Quantum Biophysical Semeiotics and mit-Genome's fractal dimension

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Abstract

In this paper we highlight the connections between Quantum Biophysical Semeiotics, mit-DNA and mit-Genome. The structure and function of n-Genome and mit-Genome are related with a well define non-Euclidean geometry called fractal geometry, and consequently with deterministic chaos. The alteration of mit-DNA has a primary importance to detect a well defined cell's cytopathy which is the *conditio sine qua* non of very important common pathologies such as cancer, T2DM and coronary heart diseases.
The advanced experimental research in genomics, developing the knowledge of fractal Genomes, both from n-DNA and mit-DNA, through the measure of its fractal dimension, will understand deeply the connection between pathologies, in progress, pre-metabolic, silent and even in their potential stage, i.e., Constitution-Dependent, Inherited Real Risk fractal structures and complex behaviors. The experimental genomics will so finally corroborate what is already given theoretically by quantum biophysical semeiotics: the complexity of biological dynamical systems can be detected through fractal dimension, which is the measure of the health condition of each subject.

"A complete set of genes of an organism, namely its genome, has a huge interconnected network, rich in feedback loops, in which genes regulate each other's actions directly or indirectly. The genome is not a linear series of independent genes (characters) but rather a tightly woven network of reciprocal effects mediated by multiple repressors and de-repressors, exons and introns, jumping genes, as well as structural proteins." (Francisco Varela)

Introduction

Several works of the last decades evidence the importance of deterministic chaos and fractals in genomics, genetics and epigenetic (Capra, 1997).

The research of Kauffman (1993), using binary networks in cellular automata, shows that the genome can be represented with a binary network at the edge of deterministic chaos, or by a network with a frozen core and islands separated from variable nodes. This is a plausible model of evolution and adaptation that has been proved correct.

By studying the complexity of biological systems, the focus has shifted from the structures to the processes that 'emerge' from them. In the past there was the view of genes as stable and clearly distinct units that transmit hereditary characteristics. Genetic stability is instead an emergent property that stems from the complex dynamics of the whole cellular network.

The stability of genetic structure is the result of a well-orchestrated dynamic process that requires the participation of a large number of enzymes, those organized in complex metabolic networks that regulate and ensure both the stability of DNA molecules, and the accuracy of their duplication. The stability of genes is not an intrinsic property of DNA molecules, but a result of complex dynamics of cellular processes.

During duplication the cell not only passes the double helix newly replicated DNA but also a complete set of enzymes, coenzymes and ions needed for metabolic processes such as membranes, including their glycocalicies, and other cellular structures: in short the entire cell's network. In this way, cellular metabolism can perpetuate itself without ever leaving the pattern of their self-generated networks.

In all living organisms there is a subtle balance between genetic stability and mutability; the ability of the organism to actively produce mutations is only acceptable if it helps evolution. The regulatory mechanisms of mutability show a growing abundance of details. The mutations, actively generated and regulated by epigenetic cell network, and evolution are an integral part of self-organization of living organisms.

The decoded human genome is nothing more than the alphabet, and is dynamic rather than static, and his combination of letters, gradually varying according to which letters are activated, denote human physiological behavior. And like any language, is destined to evolve, to change over time, while retaining its stability. The illegal extension of a genetic paradigm by the relatively simple coding and decoding to the complex genetics of cell function is an epistemological error: the genes seen as the causes of all biological phenomena is a confusion between different levels. The principle - a gene, a protein - may not be valid.

Keller discovered that the signal (or signals) that determine the specific order or pattern to which DNA must conform after recombination as a result of the final transcription process comes from those regulating complex dynamics belonging to the cell in its wholeness (Capra, 1997). From the dynamics regulating the cellular network can emerge many different proteins from a single gene, and a single protein can develop multiple functions. If we shift our attention from a single gene to the entire genome, there are many other problems that cast doubt on the idea of genetic determinism. For example, when a cell divides during

development of an embryo, each new cell receives exactly the same number of genes, but these cells then take on very different skills (muscle cells, blood, nerve, etc.). The types of cells do not differ from each other with regard to the genes they contain, but with regards to those that in each of them are actually being active in the presence of different mitochondrial kits. Genes do not act on their own behalf, but must be activated.

For example, Monod et al. (1961) introduced a theory: a distinction between structural genes that encode proteins and regulatory genes that control DNA transcription and thereby regulate gene expression.

Recent research has revealed the fractal structure of the cytoplasm (Aon, 1994), of the genome (Lieberman et al., 2009) and the chance that the electron can be represented with the typical complexity of a strange or chaotic attractor (Horwitz, 2004).

What emerges from these studies is the deeper understanding that biological processes involving genes are all regulated by the cellular network in which the genome is integrated, ruled out by a fascinating scheme. This network is a highly non-linear reality, a reality that contains multiple chains of feedback, so that patterns of genetic activity change constantly in response to changing circumstances. DNA, although certainly being an essential part of the epigenetic network, is not the only causative agent of forms and biological functions, as stated in the central dogma. The form and biological functioning are emergent properties of nonlinear dynamics of the network and we expect that our understanding of these processes of emergence will increase significantly with the application of chaos theory to the new discipline of epigenetic. Recent experiments in genetics have shown that the loss of individual genes - even if thought to be essential - has very limited effects on the functioning of the body (Capra, 1997). Under this remarkable stability and robustness of biological development, an embryo may be different from the initial stages - for example in case individual genes or whole cells are accidentally destroyed - then still reach the same mature form that characterizes the species to which belongs.

Natural selection does not operate on individual genes but on the scheme of self-organization bodies. It is possible to represent the whole process of biological evolution as a trajectory in a phase space that moves within a basin of attraction to an attractor (Medio, 1992) that describes the functioning of the body in the stable form that characterizes his adulthood. Complex systems exhibit nonlinear structural stability. A basin of attraction can be distorted or disturbed without changing the fundamental characteristics of the system. In the case of an embryo during evolution, it means that it is possible to change, to some extent, the initial conditions of the process without seriously damaging the development of the whole organism. Therefore, the stability of development, which remains a mystery from the perspective of genetic determinism, is clearly a consequence of basic properties of complex nonlinear systems.

DNA mutation and recombination are the two main way of bacterial evolution, but Margulis (1993) discovered a third way: the symbiosis. The most remarkable evidence of evolution through symbiosis - the tendency of different organisms to live in close association with each other, as the bacteria in our gut - is offered by mitochondria[i], the power plants that are found within most nucleated cells.

These fundamental components of all animal and plant cells that perform cellular respiration, contain their own genetic material and reproduce independently and at different times than the rest of the cell, and in fact have their own DNA, mitochondrial DNA[ii].

State of art

Deterministic chaos and non-local realm

Deterministic chaos has been defined[iii] as the 'stochastic or probabilistic behavior occurring in a deterministic system' and its main characteristics are the uncertainty and unpredictability, but is possible to detect and investigate it and to get qualitative information through invariant statistic measures such as LCE[iv], fractal dimension[v] and entropy[vi] (Medio, 1992).

Entropy represents the rate of uncertainty, or equivalently, the rate of variation of qualitative information of dynamical systems, and is important in the causal interpretation of quantum theory (Bohm, 1980), which supposed the electron to be a certain kind of particle which follows a causally determined trajectory[vii]. In addition to Newtonian classical potential, the particle[viii] moves according to a new potential, called Quantum Potential – QP – which is determined by the quantum wave field[ix], or wave function. QP is independent of the strength, or intensity, of the quantum field but depends only on its form, so that the information in the form[x] of the quantum wave directs the energy of the electron and even distant features of the environment can affect this movement in a deep way.

The feature, in which very distant events can have a strong influence, is what is meant by a non-local interaction. Non-locality implies an instantaneous connection between distant events and does operate in nature, as proved by Aspect et al. (1982), who provides strong evidence for a nonlocal form of interaction. This result follows in a natural way, within the causal interpretation, as a result of the nonlocal QP that directly connects distant particles.

