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Graphical Abstract

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Highlights

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- An equation of the total energy for simple genome replication is derived.
- Decreases in entropy and in Gibbs free energy can be accomplished together.
- Some factors may have favoured the emergence of self-replicating biological systems.
- Short RNA sequences made of G and C may conform to these predictions.

Information–energy equivalence and the emergence of self-replicating biological systems

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ABSTRACT

Biological processes are characterized by a decrease in entropy in apparent violation of the second law of thermodynamics. Information stored in genomes help to solve this paradox when interpreted under the relationship between information and energy stated by Brillouin in the 1950's. However, the origins of living forms from inanimate matter which have no information storage device remains an open question. In this paper, a theoretical approach is developed on this issue. The replication of a simple entity with a binary genome is assumed to require an information-equivalent energy in addition to the standard activation energy. It is found that, in some conditions, a decrease in entropy can be accomplished together with a decrease in Gibbs free energy. An equation of the total energy for the replication of this entity is derived. Three factors are predicted to lower this energy: a small number of states of the coding sequence, a lower temperature, and a high ratio of the reaction on diffusion coefficients. These factors may have favoured the emergence of evolutionary demons—information storage devices that are able to decrease entropy. It is evaluated that some short, single-stranded RNA sequences made only of G and of C may conform to this model. The consequences of this model and its predictions on the origins of life on Earth and on other planets are discussed.

We have already seen that a great deal of information is needed to specify the structure of ² a complicated nonrandom object. It may be concluded that anything that we would want to call "living" would have a high information content. This apparently simple requirement has far-reaching consequences.

⁵ Orgel (1973, p. 192)

1. Introduction

Brillouin (1949) started his article 'Life, thermodynamics, and cybernetics' by asking: "How is it possible to understand life, when the whole world is ruled by such a law as the second principle of thermodynamics, which points toward death and annihilation?" The second law of thermodynamics states that ¹⁰ a spontaneous chemical reaction implies an increase of entropy of the system; however, many chemical

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 reactions in living beings imply a decrease in entropy. For instance, the process of DNA duplication results in two DNA molecules identical to themselves thus implying a decrease in entropy. Brillouin's question might be reformulated in the following way: Which physical mechanisms might explain how living beings have evolved from inanimate matter? This question—which is essential to understand the origin of life on Earth and possibly in other natural or artificial systems—remains essentially unsolved. Life on Earth is, as far as we know today, the exception of how matter is organized in the Universe, and physical laws do not to explain this exception (Hawking and Ellis, 1973; Crick, 1981). This is well illustrated by the fact that living beings, as pointed out by Brillouin, appear to violate the second law of thermodynamics which predicts that entropy increases in a closed system. By contrast to what is expected from the second law of thermodynamics, a DNA molecule will replicate identical to itself in a predictable way, thus decreasing entropy. This paradox has attracted a lot of interest from researchers over several decades.

 Genetic information is stored in genomes which can present a great variety of structures depending on the taxonomic group (see an overview in Paradis, 2020). With a few exceptions of some virus genomes (which can be RNA sequences), genetic information is stored in DNA sequences. Although the physical structure of genomes is important, molecules of DNA are not only simple physical entities: they should be considered as information storage devices. This point is a central feature in the modern concept of life (Vitas and Dobovišek, 2019). A very general definition of an information storage device is: an ordered sequence of discrete units which may take different states. In the case of DNA, there are four such states: {A, C, G, $_{29}$ T}. In the case of binary systems, such as digital computers, there are two states: {0, 1}. The link between entropy and information was established by Shannon (1948) who made an almost strict parallel between the 31 classical measure of entropy which considered microstates of physical or chemical entities, and communi- cation exchange between communicating entities. Although the validity of Shannon's framework has been debated (e.g., Kish and Ferry, 2018), some authors, such as Bekenstein (1973), do not see a problem with this parallel. On the other hand, Brillouin (1953) formulated a link between entropy and information which states that if an experiment yields an increase in information concerning a physical system, it must be paid for by a larger increase in the entropy of the system. Brillouin's framework effectively draws links between ³⁷ the concepts of energy, information, and entropy, and helped to solve the paradox of Maxwell's demon by posing that acquiring information necessitates some energy (Szilard, 1964; Earman and Norton, 1998).

 Information storage, replication, and expression are at the core of life and evolution. These features distinguish living beings from inanimated entities (Vitas and Dobovišek, 2019). Information in living beings must be read to be used or replicated. Information replication is indispensable for survival of living beings. ⁴² Similarly, the use of stored information, in whatever form, is indispensable for living beings to interact with their environment. It appears therefore that reading information stored in living beings is an indispensable mechanism for their survival. Although the question of replicating and maintaining a genome has been extensively addressed in the literature (e.g., Lynch and Conery, 2003; Elliott and Gregory, 2015), this is generally posed in terms of energy cost with respect to genome sizes rather than in terms of informational contents (Bonnici and Manca, 2016; Manca, 2017).

