⋆ FORUM ⋆

The Biolinguistics Network

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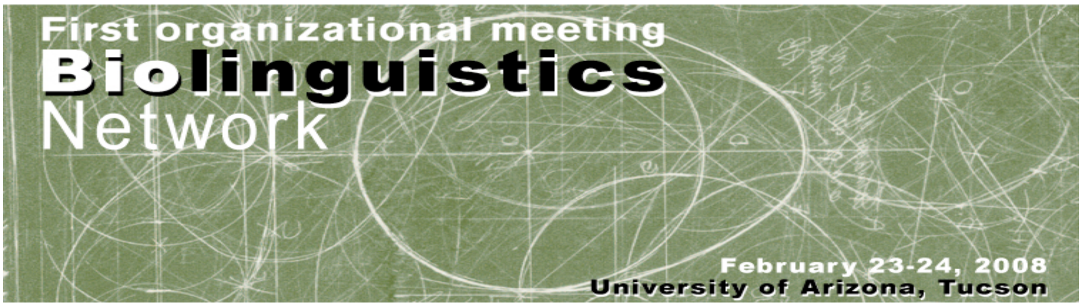
This note highlights the Biolinguistics Network, its creation, and its role as a promising avenue of research in the biological basis of the language faculty. It also provides insights into the type of material discussed by the Network's participants so far, and the questions that will be addressed in upcoming events. The Biolinguistics Network was created in 2007 to foster multidisciplinary research by setting up a dynamic space to address biolinguistic questions, including what are the principles of our knowledge of language, how this knowledge grows, how it is put to use, how it evolved, and which aspects of the machinery are unique to language as opposed to shared with other domains of knowledge. Such questions were discussed in the two conferences that led to the creation of the Biolinguistics Network. The first, *Biolinguistic Investigations*, took place in Santo Domingo in February, 2007. The second, *Biolinguistic Perspectives on Language Evolution and Variation*, was held in Venice in June of that same year. These meetings brought together a number of contributors to the field. Selected papers from these two conferences are assembled in *The Biolinguistic Enterprise: New Perspectives on the Evolution and Nature of the Human Language Faculty* (Di Sciullo & Boeckx, in press). Such events and related publications, including the multi-authored cross-disciplinary piece published in this issue (Di Sciullo *et al.* 2010), are exemplars of the catalytic role of the Biolinguistics Network in our understanding of the biology of language.

I

The first meeting of the network was held February 23–24, 2008, at the University of Arizona at Tucson. This meeting was organized jointly with Massimo Piattelli-Palmarini and sponsored by the Social Sciences and Humanities Research Council of Canada, the Université du Québec à Montréal, and the University of Arizona at Tucson.



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This meeting set out the architecture of the Biolinguistics Network, including possible websites, journals, summer schools, permanent centers, and primary roles. The network website www.biolinguistics.uqam.ca was created shortly after the Arizona meeting providing the names and web pages of the participants of the network, the links to preceding and forthcoming Biolinguistic conferences, and a thematic bibliography with downloadable papers.

The Arizona meeting provided a great venue for the presentation of current work and research programs in the understanding of the faculty of language (FLB and FLN, in the sense of Hauser *et al.* 2002) and its biological basis. The material presented at this meeting was incredibly rich and covered a wide range of biolinguistic questions. I will summarize these contributions here, referring the reader to the Biolinguistics Network website for the abstracts of each presentation.

FLB

The first session of the meeting addressed basic questions on the properties of the faculty of language in the broad sense (FLB). Marc Hauser and Ansgar Endress discussed the constraints imposed by general mechanisms of perception that influence the form that grammars can take, and reported experimental results on temporal ordering rules and edge constraints, with parallel results in humans and chimps. Tom Bever discussed some aspects of the relations between biology, learning, and evolutionary constraints on linguistic universals. He presented results on sequence learning, language learning/behavior, and fMRI studies of language behavior. Karin Stromswold talked about the 'critical period' in language acquisition and addressed three questions on the genetic, cognitive and neural bases of the 'critical period' in language acquisition. The first question is: What is the critical period? The second is: What causes the critical period? And the third question is: Why is there a critical period? Ken Wexler discussed optional infinitives in language acquisition, as well as behavioral genetic research (twin studies) showing that, even in typical development (having to do with syntactic control), there appears to be genetically linked variation. The general point of Wexler's presentation was that genetics might bear on the development and inheritance of particular properties of language, not just on language as a whole.

