

Bose-Einstein condensation of tunnelling photons in the brain cortex as a mechanism of conscious action

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Abstract

Mind is supposed to be a macroscopic quantum wave governing the dynamics of the quantum coherent cytoskeletal protein system inside the cytoplasm of the brain cortical neurons. Its dynamical timescale is determined to be that of protein dynamics (~15ps) ruling out the possibility of avoiding thermalization since catalysis is accomplished via vibrationally assisted tunneling. The cytoskeletal protein conformational states are entangled into a whole (they are quantum coherent), and effect mediated by the propagation and condensation of evanescent (tunneling) photons emitted by the ordered water that forms coherent domains in its interaction with the local electromagnetic (EM) field. Since the protein conformations rely on its hydration shells the Bose-Einstein condensation of those evanescent photons will safely transmit quantum information between the water molecules and the protein hydration shells correlating the dynamics of the cytoskeletal proteins. Special attention is paid to tubulin C-termini that are highly flexible projections from the outer microtubule surface, which organize the cytoskeletal activity via interaction with MAP structural and MAP motor proteins. In order the quantum coherent state to be realized in timescales above the thermal fluctuations the water laser system must be pumped with energy. This can be the ATP derived metabolic energy delivered to microtubules as they interact with the motor proteins, actin filaments and from cytoskeletal bound kinases and phosphatases that release energy in their catalytic action. The motor proteins are hopping along the elastic microtubules (spending ATP), leading to microtubule (and tubulin domains) vibration and F-actin contraction leads to microtubule sliding and rotation (torque). Finally the chemical (ATP-released) energy, accumulated in the microtubule elastic (acoustic) vibrations can be gained by the water molecule laser system directly from the microtubule walls and used for coherent photon emission. The created evanescent photons have negative energy and are shown to be capable of realizing group velocity v_g faster than light velocity in vacuum c . Thus optical tachyons can be essential for brain functioning. The interplay between the proteins, ordered water and EM field is considered essential for life and consciousness.

Content

Abstract	1
On protein dynamical timescale and mind action	3
Protein conformations and hydration shells	3
Structured water in cells	5
Cellular water as a laser system	6
Spontaneous symmetry breaking and Goldstone modes	9
Water laser and energy pumping	12
Quantum mechanics in the cytoskeleton	16
Tubulin tails orchestrate MAP action	21
Bose-Einstein condensation of tunnelling photons	24
Biological high-temperature superconductivity	28
Tunnelling photons are optical tachyons	28
Tunnelling photons as a definition of life	32
Where is mind? – The hard problem	33
Outline	34
References	35

On protein dynamical timescale and mind action

Since proteins are dynamical structures capable of performing all the cellular activities essential for life and possess nanoscale dimensions (and therefore are governed by the weird laws of quantum mechanics) it is tentative to speculate that mind is possibly linked to subneuronal quantum coherent activities taking part in the neuronal cytoskeletons inside the brain cortex. GEORGIEV (2003a, 2003b, 2003c) determines the dynamical timescale of mind to be the dynamical timescale of protein dynamics (10-15ps). Already GEORGIEV (2002) has shown that protein catalysis depends on *vibrationally assisted tunnelling* and possibly mind uses vibrational multidimensional tunnelling in promoting neuromediator release (exocytosis). Thus because the catalysis depends on thermal 'breathing' of proteins the coherence must be enough long to utilize the thermal fluctuations. Thus it is demanded that the coherence timescale must be comparable with the timescale of mind action (and therefore protein dynamics) in order mind to be capable to make use of the quantum effects (superpositions, entanglement, non-computability). We must conclude that any model relying on faster quantum coherent phenomena cannot be considered as 'substrate' for mind action that is why the superradiance model in microtubules developed by JIBU ET AL. (1994) is ruled out!

Mind controls protein catalytic action, which has dynamical timescale 10-15 picoseconds. Since protein catalysis utilizes protein thermal 'breathing' mind cannot rely on faster quantum coherent processes and cannot escape thermalization!

Protein conformations and hydration shells

Protein dynamics is very sensitive to slight environmental changes (temperature, pH, ions etc.) but most pronounced effect on proper protein folding have the hydration shells of proteins (i.e. the water molecules surrounding them). LEVITT & SHARON (1988) showed that simulation of the molecular dynamics of a small protein (bovine pancreatic trypsin inhibitor, BPTI) is much more realistic when water molecules were included than when in vacuum: (i) the time-averaged structure was much more like that observed in high-resolution x-ray studies, (ii) the amplitudes of atomic vibration in solution were smaller, (iii) fewer incorrect hydrogen bonds were formed and (iv) there is internal motion of proteins at picosecond timescale. In their calculation they used a simple atom-centered potential and classical mechanics to simulate a trajectory lasting 210 ps, showing that inclusion of solvent improves the agreement with experiment and gives insight into protein-water interactions. In solution, the time-averaged protein structure is much more like that observed in high-resolution x-ray studies of BPTI (deviation is 1.1 Å as opposed to 1.9 Å in vacuum) and there are fewer incorrect hydrogen bonds (1 as opposed to 14 in vacuum). A shell of water molecules with higher than normal density (1.25 g/ml) and reduced rotational freedom is found close to the protein surface!

The most dramatic effect of the protein is to more than double the number of water molecules in contact with polar and nonpolar surface relative to that expected from the

accessible surface area. This clustering of water molecules close to the protein surface increases to 1.25 g/cm³ the water density within 3-4.25 Å of the protein surface, mainly due to the large number of water molecules that are 3.75 Å from nonpolar atoms. Such increased density, which is a major effect involving about 150 water molecules (0.42 g of water per g of BPTI protein), has been observed at a flat nonpolar surface and should also be visible in well-refined electron-density difference maps of protein crystals containing sufficient water. The density calculated from the Voronoi polyhedra volume per water molecule shows that although water molecules are clustered perpendicular to the protein surface, they are not brought closer together parallel to the surface.

For a more detailed analysis of the way the protein changes the properties of the surrounding water molecules, LEVITT & SHARON (1988) divided the water molecules into four classes according to their distance from the protein surface. More than half the water molecules are in class IV. These water molecules, which are further than 10 Å from the nearest protein atom, have properties that are indistinguishable from those calculated for pure water. Their diffusion coefficient of 0.24 Å²/ps agrees with the experimental diffusion coefficient of water (0.26 Å²/ps at 300 K) and is much smaller than the value of 0.45 Å²/ps found in a simulation of trypsin in solution. The 107 water molecules in class I in the performed simulation with BPTI, which are in contact with polar groups, are most affected by the protein. These water molecules interact strongly with the protein and, as a consequence, have slightly more strained bonds and angles (by 0.39 and 0.04 kcal/mol, respectively) and much less favourable interactions with other water molecules (by 11.6 kcal/mol). Because they interact so favourably with the protein (-14.02 kcal/mol), class I water molecules have lower binding energies than bulk water (-1.9 kcal/mol). The 124 water molecules in class II, which are all in contact with nonpolar groups, have their diffusive motion restricted almost as much as those in class I. Class II water molecules do not interact very strongly with the protein (- 2.33 kcal/mol) and their binding energies are only slightly lower than in bulk water (- 0.27 kcal/mol). The lowered binding energy of water molecules in classes I and II is offset by a decrease in the entropy associated with their restricted translation and rotation. This can be quantified by comparing the distributions of water position and orientation with that expected for a completely unstructured solvent. The entropic contribution to the Gibbs energy is

$$(1) \quad -kT \sum n_i \ln \rho_i$$

where kT is Boltzmann's constant times absolute temperature, n_i is the observed number, and ρ_i is the ratio of n_i to the number expected for a uniform distribution. For the translational entropy, must be compared the actual number of water molecules found in radial shells with that expected from the accessible surface; this gives a total Gibbs energy change of 10 kcal/mol for the polar surface and 31 kcal/mol for the nonpolar surface. The distribution of the angle between a water O-H bond and the normal to the protein surface shows that for the polar surface, angles of 0° and 105° are strongly preferred, which gives a total Gibbs energy change of 74 kcal/mol, whereas for the nonpolar surface, the preferred angle is 70°, which gives a change of 17 kcal/mol. Adding the two contributions gives a Gibbs energy change per water molecule of 0.8 kcal/mol for

class I and 0.4 kcal/mol for class II. The binding Gibbs energy, which includes the entropic terms, indicates that whereas water molecules bind favourably to polar atoms (by - 1.08 kcal/ mol), their interaction with nonpolar atoms is slightly unfavourable (by 0.12 kcal/mol). LEVITT & SHARON (1988) showed that the water molecules are very mobile and move from class to class during the simulation. Because class I and II water molecules are in adjacent patches on the protein surface, the average time that a water molecule spends in each class is short, 4 ps for class I and 1 ps for class II (10 tightly bound water molecules remain in class I for the entire 100 ps period analyzed). Water molecules keep on leaving and then returning to a given class so that after 100 ps, 34% of the molecules originally in class I are still in it, whereas the corresponding number for class II is 12%. Although any structure associated with class II water molecules will be short-lived, it will have a high probability of being reformed again by the same water molecules.

Picosecond dynamics at the protein hydration shell interface determines the conformational transitions of the proteins. The dynamical water molecule ordering is crucial for proper protein function!

Structured water in cells

NMR evidence (COPE, 1975; HAZELWOOD ET AL., 1969; 1974) strongly indicates that cell water possesses more structure than liquid water, and that much of the Na⁺ and K⁺ in the cell is not free in aqueous solution, but is associated with charged sites on macromolecules (COPE, 1975). Therefore, complexed Na⁺ and K⁺ cations have been compared to valence electrons in solid conductors and free cations to conduction band electrons. With activation energy barriers and solid-liquid interfaces present in the cell, the liquid state free-cation model of the cell is clearly not applicable. A model based on structured water and associated cations is compatible with thermodynamic evidence.

A substantial part of water molecules in the cell is in the form of hydration water bound to various macromolecules. Yet another large portion exists in the so-called vicinal water form with several exotic properties. Experimental evidence shows that it freezes when the temperature is lowered beyond -70° C (KUNTZ & KAUZMANN, 1974). It is a poor solvent for electrolytes but a good one for non-electrolytes, i.e. it behaves as a non-polar solvent. It has a higher viscosity than normal water and exhibits dynamic correlations between individual molecules (COOKE & KUNTZ, 1974; FRANKS, 1975). Of great interest is the fact that most of the vicinal water surrounds the cytoskeleton. MASCARENHAS (1974) demonstrated electret properties of bound water with attendant non-linearity, hysteresis effects and long relaxation times on the order of 1s and activation energies of about 7.0-9.0 kcal/mol have been measured, all of which would tend to indicate the presence of long-range dipolar order leading to the formation of internal electric fields or perhaps collective oscillations of electric fields (DEL GIUDICE ET AL., 1986a).

