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Biolinguistics yesterday, today, and tomorrow

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3.1 Introduction

Much too generously, Noam Chomsky (Chomsky 2007c, 2009) credits me for having coined the term biolinguistics, and for having organized, in May 1974, at Endicott House in Massachusetts (Piattelli-Palmarini 1974), the first meeting in this (then) new field. He is too generous on two counts, because I did not think I was coining a new term, but rather that I was just spelling out in an obvious way what existed already, at MIT, and because Noam and Salva Luria organized that meeting at least as much as I did (Chomsky 2007c). Chomsky and Luria (a Nobel laureate and one of the main architects of modern molecular genetics) had organized a weekly seminar at MIT where biologists and linguists engaged in a constructive exchange of ideas. What could that have been, if not bio-linguistics?

Later that month, during a grand tour of private foundations in the US, trying to raise funds for the Royaumont Center in Paris, of which I was the director and Jacques Monod (French Nobel laureate and a main participant in the Endicott House meeting) the president, I learned that one of those foundations only gave grants to institutions in the US, but not to entities outside the US. I mentioned the biolinguistics venture started at MIT and the officer in charge instantly manifested great interest in it and the concrete possibility of giving a grant. I contacted Luria and suggested that a grant application be sent. It was sent and it was accepted, and it fueled research, fellowships, and meetings in biolinguistics at MIT for several years to come.[1]

One episode that happened the following year is, I think, sympto-matic of the early development of the field. While on a short visit of two weeks to the Department of Linguistics and Philosophy of MIT, an undergraduate student in biology came to see me and said he was greatly interested in working on biolinguistics. I suggested that he con-tact Luria, and he did. He told me a few days later, to my astonishment,

that Luria had discouraged him to enter the field. I then asked Luria why he had been so dismissive, and he told me candidly that no results were to be expected for many years to come, the problems were too complex, the possibility of real experiments too remote, and a young researcher was destined to be disillusioned. Luria added (in Italian, I am translating): "When you start a career as a scientist, you want to tackle a problem that has a good chance to be solved in three or four years, not in decades. It's ok for old schnooks like myself to have a side interest in big problems, but a young researcher must not be encouraged to thread into those waters." Being then young myself, and thoroughly enthusiastic about the new field, I was disappointed, but Luria did not budge from his pessimistic forecast. Nonetheless, soon after, he and Chomsky sent me a glowing letter of reference for Mary Louise Kean, an MIT post-doc who had done seminal work on the phonological aspect of aphasia, and who would be spending a semester in Paris, thanks to the grant I mentioned above. So, after all, young researchers could get results in a short time. I was delighted.

There was, however, wisdom in what Luria told me. In hindsight, almost 40 years later, one must confess that the development of biolinguistics has indeed been slow, though fascinating, and that it's still an inchoate field of inquiry. Inevitably, as time went by, it has been conditioned by several major changes in biology, in linguistics, and in the difficulty in bridging the gap between them.

3.2 Biolinguistics: The early years (Lenneberg's dream)

The pioneering monograph by Eric Lenneberg on the biological foundations of language (Lenneberg 1967) reviewed what was then known, and sketched a "dream" (Wexler 2003) of the integration between biology and linguistics. In the mid 1970s, biology was starting an exploration of the regulatory mechanisms that determine the activation and inactivation of genes. The pioneering work of Jacques Monod and François Jacob in the 1960s had startled the field by revealing that genes could be switched on or off by other genes, that one string of DNA acted as a comptroller of the expression of another string of DNA. For a long time, historically, genes had been conceptualized as catalysts. Indeed, when genes code for enzymes, their products, though not the genes themselves, are literally catalysts. That idea had long passed its time, in the early 1960s, but the notion that there existed genes acting as switches was indeed revolutionary (the 1965 Nobel Lectures of Jacob and Monod retrace this experimental as well as conceptual development). Moreover, Jacob had explicitly stressed the universality of the basic molecular components of all living organisms, from the fruitfly to the elephant, and the crucial role in evolution of the different ways to recombine and shuffle the fundamental

bricks. His masterful metaphor was evolution as tinkering (*bricolage*). (Jacob 1977).

