KNOWLEDGE RECOMBINATION ON THE INFORMATIONAL ADAPTABILITY OF CELLS, NERVOUS SYSTEMS, AND SOCIETIES

Pedro C. Marijuán

Abstract: *New abstractions and new procedures for abstraction are needed in information science. Some of them should concern the nature and function of knowledge regarding the adaptability of complex, informational entities. Knowledge "in action" manifests itself as an improved adaptability of the informational entity to its environment, and as a redirection and enlargement of its self-construction processes. If taken beyond its usual anthropocentric conception, knowledge not only underlies the guidance of human actions and perceptions within appropriately restricted cognitive settings (or disciplinary fields), it also orientates –among others– the biomolecular happenstances of cells, and the processual workings of individual nervous systems. And it does so, as will be argued here, by incurring in a peculiar dynamics of similar recombination processes performed upon heterogeneous repositories of very different physical nature, which factually increase the cognizing reach of the concerned informational entity and leverage the conquest of further adaptability niches and complexity developments. Actually the growth of informational complexity of cells, nervous systems, and societies along their respective evolutionary, ontogenetic, and historical trajectories has been based on the cumulative consequences of knowledge recombination phenomena. However, the recognition of this commonality has been obscured, among other causes, by the structural and dynamic heterogeneity of repositories in the different informational entities, and by being subject of quite separated scientific disciplines: molecular and evolutionary biology, cognitive neurodynamics, philosophy of science/"geography" of science. In the extent to which such commonalities may be elucidated from a new vantage point, it would help in the development of information science itself, as well as in the pragmatics of education, in the social organization of science, and in the research effort of contemporary societies. Finally, the new term of "scientomics" is proposed in order to capture the knowledge combinatory processes and disciplinary mixings within the sciences.*

Keywords: *Information science, Knowledge recombination, Cells, Nervous systems, Neurodynamic central theory, Scientific recombination, Scientomics*

1. Introduction

The literature about information is growing at an accelerated pace. A good portion of it, however, is still devoted to a very traditional and controversial game: the definition of information. The concept was left factually undefined in its most controversial aspects (at least in its connection with meaning, knowledge, and intelligence) by the founding fathers of the field in the 40's and 50's; and not much progress has been achieved afterwards, in spite of the successive workings of almost two generations of scholars. On the one side, the boom of new computer science fields like artificial intelligence, artificial life, and biocomputing during the 70's and 80's, together with the expansion of complexity sciences during the 90's, did not leave many relevant scholars interested in further explorations of the information paradigm (with the exception of technical applications in communication engineering, encoding and computing, DNA & molecular machines, etc.). On the other side, the dominant position of information technologies and the collective hype and "tunnel vision" promoted by techno-utopians, icompanies, e-learning, information society theoreticians, etc., were not very helpful for enlightening the debate either. Why should theoreticians of the proclaimed "information society" take care about misunderstandings and paradoxes of the i-term within the sciences? (Castells, 2000).

Is information *definable*? Rather then continuing with narrow discussions focused on a single concept (for which hundreds of definitions have been proposed along these decades!) some parties were proposing an alternative course, to be focused on rigorous disciplinary development (Conrad, 1996; Marijuán, 1996; Scarrott, 1998): *"From its very beginnings in early 90's, the FIS initiative (Foundations of Information Science) has been an attempt to rescue the information concept out from its classical controversies and use it as a central scientific tool, so as to serve as a basis for a new, fundamental disciplinary development –Information Science... At FIS, rather than the discussion of a single particularized concept, information becomes the intellectual adventure of developing a 'vertical' or 'transdisciplinary' science connecting the different threads and scales of informational processes, which demands both a unifying and a multi-perspective approach. Above all, the solution of the numerous conundrums and conceptual puzzles around information becomes the patient task of a community of scholars, in which the ideas and speculations of each individual thinker can be shared and experienced upon by the other colleagues, so that a sort of 'group mind' develops (paraphrasing L. Hyde, 1979): one that is capable of cognitive tasks beyond the power of any single person."* (see Marijuán, 1996, at: http://infoscience-fis.unizar.es/c_1.html)

The position of this paper is that the advancement of information science has to produce new kinds of abstractions. Some of them will refer to information itself (and to its relationship with meaning), others to intelligence, and as a sort of bridge between the two, there should be new abstractions on the obtention and validation of knowledge (Marijuán, 2010; Yixin, 2010). This trio of "impossible" concepts —information, knowledge, intelligence— conform the pillars upon which a future information science has to be properly founded.

Herein, rather than attempting a definition of the knowledge concept, or setting its reach in an arbitrary way, we will consider it throughout its performances *in action.* We will point to three different realms, apparently quite heterogeneous and incongruous ones, where knowledge repositories and processes of very different nature can be detected as forming part of a nucleus of informational combinatory processes that grant the adaptability of the concerned entity to its environment. Notwithstanding the enormous dissimilarity of cells, nervous systems and human societies, in all of them heterogeneous recombination processes are performed at very different time scales upon a variety of knowledge-repository supports, either molecular encodings, memory constellations, or scientific-disciplinary contents, which somehow recapitulate each other along convoluted dynamic and evolutionary hierarchies.

