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Information loss in transcribing genetic sequence from DNA into protein

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Abstract: The main question is the probability of information loss in binding site of DNA due to interaction between DNA bead charges? Information loss in the gene expression disrupts the cellular dynamics and can lead to serious defects, including cancer. Using quantum biology ,a mechanism for calculating the amount of information loss in transcribing genetic sequence from DNA to protein is proposed. In this proposal, there are three different Hilbert spaces that belong to degrees of freedom of protein, binding site, and unbinding site of DNA. At first stage it is shown that the internal stationary state of the cell can be represented by a maximally entangled two-mode squeezed state of DNA and protein. At second stage,the state of the DNA is described by a maximally entangled two-mode squeezed state of DNA binding site and DNA unbinding site. Finally it is shown that the entanglement between protein and DNA is degraded due to interaction between DNA binding site and DNA unbinding site and consequently information is lost.

Keywords: Gene Expression ,Unbinding Site, Information Loss

1. Introduction

Although great advances have been made in genetics in the last decades and the genomes of several species are now completely mapped, there is still a lot of discussion on how gene expression takes place[1].Gene expression is regulated in both prokaryotes and eukaryotes by proteins called transcription factors, which bind to chromosomal DNA at specific sites [2]. Protein binding on DNA plays a fundamental role in many cellular and viral functions, including gene expression [3]. The binding proteins can act either as activators, which means they increase the rate of expression of the genes, or as repressors that decrease the rate of expression of the regulated genes. According to the recent model, the probability of proton binding on DNA is directly proportional to temperature [3,4].

Newly, the connection of the quantum entanglement entropy to the entropy of bubbles in DNA melting is shown[5].It is argued that the absence of any extensively requirement in time makes this negative entropy an inevitable consequence of quantum mechanics in continuum. Also ,some authors attempt to treat the DNA-based biomolecular solution for the SAT problem from the quantum mechanical perspective with a purpose to explore the relationship between DNAC and quantum computation (QC)[6].Furthermore, by assuming that not only counterions but DNA molecules as well are thermally distributed according to a Boltzmann law, some researchers propose a modified Poisson-Boltzmann equation at the classical level as starting point to compute the effects of quantum fluctuations of the electric field on the interaction among DNA-action complexes[7].The main question is the probability of information loss in binding site of DNA due to entanglement between DNA bead charges? Using entanglement of Dirac fields in non non-inertial frames [8-13] we suggest a mechanism to calculate the amount of information loss in transcribing genetic sequence from DNA to protein..In our proposal, there are three different Hilbert spaces that belong to degrees of freedom of DNA binding site, DNA unbinding site, and protein. We define annihilation and creation operators for information in each space and obtain the relation between these operators during transcribing genetic sequence of the DNA binding site into protein. We derive the entangled state on DNA and protein spaces at first stage and the entangled state on DNA binding site and DNA unbinding site spaces at second stage. Finally we show that the entanglement between protein and DNA is degraded

due to interaction between DNA binding site and DNA unbinding site.

The outline of the paper is as follows. In section 2 we obtain the entangled two-mode squeezed states on DNA and protein Hilbert spaces of cells. Then we study the entangled two-mode squeezed states on DNA bead1 and DNA bead2 spaces of the cells in section 3. Finally we calculate the amount of information loss in transcribing genetic sequence from one DNA bead to protein in secion4. The last section is devoted to summary and conclusion.

2. The Radiation of Information from DNA

In this section we extend the results of the derivation of Hawking radiation for Dirac fields in black holes[9] to the information in DNA beads.First we construct one field theory for information in biological system.