This suggested to Chomsky the very idea of parametric change as a model for linguistic variation (Chomsky 2009), which was to find its way first in his Kant lecture at Stanford in 1978 and then in *Rules and Representations* (1980). The technical developments of linguistic theory in those years pointed to increasingly abstract principles, covering apparently heterogeneous phenomena in a variety of languages and dialects. The requirement of explanatory adequacy became a *sine qua non*, grounding all linguistic hypotheses onto what is naturally accessible to the child, that is, at least implicitly, on the biology of our species. A further interesting parallel between biology and linguistics in those years is to be found in what can count as the syntactic equivalent of switches, independently developed. New analyses of phenomena like syllabification, the assignment of tonic accent, and prosody (Bromberger and Halle 1994; Chomsky and Halle 1968) and affix hopping (for a later review and historical reconstruction see Lasnik 2007), steered syntactic theory away from the traditional notion of applying rules to that of highly constrained computations, activated (in a sense, therefore, switched on) by the very nature of the input. The notion of syntactic movement was progressively transformed, from an optional transformation, to a mandatory computation, driven by the need to locally assign thematic roles and Case.

As a result of this progress, the very idea that communication might have been the shaping factor in language evolution faded more and more. Growing emphasis was given on the poverty of the stimulus, internal computational constraints, modularity and innateness (for a recent update and counters to criticism see Berwick *et al.* in press). Other ways to account for language evolution seemed inevitable, but as yet poorly defined.

The study of language pathologies, notably aphasia, became increasingly relevant and researchers with a solid background in linguistic theory started having a closer look. Agrammatic aphasia became a field of inquiry and it was possible to collect evidence from pathology bearing on rather specific syntactic hypotheses. (For a later review, see Grodzinsky 1985.)

The study of sign languages from the perspective of universal grammar soon came of age (Klima and Bellugi 1979), showing that the fundamental principles of language design were largely independent of the modality of externalization.

Early studies in language acquisition contributed to divorce the spontaneous growth of language in the child from any kind of inductive trial-and-error mechanism. Remarkable discontinuities in the acquisition of syntactic processes and the identification of critical periods, uniform across children and across languages, stressed the crucial role of brain maturation, making the traditional notion of learning inapplicable. An early anthology of such studies (Wanner and Gleitman 1982) made all this

transparent. As to the genetics of language, detailed studies of the differences between monozygotic and fraternal twins for different components of language (notably lexicon versus syntax) did show a clear pattern of heritability (corroborated by the rediscovery of early studies, published in the 1930s, by Ella J. Day (Day 1932) (for a later comprehensive review, see Stromswold, 2001, 2006). The identification of language-related genes, however, was yet to come.

In view of what we will be seeing here below, it needs to be stressed that the kind of genetics on which linguists based their collaboration was of a rather traditional, Mendelian kind. In hindsight, we see that the attempt was to grasp (in Sean Carroll's felicitous expression (Carroll 2005a) "the low-hanging fruits of the tree." That is, the one-mutation/one phenotype model, so prevalent until very recently.

3.3 The middle period (circa 1985–2000: the low-hanging fruits of the tree)

The genetic regulation of higher cells, unlike that of bacteria (the domain studied by Monod and Jacob) soon appeared to present an altogether higher order of complexity (Britten and Davidson 1969). Over and above "operator" genes controlling other genes, there were inducers, integrators, sensors, promoters, batteries of genes. Further regulatory mechanisms were to come, but it was already acknowledged that this complexity in gene regulation was bound to have decisive and innovative consequences for evolution. Regulatory elements or factors were rapidly turning into whole regulatory networks (Davidson 2006, 2010). Evolution appeared increasingly to have been the evolution of these networks. The intimate integration between the study of evolution and the study of development (later to be called evo-devo) was rapidly developing, on its way to becoming a whole new field (Raff 2000).

