BIOMOLECULAR RECOGNITION:
ON POSSIBLE QUANTUM APPROACHES

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Abstract. Two unresolved issues of the (semi)classically addressed problems in molecular biophysics are unreasonably long time necessary for the change of biopolymer conformations and long-range directedness of selective biomolecular recognition processes – implying their essential quantum origin. In this paper several possible quantum approaches to biomolecular recognition are considered: Theory of Non-Radiative Resonant Structural Transitions, Model of Quantum Decoherence, and Resonant Recognition Model. These approaches might be of fundamental importance in understanding underlying macroscopic quantum-holographic Hopfield-like control mechanisms of morphogenesis, and their backward influence on the expression of genes, with significant potential psychosomatic implications.

Key words: Biomolecular Recognition, Conformational Transitions, Quantum Biophysics, Quantum Bioinformatics.

1. Introduction

Conformational properties of enzymes are essentially important for understanding of enzyme catalytic activity. The *conformational lability of a protein* makes its *specific interaction* with *substrates* possible. As the substrate is (most frequently) low-molecular, and the enzyme is (high-molecular) protein, then the substrate directly interacts with a particular small part of the enzyme molecule – its *active site* (group and distribution of

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amino acid residues and cofactors (coenzymes, vitamins, metal-organic complexes, hormones)).

In the *enzyme-substrate complex* (ESC) the *induced structural correspondence* of the enzyme and substrate is dynamically established, thus providing the optimal value of the free energy of interaction. The *conformational transformations* involved lead to a structural fit between the enzyme and the substrate, i.e. *biomolecular recognition*. The enzyme-substrate interaction is a *weak chemical bond* (Van der Waals, hydrogen, hydrophobic, ...), which is, however, very *enhanced* due to *hydrophobic active site of the enzyme*: namely, relative dielectric permittivity ε_r of the cavity of active site of the enzyme is much less ($\varepsilon_r \sim 3 \div 4$) compared to water environment ($\varepsilon_r \sim 81$), which significantly facilitates the occurrence of electric interactions ($F \sim q_1 q_2 / 4\pi\varepsilon_0\varepsilon_r r^2$) between the substrate and the active site of the enzyme. Practically, *electrostatic* interactions within *hydrophobic cavity* (active site) *of the enzyme* provide the main contribution to bioenergetics of enzyme catalysis, i.e. *to the reduction of the activation barrier* in the enzyme-substrate complex. The energy necessary for conformational changes of the enzyme structure is liberated upon binding of the substrate to the enzyme.

During enzyme-substrate interaction and formation of the enzyme-substrate complex, the states of the electronic shells of the substrate and of the atomic groups of the active site of the enzyme are excited. In the enzyme-substrate complex the energy of electronic excitation is converted to the work of *displacement of atomic nuclei*. Among the movements of atomic nuclei the *lowest energy* is demanded by *low-frequency deformational vibrations* and *rotations around single bonds*, i.e. *conformational changes*! Hence, the interactions of electronic and conformational degrees of freedom – *Volkenshtein's electronic-conformational interactions* (ECI) are the most significant for *enzyme catalysis*, cf. Figure 1.
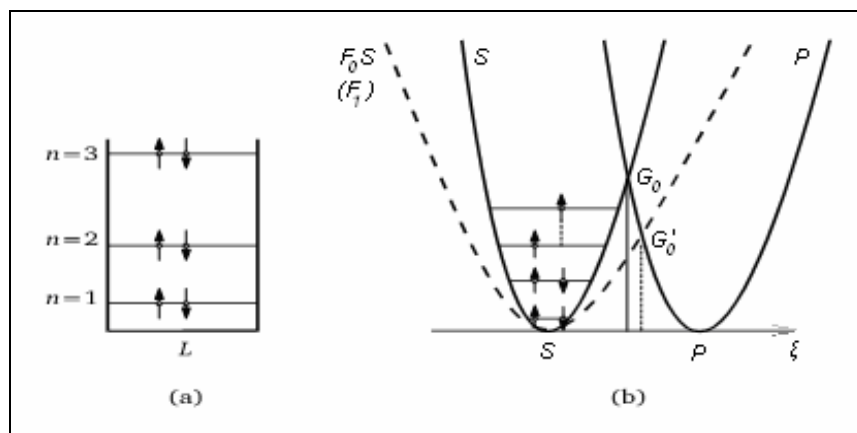