In each DNAbead,information states can be encoded by two numbers(zero or one).This property of information states is similar to Dirac field states property.

$$\left|\inf\right\rangle = \alpha\left|0\right\rangle + \beta\left|1\right\rangle \tag{1}$$

in which

$$\left|\alpha\right|^2 + \left|\beta\right|^2 = 1 \tag{2}$$

We introduce two annihilation and creation operators in related to information states as following:

$$\begin{aligned} &\inf\left|0\right\rangle = 0 \qquad \inf\left|1\right\rangle = \left|0\right\rangle \\ &\inf^{\dagger}\left|0\right\rangle = \left|1\right\rangle \qquad \inf^{\dagger}\left|1\right\rangle = 0 \end{aligned} \tag{3}$$

These equations lead us to following anti communication relations between information operators:

$$\{\inf,\inf\} = 0 \qquad \{\inf^{\dagger},\inf^{\dagger}\} = 0 \qquad \{\inf,\inf^{\dagger}\} = 1 \tag{4}$$

Now we can describe the information quantization, using the information field operator

$$INF(x) = \int \frac{d^3k}{(2\pi)^3\sqrt{2\omega(k)}}[\inf e^{-ikx} + \inf^{\dagger} e^{ikx}] \tag{5}$$

whereINF is the information field that determines the amount of information at each point.

Using above field theory, we will show the ground state for information in cell is a maximally entangled two-mode squeezed state on Hilbert spaces of binding sites of DNA and proteins.

The information transformation of DNA bead to protein is described by the following metric:

$$ds^2 = -(1-V_{DNA/protein})dt^2 + (1-V_{DNA/protein})^{-1}dr^2 + r^2 d\Omega^2 \tag{6}$$

Where the potential between a protein and a DNA bead is given by[1]:

$$V_{DNA/protein} \sim \frac{e_{DNA}e_{protein}}{r} \tag{7}$$

The information equation in DNA bead space-time can be written similar to Dirac equation[9]:

$$[i\gamma^{\mu}(\partial_{\mu} + \Gamma_{\mu})]INF = 0 \tag{8}$$

The affine connection is given by[9]:

$$\Gamma_{\mu} = -\frac{1}{4}\gamma_{\nu}(\partial_{\mu}\gamma^{\nu} + \Gamma^{\nu}_{\mu\lambda}\gamma^{\lambda}) \tag{9}$$

The gamma matrices are defined by $\gamma_{\mu} = e^{a}_{\mu}\overline{\gamma}_{a}$ where e^{a}_{μ} are tetrads , $\overline{\gamma}_{a}$ are the gamma matrices for the inertial frame and the Levi-Civita connection coefficients $\Gamma^{\nu}_{\mu\lambda}$ can be calculated by the Lagrange method[9,10].

In Kruskal coordinates the metric of theDNA bead becomes[9,11]:

$$ds^2 = -e_{DNA}e_{protein}\frac{e^{-r/e_{DNA}e_{protein}}}{r}d\bar{u}d\bar{v} + r^2 d\Omega^2 \tag{10}$$

$$\bar{u} = -2e_{DNA}e_{protein}e^{-u/2e_{DNA}e_{protein}}, \bar{v} = -2e_{DNA}e_{protein}e^{-v/2e_{DNA}e_{protein}}$$

$$u = t - r^*, v = t + r^*, r^* = -r - e_{DNA}e_{protein}\ln\left|r - e_{DNA}e_{protein}\right|$$

The positive frequency normal mode solution of equation(8) in Kruskal coordinate is approximated by[9,11] :

$$INF \propto \begin{cases} (-\bar{u}/2e_{DNA}e_{protein})^{-i2e_{DNA}e_{protein}} & region\ I \\ (\bar{u}/2e_{DNA}e_{protein})^{-i2e_{DNA}e_{protein}} & region\ II \end{cases} \tag{11}$$

In Eq. (11), we can use the fact that $(-1)^{-i2e_{DNA}e_{protein}} = e^{2\pi e_{DNA}e_{protein}}$. Using this equation we observethat the information operators in binding site satisfy the following condition:

$$\begin{aligned} &(\inf_{protein} - \tan r_{\omega}\inf^{\dagger}_{DNA})\left|0\right\rangle_{k,cell} = 0 \\ &\tan r = e^{-2\pi e_{DNA}e_{protein}} \end{aligned} \tag{12}$$

which $\inf_{protein}, \inf^{\dagger}_{DNA}$ are annihilation ,creation operators that act on DNA and protein Hilbert spaces of cell respectively.