Sub-quantum behaviors and biological systems dynamics are usually considered as separated and different worlds, but there are some interesting works as Lory's experiment (Stagnaro, 2008a) that open new perspectives about the presence of non-local realmin biological systems. Furthermore, since life system is based on the communication system, DNA functioning can not only be seen as a storage of genetic information. We can consider DNA/RNA dynamic system as an Information Energy – EI – catalyst (Manzelli, 2009) able to transmit and receive bio-physical quantum signals to and from the proteins in the living cells, so DNA can be thought as an "antenna" transmitting nonlocal information[xi] through 'gene quantum signals'(Stagnaro et al. 2007, Stagnaro 2010b).

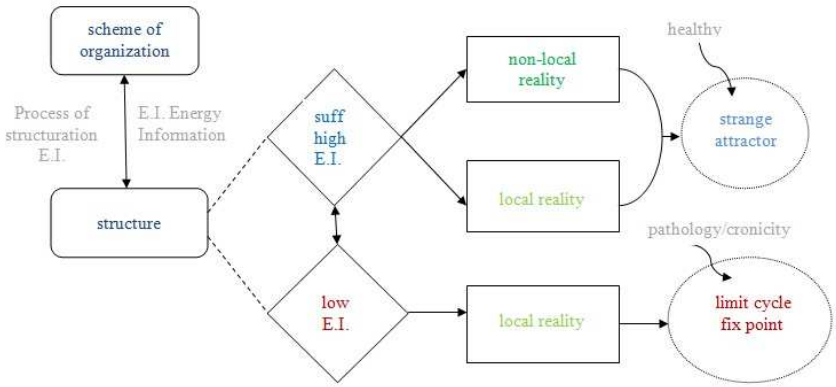
In biology, Varela et al. (1974) proposed the theory of autopoiesis, useful to understand the connection between organization and structures in living systems. An autopoietic system, so as described by Maturana and Varela, is based on a scheme of autopoietic organization through a process of structuring which can lead to different structures. The autopoietic organization is conservative and always acts on itself: self-production, self-regulation, self-referential, recursion, circularity. The scheme of organization works relentlessly to achieve the

autopoiesis through a continuous process of structuring, generating dissipative structures with non-linear dynamics (Prigogine, 1967).

There is structural coupling between organization (conservative) and structure (dissipative) to always achieve the autopoiesis. If there was a tendency to disease (or if there is pathology), the organization would always be orientated towards the survival, materializing and engaging compensatory mechanisms to restore groped the simultaneity and synchronicity.

In a previous work (Caramel et al., 2010a) we tested successfully in biological systems the hypothesis of the correlation between nonlocal reality and deterministic chaos, of the co-presence of local reality and non-local reality in physiological states, and of a sufficient high amount of information energy – EI – as catalytic process to maintain non-locality in the autopoiesis.

If the system were fully healthy, there would be actually a non-local reality (parallel to the local reality) - simultaneity and synchronicity - and the presence of deterministic chaos (chaotic or strange attractor). If there was disease, the autopoiesis would still be present, but the non-local reality and the correlated strange attractor equilibrium, corroborating the presence of deterministic chaos, would disappear so that we would observe just limit cycle equilibrium in the case of pathology, and fixed points in case of chronic diseases.



Scheme 1. Autopoiesis and Energy Information

Most of metabolic processes are catalyzed by enzymes and receive energy through special molecules known as organic phosphate or ATP, of mitochondrial origin. All cellular structures exist in conditions far from thermodynamic equilibrium: they are dissipative, far from equilibrium with their own stability, spontaneous emergence of new forms of order. As the flow of energy increases it is possible that the system encounters an instability - fork - at which the system itself can enter into a completely new state, where new structures and new forms of order can emerge - emergences - or self-organization.

Creativity is a key property of all living systems, and if cell metabolism does not use a constant flow of energy to repair structures as soon as they are damaged, quickly they would decay to steady-state: the cell would die (from chaotic attractor to limit cycle to fixed point). If the blood flow is reduced in an artery, the microcirculation would activate itself, but the fractal dimension would be reduced. We then describe the cell as an open system. Living systems are closed at the level of organizational structure (they are autopoietic networks), but open in terms of materials and energy. "*The cell enter in connection automatically with other bodies. If it expels something, there will be any other body that will absorb it*" (Lynn Margulis)

Mitochondria and mit-DNA

DNA mutation and recombination are the two main way of bacterial evolution, but Margulis (1993) discovered a third way: the symbiosis. The most remarkable evidence of evolution through symbiosis - the tendency of different organisms to live in close association with each other, as the bacteria in our gut - is offered by mitochondria[xii], the power plants that are found within most nucleated cells.

Margulis believes that mitochondria were originally bacteria floating freely. In ancient times these bacteria invaded other microorganisms so that they first settled in them. These bodies fused together then evolved into more complex life forms, breathing oxygen. There was therefore, in this case a more abrupt evolutionary mechanism of mutation: a symbiotic alliance that became permanent.

These fundamental components of all animal and plant cells that perform cellular respiration, contain their own genetic material and reproduce independently and at different times than the rest of the cell, and in fact have their own DNA, mitochondrial DNA[xiii]. In the cell there are therefore two DNA: nuclear DNA (n-DNA) and mitochondrial DNA (mit-DNA), and parallel to the nuclear genome there is mitochondrial genome. Men and women inherit the mitochondrial genetic code almost entirely from the mother: this is because the mitochondria in the sperm are present only in the tail, which does not enter the oocyte.

In mitochondria a relative abundance of inorganic ions, potassium, magnesium and phosphate is present plus in mit-DNA, cytosine and guanine content is higher than in n-DNA. Indeed, part of the mitochondrial proteins are synthesized within the mitochondrion itself, under the control of its mit-DNA, which replicates autonomously, since it contains the necessary information - a particular genetic code - for the synthesis of the inner mitochondrial membrane enzymes. Mutations and alterations in mit-DNA occur six to seven times more often than in n-DNA, presumably due to the lack of protective histones in mitochondria and because of the fact that the mit-DNA is closer to the electron transport chain, exposing high concentrations of free radicals, which can damage the nucleotides. Furthermore, in mitochondria the DNA repair mechanisms are lacking, so that mutations in t-RNA, r-RNA, and in the transcription of proteins are more frequent than in the rest of the cell. The basic elements to build DNA, RNA and enzymes, the power's vectors which supply each one of the above mentioned processes, are given by the mitochondrial activity.

Quantum Biophysical Semeiotics: consequences of mit-DNA alteration

According to Stagnaro (2004a), genome's information are transmitted simultaneously both to parenchyma and related micro-vessels, so that mutations in parenchymal cell n-DNA and mit-DNA are the *conditio sine qua non* of the most common human disorders, like diabetes, CAD, and cancer, today's epidemics.

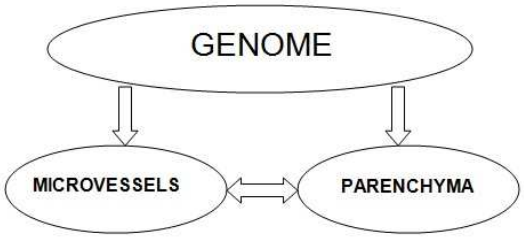
In fact, all these diseases are based on a particular congenital, functional, mitochondrial cytopathy, mostly transmitted through mother, and defined Congenital Acidosic Enzyme-Metabolic Histangiopathy, CAEMH (Caramel et al., 2010a).

The contribution of these modifications to the relative pattern of diabetic syndrome, based always on genetic or inborn errors – CAEMH - is different from patient to patient and during the disorder's evolution. For instance, in case of diabetic syndrome, insulin-secretion increases silently for years or decades, before appearing as Type 2 Diabetes Mellitus - T2DM, at the fifth and final stage of its natural history (Stagnaro, 2010c).

This pre-clinical stage is not detectable through usual clinical tests, so it is necessary to explore new approaches, such as that introduced by Quantum Biophysical Semeiotics – QBS – (Stagnaro, 2007b), which through bed-side evaluation, can assess the existence of pre-metabolic syndrome[xiv], that can last for years or decades, pre-clinical stage of the disease still potential or on training (evolution to pathology, pre- morbid state or gray area), so allowing an effective prevention (Scheme 3).