The microtubule cavities and the vicinal water have been modelled in the framework of the quantum field theory (QFT) revealing two important phenomena that could take place in the cell: (i) *collective photon emission* by water molecules (JIBU & YASUE, 1997) and

(ii) *Rabi coupling* between the water molecules inside the cavity regions near the microtubule walls and the tubulins that build up the microtubule walls (MAVROMATOS & NANOPOULOS, 1997; 1998; MAVROMATOS, 2000; MAVROMATOS ET AL., 2000, 2002).

According to GALLO ET AL. (2000) there is substantial degree of slowing down of water when confined in the proximity of a polar surface. Particularly significant in this context are the indications of a transition of adsorbed water to a *glassy state*, which is supposedly driven by the protein surface. Simulation studies of water close to the surface of a protein evidenced a typical spectral glassy anomaly, the so-called boson peak, which is related to protein-solvent coupling. The boson peak is an excess of vibrational modes present in many glasses at frequencies around 1THz. When this glassy anomaly appears in a liquid phase, it is usually considered as a precursor to the actual glass transition.

GALLO ET AL. (2000) performed a shell analysis of the dynamic behaviour of water confined in a cylindrical silica pore (with radius $\sim 2\text{nm}$) at the higher hydration levels, and have found in these cases that the contribution to the boson peak comes only from water molecules, which are not in the first layer! This fact, and the fact that the silica pore is a rigid framework, is an indication that the boson peak is a feature of liquid water, which is not induced by the substrate dynamics (the silica pore). Boson peak for the system water/Vycor glass pore has been detected recently at energies around 3.5meV. This is exactly the energy ε between the two principal eigenstates of the water molecule, which is roughly approximated by MAVROMATOS & NANOPOULOS (1998) to be 4meV.

Water inside cells is structured! It is in spin-glass state and manifests boson peak at 3.5 meV, which is related to the protein-solvent coupling! The boson peak is a feature of the liquid water molecules that are not in the first layer immediately adjacent to protein and describes a novel spin glass state. Since the hydration shell of the protein is composed from several water molecule layers and the first layer is rigid (not easily mobile) we can be sure that protein conformational dynamics is mostly affected by the spin glass state water that exhibits long-range ordering and quantum coherent dynamics.

Cellular water as a laser system

JIBU ET AL. (1994, 1997) describe the water around the cytoskeleton and in the perimembranous regions using the *quantum field theory* (QFT). Here we will describe briefly their approach. Let us denote the spatial region surrounding the cytoskeleton by V . After introduction of a Cartesian system of coordinates $Oxyz$, any point in the region V can be labelled by giving its coordinates $r = (x, y, z)$. We will consider the ideal case in which the existence of molecules other than those of water can be neglected. Indeed this could be the case because Na^+ and K^+ ions do not disturb the dynamically ordered water since their diameter is comparable with the diameter of the water molecules or smaller. The only relevant ion that has diameter greater than the diameter of the water molecules is the chloride ion Cl^- so it can suppress the dynamical order of water molecules. However its intracellular concentration is usually extremely small (it should be noted

however that its intraneuronal concentration is increased under anaesthetic binding to GABA receptors and anaesthetic action can be therefore explained via interfering with the quantum brain dynamics!). Considering the ideal case in which we describe only water molecules it is most likely that the density of water in the region V remains almost constant. Therefore, we may be allowed to fix the total number of water molecules in the region V, say N.

Let us take a look at a typical water molecule, say the j th water molecule. Here, j running from 1 to N denotes the fictitious number labelling the N water molecules in question. Its position is given by coordinates $r^j = (x^j, y^j, z^j)$. From a physical point of view, a water molecule has a constant electric dipole, and so it can be seen as a quantum mechanical spinning top with an electric dipole moment. The average moment of inertia and electric dipole moment of a water molecule are estimated to be $I=2m_p d^2$ with $d \sim 0.82 \text{ \AA}$ and $\mu=2e_p P$ with $P \sim 0.2 \text{ \AA}$, respectively. Here, m_p denotes the proton mass and e_p the proton charge. Due to the electric dipole moment μ , the water molecule interacts strongly with the quantized electromagnetic field in the spatial region V. Although the water molecule has as many energy eigenstates as a quantum mechanical spinning top and so it can exchange energy between the quantized electromagnetic field in many different values, it was revealed that the processes in which only the two principal energy eigenstates take part in the energy exchange are dominant (DEL GIUDICE ET AL., 1988).

Then, one sees immediately that the quantum dynamics of the j th water molecule can be well described by a spin variable $s^j=1/2\sigma$, where $\sigma=(\sigma_x, \sigma_y, \sigma_z)$ and σ_x 's are Pauli spin matrices denoting the three components of the angular momentum for spin $1/2$. Let ε be the energy difference between the two principal energy eigenstates of the water molecule. Then, the Hamiltonian governing the quantum dynamics of the j th water molecule is given by εs_z^j , and so the total Hamiltonian for N water molecules becomes

$$(2) \quad H_{WM} = \varepsilon \sum_{j=1}^N s_z^j$$

Two energy eigenvalues of the former Hamiltonian are $-1/2 \varepsilon$ and $1/2 \varepsilon$ reflecting the fact that only the two principal energy eigenstates with energy difference ε are taken into account.

Now, let us consider the quantized electromagnetic field in the spatial region V. It is convenient to describe the quantized electromagnetic field in terms of an electric field operator $E = E(r, t)$. Let us assume for simplicity that the electric field is linearly polarized, obtaining $E = eE$, where, e is a constant vector of unit length pointing in the direction of linear polarization. Then, the quantized electromagnetic field in question comes to be well described by a scalar electric field $E = E(r, t)$ governed by the usual Hamiltonian

$$(3) \quad H_{EM} = \frac{1}{2} \int_V E^2 d^3r .$$

Next, we take the interaction between the quantized electromagnetic field and the totality of water molecules by which they can exchange energy in terms of creation and annihilation of photons. Let us divide the electric field operator into positive and negative frequency parts

$$(4) \quad E = E^+ + E^-$$

Then, the interaction Hamiltonian of the quantized electromagnetic field and the totality of water molecules becomes

$$(5) \quad H_I = -\mu \sum_{j=1}^N \left\{ E^-(r^j, t) s_-^j + s_+^j E^+(r^j, t) \right\},$$

where

$$(6) \quad s_{\pm}^j = s_x^j \pm i s_y^j$$

The total Hamiltonian governing the quantum dynamics of the electromagnetic field, the dipolar vibrational field of water molecules, and their interaction is given by

$$(7) \quad H = H_{EM} + H_{WM} + H_I$$

Since the spatial region V in the vicinity of a cell may be considered as a cavity for the electromagnetic wave, it is convenient to introduce the normal mode expansion of the electric field operator $E=E^+ + E^-$, obtaining

$$(8) \quad E^{\pm}(r, t) = \sum_k E_k^{\pm}(t) \exp[\pm i(k \cdot r - \omega_k t)]$$

Here, ω_k , denotes the proper angular frequency of the normal mode with wave vector k. We are mainly interested in the ordered collective behavior among the water molecules and the quantized electromagnetic field in the cavity region V. Let us hence introduce collective dynamical variables S_k^{\pm} and S for water molecules by

$$(9) \quad S_k^{\pm}(t) \equiv \sum_{j=1}^N s_{\pm}^j(t) \exp[\pm i(k \cdot r^j - \omega_k t)]$$

$$(10) \quad S \equiv \sum_{j=1}^N s_z^j$$

Then, the total Hamiltonian from Eq. (7) becomes

$$(11) \quad H = H_{EM} + \varepsilon S - \mu \sum_k (E_k^- S_k^- + S_k^+ E_k^+)$$

This total Hamiltonian for the system of N water molecules and the quantized electromagnetic field in the region V inside the cell is essentially of the same form as Dicke's Hamiltonian for the laser system (DICKE, 1954). Therefore, it can be expected that water molecules in the region V manifest a laser-like coherent optical activity, that is, the water laser if energy above a certain threshold is supplied!

Spontaneous symmetry breaking and Goldstone modes

The interaction between the water dynamical system and the local electromagnetic field is considered to be crucial for quantum brain function because the electric impulses input sensory information! GEORGIEV (2003d) has calculated the electric intensity inside neurons to be 1-10 V/m and the magnetic flux density to be 10^{-10} - 10^{-7} T and suggested that there must be mechanism for translation of the entering the brain cortex electrophysiological information down to the molecular level into quantum coherent states. Since the electric field intensity is small it suggested that it interacts with *electrically ordered molecules forming giant dipoles!* This is so because the interaction energy U is proportional to the electric dipole moment p and the electric intensity E ($U = -p \cdot \vec{E}$).

JIBU ET AL. (1997) explain the macroscopic water molecule dipole ordering with reference to well known in the QFT phenomenon called *spontaneous symmetry breaking* (SSB) that leads to generation of *Nambu-Goldstone bosons*, which are long-range coherence mediating quanta. Crucial condition for the generation of those Nambu-Goldstone modes is the interaction between the biological water and the quantized electromagnetic (EM) field!

A physical inspection of the form of the total Hamiltonian from Eq. (11) reveals that it manifests a dynamical symmetry property not evident in the ground state and so the resulting quantum dynamics is known to involve certain long-range order creating phenomena due to SSB (RICCIARDI & UMEZAWA, 1967; STUART ET AL., 1978, 1979; UMEZAWA, 1993; JIBU & YASUE, 1995). The spatial dimension of this long-range order, that is, the coherence length l_c , can be estimated to be inversely proportional to the energy difference, obtaining $l_c \sim 50 \mu\text{m}$. Among those long-range order creating phenomena we may find a specific one in which the collective dynamics of the majority or water molecules in the spatial region V of the size $< 50 \mu\text{m}$ in length can give rise to cooperative interaction with the imposed external electromagnetic field. Such a spatial region is called a dynamically ordered region of water.

