**OUTLINING A DIALECTICAL HYPOTHESIS ON THE C-VALUE PARADOX IN THE LIGHT OF QUANTUM CHEMISTRY**

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**Abstract**

This article presents a hypothesis on the C-value paradox from a dialectical materialism perspective and considers issues related to quantum chemistry. The C-value paradox arises from the divergence between the amount of DNA per haploid genome and the presupposed amount of information contained within the genes. The dialectical nature of the existing totality is proposed to establish the philosophical basis of the article’s arguments, and the limitations of sigma-additive functions and their natural generalization for counting genes in terms of the existence of non-linear dynamics underlying genetic processes are discussed. By considering eight key aspects of the underlying molecular development process involved in the formation of the genetic structure, a solution to the paradox is proposed that can be experimentally verified or refuted. The article concludes by emphasizing the importance of a dialectical approach to understanding the C-value paradox and the current computational limitations for exploring the proposed hypothesis.

**Keywords:** Philosophy of chemistry, quantum chemistry, C-value paradox, G-value paradox, dialectical materialism, molecular biology.

1. **Introduction**

Since J.B.S. Haldane's works harmoniously unified Darwin’s and Mendel’s theories, and chemistry, especially molecular chemistry, has become a fundamental science for understanding how genetic issues condition and are conditioned by the biological evolution of organisms. One of the long-standing biological puzzles is the link between the complexity of the organism as a whole and its genetic structure (Choi, Kwon y Kim 2020, 699). Intuitively, as in prokaryotic organisms, it is expected that a greater number of genes implies that a eukaryotic organism is more complex. However, the C-value (genome size) and G-value (number of genes) paradoxes not only challenge that intuition but also our overall understanding of the relationship between the amount of DNA per haploid genome and the complexity of the organism to which that amount belongs.

As (Choi, Kwon y Kim 2020, 13s) point out, “Genome size affects various levels of phenomes, and genome size variations exist among species from different niches. In this respect, genome size is an important subject because many species are driven to new habitats from climate change.” This constitutes one of the reasons why resolving the paradox, approaching a solution, or simply deepening our understanding of it is important in the framework of the life sciences and related sciences.

We consider that there are two fundamental aspects that should guide the study of the C-value paradox. First, the philosophical perspective under which a problem is approached because it determines the epistemological structure of its investigation and, therefore, also determines the methodology used in the study of the phenomenon of interest. Second, although chemistry is not (formally or factually) a branch of physics (Bunge 1982, 209), which is also true for quantum chemistry, it is closely linked to it because it is based on it (Bunge 1982, 216) and regarding the molecular structure of matter, they can form a unified nonreductionist body (Seifert 2017, 209). This implies the need to consider the quantum aspects of matter when studying molecular structures, which in turn implies that the study of the C-value paradox must be approached from quantum chemistry.

The present research focuses on dialectically developing a hypothesis that allows for an explanation of the C-value paradox in terms of the molecular processes underlying the conformation of the genetic structure, considering the implications of the involvement of the time-independent Schrödinger equation in the analysis of DNA structure.

1. **The Dialectical Nature of Existence**

It is convenient to establish some subtle but fundamental differences about the concepts that allow us to understand the intrinsically material and objective general structure of which we are part, *i.e.*, the existence or material and objective reality. What should we understand by “existence”? What does it mean that existence is a general structure intrinsically material and objective? Is “the real” equivalent to “reality” and vice versa?

First, we must address the question about the definition of existence. We should understand by “existence” the organic synthesis[[1]](#footnote-2) of what is, what is not, what will be, what will not be, the probable, the possible and the purely logical[[2]](#footnote-3) (Hegel, Ciencia de la Lógica 1976, 56, 75, 80, 81, 82, 85-86, 90, 92-93, 94), (Rosental y Iudin 1971, 163), *i.e.*, the present and future development tendencies inherent and contrary (in the sense that they are in contradiction) to the studied thing along with their probable, possible or purely logical trajectories. This denotes the dialectical principle that things are not only what they are in terms of their current state of development, but also their potential, which is also reflected in the concepts of kinetic and potential energy in the context of physics, as well as in the prior and posterior distributions in the context of Bayesian statistics, allowing for the construction of probability models such as Hamiltonian systems of Markov chain Monte Carlo, because it is the same logic that underlies both theoretical constructions and the respective phenomena of reality that these constructions represent. As will be seen later, this logical commonality occurs among many other systems.

What should we understand by “contradiction”? Given a thing with different integrating components, the contradiction is precisely the inherent complementary and mutually exclusive development tendencies of the given thing, where the degree of mutual exclusion determines whether they are antagonistic contradictions or nonantagonistic contradictions. As we see, the above definition of contradiction is aligned with Bohr’s complementarity principle, which establishes that a complete knowledge of a quantum phenomenon requires a description of both wave and particle properties[[3]](#footnote-4), and which can be established in general as it follows: to reproduce the integrity of a phenomenon, it is necessary to apply complementary and mutually exclusive classes of concepts to knowledge (Rosental y Iudin 1971, 374-375); this implies unity and struggle of opposites, where struggle is the factor that generates change. In fact, the above definition of contradiction can be seen as a philosophical generalization of the complementarity principle in the broader context of dynamical systems and formally transcends the border of the gnoseological to also be an ontological postulate, linking the ontological and the epistemological through logic, dialectical logic.

Therefore, what is nothingness? Nothingness refers to all those developmental tendencies that were not realized because they were annihilated (annihilation always involves a partial conservation of the annihilated in the annihilator, a partial conservation that is the key to the purification or dialectical leap that the act of annihilation allows the annihilator to make) by the tendencies that did succeed.