A homogeneous description is out of hand—these informational entities belong to conceptual disciplines worlds apart. Thus the strategy of this paper will consist in attempting an independent description of information-knowledge processes for each one of the entities, to be followed then by some tentative abstractions/conclusions interrelating them "vertically", so to speak (Conrad, 1996). As will be argued, the main emphasis in this too brief a paper should be put on the close relationships between the evolutionary handling of molecular knowledge or *domain recombination* —combinations of protein domains throughout successive generations of living cells— versus the most sophisticate kind of cognitive games socially performed on scientific knowledge: the *interdisciplinary* recombination process performed within the system of sciences (Marijuán, 1996; Scott, 1998). In this sense, the development of a genuine *scientomics* borrowing concepts and techniques from bioinformatics will be proposed.

2. The Cell as an informational paradigm

The comparative advantage of the cellular information paradigm is that it can be properly described molecularly, almost to completion. At least in prokaryotic cells, almost all the molecular components are relatively well known, either as metabolites, or as protein-enzyme components, molecular machines, genomic sequences, etc. Evolutionarily, the living cell has been the first *informational* entity: endowed with self-production processes, communication with the environment, and an inner population of protein-agents coded into a genome. However, the extraordinary multiplicity of informational processes within the cell goes far beyond any traditional conceptualization of biological information either as code, communication, or structure. It is a dynamic world teeming up with millions of specific molecular recognition events, multiple codes, transcriptions, translations, processors, signalling systems, messengers, effectors, second messengers, regulators, interferences, complexes, connectivity networks… A very brief synthesis of its basic information processes will be discussed in what follows.

2.1. Cellular self-production

Essentially the cellular game is about a collective problem-solving dynamics applied to self-production of the own structures —implying both synthesis and degradation— which is performed by a “network society” of specialized enzyme and protein agents, continuously exchanging information about their specific activities thanks to the especial solvent properties of the water matrix. In response to *communicational* signals of the environment, thousands of *constitutive* enzymes and proteins, “nanomolecular processors” endowed with a peculiar modular structure, are synthesized (and also degraded) out from the sequential *generative* information of the DNA and RNA “data bases”, which are themselves incessantly subject to evolutionary combinatory games (Marijuán, 2002).

There appear multiple varieties of biomolecular information to distinguish (at least, the three broad categories mentioned: *constitutive*, *generative*, and *communicational*). In the interplay of all those varieties of information, the tides of self-production processes are orchestrated in a complex and flexible way, harmoniously engaging synthesis and degradation on an equal footing —the functional importance of both “negative phenomena”, protein & RNA degradation and apoptosis, or cell death, cannot be overestimated. The whole productive-informational processes culminate in the regularity of a specific cell-cycle that is *open* to the environment, both in terms of energy and information.

The elements of the constitutive architecture (“diluted” enzymes and proteins) are all of them coded into the generative architecture (“sequential” DNA & RNA), and the functional control of the latter by the former provides the core self-production and self-modification capabilities of the system —how gene expression is controlled by transcription factors. Traditionally most studies have focused in the expression of individual genes and not in the overall network and systemic instances of control. Currently, however, massive transcriptional regulatory networks are built for different prokaryotic microorganisms and eukaryotic cellular functions and specialized cell-types.

As an instance of such networks, the author’s research team has cooperated in compiling a large-scale *M. tuberculosis* transcriptional regulatory network, which has been built upon a previously published TR network (Balázsi et al., 2008) the largest to date, with further addition of different kinds of resources pertaining to publicly available sources: DNA microarrays, operons, orthology approaches, and synthetic biology experiments (Navarro et al., 2010). See Figure 1.