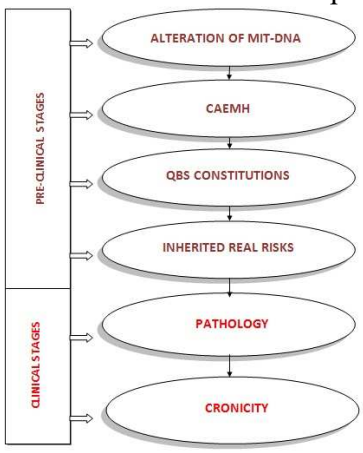
In addition, parenchymal gene mutations cause local microcirculatory remodeling, so doctor can evaluate it at the bedside in a reliable manner, gathering indirect information on inherited modifications of relative parenchymal cell, since biological system functional modifications parallel gene mutation, according to Angiobiopathy theory (Stagnaro, 2008i).

The presence of intense CAEMH – termed CAEMH-'alfa' - in a well-defined area, i.e., myocardium, involved by gene mutations in both n-DNA and mit-DNA, is the ground for one or more biophysical semeiotics constitutions[xv] (Stagnaro, 2004c) which could brings about their respective congenital Real Risks - RR (Scheme 4) characterized by microcirculatory remodeling from QBS viewpoint, especially intense under environmental risk factors.



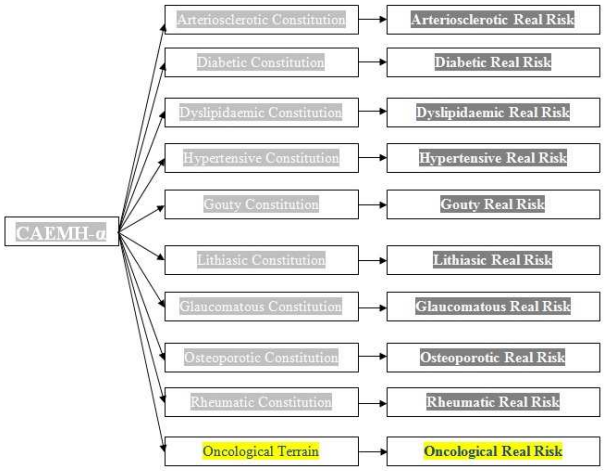
Scheme 2. Genome affects both micro-vessels and parenchyma

In Scheme 2 it is shown that genome affects both micro-vessels and parenchyma, according to Stagnaro's Angiobiopathy theory (Stagnaro, 2009a). Investigating the micro-vessels, whose behavior is typical of dissipative systems far from equilibrium, this is a way to get indirect information from the state of health of their respective parenchyma.



Scheme 3. Pre-clinical and clinical stages of diseases depending on mit-DNA alteration

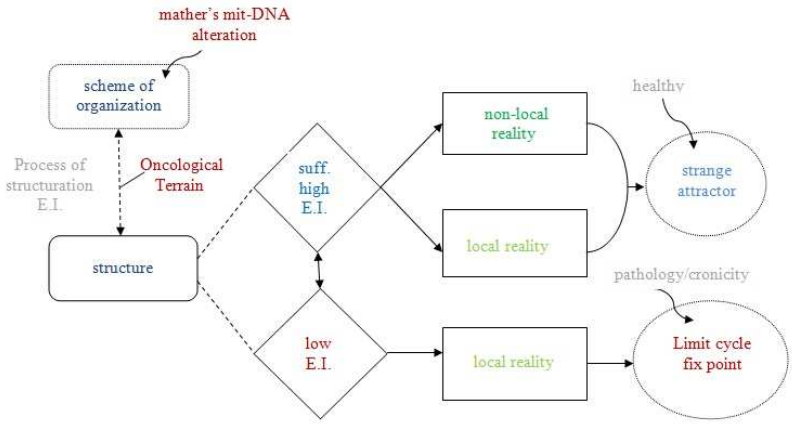
The congenital micro-vascular remodeling, shows since birth interesting structures, i.e., newborn-pathological, type I, subtype b), Endoarteriolar Blocking Devices, EBD, localized in small arteries, according to Hammersen (1968). As a consequence of above, briefly referred remarks, physicians are able nowadays to demonstrate the presence of typical pathological EBD in well defined micro-vessels, which play a central role in Inherited Real Risks.



Scheme 4. CAEMH-α, QBS constitutions and associated real risks

Through the objective QBS examination, it is possible to recognize in a few minutes and quantify if a patient has got any QBS constitution and congenital Real Risk (RR) to have a disease.

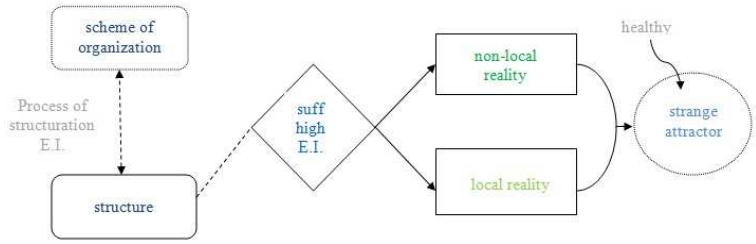
Summarizing, through QBS the doctors are able to evaluate the pre-clinical stages of the process of oncogenesis, and of many other diseases, of their patients, as shown in Scheme 3, so it is possible a pre-clinical diagnosis of the potential pathology, at bed-side, before the clinical diagnosis[xvi], i.e. the activation of 'sleeping' cancer cells (Stagnaro, 2004a), which start the clinical process of oncogenesis.



Scheme 5. Autopoiesis and Energy Information in presence of Oncological Terrain (OT)

As shown in Scheme 5, the QBS is able to diagnose the presence or absence of Oncological Terrain (OT) at birth, before the disease can appear, at an intermediate time between scheme and structure, allowing proper and timely preventive measures. If absence of

OT is detected at birth, it is clear that no scheme could never be structured in any of the cancerous diseases, identified by Stagnaro. This is the boundary line.



Scheme 6. Autopoiesis and Energy Information in absence of Oncological Terrain (OT)

Scheme 6 shows that in human bodies there is physiologically the healthy co-existence of two different realities: local reality and non-local reality. The non-locality disappears if the mitochondrial respiratory activity, and consequently EI, significantly decreases. For example, Lory's experiment (Stagnaro 2008b) fails if a stimulation is applied in a subject, following the Apnea test, with the result of an impaired mitochondrial activity. The compensation takes place because of 'nuisances' involving dissipative structural changes, but always subject to the power system's and its inherent conservative autopoietic organization.

The QBS congenital Real Risk therefore arises at an intermediate stage between the scheme of organization and the structure, a first 'structuration' from the scheme (not observable) on which we can identify it (in case there was) using simple clinical tests at bedside, in a vision in which if there were RR, it would be able to tend to a pathology (potential disease), a pathology which, if it occurred, would amount to a fully 'structuration' of the scheme of organization (i.e., genetic alteration of mit-DNA) to disease. RR, if pathologically evolving, is the slow 'event eventing' of disorders. Also considered in itself, whether static, it is a manifestation of the structuring process of the organization. The process is reversible in the sense that - through melatonin-conjugated[xvii], administration of energy (i.e., NIR-LED, Near Infra Red light-Led), and proper diet understood in the etymological sense, etc. the RR can become "residual", so that it will not disappear nor will evolve towards the structure.

The principle of the process is the Energy-Information (EI), which is catalytically in nature. The level of Vibration-Energy (EV) related to energy-information (EI) from the perspective of QBS is measured on the level of tissue oxygenation: namely the latency time of reflex, which is not a reflex in true. Indeed, stimulating the trigger-points of a biological system, such as the liver, "simultaneously" there is built up a sympathetic hyper-tonicity after a latency time dependent on the intensity of the stimulus: this is related to the intensity of liberation of adrenaline and nor-adrenaline in the biological system, so that we can observe the nonspecific gastric reflex, the stomach swells, "simultaneously" when the critical level of low energy or low oxygen is reached.

Under these conditions, in fact the biological system has become thermodynamically isolated. We are in this case, in the non-local reality: there is simultaneity and synchronicity. On a completely healthy human being (without RR) EI is in fact high enough, and then there is simultaneity of information. Local and non-local reality co-exist, exist simultaneously but in parallel, they do not overlap. When EI decreases, EM –Energy Matter – as a consequence

increases, and whether EI falls below a certain threshold, non-local reality "disappears" and we can observe just local reality. Summing up, if there is enough high EI, there is not RR, while if there is low EI, non-transitory and not occasional - low EI in transient form, for instance, is with the Apnea test in completely healthy individuals without RR – since but permanent, then there is RR (associated, i.e., with Oncological Terrain).