From the later definition of existence, we can define “the real” as the being of things in contrast with not being and with other forms (possible, probable, and so on) of being and, we can define “reality” as that which truly exists and develops, it contains its own essence and its own laws, as well as the results of its own action and development. Such reality is objective reality in all its concreteness, the essence of the given thing (Rosental y Iudin 1971, 391), the foundation of existence itself (Hegel, Filosofía de la Lógica 2006, 127-139). Therefore, the difference between “reality” and “the real” is that “reality” not only contents the essence of the existence (“the real”) but also the results of the development of the essence (Rosental y Iudin 1971, 391), its phenomenology, because phenomenon is the complete manifestation of the essence, *i.e.*, is reality (Hegel, Ciencia de la Lógica 1976, 12). But things cannot be reduced only to their essence and to the development consequences of their essence: there’s not essence isolated of non-essential (purely phenomenological), like there’s not concept darkness isolated of light, because essence and phenomenon constitute a unity: there are no “pure” essences that do not appear, neither “pure” phenomena lacking essence, *i.e.*, essence appears, and phenomenon is essential (Hegel, Ciencia de la Lógica 1976, 12, 37-38), (Rosental y Iudin 1971, 148). The unity between essence and phenomena is established in the concept of “material and objective reality”. Thus, the dichotomy between essence and phenomenon, between form and content, is overcome (Hegel, Ciencia de la Lógica 1976, 12).

What should be understood by “material and objective reality”? This should be understood as the entire material world as a whole or totality, in all its forms and manifestations. The concept of “material and objective reality” is relative in the sense that, regarding the individual it is everything that exists outside of his consciousness and is reflected by it; however, the individual itself, with its awareness, will be objective reality with respect to other people, and so on, which is not more than a philosophical generalization of the “observer” concept of the relativistic theoretical framework. Therefore, abstracting from the individual vision of the world it can be said unambiguously that material and objective reality[[4]](#footnote-5) converges with reality in general (Rosental y Iudin 1971, 391), with existence.

Is the existence intrinsically material? As (Vopson, The mass-energy-information equivalence 2019, 1) notes, it was Landauer who, in 1961, proved that information has a physical (*i.e.*, material) nature, following the mathematical definition provided by Shannon in 1948. From the Landauer Principle and from the equivalence between mass and energy established by Einstein, (Vopson, The mass-energy-information equivalence 2019, 3) it is established as the equivalence between mass, energy, and information, which is the extended Landauer principle or Landauer-Vopson principle.

Two years later, (Vopson, Estimation of the information contained in the visible matter of the universe 2021, 3) established the existence of intrinsic information that sustains the fundamental properties of elementary particles, which implies that stable elementary particles of nonzero rest mass store a fixed and quantifiable value of information about themselves, specifically each particle of the observable universe contains 1.509 bits of information and there are $6×1080$ bits of information stored in all particles of the observable universe. This implies that information is a form in which matter exists, called by Vopson “the fifth state of matter” or “fifth element”. The two previous statements that supports the claim that information is state of matter are called “information conjectures”[[5]](#footnote-6).

One year later, (Vopson, Experimental protocol for testing the mass–energy–information equivalence principle 2022, 3-4) established an experimental protocol[[6]](#footnote-7) that allows empirical verification of information conjectures because it allows confirmation of the expected content of information in elementary particles, which implies that all states of matter (in the sense of physical systems) can be translated in terms of information. Therefore, existence is intrinsically physical because all physical states of matter can be expressed in terms of information and information is physically defined.

Of course, physical existence is not existence in general, but existence in its most general sense. Following the latter definitions of existence, reality and the real, when Aristotle established his four causes (material, teleological, formal, and efficient causes) he implicitly established that things exist in different concrete senses broader than physical existence. For example, wood is the material cause of a table, the design is its formal cause, being a place to eat its teleological cause and carpentry is its efficient cause. But that means a table, as a concrete physical existence, is simultaneously a piece of wood, also a semi-processed raw material in some productive chains (a kind of mean of production called circulant capital), that, if being a place to eat is in the context business activity, the table is a mean of production (fixed capital) or a mean of consumption if it is used by a household, and can also be considered as concrete labor because it is the product of a designer’s labor and a carpenter’s labor, and also as abstract labor because the designer’s and carpenter’s labor are expressed in a general common measure of labor. The former analysis can become more complex and extensive depending on the object being analyzed. Even Comte, as devoid of historical reasoning as a positivist can be (and as supplied with linear and mechanistic reasoning as a positivist can be), understood that the more concrete sciences include their less concrete predecessors (Comte 2000, XVI), just as quantum chemistry includes the laws of quantum physics and its own laws, irreducible to the laws of quantum physics[[7]](#footnote-8).

(Landau y Lifshitz 1950, 1-2) point out that with a sufficient increase in the number of degrees of freedom, the laws of purely mechanical systems give way to the qualitatively new laws of statistical-mechanical systems. Following their logic and making a philosophical generalization of it based on Aristotelian reasoning and its implications, we can conclude that when the physical existence (the inorganic matter in its most basic sense) evolves, it gives way to qualitatively new and more complex forms of existence with their own laws which, as they evolve, gives way to another new and even more complex forms of existence with their own laws and so on. All these forms of existence coexist overlapping themselves in an organic[[8]](#footnote-9) and irreducible way and this evolutionary process is a transition historically conditioned (Haldane 2022, 4), (A. Oparin 2021, 13-14).

This logic of gradual perfection of matter and the resulting qualitative evolution is also present in the proposals of Oparin and Haldane on the origin of life on Earth (A. I. Oparin 1969, 4), (Haldane 2022, 10), which was repeatedly proven experimentally by (Miller 1953, 528-529), (Matsuo y Kurihara 2021, 1-3) and others, as documented in (Bada 2013, 2188, 2190, 2191).

The above implies periodic leaps from the quantitative to the qualitative, starting from a certain quality. These leaps occur, as will be seen below, in the context of systems that evolve without external intervention, in which emergence exists, where the whole is more than the sum of its parts, where essence (as the foundation of existence) manifests itself, ultimately, in the totality and long-term development, where periodic processes occur (whether regular or irregular, i.e. seasonality or cycles), and where the continuous and the discrete condition each other reciprocally, but ultimately, continuous processes contain the discrete ones because existence is "of a single piece," which implies the organic unity of its components.