 In this paper, I present a theoretical approach linking information theory and the evolution of informa- tion processing at the storage level. The rationale of this framework is the link between information and energy derived from Brillouin's formula on negentropy. The consequences of this framework for genomic evolution and the origins of life are discussed.

52 2. Theory and models

 The approach adopted here is based on a basic model of replication. This is justified in order that the present model and the inferred conclusions are not restricted by the specific physical nature of the information coding structure. Besides, considering that the exact nature of the first living beings on Earth is unknown, an abstract model is probably a good approach here.

 The present model considers a symbolic representation of a self-replicating entity which is denoted as 58σ z. It is assumed that there are several copies in the environment that are not identical. We assume that z is made of two basic elements, the first element is written X and is constant for all copies of the entity, and the 60 second element is either 0 or 1. So we can write $z = \{X0, X1\}$. We assume that the environment contains copies of X, 0, 1 with no limitation.

62 2.1. Information, energy, and replication

 ϵ ₆₃ The physical nature of z is not important: what is relevant here is that it can be either X0 or X1. Unless this entity is perpetual or eternal, it will eventually die or decay. Therefore, to be able to maintain its existence, it has to reproduce through a process of replication. To be effective, this process must be faithful: ⁶⁶ entities with $z = X0$ must replicate to result in two entities with $z = X0$, and entities with $z = X1$ must do the same to entities with $z = X1$. This faithfulness of the replication process is a prerequisite for life. Another prerequisite is that the physical unit of the information storage must be present in the environment to permit its replication. Therefore, a living entity with a one-bit information storage must acquire at least two bits of information to replicate itself: one bit for the value of z, and one bit from the environment.

The equivalence between energy and information stemming from Brillouin's derivation of the negentropy principle states that acquiring one bit of information requires an energy at least proportional to k_B ln 2 joules where k_B is the Boltzmann constant (Brillouin, 1953, 1959). More specifically, we may write that acquiring one bit of information requires at least ΔE joules and a lower bound for this quantity is given by:

$$
\Delta E \geqslant k_{\text{B}} T \ln 2,\tag{1}
$$

where *T* is the temperature in kelvins. Taking $T = 310.15 \text{ K} (= 37 \text{ °C})$ and $k_B = 1.380649 \times 10^{-23} \text{ J.K}^{-1}$, one finds $\Delta E \ge 2.968\ 114 \times 10^{-21}$ J for one bit of information. This value is actually meaningful at the microscopic level, that is considering a bit in isolation. At the macroscopic level, we have to consider a large number of information bits and multiply this quantity of energy by Avogadro's number $N = 6.02214076 \times$ 10^{23} , so that we have:

$$
\Delta E \ge 1787.44 \text{ J.mol}^{-1}.\tag{2}
$$

 The relevance of these equations for living beings appears when considering that living systems, such as DNA molecules, must replicate themselves by acquiring information about their surrounding environment. As mentioned previously, two bits of information must be acquired for the replication of z: one bit to know the state of z and one bit from the environment. Therefore, the right-hand side term of (2) must be multiplied by two. At this point, it is still an open question what is the source of the energy required to acquire these information bits: the system may lower its internal energy level, thus releasing some energy, or energy may be input from outside the system. The crucial point is that the system requires a source of energy which can be used as information.

⁷⁹ Let us consider again our hypothetical living being as above where the information storage is made of a $\frac{1}{80}$ single bit of information so that z takes the value X0 or X1. We also assume that the surrounding environ-81 ment contains many available copies of 0's and 1's in equal proportions; in other words, this environment ⁸² has high (thermodynamic) entropy. In order to replicate itself, our hypothetical simple living being must ⁸³ acquire information about which molecule is 0 and which molecule is 1. According to the above equations, 84 this has an energy cost given by ΔE . In a simple system, this cost can be met by decreasing the energy level ⁸⁵ during information acquisition. Hydrogen bonds (H-bonds) provide a mechanism that seems suitable for ⁸⁶ this. These bonds are ubiquitous in chemical systems (e.g., in water), do not require high energy inputs to be ⁸⁷ created (unlike common molecular bonds), and decrease the overall energy level of these systems. There-⁸⁸ fore, we predict that a simple living system with its information stored in a single bit may be self-replicating ⁸⁹ if matching 0's and 1's create H-bonds that decrease energy by at least 2 × 1787*.*44 = 3574*.*88 J.mol⁻¹. This simple model may be extended to nucleic acids (DNA and RNA) since information acquisition in

these molecules is based on H-bonds. In the case of DNA sequences, ln 2 in (1) must be replaced by ln 4 because there are four possible bases instead of two. This is equivalent to multiply the previous quantity by two (since $\ln 4 = 2 \ln 2$). Therefore, we have for DNA sequences:

$$
\Delta E \ge 7149.759 \text{ J.mol}^{-1}.\tag{3}
$$

⁹⁰ This prediction can be compared with values from the literature about the energy levels linked to base pair-91 ing in DNA. Mo (2006) estimated these energies at the following values:

92

93

$$
\Delta E(\text{CG}) = 106.17 \text{ kJ.mol}^{-1} (= 25.4 \text{ kcal.mol}^{-1})
$$

$$
\Delta E(\text{AT}) = 51.83 \text{ kJ.mol}^{-1} (= 12.4 \text{ kcal.mol}^{-1})
$$

⁹⁴ These are in agreement with the above value, and even much larger. We will come back to this point below. We now attempt to establish the overall energetic needs of replicating our hypothetical living entity. Our model assumes that replication requires a chemical reaction in order to link X with either 0 or 1. The assumption of the need for a chemical reaction for the replication of living beings is likely to be true in many cases (Crick, 1981). We may use Eyring (1935) equation that defines the rate of a chemical reaction denoted as ρ :

$$
\rho = \frac{\kappa k_{\rm B} T}{h} \exp\left(-\frac{\Delta G \ddagger}{RT}\right),\tag{4}
$$

where κ is the diffusion coefficient of the reaction, *h* is the Planck constant, ΔG : is the activation energy, and \vec{R} is the gas constant. This activation energy is the quantity of energy that must be provided to the system so that the reaction occurs. In most chemical reactions occurring in living cells, this energy is provided by coupled chemical reactions, such as the hydrolysis of adenosine triphosphate (ATP), and catalyzed by enzymes which lower ΔG : (Ji, 1974, 2000). In the present simple model of replication, the activation energy must be provided in addition to the energy needed to read information as examined above. By rearranging (4), the activation energy can be written:

$$
\Delta G^{\pm} = -RT \ln \left(\frac{\rho h}{\kappa k_{\rm B} T} \right).
$$

A chemical reaction is also characterized by the overall change in energy level of the system which is called the Gibbs free energy (Gibbs, 1873), and is defined by:

$$
\Delta G^{\circ} = \Delta H^{\circ} - T \Delta S^{\circ},
$$

where H and S denote the enthalpy and the entropy of the system, respectively, so that ΔH° is the overall ⁹⁶ change in enthalpy during the reaction, and similarly for ΔS° regarding the entropy of the system (Truhlar

 97 et al., 1983). The enthalpy of a system is defined by $H = U + pV$ where U is the internal energy of the 98 system, p is the pressure, and V is the volume. Assuming that p and V do not change during the reaction, 99 we can write $\Delta H^{\circ} = \Delta U^{\circ}$, the overall change in enthalpy of the system is equal to the overall change in ¹⁰⁰ internal energy of the system and we can write $\Delta G^{\circ} = \Delta U^{\circ} - T \Delta S^{\circ}$.

Both quantities of energy considered above are important to predict whether a chemical reaction is likely to happen: spontaneous reactions have a negative change in free energy (ΔG° < 0); however, if the activation energy is too large such reactions require a similarly large quantity of external energy such as heat or work to happen (Fig. 1). The second law of thermodynamics states that a spontaneous chemical reaction implies an increase in entropy of the system (i.e., $\Delta S^{\circ} > 0$). However, the replication of z implies by definition a decrease in entropy (as is also the case during replication of living beings). Since a spontaneous reaction is characterized by $\Delta G^{\circ} < 0$ which implies, in this case, that $\Delta U^{\circ} < T \Delta S^{\circ}$. However, we assume here that the second law of thermodynamics is not respected, thus $\Delta S^{\circ} < 0$ and since T is always strictly positive, we have $-T\Delta S^{\circ} > 0$. Therefore, to satisfy $\Delta G^{\circ} < 0$, the following inequalities must hold:

$$
\Delta U^{\circ} < 0
$$
\n
$$
|\Delta U^{\circ}| > T |\Delta S^{\circ}|.
$$

¹⁰¹ In other words, the decrease in internal energy of the system must be greater than the decrease in entropy ¹⁰² multiplied by the temperature.

free energy (ΔG°). In this hypothetical example, the reaction produces energy ($\Delta G^{\circ} < 0$). **Figure 1:** Changes in energy level during a chemical reaction showing the activation energy (Δ $G[±]$) and the

