Life Sciences, Information Sciences

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Life Sciences, Information Sciences
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The Centre Culturel International de Cerisy proposes, each year from the end of May to early October and within the welcoming context of a 17th-Century castle, an historic monument, meetings to bring together artists, researchers, teachers, students, social and economical actors, as well as the wider public interested in cultural and scientific exchanges.
A long cultural tradition

– Between 1910 and 1939, Paul Desjardins organized the famous “decades” in Pontigny abbey, to unite eminent personalities for debates on literary, social and political themes.

– In 1952, Anne Heurgon-Desjardins, while repairing the castle, created the Centre Culturel and continued, with her own personal touch, the work of her father.

– From 1977 to 2006, her daughters, Catherine Peyrou and Edith Heurgon, took the lead and brought a new dimension to the activities.

– Today, after the departure of Catherine and then of Jacques Peyrou, Cerisy continues under the management of Edith Heurgon and Dominique Peyrou, supported by Anne Peyrou-Bas and Christian Peyrou, also part of Cerisy castle’s Civil Society, as well as with the support of an efficient and dedicated team led by Philippe Kister.

A like-minded original project

– They receive, in a prestigious setting far removed from urban disturbances and for a relatively long time period, people who are animated by the same attraction for discussion, in order to, through communal contemplation, invent new ideas and weave lasting connections.

– The Civil Society graciously puts the premises at the disposal of the Association des Amis de Pontigny-Cerisy, with no lucrative purpose and recognized for its public interest, currently presided over by Jean-Baptiste de Foucauld, the inspector general of finances.

A regularly supported action

– The Centre Culturel, the main means of action of the Association, has organized nearly 750 symposiums broaching, through completely independent routes, the most diverse of themes. These symposiums have given rise, through various editors, to the publication of approximately 550 books.

– The Centre National du Livre ensures continuous support to the organization and publication of the symposiums. The territorial collectivities (Normandy Region, department Council of the Manche, Coutances Mer and Bocage) and the regional directorate of cultural affairs bring their support to the Center, which also organizes, alongside the Universities of Caen and Rennes 2, encounters on themes concerning Normandy and the Great West.
– A Cercle des Partenaires, circle of partners, formed of enterprises, local collectives and public bodies, supports and even initiates prospective encounters on the main contemporary challenges.

Since 2012, a new modern and accessible conference room has allowed for a new formula: the “Entretiens de la Laiterie”, days for exchanges and debates, a collaborative effort from the partners of the Association.

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Déterminismes et complexités (autour d’Henri Atlan), La Découverte, 2008.


Bachelard, UGE, 10-18, réédition, Hermann, 2011.


Connaissance, activité, organisation, La Découverte, 2005.


Imaginaire, industrie, innovation, Manucius, 2016.

L’industrie, notre avenir, Eyrolles, 2015.

Intelligence de la complexité, L’Aube, réédition Hermann, 2013.

One Hundred Years of Intuitionism (1907-2007), Birkhäuser Verlag AG, 2008.


Des possibles de la pensée (itinéraire philosophique de F. Jullien), Hermann, 2014.


Ouvrir la logique au monde, Hermann, 2009.


Temps et devenir (autour d’Ilya Prigogine), Patiño, réédition, Hermann, 2012.


Logos et théorie des catastrophes (autour de René Thom), Patiño, 1988.


Introduction

The organizers of the Cerisy SVSI (*Sciences de la vie, sciences de l’information*) week wagered that high-caliber researchers from different disciplines, ranging from life sciences on the one hand to information sciences on the other, would have subject material to discuss in *Château de Cerisy* - this exceptional location conducive to reflection – and would be happy to exchange their respective thoughts on the fundamental question of the link between life and information, an intangible element that is even more elusive than life. Several philosophers and ethologists have also brought us their vision. We hope that you will agree, by reading this book, that the wager paid off.

