OPEN ACCESS
Global Journal of Research in Medical Sciences
ISSN: 2583-3960 (Online)
Volume 04 | Issue 04 | July-Aug. | 2024
Journal homepage: https://gjrpublication.com/gjrms/
Research Article

# Biopolymerization chain reactions in protein synthesis

*Jelenka Savković Stevanović

Faulty of Technology and Metallury, Belgrade University, Karnegijeva 4, 11000 Belgrade

**DOI:** 10.5281/zenodo.13617714 **Submission Date:** 11 July 2024 | **Published Date:** 30 Aug. 2024

***Corresponding author:** Jelenka Savković Stevanović
Faulty of Technology and Metallury, Belgrade University, Karnegijeva 4, 11000 Belgrade

## Abstract
In this paper biopolymerization reaction of DNA molecules was studied. Chemical and mathematical models were considered. A complex mathematical model of biopolymerization generating microscopic and macroscopic balances of probability distribution function was derived. The three stages initiation, elongation and termination reactions were examined. The distribution function of the oligomers specifies concentration, and temperatures in the spatial coordinates and time and length of the oligonucleotide's chains. The algorithm for oligomers concentration distribution and temperature distribution functions simulation was derived.

**Keywords:** Biopolymers, oligomers, distribution, concentration, temperature.

## 1. Introduction
The molecule that conveys biological information from one generation to the next takes the three dimensional form of a double helix [1]-[3]. 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 last century. 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) monophosfates, 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].

In this paper mathematical model for biopolymerization chain reactions which including microscopic and macroscopic description of the problem were derived. This model includes the general mass and heat balances of $\beta-$ distribution functions including reaction and heat rate.

## 2. Oligomers
Bases that occur in the nucleotides are derived by substitution on the ring structures of the parent substances, purine and pyrimidine. The three major pyrimidine bases present in the nucleotides of both procaryotes and eukaryotes are cytosine,


*Corresponding author: Jelenka Savković Stevanović

thymine, and uracil. The purine bases adenine and guanine are the two major purines found in living organisms. Two other purine bases, hypoxanthine and xanthine, occur as intermediates in the metabolism of adenine and guanine. In humans, a completely oxidizes purine base, uric acid, is formed as the end product catabolism.

In natural materials, unusual bases occur in the addition to the 5 major described bases. Some of these unusual substituted bases are present only in the nucleic acids of bacteria and viruses, but many are also found in the DNA and transfer RNAs of both prokaryotes and eukaryotes. For example, both bacterial and human DNA contain significant quantities of 5-methylcytosine, bacteriophages contain 5- hydroxyl-methyl-cytosine. Unusual bases presenting the messenger RNA molecules of mammalian cells include $N^6$, $N^6$-dimethyladenine, and $N^7$-methylguanine. An uracil modified at the $N_3$ position by the attachment of an (α-amino, α-carboxyl)-propyl group has also been detected in bacteria.

In plants, a series of purine bases containing methyl substituents occurs. Many have pharmacologic properties. Examples are coffee, which contains caffeine (1,3,7 –trimethylxanthine), tea, which contains theophylline (1,3-dimethylxanthine).

Because of keto-enol tautomerism, theses aromatic molecules can exist in a lactim or lactam form, the latter is by far the predominant tautomer of guanine or thymine under physiologic conditions.

At neutral pH, guanine is the least soluble of the bases, followed in this respect by xanthine. Although uric acid as urate is relatively soluble at a neutral pH, it is highly insoluble in solutions with a lower pH, such as urine. Guanine is not a normal constituent of human urine, but xanthine and uric acid do occur in human urine. These latter 2 purines frequently occur as constituents of urinary tract stones.

## 3.The protein synthesis

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 → RNA→Protein.

### 3.1 Biopolymerization kinetics

*Transcription* is the first part of the central dogma of molecular biology: DNA→RNA. It is the transfer of genetic instructions in DNA to mRNA. During transcription, a strand of mRNA is made to complement a strand of DNA.

Transcription uses the sequence of bases in a strand of DNA to make a complementary strand of mRNA. Triplets are groups of three successive nucleotide bases in DNA. Codons are complementary groups of bases in mRNA.