We now introduce the energy-information equivalent required for replication, denoted as \mathfrak{E} , and is

defined as the sum of Brillouin's information given by (1) and the activation free energy ΔG :

$$
\mathfrak{E} = 2Nk_{\text{B}}T \ln Z - RT \ln \left(\frac{\rho h}{\kappa k_{\text{B}}T} \right),
$$

where Z is the number of states of the basic information storage (i.e., $Z = 2$ for the hypothetical entity z, $Z = 4$ for RNA and DNA). The second term of the right-hand side can be split to isolate the two coefficients of the reaction (ρ and κ):

$$
\mathfrak{E} = 2Nk_{\mathrm{B}}T\ln Z - RT\ln\frac{\rho}{\kappa} - RT\ln\left(\frac{h}{k_{\mathrm{B}}T}\right).
$$

It is a central point of the present hypothesis that the energy required by replication is provided in the above theoretical model by the lowering of internal energy of the system, so this implies:

$$
\mathfrak{E} \leq -\Delta U^{\circ}.
$$

In other words, during the chemical reaction involved in replication, the decrease in internal energy must be at least equal to the activation energy of the reaction plus the energy defined by Brillouin's equation, $k_B T \ln 2$. Therefore, any factor that will lower the value of $\mathfrak G$ will stimulate chemical reactions leading to self-replication. Let us define three coefficients A , B , and C that depend only on T and on the constants previously defined $(k_B, h, \text{ and } R)$:

$$
A = 2Nk_{\text{B}}T
$$

\n
$$
B = RT
$$

\n
$$
C = -RT \ln \left(\frac{h}{k_{\text{B}}T}\right).
$$

Since $h = 6.62607015 \times 10^{-34}$ J.Hz⁻¹, then $h/k_B \approx 5 \times 10^{-11}$, and thus C will be greater than zero for all realistic values of T. Additionally, A and B are also strictly positive ($R = 8.314\,462\,618\,153\,24\,\mathrm{J}$.mol⁻¹.K⁻¹). ¹⁰⁵ The energy-information equivalent of replication is now written as:

$$
\mathfrak{E} = A \ln Z - B \ln \frac{\rho}{\kappa} + C.
$$

106 It appears that three factors are likely to influence the value of \mathfrak{C} . First, the lower the value of Z , the 107 lower the value of $\mathfrak C$ (since $Z \ge 2$, then $A \ln Z > 0$). Second, the ratio ρ/κ will always be positive (both ¹⁰⁸ parameters are always positive) so that the crucial point is whether this ratio is less than, equal to, or greater ¹⁰⁹ than one:

$$
\frac{\rho}{\kappa} > 1 \Rightarrow \ln \frac{\rho}{\kappa} > 0
$$

$$
\frac{\rho}{\kappa} = 1 \Rightarrow \ln \frac{\rho}{\kappa} = 0
$$

$$
\frac{\rho}{\kappa} < 1 \Rightarrow \ln \frac{\rho}{\kappa} < 0.
$$

¹¹⁰ Interestingly, the absolute values of these two parameters are not important, only their ratio. The reaction 111 coefficient ρ determines the "speed" of the reaction, so that the larger its value, the more efficient is the reac-112 tion. The diffusion coefficient κ can be compared to the diffusion parameter of a particule or a molecule as ¹¹³ considered in the early developments of modern physics (Einstein, 1905; Sutherland, 1905) and determines 114 how fast the molecules move in the environment. Therefore, it makes sense that the ratio ρ/κ is important ¹¹⁵ as it quantifies the opposite actions of reaction and diffusion. Third and finally, temperature has an almost 116 linear effect on \mathfrak{E} (Fig. 2). The ratio ρ/κ influences the position of this quasilinear relationship: the higher 117 this ratio, the lower the value of $\mathfrak G$ for a given value of T. The predicted values for $\mathfrak G$ vary between 65 and ¹¹⁸ 90 kJ.mol⁻¹ for temperatures varying between 270 and 330 K and a ratio ρ/κ between 0.1 and 10.

119 2.2. Self-Replicating RNA and Information

 In this section, we consider a real system that might conform to the previous theoretical model. Orgel (1992) discussed the case of self-replicating RNA molecules with the particular case of the hexamer GC- CGGC. This single-stranded RNA molecule can self-replicate *in vitro* through the ligation of the two trin- ucleotides GCC and GGC (Sievers and von Kiedrowski, 1994). Interestingly, this hexameric molecule is palindromic: it is identical to its Watson–Crick complement so that a pool of these molecules can form double stranded RNAs, a fact which plays a role in its self-replication process (Orgel, 1992). Another in- teresting fact about palindromic nucleic acid sequences is that they may form Watson–Crick pairs within themselves (i.e., hairpins) if they are sufficiently long. The sequence GCCGGC is too short to form a hair- pin (Fig. 3A); however, the insertion of two nucleotides, for instance GC, in the middle of this hexamer, is enough to result in a molecule which is predicted to make a hairpin (Fig. 3B). The resulting hairpin is made of two base pairs. Inserting two other nucleotides C and G result in a decamer which also forms a hairpin this time with three base pairs (Fig. 3C). These two hypothetical octomer and decamer are also 132 palindromic. Nevertheless, whether these longer RNA molecules are able to self-replicate in the same way than the GCCGGC sequence is unknown.