In the context of cosmological models, (Haferkamp, y otros 2022, 530) proved theoretically for physical systems (locally) that the universe evolves from a linear growth to a complex one, and (Alexander, y otros 2021, 1, 7-12) established theoretically that the universe is self-organized, deterministic, historically determined, and evolves learning in an autodidactic way its own laws (in the sense of an unsupervised deep recurrent cyclic neural network) by applying itself a process physically equivalent to biological natural selection, which (a recurrent neural network) implies an algorithm adding new nonlinearities over time (Zhang, y otros 2016, 3), which can find an analogy with the concept of “emergence” in complex systems, *i.e.*, a spontaneous appearance of new information because of the dynamics of the system. This also implies that the laws of physics could be subject to higher-order laws which control them in the same sense that a logic of a certain order is subject to the rules of a higher-order logic, and that the teleological cause (practical purpose) conditions the mechanical or efficient cause without the need for the existence of will or intellect (as was previously assumed about teleology).

All the above corresponds to the ontological, epistemological, and methodological dialectical-materialist principle that establishes that knowledge goes from the simple to the complex, as the reflection of the material world that undergoes the same transition.

Despite the fact that the Zhang’s et al.’s research does not present a philosophical explanation about the existence of a self-taught universe, in light of what Oparin and Haldane have proposed regarding the origin of life, it is reasonable to conceive that intrinsic teleology (that is, final teleology, as opposed to extrinsic teleology, which is intermediate) is always, in its most general form, that systems/processes move from antagonistic to nonantagonistic contradictions. This is due to the inherent stabilization requirement of systems: the contradiction consists of the developmental tendencies of the elements that compose the analyzed object, which are nonstructural (nonantagonistic, because they imply relative stability) or structural (antagonistic, because they imply absolute instability, which will result in the collapse of the internal structure of the given object and its emergence as something superior that reconciles those antagonistic contradictions), whether in the short or long term, whether at a partial or a total level. Therefore, systems must stabilize in terms of their evolutionary process to preserve themselves.

Therefore, there exists a metalogic[[9]](#footnote-10) (the logic of the existence) that unifies and is unified by the logic of all concrete systems that conforms the existence, which cannot be other than the same logic that we have been using to arrive here: the materialist version of the dialectic logic, where the adoption of the materialist version instead of the idealist version is justified by the physical nature of information as a state of matter into which all other states can be translated. There are some previous research studies, such as (Vitiello 2014, 203), which from the framework of formal logic (since topology founded by set theory is based on formal logic) establish that there is an isomorphism (which can be conceived as an equivalence between the internal or fundamental structures of two systems) between dissipative systems, self-similar fractal systems, and electrodynamic systems, which, according to his words, raises an “integrated view of Nature”.

What does the above mean? It basically means two things. The first is that existence has multiple forms of manifestation, forms that each possess and are subordinated to a specific content, that is, existence is made up of various qualitatively different systems, such as political economy systems, physical systems, chemical systems, and geological systems, among others. These qualitative differences and distinctions between the various systems have an objective and material character, which implies that they express qualitatively different objective and material states (in a broader way than physical states). The second meaning is that, despite such differences and distinctions, existence has a common essence and a metalogic inherent to it (the essence as the foundation of existence, a common essence, dynamic and at the same time metalogical-invariant), for which existence is monistic or, expressed in topological terms, “in one piece” (connected space).

The totality of phenomena is the absolute, Spinoza’s essence, which is identified with the multiplicity of its determinations. Because of this identity, however, the essence cannot be an abstract and empty unity, but rather is the active producer of its determinations, the cause of its effects. Evidently, this chain of causes and effects implies the risk of an infinite reasoning process, in which the first cause can never be known, which Hegel avoids by considering that the cause contains its effect and is contained in it, so that the relationship between them is one of identity, and has its truth in reciprocal action, profound unity of the causal chain (Hegel, Ciencia de la Lógica 1976, 12), (Dib 2020, 11): the essence as the foundation of existence (Hegel, Filosofía de la Lógica 2006, 127-139).

Therefore, truth must be sought in the whole/totality because to understand the truth of the relative, the truth of the absolute must be understood: the subjective (partial) is the objective (totality) without unfolding, without developing. Because this totality as provisional absolute[[10]](#footnote-11) (Findlay 1964, 1) is composed of the relative, although not linearly, that is, the absolute is more than the mere aggregation of the relative, in the process of knowing the truth of the absolute is where we are going to know the truth of the relative. This is precisely the fundamental philosophical idea behind the wavelet-particle duality: the truth of the particle is in the wavelet, but in the process of knowing the truth about the wavelet, the truth about its constituent particles is being known.

Finally, there is another relevant implication of the mentioned corollary, which is that to know the truth of one class of systems (physical systems, for example) we must know the truth about all the other systems that make up existence, or at least the most important. The autodidactic universe that in its learning process applies “cosmological natural selection” to itself is a proof of the above.

1. **Sigma-Additive Functions**

Following (Kolmogórov y Fomin 1978, 309-313), let be $ϕ$ a real function and let $S$ be a $σ−Álgebra$. The function $ϕ$ is $σ−aditiva$ or countable-additive when:

$$ϕ\left(S\right)=\sum\_{i=1}^{\infty }ϕ(S\_{i}),whereS\in S;S=i=1\infty S\_{i},S\_{i}S\_{j}=0$$

The above means that for a finite set of sequences of disjoint sets (without common elements), the length of the union of these sets is equal to the sum of the distances (which are quantitatively express ed in lengths) of these sets.

The function $ϕ$ is countable subadditive when:

$$ϕ\left(S\right)\leq \sum\_{i=1}^{\infty }ϕ(S\_{i}),whenS\in S;S⊆i=1\infty S\_{i}$$

The previous means that the infinite union $i=1\infty S\_{i}$ can contain elements that are not necessarily in $S$. Thus, a subadditive measure is a function that defines the sum of two sets within a domain as one whose result will always be another element less than or equal to the sum of the values of the functions evaluated on each set.

The difference between both types of functions is the restriction on the result they impose in additive functions, the result must be equal to the sum of the inputs, while in subadditive functions, the result must be less than or equal to the sum of the inputs. Therefore, additive functions are a particular case of sub-additive measures.