This book begins by questioning the link between the information contained within the genome and the resulting phenotype. This challenging question does not have a simple and unambiguous answer as was initially thought following the discovery of DNA’s double helix. Indeed, Antonio LaZcano reminded us that, shortly after its discovery, Crick said to his son: “The gene is a code”. This is based on the assumption that a cell follows the program written with the four letters of the genome. It is, however, not so simple, as we now know that the follow-up of the process of genome to individual is in no way a straightforward path. Since the 1960s, we have begun to understand that the environment affects gene expression and that in consequence, in a certain sense, the environment influences the phenotype. With the progresses made in epigenetics, it is now well established that methylation affects gene activation and that, in consequence, the same genome can lead to different genotypic traits.
Let us remind ourselves that genes contain sequences of nucleotides, assembled three by three in messenger RNA (transcribed from DNA), and are the “control signals” for any transfer RNA (tRNA), which in turn carry an amino acid. Transported by tRNA to the ribosome, amino acids bind to each other and form a protein. This correspondence system that we call the “genetic code” is “globally deterministic”, but at each stage remains subject to the physiochemical variations of molecules and to the fact that a tRNA can recognize several well-defined nucleic bases (wobble pairing).

We are far from the working principle of a von Neumann computer program, or more precisely a series of instructions (program) transformed by a compiler into machine language that controls elementary operations on data (input) and produces a result (output) or an action. To spell out this analogy, DNA is the program (the instructions); a compiler, tRNA, reads the instructions that are carried out in an assembly machine (the ribosome), which then puts the material (amino acids) together. The proteins represent the result of the program. Unlike von Neumann’s program, as we saw during this symposium, there are many variations that come between DNA and proteins. It is more like a software program, *horresco referens*, which randomly jumps or modifies some instructions, a compiler so poorly made that it is sensitive to external interventions, but so roundabout that it always leads to the production of machine instructions and therefore results!

To return to biology, the first thing that Bernard Dujon demonstrated was that the genome contains a lot of other “information” than the nucleic bases use for their immediate function. It contains ancient “relic” sequences, redundant parts, forgotten parts and bits of genes of undetermined origins. Bernard Dujon’s presentation gives an idea of the immense mish-mash that is the genome. If software programs were like this, not a single application would work!

Bernard Dujon also showed us that evolution mostly works through regression events, a far cry from notions of “progress” and from the linear phylums often cited from a determinist-finalist perspective and in graphic representations of evolution. Bernard Dujon gave us a simple number to show that the size of the genome does not indicate its place in evolution nor the organism’s complexity – *Paramecium* has 49,000 genes whereas *Homo sapiens* have 23,000.

Giuseppe Zaccai, Marie-Christine Maurel, Ada Yonath, András Páldi, Alessandra Carbone and Frédéric Ducongé’s presentations demonstrated the complexity of the

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1 Here, we refer only of protein-coding genes, since there are other genes whose products remain in the form of RNA that are very important at the functional level in cells, but that are never translated into proteins.
operations from DNA to protein and to phenotype. The DNA $\rightarrow$ RNA $\rightarrow$ protein $\rightarrow$ phenotype pathway, although globally deterministic, undergoes undeniable variations due to the external environment and internal chaos due to inevitable anomalies arising from such a complex process. As such, in each DNA to RNA, RNA to protein and protein to phenotype pathway, information from outside of the genome sequence has a role. The environment plays a part in the DNA to RNA process by acting on gene expression, the organism’s external environment and the cell environment. In particular, several papers highlighted the role of physical constraints, thermodynamics and molecular arrangement and pairing dynamics (Giuseppe Zaccai, Alessandra Carbone and Vincent Fleury’s papers). Antonio Lazcano, for his part, demonstrated the essential role of RNA in the origin of life. To finish, Jean Fourtaux paints a rapid picture of evolution whose richness is illustrated by the prodigious diversity of planktonic life, discovered by the “Tara” expedition presented by Christian Sardet.

The second part of these presentations revolves around the notion of variability, randomness, probability and species. As András Páldi wrote: “Variation is an intrinsic property of the living […]. It is stability that must be explained”. This opinion is shared by Philippe Kourilsky who returns to the evolutionary consequences of the principle of variation, the central focus of Maël Montévil, Giuseppe Longo and Ana Soto’s presentations who also remind us that, in Philippe Kourilsky’s words, it is a matter of “freedom under constraint”. We often forget, as Guillaume Lecointre pointed out, that the preservation of species through individual variation is one of the concepts underlaid by Darwin’s famous book on the origin of species. It must be said that the role of randomness in biology is often poorly understood, so what can be said about probability? This is one of the subjects touched on by Cédric Villani.