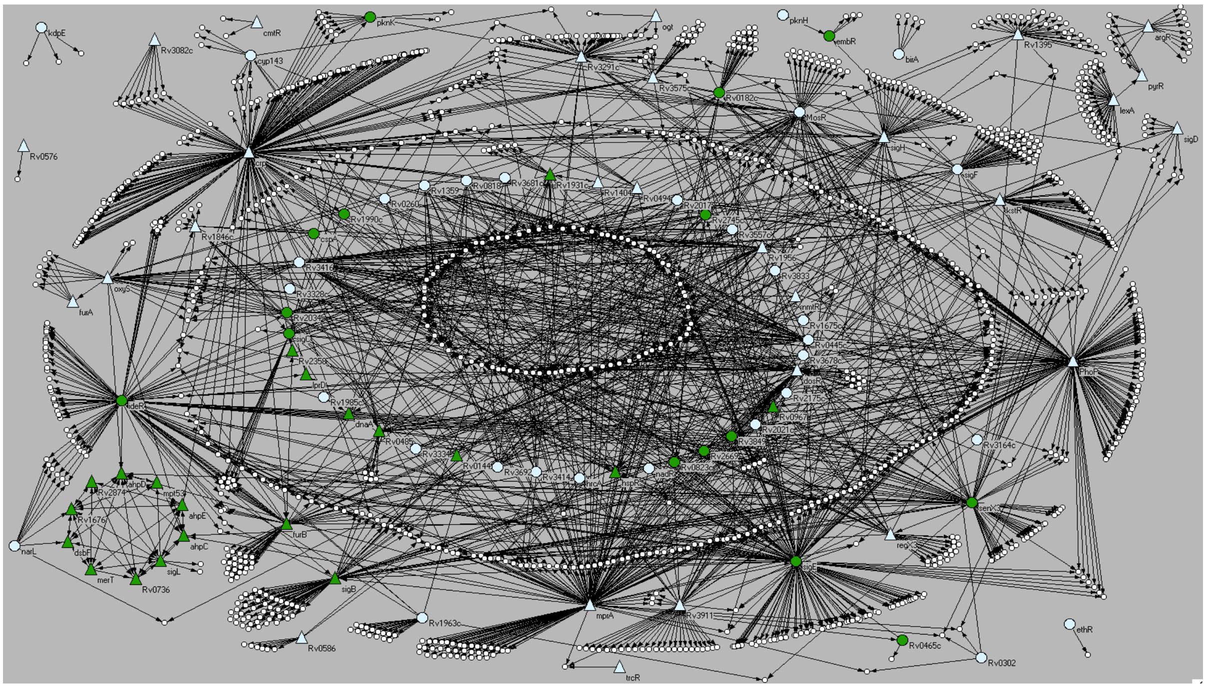

Figure 1. The Transcriptional-Regulatory (ETR) Network of *M. tuberculosis*.

In Figure 1, nodes represent *Mt*’s genes, and links represent their regulatory interactions. Transcription factors appear either green or blue, depending on whether they have known transcriptional regulator or not. The white nodes represent output elements without transcriptional activity. The triangle nodes represent protein transcription factors that auto-regulate their own expression. Approximately 35% of the genome is covered by this network. (Modified from: Navarro, 2010).

The 1,400 network nodes represented correspond all of them to specific genes of *M. tuberculosis* and their protein products, while the 2,304 links correspond to gene expression regulatory interactions by 94 transcription factors. The network shows a clear organization in structural levels that correspond with the complex functions and life-cycle stages of this highly sophisticate pathogen. Overall, the genome of the bacillus contains more than 4,000 genes and close to 190 transcription factors. In general, an increased number of transcription factors per genome translate into greater genetic network connectivity, which is correlated with increased complexity of the microorganism structures and life cycle (Levine & Tjian, 2003).

2.2. Cellular signaling

By itself the transcription network is “blind”. In other words, the coupling between the sequential and the diluted architectures needs the injection of further adaptive capability to respond to environmental demands. This is done by means of signaling guidance, so to partially deploy the genetic circuits in response to relevant happenstances of the environment or from within the cell. The *topological governance* of the transcription regulatory network, the decision of what parts should be activated or what particular circuits should be inhibited, is achieved thus by the cellular signaling system or *signalome.*

In prokaryotes, a variety of molecular systems are involved in the signalome, ranging from simple transcription-sensory regulators (a single protein comprising two domains), such as the well-known *embR, alkA* or *furB*, to those systems of multiple components and interconnected pathways that regulate key stages of the cell cycle, such as latency, pathogenesis, replication, and dispersion. A basic taxonomy of bacterial signaling systems was proposed somewhere else (Marijuán et al., 2010), which was centered on "the 1-2-3 scheme."

In eukaryotes, the signaling system comprises many hundreds of different classes of dedicated molecular agents (receptors, ion channels, transducers, amplification cascades, second messengers, intermediate effectors, final effectors) that can be arranged differently in each tissue. Particularly throughout the very fast changes in second messenger concentrations, an integrated perspective (measurement) of the different internal and external influences at play is obtained within the cell, and is subsequently passed towards intermediate chains and the final effectors.

At the end of the signaling command-chain, the gene expression machinery is waiting to be fed with a combination of *ad hoc* signals in order to change the transcriptional status of the genome –so that the well measured signals from the cytoplasmic signalome may be finally enacted as a new transcription program in relation with the advancement of the cell cycle or with the specialized function of the cell (Janes et al., 2005).