Figure 1 (a) *In order to understand the nature of ECI, it is helpful to make use of a simplified model of the interaction between electrons and atomic nuclei –*

electrons in a potential box with infinitely high mobile walls, wherefrom the electron pressure force exerted on the wall is easily obtained: $f_e = |dE/dL| = n^2h^2/4m_eL^3$. A change in equilibrium results either from the excitation of electrons in the system (arises n) or from the addition of electrons (arises number of electrons, i.e. number of hits upon the walls of the box), when the walls of the box move and pass to a new equilibrium position, at an increased distance from each other, $L + \Delta L$. (b) On the other hand, if one considers a parabolic well with mobile walls, it will be easy to show how ECI lower the activation barrier (G_a). The expansion of the parabola of the initial reagents of the biochemical reaction, brought about by the added pressure forces of the electrons, results in the shift of the point of intersection with the second parabola of the products of the biochemical reaction, i.e. to decrease of the free energy of activation ($G_a' < G_a$)! Such semi-classical consideration of ECI (Volkenshtein, 1975; 1983), demonstrates that the energy of electronic excitations is converted to the work of displacement of the nuclei, i.e. to the conformational energy. As a result, the biochemical reaction is accelerated.

2. Quantum Models of Electronic-Conformational Interactions and Biomolecular Recognition

Two *unresolved issues* of the (semi)classically addressed problems in molecular biophysics are *unreasonably long time* necessary for the *change* of biopolymer conformations (Levinthal paradox (Levinthal, 1968)) and a *long-range directedness* of selective biomolecular recognition processes – implying their essential *quantum origin* (Raković, 2008; 2009).

The quantum nature of *biomolecular recognition* might be supported by: (1) *The Theory of Non-Radiative Resonant Structural Transitions* (Gribov, 2001), through intermediate quantum-coherent superposition of the externally activated electronic-vibrational states of the participating biomolecules; (2) *Model of Quantum Decoherence* (Raković, Dugić, & Plavšić, 2004; Dugić, Raković, & Plavšić, 2005; Raković, Dugić, & Plavšić, 2005; Raković et al, 2006; Raković, 2007; Raković & Vasić, 2008), through environment-induced conformational transitions in biomolecular recognition, with possibility to consider cellular biomolecular recognition as a Hopfield-like quantum-holographic associative neural network (by treating all biomolecules of the same type within a cell as *dynamically coupled identical quantum particles,* thus implying deeper *quantum holism of the cell*); and (3) *Resonant Recognition Model* (RRM) (Cosic, 1994; 1997; Pirogova, Akay, & Cosic, 2002; Veljkovic, 1980; Veljkovic & Slavic, 1972), based on findings that *informational* biomolecules and their targets have common RRM-frequency peak but almost opposite phases – which will be elaborated in detail further on.

The Theory of Non-Radiative Resonant Structural Transitions (Gribov, 2001), within the framework of standard *quantum-chemical* Hamiltonian (including kinetic energies and Coulomb interactions of all biomolecular electrons and nuclei) and Born-Openheimer *adiabatic approximation* (of separated biomolecular electronic and vibrational degrees of freedom), replaces the (quasi)classical problem of many-electron hyper-surface $E_e(\phi_e^{(k)})$, not adiabatically well-defined when traversing between two adjacent local minima, by better defined problem of two (virtually intersecting) isomeric many-electron hyper-surfaces (hyper-paraboloids) serving as potential hyper-surfaces for two vibrational (isomeric) problems, cf. Figure 2.