The production of EI may be endogenous - it is created endogenously in humans through a transformation of breath in subtle and vital energy, and through mitochondrial activity - or exogenous - through the release of substances like melatonin, the adoption of an appropriate diet, NIR-LED (near infrared light) – that stimulates the mitochondrial respiratory function[xviii], i.e., oxidative phosphorylation.

The endogenous EI is born and formed in the mitochondria, the power plant of human body. The autopoietic system self-produces EI, by transforming EM, including food, water and O_2 - which is converted into EV-EI. Endogenously we produce ourselves the EV-EI indirectly with the breath, in the sense that vital energy is a subtle energy that occurs through breathing (it is not air, it is not breath, but it travels and is created together with it).

Exogenously the EI is created by chemical transformations and biological properties of certain food we eat or through the release of specific substances (e.g., conjugated - melatonin) or certain stimuli (e.g., LLLT, including NIR-LEDs) to improve the mitochondrial respiration.

In biological systems the Energy-Information can be transmitted chemically - through metabolic processes - and/or electrically - with the neurotransmitters - peptides. The peptides can be imagined as an "antenna", which carry information (waves) non-locally, simultaneously and synchronously by resonance (in case of non-local reality with high EI), or locally in space-time.

In biological systems the EI is transmitted through the classic routes in the local reality, using substrates that reach the target tissue via blood, lymphatic, venous (hormones, cytokines, etc.) or through the nerve pathways (neurotransmitters) characterized by polarization - depolarization: there is time and energy consumption (if I move a substance from A to B, this implies waste of energy, and spending time). On the contrary, in non-local reality pure and catalytic EI acts according to what is known in the microscopic world, expression of entanglement, observable with the QBS, of both worlds. DNA, like an antenna, starts to "vibrate", simultaneously to "intense" stimulation on certain trigger - points, catalyzing the reactions without energy expenditure, between the compound A and B, with production of C. For example: abdominal lateral pinch of fat "simultaneously" active function of liver PPAR (the mill that burns fat and glucose) revealed by the "simultaneous" local microcirculatory activation[xix].

There is a continuous structural coupling of bodies-environment in all directions. If there is a tendency to disease (RR), the complex dynamics in biological system decreases: there is no chaos or lesser according to the fractal dimension (fD), detectable through the diagnostic-percussio-auscultatory-reflex (Stagnaro, 2004a), with the simple use of the stethoscope, measuring the latency, intensity and duration of reflexes. The absence of the strange attractor or of deterministic chaos, is signal of low EI, the entropy is tending to zero, then in this case there is a local reality of information transmission, there is not the non-local reality. We must therefore enter EI (or create the conditions to increase it) in order to restore a sufficiently high

level of EI. In accordance to Angiobiopathy (Stagnaro, 2009a), by improving mitochondrial activity in the parenchyma and in micro-vessel intracellular free energy cells is involved favorably and various biological activities are improved: the microcirculation will be normalized, if not activated in a physiological way (type I, associated, microcirculatory activation).

QBS allows accurate and direct study of well being and functioning of micro-vessels and only indirectly of the related parenchyma[xx]. If it improves the way of being and functioning of the microcirculation this does mean that it also improved the way of being and functioning of its parenchyma. This is done by stimulating the activity of mitochondria by acting on the vehicles that transmit EI: metabolism (chemical process), peptides' net (electric-electronic process), but also by improving, normalizing tissue oxygenation, expression of the normal operation of mitochondrial oxidative phosphorylation. Indeed, the mitochondrial functional cytopathy is the *sine qua non* of the more frequent and severe human disease and not.

Exogenous prevention and therapy (with environmental action) is done directly on EI (and related EV) at chemical level: proper diet, conjugated melatonin, NIR-LED, or at electric level: such as acupuncture, which also acts on neurotransmitters or peptides. Endogenous prevention and therapy (autopoietic) can be implemented for example through: improving the quality of breath, improvement of lifestyles and slow pace of the same (e.g., eating serene, calmly, as appropriate as possible) choice of appropriate physical activities (exercise, sports), yoga, meditation, prayer.

We are composed of a continuum of biological systems which interpenetrate and interact one other, and in health conditions show a chaotic behavior, measured by the fractal dimension, as shown in Table 1.

Fractal Dimension fD	**Equilibria**	**State of health**
fD = 1	fix point	Chronic disease – chronic and acute pathology
1 < fD < 1.9	limit cycle tending to fix point	pathology – tendency to chronic disease State of variable severity of disease evolution
1.9 ≤ fD < 3	limit cycle	initial implementation of the tendency to disease /potential pathology- i.e. Oncological Terrain (TO) – initial evolution to disease
3 ≤ fD < 3.81	limit cycle tending to strange attractor	tendency to physiologic condition (only potential phase)
fD ≥ 3.81	strange or chaotic attractor	Physiologic condition – healthy state

Table 1. State of health, equilibriums and fractal dimension

Legend: the fractal dimension (fD) is calculated as the time of the disappearance of gastric aspecific reflex, before the appearance of the next. It is important that the fD is directly related to (d) or inversely (INV) related with:

A) (d) the local microcirculatory functional reserve - (vasomotility and vasomotion) and then

B) (d) with the presence, or not, of the local congenital Real Risk;

C) (d) with the latency time of gastric aspecific reflex and then with tissue pH;

D) (INV) with the duration of the gastric aspecific reflex

In the autopoietic living biological system (e.g., nervous system, immune system), if there were a disease, the autopoiesis would still function. The organization would remain intact, it is stable, continuous, always on, it is a conservative system, and if it there were not, the structure and the system would disintegrate, life itself would disappear! In macro-interacting biological systems there is a "mind" synthesis of an autopoietic system that is based on a composite unit (i.e., psycho-neuro-endocrine-immune system).

If the system were fully healthy, there would be actually a non-local reality (parallel to the local reality) - simultaneity and synchronicity - and the presence of deterministic chaos (chaotic or strange attractor). If there were disease, the autopoiesis would still be present, but the non-local reality and the correlated strange attractor equilibrium, corroborating the presence of deterministic chaos, would disappear so that we would observe just limit cycle equilibrium in the case of pathology, and fixed points in case of chronicity. The presence of just the local reality is a consequence of the reduction of EV and EI, but with proportional increase of EM.

Chaos appears to be one of the sources of life. If chaos is not (or is missing) we can create the conditions for it to emerge again. Chaos in biology is related to life: where it is missing and at the same time we cannot restore it, it is the end. For example, through the use of melatonin conjugated, the energy level raises and then EV-EI increase fostering and perpetuating the non-local reality parallel to local reality. If there were only local reality (which denotes a tendency to disease or pathology or potential disease) it would then need to return to a more complex order (chaotic attractor), but only if there is deterministic chaos arising from well-functioning mitochondria.

1st Conjecture: reversibility of mit-DNA's alteration for future generation

If a patient is positive for Oncological Terrain - OT, detected by mean of a QBS diagnosis, he/she has the opportunity to make an effective primary prevention, especially in the case of Inherited Real Risk of Cancer, so that his/her Real Risk becomes "residual", i.e., not dangerous. This means that the QBS constitution(s), i.e., the Oncological Terrain will not disappear, but with a proper prevention, his/her Real Risk will become residual: he/she will never be affected by a cancer. The point is that the alteration of mit-DNA, evidenced by ICAEM, still exists, so that it will be transmitted, mostly by mothers, to future generations. While it is almost sure that a mother with positive OT will transmit her mit-DNA's alteration to sons and daughters, what about a mother or future parents both with positive OT under an effective preventive treatment in order to make residual their Inherited Real Risk? What about their children? Will they be born with negative or positive Oncological Terrain? These were the questions made by Stagnaro (2004c) in order to understand the reversibility, or not, of mit-DNA's alteration for future generation.

The Stagnaro hypothesis (1st Conjecture) was that *the alteration of mit-DNA is reversible for future generation*: if future parents, both positive for OT, accept to make an effective preventive therapy before procreation, their children will be negative for OT, they will never suffer of any cancer, both solid and liquid, in the study cases of QBS.