Now, we assume that the Kruskal vacuum $\left|0\right\rangle_{k,cell}$ is related to the cell vacuum $\left|0\right\rangle_{c}$ by

$$\left|0\right\rangle_{k,cell} = F(\inf_{protein}, \inf^{\dagger}_{DNA})\left|0\right\rangle_{c} \tag{13}$$

where F is some function to be determined later.

From

$$\left\{\inf_{protein}, \inf_{DNA}^{\dagger}\right\} = 1$$

we obtain

$$\left\{\inf_{protein}, (\inf_{DNA}^{\dagger})^{m}\right\} = \frac{\partial}{\partial \inf_{protein}^{\dagger}} (\inf_{DNA}^{\dagger})^{m}$$

and

$$\left\{\inf_{protein}, F\right\} = \frac{\partial F}{\partial \inf_{protein}^{\dagger}}$$

Then using equations (12) and (13), we get the following differential equation for F.

$$\left(\frac{\partial F}{\partial \inf_{protein}^{\dagger}} - \tan r \inf_{DNA}^{\dagger} F\right) = 0 \tag{14}$$

and the solution is given by

$$F = e^{\tan r \inf_{protein}^{\dagger} \inf_{DNA}^{\dagger}} \tag{15}$$

By substituting (15) into (13) and by properly normalizing the state vector, we get:

$$\begin{aligned} &|0\rangle_{k,cell} = e^{\tan r \inf_{protein}^{\dagger} \inf_{DNA}} |0\rangle_{c} = \\ &\cos\ r \sum_{m=0,1} \tan^{m} |m\rangle_{DNA} \otimes |m\rangle_{protein} \end{aligned} \tag{16}$$

where $|m\rangle_{DNA}$ *and* $|m\rangle_{protein}$ are orthonormal bases (normal mode solutions) for H_{DNA} and $H_{protein}$ respectively. We observe the ground state for information is a maximally entangled two-mode squeezed states on DNA and protein Hilbert spaces of cell. The probability of transcribing information of DNA into protein can be obtained as following:

$$\begin{aligned} n_1 &= {}_{k,cell}\langle 0|\inf_{protein}^{\dagger} \inf_{protein}|0\rangle_{k,cell} \\ &= {}_{protein}\langle m|\,{}_{DNA}\langle m|\cos^2 r \inf_{protein}^{\dagger} \inf_{protein} \\ &\times \sum_{m=0}^{1} \tan^{2m}(r)|m\rangle_{DNA}|m\rangle_{protein} \\ &= {}_{protein}\langle m-1|\,{}_{DNA}\langle m|\cos^2 r \\ &\times \sum_{m=0}^{1} \tan^{2m}(r) m |m\rangle_{DNA}|m-1\rangle_{protein} \\ &= \cos^2 r \sum_{m=0}^{1} \tan^{2m}(r) m \\ &= \sin^2(r) = \frac{e^{-2\pi e_{DNA} e_{protein}}}{1+e^{-2\pi e_{DNA} e_{protein}}} \end{aligned} \tag{17}$$

This probability depends on the protien and DNA charges.If charges of DNA and protein have opposite signs, this probability increases with increasing charges.However if the sign of two charges are the same,this probability decreases with increasing charges.

3. The information Transformation from One Bead to Another in DNA

In this section we show the ground state for information in DNA is a maximally entangled two-mode squeezed state on Hilbert spaces of binding sites and nonbinding site of DNA.

The metric for information transformation inside the DNA is given by

$$\begin{aligned} ds^2 &= -(1 - V_{DNAbead/DNAbead}) dt^2 + \\ &(1 - V_{DNAbead/DNAbead})^{-1} dr^2 + r^2 d\Omega^2 \end{aligned} \tag{18}$$