2.3. Cellular knowledge in action

The living cell enacts a new way of existence, an active "informational" one that is based on the capability to keep the own structures in a permanent state of "flow", piling up synthesis and degradation processes in a way that reminds critically self-organized phenomena (Marijuán, 2004). Thus, the living cell may systematically respond to signals from the environment, and produce the "meaning" they imply, by letting the signals themselves to interfere with the ongoing molecular dynamics of the cellular self-production "flow". Therefore, *meaning* may be defined throughout molecular *mining*: as the (signal) induced changes in components and connectivity of the constitutive enzyme-protein populations and the associate metabolites and substrates. The *relevance* and *value* of the signal can subsequently be considered and gauged —cellularly, this would correspond to second messengers and the cycle "checkpoints". Completion of the cell cycle always appears as the fundamental reference. The phenomenon of *knowledge* may be appended too, once the generative codes of the elements implementing successful responses have been evolutionarily selected, refined, and cohered within the life cycle (Marijuán & del Moral, 2007).

"Evolvability", understood as computational efficiency in the elaboration of DNA adaptive knowledge, has been largely increased along the evolutionary process itself. Because of the DNA modular organization of its domain based "addresses", the evolutionary genetic algorithms for physiological problem solving become largely parallelized. The different components of the biomolecular solutions may be separately tinkered with in different domains, and linked together later on (Peisajovich et al. 2010). Besides, every molecular stage (transcription, folding, transportation, modification, complexes, degradation), specifically coded onto DNA addresses, may be used as a new functional element of control. Solutions may be chosen, then, from an augmented set of molecular building blocks. The so called "Central Dogma" of classical molecular biology should not be taken as a closed, linear production-chart; rather the successive stages and intermediate transcripts could participate as legitimate molecular partners, each one endowed with endogenous recognition capabilities, within a whole *transmolecular matrix* of controlling interactions (Marijuán, 2002, 2004). We might argue that prokaryotes have used those very capabilities mostly towards the direct solution of *molecular assimilation* problems (in their encounter with environmental substances), while eukaryotes have tamed a fascinating developmental complexity by evolving towards the general solution of *molecular organization* problems.

Most of that complexity growth has been built by tinkering upon multi-domain enzymes and proteins, so that primary function codes or addresses and secondary addresses regarding the circumstances of the primary functions have been put together (though often in separate domains) onto the same DNA memory bank. Then the parallel with the von Neumann scheme of modern computers seems unavoidable: for memory addresses and logical functions are also put together into the CPU memory of computers. Further interpretations of cellular organization in "computer terms" have recently been made: Danchin (2009) about analogies with Turing machines, and Yan (2010) on operating systems.

From the knowledge perspective of this article it is important realizing that, by means of bioinformatic tools, one can track down how the different combinations of protein domain families have been progressively formed within genes, generating new protein domains and new gene families in a sort of "bing bang" of protein evolution, from the early forms of life to the more modern genera. Very old domains can be visualized as they have interpenetrated and recombined with recent domains within more complex proteins, following prokaryote horizontal gene transfer as well as genetic recombinations of all kind in both prokaryotes and eukaryotes, systemically *putting into action* more efficient genomes with improved sets of protein domain functionalities (primary functions plus the retinue of accompanying functional circumstances). The existing protein domains coded into the genomic DNA and their combinatory processes may be seen as the stock of knowledge of each species and, globally, of the biosphere as a whole. Genomes are continuously in the making, self-adapting and trying new knowledge solutions for each individual species as an existential answer to the selective demands posed by every particular niche.

3. Brains and knowledge: Towards a Neurodynamic Central Theory

The transition from cells to brains implies an important change concerning the disciplinary backgrounds –and even more concerning the problems to be tackled. In information terms, the study of information-knowledge in advanced brains bears a significant disadvantage, notwithstanding the anthropocentric familiarity it inevitably conveys. Arguably, one of the most dramatic absences in contemporary science concerns the lack of a central theory in the neurosciences. The revolutionary changes occurred in most neuroscientific disciplines (computational, cognitive, physiological, behavioral, network analysis, neuropsychiatry...) during recent decades have not been accompanied by the development of integrative theories yet, capable of introducing a new sense and a new order upon the data deluge received. The absence of a *central neurodynamic theory*, similar to the Darwinian Theory central role in the biological realm (or classical mechanics in physics), is creating an intellectual vacuum that negatively influences in the neurosciences themselves, as well as in their relationships with other technological and social disciplines. The basis of a possible theoretical development in that direction, related with knowledge production too, will be drafted in what follows.

3.1. Development of an integrative attempt

The NCT scheme ("Neurodynamic Central Theory") addresses a new way of explaining the organization of brain information processes (Marijuán & Panetsos, 2011). It establishes the correspondence between neurodynamics and behavior by means of a central theory grounded on dynamic connectivity (conectome) and on optimality (principles of brain economy). As the core of this theory, it is proposed the development of an informational "behavioral-processual engine" ingraining the multidimensional operations of composition-decomposition of sensorimotor afferences and efferences with the realization of an action/perception cycle, producing adaptive behavior and associative learning (efficient knowledge) as outcomes. A number of disparate behavioral and cognitive aspects might be unified out from the development of this theory, including the recently coined brain's "dark energy" (Raichle, 2006, 2010) and the global "workspace" proposed by Changeux, Dehaene, and others (Dehaene et al., 2001).

