



How becomes life on the Earth

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Abstract

In this paper how becomes life on the Earth was studied. The molecule that conveys biological information from one generation to the next takes the three dimensional form of a double helix. Activities and interactivities very complex gene and their product proteins are studied. Oligonucleotides transfer in space and time as well as for some properties was developed. The hybridization was determined by probabilities of reactions between oligonucleotides. Complex biopolymerization reactions of probability distribution functions specifying concentration and temperature were expressed. This article helps to understand how life becomes on the Earth.

Keywords: bioinformation, gene, biopolymers, life, distribution, conditional probability.

1. Introduction

The discovery that genetic information is coded along the length of a polymeric molecule composed of only four types of monomeric units is one of the major scientific achievements of the twentieth century [1]-[3]. The structure and function of the purines and pyrimidines and their nucleosides and nucleotides were studied in literature [4]-[6]. The heterocyclic bases purine and pyrimidine are the parent molecules of nucleosides and nucleotides. Nucleotides are ubiquitous in living cells, where they perform numerous key functions. Examples include incorporation, as their ribose (RNA) or deoxyribose (DNA) monophosphates, into nucleic acids, energy transduction (ATP), parts of coenzymes (AMP) acceptors for oxidative phosphorylation (ADP) all osteric regulators of enzyme activity, and second messengers (cAMP), (cGMP). The probability of mismatched hybridization is identified with the probability of error in the transmission of information. The connection is made between the free energy and species concentrations and the information transmission through DNA hybridization [7]-[8]. The probabilities of different chemical species are related to their relative occurrence in the reaction bath and quantified as their mole fractions.

An initial population is chosen, randomly. The amount of information that can be transmitted without error is bounded by the capacity of the hybridization channel [9]. The capacity of the hybridization channel is determined by the probabilities of reactions between oligonucleotides, which are related to the change in Gibbs free energy for the reaction.

Mathematical model of free radical frontal polymerization phenomenon consists of the kinetic equations, which representing mass balances for the reacting species was derived [10]. Complex model of polymerization and complex population model were built [11]-[15].

How this approach helps to understand begin human life on the Earth shows in this paper. Light has made appropriate conditions and information has been transferred with frequency change of electromagnetic waves.

2. Quant formation

Energy of quant can form on the probabilistic manner. The quant energy term can be derived according to following equation:

$$\Delta p \Delta q = \varepsilon \Delta t \quad (1)$$

where p - probability of position, q - probability of time, ε - quant energy, J and t - time, s .

To set the start frequency is very important. The maximum stop frequency can measure by the measurement hardware.

Then vibration change can be defined as:

$$\Delta f = \frac{\varepsilon}{h} \quad (2)$$

where f - frequency, $1/s$ and $h = 6.62 \cdot 10^{-34} Js$ universal Plank's constant.

Like other waves, electromagnetic waves have properties of speed, wavelength, and frequency.

Information value was transfer varying frequencies and disturbance regulation [16] - [18].

Interaction the electromagnetic waves various frequencies produce information - word. Quality of information, letters, length of word, pause and the others attributes (insertion, deletion) determine frequency variability and interactions between different frequencies.

3. Gene transition

Need to study space and time activities and interactivities very complex gene formation and their products proteins.

The system pool or component interconnections are defined by the process connections of the functional working model. The equations for gene transfer and mass and energy distribution have given by equations (4) and (5).