As (Huang y Mackay 2016, 3) point out, an additive genetic model refers to the situation where $d=0$ and, therefore, there is a perfect linear relationship between the genotypic value and the number of copies of the $A$ alleles, which implies that there is no dominance since the value of the heterozygote ($d$) is zero. Thus, additive functions or measures are those that serve to quantify relationships of completely linear nature between certain variables, such as the relationship between genotypic value and phenotypic value under the assumptions defined above.

1. **The C-Value Paradox**

Formally, the C value is the amount of nonreplicated nuclear DNA in the gametic nucleus, regardless of the species ploidy level (Fleury, Baumann y Langridge 2012, 83), *i.e.*, genome size. A paradox is often what a science sets aside with interest, amusement, and distant courtesy those things that are too solid to be purely or simply rejected and too contradictory to be adopted (Emmanuel 1972, 14).

As (Latorre y Silva 2013) point out, the genome of an organism is the total content of DNA in its cells, including genes and intergenic regions. In prokaryotes (Archaea and Bacteria), there is generally a linear relationship between genome size and the number of genes[[11]](#footnote-12). The smallest genomes are found in symbionts and parasites, as they undergo a process of gene degradation during adaptation to their new lifestyle. However, in eukaryotes, there is no correlation between genome size and organism complexity. This is known as the *C-value paradox*.

The largest genome is found in an amoeba, a unicellular organism, with 686,000 Mb, 200 times larger than the human genome and 20,000 times larger than that found in yeast (Latorre y Silva 2013). Currently, it is known that most of the excess DNA is repetitive DNA, which, at the time Latorre and Silva wrote the cited article (2001), apparently did not have a function and whose possible role in genome evolution was unknown. Because of that, the authors established that this type of DNA is known as *selfish DNA*, a term that refers to genetic segments that can enhance their own transmission at the expense of other genes in the genome, even if this does not have a net positive or negative effect on the fitness of the organism. As (Werren 2011, 10863) points out, these genes can only be harmful or neutral to the organism. The next section will address its role in genomic evolution.

**Figure 1**

*Range of Genome Size in Organisms of the Three Domains of Life*

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*Source:* (Latorre y Silva 2013).

As (Latorre y Silva 2013) point out, “genome size in eukaryotes is defined as the C-value or amount of DNA per haploid genome, such as that which exists in the nucleus of a spermatozoon”. It is called C because this amount is virtually constant within a species and characterizes them.

As Figure 1 shows, in general, eukaryotes have much larger genomes than prokaryotes, with only one exception. It can also be observed in the figure that there is a very wide range of sizes, much larger than that of prokaryotes (more than 80,000-fold larger. However, is there, as in prokaryotes, a relationship between genome size and organism complexity?

**Table 1**

*Genome Size, Gene Number and Gene Density*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Organism** |  |  |  |  |  |
| Common name or class | Scientific name | Genome size(Mb) | Number of genes | Gene density(genes/Mb) |  |
|  |
| **Eukaryotes** | *Saccharomyces cerevisiae* | 12 | 6,241 | 480 |  |
| Baker’s yeast |  |
| Nematode | *Caenorhabditis elegans* | 97 | 18,424 | 190 |  |
| Cruciferous | *Arabidopsis thaliana* | 125 | 25,498 | 204 |  |
| Fruit fly | *Drosophila melanogaster* | 180 | 13,601 | 75 |  |
| Pufferfish | *Fugu rubripes* | 400 | 35,000 | 100 |  |
| Rice | *Oryza sativa* | 450 |  |  |  |
| Sea urchin | *Strongylocentrotus purpuratus* | 900 | 27,350 | 30 |  |
| Maize | *Zea mays* | 2,400 |  |  |  |
| Human | *Homo sapiens* | 3,400 | 35,000 | 10 |  |
| Onion | *Allium cep* | 18,000 |  |  |  |
| Amoeba | *Amoeba dubia* | 686,000 |  |  |  |
| **Archaea** | *Aeropyrum pernix* | 1.55 | 1,522 | 981 |  |
| Crenarchaeota |  |
| Euryarchaeota | *Methanococcus jannaschii* | 1.66 | 1,715 | 1033 |  |
| Euryarchaeota | *Archaeoglobus* | 2.18 | 2,420 | 1110 |  |
| **Bacteria** | *Buchnera sp. CCE* | 0.45 |  |  |  |
| Proteobacteria |  |
| Gram positive | *Mycoplama genitalium* | 0.58 | 479 | 831 |  |
| Proteobacteria | *Buchnera sp. APS* | 0.64 | 564 | 881 |  |
| Gram negative | *Haemophilus influenzae* | 1.8 | 1,727 | 959 |  |
| Cyanobacteria | *Synechocystis sp.* | 3.6 | 3,168 | 880 |  |
| Gram positive | *Bacillus subtilis* | 4.2 | 4,100 | 976 |  |
| Proteobacteria | *Escherichia coli* | 4.6 | 4,288 | 932 |  |

*Source:* (Latorre y Silva 2013).

In Table 1, the range of C values is presented for several representative groups of eukaryotic organisms. In this table, the following is observed:

“(…) unicellular protists such as amoebae show the greatest variation in C-values (23.5 Mb to 686.000 Mb, with a ratio of 29,191 between the largest and the smallest), while mammals, birds and reptiles show less variation in the size of their genome (a ratio of only 4, 1 and 4, respectively). Furthermore, the large variation in genome sizes between eukaryotic species does not seem to have a relationship with either the complexity of the organism or the number of genes they contain. For example, amoebae, which have the largest genomes, have 200 times more DNA than humans (3,400 Mb) and an amoeba cannot be more complex than a human. Moreover, it would be expected that mammals, more complex organisms, present larger genomes. However, many other organisms, such as fish, amphibians, or plants, have much larger genomes. Even when we compare the sizes between organisms that appear similar in terms of complexity, there are also wide differences in their C-values. For example, flies and locusts, onions, lilies, etc. have considerable variations in the sizes of their genomes. Amphibians as a group have variations of up to 91 times and it is hard to believe that this may reflect variations of nearly 100 times the number of genes necessary to give rise to the corresponding amphibians, or that onions need 200 times more DNA than rice.” (Latorre y Silva 2013).