Since variability is intrinsic to life, it is not surprising that the notion of a species becomes difficult to define, as shown by Philippe Grandcolas. Computer science teaches us that the class, like the species, is a category (Guillaume Lecointre) or a representation, according to Kavé Salamatian, whose term is useful for simplifying the work of programmers or scientists. We are in full nominalism, as reminded by Guillaume Lecointre. However, categories or species are just simplifications, with no tangible existence, and Kavé Salamatian warns us against (Babel’s) temptation of considering programming as a universal representation, which would be very limiting. To avoid intentional categorization, all the elements of a category should be enumerated, for example all elephants with an electronic chip. It is exactly this enumeration that we wish to avoid, despite its potential for certain species on their way to rarefaction! To return to the notion of a species, it is therefore not surprising that several papers returned to this problematic (Philippe Grandcolas, Régine Vignes Lebbe and Guillaume Lecointre). Although it seems very complicated, it is simply because we cannot say that there is an exact correspondence between the genome and the species. Bernard Dujon reminds us that the genomes of two
representatives of the same species are not exactly identical, although they have approximately 95% of their base pairs in common.

From another viewpoint, computer scientists interpret any program as a function that combines an output with all inputs in a determinist manner, following a more or less complicated algorithm. For a given input, regardless of the machine and the environment, the output will always be the same. As pointed out by Gérard Berry, what characterizes this algorithm is its independence from the machine, just as the information is independent of the medium. The algorithm is non-substantial according to Heinz Wismann. He explains how the notion of function arose in the Middle Ages to allow the transmission of ecclesiastic rights at the death of the holder, such as with episcopal function. There is a dialectic between a non-substantiality and incorporation, which refers to the materialization of the function-program on any machine. Cédric Villani returns to this important notion of function by questioning the specific function expressed in a network of neurons, a function that is neither analytical nor definable by extension (contrary to the role of a bishop) because it contains several thousand parameters. What epistemological status should we give to such functions that explain nothing, but that are now widely used?

The property of non-dependence of information on a medium makes it such that, as illustrated by Gérard Berry in his report, algorithms are everywhere, including in life sciences (images, three-dimensional representations, models). Although gigantic, databases do not create knowledge or good representations without algorithms (Maël Montévil and Giuseppe Longo, Régine Vignes Lebbe, Cédric Villani). However, modeling in life sciences poses very specific problems, since life has but very distant links with the automatons of artificial life described by Hugues Bersini, despite some spectacular convergences of form. Life is not totally “determinist” in the traditional sense of the term. It is much more “analogue” than discrete, hence the great interest in research on analogical simulators such as those presented by François Fages and Guillaume Le Guludec, and from which the importance placed on computer reconstructions of chemical reactions (A. Marco Saitta) that shed precious light on prebiotic reactions.

If we return to the cell, there is no doubt that it expresses its genes, but with sufficient variability that we cannot seriously support the analogy with a computer software program. It is a return to function, because even if the DNA molecule is perfectly defined at the chemical level, in the cell its function is subject to the variations in all the other molecules present in the cell, unlike computer programs that are also based on function, but are not subject to variation but to potential errors! It is precisely the conservation through variation that makes the cell different to the machine. The machine’s motto would more likely be: “Conservation through immutability”. Cédric Villani, from his standpoint, also insists on the differences between biology and mathematics in terms of sciences.
However, the process of reproduction as a whole is robust: the daughter yeast resembles the mother yeast and assumes the same functions, the \( n \)th generation drosophila resembles its distant ancestor as though they were two drops of water. This being said, although we can say that one drop of water resembles another, there are still many differences at the macro and nano levels. Life is stable in its variation (Guillaume Lecointre), that is to say variability is the very source of robustness. With all its more or less successful proteins, more or less folded, there will always be some, or often one, that binds to the right place, as demonstrated by Alessandra Carbone.