In this approach, by *external perturbation* of the isomers, at this very intersection the conditions for electronic-vibrational non-radiative resonant transitions between the two isomers (*i, f*) are achieved: these resonance electronic-vibrational states of two isomers are transformed from the corresponding (non-perturbed) products of electronic and vibrational wave functions ($\phi_e^{(i)} \phi_v^{(i)}$, $\phi_e^{(f)} \phi_v^{(f)}$) into (perturbed) symmetrized superposition ($\phi_e^{(i)} \phi_v^{(i)} \pm \phi_e^{(f)} \phi_v^{(f)}$)/√2, and their (non-perturbed) energies from resonating (equal) superpositions of the ground electronic energies of corresponding minima of many-electron hypersurface and vibrational energies of higher excited states ($E_e^{(i)} + E_v^{(i)} = E_e^{(f)} + E_v^{(f)}$) into (perturbed) slightly split energy doublet ($E_e^{(i)} + E_v^{(i)} + \frac{1}{2}\Delta E$, $E_e^{(f)} + E_v^{(f)} - \frac{1}{2}\Delta E$), with $\Delta E = 2(E_e^{(i)} + E_v^{(i)})S_{ev}^{(i,f)}$ (where electronic-vibrational overlap integral between the two resonating isomeric states (*i, f*) is $S_{ev}^{(i,f)} = \iint \phi_e^{(f)} \phi_v^{(f)} \phi_e^{(i)} * \phi_v^{(i)} * dV_e dV_v \approx S_v^{(i,f)} S_e^{(i,f)}$, while $S_v^{(i,f)}$ and $S_e^{(i,f)}$ are corresponding overlap integrals of vibrational and electronic components). In the first approximation, the matrix element of *dipole transition* from *i*-th to *f*-th isomer is given by $\boldsymbol{\mu}^{(i,f)} \approx \iint \phi_e^{(f)} \phi_v^{(f)} (\boldsymbol{\mu}_e + \boldsymbol{\mu}_v) \phi_e^{(i)} * \phi_v^{(i)} * dV_e dV_v \approx \boldsymbol{\mu}_e^{(i,f)} S_v^{(i,f)} + \boldsymbol{\mu}_v^{(i,f)} S_e^{(i,f)}$, where $\boldsymbol{\mu}_e$ and $\boldsymbol{\mu}_v$ are corresponding electronic and nuclear components of the operator of total dipole moment. It is obvious that transition between two isomers will be allowed when components of corresponding dipole moments, $\boldsymbol{\mu}_e^{(i,f)}$ and $\boldsymbol{\mu}_v^{(i,f)}$, *and* overlap integrals, $S_v^{(i,f)}$ and $S_e^{(i,f)}$, *do not vanish*!
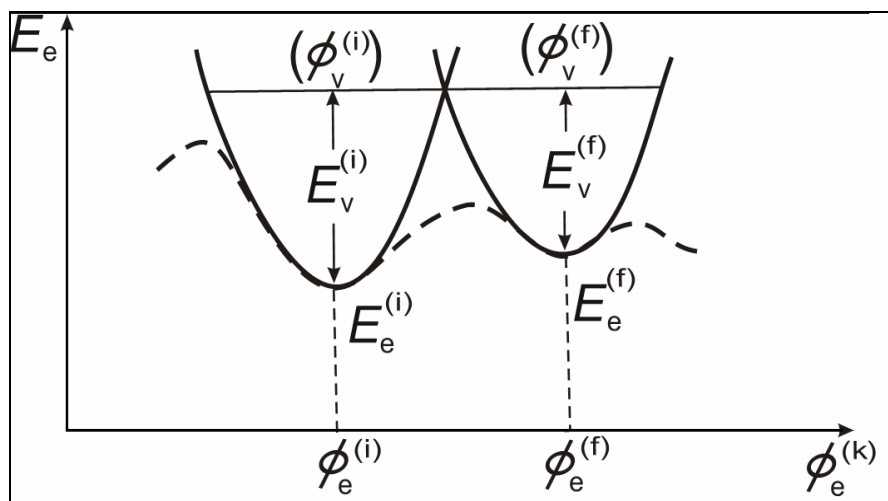
Figure 2 *The (semi)classical problem of many-electron hyper-surface $E_e(\phi_e^{(k)})$ as a potential energy for adiabatically decoupled Q1D vibrational and conformational system (with local minima as semi-classical 'positions', i.e. many-atomic isomer configurations on many-electron hyper-surface (broken line in the figure)) – not adiabatically well-defined when traversing between two adjacent local minima – is replaced within the framework of the theory of non-radiative resonant transitions* (Gribov, 2001) *by better defined problem of two (virtually intersecting) isomeric many-electron hyper-surfaces (hyper-paraboloids) serving as potential hyper-surfaces for two vibrational (isomeric) problems (full line in the figure). In this approach, by external perturbation of the isomers, at this very intersection the conditions for electronic-vibrational non-radiative resonant transitions between the two isomers (i, f) are achieved: in the first approximation, the matrix element of dipole transition from i-th to f-th isomer is given by* $\boldsymbol{\mu}^{(i,f)} \approx \boldsymbol{\mu}_e^{(i,f)} S_v^{(i,f)} + \boldsymbol{\mu}_v^{(i,f)} S_e^{(i,f)}$, *and it is obvious that transition between two isomers will be allowed when components of corresponding electronic and vibrational dipole moments,* $\boldsymbol{\mu}_e^{(i,f)}$ *and* $\boldsymbol{\mu}_v^{(i,f)}$, *and electronic and vibrational overlap integrals,* $S_v^{(i,f)}$ *and* $S_e^{(i,f)}$, *do not vanish. Also, during these resonant transitions the perturbed biomolecular system is shortly described by quantum-coherent superposition* $(\phi_e^{(i)} \phi_v^{(i)} \pm \phi_e^{(f)} \phi_v^{(f)})/\sqrt{2}$, *before its quantum decoherence into final electronic state* $\phi_e^{(f)}$ *or into initial electronic state* $\phi_e^{(i)}$ *(with subsequent de-excitations into lower vibrational states).*