Transcription begins when the enzyme RNA polymerase binds to a region of a gene called the promoter sequence. This signals the DNA to unwind so the enzyme can “read” the bases of DNA. The two strands of DNA are named based on whether they will be used as a template for RNA or not. The strand that is used as a template is called the template strand, or can also be called the antisense strand. The sequence of bases on the opposite strand of DNA is called the non-coding or sense strand, Once the DNA has opened, and RNA polymerase has attached, the RNA polymerase moves along the DNA, adding RNA, nucleotides to the growing mRNA strand. The template strand of DNA is used as to create mRNA through complementary base pairing. Once, the mRNA strand is complete, and it detaches from DNA. The result is, a strand of mRNA that is nearly identical to the coding strand DNA – the only difference being that DNA uses the base thymine, and the mRNA uses uracil in the place of thymine.

In eukaryotes, the new mRNA is not yet ready for translation. At this stage, it is called pre-mRNA, and it must go through more processing before it leaves the nucleus as mature mRNA. The processing may include splicing, editing, and polyadenylation. These processes modify the mRNA in various ways. Such modifications allow a single gene to be used to make more than one protein.

Splicing removes introns from mRNA. Introns are regions that do not code for the protein. The remaining mRNA consists only of regions called exons that do code for the protein. The ribonucleoproteins in the diagram are small proteins in the nucleus that contain RNA and are needed for the splicing process.

Editing changes some of the nucleotides in mRNA. For example, a human protein called APOB, which helps transport lipids in the blood, has two different forms because of editing. One form is smaller than the other because editing adds an earlier stop signal in mRNA.

5′ Capping adds a methylated cap to the "head" of the mRNA. This cap protects the mRNA from breaking down, and helps the ribosomes know where to bind to the mRNA.

Polyadenylation adds a "tail" to the mRNA. The tail consists of a string of as (adenine bases). It signals the end of mRNA. It is also involved in exporting mRNA from the nucleus, and it protects mRNA from enzymes that might break it down.

Pre-mRNA processing is it when mRNA requires processing before it leaves the nucleus.

*Translation* is the second part of the central dogma of molecular biology: RNA→Protein. It is the process in which the genetic code in mRNA is read to make a protein. After mRNA leaves the nucleus, it moves to a ribosome, which consists of mRNA and proteins. The ribosome reads the sequence of codons in mRNA, and molecules of tRNA bring amino acids to the ribosome in the correct sequence.

Translation occurs in three stages: initiation, elongation and termination.

**Initiation:** After transcription in the nucleus, the mRNA exits through a nuclear pore and enters the cytoplasm. At the region on the mRNA containing the methylated cap and the start codon, the small and large subunits of the ribosome bind to the mRNA. These are then joined by a tRNA which contains the anticodons matching the start codon on the mRNA. This group of molecules (mRNA, ribosome, tRNA) is called an initiation complex.

**Elongation:** tRNA keep bringing amino acids to the growing polypeptide according to complementary base pairing between the codons on the mRNA and the anticodons on the tRNA. As a tRNA moves into the ribosome, its amino acid is transferred to the growing polypeptide. Once this transfer is complete, the tRNA leaves the ribosome, the ribosome moves one codon length down the mRNA, and a new tRNA enters with its corresponding amino acid. This process repeats and the polypeptide grows.

**Termination:** At the end of the mRNA coding is a stop codon which will end the elongation stage. The stop codon doesn't call for a tRNA, but instead for a type of protein called a release factor, which will cause the entire complex (mRNA, ribosome, tRNA, and polypeptide) to break apart, releasing all of the components.

## 4. Biopolymerization rate

A distribution function of biopolymers can be expressed:

$$\psi_c(x, y, z, \xi_i, ....., \xi_n) \qquad (1)$$

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

For an arbitrary region in this $3+n$ space $R$, 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:

$$\int_R \frac{\partial \psi_c}{\partial t} + \frac{\partial (v_x \psi_c)}{\partial x} + \frac{\partial (v_y \psi_c)}{\partial y} + \frac{\partial (v_z \psi_c)}{\partial z} +$$

$$\sum_{j=1}^{n} \frac{\partial (v_i \psi_c)}{\partial \xi_i} - D\left(\frac{\partial^2 \psi_c}{\partial x^2} + \frac{\partial^2 \psi_c}{\partial y^2} + \frac{\partial^2 \psi_c}{\partial z^2}\right) + \qquad (2)$$