2nd Conjecture: Genome's chaotic dynamics and fractal structure

The differences appear to be structured in patterns of gene expression rather than the genes themselves.

The above mentioned theory of autopoiesis based on 'scheme of organization and structure' can be extended to triad: organization, structure, process (Capra, 1997). We often hear that genes contain the information that characterizes a living being. We can say that this is a mistake for two main reasons. First, it confuses the phenomenon of heredity with the replication mechanism of certain cellular components (DNA) that have greater stability through the generations. Second, because if we say that DNA contains what is necessary to characterize a living being, we leave apart these components (part of the autopoietic network) from their interactions with the rest of the network.

The network of interactions in its entirety is what constitutes and specifies the characteristics of a particular cell, not just one of its components. The fact that changes in these components called genes have a tragic consequence for the structure of a cell is certain, however. The mistake is to confuse the essential with the sole responsibility of participation. By the same reasoning one could say that the political system of a country determines its history. This is patently absurd: the political system is an essential component of whatever the story, but does not contain information that specifies this story.

In the theory of autopoiesis, Maturana and Varela speak of single scheme, which is followed by different structures. Capra supports this theory by introducing what links structure to scheme, namely the process (the principle of which in QBS is identified with the Energy Information by Manzelli). While speaking of the cells, Capra is sticking to Maturana and Varela (a scheme, different structures); now dealing with DNA and genes and the genome, he is in trouble, and says that there are more schemes of organization.

What line to follow? From each organization scheme certainly different structures can arise, but it is true that an organization scheme can itself be a structure that is derived from a scheme of organization upstream, so in this case it can take different structures, such as human genome (either n-genome or mit-genome).

Each structure refers to an unique scheme of organization: there is an underlying determinism, an accurate divine plan, conservative, albeit in a series, a 'Shiva's' dance of creation and destruction, which as an old wise-man is always tending towards a cosmic stability, with its wisdom. Any scheme of organization may lead to different structures: in QBS the process of structuring the scheme favored by EI. If EI (Energy Information) decreases, because EV (Vibratory Energy) decreases and the EM (Energy Matter) increases, then the structure changes.

This is because we firstly look at the structure, not knowing the scheme, so we see this diversity in the relationships between components, in the relationships that develop between the different genes (activated or not): the relationships between components denote the structure. What produces rather different relationships between genes, what gives diversity and differentiation in the structure? This is given by the process of structuring, whose principle is Energy Information. *In the light of chaos theory can be conjectured* - 2nd conjecture - *that the Energy Information "called" informational parameters* (learning parameters, adaptive parameters, flexible, changeable parameters seen as pseudo - variables in a continuous learning process) *leading to ever active different configurations.*

Some parameters should be of type 0-1 (on-off), while others may be different in nature as defined in accordance with the scheme of organization. How does complex dynamics of chaos theory work? Through computer simulation, it is possible to observe in a monitor the bifurcations or attractors dynamics of a system, varying its qualitative parameters. Varying even just one parameters, is possible to look at how dumb the configuration of the attractor. The attractor, which shows fractal pattern in the case it were strange, is the image of the structure, the scheme's 'structuring' (Figure 1). The continuous process of structuring, from scheme to structure, is given by the experimental simulation, i.e., caused by a change in the parameters (by holding one while the other are fixed, or more at a time). Entering different Information (different input parameters, gradually), we can say that we enter Energy Information.

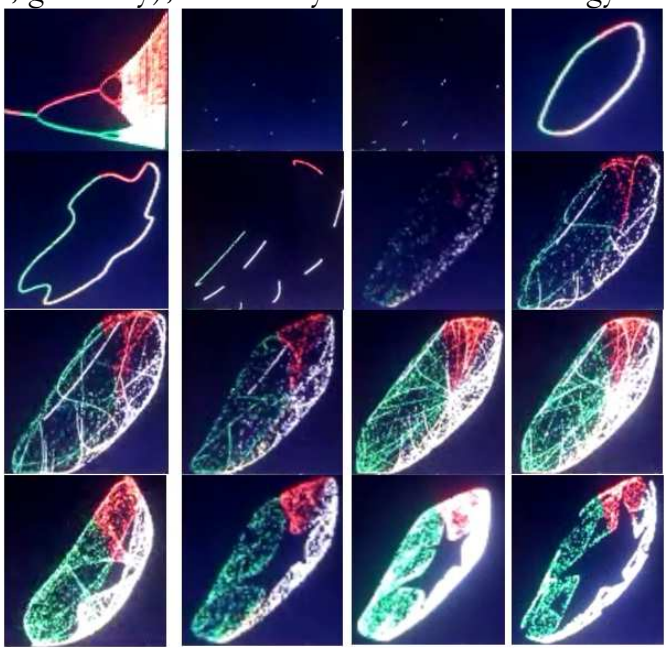


Figure 1. Attractor dynamics

Attractor's dynamics evidence a structure, an ever changing cloud of points showing a harmony, a structured order, which "zoomed" always gives the same designs on scales more small: *is a fractal*. Connecting these dots with lines, we have a network of lines, which following the initial setup, using some imagination, show the links between different genes. If just one parameter is very little modified, we can look at significant qualitative changes in the cloud of observed points, denoting the activation of such new points - activation of new genes - and off a few points just seen on - off of old genes just observed (Figure 2).

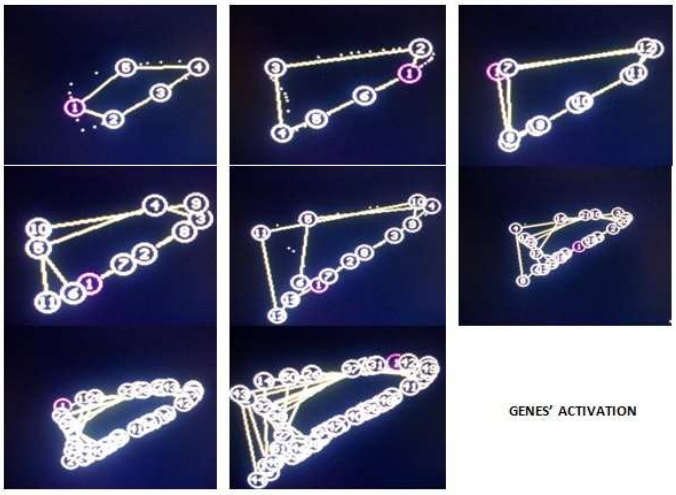


Figure 2. Genes' connections

From this last observation we can say that it is not essential that in EI there is a direct correlation with the genes (the above hypothesis about parameters on/off is not essential and indispensable). In fact, the 'on-off' is given simply by the configuration of the parameters operating on the scheme of organization, which let observe the final structure in some way, from time to time, and which is a network of interrelated genes, in a feedback interactive relation one another. Therefore not always the same assets is given: i.e., if the parameter a = 0.0000000278 changes to a = 0.0000000277, we do not know yet what effect will be produced on genes, we do not know which genes are induced from this parameter to switch on and which ones to shut down. This will be known lately looking at the final structure). We must follow the temporal evolution of the event, because we will never perfectly know the initial conditions, which would enable the accurate prediction!

This hypothesis is perhaps more likely, because although there is an underlying determinism (scheme of organization) there is extreme sensitivity, adaptability, flexibility, mutation. Should we also think about a moment by moment determinism which says at every step: "these genes be active, these not"? Bohm says that there is moment by moment, a causal background, as the implicate order, but not strictly deterministic, and that is why there is vagueness, unpredictability, and space for creativity. It is our observation that builds relationships, functions, interpretations of cause and effect, but in the theory of dissipative systems it is quite clear that everything happens in a self-regulating way, there are always balances complex structures, far from equilibrium named emergencies.

And these emergencies seem spontaneous. Spontaneity is not random, it has a fund of determinism behind, given by the scheme of organization, it is nor causal in the strict sense, because there is spontaneity. There may be an ex-post causality in the sense of definition given by an observation according to its cognitive domain and its global observation in the context of the structural coupling observed (Causality not as fact but as a mere ex-post interpretation' saied Nietzsche): biological system - environment - observer, which is a causality in the sense of Bohm due to the existence of underlying hidden order (and still unknown to science) generative and implicative of varying degrees, hierarchically intricate.