¹³⁴ The hairpin structure of single-stranded RNAs is important because it helps to stabilize these molecules ¹³⁵ by lowering their energy level. Furthermore, these structures are reminiscent of those observed in ribozymes

ture (T in kelvins) for three different values of the ratio of reaction on diffusion coefficients (ρ/κ). The values Figure 2: Variation of the equivalent energy of replication ($$$ in kilojoules per mole) with respect to temperawere calculated with $Z = 2$ and the values of the constants as given in the text.

 (Kruger et al., 1982). Indeed, in ribozymes the hairpins and loops making the secondary and tertiary struc-137 tures are crucial for their enzymatic activities (Lilley, 2011). Furthermore, Lincoln and Joyce (2009) showed that ribozymes can be self-replicating.

139 2.3. Information and the evolution of complexity

 The previous section considers the information–energy equivalence from the standpoint of replication. The present section starts from this relation between information and energy and considers some of the consequences in terms of information contents. A hypothetical living system with information stored on a single bit (like the one considered in the previous section) cannot code more than two states. However, if the information storage is made of several bits, it could be that more complex information can be coded. Take the simple case of a sequence with two bits; there are two ways to consider the information coded by this sequence. The first way is to assume that each bit codes separately for one information each, thus, with 147 a single bit with a energy-equivalent of $2k_BT \ln 2$. The second way to consider the information coded by two bits is that they may also interact so that the

 four possible states (00, 01, 10, 11) may also content new information. The energy of these two interacting bits can be calculated similarly as they code for a four-state information content by substituting ln 2 by ln 4:

Figure 3: (A) This sequence of six nucleotides can self-replicate (see Orgel, 1992) and is predicted to make a single loop. The insertion of (B) two or (C) four nucleotides results in a more complex secondary struture with a loop and a hairpin. The inserted nucleotides are highlighted on a light blue background. The secondary structures were predicted from the primary structures using <http://rtools.cbrc.jp/>.

 $k_{\rm B} T \ln 4 = 2k_{\rm B} T \ln 2.$

 It might seem logical that the two ways just described are exclusive. Two bits of information may be either additive or interactive, but cannot be both. However, in a general approach of modelling interactions and complexity in the context of information storage, we consider that this last possibility ("both") is not excluded. This approach makes possible to define an upper bound to the information contents of a sequence of bits. Therefore, the overall energy–information content of a sequence of two bits is given by:

 $\Delta E \geqslant 4k_{\rm B}T \ln 2$.

156 We now consider the more general case of a sequence made of n bits. Each bit has a binary information

157 content so that the total information content of this sequence is $nk_BT\ln 2$. Let us assume that some of 158 these bits interact to create new information. We introduce a new parameter, denoted as ξ , defined as the 159 proportion of bits that interact to procude new information content ($0 \leq \xi \leq 1$). These interactions could ¹⁶⁰ be of order two (i.e., involving two bits) or of higher orders. We will thus write this new parameter as a vector ξ _o where the subscript gives the order of the interactions ($o = 2, ..., N$). Let use define the potential ¹⁶² sequence information (denoted as Ψ) by:

$$
\Psi = nk_{\rm B}T \ln 2 + \sum_{o=2}^{N} \frac{\xi_o n}{o} k_{\rm B}T \ln 2^o
$$

$$
= nk_{\rm B}T \ln 2 \left(1 + \sum_{o=2}^{N} \xi_o \right).
$$

¹⁶³ Thus, the additional information content provided by interactions among the bits in a sequence can be ¹⁶⁴ increased by the proportion of interacting bits.

165 We consider now a specific model of two bits with a special type of interaction: regulation. We assume that the first bit codes for a phenotype (hereafter denoted as either ϕ_0 or ϕ_1), whereas the second bit codes ¹⁶⁷ for the regulation of the expression of this phenotype. Using the same notation as above, we write:

$$
x = \begin{cases} 0 \to \phi_0 \\ 1 \to \phi_1 \end{cases}
$$

 168 The second bit is denoted as r and regulates whether x is expressed or not:

$$
r = \begin{cases} 0 \to x \text{ is repressed} \\ 1 \to x \text{ is expressed} \end{cases}
$$

169 We have now a phenotype space for each possible sequence of these two bits:

$$
xr = \left\{ \begin{array}{l} 00 \rightarrow \emptyset \\ 10 \rightarrow \emptyset \\ 01 \rightarrow \phi_0 \\ 11 \rightarrow \phi_1 \end{array} \right.
$$

 However, to be effective the regulatory system needs to acquire information, for instance from the environ-171 ment. If the information acquired is binary, the associated energy cost is at least $k_B T \ln 2$. Consequently, the energy cost of the phenotypic expression requires to acquire three bits of information: one bit from the environment and the two bits from the sequence. The energy equivalent is:

$$
\Delta E \geqslant 3k_{\text{B}}T\ln 2.
$$

174 In the general case, if there are n_x bits for the phenotypes, and n_r bits for the regulatory systems:

$$
\Delta E \ge (n_x + n_r)k_\text{B}T \ln 2 + n_r k_\text{B}T \ln 2
$$

$$
\ge (n_x + 2n_r)k_\text{B}T \ln 2.
$$

 So the energetic costs of regulatory systems is predicted to be twice larger than for phenotype coding sequences.