$$(r) dR = 0$$

where $dR = dxdydzd\xi_i, ...., d\xi_n$; $(r)$ *is* reaction rate, $\psi_c$ is concentration distribution function of reacting species, and $D$ is effective diffusion coefficient of reacting spaces. 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 $\xi_l$ should be considered as a property, is deriving final macroscopic model:

$$\frac{1}{V}\frac{\partial(\psi_c)}{\partial t}+\sum_1\frac{\partial(v_i\psi_c)}{\partial\xi_i}+(r)=\frac{1}{V}(\psi_{c(in)}-\psi_{c(out)}) \quad (3)$$

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:

$$\psi_c=1/V\int_V\psi_c dV \quad (4)$$

## 5. Chemical and mathematical model of biopolymerization reactions

Standard methods of molecular biology include hybridization, ligation, melting, and annealing, restriction enzymes, polymerization chain reaction, nucleases, and repair enzymes.

In this paper simplify biopolymerization chain reactions was studied.
The phenomenon of free radical frontal polymerization involves the basic free radical mechanism of oligomers:

$$I \xrightarrow{k_i} 2fX_0 \quad \text{(initiation)} \quad (5)$$

$$X_n + M_i \xrightarrow{k_e} X_{n+1} \quad \text{(elongation)} \quad (6)$$

$$X_n + X_m \xrightarrow{k_t} P \quad \text{(termination)} \quad (7)$$

where $I$, $M$, $X_n$, $P$ denote initiator, monomer, growing strand, and dead polymer species, respectively, $i=1,2,3,4$, $f$ is the initiator efficiency factor, and $X_n$, $n=0,1,2,..$ denotes a radical containing $n$ monomer molecules.

The reaction rate constant has the form of exponentials:

$$k_j=k_j(T)=k_j\exp(\frac{E_j}{R_gT}) \quad j=i,e,t \quad (8)$$

where $R_g$ is the universal gas constant, $T$ is the temperature of the medium, $k_j$ and $E_j$ are the frequency factor and activation energy, respectively, of the reaction designated by $j$.

$$(r_i)=-2k_i\psi_{cI}$$
$$(r_e)=2fk_I\psi_{cI}-2k_e\psi_{cX}^2\psi_{cM}$$
$$(r_t)=-k_t\psi_{cM}\psi_{cX} \quad (9)$$

where $\psi_c$ is concentration of reacting species, $k_i$ is the initiation, decomposition, reaction rate constant, $k_e$ is the elongation, propagation, reaction rate constant, and $k_t$ is the termination reaction rate constant.

If include all reactions has given by equations (5)-(7), equation (2) can be written as follow:

$$\int_R \frac{\partial \psi_{cI}}{\partial t} + \frac{\partial (v_x \psi_{cI})}{\partial x} + \frac{\partial (v_y \psi_{cI})}{\partial y} + \frac{\partial (v_z \psi_{cI})}{\partial z} + \sum_{j=1}^{n} \frac{\partial (v_i \psi_{cI})}{\partial \xi_i} - D\left(\frac{\partial^2 \psi_{cI}}{\partial x^2} + \frac{\partial^2 \psi_{cI}}{\partial y^2} + \frac{\partial^2 \psi_{cI}}{\partial z^2}\right) + (r_I) dR = 0 \quad (10)$$

$$\int_R \frac{\partial \psi_{cM}}{\partial t} + \frac{\partial (v_x \psi_{cM})}{\partial x} + \frac{\partial (v_y \psi_{cM})}{\partial y} + \frac{\partial (v_z \psi_{cM})}{\partial z} + \sum_{j=1}^{n} \frac{\partial (v_i \psi_{cM})}{\partial \xi_i} - D\left(\frac{\partial^2 \psi_{cM}}{\partial x^2} + \frac{\partial^2 \psi_{cM}}{\partial y^2} + \frac{\partial^2 \psi_{cM}}{\partial z^2}\right) + (r_p) dR = 0 \quad (11)$$

$$\int_R \frac{\partial \psi_{cX}}{\partial t} + \frac{\partial (v_x \psi_{cX})}{\partial x} + \frac{\partial (v_y \psi_{cX})}{\partial y} + \frac{\partial (v_z \psi_{cX})}{\partial z} + \sum_{j=1}^{n} \frac{\partial (v_i \psi_{cX})}{\partial \xi_i} - D\left(\frac{\partial^2 \psi_{cX}}{\partial x^2} + \frac{\partial^2 \psi_{cX}}{\partial y^2} + \frac{\partial^2 \psi_{cX}}{\partial z^2}\right) + (r_t) dR = 0 \quad (12)$$