To reiterate, a new integrative theory is badly needed, a radically whole new approach rather than the piece-meal approach followed in most theoretizations of neuroscientific disciplines. The ongoing neurocomputational, neuromolecular, neuroinformatic and neuroimaging revolutions (to name but a few of the emerging disciplines responsible of the enormous experimental data-accumulation taking place in neurosciences) have not been accompanied by any parsimonious synthetic approach yet. Very recent findings about the "Conectome" need to be elaborated and generalized, both in their theoretical interpretation and in their experimental content (Zamora-López, 2010; Sporns, 2011). The dynamic "Conectome" has to be interpreted in terms of supersystem configurations of an information processing engine realized by cortical areas and medial nuclei, along an optimization process of local/global nature, and following symmetry-breaking/symmetry-restoration operations that make each cortically stored information unique and recoverable (Collins, 1991; Collins & Marijuan, 1997; Turvey, 2004). In the optimality aspect, the NCT scheme integrates those findings with principles of maximum economy in space and time, and with symmetry-breaking and group theory concepts for distributed processes that will configure a hierarchical-heterarchical scheme of information processing, learning and adaptive behavior (Marijuán, 2001).

The NCT paradigm gives sense to a number of recent studies on cortical connectivity, which are disclosing a highly complex panorama of neural activations in multiple areas and regions that are integrated into transient constructs of almost unknown behavioral functionality (where the phenomenon of consciousness might be appended). Some of these works about the "Conectome" have pointed at the emergence of dynamic core aggregates that fleetingly appear and disappear in milliseconds after any complex stimulus or mental process (originated either from the "outside" or from the "inside"). Such unending dynamics of fleeting aggregates has recently been dubbed as the brain's *"dark energy"*, and different cognitive-behavioral interpretations have been suggested, but until now they have not conduced to any sensible scheme (Raichle, 2006, 2010).

The NCT opens up a new research direction in the genuine organizational principles of *autonomy* that have guided the evolution of information processing in the vertebrate CNS. The "virtual reality" generated by the CNS out from the open-ended internal and external data affordances represents but the fitness occasions that the animal confronts as an autonomous agent in its environment. Autonomous agent theory, as well as the development of non-von-Neumann architectures (parallel processing), are closely related to this new type of information processing "engines".

3.2. A new approach to human knowledge

In the human case (and in most advanced central nervous systems), it is the *action/perception* cycle what serves as the universal substratum for organizing behavior and subsequently tending the fabrication of meaning, categories and knowledge. Seemingly, we confront the world in accordance with such action/perception cycles or oscillations, regularly switching between dominant modes of behavior (motor centered versus sensory centered). The advancement of the cycle is based on a global minimization process performed upon an entropic global/local variable that cortical columns and medial nuclei cooperatively create and annihilate upon a local basis, but also mediated by the organization of variable supersystem configurations, and implying formal rules of symmetry-breaking and symmetry-restoration. It is the informational *"behavioral-processual engine"* that ingrains the multidimensional operations of composition-decomposition of sensorimotor afferences with the realization of an action/perception cycle, producing (thalamicaly mediated) adaptive behavior and associative learning outcomes.

The brain appears as an abstract problem-solving playground where topologically distributed variables (“tuning precision voids”) occurring at the neuronal columns of cerebral maps are processed as some overall entropy that different brain substructures and specialized modules tend to minimize. Because of the evolutionary design of nervous systems (e.g., the vertebrate phenomenon of *decussation* of the nerve fibers) internal and external organismic “problems” locally increase that entropy value. The subsequent blind (abstract) minimization by the nervous system’s topological mechanisms and modular specialized subsystems produces as a byproduct the adequate behavioral and learning outputs. A problem-solving behavior well adapted to the advancement of the individual’s life cycle emerges from all those distributed processes and minimization operations (Marijuán, 1996b).

It is of particular interest in the human case that the combined system formed by the frontal and prefrontal areas with their massive increase in connectivity are breaking the brain’s reliance on modular specialized subsystems and maximally expanding the combinatory possibilities. Following Dehaene (2009), a “neuronal workspace” emerges whose main function is to assemble, confront, *recombine, and synthesize knowledge.* This system is further endowed with a fringe of spontaneous fluctuation that allows for the testing of new ideas, related to both the emergence of reflexive consciousness and the human competence for cultural invention. Although conscious brain activity fluctuates stochastically it does not wander at random. Selection mechanisms stabilize the combinations of ideas that are most interesting, useful or just “contagious”: privileged neuronal projections coming from the evaluation and reward circuits of orbitofrontal and cingulate cortex as well as the subcortical nuclei of amygdala and the basal ganglia are participating in this process.