In the theory of extended autopoiesis, including the structuring process, as we talk about open systems far from equilibrium, one might think that the EI interacts (communicating) with all biological systems derived from the same embryo in the body - this is

allowed in case of EI's high level because the non-local realm and simultaneity; there is not energy's consumption - and then with all the systems seen as continuously connected to the network, i.e., PNEI system, taking the information from this interaction, which goes to denote the Energy Information at any moment of the autopoietic process - hence the continuous updating of the parameters that shape the underlying scheme in the human genome, seen just as a network of complex non-linear relationships between the various genes that may be active or not.

Moreover, the initial hypothesis - on/off parameters to set step by step genes activation - is likely because what we see on the monitor, the cloud of dots, are not genes, but is a mathematical abstraction - previously metaphorically identified as genes, for ease of explanation. And the hypothesis of 'zero-one' parameters is consistent with a vision of determinism background (scheme or pattern), but not marked (step by step), because the 'zeros-ones' are not given from something already written at the time of creation (at least in the strict sense), but by the interaction of EI with all biological systems of the body (learning themselves, in turn interacting with the environment, in turn autopoietic, but closely related and interacting with one another, in turn adaptive, flexible, changeable learners) and the external environment. These parameters should denote moment by moment the synthesis of the present moment (in case of high EI, non-local reality) so that an optimal parametric configuration of the scheme is created, which is structured simultaneously, moment by moment, in the structure that we observe.

A connection between chaos theory and human genome's functioning is also evidenced by the fact that there are relatively few genes than was thought, and they regulate numerous configurations and behaviors. The basis of the observed complexity is disarmingly simple, as the simple basic rules that govern the behavior of quarks. So that simplicity and complexity are intertwined in a wonderful way, as is known.

As mentioned in the previous conjecture, 'entering Energy Information - EI' in the mother before conception, if the child is born without TO means that, with the help of further EI, both scheme and structure of nuclear and mitochondrial genome were favorably affected! EI and its distribution throughout the body could be related to the genetic code of mitochondria with their carriers of energy. All this is well more than the sum of its parts, as mentioned in prisms, according to Adorno.

Most diseases have multiple underlying genetic mutations. The genes are fragmented, there are the coding segments, interspersed with lengthy and repetitive sequences that do not say anything, and whose function is obscure (superficially classified as junk DNA). But everything makes sense, there is no chance and futility. Their distribution suggests that some of these non-coding sequences may contribute to the overall regulation of gene activity.

For example, Oncological Terrain is such because there are some alterations in n-DNA and mit-DNA. However, if we correct the functional mitochondrial error (CAEMH) with melatonin, NIR-LED, regular life, etc., the disease generally does not arise. Then, the onset of diseases such as diabetes, cancer, hypertension, CAD, is observed when there is both an alteration of the n-DNA and mit-DNA and a decreased EV (tissue acidosis). Consequently, with a proper increase of EV, mitochondria start to work well again, and consequently EI

increases restoring the non-local reality, so that disease does not arise, at least in most cases: reduced EI is sign of genome's alteration, as implicit in the 1st conjecture.

As stated in the idea of 'DNA antenna' by Manzelli resonance signals, which simultaneously activate the DNA, are synchronous because the reality is not - local (Stagnaro et al., 2007).

For these reasons, unable to "see" the nuclear and mitochondrial DNA, we look at the final changes, induced on the activities of biological systems (Stagnaro, 2004).

This clearly contrasts with the genetic determinism. What makes that development follows a certain route? As mentioned above, this is because there is lack of EV and then of EI, due to impairment of mitochondrial respiration: CAEMH!

Experimental evidence of 1st conjecture

The 1st conjecture - reversibility of mit-DNA alteration for future generation – formulated by (Stagnaro, 2004c), has been confirmed by Stagnaro (2010a). This experimental evidence has been called 'Manuel's Story'.

In April 2010, Manuel is the first newborn in the world NEGATIVE for Oncological Terrain even if both parents are POSITIVE for Oncological Terrain. In spite of the fact he is son of a mother and a father both involved by Oncological Terrain, his parents underwent a Conjugated-Melatonin treatment a lot of months before pregnancy began. Technically speaking, his parents became positive exclusively for the residual variant form of predisposition to malignancy, which is not dangerous at all, because mitochondrial respiratory chain is perfectly functioning, so that endogenous-cellular energy level in every biological system results high. Broadly speaking, under preventive therapy, their Inherited Real Risk of cancer became residual, even if they will still have for ever OT: it means that they can continue to live without any risk of cancer appearing. Furthermore their son is negative for OT: it means that his son hasn't got any OT, any real risk of cancer, therefore he does not need of any preventive therapy: none of the tumors studied by QBS will never hurt him in life. The first experimental evidence confirms that the 1st QBS Conjecture is true. A widely experimental research could confirm the truth, or not, of 1st QBS Conjecture for a wide range of study cases.

Experimental evidences of 2nd conjecture

The 2nd Conjecture formulated by Caotino et al. (2008) finds its experimental evidence in a recent article (Lieberman et al., 2009).

By breaking the human genome into millions of pieces and reverse-engineering their arrangement, researchers have produced the highest-resolution picture ever of the genome's three-dimensional structure (Figure 3). The picture is one of mind-blowing fractal glory, and the technique could help scientists investigate how the very shape of the genome, and not just its DNA content, affects human development and disease. It's become clear that the spatial organization of chromosomes is critical for regulating the genome. This opens up new aspects of gene regulation that weren't open to investigation before. It's going to lead to a lot of new

questions. As depicted in basic biology textbooks and the public imagination, the human genome is packaged in bundles of DNA and protein on 23 chromosomes, arrayed in a neatly X-shaped form inside each cell nucleus. But that's only true during the fleeting few moments when cells are poised to divide. The rest of the time, those chromosomes exist in a dense and ever-shifting clump. Of course their constituent DNA strings are clumped, too: If the genome could be laid out end-to-end, it'd be six feet long. For decades, some cell biologists suspected that the genome's compression wasn't just an efficient storage mechanism, but linked to the very function and interaction of its genes. But this wasn't easy to study: Sequencing the genome destroys its shape, and electron microscopes can barely penetrate its active surface. Though its constituent parts are known, the genome's true shape has been a mystery. In April 2009, a paper published in the *Proceedings of the National Academy of Sciences* linked patterns of gene activation to their physical proximity on chromosomes. It still provided the most persuasive evidence to date that genome shape matters, even though the researchers' chromosome map was relatively low-resolution. The topography described in the latest research, published in *Science*, is far more detailed. It's going to change the way that people study chromosomes. It will open up the black box. Researchers didn't know the internal organization. Now they can look at it in high resolution, try to link that structure to the activity of genes, and see how that structure changes in cells and over time. To determine genome structure without being able to directly see it, the researchers first soaked cell nuclei in formaldehyde, which interacts with DNA like glue. The formaldehyde stuck together genes that are distant from each other in linear genomic sequences, but adjacent to each other in actual three-dimensional genomic space. The researchers then added a chemical that dissolved the gene-by-gene linear sequence bonds, but left the formaldehyde links intact. The result was a pool of paired genes, something like a frozen ball of noodles that had been sliced into a million fragmentary layers and mixed. By studying the pairs, the researchers could tell which genes had been near each other in the original genome. With the aid of software that cross-referenced the gene pairs with their known sequences on the genome, they assembled a digital sculpture of the genome. And what a marvelous sculpture it is. There's no knots. It's totally un-entangled. It's like an incredibly dense noodle ball, but is possible to pull out some of the noodles and put them back in, without disturbing the structure at all. In mathematical terms, the pieces of the genome are folded into something similar to a Hilbert curve (Figure 4), one of a family of shapes that can fill a two-dimensional space without ever overlapping — and then do the same trick in three dimensions. How evolution arrived at this solution to the challenge of genome storage is unknown. It might be an intrinsic property of chromatin, the DNA-and-protein mix from which chromosomes are made. But whatever the origin, it's more than mathematically elegant. The researchers also found that chromosomes have two regions, one for active genes and another for inactive genes, and the un-entangled curvatures allow genes to be moved easily between them. The configuration likes to the compressed rows of mechanized bookshelves found in large libraries: they are like stacks, side-by-side and on top of each other, with no space between them. And when the genome wants to use a bunch of genes, it opens up the stack. But not only does it open the stack, it moves it to a new section of the library.