Linguistic theory had consolidated further and had found a comprehensive framework (the Theory of Government and Binding). The idea of parametric variation had been refined and had found several applications. A restricted number of syntactic modules had been identified and their fine inter-digitation explained the nature of distinct levels of representation, and the licensed operations on these. The detailed analysis of agrammatism revealed specific disruptions, establishing solid bridges between linguistic theory and neuroscience (Grodzinsky 2000). It was becoming more and more frequent, and more and more relevant, to find evidence pro or con specific syntactic hypotheses in brain data and in data on language acquisition (Wexler 1994). Continuing progress in brain imaging (PET, fMRI, EEG, then MEG) started producing numerous publications on brain and language, of unequal level of interest.

Basically, however, it became clear that distinct linguistic tasks were differently localized in the brain, confirming what had been known all along, but on different bases.

Language pathologies other than aphasia were discovered and finely analyzed: Specific Language Impairment, Williams Syndrome, Turner Syndrome, Spina Bifida, and the case of savants. Cumulatively, these data corroborated the notion that language is modular, both at the "large" level and the "fine" level (for an impressive recent review see (Curtiss in press)). On the front of the genetics of language, a new case opened up, that of FOXP2, raising both legitimate interest and exaggerated hopes (Piattelli-Palmarini and Uriagereka 2011).

The rise of the Minimalist Program (ever since Chomsky 1995b) created new opportunities for a biolinguistics concerned with more abstract properties of language and their plausible correlates in brain and in acquisition. The mandatory character of linguistic computations and of their natural constraints (criteria of no-tampering, last resort, strict locality), became evident, further corroborating an implicit parallel with the biological notion of switches and regulation. This opened the present period.

Painting with a broad brush the scene of the intermediate period, I think that we have witnessed the end of any lingering doubts about the legitimacy and the interest of exploring the biological correlates of language. The initial program of biolinguistics had become, as a matter of fact, a full domain of inquiry, with several anthologies and, later on, its own scholarly journal (*Biolinguistics*). Evidence from different sources had converged onto a better picture of modularity, maturation, and the poverty of the stimulus. The "low-hanging fruits" had been collected. A very fine summary of this period and its main successes is to be found in a book by Lyle Jenkins and in a volume edited by him (Jenkins 2000, 2004), terminating with a most illuminating chapter: a synthesis and a brief historical reconstruction by Chomsky (for a comprehensive recent panorama see Di Sciullo and Boeckx 2011).

3.4 The present period (ever since circa 2000: the higher fruits)

Biology is undergoing a further revolution. Not only is the study of gene-environment interactions becoming a puzzle of increasing difficulty, but the issue of "missing heritability" (Maher 2008; Manolio *et al.* 2009) lingers and is, for the time being, unresolved. This means, in extremely simple terms, that the classical Mendelian picture of one gene/one phenotype is rather the exception than the rule, and that, typically, the identification of dozens of genes related to a disease (the best studied case, for obvious reasons) only accounts for 3% or 7% of the genetic risk for that disease.

No one has doubts that there is a genetic component to the disease, but the complete picture of the interaction is presently "missing." The key appears to be several complex interactions between common variants and rare ones for each of those genes, and how those genes interact with the rest of the genome.

Over 25 genes have been identified already as being, in one way or another, linked to language, some of which regulating other genes also linked to language (as is the case of *FOXP2*). Moreover, epigenetics is actually a field in full expansion, and it's far from evident how this will one day connect to linguistics (Vercelli 2009). Collecting the higher fruits of the tree seems to require a significantly greater effort than ever imagined.

The panorama of evolutionary theory is slowly but significantly moving away from classical neo-Darwinism (Fodor and Piattelli-Palmarini 2011), though there is great resistance to admit that it is so, and this momentous change, destined to accelerate in the years to come, is conveniently and prudently presented as an "extension" of the classical theory (Pigliucci 2009).