Let us investigate the collective dynamics of water molecules in the region V starting from the total Hamiltonian (Eq. (11)). We want to see the dynamical symmetry inherent in the quantum dynamics governed by the total Hamiltonian (Eq. (11)). For this it is convenient to introduce the canonical variables or the electromagnetic field through the relation:

$$(12) \quad P_k(t) = \sqrt{\frac{\hbar\omega_k}{2}} i(E_k^- - E_k^+)$$

$$(13) \quad Q_k(t) = \sqrt{\frac{\hbar}{2\omega_k}} i(E_k^- + E_k^+).$$

Those canonical variables satisfy the canonical commutation relations:

$$(14) \quad [P_k(t), Q_h(t)] = -i\hbar\delta_{kh}$$

$$(15) \quad [P_k(t), P_h(t)] = [Q_k(t), Q_h(t)] = 0$$

$$(16) \quad P_k^*(t) = P_{-k}(t)$$

$$(17) \quad Q_k^*(t) = Q_{-k}(t)$$

Here, A^* denotes the adjoint operator of A .

In terms of the canonical variables, the total Hamiltonian (Eq. (11)) becomes:

$$(18) \quad H = \frac{1}{2} \sum_k \{P_k^*(t)P_k(t) + \omega_k^2 Q_k^*(t)Q_k(t)\} + \varepsilon \sum_{j=1}^N s_z^j - \sqrt{\frac{2}{\hbar}} \mu \sum_{j=1}^N \sum_k \left\{ \sqrt{\omega_k} Q_k(t) s_x^j - \frac{1}{\sqrt{\omega_k}} P_k(t) s_y^j \right\}$$

which is identical with Takahashi's Hamiltonian used to investigate the distributed memory mechanism in the brain (STUART ET AL., 1979). Thus, it is seen that this total Hamiltonian, governing the quantum dynamics of electromagnetic field and the electric dipole field of water molecules interacting with each other, remains invariant under the transformation of canonical variables given by

$$(19) \quad Q'_k(t) = Q_k(t) \cos \theta - \frac{1}{\omega_k} P_k(t) \sin \theta$$

$$(20) \quad P'_{-k}(t) = \omega_k Q_k(t) \sin \theta + P_{-k}(t) \cos \theta$$

$$(21) \quad s_x'^j(t) = s_x^j(t) \cos \theta + s_y^j(t) \sin \theta$$

$$(22) \quad s_y'^j(t) = -s_x^j(t) \sin \theta + s_y^j(t) \cos \theta$$

$$(23) \quad s_z'^j(t) = s_z^j(t)$$

for a continuous parameter θ . This transformation corresponds to a continuous rotation around the third axis and can be regarded as belonging to a continuous group or rotation SO(2) in the two-dimensional space.

Now let us look for a time-independent solution to the Heisenberg equations for canonical variables in order to investigate the dynamically ordered state of the system of electromagnetic field and water molecules in the region V. The Heisenberg equations are given by

$$(24) \quad \frac{dQ_k(t)}{dt} = \frac{1}{\hbar} [Q_k(t), H]$$

$$(25) \quad \frac{dP_k(t)}{dt} = \frac{1}{\hbar} [P_k(t), H]$$

$$(26) \quad \frac{ds_x^j(t)}{dt} = \frac{1}{\hbar} [s_x^j(t), H]$$

$$(27) \quad \frac{ds_y^j(t)}{dt} = \frac{1}{\hbar} [s_y^j(t), H]$$

$$(28) \quad \frac{ds_z^j(t)}{dt} = \frac{1}{\hbar} [s_z^j(t), H]$$

and the time-independent solution is obtained as follows:

$$(29) \quad P_k(t) \equiv 0$$

$$(30) \quad Q_k(t) \equiv Q_k^0$$

$$(31) \quad s_x^j(t) \equiv u$$

$$(32) \quad s_y^j(t) \equiv 0$$

$$(33) \quad s_z^j(t) \equiv w$$

Here, Q_k^0 is a constant taking a different value for a different value of wave number k, and u and w are also constants. Each spin variable $s^j = (s_x^j, s_y^j, s_z^j)$ describing the jth water molecule is found to be aligned in one and the same direction pointed by a constant vector (u,0,w). Such a *long-range alignment of spin variables* is nothing but a manifestation of a dynamical order of the system of the quantized electromagnetic field and water molecules. Namely, there exists a long-range order so that the spin variable of water molecules in the region V is systematized globally to realize the uniform configuration.

It is interesting to see that this time-independent solution, representing a dynamically ordered state of the system of the quantized electromagnetic field and water molecules in the region V , is no longer invariant under the continuous transformation of canonical variables Eqs. (19)-(23). The aligned direction is transformed into another direction under such a continuous rotation around the third axis. Thus, a strange situation is realized in which the total Hamiltonian, governing the quantum dynamics of canonical variables, is invariant under a certain compact continuous transformation, whereas it admits to a stable time-independent solution which is not invariant under the same transformation. In quantum field theory, such a situation is known as spontaneous symmetry breaking, and several interesting quantum phenomena are known to emerge (UMEZAWA, 1993; JIBU & YASUE, 1995). Namely, the *Nambu-Goldstone theorem* in QFT asserts that in such a situation of spontaneous symmetry breaking cooperative excitations of the symmetry attributes appear as long-range correlation waves and behave as bosons (i.e. quanta obeying Bose-Einstein statistics) whose minimum energy is zero (UMEZAWA, 1993; JIBU & YASUE, 1995). They are called *Goldstone bosons* or *Goldstone modes*. Since the Goldstone boson manifests a continuous energy spectrum above zero, it is also called a *gapless mode* or *massless boson* because there exists no energy gap in the spectrum.

In the actual case of the system of the quantized electromagnetic field and water molecules, aligned uniformly in the dynamically ordered state of spontaneous symmetry breaking type are the spin variables standing for electric dipoles of water molecules (JIBU ET AL., 1994; HAGAN ET AL., 1994). Goldstone bosons created there with almost zero energy requirement are nothing but quanta of long-range correlation waves of aligned electric dipoles. They are coherent electric dipolar waves called '*soft polaritons*' in the case of a general ferroelectric material created by even a very weak perturbation and propagate over a long distance up to the coherence length of about 50 μm .

The interaction between the water molecules and the local EM field in neurons generates Nambu-Goldstone bosons, which are quanta of long-range correlation waves of aligned electric dipoles! Since the hydration shells are coupled to the protein conformational states and the picosecond protein dynamics it is likely that the EM field carried electrophysiological information can directly affect cytoskeletal protein function (i.e. input information to the neuronal cytoskeleton)!

Water laser and energy pumping

Among the long-range order creating phenomena resulting from the interaction between the water dipoles and the local electromagnetic field we may find a specific one in which the collective dynamics of the water electric dipole field in the spatial region of linear dimension up to 50 μm can give rise to cooperative emission of coherent photons given energy by certain systems external to the quantum system of electromagnetic field and water electric dipole field. JIBU ET AL. (1994) suggested that mind could operate via conversion of incoherent energy into emission of coherent photons, a process known as *superradiance*. Since the superradiance operates at 10^{-14} s and escapes thermalization it is

ruled out to mediate long-range coherence between proteins, since their dynamical action is in the order 10^{-11} s. Thus in order to understand how mind operates we should investigate the case in which the collective dynamics has characteristic time comparable to that of thermally disordered dynamics and suffers from thermal fluctuation and dissipation. It will be shown that the laser-like emission of coherent photons can be realized even in such a case with thermal noise and loss provided that the electric dipoles of protein molecules of the microtubule manifest a certain collective dynamics sufficient to ‘pump up’ the water electric dipole field. JIBU & YASUE (1997) noted that in such case the *Heisenberg-Langevin equation* for water laser system requiring pumping could be of crucial importance. If we take into account the thermal interaction with the disordered external systems at body temperature T, the Heisenberg equations of motion must be replaced by either the Heisenberg-Langevin equation or the Schrödinger-Langevin equation (YASUE 1976, 1977, 1978a, 1978b, 1979).

First we will assume for simplicity that only one eigenmode with a specific eigenvalue; say ω_{λ_0} resonates with the energy difference ε between the two principal energy eigenstates. Namely we have $\varepsilon = \hbar\omega_{\lambda_0}$, and all the other eigenmodes are neglected. In the conventional laser theory, this is known as a single mode laser. Since we have only one eigenmode with eigenvalue ω_{λ_0} we may omit all the eigenvector indices of the dynamical variables. The three collective dynamical variables, S and S^\pm , for water electric dipole field and the two variables, a^* and a, for electromagnetic field are given by the *Heisenberg-Langevin equations*:

$$(34) \quad \frac{dS}{dt} = -\gamma(S - S_\infty) - i\frac{f}{\hbar}(a^*S^- - S^+a) + \eta$$

$$(35) \quad \frac{dS^+}{dt} = i\frac{2f}{\hbar}Sa^* - \gamma_0S^+ + i\frac{\varepsilon}{\hbar}S^+ + \eta^+$$

$$(36) \quad \frac{dS^-}{dt} = -i\frac{2f}{\hbar}Sa - \gamma_0S^- - i\frac{\varepsilon}{\hbar}S^- + \eta^-$$

$$(37) \quad \frac{da^*}{dt} = -\gamma_{EM}a^* - i\frac{2\pi\varepsilon f}{\hbar V}S^+ + \eta^*_{EM}$$

$$(38) \quad \frac{da}{dt} = -\gamma_{EM}a + i\frac{2\pi\varepsilon f}{\hbar V}S^- + \eta_{EM}$$

Here, γ and γ_0 are damping coefficients for the water electric dipole field, γ_{EM} is a damping coefficient for the electromagnetic field, η and η^\pm are thermal fluctuations for the water electric dipole field, η^*_{EM} and η_{EM} are thermal fluctuations for the electromagnetic field, and S_∞ is a parameter designating the rate of pumping due to the interaction with a certain collective dynamics of the electric dipoles of protein molecules of the microtubule. In this case, the collective dynamical variables of water electric dipole field can be deleted in the adiabatic approximation, and the Heisenberg-Langevin

equations Eqs. (34)-(38) can be reduced approximately to the Heisenberg-Langevin equations for the quantized electromagnetic field, that is

$$(39) \quad \frac{da^*}{dt} = \alpha a^* - \beta a a^* a^* + \xi^*$$

$$(40) \quad \frac{da}{dt} = \alpha a - \beta a^* a a + \xi.$$

Here, α and β are constants given by

$$(41) \quad \alpha = -\gamma_{EM} + \frac{4\pi\epsilon f^2 S_\infty}{\hbar^2 V \gamma_0}$$

$$(42) \quad \beta = \frac{16\pi\epsilon f^4 S_\infty}{\hbar^4 V \gamma_0^2 \gamma}$$

and ξ^* and ξ are effective thermal fluctuations for the quantized electromagnetic field.