Therefore, in the extent to which those premises are correct, a compact approach to *knowledge automation and recombination* by the central nervous system seems achievable, and further, a new “Theory of Mind” could be contemplated. It will be close to current attempts on formulating a motor-centered epistemology, which has been deemed by relevant neuroscientists as one the best foundations for explaining our "automated cognition". See different expostulations about the organization of action and advanced cognition (Allman, 1999; Berthoz, 2000; Edelman & Tononi 2000; Arbib, 2001; Fuster, 2003; Changeux, 2004; Buzsáki, 2006; Dehaene, 2009; Nunez, 2010).

4. The Sciences

Is "recombination" too narrow a window when we enter into the organization of the social-cognitive dynamics? Not at all. Although we still lack adequate “theories of mind” to rely upon (as already said, a very unfortunate theoretical void), approaching science itself as a composite informational construction and particularly as *knowledge recombination* looks feasible.

We can quote from Brian Arthur (2009), in his recent approach to the nature of technological change, which is so close to the dynamics of science itself: *"Conventional thinking ascribes the invention of technologies to ‘thinking outside the box’, or vaguely to genius or creativity, but this book shows that such explanations are inadequate. Rather, technologies are put together from pieces — themselves technologies — that already exist. Technologies therefore share common ancestries and combine, morph, and combine again to create further technologies. Technology evolves much as a coral reef builds itself from activities of small organisms — it creates itself from itself; all technologies are descended from earlier technologies..."*

Mutatis mutandis, the recombination idea would apply to science as well. The “natural” division of work within scientific communities seems to reflect the presence of knowledge recombination processes: the need of specialized disciplines and the reliance on paradigms, the fracture and emergence of new fields, the systematic increase in the number of disciplines during last centuries, the clusters and citation networking structures within scientific publications... Disciplines, rather than being isolated fields, are continuously mixing and rearranging their contents, *recombining* them, for the sake of the problems they have to solve, and factually giving birth to successive generations of inter-disciplines (e.g., information-physics, physical chemistry, biophysics, biochemistry, bioenergetics, bioengineering, socio-physics, sociobiology, psycho-sociology, neuro-psychiatry, socio-information, etc.). However, the *recombination of knowledge* has passed almost unnoticed in traditional philosophy of science, notwithstanding the massive presence of the phenomenon in contemporary scientific-technological societies (Scott, 1998). It has been estimated that after the industrial revolution the number of scientific fields has doubled with each passing generation: during the last 30 years, the number has increased from around 3000 disciplines and sub-disciplines in the 70’s, to almost 7000 nowadays. Indeed, science has become too complex a system, and we badly need fresh theoretical new views on how societies create, use, and recombine such a number of fields of knowledge.

The way different disciplines “process” their specific information and create new knowledge, and keep it in record while at the same time this knowledge is widely disseminated so that it can be put into action, and again combined and recombined with elements of all the other disciplines, neatly becomes another information paradigm. Reliable knowledge mediates action/perception cycles of individuals and prolongs them, supra-individually, making possible a more cogent and integrated closure at the social scale. The social creation of knowledge paradigmatically becomes an informational process, ultimately derived from knowledge recombination processes in the cerebral “workspace” of individuals. We really see a “collective nervous system”, a “social workspace” in action. Indeed the “swarm intelligence” that emerges goes far beyond the perception and action capabilities of the limited individual. In point of fact, the strict conditions put by the scientific method are also efficient protocols that grant the social decomposability of problems (Rosen, 2000). The scientific method itself appears from this perspective as the conditions to be met for a coherent decomposition of problems by communities of problem-solvers whose workings are separated in time and space. Standards, measurements, mathematical operations, formalizations, and so on become ways and means to extrovert mental operations out of the individual’s nervous system and directly interconnect perceptions and actions at a vast institutional-social scale (Hobart & Schiffman, 1998). The success of science in this informational jumping over the individual’s limitations has been rationalized as the superiority of the scientific method (leaving aside any communication and thought-collective aspects) or directly attributed to “*the unreasonable effectiveness of mathematics*” (Wigner, 1960). However, there is not much understanding of the underlying “informational” causes (Lanham, 2006; Wright, 2007).

In the same way that we have already developed philosophy of science, history of science, and psychology & sociology of science, we would also need a genuine informational approach to science. Otherwise global visions of the scientific enterprise will oscillate in between the mythical-parochial reductionism (Marijuán, 1996) and the bureaucratic pragmatism of “*seeing like a state*” (Scott, 1998). A well-developed information science should encourage a non-hierarchical relationship between the major disciplines, highlight their mutual interactions, and should also systematically promote the *knowledge recombination* processes, educating for a better and more “real” social usage of multidisciplinary knowledge. Information science should take full responsibility in advancing a new understanding on the integration mechanisms at work in the individuals’ knowledge and a new view on the sciences themselves, which quite probably will be of importance for the future achievement of really sustainable, knowledge-based societies.