From the above consideration, it can be concluded that *allowed transitions* between isomeric states (*i, f*) are possible only for close states with *non-vanishing* overlap integrals $S_v^{(i,f)}$ and $S_e^{(i,f)}$, or in *cascade* resonant transitions between *close intermediate* participating isomeric states, which might be related to non-dissipative

polaron/soliton-like transport (Raković, 2008; 2009; Keković, Raković, & Davidović, 2007).

Also, during these resonant transitions the perturbed biomolecular system is shortly described by *quantum-coherent superposition* $(\phi_e^{(i)} \phi_v^{(i)} \pm \phi_e^{(f)} \phi_v^{(f)})/\sqrt{2}$, before its *quantum decoherence* into final electronic state $\phi_e^{(f)}$ or into initial electronic state $\phi_e^{(i)}$ (with subsequent de-excitations into lower vibrational states).

Model of Quantum Decoherence (Raković, Dugić, & Plavšić, 2004; Dugić, Raković, & Plavšić, 2005; Raković, Dugić, & Plavšić, 2005; Raković et al, 2006; Raković, 2007; Raković & Vasić, 2008) fits nicely within the previously described picture of short-lasting description of *quantum-coherent superposition* of states of the two isomers before its quantum decoherence into one of the two final isomer states. It generally allows the reproduction of both *existence and stability* of the (stationary) ligand-proteins/target-receptors key/lock mismatching and matching conformations, and the *short time scales* for the quantum-mechanical processes resulting effectively in (nonstationary) mismatching-to-matching conformational transitions in selective ligand-proteins/target-receptors key/lock *biomolecular recognition processes* under external (e.g. compositional/chemical, thermal, optical ...) influences on the cell's complementary cytoplasmatic environment.

Dynamic modification of (many-electron) energy-state hyper-surface $E_e(\phi_e)$, of the *cell's quantum-ensemble* protein/substrate biomolecular macroscopic open quantum system (through changes in operator of density of states $\hat{\rho}_e(t)$), is a natural consequence of coupled electronic-conformational processes – which implies potential possibility to consider cell's biomolecular recognition as *Hopfield's quantum-holographic associative neural network*. This approach assumes *standard cell's local treatment of quantum ensemble of non-interacting dynamically non-coupled N distinguishable* quantum biomolecular proteins of the same type (and their corresponding biomolecular classes of substrates) (Raković, Dugić, & Plavšić, 2004; Dugić, Raković, & Plavšić, 2005; Raković, Dugić, & Plavšić, 2005; Raković et al, 2006; Raković, 2008; 2009).