The Heisenberg-Langevin equations Eqs. (39)-(40) governing the collective dynamics of the quantized electromagnetic field in the region V can be reduced to the Langevin equation if Glauber's coherent state representation is adopted (KLAUDER & SUDARSHAN, 1968; JIBU & YASUE, 1997):

$$(43) \quad \frac{dZ}{dt} = \alpha Z - \beta \bar{Z} Z^2 + B.$$

Here, $Z = Z(t)$ is a Markov process in the complex plane denoting the complex eigenvalue of the electromagnetic field operator a , $B = B(t)$ is a complex Gaussian white noise representing the thermal fluctuation of the quantized electromagnetic field and \bar{z} denotes the complex conjugate of a complex number z . The mean and variance of the complex Gaussian white noise are given by

$$(44) \quad \langle B(t) \rangle = 0$$

$$(45) \quad \langle \overline{B(t)} B(s) \rangle = 2D \delta(t-s)$$

respectively, where $\langle \rangle$ indicates the expectation value, $\delta(t)$ is the Dirac delta function and D is a diffusion constant given by

$$(46) \quad D = \frac{M\pi^2\varepsilon^2 f^2 \gamma_0}{2\gamma_{EM}^2 \hbar^2 V^2} + \frac{2\pi \gamma_{EM} \varepsilon}{V} \left(\frac{1}{\exp\left(\frac{\varepsilon}{k_B T}\right) - 1} + \frac{1}{2} \right)$$

with k_B the Boltzmann constant.

The Langevin equation Eq. (43) is equivalent to the Fokker-Planck equation

$$(47) \quad \frac{\partial}{\partial t} f = -\frac{\partial}{\partial z} \left[(\alpha z - \beta \bar{z} z^2) f \right] + D \frac{\partial^2}{\partial z \partial \bar{z}} f$$

for the probability distribution function $f = f(z, \bar{z}, t)$ of the complex Markov process $Z(t)$. The stationary solution of the Fokker-Planck equation Eq. (47) can be obtained immediately;

$$(48) \quad f = C \exp \left[\frac{2\alpha \bar{z} z - \beta (\bar{z} z)^2}{2D} \right]$$

where C is a normalization constant such that

$$(49) \quad \iint f(z, \bar{z}, t) dz d\bar{z} = 1$$

holds.

This stationary solution Eq. (48) of the Fokker-Planck equation Eq. (47) is nothing but the unique equilibrium probability distribution function of the Markov process $Z(t)$. By the explicit form given by Eq. (48), it is immediately clear that the characteristics of the equilibrium probability distribution of the Markov process $Z(t)$, denoting the dynamics of the quantized electromagnetic field in the region V , depend sensitively on the rate of pumping S_∞ provided by the dynamics of electric dipoles of the microtubule proteins. Namely for smaller values of S_∞ such that $\alpha < 0$, the most probable value for the intensity of the electromagnetic field $I = \sqrt{Z\bar{Z}}$ vanishes, while it becomes nonvanishing for larger values of S_∞ such that $\alpha > 0$, obtaining

$$(50) \quad I = \sqrt{\frac{\alpha}{\beta}}.$$

JIBU & YASUE (1997) have shown that the collective dynamics of the quantum system of electromagnetic field and water electric dipole field in the region V manifests a long-range cooperative phenomenon of photon emission even if the thermal fluctuation and dissipation are taken into account. Excitation of the quantized electromagnetic field, that is, emission of photons in the region V is induced by the interaction with the dynamics of electric dipoles of tubulins if the pumping rate S_∞ exceeds the determined above threshold value,

$$(51) \quad S_\infty > \frac{\hbar^2 V \gamma_0 \gamma_{EM}}{4\pi\epsilon f^2}$$

It is therefore interesting to find out a specific ‘pumping’ mechanism that can be safely realized within neurons by cytoskeletal protein dynamics.

Quantum mechanics in the cytoskeleton

The cytoplasmic structural and dynamical organization of cells is due to the presence of networks of interconnected protein polymers, referred to as the *cytoskeleton*. The cytoskeleton consists of microtubules, actin microfilaments, intermediate filaments and an organizing complex, the centrosome with its chief component the centriole, built from two bundles of microtubules in a separated T-shape.

Microtubules are hollow cylindrical tubes, of about 25 nm in diameter on the outside and 14 nm on the inside, whose walls are polymerized arrays of protein subunits. Their lengths may range from tens of nanometers during early assembly, to possible centimeters in nerve axons within large animals. The protein subunits assemble in longitudinal strings called protofilaments, 13 parallel protofilaments laterally align to form the hollow tubules. The protein subunits are “peanut” shaped dimers, which in turn consist of two globular proteins, monomers known as α - and β - tubulin. The α - and β -tubulin monomers are similar molecules with identical orientation within protofilaments and tubule walls. In the polymerized state of the MT, one monomer consists of 40% α -helix, 31% β -sheet and 29% random coil. Each monomer consists of about 500 aminoacids, is about 4nm x 4nm x 4nm and has a local polarity.

The *centrosomal microtubules* are unstable and undergo intense dynamics. Much of the dynamic nature of microtubules is attributed to regulated growth and shrinkage of the polymer plus ends (dynamic instability) or to the addition of subunits at the plus end while they are simultaneously lost from the minus end (treadmilling). However in neurons the microtubule severing by specific enzyme called *katanin* (QUARMBY, 2000) is important for the production of *non-centrosomal microtubules*, which are stable and thus good candidate for quantum computation. In neurons, a large number of non-centrosomal microtubules are required for the growth and maintenance of neuronal processes (AHMAD ET AL., 1999). Injection of an anti-katanin antibody into neurons leads to an accumulation of centrosomal microtubules and a loss of neuronal processes, which indicates that *centrosomal katanin*, is important for the production of non-centrosomal

microtubules primarily through severing of the microtubules near the centrosome. In the neurons the minus end might be capped, which would allow the persistence of centrosome-free microtubules (RODIONOV ET AL., 1999).

HATORI ET AL., 2001 have shown that *actin filaments* (F-actin) sustain magnetic coherence in muscle contraction, so it is not surprising that in neurons actin filaments could behave in similar manner. MATUS (1999; 2000) reports that actin based plasticity is essential for dendritic spine reorganization. BARBAYANNIS ET AL. (1998) report that sufferers from Williams syndrome exhibit mental retardation and a defect in visio-spacial constructive cognition - the ability to integrate individual objects into whole picture. One copy of the gene encoding LIM-kinase1 (LIMK1) has been lost from genomes of these patients. LIMK1 is expressed in high concentrations in neurons and regulates the structure of the actin cytoskeleton. So it is interesting to explore the possibility for microtubule <-> actin filament interaction and transfer of quantum information.

HOLMES ET AL., (1990) have found that F-actin can be viewed either as a *left-handed single helix* with a rise per monomer of 27.5 Å and 13 subunits that repeat after six turns or as a *right-handed double helix* with a rise per monomer on each helix strand of 55 Å and a repeat every 72 nm. The maximum diameter of the filament varies between 90 Å and 95 Å. FUCHS & KARAKESISOGLOU (2001) show that the actin filaments are attached to microtubules via cross-linking proteins called *plakins*. The plakins are family of sequence-related cross-linker proteins that include plectins, the bullous pemphigoid antigen-1 proteins (BPAG1s), ACF7 (referred to as kakapo in lower eukaryotes), desmoplakin, envoplakin, and periplakin. Plakins are enormous (200-700 kD) proteins that anchor cytoskeletal networks to each other and/or to cellular structures such as adhesive junctions. The cross-linking between the microtubules, intermediary filaments (IFs) and actin allows for rapid communication (informational transfer) via solitons, a possibility for microtubules to drive the self-organization (assembly/disassembly) of the cytoskeleton.

JAROSCH & FUCHS (1975); SCHULZ & JAROSCH (1980); JAROSCH & FOISSNER (1982); JAROSCH (1986a; 1986b; 1991) have described actin-MT interactions which suggest that (i) contractile actin filaments are spirally wound around microtubules, (ii) coordinated contraction of the actin filaments imparts a rotational torque to MT, somewhat like a spinning top, (iii) actin filaments wound in opposite directions on the same MT can cause rotational oscillations of the MT. Thus JAROSCH (1986a; 1986b; 1991) provides us with a picture of a dynamic cytoplasmic network in which the cytoskeleton may be twisting back and forth, even *rocking-and-rolling!* Perturbation of any part of such a tensegrity network could have dynamic consequences throughout its domain. Transient changes in *tension*, *compression*, or *oscillatory rhythm* caused by a variety of factors would be detectable and possibly amplified throughout the cytoskeleton.