Where the interaction between two DNA beads is described by following potential [1]:

$$V_{DNAbead/DNAbead} \sim \frac{e_{DNA}^2}{r} \tag{19}$$

In Kruskal coordinates the metric of information transformation inside the DNA becomes[8-13]:

$$ds^2 = -e_{DNA}^2 \frac{e^{-r/e_{DNA}^2}}{r} d\bar{u} d\bar{v} + r^2 d\Omega^2 \tag{20}$$

$$\bar{u} = -2e_{DNA}^2 e^{-u/2e_{DNA}^2}, \bar{v} = -2e_{DNA}^2 e^{-v/2e_{DNA}^2}$$

$$u = t - r^*, v = t + r^*, r^* = -r - e_{DNA}^2 \ln\left|r - e_{DNA}^2\right|$$

The solution of information equation(equation8.) in this coordinate is approximated by[8-13]:

$$\inf \propto \begin{cases} (-\bar{u} / 2e_{DNA}^2)^{-i2e_{DNA}^2} & region\ \ I \\ (\bar{u} / 2e_{DNA}^2)^{-i2e_{DNA}^2} & region\ \ II \end{cases} \tag{21}$$

In Eq. (21), we can use the fact that $(-1)^{-i2e_{DNA}^2} = e^{2\pi e_{DNA}^2}$. Using this equation we observethat the information operators in DNA satisfy the following condition:

$$\begin{aligned} &(\inf_{DNA\ bead1} - \tan r' \inf_{DNA\ bead2}^{\dagger})|0\rangle_{DNA} = 0 \\ &\tan r' = e^{-2\pi e_{DNA}^2} \end{aligned} \tag{22}$$

which $\inf_{DNA\ bead1}, \inf_{DNA\ bead2}^{\dagger}$ are annihilation ,creation

operators that act on DNA bead 1 and DNA bead2 Hilbert spaces respectively. With similar calculations to section 2 we get:

$$|0\rangle_{DNA} = e^{\tan r' \inf^{\dagger}_{DNA\ bead1} \inf^{\dagger}_{DNA\ bead2}} |0\rangle_c = \cos\ r' \sum_{m=0,1} \tan^m r' |m\rangle_{DNA\ bead1} \otimes |m\rangle_{DNA\ bead2} \quad (23)$$

where $|m\rangle_{DNA\ bead1} \otimes |m\rangle_{DNA\ bead2}$ are orthonormal bases (normal mode solutions) for $H_{DNA\ bead1}$ and $H_{DNA\ bead2}$ respectively. We observe the ground state for information is a maximally entangled two-mode squeezed states on bead1 and bead2 Hilbert spaces of DNA. The probability of transcribing information of DNA bead1 into DNA bead2 can be obtained as following:

$$\begin{aligned} n_2 &= {}_{DNA}\langle 0|\inf^{\dagger}_{DNA bead2} \inf_{DNA bead2}|0\rangle_{DNA} \\ &= {}_{DNA bead2}\langle m|\,{}_{DNA bead1}\langle m|\cos^2 r' \inf^{\square}_{DNA bead2} \inf_{DNA bead2} \\ &\times \sum_{m=0}^{1} \tan^{2m}(r')|m\rangle_{DNA bead1}|m\rangle_{DNA bead2} \\ &= {}_{DNA bead2}\langle m-1|\,{}_{DNA bead1}\langle m|\cos^2 r' \\ &\times \sum_{m=0}^{1} \tan^{2m}(r') m |m\rangle_{DNA bead1}|m-1\rangle_{DNA bead2} \\ &= \cos^2 r' \sum_{m=0}^{1} \tan^{2m}(r') m \\ &= \sin^2(r') = \frac{e^{-2\pi e^2_{DNA}}}{1+e^{-2\pi e^2_{DNA}}} \end{aligned} \quad (24)$$

This probability depends on the DNA bead charges.

4. The Information Loss in Transcribing Genetic Sequence from One DNA Bead to Protein

Now we can calculate the information loss in transcribing genetic sequence from DNA to protein due to interaction between DNA beads. At first stage, there is an entanglement between the DNA and protein spaces of cell(see equation16.).

$$|0\rangle_{k,cell} = \cos r|0\rangle_{DNA}|0\rangle_{protein} + \sin r|1\rangle_{DNA}|1\rangle_{protein} \quad (25)$$

At second stage,we can describe the state of the DNA as an entangled state of both DNA bead1 and DNA bead2 (see equation 23.) .

$$|0\rangle_{DNA} = \cos r'|0\rangle_{DNA\ bead1}|0\rangle_{DNA\ bead2} + \sin r'|1\rangle_{DNA\ bead1}|1\rangle_{DNA\ bead2} \quad (26)$$