The segregation of active and inactive genes adds to evidence that genome structure affects gene function. It is a great description of the structure of the nucleus, and putting that on top

of what it has been done, it forms the big picture. The paper linked rough outlines of chromosome arrangement to gene activation. Whereas that study only looked at a few chromosomes, the *Science* paper looks at fine resolution over the whole genome. Now is possible to produce these genome maps, and superimpose them with genome-wide analyses of gene expression. The question is now how changes in spatial organization relate to changes in genes turning on and off, for instance in the studies how glitches in chromosome structure may turn cells cancerous. Connecting genome shape to gene function could also help explain the connection between genes and disease, which remain largely unexplained by traditional, sequence-focused genomics. It is perfectly reasonable and almost inevitable that the 3-D structure of DNA is going to influence how it functions. Researchers also want to study how genome shape is altered. That appears to happen constantly during the transition from stem cell to adult cell, and then during cell function. How much variation is there in structure across cell types? What controls it? Exactly how important is it? This is a new area of science.

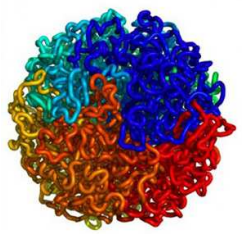


Figure 3. 3D structure of genome

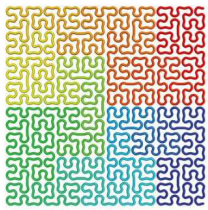


Figure 4. 2D Hilbert's curve

Image: From Science*, a two-dimensional Hilbert curve, and the three-dimensional shape of a genome.*

3rd Conjecture: mit-Genome's fractal dimension as topic measure for metabolic and pre-metabolic syndromes

Connecting the shape of the genome with gene function could also help explain the connection between genes and disease, which remains largely unexplained by traditional genomics, focusing on the sequence.

In case of ICAEM there is alteration of mit-DNA. As n-DNA is linked with n-Genome, mit-DNA is linked with mit-Genome.

From Science article (Lieberman, 2009), experimental evidence of 2nd Conjecture, we know of 3D fractal shape. So, we can formulate the following 3rd conjecture*: if there is alteration of mit-DNA, then there is alteration of mit-Genome, i.e., a lower fractal dimension*. If we would not be able to measure the fractal shape of genome by mean of fD, then it possible to deduce the complexity of genome's fractal structure by looking at the alteration of mit-DNA through QBS diagnosis.

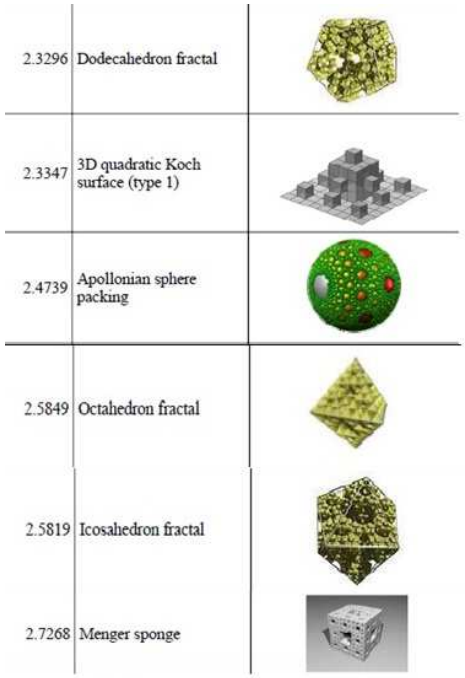


Figure 5. fractal dimension of some 3D structures

If there is functional alteration of mit-DNA, then there is alteration of shape and structure of the correspondent mit-genome.

In the studies about genome the attention is now paid on shape-position-function in the space instead of sequence-content-structure: function and structure are anyway the two poles of the same equation: If you change one the other will inevitably change. The spatial position of activated genes shows an ever changing gene's networking, so that varying the genome's fractal structure, then genome's function is modified. For example, if a subject with positive Oncological Terrain is located on Curri or Hartmann nodes, telluric currents significantly worsen the biology of neural centers PNEI, due to changes in stoichiometric nuclear site, despite the effective treatment (Stagnaro, 2004a).

One more example about the connection between energy and qualitative active information and structures is given by David Bohm talking about the electron.

The information which shows the chaotic behavior of a system, i.e. entropy which means the rate of change of qualitative information in a dynamical system, is itself guiding it. There is active information, i.e., a form with a little energy enters and guides a greater energy. There is an energy-form which in-form, as with the genome fractal - a form in-forms. This energy is in a not size state, is potentially active everywhere, and it has now become active when its form enter in the classical energy. Consider the example of a radio wave, the shape of which carries a signal, such as the voice of a disk-jockey. The energy of the sound being heard by the radio receiver is not from this wave, but from the battery unit. The subtle and hidden energy is in its essence not-formed, but takes the form of the information contained in the radio wave. This information is potentially active everywhere but only becomes active when its current form comes into the power of the radio. The analogy with the bohmian causal interpretation is clear. The quantum wave carries information and is therefore potentially active everywhere, but becomes active only when and where this energy goes into the energy

of the particle. The electron has got therefore a complex and hidden structure that is at least comparable to that of a radio.

Recently, the discover of Psychokinetic Diagnostic (Caramel et al., 2010b) gives strong evidence of the connections between structures – forms and in-formation without any shape. In PD, the thought of the examiner links the radio (the examiner itself) and the source of in-formal energy, just in case of enough empathy between the 2 parts.

What QBS is already able to do from the bottom and with a simple stethoscope - investigating the micro-vessels and the microcirculation by calculating its fractal dimension, being able to say already if there is genetic alteration of mit-DNA - will be in the future confirmed by an advanced more sophisticated research, directly by measuring the fractal dimension of the genome gradually noted - when able to calculate it.

One more difference between the research published in Science and QBS is that the first one deals with nuclear Genome while QBS deals with both n-DNA and mit-DNA so that this 3rd conjecture can be experimentally evaluated when the advanced research will deepen the function of mit-DNA and its proper genome.

By measuring the fractal dimension of the mit-Genome the simple diagnosis will be invigorate that is already given by the QBS functional genetic investigation of mit-DNA, which denotes in case it were altered, CAEMH in its degree of intensity, QBS Constitutions, inherited real risks of linked disease, and so on. A low fractal dimension of the mit-genome - compared to its baseline - will be index of genetic modification of mit-DNA and of course with all that it implies in agreement with the QBS.

Conclusions

The structure and function of n-Genome and mit-Genome are related with a well defined non-Euclidean geometry called fractal geometry, and consequently with deterministic chaos, really helpful for QBS diagnosis.

In the 1st Conjecture of this paper it is explained Stagnaro's hypothesis formulated in 2004 about reversibility of mit-DNA's alteration for future generation. This hypothesis has been experimental recently verified, when Manuel was born in April 2010 with negative Oncological Terrain from parents both positive OT; aware of their QBS constitution they began an effective preventive therapy before conception, confident upon Stagnaro's guess. Without any prevention Manuel would be born with positive OT, as his parent are.

In 2008 Caotino and Stagnaro agreed with the 2nd Conjecture, which assumed chaotic deterministic dynamics and fractal structure of human Genome.

This second hypothesis has been experimentally verified in 2009 by some researchers as evidenced in the paper published in Science.

The 3rd Conjecture formulated in this paper is about the fractal dimension of mit-Genome: *: if there is genetic alteration of mit-DNA, then there is alteration of mit-Genome, i.e., a lower fractal dimension*.

This conjecture is partially confirmed by QBS, which through a well defined diagnosis is able to state if there is genetic alteration of mit-DNA, but could be corroborated during advanced

future research able to effectively measure the fractal dimension both of n-Genome and mit-Genome.

Thanks to second guess, Caotino et al. (2008) anticipated the excellent work of Lieberman et al. (2009). In fact, the alteration of the mit-DNA is, on the one hand, the indirect expression of the n-DNA, i.e., the proteins present in mitochondria, but derived from nucleus, and secondly, it is expressed in CAEMH and in early alterations in the different glycocalyx, synthesized by the cell itself on indications given by the n-DNA and mit-DNA.
The early altered functions of the glycocalyx of the different cells, are now able to be clinically precisely evaluated by QBS.