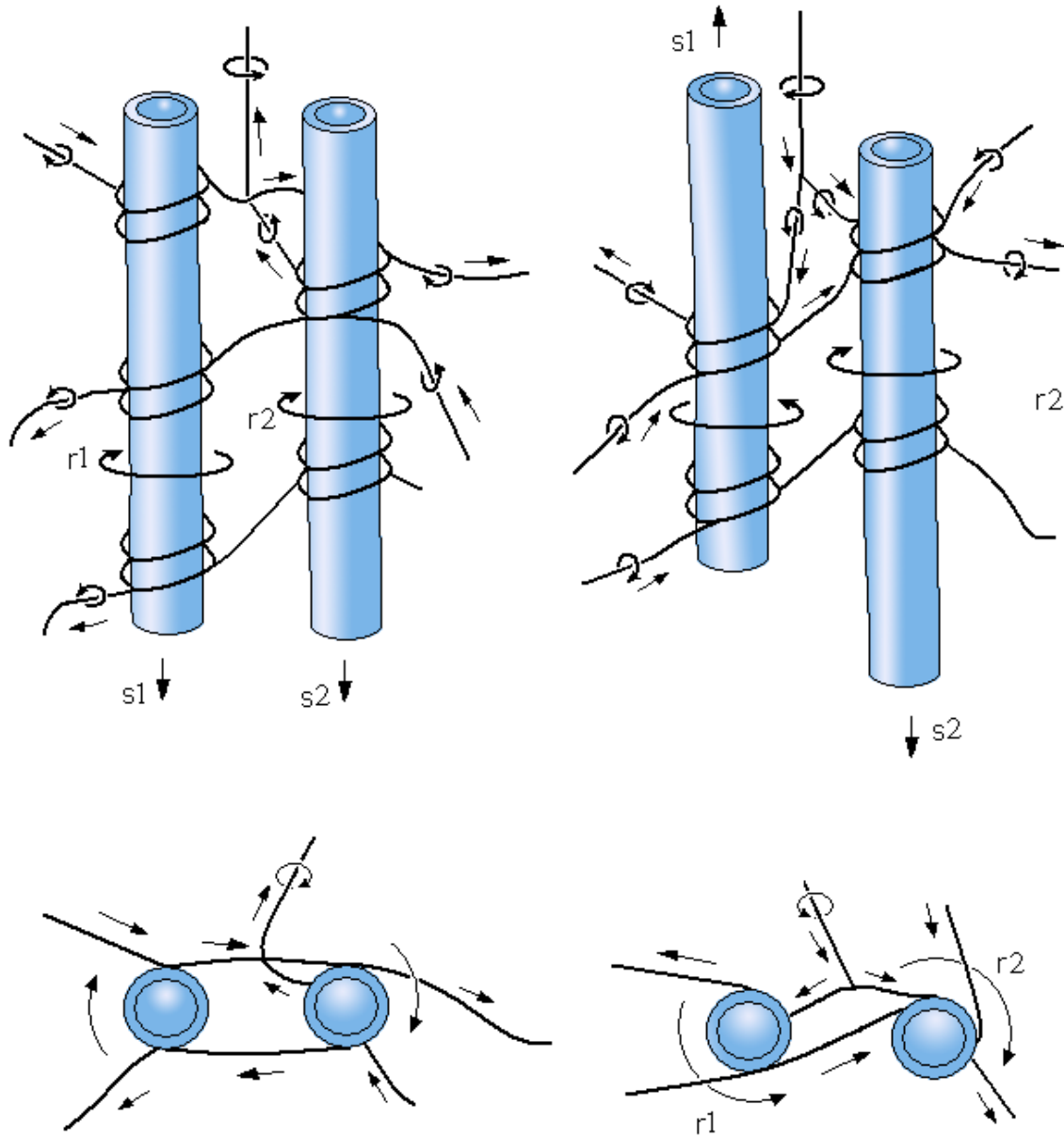


FIG. 1 Microtubule rotation and sliding driven by the actin filaments. Since the F-actin is right handed double helix the mechanical force applied on microtubule and the torque (or the direction of actin helix rotation) constitute right-handed system. The rotation and sliding of microtubules however depends on the actin attachment sites and the actin filament contraction/relaxation that is why microtubules can slide and rotate in any direction. Legend: microtubules in blue; F-actin in black; r, rotation; s, sliding.

GEORGIEV (2003e) has shown that the tubulin-bound GTP cannot be used as a pump to deliver energy to microtubules. This is because α -tubulin bound GTP is not hydrolyzable, and in contrast β -tubulin GTP is hydrolyzable, but neither can undergo GDP \rightarrow GTP exchange, nor can be phosphorylated, thus no ‘pumping cycle’ is available! Therefore we need alternative mechanism. Such could be using of primed energy accumulated in the microtubule acoustic vibrations (and tubulin domain GHz vibrations). Essential could be the motor protein (kinesin, dynein) ‘hopping’ along the microtubules that converts the released ATP (chemical) energy into motor protein and vesicle motion and microtubule acoustic vibration induced by the motor protein (kinesin) walk. The interaction between microtubules, motor proteins and F-actin can lead to high frequency acoustic vibrations of the cytoskeletal network, and the acoustic energy can be used to pump the water laser!

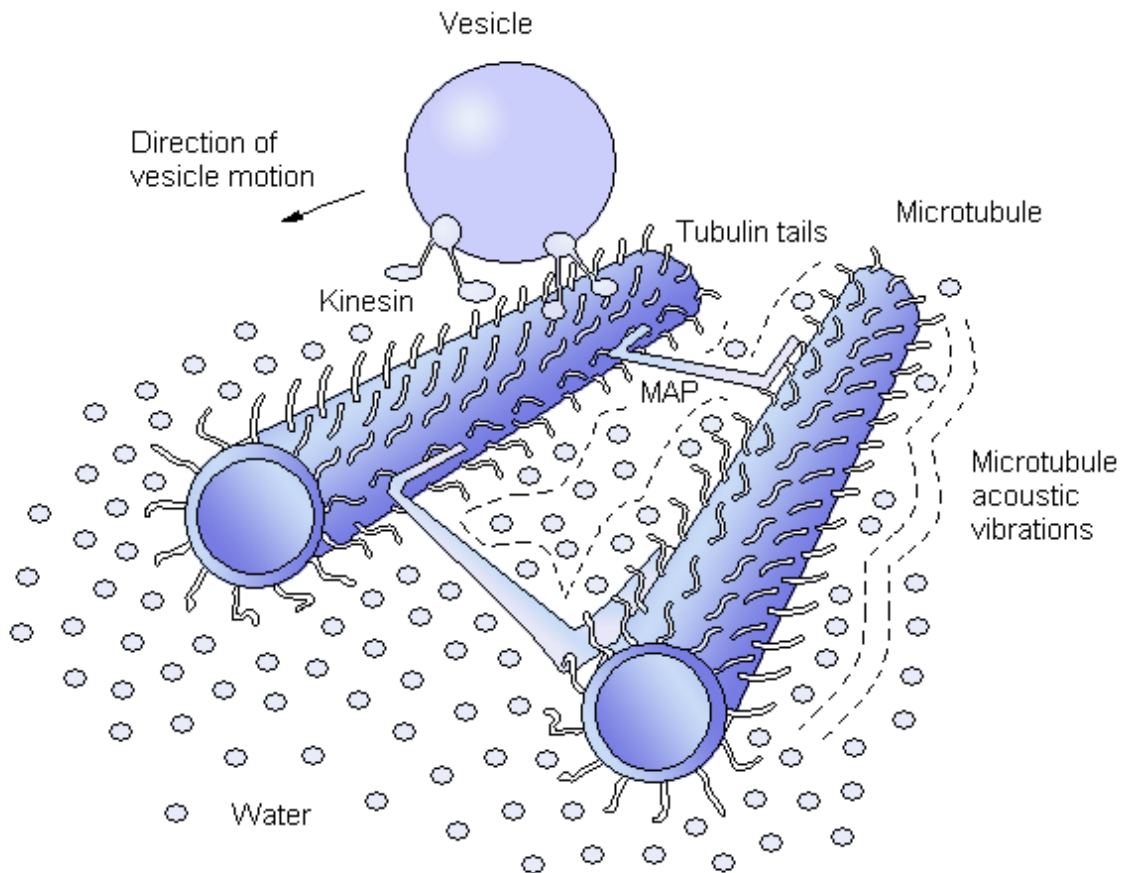


FIG. 2 Microtubules and vesicle motion: (i) motor protein hopping makes cytoskeletal microtubules to vibrate because of their elastic walls. Thus they convert the ATP spent energy by the motor proteins into acoustic mechanical energy of the microtubule wall. (ii) The energy of the acoustic vibrations could be further used to pump the water laser system surrounding the cytoskeletal proteins and coherent emission of photons to follow.

Large deformability of microtubules at low stress and formation of the ionic layer at their surface are important physical properties for *slip boundary conditions* that minimize damping effects of cytosol viscosity. Theory based on no-slip (stick) boundary conditions (FOSTER & BAISH, 2000) neglected the physical properties of microtubules, did not adequately represent conditions in which microtubules exist in the cell, and, therefore, claimed that excitation of vibrations is not possible. POKORNY (2003) showed that in the living cells the *slip boundary conditions* enable excitation of vibrations at least in the frequency domain 1-100 MHz. Ions from the cytosol are attracted to tubulin heterodimers with electric dipoles and create a charge layer around the surface of the microtubule. Because of the *slip boundary conditions* in the surface layers of the microtubule and in the adjacent charge layer dissipative effects of viscous damping on vibrations are diminished. At the frequency 10 MHz the relaxation time may be more than 100 times greater than the period of oscillations. Thus excited vibrations and generated electromagnetic field may have fundamental role in organization of a cell.

KESKIN ET AL. (2002) showed that the slow, large-amplitude motions, also referred to as *global motions*, are conceived to be essential for protein function. It is known that the low-frequency modes make major contributions to thermal conformational fluctuations. Such motions can influence the interactions of proteins with other molecules and its environment. Higher frequency fluctuations, in contrast, are more localized, involve only a few residues, and can play an important role in signal transmission, enzyme reactions, and other internal processes. Using new developed computational method for protein simulation KESKIN ET AL. (2002) observed three highly correlated regions for each of the tubulins in the dimeric form. Studying the relative motions between domains finds that the N-terminal, intermediate, and C-terminal domains of the α -subunit are negatively correlated (or anticorrelated) with their counterparts in the β -subunit. This means that each tubulin monomer shows symmetrical, opposite direction, movements with respect to the dimer interface. Meanwhile within each separated monomer, the N- and C-termini exhibit some tendency to move in the same direction (except for the peptide segment 10-80) whereas the intermediate domain of the molecule undergoes mostly opposite direction motions.

SAMSONOVICH ET AL. (1992) modelled *gigahertz (!) phonon coherent excitations* in microtubules and showed that these acousto-conformational transitions produce standing waves along the microtubule in a way that some tubulins focus the energy of the excitation. These local maxima along the microtubule lattice match the MAP attachment sites on microtubules. Although SAMSONOVICH ET AL. (1992) modelled the whole tubulin monomer as a single oscillator their results are very important. Since the β -tubulin bound GTP is hydrolyzed as soon as the successive dimer is incorporated in the growing microtubule and the released energy is accumulated in the microtubule lattice as mechanical strain, the increased elasticity of the microtubules could be in some way crucial for the proper microtubule function. Increasing the elasticity theoretically reduces the amplitude of vibrations but increases the frequency. As POKORNY (2003) has shown the damping from the surrounding cytosol is diminished when the vibrational frequency exceeds 10 MHz, so the suggested water laser pumping by the acoustic vibrations of microtubules seems biologically feasible.

Tubulin tails orchestrate MAP action

GEORGIEV (2003c, 2003d) suggested that the *tubulin tails* are essential elements from microtubules sensitive to the local electric field, intensively modified via GPCR-linked biochemical cascades - possibility for MAP attachment regulation and converting of the short term memory into long term memory. Thus propagating solitons of evanescent photons can affect the tubulin tail conformational states, since the tubulin tails are highly flexible and their conformation is expected to be extremely sensitive to the status of their hydration shells!