¹⁷⁷ 3. Discussion

 Information theory is concerned with the mechanisms of information transmission and interpretation (e.g., coding and decoding; Cover and Thomas, 2006). Among the many applications of information theory in physical sciences, the Landauer's principle predicts that information acquisition and erasure in comput- ing machines entail a rise in entropy, therefore linking thermodynamics and information theory (Landauer, 1961). Experimental evidence has been recently found to support this conjecture (Toyabe et al., 2010; Bérut et al., 2012; Hong et al., 2016), although the interpretation of these experimental results has been disputed (Kish and Granqvist, 2012). As an extension of Landauer's principle, theoretical physicists recently at- tempted to quantify the mass of a bit of information (Herrera, 2014; Vopson, 2019), therefore effectively linking information theory with special relativity. Although the idea of entropy seems ubiquitous enough to be used in different contexts, it is important to differentiate clearly those applications. Recently, Vopson and Lepadatu (2022) clarified this point by stating the law of infodynamics where the total entropy of a system is defined as the sum of its physical entropy (in its traditional thermodynamic meaning as the sta- tistical distribution of microstates) and its information entropy (defined with Shannon's classic formula). Their law has been applied to analyse genetic mutations of the SARS-CoV2 viruses within a deterministic framework (Vopson, 2022). When considering biological systems, the distinction between both forms of entropy is indeed important. Thermodynamic entropy considers the spatial distribution of entities which can

 differ in any relevant characteristic (e.g., the velocity of gas molecules in Maxwell's hypothetical demon experiment) but this quantity has no implicit or explicit consequence in terms of information. On the other hand, Shannon's entropy considers the relative frequencies of these entities (i.e., their diversity) as potential information bearers. Both concepts are crucial for biological processes and cannot be used interchangeably. The present paper starts from Brillouin's equation of information to assess the energy requirements of two fundamental aspects of living systems: replication and phenotype expression. The goal of this work is to find the conditions or requirements that permitted the emergence of life even though the underlying physical and chemical processes follow the second law of thermodynamics.

 The problem of replication of living beings, and in particular the replication of genomic sequences, is the perfect illustration that the chemical reactions involved in this process do not respect the second law of thermodynamics, by defintion, since genomes are replicated identical to themselves resulting in a decrease in entropy of the system. The challenging question is: How this process was initiated during evolution? The model developed in this paper proposes a mechanism based on the energy requirements involved in the reactions of replication: the process of information recognition during replication lowers the internal energy of the system and can provide the necessary energy for replication and information duplication.

 Initially during evolution, there was no blueprint similar to the current genomic information, so repli- cation could not occur by producing identical invididuals. Instead, replication could have happened by 211 mechanical or physical replication. Such mechanisms do not involve any biological processes; however, they are known to favour the replication of some entities by simple preferential pairing of elements (e.g., Penrose and Penrose, 1957; Griffith et al., 2005). This mechanical process of self-replication can be re- lated to some results on the replication of small RNA sequences (Orgel, 1992; Sievers and von Kiedrowski, 1994).

 It is interesting to note that the synthesis of small RNA molecules can be achieved through coupled cyclical reactions (Sievers and von Kiedrowski, 1994; Robertson and Joyce, 2012). Liu and Sumpter (2018) reviewed coupled chemical reactions and suggested that they may have had an important role in the early developments of life. One prediction from the present paper is that short, self-replicating RNA sequences may have been synthesized by accumulating nucleotides and result in molecules with enzymatic activities $_{221}$ similar to those observed in current ribozymes (Kruger et al., 1982; Lincoln and Joyce, 2009; Lilley, 2011). ²²² It has been shown that even some very short RNA sequences, up to five nucleotides, can have an enzymatic activity (Turk et al., 2010). It remains to be shown that the short sequences that are able to self-replicate are also able to have enzymatic activities. That would bridge the gap between replication and (bio)chemical activity.

 In living beings, information stored in genomes can be interpreted as a device providing energy since, ₂₂₇ in the case of enzyme-coding sequences, the protein that are coded and eventually synthesized contribute to lower the activation energy of the reactions in the cell (Ji, 1974, 2000). Therefore, there is a conversion from information into energy. Before the evolution of genomes, this flow could not happened in this direction, and it seems we need to hypothesize that energy was converted into information in a way or another.