It would be anyway a paradox if a not fractal thermodynamic structure (n-DNA and mit-DNA) could give rise to structures (micro-vessels, glycocalyx) with fractal function. Structure and function are in fact the poles of the same equation.

The genome structure, both from n-DNA and mit-DNA, derives from a scheme of organization behind (implicated order, hidden variables). the genome structure is itself the organization scheme for glycocalyx and micro-vessels.

We have a hierarchy of structures and schemes of organization; each organization scheme can be in turn structure, or indeed any structure can be both scheme of organization which defines the lower-order structures, and the image of a process of structuring led by an upstream scheme.

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[i] Mendel (1822-1884), studying the behavior of chromosomes in the nucleus, showed that the hereditary characters are transmitted as a unit. Chromosomes are located in individual hereditary characteristics of these units, then called genes. The transmission of characteristics from parents to offspring is called heredity: the majority of such characters of an organism passes from parents to children when organisms reproduce. But he had no knowledge of the existence of mitochondria described by Altmann in 1894 and rediscovered by Benda in 1897, who baptized them with their current name.

[ii] The human mitochondrial DNA is inherited by matrilineal (not Mendelian inheritance) as during the process of fertilization of sperm mitochondria are marked with ubiquitin, a protein that binds to other proteins to be degraded. As a result, the mitochondrial genome of the offspring will be almost equal to the mother (subject to possible mutations) and also if the mother is suffering from a mitochondrial disease transmission, then all children inherit. In literature there are very few reported cases in which the mitochondrial DNA seems to derive from the father or both parents.

[iii] The Royal Society, London, 1986

[iv] Lyapunov Characteristic Exponents – LCE – is a statistic measure to test the presence of 'sensitive dependence on initial conditions' – SDIC – in a system. SDIC is at the root of the 'disorderly' behavior of deterministic dynamical systems and is responsible for their random appearance and unpredictability.

[v] Fractal dimension is a measure of the way orbits fill the phase space under the action of a flow or a map, suitable for fractal objects, characterized by a non-integer dimension.

[vi] Entropy is a measure of the uncertainty in deterministic dynamical systems, or equivalently is the amount of information we get on the average by making an observation. In particular, the presence of positive entropy indicates that the observation of the system continues to generate information for an arbitrary long interval of time. Consequently, unless the position of the system can be observed with absolute precision, there will forever remain uncertainty about its future course, even when the dynamical rule governing the system is known with precision. Zero entropy is interpreted as absence of chaotic or complex behavior, typical of linear or periodic systems with fixed point or limit cycle equilibrium, so that they are fully and exactly predictable: none new quality information emerges for an arbitrary long interval of time.

[vii] The particle paths fluctuate chaotically, so that causal interpretation is not strictly deterministic as in Newton physics: unpredictability and uncertainty are intrinsic property of the deterministic dynamical systems observed, as in chaos theory, and not random or casual like in classical interpretation of N. Bohr.

[viii] This electron turns out not to be a simple structureless particle but a highly complex entity that is effected by the quantum potential – QP - in a extremely subtle way. Indeed QP is responsible for some novel and highly striking features which imply qualitative new properties of matter that are not contained within the conventional quantum theory.

[ix] Unlike the particles of Newtonian physics, the electron is never separated from a certain quantum field which fundamentally affects it, and exhibits certain novel features. This quantum field satisfies Schrödinger's equation, it is therefore causally determined.

[x] The form of QP can dominate behavior: information contained within QP will determine the outcome of a quantum process. There is an active information, a form having very little energy enters into and directs a much greater energy. There is an energy form acting to inform.

[xi] Information, from the latinum verb 'in-formare', which means 'to give a form' is a truly more primitive fundamental activity than energy and matter, is something that precedes every physical form (Aristotele). Information's action is therefore related to the potential codification plan of producing an objective form and in turn we can perceive an object as form's of information transmission.

[xii] Mendel (1822-1884), studying the behavior of chromosomes in the nucleus, showed that the hereditary characters are transmitted as a unit. Chromosomes are located in individual hereditary characteristics of these units, and then called genes. The transmission of characteristics from parents to offspring is called heredity: the majority of such characters of an organism pass from parents to

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[xiv] Metabolic syndrome is a combination of medical disorders that increase the risk of developing cardiovascular disease and diabetes. It is also known as metabolic syndrome X, syndrome X, insulin resistance syndrome, Reaven's syndrome. The pre-metabolic syndrome, as defined by Stagnaro, is the syndrome that precedes the metabolic one, and is linked with congenital real risks and their associated biophysical semiotics constitutions.

[xv] Biophysical semeiotic constitutions, detectable since birth, are the inherited congenital ground or terrain of well defined potential diseases clinically hidden, which can last several years before appearing, in the slow transformation process from potential (pre-metabolic syndrome, pre-clinical stages) to effective pathology (metabolic syndrome)

[xvi] Metabolic syndrome is a combination of medical disorders that increase the risk of developing diseases. The pre-metabolic syndrome, as defined by Stagnaro, is the syndrome that precedes the metabolic one, and is linked with congenital real risks and their associated biophysical semiotics constitutions.

[xvii] Melatonin is a natural substance that our body produces itself. It is produced by synthesis in the laboratory and placed in the body is to act on mitochondria, especially increases mitochondrial phosphorylation, it produces more EV and therefore greater EI and this must be for the benefit of the entire body, improves breathing (especially at night; we produce melatonin mainly from the early hours of the night until around dawn), and therefore this is a hormone that is universal and is good for the treatment of multiple diseases, or tendencies to pathology, and then to make the RR residual. It is also a good neurotransmitter.

[xviii] In therapy, based on what has been observed in patients with Oncological Terrain places on the nodes of Curry or Hartmann (worsening of PNEI - psycho-neuro-endocrine-immune system), these energies released will improve and normalize respectively, by their influence on the alignment device, the orbital motion of subatomic particles, including the mitochondrial respiratory chain, which first reacts.

[xix] Lory's experiment is based on the fact that "all" subatomic components and then atomic and molecular structured to form a cell and the whole cell or parenchyma, are correlated between themselves and with "all" the other branch of the same embryological in a four-dimensional space, like they are just "plot" (entanglement) two electrons observed by Aspect in his famous experiment. The effect of' entanglement means that the information takes on a "non-local" dimension. Lory's experiment is as follows: if it is done a digital pressure applied over a parotid gland, or a salivary gland sublingual, of a "single ovular" twin sister, simultaneously it is observed microcirculatory activation type I associated in the pancreas of the other twin sister, regardless of the distance that separates them: meters or kilometers (see in the references Manzelli and Stagnaro).

[xx] The micro-circulatory remodeling is directed by the way of living and working on the parenchyma: if the subject is healthy, is healthy the related parenchyma on the microcirculation (see angiobiopathy theory, dealing with diseases of blood and lymph vessels in accordance with the semiotics biophysics). Certainly a loss, rheumatism, immune, infectious, can act both directly and indirectly. See [http://www.semeioticabiofisica.it/microangiologia/common.htm]. It may be that in the long run re-organization becomes difficult or impossible because the flow decreases more, and then are built up of feedback mechanisms for which are to activate dormant cancer cells. Aging with free radicals that accumulate contributes to further damage both micro vascular and parenchymal: even endothelium (cell layers lining the inner surface of blood vessels and heart chambers) and smooth muscle cells possess mitochondria. Remodeling micro circulatory type cancer is an expression of mutations of genes within cells in that forum: any change in gene expression - cell finds its expression in the parallel alteration of its microcirculation (microvascular tissue units): the tissue here is around the vessels, interstitial, not the parenchyma! If these processes are blocked, stops the entire organization. Very important is that if there are congenital abnormalities, genetically transmitted through the mother (see CAEMH, mitochondrial cytopathy or mitochondrial functional pathology in the site www.semeioticabiofisica.it) amending the unfolding vital physiological processes occur the most serious human diseases, and not, now real epidemics. Autopoietic networks must therefore regenerate themselves continuously in normal and physiological way, to maintain its organization.