The increasing success of evo-devo suggests entirely new ways of looking at the evolutionary relation between genes, mostly paying attention to regulatory genes, across species and phyla (Carroll 2005a). The invariance of the fundamental bricks in evolution goes way beyond what Jacob had intuited, now covering whole developmental and evolutionary modules that we find highly conserved even across distant species and phyla (Schlosser 2004; Wagner 2005). A consequence is that, in the domain of language, as in other domains, it is perfectly legitimate, and often very productive, to compare genes, phenotypes, and patterns of regulation in distant species. For instance humans and songbirds for the development of the control of complex vocalizations (Scharff and Haesler 2005; White et al. 2006), just as is the case for vertebrates and jellyfish for the development of globular eyes (Piatigorsky and Kozmik 2004). Moving away from the poor analogies between human language and the painful learning of sign languages by chimps, surely close relatives, we may want to explore more productive comparisons with songbirds, of which we are only distant relatives.

In fact, one consequence of the modularity of development and the modularity of mind, is that one module, once activated, may well remain encapsulated, regardless of its utility for the species, and regardless of the lack of other organs that may profitably interface with it. The many complete globular eyes of the box jellyfish encounter no optic nerve and no brain, though they each have a lens, a cornea, and a retina. The genetic explanation of what has happened in evolution to produce this anomaly is well reconstructed. Further surprises of this kind are likely to come from evo-devo. Evolution and development will probably be better understood in the future one module at a time.

Brain imaging has reached greater sophistication and new methods are available (such as MEG and near infrared imaging). We may, thus, hope to go beyond the brain confirmations of long-held hypotheses, interesting as these confirmations are. It has been reassuring to ascertain, via separate brain activations, that real syntactic computations are different from superficially similar ones, only possible as an abstract exercise (Musso *et al.* 2003) and that real sentences, as well as Jabberwocky sentences, activate brain areas that are quite distinct from those activated by a list of words (Pallier, Devauchelle, and Dehaene 2011). In the future, it will be even more interesting to learn, perhaps, that linguistic tasks about which we are not so sure (deriving a phase versus a non-phase) are indeed different, or are not, at the brain level. But, just as only the revolution in the more basic science (physics) has once produced a revolution in the less basic one (chemistry), so we can expect that only a revolution in the neurosciences will produce a major one in biolinguistics. No one knows at present why the different brain modules, whose existence leaves no doubt, do different things. All we can do at present is to link, phenomenologically, one brain region to a cognitive task, but that's where the buck stops. Unlike, say, the eye or the kidneys, whose different functions can be seen directly in their different structure, the brain looks to us much the same everywhere. Surely this is not the case, deep down, but we do not know why. Possibly the key will be the synchronicity of signals, phase slippages, selective group coordination, micro-cascades of excitations, or the reverberation of quantum phenomena inside neurons. The younger generations will one day know.

On a different front, quite encouraging are, in my opinion the studies of the abstract invariants of language, at different levels, from the syllable to phases. (Medeiros, 2008; Piattelli-Palmarini and Uriagereka 2008). These are the "third factor" in language design (Chomsky 2005), more akin to a physico-linguistics than to biolinguistics. The road to travel is still long, but we have the impression of having opened a Pandora's box. More and more, such deep regularities, instances of optimization, do appear in language as we look into it (Medeiros 2012, Uriagereka 2012). Synergistically, though for the time being mostly independently, deep invariants and instances of optimization emerge also elsewhere in biology (Cherniak *et al.* 2004) (for a brief census, see Part 1 of Fodor, and Piattelli-Palmarini 2011 reviving a tradition of search for structural invariants that dates back to D'Arcy Thompson).

A question comes to mind, when witnessing that so much of biological structure is derived "for free, from physics" (as Chris Cherniak likes to say) and that there is so much that is explained by a "non-genomic nativism." The question, simply and radically put, is: why do we also need DNA and proteins? This is a very hard question to answer, for anyone. In fact, one of the modern pioneers in this field, Stuart Kauffman,

acutely says (Kauffman 1993) that "no body of knowledge" today can combine the physical and computational deep invariants of biological systems with the mechanisms of genetics and development. Kauffman's characterization is important: no body of knowledge does it, a much more serious default than that of just lacking a theory or hypothesis, or even a whole discipline. The future generations, bless them, will one day fill this great gap.