Space and time expressions which including attributes at the oligonucleotides transfer are:

$$\int_V \left\{ \frac{\partial \psi_c}{\partial t} + v_x \frac{\partial \psi_c}{\partial x} + v_y \frac{\partial \psi_c}{\partial y} + v_z \frac{\partial \psi_c}{\partial z} + \sum_{i=1}^n \frac{\partial (v_i \psi_c)}{\partial \xi_i} - D_f \left(\frac{\partial^2 \psi_c}{\partial x^2} + \frac{\partial^2 \psi_c}{\partial y^2} + \frac{\partial^2 \psi_c}{\partial z^2} \right) + (r) - D \right\} dV = 0 \quad (4)$$

Energy changes are:

$$\int_V \left\{ \rho C_p \left(\frac{\partial \psi_T}{\partial t} + v_x \frac{\partial \psi_T}{\partial x} + v_y \frac{\partial \psi_T}{\partial y} + v_z \frac{\partial \psi_T}{\partial z} + \sum_{i=1}^n \frac{\partial (v_i \psi_T)}{\partial \xi_i} \right) - \lambda \left(\frac{\partial^2 \psi_T}{\partial x^2} + \frac{\partial^2 \psi_T}{\partial y^2} + \frac{\partial^2 \psi_T}{\partial z^2} \right) + S_r \right\} dV = 0 \quad (5)$$

where t - време, s, x , y and z , - space coordinates, m, V - space volume, ξ - attribute, ψ_c - concentration probability distribution, mol/m^3 , v - geometrical velocity, m/s , D_f - diffusion coefficient, $m^2 s^{-1}$, r - hybridization reaction, D - denaturation, ρ - density, kg/m^3 , C_p - heat capacity, $J/Kmol$, ψ_T - temperature probability distribution, K, λ - conductivity coefficients, J/mK and S_r - heat generation, J.

These equations help to better understand mechanisms of gene transition and have published by Savkovic Stevanovic the first time in the literature from 1999 to 2002 [1]-[4], [8].

Frequency of the sun light changes in z direction can be described as:

$$\frac{\partial f}{\partial t} + v_x \frac{\partial f}{\partial x} + v_y \frac{\partial f}{\partial y} + v_z \frac{\partial f}{\partial z} = D_f \left(\frac{\partial^2 f}{\partial x^2} + \frac{\partial^2 f}{\partial y^2} + \frac{\partial^2 f}{\partial z^2} \right) + \frac{f}{z} g \quad (6)$$

where f - frequency, $1/s$, g - gravity, m/s^2 .

3.1 How information are coded

The complex structural organization of an organism is specified by an inherited script conveying an enormous amount of coded information. A particular sequence of nucleotides says the same thing to one organism as it does to another, differences between organism reflect genetic programs of different nucleotides sequences [20]-[22]. The chemical reaction in which two single strands of DNA, oligonucleotides, are hydrogen bonded is called hybridization reaction. The hybridization reaction is modelled by random noisy channel [21].

The hybridization tube was determined by probabilities of reactions between oligonucleotides. The presence of massive numbers $\sim 10^{12}$ of molecules representing each particular edge and vertex of the graph allowed for all possible molecular combinations to form simultaneously within their reaction bath. DNA information processing which involving equilibrium constants was examined in the work [22].

In this paper free energy of the oligonucleotides recombination and random noisy as conditional probabilities were investigated and developed.

4. DNA hybridization

Along the length of the molecules, information is encoded in the specific sequences of nucleotides, the chemical building block of DNA – deoxyribonucleic acid. Specific sequential arrangements of nucleotides, these four chemical letters (A-adenine, T-thymine, C-cytosine, G-guanine), encode the precise information in a gene. If the entire library of genes stored within the microscopic nucleus of a single human cell were written in letters the size of those you are now reading, the information would fill more than a hundred books as large as this one. Thus, the complex structural organization of an organism is specified by an inherited script conveying an enormous amount of coded information.

A particular sequence of nucleotides says the same thing to one organism as it does to another, differences between organisms reflect genetic programs of different nucleotide sequences.

The probability of mismatched hybridization is identified with the probability of error in the transmission of information. When this is incorporated into the information theoretic analysis, the connection is made between the free energy and species concentrations and the information transmission through DNA hybridization. The probabilities of different chemical species are related to the relative occurrence in the reaction bath and quantified as their mole fractions. An initial population is chosen, randomly.