However, there is an alternative possibility of *holistic cell's non-local treatment of quantum system of non-interacting dynamically coupled N in-distinguishable* quantum biomolecular proteins of the same type (and their corresponding biomolecular classes of substrates) (Raković, 2007; Raković & Vasić, 2008; Raković, 2008; 2009). Then dynamical modification of many-electron energy-state hyper-surface of cell's biomolecular protein macroscopic open quantum system (and analogously their corresponding biomolecular classes of substrates), can be best represented in the formalism of *second quantization*, which treats *all biomolecules of the same atomic configuration* as *in-distinguishable quantum particles* which *occupy different isomeric-conformational states,* and considers such cell's *N-particle protein quantum state* in quantum-mechanical *occupational basis* which describes *number of proteins*

that occupy subsequently all states *of complete basis set of single-particle isomeric-conformational protein states.*

The second approach provides a *plausible quantum-holistic* picture of biological cell, and especially *phenomenologically approved quantum-holographic (fractal) coupling of various* hierarchical quantum levels – from-biological cell-to-acupuncture system/consciousness (Raković, 2008; 2009). This implies Hopfield-like quantum-holographic feedback influence of the EM field of acupuncture system on cells' conformational protein changes and genes' expression (so called macroscopic 'downward causation'), and not only reversed (microscopic 'upward causation'), with mutual quantum-informational control of ontogenesis/embryogenesis and morphogenesis, starting from the first division of the fertilized cell when differentiation of the acupuncture system begins – with significant *psychosomatic and cognitive bio-informational implications* (Raković, 2007; Raković & Vasić, 2008; Raković, 2008; 2009).
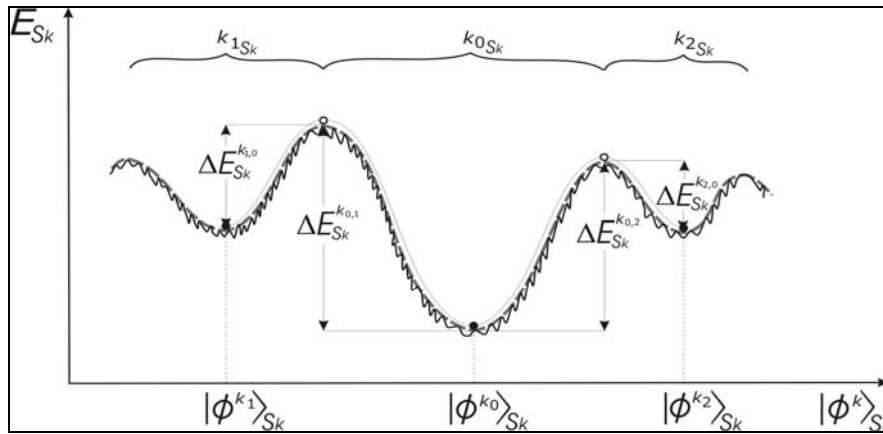

Figure 3 *Schematic presentation of the memory attractors in the energy-state ($E_{S_k}(\phi^k)$) hyper-surface of the quantum-holographic memory/propagator of the open macroscopic quantum system S_k (cell's protein/ target biomolecular one* (Raković, 2008; 2009)):

$$G(r_2,t_2;r_1,t_1) = \sum_{i=1}^{P} \phi^{k_i}(r_2,t_2)\phi^{k_i*}(r_1,t_1)$$

$$= \sum_{i=1}^{P} A_{k_i}(r_2,t_2)A_{k_i}^{*}(r_1,t_1)e^{\frac{i}{\hbar}(\alpha_{k_i}(r_2,t_2)-\alpha_{k_i}(r_1,t_1))}$$

It should be pointed out that quantum decoherence presumably plays fundamental role in biological quantum-holographic neural networks, through presented energy hyper-surface shape adaptation (in contrast to low-temperature artificial cubit quantum processors where it must be avoided until the very read-out act of

quantum computation) – which implies that Nature presumably has chosen elegant room-temperature solution for biological quantum-holographic information processing, permanently fluctuating between quantum-coherent states $\left|\phi^k(t)\right\rangle_{S_k} =$