3.5 Design for a curriculum in biolinguistics

Speaking of future generations, when hopefully biolinguistics will turn into a domain such that BS or BA majors will exist in some universities, I will indulge in designing a curriculum, in broad terms. Most of these courses will have to be created from scratch, as the telegraphic description I am giving may make clear. So, it's an ambitious plan, as the new discipline requires.

3.5.1 Basic courses

Introduction to language. Covering the main components: phonology, morpho-lexicon, syntax, and semantics. With special emphasis on invariants, universal grammar, and parametric change.

Introduction to biology. With special emphasis on common Baupläne, gene regulatory networks, developmental, and genetic modules.

Introduction to computational mechanisms. Quite different from the standard computer science basic courses (where students are mostly taught to program in Java). Mechanisms for divide-and-conquer and recursion; memorization (remembering the results of repeated computations); dynamic programming and data organization (for efficient access and search, indexing, graphs); parallelism (process communication, embarrassingly parallel problems, map-reduce); functions and their inverses (one-to-many, many-to-one, one-way, cryptographic basis); finite state machines, stacks, tapes; Turing computability (how to think about these mechanisms or building blocks). Key relevant concepts include: determinism/non-determinism, computational complexity, etc.

Introduction to physics. Basically, the physics needed to understand the nervous impulse, and the principles of functioning of MRI, fMRI, MEG, EEG, and near infrared.

Basic calculus. The analysis of functions, elementary differential equations, maximization and minimization, variational calculus.

Introduction to logic. Sets, operations on sets, propositional calculus, predicate calculus, quantifiers, scope.

3.5.2 Intermediate level courses

Neurobiology. Special emphasis on the modular evolution of the nervous system. Synaptogenesis, stability and instability of neuron networks, interactions of synaptic potentials. Neuroimaging techniques.

Human genetics. History of the domain, from inborn errors of metabolism to the present scene. Special emphasis on the different kinds of genotype–phenotype relations and on gene-environment interactions. The study of twins. Epigenetics, the case of missing heritability, main techniques of gene identification and of estimating variation, common variants versus rare variants, estimates of genetic risk.

Brain imaging. The different techniques, their advantages and their limitations with special attention to language-related data. Critical evaluation of the statistical analyses adopted and of the conclusions they allow or do not allow.

Language pathologies. Various kinds of aphasia, SLI, Williams Syndrome, the case of savants, Turner Syndrome, Spina Bifida. All these cases analyzed in the light of precise linguistic hypotheses, as evidence pro or con such hypotheses.

Linguistics. Intermediate courses, with special emphasis on syntactic theory and the semantics of natural language.

Language acquisition. With special emphasis on the relation between linguistic hypotheses and longitudinal data on acquisition, in several languages.

3.5.3 Advanced courses

Theories of evolution. A critical historical panorama of evolutionary theories, from early Darwinism to neo-Darwinism and the modern synthesis. Evo-devo and its consequences. Modularity, robustness, and evolvability. The search for the laws of form, deep invariants, instances of optimization.

Neuroscience. Principles of brain evolution. The physics of neurons and neuronal networks. Comparative ontogenesis of the brain across phyla. Ablation, regeneration, gene regulatory mechanisms. Computer models of brain modules.

Philosophy of linguistic theories. Critical historical reconstruction of the central concepts in linguistic theory. Representations, derivations, constraints, locality. Principles and parameters yesterday and today. Formal analyses (the hierarchy of automata) versus virtual conceptual necessity. Explanatory adequacy and beyond.

Quantum physics. Room at the bottom, inside the neuron. Microtubules and quantum coherence. Fundamentals of quantum computation and its biological correlates.

<u>The mathematics of life</u>. Fractals, attractors, strange attractors. Fibonacci series. Bifurcations, instabilities, pattern formation. Scale invariants.

<u>Biolinguistics</u>. Bringing all this together. Revisiting the canonical cases with a new eye. Classics of biolinguistic inquiry, old and new problems, puzzles, and mysteries.