5. Evolutionary conclusions: from genomics to *scientomics*

It can be argued that the growth of informational complexity of cells, nervous systems, and societies along their respective evolutionary, ontogenetic, and historical trajectories has been based on the cumulative consequences of knowledge recombination phenomena. From the point of view of “natural computing” there could be some lessons to learn on how very limited “agents” are capable of developing a collective processing that goes far away from the computing bounds of each single agential entity, and that process includes relying on combinations of successful interactive memories of past experiences —knowledge recombination. The recognition of this commonality, however, has been obscured, among other causes, by the structural and dynamic heterogeneity of repositories in the different informational entities, and above all by being subject of quite separated clusters of scientific disciplines: molecular and evolutionary biology, cognitive neurodynamics, philosophy of science/”geography” of science. Seemingly, increased epistemic distance translates into more difficult and less frequent interrelation processes.

At the time being, putting into practical test the recombination idea might be achieved rather partially. There is insufficient development in the neurosciences yet about the set of concepts mentioned (“workspace”, “behavioral-processual engine”, “dark energy”). But there might be sufficient room to compare the biological evolution of DNA codes of protein domains and the social-historical evolution of scientific disciplinary contents. Do cognitive “modules” exist within disciplines that travel to other disciplines and generate new fields there? If so, could the “combinatory” processes in both realms be interrelated?

Culturomics might have already paved part of the way. Borrowing the main concepts and techniques from evolutionary biology, J.B. Michel & E.L. Aiden were able to track the growth, change, and decline of the most meaningful *published words* during last centuries (Michel et al. 2011). The new term they have coined, *culturomics*, means the application of “genomic techniques” of high-throughput data collection and analysis to the study of human culture, as sampled in a vast mapping of words from a corpus of digitized books, containing about 4% of all printed books ever published. Further sources might be incorporated to the culturomic stock:

newspapers, manuscripts, maps, artwork, etc. Analysis of this corpus enables a new qualitative and quantitative investigation of cultural trends, social and political influences, fashions, and all sort of cultural phenomena...

Thus, the knowledge recombination hypothesis applied to the historical evolution of science might be considered in *scientomic* terms, as an evolutionary quest on the combinatory activity of disciplinary modules or domains of theoretical-practical knowledge travelling to other disciplines and changing there the local textures of knowledge, altering the regional maps of science, and the whole complexion of the world of knowledge at large. In other words, influential modules such as Euclidian geometry, Newtonian mechanics, differential equations, genetics, and so on (and a multitude of other minor modules), would have generated the history of sciences, not only "developmentally" inside their own fields, but even more "combinatorially", propelling the multidisciplinary evolution and cross-fertilization among scientific disciplines. In terms of education science something similar would happen too, for an abridged recapitulation resembling Haeckel's law seems to be taking place in the ontogenetic development of an individual's knowledge, which somehow recapitulates the fundamentals of the social acquisition of knowledge along history.

Scientomics, which we are suggesting will be an important future task for the consolidation of information science, appears as a multidisciplinary research-project running in parallel to current achievements of culturomics in the cultural realm, though pointing at some more ambitious epistemic goals. Indeed the creation of a proficient *"scientomics"* new field would help to make sense of the historical processes of science, and of human knowledge in action.

Bibliography

Allman J.M. 1999. *Evolving Brains.* Scientific American Library, New York.

Arbib M.A. 2001. The Co-evolution of Human Consciousness and Language. *Annals of the New York Academy of Sciences,* 929, 195-220.

Arthur B.W. 2009. *The Nature of Technology: What it Is and How it Evolves*. The Free Press and Penguin Books. New York.

Balázsi G., Heath A.P., Shi L., Gennaro M.L. 2008. The temporal response of the *Mycobacterium tuberculosis* gene regulatory network during growth arrest. *Molecular Systems Biology,* 4: 225.

Berthoz A. 2000. *The Brain's Sense of Movement.* Harvard University Press, Cambridge (Mass).

Buzsáki G. 2006. *Rhythms of the Brain.* Oxford University Press, New York.

Danchin A. 2009. Bacteria as computers making computers. *FEMS Microbiol Rev,* 33: 3-26.

Changeux J.P. 2004*. The Physiology of Truth.* Cambridge, MA

Dehaene S., Kerszberg M., Changeux J.P. 2001. A Neuronal Model of a Global Workspace in Effortful Cognitive Tasks. *Annals of the New York Academy of Sciences* vol. 929, 152-165.

Dehaene S. 2009. *Reading in the brain.* Penguin, New York.

Collins K.P. 1991. On the Automation of Knowledge within Central Nervous Systems. Poster and Manuscript presented at the 1991 Meeting of the American Association for the Advancement of Science, Washington.

Collins K.P., Marijuán P.C. 1997. *El Cerebro Dual: Un Acercamiento Interdisciplinar a la Naturaleza del Conocimiento Humano y Biológico.* Barcelona: Editorial Hacer.