$\sum_i c_{k_i}(t)\left|\phi^{k_i}\right\rangle_{S_k}$ *and classically-reduced states* $\hat{\rho}_{S_k}^k(t) = \sum_i \left|c_{k_i}(t)\right|^2 \left|\phi^{k_i}\right\rangle_{S_k S_k} \left\langle\phi^{k_i}\right|$ *of cell's biomolecular open macroscopic quantum system S_k, through nonstationary interactions with farther bodily environment and through decoherence by bodily closer environment. The same might be related to higher hierarchical quantum-holographic macroscopic open acupuncture system/consciousness level, thus providing natural framework for quantum-holographic coupling with lower cellular level, thus changing the expression of genes.*

To be more specific, in the formalism of second quantization – the mentioned cell's *N*-particle protein quantum state is considered in quantum-mechanical *occupational basis* (generally bosonic, because of protein-substrate integer spin due to even number of their covalent bonded electrons!), describing number of proteins which occupy complete set of *single-particle protein-substrate isomeric/conformational states*: $\left|n_0 n_1 n_2 ...\right\rangle_e$, with conditions $N = n_0 + n_1 + n_2 + ...$ and $E_{S_e} = n_0 E_e^{(0)} + n_1 E_e^{(1)} + n_2 E_e^{(2)} + ...$ (where E_{S_e} is the many-electron energy of the total cell's *N*-particle-protein quantum state, while $E_e^{(0)}$, $E_e^{(1)}$, $E_e^{(2)}$ ... are the many-electron energies of the protein single-particle quantum isomeric/conformational states 0, 1, 2, ...). An many-electron energy-state hyper-surface of such protein *N*-particle-isomeric/conformational state has a schematic representation in Figure 3, where the internal surface of every minimum is proportional to the partial energy ($n_i E_e^{(i)}$) of the *i*-th protein single-particle-isomeric/conformational state occupied by n_i isomers of the same form (i = 0, 1, 2, ...), so that total energy ($E_{S_{ke}}$) of the cell's protein *N*-particle-isomeric/conformational state is proportional to the sum of internal surfaces of the all minima of the many-electron hyper-surface.

It should be noted that inclusion of *vibrational degrees of freedom (phonons) of all possible isomeric/conformational states*, requires their consideration in quantum-mechanical *occupational basis* (also bosonic, because of phonon's integer spin!) – describing number of phonons occupying complete set of single-particle *phonon states* of the all protein-substrate isomers/conformations: $\left|n_1^{(0)} n_2^{(0)} ... n_{3N-6}^{(0)} n_1^{(1)} n_2^{(1)} ... n_{3N-6}^{(1)} n_1^{(2)} n_2^{(2)} ... n_{3N-6}^{(2)} ...\right\rangle_v$ where every isomeric protein-substrate complex composed of N_i atoms has generally $3N_i$-6 vibrational degrees of freedom (phonon types), out of which every phonon state can be occupied by an unlimited number of phonons (which is characteristic of all bosons, i.e. particles of integer spin). It should be pointed out that an energy hyper-surface of multi-dimensional

phonon quantum state has also a schematic representation in Figure 3, with potentially unlimited number of phonons in every single-phonon state. So, at the cellular level, there would exist *two* (interacting) macroscopic quantum subsystems for *every set of identical molecules* – first with *modifying many-electron hypersurface* $E_e(\phi_e)$ and second with *modifying EM multi-phonon hypersurface* $E_v(\phi_v)$ (where the second one might also include low-energy long-range coherent microwave Fröhlich excitations (Fröhlich, 1968; 1991) – created as a result of interaction of electronic and phonon isomeric subsystems, of particular significance in *microwave resonance therapy* (MRT) of a dynamic modification of the EM multi-phonon (and related many-electron) *acupuncture* macroscopic quantum subsystem).