Genes

The second section of the conference focused on genes, and in particular on our understanding of the role of the *FOXP2* gene, previously thought by some as being the 'language gene'. Lyle Jenkins pointed out that interdisciplinary work in a large number of subfields of biolinguistics in recent years has provided a preliminary and partial sketch of the mapping of the *FOXP2* gene to its phenotype (including language and cognition). However, he noted that the following questions remain unanswered. What exactly is the phenotype of the developmental verbal dyspraxia caused by *FOXP2*? How can we sharpen the distinction between the linguistic features of the phenotype from other cognitive problems? How can we determine what genes involved in language are downstream from *FOXP2*? And what can we learn about the brain areas and circuits sub-served by language? Robert Berwick suggested three separate lines of experiments regarding *FOXP2* in order to extend the domain of evidence, relating *FOXP2* to sign language and motor serialization, to evolution, and to the 'songeme' analysis of normal and knock-down zebra finches. Massimo Piattelli-Palmarini and Juan Uriagereka's talk, 'Spellbound: The birds', suggested that the narrow language faculty may have evolved as a procedure that 'externalizes' a more ancient form of recursion. To address the parsing problem that results, they discussed the role of songbirds' Area X, the functional equivalent of our caudate nucleus, which is responsible for the acquisition and the production of the singing behavior, and the role of songbird *FoxP2* in this area. In his second talk, Robert Berwick also pointed out that even though recent research has suggested that *FOXP2* has undergone strong natural selection within the last 100,000 years, the differences we observe between human *FOXP2* and *FoxP2* in non-human primates could just as easily be due to chance alone.

FLN to FLB

The last section of the conference was devoted to the bridging FLN to FLB. I focused on linking the basic Minimalist operator, Merge, to experimental results. I presented the results of behavioral and ERP experiments indicating that there are differences in the processing of morphological expressions with the same linear properties but different in their hierarchical structure. I proposed that "deep asymmetry effects" follow from the computation of Merge by the brain. Cedric Boeckx stressed the need for biolinguists to take very seriously the recent (minimalist) trend that seeks to "approach UG from below" and uncover basic, primitive operations, such as Merge. He focused on the syllable and the phase, and argued that the minimalist search for basic relations is the best bet we have for formulating 'linking hypotheses' in the domain of neurolinguistics and evolutionary linguistics. Lisa Cheng's presentation focused on syntax–phonology (mis)matches and their mappings at different interfaces. The questions she considered included the following: How is syntactic phrasing mapped with phonological phrasing? Or how does syntactic phrasing feed phonological phrasing? One extension of this program is at the domain of psycho-/neuro-linguistics: How does sentence planning work, taking into consideration the syntax–phonology interface? Elly van Gelderen discussed which insights historical syntax provides regarding economy principles, when couched within a biolinguistic framework. She raised the following question: How is cyclical change from analytic to synthetic to analytic relevant to the claim that "the conflict between computational efficiency and ease of communication" is resolved "to satisfy the CI interface"? Heidi Harley & Andrew Wedel presented work on the mapping of the hierarchical structure of syntax onto the linear structure of the utterance. They investigated this mapping by contrasting the cross-linguistically uniform selectional/hierarchical relationship between verbs and their objects with the cross-linguistically varying temporal relationship between verbs and their objects in SOV and SVO languages. Jim McGilvray discussed linguistically expressed concepts (HOUSE, TIGER, MOST, SILLY, WASH…), pointing out that the study of such concepts requires the kind of internal machinery that exploits resources within the mind/head, each of which develops according to some internally set agenda. This agenda is multifaceted, and calls upon the study of internal systems (computational theories of vision, for example), developmental data, evidence concerning how linguistic concepts are employed by/within other systems, and evo–devo materials.

In addition to the setting of the organizational aspect of the Biolinguistics Network, two publications came out of the discussions of the first meeting of the network: Hauser & Bever (2008) and Di Sciullo *et al*. (2010). These papers resulted from a collective effort to address biolinguistic questions, to showcase the advances, and to point to open questions for a larger public, encompassing linguistics and biology, as well as cognitive and computational sciences.

II

The upcoming meeting of the Biolinguistics Network, *The Language Design* conference, will be held this spring at the Université du Québec à Montréal (May 27–30, 2010). Its purpose is to address further biolinguistic questions, and in particular the factors entering into the human language design stemming from linguistic theory, biolinguistics, and biophysics. This workshop will bring together participants from a broad array of disciplines to discuss topics that include the connection between linguistic theory and genetics, evolutionary developmental biology and language variation, and computer science/information theory and the reduction of uncertainty/complexity. While the first meeting of the network addressed general questions on FLB, FLN–FLB, and genetics, the questions raised by the forthcoming event are more fine-grained. The themes that will be discussed include the role of properties of grammars, operations, relations, complexity reducing factors, brain studies, as well as studies in language variation and change on our understanding of the biology of language. The following paragraphs outline some of the questions that will be addressed.

Formal Grammars and Human/Animal Comparative Studies

Recent work on Chomsky's hierarchy of formal grammars, as well as on formal grammars and human/animal comparative studies, brings to the fore issues that go back to the 1950s on the sort of grammars/automata that specifically describe/generate human language (Chomsky 1956). Several questions arise, including whether more than one sort of formal grammar is part of the language design, perhaps distributed in different components (Bergelson & Idsardi 2009), or possibly available within narrow syntax itself (Lasnik, in press). Recent human/animal comparative studies on learnability raise similar questions (Fitch & Hauser 2002, Jarvis 2004, 2006, Saar & Mitra 2008, Friederici 2009). To what extent do such studies shed light on the specificity of human language?