FUJII & KOIZUMI (1999) studied the associations of MAPs with tubulin. They found tubulin to undergo many posttranslational modifications at or near the carboxyl termini of the subunits. These C-termini are rich in acidic amino acids and have been shown to be involved in tubulin binding to MAPs. Specifically, they found the MAPs to bind α -tubulin at amino acid sequences Lys430-Glu441 and β -tubulin at amino acid sequences Tyr 422-Gly 434. C-termini of α - and β -tubulin known as *tubulin tails* are rich in acidic amino acid residues that is why the tubulin tails are highly flexible, mobile, susceptible to proteolysis, and exposed to the solvent (SARKAR ET AL., 2001). The β -tubulin C-terminus binds MAP2 or tau, whereas the α -tubulin C terminus binds these proteins only weakly. The amino acid sequences encoded by β -tubulin genes have revealed a high level of overall similarity, but significant divergence between their C-termini. The pattern of expression of the β -tubulin genes has been studied in several different human cell lines and has revealed varying levels of and differential expression in different cell lines. It appears that distinct human β -tubulin isoforms are encoded by genes whose exon size and number has been conserved evolutionarily, but whose pattern of expression may be regulated either coordinately or uniquely (HALL ET AL., 1985). The tubulin C-termini are prone to intense modification and regulation by different biochemical pathways inside neurons. In mammalian cells, both α - and β -tubulin occur as seven to eight different genetic variants, which also undergo numerous posttranslational modifications (ROSENBAUM, 2000). The main control of the microtubule function is achieved via covalent modifications (BANERJEE, 2002). Indeed in organisms such as the protists that express identical α - and β -tubulins posttranslational modifications provide the only source of variation (SILFLOW, 1991). Modifications such as acetylation, palmitoylation, phosphorylation and polyglutamylation are posttranslational modifications found on other proteins; others such as detyrosination and polyglycylation appear to be tubulin specific.

Tyrosination-detyrosination is one of the major posttranslational modifications in which the C-terminal tyrosine residue in α -tubulin is added or removed reversibly. The tubulin tyrosination cycle involves the enzymatic removal of the C-terminal tyrosine residue present on some α -tubulin isoforms by a specific carboxy-peptidase, and its subsequent restoration by a tubulin-tyrosine ligase (IDRISS, 2000). Although the functional relevance of this modification is not always clear, highly stable microtubules such as those of the axoneme are detyrosinated, and this appears to reflect the length of time the individual α -tubulin substrate molecule has spent in a microtubule. Although tyrosination does not alter the assembly activity of tubulin in vitro, these two forms of tubulin have been found to be distributed differently in vivo and are also correlated with MT stability. Recent

evidence indicates that detyrosination of tubulin can regulate interaction of MTs with vimentin intermediate filaments by a kinesin-dependent mechanism (KREITZER ET AL., 1999). Removal of the penultimate glutamate residue from the α -tubulin polypeptide produces $\Delta 2$ -tubulin, a derivative that is unable to act as a substrate for tubulin-tyrosine ligase, and this truncated protein is therefore removed from the tyrosination cycle. $\Delta 2$ -tubulin is particularly prevalent on microtubule structures such as the axonemes of flagella and cilia and also in mammalian brain cell microtubules.

The tubulin modifications *polyglutamylation* and *polyglycylation* involve the attachment of oligoglutamyl and oligoglycyl side chains of variable length to specific glutamate residues located near the C-terminus of both α - and β -tubulin. Polyglutamylation and polyglycylation are particularly associated with stable microtubule structures such as the axonemes of cilia and flagella. Centriolar microtubules appear to be polyglutamylated but not polyglycylated (MILLION ET AL., 1999). Polyglutamylation appears to be critical for the stability of centriolar microtubules, since microinjection of monoclonal antibodies specific for polyglutamylated tubulin isotypes, results in the transient disappearance of centrioles in mammalian cells (BOBBINEC ET AL., 1998). Polyglutamylation also represents the major posttranslational modification of axonal tubulin in neuronal cells, where it appears to regulate the differential interaction between microtubules and MAPs. For instance, MAPs such as tau and kinesin exhibit optimal binding to tubulin modified by ~ 3 glutamyl residues, binding affinity decreasing with increased polyglutamyl chain length (BOUCHER ET AL., 1994; LARCHER ET AL., 1996). In contrast, increasing polyglutamyl chain length does not appear to affect the binding affinity of MAP1A significantly. BONNET ET AL. (2001) suggest that the differential binding of MAPs to polyglutamylated tubulin could facilitate their selective recruitment to distinct microtubule populations and thereby modulate the functional properties of microtubules.

In the variety of C-termini functions is observed and chaperon-like activity (SARKAR ET AL., 2001). Within the cell exist proteins called *molecular chaperones* that act as catalysts for proper protein folding. Polypeptides in the cell could fold in multiple ways, some of them biologically useless (aggregation), thus there is always a kinetic competition between the correct folding and the aggregation. The yield of the folded protein will depend upon the relative rate of two processes. Therefore, for successful folding of a protein, chaperones minimize the rate of aggregation.

Additionally microtubules (tubulin) interact with G-proteins in direct protein-protein interactions providing link between the membrane GPCR-signalling and the cytoskeleton. Even more important is the fact that microtubules can be attached to membrane bound proteins (ion channels, GPCRs, proteins forming tight- and gap-junctions, etc.). Thus it appears that the cytoskeleton does not only organize the intracellular space but in concert with cytoskeletal scaffold proteins provides basis for membrane organization and reorganization. This last possibility is crucial for the synaptic function and the synaptic based learning.

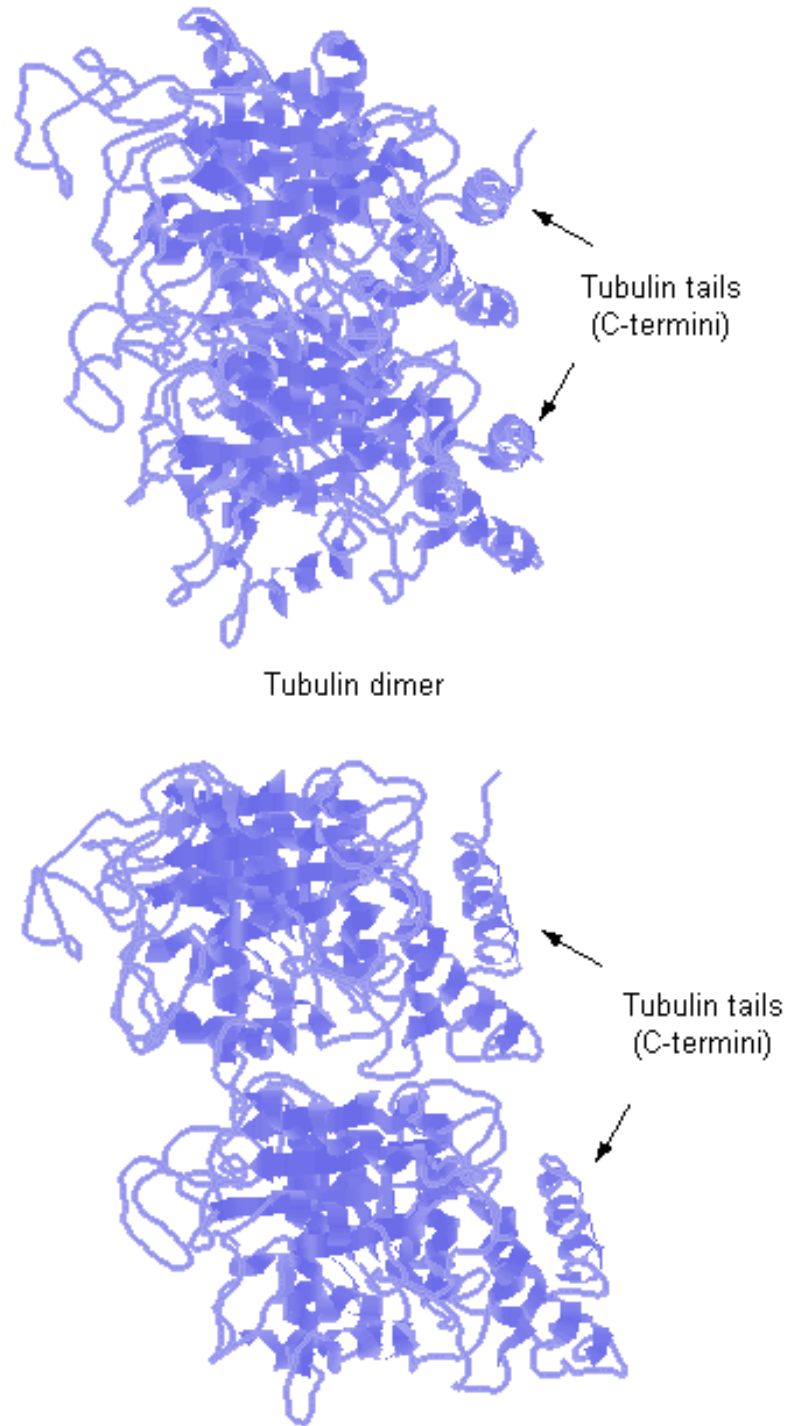


FIG. 3 Microtubules interact with MAP-structural and MAP-motor proteins mainly via the tubulin C-termini. The tubulin tails are flexible projections extending from the microtubule outer surface and their conformations are sensitive to the local electromagnetic field. The image is generated using the ITUB protein databank entry.

Bose-Einstein condensation of tunnelling photons

JIBU & YASUE (1997) revealed that the quantum system of electromagnetic field and water electric dipole field manifests long-range ordered dynamics due to the *spontaneous symmetry breaking* in quantum field theory even though it suffers from interaction with thermally disordered dynamics of the external systems of biomolecules. We already have discussed how the normal mode of the local EM field takes part in realization of the dynamical ordering of water molecules. Now let us focus our attention how the local EM field interacts with the already ordered water! A novel phenomenon occurs: namely the *Goldstone bosons condense with ordinary photons and make them massive*. The resulting species are confined within the water and propagate only due to the *tunnelling effect*.