Resonant Recognition Model (Cosic, 1994; 1997; Pirogova, Akay, & Cosic, 2002; Veljkovic, 1980; Veljkovic & Slavic, 1972) is confirmed on more than 1000 proteins from more than 30 functional groups – with numerous potential practical advantages in the fields of molecular biology, biotechnology, medicine, agriculture and nanotechnology. It is based on findings that there is significant correlation between spectra of the numerical presentation of constitutive elements of primary sequences (amino acids, nucleotides) and their biological activity or interaction in corresponding biomolecules (proteins, DNAs). The RRM model interprets this linear information by assigning the electron-ion interaction potential (EIIP) value to each constitutive element of primary sequence thus describing their average energy states of valence electrons, with subsequent using signal analysis methods in fast Fourier transform transforming this numerical series into single-electron wave number/RRM frequency domain and determining the common frequency components as peak frequencies in the multiple cross-spectral function for a group of primary sequences. The presence of peak with significant signal-to-noise ratio in a multiple cross-spectral function of a group of sequences with the same biological function means that all of the analysed sequences within the group have this single-electron RRM frequency component in common, with the following general conclusions: (1) such a peak exists only for the group of biomolecules with the same function; (2) no significant peak exists for biologically unrelated biomolecules; (3) peak frequencies are different for different biological function; (4) ligand-proteins and their biomolecular target-receptors have the same characteristic frequency in common but almost opposite phase – providing also novel theoretical possibilities for protein *de novo* design with desired functions!

In the context of the RRM-model, the same characteristic single-electron RRM frequency, and almost opposite phase, presumably characterises not only biomolecular protein and target general function, but also their *macroscopic quantum biomolecular recognition interaction* on the level of biological *cell* – possibly by externally *activated* (compositionally/chemically, by averaged intermolecular approaching of proteins and targets necessary for non-vanishing overlap integrals of the corresponding electronic and vibrational wave functions, or thermally/optically, by supplying vibrational energy necessary for making conditions for electronic-vibrational non-radiative resonant

transitions between two isomers (i, f), cf. Figure 2) ligand-proteins/target-receptors RRM quantum-resonantly electron-electron coupling *accompanied* by $\phi^{(i)}$-annihilation and $\phi^{(f)}$-creation of conformones' quanta in two-conformational transitions $\phi^{(i)} \rightarrow \phi^{(f)}$ (giving rise to (energy-favourable) many-electron energy-deepening of the final state $\phi^{(f)}$ and many-electron energy-shallowing of the initial state $\phi^{(i)}$ on the macroscopic quantum level of cell, i.e. to *dynamic modification of the many-electron hyper-surface $E_e(\phi^{(k)})$ of the cell's protein macroscopic quantum system* (cf. Figure 3 (Raković, 2007; Raković & Vasić, 2008; Raković, 2008; 2009)).

Considered within the framework of Hückel-like theory of molecular orbits (Keković et al, 2008; Raković, 2008; 2009), the quantum approach to the RRM-model shows that discrete Fourier transform in the RRM model is basically related to sequential contributions to the first order correction of energy (i.e. *primary sequence of amino-residues*, but not to (single electron) energy of the periodic part of protein's chain). So, the results of the RRM model imply that on the bio-molecular level an information processing is going on in the *inverse space* of Fourier spectra of the primary sequences of bio-molecules, bearing resemblance to quantum-holographic ideas that cognitive information processing is going on in the *inverse space* of the Fourier spectra of the perceptive stimuli (Pribram, 1971; 1991), thus supporting picture of *quantum-holographic fractal coupling* of various hierarchical levels in biological species, with significant potential psychosomatic implications (cf. Figure 3).

3. Conclusions

The two unresolved issues of the (semi)classically addressed problems in molecular biophysics are unreasonably long time necessary for the change of biopolymer conformations and long-range directedness of selective bio-molecular recognition processes – implying their essential quantum origin. In this paper several possible quantum approaches are considered: the Theory of Non-Radiative Resonant Structural Transitions, through intermediate quantum-coherent superposition of the externally activated electronic-vibrational states of the participating bio-molecules; the Model of Quantum Decoherence, through environment-induced conformational transitions in bio-molecular recognition, with possibility to consider cellular bio-molecular recognition as a Hopfield-like quantum-holographic associative neural network; and the Resonant Recognition Model (RRM), based on the findings that informational bio-molecules and their targets have common RRM-frequency peak but almost opposite phases. These approaches might be of fundamental importance in understanding the underlying macroscopic quantum-holographic Hopfield-like control mechanisms of morphogenesis, and their backward influence on the expression of genes, with significant potential psychosomatic implications.