The lack of a defined pattern between C-values and the presumed amount of genetic information contained in the organism’s genome was called the *C-value paradox*.

Since it is not logical to assume that a species possesses less DNA than the amount required to specify its vital functions, it must be explained why many species contain such an excess of DNA. Therefore, the first question to be clarified is whether there is a correlation between genome size and the number of genes. That is, are differences in genome size due to gene or nongene DNA?

(Latorre y Silva 2013) point out that it has been known since the late 1960s that the eukaryotic genome is composed of a large amount of repetitive DNA. Additionally, since the late 1970s, it has been known that genes are interrupted by noncoding sequences, introns, which must be removed before the ribosome synthesizes the protein. In both cases, it is apparently superfluous DNA that contributes to the wide variation in C-values and, therefore, explains the apparent paradox. However, as previously mentioned, recent research such as (Werren 2011, 10863) indicates that this DNA is not superfluous (or, at the very least, there are strong indications that it is not), but rather these genes can only be harmful or neutral to the organism. As a result, a genetic conflict arises between selfish genetic elements (SGEs) and other genetic elements of the genome, highlighting a dialectical relationship between the two types of genes as will be shown below.

(Werren 2011, 10866) states that there is increasing evidence that SGE and the resulting genetic conflict are important drivers of evolutionary change and innovation, describing the types of SGE and their evolutionary consequences, including how these elements shape basic biological features such as genome structure and gene regulation, the evolution of new genes, the origin of new species, and mechanisms of sex determination and development. This highlights a dialectical relationship between both types of genes, which are in perpetual unity and struggle, thereby generating evolutionary change. That is why we consider it convenient to call them *negative genes* (in the sense of dialectically conceived negativity) or NGs instead of selfish genes.

(Werren 2011, 10868-10869) also considers the dynamics of NGs, including their possible “evolutionary functions”. This implies that the C-value paradox remains open as such, as a paradox.

The size and number of introns vary widely across the evolutionary scale, with mammals having the highest number and largest size. Repetitive DNA also varies among organisms. This DNA is traditionally classified as highly repetitive, with sequences such as microsatellites and minisatellites, and moderately repetitive, which includes transposable elements (also known as "transposons"), sequences that constitute the clearest example of selfish DNA.

As pointed out by (Pray 2022), the question "How many genes are there in a genome?" surprisingly "(...) is not very important, and the current paradigm of molecular biology holds that it has nothing to do with the complexity of the organism. There is more to genomes than genes that encode proteins alone. Obviously, this is a case of systems with enough complexity so that the whole is more than the sum of the parts, which suggests the inadequacy of additive functions for gene counting.

The current paradigm about the eukaryotic nuclear genome establishes the following (Pray 2022):

1. The eukaryotic nuclear genome is linear, unlike the typically circular DNA of bacterial cells. This means that it adheres to the structural double helix model of Watson-Crick.
2. Additionally, it is embedded in nucleosomes, complex structures of DNA-protein that group together to form chromosomes.
3. Eukaryotic genomes vary dramatically in terms of size and number of genes. Nonetheless, the size of the genome and the number of genes present in an organism reveal little about the complexity of that organism.

**Figure 2**

*Chromatin has a highly complex structure with several levels of organization. The simplest level is the double-helical structure of DNA*



*Source:* (Pray 2022).

**Table 2**

*Genome Size and Number of Protein-Coding Genes for a Select Handful of Species*

|  |  |  |
| --- | --- | --- |
| **Species and Common Name** | **Estimated Total Size of Genome (bp)\*** | **Estimated Number of Protein-Encoding Genes\*** |
| *Saccharomyces cerevisiae* (unicellular budding yeast) | 12 million | 6,000 |
| *Trichomonas vaginalis* | 160 million | 60,000 |
| *Plasmodium falciparum* (unicellular malaria parasite) | 23 million | 5,000 |
| *Caenorhabditis elegans* (nematode) | 95.5 million | 18,000 |
| *Drosophila melanogaster* (fruit fly) | 170 million | 14,000 |
| *Arabidopsis thaliana* (mustard; thale cress) | 125 million | 25,000 |
| *Oryza sativa* (rice) | 470 million | 51,000 |
| *Gallus gallus* (chicken) | 1 billion | 20,000-23,000 |
| *Canis familiaris* (domestic dog) | 2.4 billion | 19,000 |
| *Mus musculus* (laboratory mouse) | 2.5 billion | 30,000 |
| *Homo sapiens* (human) | 2.9 billion | 20,000-25,000 |

*Source: (Pray 2022)*.

From Figure 2 and Table 2, the following it can be verified:

1. The simplest level of chromatin, whose DNA organization order is lower than the chromosome, is the DNA double helix.
2. There is not even a clear correspondence between genome size and the number of genes encoding proteins, another indication that the number of genes in a eukaryotic genome reveals little about the complexity of the organism.

Alternative splicing was the first phenomenon that scientists discovered that made them realize that genomic complexity cannot be judged by the number of genes that code for proteins. As (Pray 2022) notes,

“During alternative splicing, which occurs after transcription and before translation, introns are removed, and exons are spliced together to make an mRNA molecule. However, the exons are not necessarily all spliced back together in the same way. Thus, a single gene, or transcription unit, can code for multiple proteins or other gene products, depending on how the exons are spliced back together. In fact, scientists have estimated that there may be as many as 500,000 or more different human proteins, all coded by a mere 20,000 protein-coding genes”.

Therefore, the complexity of an organism is the result of much more than simply the number of nucleotides that make up a genome and the number of coding sequences in that genome. As (Pray 2022) notes,

“Not only may one coding sequence encode a large number of separate protein products via alternative splicing, but many genomes are also rich with noncoding RNA sequences that work to coordinate gene expression. When one combines these elements with other regulatory elements, such as enhancers and promoters, as well as with potential sequences that remain uncharacterized, it becomes clear that while size is one component of organismal complexity, its contribution to that complexity is small.”