In order to explain how this happens we have to describe the SSB phenomena in the dynamically ordered region of water within the fully quantum field theoretical framework. In spite of introducing a finite number of water molecules explicitly, a molecular field represented by a two component spinor field

$$(52) \quad \psi(r,t) = \begin{pmatrix} \psi^+(r,t) \\ \psi^-(r,t) \end{pmatrix}$$

is introduced to prescribe the quantum dynamics of water in the region V. Here, $\psi^+(r,t)$ and $\psi^-(r,t)$ are upper and lower spinor components corresponding to the probability amplitudes of water molecules in the first excited state and the lowest energy state of rotation, respectively. This molecular field will be called the water molecular field. Density of the electric dipole of water molecules can be given by

$$(53) \quad D(r,t) \equiv \tilde{\psi}(r,t) \frac{\hbar}{2} \sigma \psi(r,t)$$

where

$$(54) \quad \tilde{\psi}(r,t) = (\psi^+(r,t)^* \psi^-(r,t)^*)$$

is the adjoint spinor field. The explicit form of the Pauli spin matrices $\sigma = (\sigma_1, \sigma_2, \sigma_3)$ is given by

$$(55) \quad \sigma_1 = \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}, \quad \sigma_2 = \begin{pmatrix} 0 & -i \\ i & 0 \end{pmatrix}, \quad \sigma_3 = \begin{pmatrix} 1 & 0 \\ 0 & -1 \end{pmatrix}.$$

Clearly, we have

$$(56) \quad D(r^j, t) = \hbar s^j = \frac{\hbar}{2} \sigma$$

when the water molecular field $\psi(r, t)$ manifests localization in a sense that $\psi(r, t) \neq 0$ only in each position $r = r^j$ of the j th water molecule. This is the case we treated in the preceding section in which spontaneous symmetry breaking was investigated by means of Heisenberg equations Eqs. (24)-(28) with respect to Takahashi's Hamiltonian Eq. (18). There, the dynamically ordered state of the system of the quantized electromagnetic field and water molecules in the region was represented by the time-independent solution Eqs. (29)-(33). Let us denote the corresponding quantum state by $|0\rangle$ in the quantum field theoretical Hilbert space. As each energy spin variables s^j is aligned in one and the same direction given by a constant vector $(u, 0, w)$ in the dynamically ordered state, the expectation value of the electric dipole density does not vanish, obtaining

$$(57) \quad \langle 0 | D(r, t) | 0 \rangle = (u, 0, w) \neq 0$$

The rotational transformation of spin variables Eqs. (21)-(23) around the third axis is represented by the U(1) subgroup of SU(2) rotations for the water molecular field $\psi(r, t)$;

$$(58) \quad \psi(r, t) \rightarrow \psi'(r, t) = \exp\left(\frac{i\theta\sigma_z}{2}\right)\psi(r, t).$$

The dynamically ordered state $|0\rangle$ of the system of the quantized electromagnetic field and the water molecular field in the region V cannot be U(1) invariant, since it has to carry the nonvanishing electric dipole density (Eq. (57)). Namely, the U(1) rotational symmetry around the third axis is spontaneously broken in the dynamically ordered state $|0\rangle$. However, the dynamically ordered state $|0\rangle$ can still have local U(1) rotational symmetry under the transformation

$$(59) \quad \psi(r, t) \rightarrow \psi'(r, t) = \exp\left(\frac{i\theta(r, t)\sigma_z}{2}\right)\psi(r, t)$$

with a space-time dependent parameter $\theta = \theta(r, t)$. This is a local gauge transformation for the water molecular field $\psi(r, t)$, and it is immediately seen that such a local U(1) rotational symmetry can be ensured by the corresponding gauge transformation of electromagnetic field

$$(60) \quad A(r, t) \rightarrow A'(r, t) = A(r, t) - \nabla\theta(r, t).$$

Here, $A(r, t)$ is the vector potential of the electromagnetic field such that the electric field $E(r, t)$ is given by $E = -\frac{\partial A}{\partial t}$. The space-time dependent parameter $\theta(r, t)$ thus restore the

broken U(1) rotational symmetry and can be regarded as the *Goldstone mode* whose energy quanta are *Goldstone bosons*.

The dynamically ordered state of the system of the quantized electromagnetic field and the water molecular field in the region V thus create a longitudinal mode of the electromagnetic field, that is, the *Goldstone mode*, so that the broken symmetry is restored. In other words, the additional longitudinal mode must be superposed on the vector potential in the region V, and consequently energy quanta of the electromagnetic field (i.e., photons) come to have nonvanishing (effective) mass due to the *Higgs mechanism* in gauge theory (UMEZAWA, 1993). The interaction between the ordered water and the quantized electromagnetic field makes photons (effectively) massive. This means that the gauge transformed vector potential $A'(r,t)$ is subject to the modified Maxwell equation with mass term:

$$(61) \quad \left(\square + \frac{M^2 c^2}{\hbar^2} \right) A'(r,t) = 0,$$

$$(62) \quad \square \equiv \left(\frac{1}{c^2} \frac{\partial^2}{\partial t^2} - \nabla^2 \right)$$

\square denotes the d'Alembertian operator, and M stands for the effective mass of a photon.

The electric field $E(r,t)$ is also given by $E = -\frac{\partial A'}{\partial t}$ in this gauge and so subject to the same modified Maxwell equation with mass term

$$(63) \quad \left(\square + \frac{M^2 c^2}{\hbar^2} \right) E(r,t) = 0$$

in the dynamically ordered region of water.

Recall that the normal mode of the quantized electromagnetic field subject to the Maxwell equation (without mass term) took part in realizing the dynamically ordered region of water. Once such a dynamically ordered region of water is created, then a longitudinal mode of the quantized EM field carrying photons interacting with ordered water to display a non vanishing effective mass emerges by means of the Higgs mechanism: the emergence of Goldstone bosons restoring the spontaneously broken symmetry can be shielded by making gauge bosons, that is, photons, massive. This mode of the quantized electromagnetic field is called an *evanescent mode*.

Energy quanta of the evanescent mode of the quantized electromagnetic field with nonvanishing mass will be called *evanescent photons* or *virtual photons*. The modified Maxwell equation Eq. (63) yields the evanescent mode characterized by imaginary wave vectors. They are also called *tunnelling photons* designating the fact that they are moving ‘evanescently’ in the dynamically ordered region of water by means of the quantum tunnelling effect.

Since the effective mass of the evanescent photon is essentially a spatial damping factor for the evanescent mode of the quantized electromagnetic field in the dynamically ordered region of water, it is of the order inversely proportional to the penetration depth of the evanescent mode (DEL GIUDICE ET AL., 1982, 1985, 1986b, 1988, 1989), obtaining

$$(64) \quad M \approx \frac{\hbar}{c\delta} \approx 13.6 \text{ eV}$$

$$(65) \quad \delta \sim 25 \text{ } \mu\text{m}$$

The penetration depth δ is of the same order as the coherence length l_c .

As was clarified UMEZAWA (1993) collective modes of long-range ordered dynamics are nothing but macroscopic objects of quantum origin. Crystals, magnetic media and superconducting media are familiar examples of such macroscopic objects, but it seems difficult to get a correct image of the macroscopic object realized by a collective mode of the quantum system of electromagnetic field and water electric dipole field. Of course, the collective mode in question was shown to induce coherent photon emission phenomena. However, it must be emphasized that those photons are not ordinary ones but specific ones, which cannot go away from the spatial region occupied by the macroscopic object. In other words, those photons are associated not to the usual advancing plane wave mode but to the evanescent wave mode of the quantized electromagnetic field wrapping the localizations of water electric dipole field, and they can exist only in conjunction with water. We call such photons *evanescent photons* in water.

Since the evanescent photons in water are not associated to the advancing plane wave, we cannot see them from the outside as light. Therefore, JIBU & YASUE (1997) suggested that it is demanded to put the finest optical fiber or metallic fiber into the region of macroscopic object made of evanescent photons in water, so that energy quanta of the trapped evanescent wave mode are scattered into the advancing plane wave mode and finally detected as light. As the evanescent wave mode of the quantized electromagnetic field is maintained by the ordered dynamics of water electric dipole field strongly coupled to it, the evanescent photons accompany the coupled wave of water electric dipole field and can be seen as charged quanta. Namely, unlike the usual concept of photons, the evanescent photons in water have effective electric charge e^* and effective mass m^* , and behave as *Bose quanta* (JIBU & YASUE, 1997). For now the direct measurement of the evanescent photons was not been achieved, however there is possibility to be registered secondary evoked processes by the tunnelling photons.

Biological high-temperature superconductivity

It may be of certain help for giving a correct image of the macroscopic object of a collective mode of the quantum system of electromagnetic field and water electric dipole field if we call it *evanescent photon water*. Namely, evanescent photon water is a typical macroscopic object in brain cells, which can be regarded as a macroscopic condensate of evanescent photons with certain effective charge and mass. The physical situation is similar to that of superconducting media in which a macroscopic Bose-Einstein condensate of pseudo-particles called *Cooper pairs* with certain effective charge and mass is realized. The macroscopic condensate of Cooper pairs is realized only at lower temperature close to absolute zero, and so superconductive phenomena of Cooper pairs can hardly be realized in macroscopic objects at body temperature! This fact had been referred to as a common negative claim against the possibility of superconductive phenomena in living matter. However, because the macroscopic condensate of evanescent photons has been shown to be realized even at body temperature in the vicinity of structured biomolecules as cytoskeletal microtubules, we can expect the possibility of superconductive phenomena of evanescent photons in living matter, especially in the brain. Simply put, as the evanescent photon has mass nonvanishing but much smaller than that of the *Cooper pair of electrons*, the macroscopic condensate of evanescent photons has the critical temperature higher than the body temperature, and we still have superconducting phenomena in *evanescent photon water* in the brain at body temperature (JIBU ET AL. 1996).

Just for illustration we will provide the masses of a *Cooper electron pair* $M' \sim 1021997.8$ eV and the already calculated mass of the *evanescent photon* $M \sim 13.6$ eV. The mass difference of 5 orders of magnitude rules out the older suggestion for electron superconductivity in biological matter supposed by HAMEROFF ET AL. (2002). The Cooper pair condensation requires extreme cold since Cooper pairs are too massive. In contrast the critical temperature of the boson condensate of evanescent photons with effective mass $M \sim 13.6$ eV can be estimated to be much higher than the body temperature, since it is inversely proportional to the boson mass (JIBU ET AL., 1996)

Therefore, it seems highly plausible that it is not the microscopic quantum mechanical system of electrons in biomolecules but the macroscopic quantum ordered dynamical system of evanescent photons in water, which plays the essential role in realizing the long-range biological order in living matter!

Tunnelling photons are optical tachyons

Tunnelling (evanescent) photons propagate with zero time inside the tunnelling region that is with infinite velocity $v \rightarrow \infty$ (ENDERS & NIMTZ, 1992; 1993a; 1993b; NIMTZ ET AL., 1994; NIMTZ, 1998). Solitons composed from tunnelling photons (which are quantum waves that do not dissipate) therefore can propagate with infinite velocity inside the tunnelling region too. The evanescent photons in QBD cannot be seen as light from

outside since their existence is possible only in the dynamically ordered water that has created them (JIBU & YASUE, 1997).