An overview of the presentations led to the idea that the emergence of life and its development are the result of constant trial and error, devoid of sense, in which what “works” best has the ability to supplant the other inhabitants of a niche and last there as long as there are nutritional resources within it. As we were told by Giuseppe Zaccai, “in physics there are laws, in biology there are only exceptions”.

We return to Darwinism at this stage, but at the heart of the organism at the cell level, this cellular Darwinism opens up therapeutic perspectives in the fight against cancer as indicated by Guillaume Lecointre. However, as Philippe Kourilsky says, this trial and error has its rules (as we have just mentioned) and its constraints (notably that of its environment). It is therefore necessary to complete Giuseppe Zaccai’s comment by saying that the exceptions do however obey laws and are subject to constraints.

In terms of evolution, as evoked by Bernard Dujon, there is a lot of destruction and creation of species through crises. The analogy that springs to mind is that of the creative destruction of Schumpeter. If we were to latch back onto programming, evolution is like an algorithm of simulated annealing, aptly named genetic algorithm. We optimize locally and, from time to time, we jostle the system randomly to prevent from finding ourselves trapped in a minimum local (let us call this an evolutionary impasse). On this topic, Cédric Villani spoke of the “Metropolis” algorithm that is a precursor of genetic algorithms. He did, however, also underline the limitations of simulations and Monte Carlo type algorithms: in the end, what can we understand without a model?

Between DNA and the individual, there are many variations, leading to the question of individuality from a Simondonian perspective. This reflection is introduced by Vincent Bontems. In the process of individualization, several presentations insisted on the role of interaction and instruction. Dominique Guillo introduced the notion of interspecies interaction and the transmission of associated knowledge. Mathieu Lihoreau, Jean-Claude Barrey and Pedro Ferrandiz, Michel Duhamel and Joël Sternheimer team put these exchange processes back into an ecological and ethological perspective.
Such rich exchanges between different disciplines lead to astronomical queries (Michel Cassé) and philosophizing on the roles of the living and the artificial (inforgs) that populate the infosphere (Jean-Gabriel Ganascia). The philosophers question themselves on the possibility of creating informational organisms (inforg) with the attributes of life: is it feasible? Desirable? The answers from Bernadette Bensaude Vincent and Jean-Michel Besnier are clearly and resolutely negative. As we are reminded by Jean-Michel Besnier, in a well established philosophical tradition, humanism is the power to say “no”. Coming from the symposium, there was a desire to add that individualization is, in this sense, the obligate passage of humanism and this power to say “no” begins in the cell with the possibility to not completely obey the genes. From this single action, the cell is most definitely not an automaton.

In a metaphorical sense, let us say that life appears to constitute tremendous trial and error, an intense handiwork fluctuating with the whims of Darwinian selection and varying interactions in a limited and unstable environment. We are very far from a program, but what appears clear is that it is just as important to have information as it is to have matter and that the information is not read the same way at each level. At the genome and cellular levels, there is information that resembles a code but is not one in terms of its execution, which is neither essential nor certain. It is the passage of DNA to phenotype and, finally, to that which characterizes a species, that is the object of the first part of this book: From Gene to Species.

The programming vision is formulated around the notion of an algorithm as explained by Gérard Berry. The algorithm does not vary (or according to another algorithm), which differentiates it radically from the living. Unvarying, it does not individualize itself and this leads to reflections on the notion of individualization and the individual uniqueness in life sciences. This draws a boundary between the automaton and the living, even if they are each informational organisms that interact in the infosphere. The interaction then becomes a central concept in the construction of knowledge. From program to life passing through individualization, interaction and philosophy, such is the main thread for the second part of this book.

**Acknowledgments**

In addition to the countless individual encouragements and support, the organizers would like to thank the following institutions without whose support this symposium could not have occurred: Électricité de France (Region of Paris), Centre National de la Recherche Scientifique (CNRS), Commissariat à l’énergie atomique (CEA), Institut National de Recherche en Informatique et en Automatique (INRIA), Association Reso, Délégation Générale à la Langue Française et aux Langues de France (DGLFLF), Centre des Monuments Nationaux (Administration de l’Abbaye du Mont Saint-Michel) and ISTE Group.