 Since the "RNA World" hypothesis has been formulated, several studies have provided a range of evi- dence for its support (Robertson and Joyce, 2012). Similarities between the sequences of different types of RNA found in the cells have been noted by some authors several decades ago. Even before the discovery of the ribozyme, Mizutani and Ponnamperuma (1980) noted "that the ancestral form of tRNA's could have been composed of 17 nucleotides of which 7 nucleotides formed a loop and of which two pentanucleotides at either end of the loop constituted complementary double helical structure." However, these authors did not favour the hypothesis of "RNA first" and thought that "it is reasonable to suppose that small peptides and small oligonucleotides as well as their precursors existed and interacted in the 'soup'." See also White (1980) who hypothesized the peptides and nucleotide oligomers interacted closely to generate the first living cells.

²⁴¹ The discovery of enzymatic activity in some RNA molecules changed the perspective that initial living beings had to rely on proteins. Lacey et al. (1992) reviewed some of the literature following this discovery and pointed out to the similarity between the sequences and structures of ribozymes and tRNAs: "Maybe 5'- CA-3' is one of the simpler (and most important) ribozymes and maybe AMP by itself is just not sufficient. We shall see." These authors also noted that similarities between the different types of RNA pointed to a common origin of these molecules: "More recent homology studies (Staves and Lacey, 1989) support the idea of a common ancestor for tRNAs and 5S rRNA." A recent review by Tamura (2015) seems to confirm that rRNA could have evolved from ancestral tRNA. Finally, Becker et al. (2019) showed that all purines, pyrimidines, and ribose (i.e., the building blocks of ribonucleotides and then of RNA) can be synthesized in realistic prebioric conditions driven by wet-dry cycles, further supporting that RNA-based living entities may have been the first to evolve on Earth.

 These findings could seem intriguing giving the fact that current rRNA and tRNA molecules interact closely with many proteins. For instance, the ribosome is made of several rRNA molecules and several proteins. However, it has been shown that a ribosome made of rRNAs only can be functional:

 The most obvious source of energy comes from peptide bond formation; peptidyl transfer re- sults in formation of a peptide amide bond from an activated ribose ester linkage, accompanied by a large change in free energy. How can this free energy change be coupled to transloca- tion? The answer most likely lies in the changing chemical nature of the acceptor end of the tRNA as it moves through the ribosome (Spirin 1985). [. . .] This finding shows that thermal energy alone is sufficient to drive the intersubunit rotation underlying translocation. $[\dots]$

These findings show that even the complex, large-scale molecular movements associated with

translocation can be driven by thermal energy, obviating the need for special energy-generating

steps in protein synthesis by the first ribosomes. (Noller, 2012)

 It appears therefore that evolution may have started well before DNA genomes appeared. In a more recent study, Goldman et al. (2010) found that even RNA genomes may have interacted and coevolved with proteins that are still in use in cells today. In particular, they found that "translation proteins underwent major evolutionary expansion well before the first species diverged from LUCA (last universal common ancestor) and even before the DNA genome was established."

 The present work agrees with the RNA World hypothesis since it predicts that an entity can be replicated ₂₇₀ where the required energy is provided by the lower energy level of the system during information reading. 271 Self-replicating RNA molecules seem a good empirical model of such entities.

 Another line of evidence is found from coupled chemical reactions. In living cells, coupled reactions occur frequently so that a thermodynamically favoured reaction (e.g., hydrolysis of ATP into ADP) releases energy for a second reaction which is thermodynamically less favoured (e.g., binding of an amino acid to a peptide). Liu and Sumpter (2018) reviewed models of coupled chemical reactions and found that some systems are catalytic while others are self-replicating. More importantly, they found that "it is possible to construct a self-replicating system in which the entropy of some parts spontaneously decreases." Recent works have proposed several experimental systems of self-replicating chemical systems that could be mod- els of prebiotic evolution (Komáromy et al., 2017; Colomer et al., 2018; Morrow et al., 2019; Liu et al., 2020). It is still not yet clear whether one of these systems could be the precussor of biological evolution on Earth, or whether several of these systems could have coexisted on Earth before one of them (based on RNA self-replicating molecules) evolved.

