations.

Jackendoff's proposal does differ from some other specific proposals in the Minimalist Program, as in Chomsky (2005) and Di Sciullo and Boeckx (2011) on Principles not specific to the faculty of language, the so-called third-factor principles. He does seem to have objections to what Chomsky 2005 calls Third factor principles, what Jackendoff calls "first principles" – Principles not specific to the faculty of language. He regards this as misguided effort to "eliminate the role of natural selection": "The situation parallels streamlining in dolphins. The advantage of streamlining is a consequence of natural law. But dolphins still had to evolve this shape, presumably through natural selection. In other words, in these cases, natural law does not eliminate the role of natural selection, as Chomsky is suggesting; rather, it shapes the adaptive landscape within which natural selection operates." (ibid, pg. 604) Jackendoff appears to be objecting to introducing considerations of natural law into the study of biology of language: ''The biolinguistic approach seeks to derive properties of language from what is called "natural law" or "third factor considerations," so that they are somehow not a burden on natural selection.'' What is meant here by "burden on natural selection?" Jackendoff elaborates with an example, noting that natural law (or physics) is involved in digitizing vocal signals: "But notice that this does not take the burden off evolution." (ibid, pg, 604). He seems to believe that the reason physics laws are introduced into biology is to take the burden off evolution. In other words, if we have an explanation in terms of physical laws, then we can "eliminate natural selection," even evolution from our explanatory accounts. Nothing could be further from the truth: what the biolinguist and the biologist more generally are trying to do is not eliminate natural selection, much less evolution, but rather to understand evolution, and to do that one must understand how various principles from physics, chemistry and biology interact with one another.

Finally, contrary to common assumptions, the search for the principles of evolutionary and developmental biology that could have led to a language faculty is not premature, as links have already been identified between what we know of the nature of linguistic structure and what is known about the genetic basis of biological development. The unification of linguistics with biology and physics is often misunderstood. By introducing considerations of physics and mathematics ('the Galilean method') into linguistics, and other areas of biology, it will be possible to derive the properties of language from deep and simple principles. The program initiated by D'Arcy Thompson (1992) and Turing (1952), among others, which noted the importance of physical factors in understanding the mechanisms, development and evolution of biological organisms has become increasingly important for the analysis of biological systems as a whole, and are under intensive study in a number of areas, now familiar as "systems biology", "self-organization," etc.

5. Conclusion

Biolinguistics is in our view a most promising field bridging discoveries in linguistics and the natural sciences to further our understanding of the human language faculty as a unique biological object. By focusing on core aspects of this field, pointing to the relevance of core notions in current generative grammar to the biological study of language and bringing to the fore new developments, we hope to foster further contributions to this research program.

In the past sixty years or so, we have seen an explosion of interdisciplinary work in the various subfields of biolinguistics (a partial list): theoretical linguistics (syntax, semantics, morphology, lexicon, phonology, phonetics, pragmatics, etc.), computational linguistics (parsing, etc.), child language acquisition, multi-language (bilingual, etc.) acquisition, perceptual studies, language change, comparative linguistics (typology, etc.), sign language, language contact (pidgins, creoles, etc.), speech disorders (dyslexia, developmental verbal dyspraxia, specific language impairment, etc.), language savants, language neurology (function, anatomy, architectonics, etc.), cross-species comparative work (non-human primates, songbirds, etc.), mathematical modeling and simulation (language change, development, evolution, etc.) and other cognitive domains (mathematics, vision, music, etc.). All of these areas are currently foci of active research.

It is sometimes useful to apply a kind of litmus test for the state of biolinguistics. Many years ago (1976), Chomsky said the following, at a symposium in honor of Eric Lenneberg:

"The study of the biological basis for human language capacities may prove to be one of the most exciting frontiers of science in coming years'' (Chomsky 1976).

The litmus test is to ask whether this statement still holds today. We think it is safe to say that many more exciting years for biolinguists lie ahead.

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