Also,using equation(22)we can write the Bogoliuobov transformation between DNA creation- annihilation operator and creation -annihilation operators in DNA bead 1 and DNA bead 2:

$$\begin{aligned} \inf_{DNA} &= \cos r' \inf_{DNA\ bead1} - \sin r' \inf^{\dagger}_{DNA\ bead2} \\ \inf^{唵}_{DNA} &= \cos r' \inf_{DNA\ bead1} - \sin r' \inf_{DNA\ bead2} \end{aligned} \quad (27)$$

The excited state of DNA can be obtained as following:

$$|1\rangle_{DNA} = \inf^{\dagger}_{DNA}|0\rangle_{DNA} = |1\rangle_{DNA\ bead1}|0\rangle_{DNA\ bead2} \quad (28)$$

By substituting equations(28)and (26) in equation(25) we can get:

$$\begin{aligned} |0\rangle_{cell} &= \cos r(\cos r'|0\rangle_{DNA\ bead1}|0\rangle_{DNA\ bead2} + \\ &\sin r'|1\rangle_{DNA\ bead1}|1\rangle_{DNA\ bead2})|0\rangle_{protein} + \\ &\sin r|1\rangle_{DNA\ bead1}|0\rangle_{DNA\ bead2}|1\rangle_{protein} \end{aligned} \quad (29)$$

Since protein is binding to DNA bead 1 and causally disconnected from DNA bead2, we take the trace over the mode in this region, which results in a mixed density between DNA bead1 and protein

$$\rho_{DNAbead1,protein} = \begin{pmatrix} (\cos r\cos r')^2 & 0 & 0 & \cos r'\cos r\sin r \\ 0 & (\cos r\sin r')^2 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ \cos r'\cos r\sin r & 0 & 0 & \sin^2 r \end{pmatrix} \quad (30)$$

in the basis $|00\rangle, |01\rangle, |10\rangle, |11\rangle$ where

$$|ab\rangle = |a\rangle_{DNAbead1}|b\rangle_{protein}$$

To determine whether or not this state is entangled we use the partial transpose criterion [8,12]. If at least one eigenvalue of the partial transpose of the density matrix is negative, then the density matrix is entangled. The partial transpose is obtained by interchanging DNA bead1's qubits

$$\rho^{T}_{DNAbead1,protein} = \begin{pmatrix} (\cos r\cos r')^2 & 0 & 0 & 0 \\ 0 & (\cos r\sin r')^2 & \cos r'\cos r\sin r & 0 \\ 0 & \cos r'\cos r\sin r & 0 & 0 \\ 0 & 0 & 0 & \sin^2 r \end{pmatrix} \quad (31)$$

This density has the following eigenvalues :

$$\lambda = (\cos r\cos r')^2, \sin^2 r, \frac{-(\cos r\sin r')^2 \pm \sqrt{(\cos r\sin r')^4 + 4\cos r'\cos r\sin r}}{2} \quad (32)$$

It is found that the state is entangled due to negative eigenvalue.To obtain the amount of entanglement , we calculate the logarithmic negativity. This entanglement monotone is defined as:

$$N(\rho) = \log_2 \left\| \rho^{T} \right\| = \log_2 (\cos^2 r' + \sin^2 r) \quad (33)$$

where ρ^{T} is the trace-norm of the density matrix ρ . In the limit of infinite DNA bead charges, the logarithmic negativity is zero. However in the limit of zero DNA bead charge ,it's value is converging to unity.This means that the entanglement between protein and DNA is degraded with increasing DNA bead charges and consequently information isn't extracted completely from binding site.

5. Summary and Conclusion

In this manuscript,we calculate the amount ofinformation loss in binding site sue to interaction between DNA bead charges . To this end, we introduce three Hilbert spaces that belong to degrees of freedom of DNA binding site, DNA unbinding site and protein.At first stage we show that the internal stationary state of the cell can be represented by a maximally entangled two-mode squeezed state of DNA and protein.At second stage,the state of the DNA can be described by a maximally entangled two-mode squeezed state of DNA unbinding site and protein.Finally we show that the entanglement between protein and DNA is degraded due to interaction between DNA beads .

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