Conrad M. 1996. Cross-scale information processing in evolution, development and intelligence. *BioSystems,* 38, 97-109.

Edelman G.M., Tononi G. 2000. *A Universe of Consciousness: How Matter Becomes Imagination*. Basic Books, New York.

Fuster J. 2003. *Cortex and Mind: Unifying Cognition.* Oxford University Press, New York.

Hobart M.E., Schiffman, Z.S. 1998. *Information Ages.* The Johns Hopkin University Press, Baltimore.

Lanham R.A. 2006. *The Economics of Attention.* The University of Chicago Press, Chicago.

Levine M., Tjian R. 2003. Transcription regulation and animal diversity. *Nature,* 424: 147-51.

Marijuán P.C. 1996. First conference on foundations of information science: From computers and quantum physics, to cells, nervous systems, and societies. *BioSystems,* 38, 87-96.

Marijuán P.C. 1996b. Information and symmetry in the biological and social realm: New avenues of inquiry. *Symmetry: Culture and Science*, 7, 3, 281-294.

Marijuán PC. 2001. Cajal and Consciousness: An Introduction. *Annals of the New York Academy of Sciences*, April 2001, 929, 1-10.

Marijuán P.C. 2002. Bioinformation: untangling the networks of life. *BioSystems,* 64, 11-118.

Marijuán P.C. 2004. Information and life: towards a biological understanding of informational phenomena. *tripleC,* 2(1): 9-19.

Marijuán P.C. 2009. The advancement of information science: is a new way of thinking necessary? *tripleC,* 7(2): 369-75.

Marijuán P.C., del Moral R. 2007. The informational architectures of biological complexity. In: *Computation, Information, Cognition –The Nexus and The Liminal*. Dodig-Crnkovic G. and Stuart S. (eds.) Cambridge University Press, Cambridge.

Navarro J., del Moral R. 2010. On prokaryotic intelligence: strategies for sensing the environment. *BioSystems,* 99: 94-103.

Marijuán P.C., Panetsos F. 2011. Towards a Neurodynamic Central Theory. FET 2011. Extended abstract for Poster Session.

Michel J.B., Shen Y.K., Aiden A.P., Veres A., Gray M.K.; Google Books Team, Pickett J.P., Hoiberg D., Clancy D., Norvig P., Orwant J., Pinker S., Nowak M.A., Aiden E.L. 2011. Quantitative Analysis of Culture Using Millions of Digitized Books. *Science,* 331:176-82.

Navarro J. 2010. Transcriptional Regulatory Network of *M. tuberculosis*: Functional and Signaling Aspects. Master Thesis. Universidad de Zaragoza.

Navarro J., Goñi-Moreno A., Marijuán P.C. 2010. Varieties of biological information: a molecular recognition approach to systems biology and bioinformatics. *ITHEA Intern. Journal of Information Theories and Applications,* vol. 4, 1, 56-66.

Nunez PL. 2010. *Brain, Mind, and the Structure of Reality*. New York: Oxford University Press.

Raichle M.E. 2006. The brain´s dark energy. *Science,* 324: 1249-50.

Raichle M.E. 2010. The brain´s (Dark energy). *Scientific American,* March 2010, 28-33.

Rosen R. 2000. *Essays on Life Itself.* Columbia University Press, New York.

Scarrott G. 1998. The Formulation of a Science of Information: An Engineering Perspective on the Natural Perspectives of Information. *Cybernetics and Human Knowing,* 5, 4, 7-17.

Scott J.C. 1998. *Seeing Like a State.* Yale University Press, New Haven.

Sporns O. 2011. The non-random brain: efficiency, economy, and complex dynamics. *Frontiers in Computational Neuroscience*, 5 (5): 1-13.

Turvey MT. 2004. Impredicativity, Dynamics, and the Perception-Action Divide. In: Jirsa V.K. & Kelso S. editor. *Coordination Dynamics: Issues and Trends.* Berlin: Springer-Verlag.

Wigner E. 1960. The Unreasonable Effectiveness of Mathematics in the Natural Sciences," in *Communications in Pure and Applied Mathematics,* vol. 13, No. I (February 1960). John Wiley & Sons, New York.

Wright A. 2007. Glut: *Mastering Information through the Ages.* Joseph Henry Press, Washington DC.

Zamora-López G., Zhou Ch., Kurths J. 2010. Cortical hubs form a module for multisensory integration on top of hierarchy of cortical networks. *Frontiers in Computational Neuroscience*, 4 (1): 1-13.

Yan K.K., Fang G., Bhardwaj N., Alexander R.P., Gerstein M. 2010. Comparing genomes to computer operating systems in terms of the topology and evolution of their regulatory control networks. *PNAS,* 107 (20): 9186-91.

Authors' Information

Pedro C. Marijuán
Bioinformation and Systems Biology Group
Aragon Institute of Health Sciences (I+CS), Zaragoza 50009, Spain
pcmarijuan.iacs@aragon.es