Further, macroscopic equations can be written as the following system equations:

$$\frac{1}{V} \frac{\partial (\psi_{cI})}{\partial t} + \sum_{i=1}^{n} \frac{\partial (v_i \psi_{cI})}{\partial \xi_i} + (r_I) = \frac{1}{V} (\psi_{cI(in)} - \psi_{cI(out)}) \quad (13)$$

$$\frac{1}{V} \frac{\partial (\psi_{cM})}{\partial t} + \sum_{i=1}^{n} \frac{\partial (v_i \psi_{cM})}{\partial \xi_i} + (r_p) = \frac{1}{V} (\psi_{cM(in)} - \psi_{cM(out)}) \quad (14)$$

and

$$\frac{1}{V} \frac{\partial (\psi_{cX})}{\partial t} + \sum_{i=1}^{n} \frac{\partial (v_i \psi_{cX})}{\partial \xi_i} + (r_t) = \frac{1}{V} (\psi_{cX(in)} - \psi_{cX(out)}) \quad (15)$$

Temperature changes in the bath are shown by the following equations. The microscopic heat balance with energy distribution function is:

$$\int_R \frac{\partial \psi_T}{\partial t} + \frac{\partial (v_x \psi_T)}{\partial x} + \frac{\partial (v_y \psi_T)}{\partial y} + \frac{\partial (v_z \psi_T)}{\partial z} + \sum_{j=1}^{n} \frac{\partial (v_i \psi_T)}{\partial \xi_i} - \lambda\left(\frac{\partial^2 \psi_T}{\partial x^2} + \frac{\partial^2 \psi_T}{\partial y^2} + \frac{\partial^2 \psi_T}{\partial z^2}\right) + S_R = 0 \quad (16)$$

where $S_R$ is heat of reaction, $\lambda$ thermal conductivity and $\psi_T$ a temperature distribution function.

Final macroscopic model is derived as:

$$\frac{1}{V}\frac{\partial(\psi_T)}{\partial t}+\sum_1\frac{\partial(v_i\psi_T)}{\partial\xi_i}+S_R=\frac{1}{V}(\psi_{T(in)}-\psi_{T(out)}) \quad (17)$$

where $\psi_T$ is geometrically averaged temperature distribution function

$$\psi_T=1/V\int_V\psi_T dV \text{ and} \quad (18)$$

$$v_i=d\xi_l/dt$$

Heat reaction rate expression is defined:

$$S_r=(r)(\Delta H)_r \quad (19)$$

where $\Delta H$ heat of reaction.

## 6. The algorithm for simulation

An initial population is chosen, randomly. Based upon their fitness, or how well they optimize or satisfy an external constraint, individuals are selected from a population. Fit parents are selected at random, and children formed from them through crossover. Small changes in individuals in the population are made by random mutation.

**The derived mathematical model Eqs. (10)-(19) can be solved for DNA oligonucleotides sequence simulation. The** derived algorithm has shown in Fig. 1.

The algorithm simulated concentration of initiator, monomer and growing biopolymer in time, spatial coordinates and sequence length.

Partial differential equations solution can be performed by existing software packages. Sequences growth can be simulated for different contour conditions. The partial differential can be solved by the finite difference method [13].

In Adleman's work [9] Hamiltonian path through a graph was formed through successive hybridization of oligonucleotides (oligos) which represented vertices and edges in the graph. For larger problems, however iteration may become necessary.

Savkovic-Stevanovic [2] was simulated and predicted values for free energies distribution for oligomeric duplexes using Gaussian function. Numerous layouts were tested for the case of DNA blocks (A//T, G///C, T//A, C///G).

## 7. Conclusion

In this paper biopolymerization reactions in protein synthesis were examined. The mathematical model of process initiation, elongation and termination was derived. Protein synthesis kinetics was studied.

Oligomers specifies concentration and temperature distribution in spatial coordinates and time and sequence length were predicted. Biopolymerization rates of reacting species have been defined, which can be control.