Once the philosophical and theoretical foundations for the construction of a hypothesis have been sufficiently established, it is legitimately possible to “speculate”[[12]](#footnote-13) on the possible explanation of the phenomenon being studied, which will not be an “idle speculation” because it is or will be susceptible to experimental proof or refutation when technological level permits it (Haldane 2022, 7, 12).

1. **A Hypothesis on the C-Value Paradox**

The first issue to analyze is whether DNA strands are adequately described as linear systems. Regarding this, as (Yakushevich 2001, 305) notes, for over twenty-one years, many researchers studying the large amplitude internal movements of DNA have concluded that the molecule can be considered a nonlinear dynamic system in which solitary conformational waves can be excited. The first approach to nonlinear modeling of chemical systems, which is currently the standard approach in this regard, was carried out in the form of a nonlinear Hamiltonian system. At the level of quantum mechanics, the Hamiltonian of a dynamic system is an operator that corresponds to the total energy of that system, including both kinetic energy and potential energy. Its spectrum, *i.e.*, the energy spectrum of the system or, equivalently, the set of eigenvalues of the equations that describe the energy of the system, is the set of possible results that can be obtained from a measurement of the total energy of the system. In the context of quantum chemistry, a molecular Hamiltonian is the Hamiltonian operator that represents the energy of the electrons and nuclei in a molecule.

Following (Yakushevich 2001, 305), this approach has been used to theoretically explain general issues such as the dynamic mechanisms of DNA function, dynamic mechanisms of transitions between different forms of DNA, long-range effects[[13]](#footnote-14), the regulation of the transcription processes described above, DNA denaturation[[14]](#footnote-15), protein synthesis (specifically, insulin production) and carcinogenesis (the process by which cancer develops), among other molecular phenomena, as well as brave attempts to explain different experimental data within the frameworks of nonlinear concepts, despite the heated discussion in the scientific literature, such as interpretations of experimental data on hydrogen-tritium exchange[[15]](#footnote-16), resonant microwave absorption and neutron scattering by DNA.

However, at a directly applied level, there are limitations to the use of this approach, since although it is generally assumed that solving the time-independent Schrödinger equation associated with the Coulomb Hamiltonian will predict most of the molecule’s properties, including its shape (three-dimensional structure), calculations based on the complete Coulomb Hamiltonian are very rare. The fundamental reason is that its Schrödinger equation is computationally very difficult to solve, and as a result, applications at the time Yakushevich wrote his research were restricted to small systems such as the hydrogen molecule; as will be seen later, modern numerical methods and quantum computing have changed the scope of our numerical estimates.

In Yakushevich’s research, the history of the problem in question is briefly described, as well as the main results and new arguments based on the analysis of internal movements of DNA and general principles of mathematical modeling of such movements. It has been established (Yakushevich 2001, 306) that it is necessary to use an inharmonic approach[[16]](#footnote-17) (nonlinear) when the amplitudes of the movements are not small, for example, when local unwinding of the DNA double helix occurs at the local level[[17]](#footnote-18).

Specifically, as pointed out by (Amnuanpol 2016, 69), this unwinding occurs during DNA transcription. There, base pairs open in response to enzymatic forces, separating two intertwined nucleotide strands. Consequently, double-stranded DNA (dsDNA), where two nucleotide strands are wound together, structurally transitions to single-stranded DNA (ssDNA), where two nucleotide strands are completely unwound and separated. The large separation between strands is closely related to the softening of the nucleotide strands.

Thus, it becomes evident that the source of complexity occurs around transcription, either during or immediately after it. This is because the source of complexity lies in alternative splicing processes (which are a source of complexity because a single gene codes for multiple proteins and the resulting exon splicing may not be the same as originally spliced), DNA editing, trans-splicing, and tandem chimerism. It is around this moment that the paradox of not being able to describe the complexity of the organism by the number of genomes arises, as there is no-linear relationship between the whole and its integrant parts at this moment.

From the above, it follows that to solve the C-value paradox[[18]](#footnote-19) it is necessary to take into consideration the following eight aspects:

1. What type of information is encoded by the involved genes?
2. What type of encoding is employed?
3. Should only protein-coding genes be considered or, alternatively, should greater weight be assigned to protein-coding genes compared to non-coding ones (*e.g.*, through weighting schemes)?
4. What type of transcription is performed?
5. Genes have a nonlinear internal structure, ideally involving the Schrödinger equation since in the early 20th century some chemists such as Walter Heitler and Fritz London demonstrated that covalent bonds can be understood through the lens of the quantum world and nucleotides belonging to the same strand are connected by strong covalent chemical bonds (Zdravković, y otros 2019, 1). This is the case, for example, or the Peyrard-Bishop model (Zdravkovic 2019, 11).
6. The type of gene involved.
7. Consider the role played by negative genes (discussed above) in genetic and biological evolution.
8. Consider what happens around transcription.

If the eight aforementioned factors could be taken into consideration when establishing a relationship between the number of genes and the complexity of the organism, it is very likely that the desired traces of regularity regarding the link between the number of genes and the complexity of the organism could be discovered, with a certain margin of error at a certain level of statistical confidence.

This is asserted because, due to the instrumental limitations mentioned earlier, it is most likely that modeling this phenomenon would only be possible from the theory of probabilities, which is the same approach applied to quantum mechanics and quantum chemistry. Additionally, it should be considered that eukaryotic organic systems are not mechanical systems, that is, they cannot be completely described by their mechanism; in fact, certain versions of quantum systems are not even mechanical, for example, dissipative quantum systems, which, as demonstrated by (Vitiello 2014, 203), are isomorphic (*i.e.*, topologically equivalent) to fractal systems (which are complex systems in the sense of chaos theory).