The capacity of the hybridization channel is determined by the probabilities of reactions between oligonucleotides, which are related to the change in Gibbs free energy for the reaction. Manipulation of the reaction conditions temperature, reactant concentrations and base sequence may be a good method to control DNA [19]- [21].

The basic processing of DNA based computation as suggested by Adleman [9], is in the massive number of string comparisons that occur during the template matching reactions between DNA oligonucleotides. A small instance of the so called Hamiltonian path problem – HPP was encoded in molecules of DNA and solved in a test tube using standard methods of molecular biology which include hybridization, ligation, melting and annealing, restriction enzymes, polymerization chain reaction - PCR, nucleases, and repair enzymes. Thus a fundamental step in a DNA proposal for DNA computation Boolean logic based on DNA continue to rely on the mechanism of the template matching hybridization reaction. Most assume that the hybridization between oligonucleotides occur error free.

The presence of massive numbers 10^{12} of molecules representing each particular edge and vertex of the graph allowed for all possible molecular combinations to form simultaneously within their reaction bath. A typical test tube has huge numbers of molecules 6.022×10^{23} per mole.

The oligonucleotides are considered as symbols that are communicated through a noisy channel representing the hybridization. Therefore, the transmission of sequence information occurs either without an error i.e. perfect complement base pair matching, or with an error.

The chemical reaction in which two single strands of DNA, oligonucleotides (oligos) are hydrogen bonded together is a hybridization reaction (Fig.1).

The binary reaction of hybridization is:



The hybridization reaction is modeled as a noisy channel as shown in Fig.1.

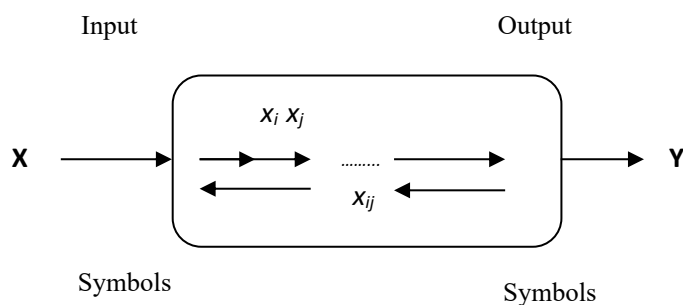


Fig. 1: Hydrogen bonding

Fig. 1 shows word formation of length n from input X and output Y through the hybridization.

There are three nano chemical species. X corresponds to the initial reactant space with mole fractions for oligos of x_i , Y is the space after the hybridization reactions, the final oligo reactant and hybridization product space, with mole fractions of the products $\langle x_i x_j \rangle$. There is the joint space where x_{ij} indicates oligo i in hybridization with oligo j .

This approach helps to understand begin human life on the Earth. Light has made appropriate conditions and information has been transferred with frequency change of electromagnetic waves as stated Savkovic Stevanovic, first time in literature 2024 and 2025 [16]-[18].

The stoichiometric equation for two arbitrary oligonucleotides, x_i and x_j given by eq. (7) where $\langle x_i x_j \rangle$ represents the hybridized oligonucleotides (Fig.2). There are many reactions like this in bath channel.

The direction of the reaction is determined by the sign of the change in the free energy,

$$\Delta G = \Delta G^0 + RT \log Q \tag{8}$$

where ΔG^0 is the free energy change under ideally dilute standard conditions of concentration and pressure, R is the universal gas constant, T is the temperature and Q is defined as:

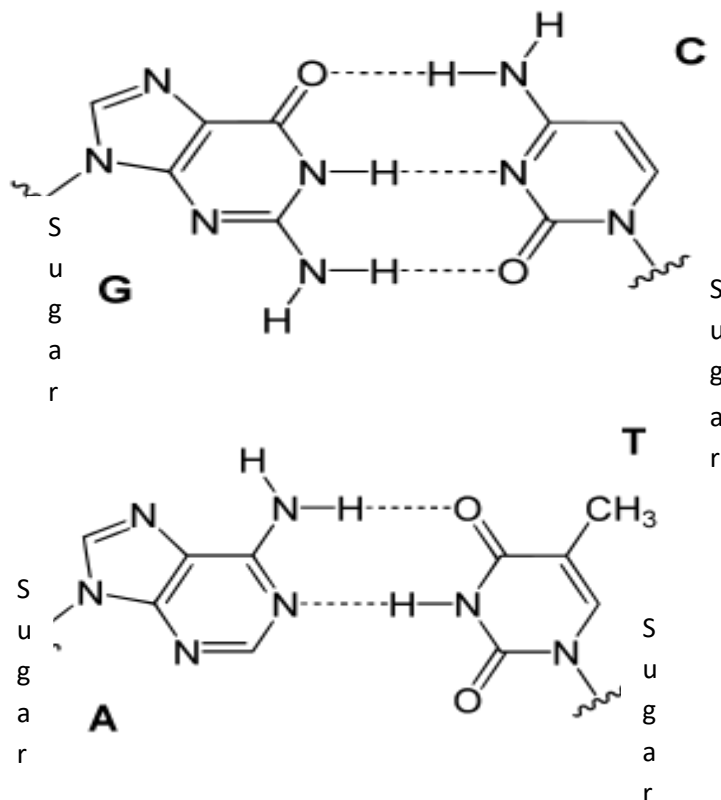


Fig.2: The nucleotides building block

$$Q = \frac{|x_i x_j|}{|x_i||x_j|} \quad (9)$$

where x indicates mole fractions, and therefore, Q is dimensionless.

The reaction will be driven towards chemical equilibrium, where the rates to the left and right side of the reaction are equal, $\Delta G=0$, translates to

$$\Delta G^0 = RT \log K_{eq} \quad (10)$$

where K_{eq} is the chemical equilibrium constant, which is given by

$$K_{eq} = \left| x_i x_j \right|_{eq} / \left| x_i \right|_{eq} \left| x_j \right|_{eq} \quad (11)$$

The Gibbs free energy is a function of temperature, pressure, and the amount, measured in moles of each component in the system. It is assumed that temperature and pressure are constant and the amounts of the components are allowed to change infinitesimally, then the infinitesimal change in G is:

$$dG = \sum_{i=1}^N (\partial G / \partial n_i)_{T,P,n_{j \neq i}} dn_i \quad (12)$$

where n_i is the mole number of the N components in the system.

The chemical potential for component i is defined as

$$\mu_i = (\partial G / \partial n_i)_{T,P,n_{j \neq i}} \quad (13)$$

The condition for chemical equilibrium is

$$\sum \mu_i dn_i = 0 \quad (14)$$

For chemical reaction general,

$$0 = \sum v_i A_i \quad (15)$$

where the v_i are the stoichiometric coefficients which are negative for reactants and positive for products. The change in the amount of species A_i in the reaction is proportional to the $v_i dn_i = v_i d\xi$, where the constant of proportionality is called the extent of the reaction ξ .

Substitution for dn_i into eq. (14) produces condition of chemical equilibrium,

$$\sum_1 v_i \mu_i = 0 \quad (16)$$

The change in G with the extent of the reaction is

$$\frac{dG}{d\xi} = \sum_1 v_i \mu_i \quad (17)$$

which is zero at equilibrium. The free energy change can be written as

$$\frac{dG}{d\xi} = \Delta G^0 + RT \log Q \tag{18}$$

where ΔG^0 is the free energy change under ideally dilute standard conditions, and $RT \log Q$ is a correction term for non-standard conditions.