The power of the new complex model was demonstrated by dispersion model which incorporating biopolymerization chain reaction in rigorous biopolymerization mechanism, diffusion and convention.

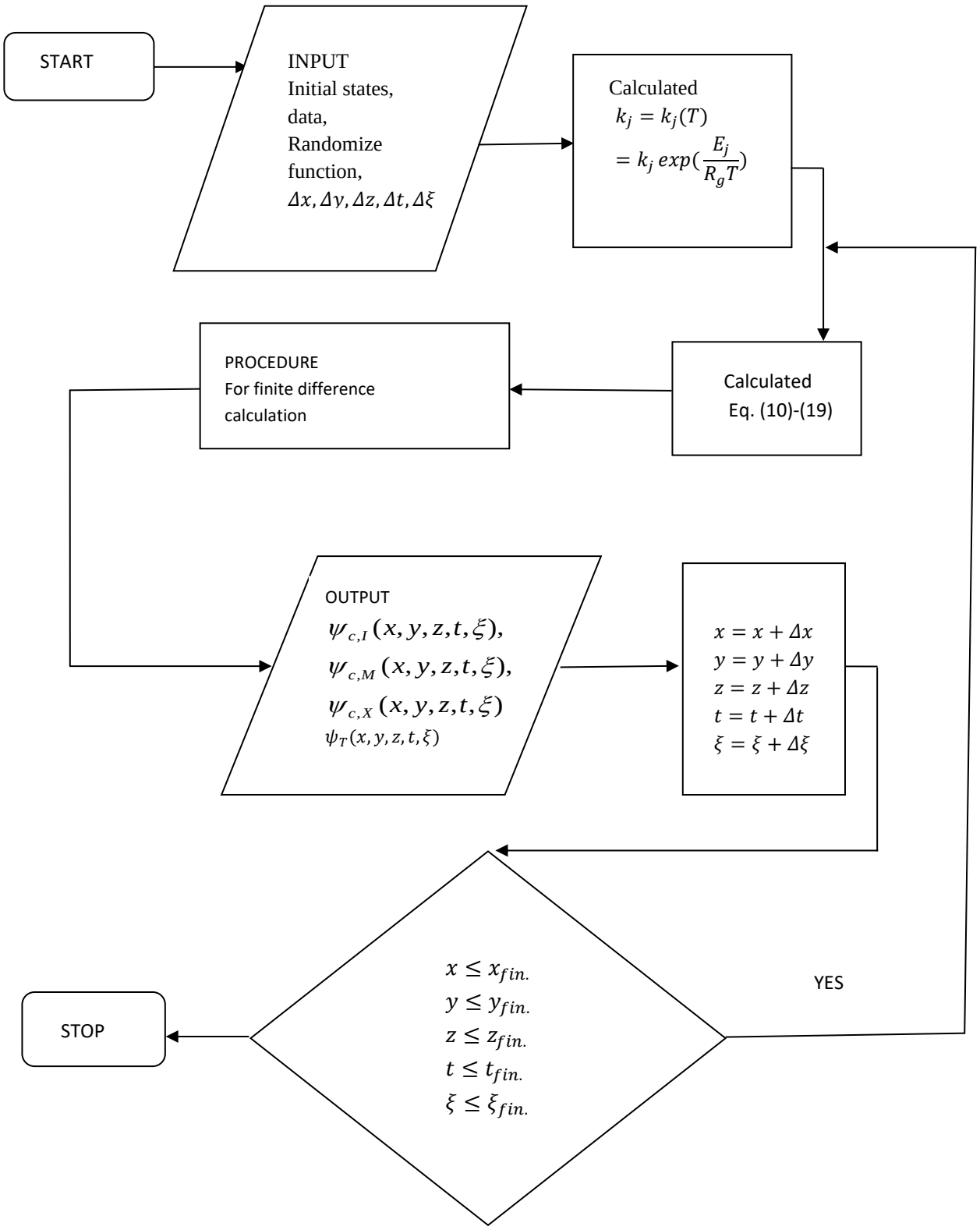


**Fig.1** The algorithm for simulation

## Notation

$I$ - initiation complex

$M$ - monomer

$P$ - product, protein

$R$ - 3+n dimensional space

$R_g$ - universal gas constant, 8.314 $J / molK$

$r$ - reaction rate, $mol / s$

$S_r$ - heat reaction rate, $KJ / mol$

$t$ - time, $s$

$T$ - temperature, $K$

$X$ - free radical

$x, y, z$ - spatial coordinates

$v$ - speed, $nm / s$

$V$ - volume, $nm^3$

### *Symbols*

$\psi$ - probability distribution function

$\xi$ - sequence length, $nm$

$\lambda$ - thermal conductivity, $Jcm^{-2}K^{-1}$

## Abbreviation

**AMP** - adenine monophosphate
**ADP** - adenine diphosphate
**ATP** - adenine triphosphate
**CTP** - cytosine triphosphate
**GMP** - guanine monophosphate

## References


1. J. Savkovic - Stevanovic, An evolutionary system modeling, Design and learning of autonomous behavior, *ESS 99-11th European Simulation Symposium and Exhibition*, Erlangen, Oct., 26-28,1999.
2. J. Savkovic – Stevanovic, Modeling and DNA sequences simulation MESM2001- 3rd *Middle-East Simulation Conference, Modeling and Simulation for Medical Applications*, Amman, Jordan, Aug. 28-30, 2001.
3. J. Savkovic - Stevanovic, A complex model for simulation of biosubstance crystalization, *ESM2001-15th European Simulation Multiconference*, BIO-3, p. 1036, Prague, June 6-9, 2001.
4. J. Savkovic - Stevanovic, Information processing in biopolymeric molecule, *MESM 2002- 4thMiddle East Simulation Conference, Modeling and Simulation for Medical Applications*, Sharjah, UAE, Sept., 28-30, 2002.
5. M. Jones, Pyrimidine nucleotide biosynthesis in animal cells, *Annu Rev. Biochem*.,49,523, 1980.