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REZIME

Dva nerazrešena pitanja semi-klasično postavljnih problema u molekularnoj biofizici jesu nerazumno dugo vreme potrebno za izmenu biomolekularnih konformacija i dugo-dometna usmerenost selektivnih procesa biomolekularnog prepoznavanja.

U radu je razmotreno nekoliko mogućih kvantnih prilaza rešavanju ovih problema. Predloženi kvalitativni scenario je dovoljno opšti i čini dobru osnovu za principijelno rešenje problema biopolimernog sklupčavanja u nativnu konformaciju pri visoko selektivnim procesima protein/receptor biomolekularnog prepoznavanja, implicirajući makroskopsku kvantnu nelokalnost na biološkom ćelijskom nivou. (Bazična nelokalnost se može proširiti i na makroskopski kvantni nivo biološkog organizma na šta ukazuje makroskopska kvantna mikrotalasna rezonantna terapija akupunkturnog sistema.) Kvantna priroda ovih procesa ilustrovana je na primeru neradijativnih strukturnih prelaza, modelu kvantne dekoherencije i modelu rezonantnog prepoznavanja uz diskusiju implementirajućeg mehanizma elektronsko-konformacione sprege u ključ-brava uklapajućim konformacionim prelazima biomolekularnog prepoznavanja protein/supstrat. Na osnovu ovih prilaza u stanju smo da reprodukujemo kako egzistenciju i stabilnost (stacionarnih) polimernih konformacija tako i kratka vremena za kvantno -mehaničke procese u konformacionim prelazima u selektivnim procesima biomolekularnog prepoznavanja. Pošto ovi procesi dovode do dinamičke modifikacije više-elektronske hiperpovrši energija-stanje ćelijskog protein/receptor ansambalskog biomolekularnog makroskopskog kvantnog sistema, to otvara mogućnost razmatranja ćelijskog biomolekularnog prepoznavanja kao Hopfildove kvantno-holografske asocijativne neuronske mreže. Ovi prilazi mogu biti od fundamentalnog značaja za razumevanje bazičnih makroskopskih kvantno-holografskih Hopfildovih kontrolnih mehanizama morfogeneze i njihovog povratnog uticaja na ekspresiju genoma.

SUMMARY

Two unresolved issues of the (semi)classically addressed problems in molecular biophysics are unreasonably long time necessary for the change of biopolymer conformations and long-range directedness of selective biomolecular recognition processes.

This paper deals with several possible quantum approaches to solving these problems. The suggested qualitative scenario is sufficiently general and makes a good basis for a principled solving of the problem of biopolymer winding up into the native conformation at highly selective processes of protein/receptor biomolecural

recognition, implying macroscopic quantum non-locality at the biological cell level. (The basic non-locality can be spread to macroscopic quantum level of a biological organism also, which is suggested by macroscopic quantum microwave resonant therapy of acupuncture system). The quantum nature of these processes has been illustrated by the example of Non-Radiative Structural Transitions, the Model of Quantum Decoherence and the Resonant Recognition Model complete with the discussion on the implementing mechanism of electronic-conformational interactions in key-lock fitting conformational transitions of protein/substrate biomolecular recognition. Based on these transitions we can reproduce both the existence and stability of (stationary) polymer conformations and the short times for quantum-mechanical processes in conformational transitions in selective processes of biomolecular recognition. Since these processes lead to dynamic modification of many-electron hyper-surface energy-state of cell protein/receptor of ensemble biomolecular macroscopic quantum system, this creates possibilities to consider the cell biomolecular recognition as Hopfield-like quantum-holographic associative neuron network. These approaches can be of fundamental importance for understanding of basic macroscopic quantum-holographic Hopfield-like control meachnisms of morphogenesis and their backward influence on genome expression.