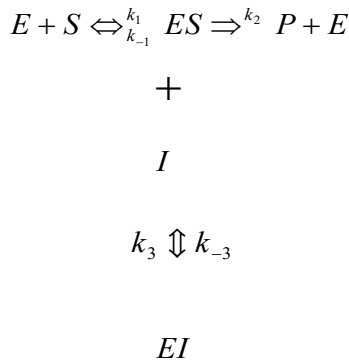
5. Biotransformation by enzymes

The structure and function of the purines and pyrimidines and their nucleosides and nucleotides were studied in numerous literature. Synthetic analogs of naturally occurring nucleotides find application in cancer chemotherapy as enzyme inhibitors and can replace the naturally occurring nucleotides in nucleic acids [22]. Therapeutic attempts to inhibit the growth of cancer cells or certain viruses have often employed administration of analogs of bases, nucleosides, or nucleotides that inhibit the synthesis of either DNA or RNA. Allopurinol, a purine analog, is widely used in the treatment of gout.

Biomedical important it neither nucleotides nor their parent purine and pyrimidine bases in the diet are incorporated into human tissue nucleic acids or into purine or pyrimidine coenzymes [8]. Even when a diet rich in nucleoproteins is ingested, human subjects form the constituents of tissue nucleic acids from amphibolic intermediates. This de novo synthesis permits purine and pyrimidine analogs with potential as anticancer drugs to be incorporated into DNA. The rates of synthesis of purine and pyrimidine oxy- and deoxyribonucleotides are subject to precise regulation. Mechanisms have evolved to ensure production of these compounds in quantities and at times appropriate to meet varying physiologic demand.

In addition to de novo synthesis, these include “salvage” pathways for reutilization of purine or pyrimidine bases released by degradation of nucleic acids in vivo. Human diseases that involve abnormalities in purine or pyrimidine metabolism include gout, Lesch-Nyhan syndrome, Reye’s syndrome, adenosine deaminase deficiency, and purine nucleoside phosphorylase deficiency.

Enzymes have significant role in oligonucleotides biotransformation.



where E - enzyme, S - substrate, ES - complex with substrate, I -inhibitor, EI - complex with inhibitor and k - biochemical constant.

6. Biopolymerization rate

A distribution function of biopolymers can be expressed [12],[13],[15]:

$$\psi_c(x, y, z, \xi_1, \dots, \xi_n) \tag{19}$$

where x, y, z represent ordinary spatial coordinates, t is time and ξ_i represents the i^{th} property.

For an arbitrary region in this $3 + n$ space, it can be defined geometric velocities: $v_x = dx / dt$, $v_y = dy / dt$, $v_z = dz / dt$ and time rate of change properties $v_i = d\xi_i / dt$ as follow:

$$\int_V \left\{ \frac{\partial \psi_c}{\partial t} + \frac{\partial (v_x \psi_c)}{\partial x} + \frac{\partial (v_y \psi_c)}{\partial y} + \frac{\partial (v_z \psi_c)}{\partial z} + \sum_{i=1}^n \frac{\partial (v_i \psi_c)}{\partial \xi_i} - D_f \left(\frac{\partial^2 \psi_c}{\partial x^2} + \frac{\partial^2 \psi_c}{\partial y^2} + \frac{\partial^2 \psi_c}{\partial z^2} \right) + (r) \right\} dV = 0 \tag{20}$$

where $dV = dx dy dz d\xi_1 \dots d\xi_n$; (r) is reaction rate, ψ_c is concentration distribution function of reacting species, mol/m^3 and D_f is effective diffusion coefficient of reacting spaces, m^2s^{-1} . The method of evolving the general microscopic balance will correspond to the integral formulation.

This model takes a distribution function of substructure for design of repetitive complex structure. For polymers population, sequences length ξ_l should be considered as a property, and is deriving final macroscopic model:

$$\frac{1}{V} \left[\frac{\partial \psi_c}{\partial t} + \sum_i \frac{\partial (v_i \psi_c)}{\partial \xi_i} + (r) \right] = \frac{1}{V} (\psi_{c(in)} - \psi_{c(out)}) \quad (21)$$

where $\psi_{c(in)}$ and $\psi_{c(out)}$ is geometrically averaged distribution function, and $v_i = d\xi_l / dt$. The geometric average distribution function is defined as:

$$\psi_c = 1/V \int_V \psi_c dV \quad (22)$$

The temperature distribution function can be described as follows:

$$\int_V \left\{ \rho C_p \left[\frac{\partial \psi_T}{\partial t} + \frac{\partial (v_x \psi_T)}{\partial x} + \frac{\partial (v_y \psi_T)}{\partial y} + \frac{\partial (v_z \psi_T)}{\partial z} + \sum_{i=1}^n \frac{\partial (v_i \psi_T)}{\partial \xi_i} \right] - \lambda \left(\frac{\partial^2 \psi_T}{\partial x^2} + \frac{\partial^2 \psi_T}{\partial y^2} + \frac{\partial^2 \psi_T}{\partial z^2} \right) + (Sr) \right\} dV = 0 \quad (23)$$

where Sr is heat of reaction, J , λ is thermal conductivity, J/mK and ψ_T a temperature distribution function, K .

Final macroscopic model is derived as:

$$\frac{1}{T} \left[\frac{\partial \psi_T}{\partial t} + \sum_{i=1}^n \frac{\partial (v_i \psi_T)}{\partial \xi_i} + S_r \right] = \frac{1}{V} (\psi_{T(in)} - \psi_{T(out)}) \quad (24)$$

where ψ_T is geometrically averaged temperature distribution

$$\psi_T = \frac{1}{V} \int_V \psi_T dV \quad (25)$$

Amazing artwork shows a process that takes place in the cells of all living things: the production of proteins. This process is called protein synthesis, and it actually consists of two processes - transcription and translation. In eukaryotic cells, transcription takes place in the nucleus. During transcription, DNA is used as a template to make a molecule of messenger RNA (mRNA). The molecule of mRNA then leaves the nucleus and goes to a ribosome in the cytoplasm, where translation occurs. During translation, the genetic code in mRNA is read and used to make a polypeptide. These two processes are summed up by the central dogma of molecular biology: DNA \rightarrow RNA \rightarrow Protein.

7. Discussion

1. In space and time interval quant forms as energy.
2. Oligonucleotide transfer by convention and diffusion have been discussed.
3. Model of hybridization channel was derived.
4. How information is coded was defined.
5. DNA polymerization chains was expressed.
6. Probability distribution function of biopolymers was derived.
7. The macroscopic model of repetitive complex structure was developed.

8. Conclusion

This paper helps to understand how becomes life on the Earth. Light has made appropriate conditions and information has been transferred with frequency change of electromagnetic waves. Genes are transferred randomly by convention, diffusion and chemical reaction.

In this paper the equations for gene transfer were developed.

Hybridization oligonucleotides in building blocks have been expressed. Free energy indicator was analyzed.

Enzymes inhibitors are very important in DNA recombination.

Distribution function for biopolymers concentration and temperature were expressed. The macroscopic models were derived.

Abbreviation

DNA - deoxyribonucleic acid
 RNA - ribonucleic acid
 AMP - adenine monophosphate
 ADP - adenine diphosphate
 ATP - adenine triphosphate
 CTP - cytosine triphosphate
 GMP - guanine monophosphate

Notation

c - concentration, mol/m^3
 C_p - heat capacity, $J/molK$
 C_0 - total strand concentration, mol/m^3
 D_f - effective diffusion coefficient, m^2s^{-1}
 g - gravity, ms^{-2}
 ΔG - free energy change, KJ / mol
 H - enthalpy, KJ / mol
 E - enzyme
 f - frequency, $1/s$
 I - inhibitor
 k, k_{-1} - specific chemical constant, s^{-1}
 P - pressure 101325 Pa
 R - gas constant, of 8.314 J/(mol·K) in SI units
 S - substrate
 ΔS - entropy, $KJ / molK$
 T - temperature, K
 x - mole fraction, mol / mol

Greek Symbols

Δ - change
 ε - error
 λ - thermal conductivity, J/mK
 ξ - attribute
 μ - chemical potential

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