6. J. Savkovic Stevanovic, R. Stevanović, Purine and pyrimidine nucleotide biosynthesis, *Global Journal of Research in Medical Sciences (Global J Res Med Sci.)*, Vol. 4 (4)5-11 (2024) ISSN2583-3960 https://doi.org/10.5281/zenodo.12689400.
7. J. Savkovic -Stevanovic, J. Adnadjevic, R. Stevanovic, Information transfer in the DNA molecules, Proceedings of the *IES2001-12th Symposium and Seminar on Information and Expert Systems in the Process Industries*, Belgrade, pp. 140-153, October 26-27, 2001.
8. J. Savkovic – Stevanovic, An integrated evolutionary model development, *ESM- 2000-14th Europen Simulation Conference, Simulation and Modeling Enablers for Better Quality of Life,* Ghent, Belgium, May 23-26, 2000.
9. L. M. Adleman, Molecular computation of solutions to combinatorial problems, *Science*, 266, 1021-1024, 1994.
10. J. Savkovic-Stevanovic, Complex modeling of interfacial gel polimerization", *ESM2002 - 16th European Simulation Multiconference*, Darmstadt, Germany, June 3-6, 2002.
11. C. Spade and V. Volpert, Mathematical modeling of interfacial gel polymerization for weak and strong gel effect, *Macromol.Theory Simul*., 9, 26-46, 2000.
12. J. Savkovic-Stevanovic, A complex population model for biopolymers formation, *Comput. Ecol. Eng*.,1(2) 128-134, 2005.

13. J. Savkovic Stevanovic, The DNA biopolymeric chains, *Comput. Ecol. Eng*., 6(2), 63-68, 2010.
14. J. Savkovic-Stevanovic, Informational macromolecule in biological systems, *MCBC2009-Mathematics and Computers in Biology and Chemistry*, Prague, March, 23-25, 2005.
15. J. *Savkovic-Stevanovic*, Genetic information in biopolymeric chain, *World Scientists Engineering and Academic Society-WSEAS, 2nd International Conference Biomedical Electronics and Biomedical Informatics*, pp.122-126, Moscow, Russia, 22-23, August, 2009, ISBN 978-960-474-100-6, ISSN 1790-5125.

**CITATION**
J. Savkovic Stevanovic. (2024). Biopolymerization chain reactions in protein synthesis. In Global Journal of Research in Medical Sciences (Vol. 4, Number 4, pp. 62–70). https://doi.org/10.5281/zenodo.13617714