The above implies the substitution of sigma-additive functions for other types of functions in the context of gene counting[[19]](#footnote-20), functions that will have to involve high-dimensional and complex-structured probabilistic systems. However, an investigation of this nature requires not only a dialectical vision of the processes as defined in Section II, but also a profound scientific-technical knowledge of the directly and indirectly studied phenomena, as well as supercomputers that may not necessarily exist or even be in the process of being developed.

Therefore, we consider it convenient to call them negative genes (in the sense of dialectically conceived negativity) instead of selfish genes. Additionally, one of the most important, if not the most important, issues is the fact that the elaboration of the different working hypotheses that allow the construction of functions or functionals with which to seek the counting of genes in such a way that the greater the number of genes, the greater the complexity of the eukaryotic organism, must be carried out within the ontological, logical, and gnoseological framework outlined in Section II.

The above has different implications. For example, it may not necessarily be a single function (or functional, if that were the case) but rather a family of functions (or functionals) that perform this task, that the problem should not be approached in a reductionist manner, that ordinary or positive genes and negative genes should be conceived as opposites in unity and struggle that generate change, that truth should not be conceived in instrumental terms (Kantian and positivist conceptions) and/or empirical results (empiricist conception) but rather such instruments and their results should be interpreted in terms of dialectical logic (whose fundamental principles have been exposed) and must be congruent with the dialectical behavior presented by the ontology of other phenomena in the same field and different fields (in the sense shown in Section II), that speculation that allows the construction of hypotheses is legitimate to the extent that it is anchored to general concrete facts[[20]](#footnote-21), that the inherent contradictions in a subject of study must be expressed as the contradiction between form and content (at the epistemological level) and the contradiction between phenomenon and essence (at the ontological level) organically linked through dialectical logic (under the monist principle of complementarity, which implies that phenomena are “of one piece” but without their components losing their identity).

The eight aforementioned factors are consistent with the findings in other research. For example, (Choi, Kwon y Kim 2020, 709) point out that “The disconnection between gene number and biological complexity may be derived from highly complex gene expression regulation, multifunctional proteins, alternative splicing, multigene families, and developmental regulation by homoeotic gene sets.” These results can also be fed back with findings of previous efforts aimed at resolving the C-value paradox. For example, (Gall 1981, 13s) proposes a model that “(…) stress that the number of active genes and transcription units need not be correlated with the total amount of DNA.” This can be considered to build new gene count functions.

On an instrumental level, the novel research by (Al, y otros 2020, 8) presents an analytical and numerical study of the Peyrard-Bishop DNA dynamic model equation, and in both cases, they obtain accurate, efficient, and versatile results in mathematical physics to solve the non-linear evolution equations (NLEEs) involved; their methods can also solve other NLEEs too. The analytical and numerical solutions seem to have a strong convergence, as shown in figure 3. This may smooth the path for the study of the C-value paradox involving the time-independent Schrödinger equation.

**Figure 3**

*Graphical Comparison of Analytical and Numerical Solutions of the Peyrard-Bishop DNA Dynamic Model Equation*



*Source:* (Al, y otros 2020, 8).

(Zdravković, y otros 2019, 1) presents a kink solution[[21]](#footnote-22) (also a localized solution) for the helicoidal Peyrard-Bishop model of DNA molecules using numerical methods that “could be a useful tool to describe DNA–RNA transcription”. This is shown in Figure 4.

**Figure 4**

*Graphical Comparison of Analytical (Dotted Lines) and Numerical (Solid Lines) Versions of Kink (Left) and Localized (Right) Solutions*



*Source:* (Zdravković, y otros 2019, 4).

Additionally, the novel research by (Boev, y otros 2021, 1) proposes a successful method for solving genome assembly tasks with the use of quantum and quantum‑inspired optimization techniques, specifically for de novo genome assembly[[22]](#footnote-23). The algorithm of the numerical method proposed by the authors is shown in Figure 5.

**Figure 5**

*Solving the de novo genome assembly problem using quantum annealers and quantum-inspired (digital) annealing algorithms*



*(a) raw reads; (b) raw reads are transformed to the overlap-layout-consensus (OLC) graph; (c) finding the Hamiltonian path for the OLC graph is reduced to the QUBO[[23]](#footnote-24) problem; (d) the QUBO problem should be embedded to the architecture of the quantum annealer (D-Wave): for this purpose each logical variable of the QUBO problem is assigned with several qubits of the quantum annealer; (e) and (f) the Ising problem in QUBO form can be solved using quantum annealers (D-Wave) and quantum-inspired algorithms (SimCIM), respectively; (g) the output is the Hamiltonian path[[24]](#footnote-25); (h) the genome sequence is obtained as the solution.*

*Source:* (Boev, y otros 2021, 3).

All the numerical methodologies mentioned above could be used to build new gene count functions that meet the eight criteria indicated.

1. **Conclusions**

This research suggests that if the eight key aspects identified in the process that shapes genomic structure are considered in light of dialectical materialism, it is possible to construct a function that counts genes in such a way that the size of the genome and the number of genes correspond to the biological complexity of the organism being studied, at least approximately. This implies a solution or an approximation to the solution of the C-value paradox. To the best of our knowledge, this is the first time that this proposal has been made.

The eight key aspects identified, especially the role of negative or selfish genes, the processes that occur around transcription, and the quantum and complex structure (dynamic and nonlinear) of DNA are the centers of gravity around which the paradox-free gene counting function (PFGCF) must be constructed. In addition, a gnoseological and methodological guide is provided to lead such elaboration, as well as numerical methods suggested to solve problems of high computational complexity in the context of molecular biology.

The results obtained are, from every perspective, insufficient both in theory and application and only seek to constitute a solid starting point on the addressed problem, specifically on which aspects and moments of the underlying set of processes should be focused to approach the construction of a PFGCF, and the general epistemological and methodological guidelines under which this approach should be carried out as well as suggestions of numerical methodologies to carry out the task.

This study, as a legitimate speculation and general guide for the construction of a PFGCF, has the limitation of not having specific proposals and, consequently, neither experimental verification of possible responses. However, this is precisely why the possibility of a wide variety of theoretical and applied research in this line is opened for the future, which will have to involve philosophers, chemists, geneticists, and physicists, as well as the use of high-capacity computational equipment.