 Darwinian evolution is dependent on the existence of information storage in living beings (Dawkins, 1996). Therefore, natural selection certainly did not play a role in the early stages of life evolution when information was not firmly established. However, once self-replicating entities with information storage have evolved, selection among them could have acted and favoured the replication of some of them. I draw here a similarity between the mechanisms of regulation and Maxwell's demon (Earman and Norton, 1998; Weinstein, 2003). As a reminder, a demon is, according to Maxwell, an entity which is able to decrease the entropy of a system without inputing energy in it by opening a gate to let the "fast" (i.e., high energy) gaz particules move in one direction and the "slow" (low energy) ones move in the other direction. However, $_{291}$ Szilard (1964) showed that the demon must acquire information about their energy levels, and given the equivalence stated in the Introduction, this requires to spend some energy. Furthermore, in Maxwell's riddle, the demon is given. We could see an analogy with living systems where regulatory mechanisms act effectively as demons by decreasing the entropy. However, Maxwell's original riddle does not say anything how the demon acquired the information that tells it to do its work. Indeed, the demon must have been "programmed" in one way or another. Similarly, in living systems the emergence of regulation during the ₂₉₇ early stages of biological evolution faces the same problem. How come these mechanisms have come to do what they do—regulate biological processes?

 An argument of the present paper is that considering the equivalence between energy and information makes possible to explain the origin of complexity from the same principle that explains the emergence 301 of self-replicating systems with information storage. Zuckerkandl (2006) emphasized the importance of higher-order interactions in biological processes, stating that information stored in DNA sequences is, in itself, not sufficient:

 The requirement for an interaction between sequence properties and higher-order structural properties of informational macromolecules however may well remain absolute for all forms of life in the universe. (p. 6)

 Zuckerkandl also noted that a "linear heteropolymer acting alternatively through its sequence and through its conformation-dependent enzymatic properties" can fulfill the dual role of information storage and biological activity.

 The energy requirements for biochemical reactions during the first stages of evolution have been an 311 unanswered question for several decades. Because of this difficulty, several authors formulated the hypoth-312 esis of panspermia which postulates that life may have been originated outside the Earth and brought on our planet through meteorites or other extraterretrial vehicles (Arrhenius, 1908; Crick and Orgel, 1973). How- ever, Orgel (1973) proposed that energy was brought to early biochemical reactions through an alternance of dry and wet environments:

 If dry thermal reactions were important for the origins of life, it is hard to understand how they were replaced by solution reactions later in the course of biochemical evolution.

 I believe that the two types of reaction occurred in close association on the primitive earth. Random polymers and reactive intermediates were formed in efficient thermal reactions. When the mixtures of products formed in this way were wetted, for example by rain or dew, they reacted further in solution. If this picture is correct, modern biological condensations evolved from these latter solution reactions. (p. 138)

 Some minerals are known to catalyze RNA polymerization (for instance, montmorillonites; Aldersley et al., 2011) and could have played a role in the early self-replication of short RNA molecules (Becker et al., 325 2019). These catalytic minerals may have been important for the early synthesis of RNA polymers before they could be used as information storage devices. Once these polymers were self-replicating, so that energy could be stored as information, the early stages of evolution could be initiated. These speculations can be related to a prediction from the above model which is that the higher the ratio of the reaction coefficient to the diffusion coefficient (ρ/κ), the lower the energy requirement for replication. Earlier researchers have noted the importance of "keeping together" the molecules involved in the first stages of prebiotic evolution:

- It is important to note that autocatalytic growth and natural selection cannot occur in this model
- unless both peptide and nucleotide oligomers remain in the vicinity of each other much of the
- time, either due to the impermeability of a membrane, to adsorption on a clay surface, or to
- some similar localization process. (White, 1980, p. 126)

 By contrast to White's model which postulates that proteins and nucleic acids were both required during brebiotic evolution, the hypothesis of RNA molecules associated with, for instance, clay minerals provides a simpler mechanism because it does not require the early presence of proteins.

 The model developed in this paper leads to the prediction that the energy requirement for replication of a bit varies between 65 and 90 kJ.mol⁻¹ for temperatures varying between 270 and 330 K (0–60 °C). Such values are close to the decrease in energy resulting from the formation of H-bonds in DNA sequences ³⁴¹ which has been estimated to be 52 and 106 kJ.mol⁻¹ for AT and GC pairs, respectively (Mo, 2006) which support the argument developed above. Additionally, it is predicted that binary sequences, i.e. with the 343 parameter $Z = 2$, have a lower energy requirement than with $Z > 2$. This suggests the possibility that initial self-replicating RNA sequences might have evolved from GC pairs only, and that AU pairs may have been incorporated later during evolution. The small hypothetical RNA molecules considered above with 346 eight or ten nucleotides are indeed made only of G and C and are predicted to form a loop and a hairpin. ³⁴⁷ It will be interesting to assess whether some RNA molecules made only of these two bases have catalytic activity.

³⁴⁹ By providing a theoretical framework, the above model can be applied to the origin of life in other environments than on Earth. The above equations were derived without assumption on the exact nature of ³⁵¹ the molecules involved. Thus, any system that agrees with the above predictions might lead to the evolution of life. It will be particularly interesting to assess whether this model can have applications for the study of extraterrestrial life.

354 Declaration of competing interest

 The author declares that he has no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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