The Properties of the Operators of FL(N)

One important question is the nature of the operators that derive the discrete infinity of human language. Merge and Agree are assumed to be the dyadic operators of the Faculty of Language. However, several questions arise with respect to their properties. Is Merge completely free (Boeckx, to appear), or is it subject to formal conditions (Frampton & Gutmann 2002)? Further questions arise on the nature of the representations derived by Merge, and whether or not these are restricted to adjunction (Hornstein & Pietroski, forthcoming). More questions arise regarding the semantics of human language, the kinds of operators that derive the interpretation, and whether the derivations are external to narrow syntax (Pietroski 2008, Higginbotham 2009, Hinzen, in press, to appear). What kind of biological evidence would support the theoretical in this regard?

The Role of (A)Symmetry in Grammar and Biology

Properties of relations such as symmetry, asymmetry and antisymmetry have been shown to be relevant in the language design. Symmetry-breaking has been proposed to drive derivations (Moro 2000, 2008) and to account for word-order differences (SVO, VSO, etc.) (Jenkins 2000, 2004, in press a, in press b); antisymmetry has been argued to be a central property in syntax, as well as for linearization (Kayne 1994), and asymmetry has been claimed to be part of Merge (Chomsky 1995, Di Sciullo 2003a, 2003b, 2005, Zwart 2006, Di Sciullo & Isac 2008a, 2008b). We know that properties of relations are used to describe the dynamics of morphogenesis in biology (Montell 2008), and to formulate laws of physics. Why should these abstract properties of form participate in the language design? What is the basis of their dynamics in human language?

Complexity-Reducing Factors in Derivations, Biology, and Physics

It is generally assumed, since Chomsky's (2005) three factors, that the factors reducing derivational complexity are external to the language design. They include mechanisms that reduce the search space and the choice points in the derivations. Phases are part of the factors reducing derivational complexity in narrow syntax (Uriagereka 1999, Chomsky 2001, 2008, Boeckx & Grohmann 2007, Grohmann 2009). Other complexity-reducing factors include the mechanisms restricting the set of possible acquirable grammars (Yang 2002, Di Sciullo & Fong 2005, Niyogi 2006, Roeper 2007), those that reduce the set of possible interpretations for linguistic representations (Reinhart 2006, Speas, in press), and those that come from limits imposed by perception and memory (Chomsky & Miller 1963, Bever 1970). Are these computational constraints related to one another? Are there correlates to complexity-reducing factors in biology or in physics?

Variation in Languages and in Biology

Advances in our understanding of language variation since Principles–and–Parameters have made it possible to derive observable differences between languages from abstract properties of the grammar and phylogenetics (Guardiano & Longobardi 2005, Longobardi & Guardiano, in press). Recent findings in the dynamics of morphogenesis, regulatory HOX genes (Gehring & Ikeo 1999, Gehring 2005), and philogenetic patterns of variance (Palmer 2004a, 2004b, 2009) are interesting from a biolinguistic perspective (Niyogi & Berwick 1997, 2009, Di Sciullo, in press). They point at the central role of asymmetry in the dynamics of variation and change in the biological world. How can our knowledge of variation and change in genetics and population biology enhance our understanding of language diversity?

Genetics, Brain Studies, and Language Impairments

From an evolutionary and comparative standpoint, *FOXP2* has been intensely analyzed as potentially shedding light on the unique characteristics of the human species, as well as on human origins. However, given *FOXP2*'s multifactorial neural influence and its role as part of the externalization system for language, it would then seem speculative at this point to base strong conclusions on such evidence (Berwick & Chomsky, in press and Piattelli-Palmarini & Uriagereka, in press). How do advances in our understanding of SLI and other genetically endowed language impairments, such as Williams–Beuren syndrome (Perovic & Wexler 2007), as well as advances in the study of brain-level mechanisms that support language (Fiorentino & Poeppel 2007, Lau *et al.* 2008), shed light on the language design?

The conference will offer a renewed opportunity to bring forward new approaches to these important questions. The confirmed speakers are: Robert Berwick, Cedric Boeckx, Roberto De Almeida, Anna Maria Di Sciullo, Sandiway Fong, Jason Ginsberg, Kleanthes Grohmann, Wolfram Hinzen, James Higginbotham, William Idsardi, Dana Isac, Lyle Jenkins, Howard Lasnik, Giuseppe Longobardi, Partha Mitra, Richard Palmer, Massimo Piattelli-Palmarini, Paul Pietroski, David Poeppel, Charles Reiss, Tom Roeper, Margaret Speas, Juan Uriagereka, and Kenneth Wexler. The abstracts will be posted shortly on the network website.

III

The Biolinguistics Network keeps track of the participants, the publications and the conferences in this field. Together with the *Biolinguistics* journal and the recently created *Biolinguistics* blog, it strengthens the links between individuals, groups and institutions interested in pushing forward our knowledge of the biology of language.

As the founder of the Biolinguistics Network, I believe that in such a dynamic space, it is likely that the biolinguistic questions will meet explanatory hypotheses and that new insights will lead to a better understanding of language as a natural object.

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