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1. “Organic” in the sense of forming a coherent whole and “synthesis” in the sense of the composition of the contradictory and complex composition of a whole by the conjunction of its parts. [↑](#footnote-ref-2)
2. The purely conceived. [↑](#footnote-ref-3)
3. We are going to expand this in the next section. [↑](#footnote-ref-4)
4. The characterization of existence in general not only as objective reality but also as material is because the idealist philosophical school has an objective variant, whose best representative is Hegel. [↑](#footnote-ref-5)
5. Judgments that are formed of something by indications or observations; such judgments are anticipated to be true but are not yet generally proven. [↑](#footnote-ref-6)
6. Detailed sequence of a scientific action process. [↑](#footnote-ref-7)
7. Of course, this characteristic is not linear. For example, we cannot expect to need quantum chemistry laws to explain capital accumulation in political economy systems, but we can expect to need knowledge of quantum chemistry laws for a better understanding of the phenomena studied in molecular biology, the laws of molecular biology for a better understanding of human neurology, the laws of human neurology for a better understanding of human psychology, the laws of human psychology for a better understanding of social psychology, and the laws of the latter for a better understanding of the ideological alignment phenomenon. Obviously, the form and degree in which this accumulation of intersystemic laws will exist and the ease with which the details of this accumulation will be visible will not be linear and will vary according to the phenomenon under study. [↑](#footnote-ref-8)
8. In the sense of a coherent whole. [↑](#footnote-ref-9)
9. A metalogic is a logic that reviews or thinks of itself, and dialectical logic is a metalogic (Findlay 1964, 2). How does dialectical logic think of itself as a metalogic? Through process which is multi-level (multidimensional, seeking to encompass relevant totality), recursive into the past (historical, long-term) and conservative of error (aspects of less developed stages of a process that have only been partially overcome -negated- and, consequently, partially preserved in earlier stages, which highlights the continuity and unity of existence as a totality). This conservation of error is not only present in the process of constructing scientific knowledge, but also in research tools as relevant as the Bayes' theorem or the Newton-Raphson method. [↑](#footnote-ref-10)
10. The only absolute certainty is uncertainty, and the only absolute constant is change. [↑](#footnote-ref-11)
11. This refers to the number of genes that are added, as seen before, in a linear manner, *i.e.*, sigma-additive. [↑](#footnote-ref-12)
12. To speculate is, philosophically speaking, to think by implication. A legitimate speculation is one that starts from material, objective, and rational bases, and which develops without ever losing its anchoring in such bases. [↑](#footnote-ref-13)
13. As pointed out in (Dekker y Misteli 2015, 1), long-range interactions can occur intrachromosomally between regions located on the same chromosome or interchromosomally between regions on different chromosomes. [↑](#footnote-ref-14)
14. As noted in (Wang, Lim y Son 2014, 1), DNA denaturation is a process of separating dsDNA (double-stranded DNA) into single strands, which are favorable for DNA hybridization. Although denaturation is a key reaction that determines the success of DNA hybridization-based bioassays, up to the time prior to the publication of the cited article, a systematic characterization of the denaturation method for dsDNA had not been attempted. [↑](#footnote-ref-15)
15. The research by Englander et al, in 1980, which was the pioneering research in proposing the nonlinearity of DNA, was precisely about this phenomenon. [↑](#footnote-ref-16)
16. An inharmonic approach is one that models the deviation of a system from being a harmonic system, that is, a system that tends towards equilibrium because any deviation from that equilibrium is restored by a force proportional to the force that caused it to deviate from equilibrium. In the context of DNA, the non-harmonic behavior is may be due to the presence of non-linear stacking forces, which make the potential energy of the interactions between the bases not proportional to the deviations of the base position from its equilibrium position. [↑](#footnote-ref-17)
17. The research by (Zdravkovic 2019, 2-28) explains some of the nonlinear models of DNA dynamics. [↑](#footnote-ref-18)
18. By “solve” we should not understand a solution of linear logic and formal foundation, but a solution that allows us to find truly relevant traces of regularity between the relationship of the number of genes and the complexity of the analyzed organism. [↑](#footnote-ref-19)
19. If the double helix is the most basic form of chromatin (and these are less complex than chromosomes) and there are strong indications non-linearity of double helix, then it implies that it is not reasonable to count genes in the conventional sense (in the additive sense). [↑](#footnote-ref-20)
20. That facts are both concrete and general is possible because Marx’s theory of knowledge, which unlike empiricism does not naturally accept empirical evidence simply as empirical fact ("raw facts"). His theory of knowledge is that of *the rationalized concrete* in terms of the logical framework of dialectics (Dussel 1985, 49-54), which also differs substantially from rationalism and its variants in that it is not limited to being an abstract expression of the empirical that is not necessarily rigorously subject to the facts and/or their power. This rationalization implies the logical unification of the ontological and the gnoseological. [↑](#footnote-ref-21)
21. A kink solution refers to a solution of a nonlinear differential equation that represents a transition region between two different states. This solution is often presented as a wave or soliton and has a topological shape that resembles a step or “kink” in the curve. In the context of DNA chain distortion, a kink solution refers to a configuration in which the structure of the chain bends at a specific point, creating a transition region or “kink”. These kink solutions are important in the study of DNA dynamics and may have implications on the stability of the molecule’s structure and biological function. [↑](#footnote-ref-22)
22. *De novo* sequencing refers to sequencing a novel genome where there is no reference sequence available for alignment which is used for the analysis of genomic rearrangements, chromosome phasing, and reconstructing genomes without a reference, require solving tasks of high computational complexity (Boev, y otros 2021, 1). [↑](#footnote-ref-23)
23. Quadratic Unconstrained Binary Optimization (QUBO), or Unconstrained Binary Quadratic Programming (UBQP). [↑](#footnote-ref-24)
24. A Hamiltonian path is a path in a graph that visits each vertex exactly once. In other words, it is a trajectory that traverses all the nodes of a graph without repeating any. [↑](#footnote-ref-25)