Tunnelling represents the wave mechanical analogy to the propagation of *evanescent modes* (NIMTZ & HAIBEL, 2002; NIMTZ ET AL., 1994; 2000a; 2000b; 2000c). Nice example of photonic barrier generating evanescent modes is the double prism with a gap of rarer refractive index with a beam falling with angle greater of the angle for total internal reflection. The latter set-up is described as *frustrated total internal reflection (FTIR)*.

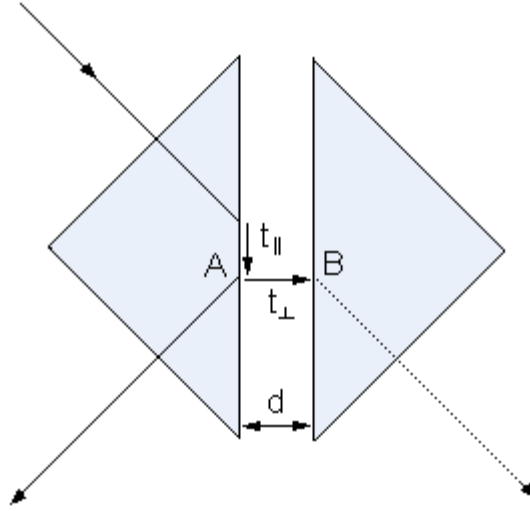


FIG. 4 The tunnelling time of the double-prism experiment consists of two components: t_{\parallel} for the Goos-Hänchen shift parallel to the prism's surface and t_{\perp} for crossing the gap in the direction perpendicular to the two surfaces of the gap.

For an angle of incidence greater than the angle of total reflection the barrier transmission time of the double-prism, or what we call here the tunnelling time can be split into two components

$$(66) \quad t_{\text{tunnel}} = t_{\parallel} + t_{\perp},$$

one along the surface due to the Goos-Hänchen shift, and another part perpendicular to the surface. The measured tunnelling time t_{tunnel} represents the group time delay, which results in the group, or signal velocity.

The first component of t_{tunnel} is related to a non-evanescent wave characterized by the real wavenumber

$$(67) \quad k_{\parallel} := k_0 n_1 \sin \theta_i$$

while the second one

$$(68) \quad k_{\perp} := ik_0 \sqrt{n_1^2 \sin^2 \theta_i - 1}$$

is related to the evanescent mode traversing the gap between the two prisms.

$$(69) \quad k_0 = \frac{2\pi}{\lambda_0},$$

where λ_0 is the corresponding vacuum wavelength, and n_1 is the refractive index of both prisms.

In the symmetrical design of the experiment displayed in FIG. 4 the reflected and the tunnelled signal leave the first and the second prisms at the same time. This result represents an experimental proof that for the tunnelling time component t_{\perp} holds $t_{\perp} = 0$. It is in agreement with the observations on other photonic tunnelling structures: the finite measured tunnelling time accrues at the entrance boundary and no time is spent inside a barrier.

Evanescent modes show some amazing properties to which we are not used to from classical physics. Apparently evanescent modes are nonlocal fields and represented by virtual photons. Evanescent modes are easily traceable through barriers some 100 wavelengths thick and they *do not spend time in the barrier*. The latter is an experimental result due to the fact that the transmission time is independent of barrier length (Hartman effect). The proof of this behaviour is observed in the case of symmetrical *frustrated total internal reflection (FTIR)* discussed above, where the reflected and the transmitted signal have the same delay time, i.e. the time spent inside the barrier is zero. The measured finite transmission time comes into existence at the entrance boundary of the photon barriers.

Compared with the wave solutions an evanescent mode is characterized by a purely imaginary wave number, so that i.e. the wave equation yields for the electric field $E(x)$

$$(70) \quad E(x) = \exp[i(\omega t - kx)] \Rightarrow E(x) = \exp[i\omega t - kx]$$

where ω is the angular frequency, t the time, x the distance, k the wave number, and $k=ik$ the imaginary wave number of the evanescent mode.

Thus evanescent modes are characterized by an exponential attenuation and a lack of phase shift. The latter means that the mode has not spent time in the evanescent region, which in turn results in an infinite velocity in the phase time approximation neglecting the phase shift at the boundary (HARTMAN, 1962). The infinite velocity of propagation of tunnelling photons and the suggested solitons is in contrast with the finite velocity $v < c$ suggested by JIBU & YASUE (1997). Indeed the infinite velocity implies non-locality and could explain the unity of mind (the so-called *binding problem* in psychology)!

Evanescent modes are characterized by extraordinary properties: Their energy is negative, they are not directly measurable, and the evanescent region is not causal in Einstein's sense since the modes traverse this region instantaneously (NIMTZ, 1999a; 1999b; 1999c). The Schrödinger equation yields a *negative kinetic energy* in the tunnelling case, where the potential U is larger than the particle's total energy W :

$$(71) \quad \frac{d^2\Psi}{dx^2} + \frac{2m}{\hbar^2}(W - U)\Psi = 0$$

The same happens to evanescent modes. Within the mathematical analogy their kinetic electromagnetic energy is negative too. The Helmholtz equation for the electric field E in a waveguide is given by the relationship

$$(72) \quad \frac{d^2E}{dx^2} + (k^2 - k_c^2)E = 0$$

where k_c is the cut-off wave number of the evanescent regime. The quantity $k^2 - k_c^2$ plays a role analogous to the energy eigenvalue and is negative in the case of evanescent modes.

The dielectric function ε of evanescent modes is negative and thus the refractive index is imaginary.

For the basic mode a rectangular waveguide has the following dispersion of its dielectric function, where $k_c = \left(\frac{\pi}{b}\right)^2$ holds and b is the waveguide width,

$$(73) \quad \varepsilon(\lambda_0) = \frac{1 - \lambda_0}{2b}$$

λ_0 is the free space wavelength of the electromagnetic wave.

In the case of tunnelling it is argued that a particle can only be measured in the barrier with a photon having energy $\hbar\omega \geq (U - W)$. This means that the total energy of the system is positive. According to Eq.(73) the evanescent mode's electric energy density ρ is given by the relationship

$$(74) \quad \rho = \frac{1}{2} \varepsilon \varepsilon_0 E^2 < 0$$

where ε_0 is the electric permeability. The analogy between the Schrödinger equation and the Helmholtz equation holds again and it is not possible to measure an evanescent mode

in the tunnelling region. NIMTZ (1998) reports for an attempt to measure evanescent modes with probes put into the evanescent region but failed. Obviously evanescent modes are not directly measurable in analogy to a particle in a tunnel. This problem is due to impedance mismatch between the evanescent mode and a probe. The impedance Z of the basic mode in a rectangular waveguide is given by the relationship

$$(75) \quad Z = Z_0 \varepsilon^{-1/2}$$

where Z_0 is the free space impedance. In the evanescent regime $k < k_c$ the impedance is imaginary.

Evanescent modes do not experience a phase shift inside the evanescent region. They cross this region without consuming time. The predicted and the measured (NIMTZ & HEITMANN, 1997) time delay happens at the boundary between the wave and the evanescent mode regime. For opaque barriers (i.e. $k \cdot x \geq 1$, where k is the imaginary wave number and x the length of the evanescent barrier) the phase shift becomes constant with $\sim 2\pi$ which corresponds to one oscillation time of the mode. In fact, the measured barrier traversal time was roughly equal to the reciprocal frequency in the microwave and is independent of the barrier length (NIMTZ & HEITMANN, 1997). The latter behaviour is called *Hartman effect*: the tunnelling time is independent of barrier length and has indeed been measured with microwave pulses thirty years after its prediction (ENDERS & NIMTZ, 1992; 1993a; 1992b).

Evanescent photons spend zero time inside the tunnelling region, cannot be directly measured and because of their infinite speed (nonlocal character) they are not Einstein causal. The tunnelling photons mediate the enforcement of long-range physical correlations so that the coherent region of proteins, hydration shells and electromagnetic fields inside the brain cortex would behave as inseparable whole!

It should be noted that the evanescent modes are proved quantum phenomenon and attempts for different applications of evanescent light are made. A recent and very successful application is the *single-molecule fluorescence imaging* that helps individual biomolecules to be studied (MOERNER ET AL., 1999; MOERNER & ORRIT, 1999; MOERNER, 2002). Therefore the fact that evanescent modes are not directly measurable inside the tunnelling region does not mean that they do not interact with the biomolecules, respectively the brain matter!

Tunnelling photons as a definition of life

It is found in quantum brain dynamics (QBD) that the *Nambu-Goldstone theorem* assures the existence of specific macroscopic objects in the brain realized by ordered states of quantized electromagnetic field, proteins and water electric dipole field interacting strongly with each other. If the emphasis is put on matter, such a macroscopic object may be understood as coherent proteins interacting with the ordered water and local

electromagnetic field in the neurons. If the emphasis is put on light, on the other hand, such a macroscopic object can be seen as being made of tunnelling (evanescent, virtual) photons enveloping the water (and protein) electric dipole field. The fact that the water laser system producing evanescent photons requires pumping explains the conjecture that existence of tunnelling photons could be physical criterion for living cell, and their absence for dead cell (JIBU ET AL., 1997). The defined protein dynamical timescale (GEORGIEV, 2003a; 2003b; 2003c) demands coherence timescale above the thermal fluctuations timescale. Since this can be achieved only via use of metabolic energy for coherence pumping it is obvious why the existence of evanescent photons could be criterion for life since it is result from life (the biochemical processes of living cells).

It is interesting to finish our presentation with results from recent investigation of the *spin-boson model applications* in biology. GILMORE & MCKENZIE (2004) give a theoretical treatment of the interaction of electronic excitations (excitons) in biomolecules and quantum dots with the surrounding polar solvent. They have shown significant quantum decoherence to occur due to the interaction of the electric dipole moment of the solute with the fluctuating electric dipole moments of the individual molecules in the solvent. The introduced spin boson model by GILMORE & MCKENZIE (2004) could be used to describe the effects of decoherence on the quantum dynamics of biomolecules and the preliminary results show that exactly fluctuating dipole moments in the water will lead to decoherence of the cytoskeletal quantum coherent states. In the updated QBD model the water <-> local EM field interaction is crucial piece of the whole quantum coherent process of cytoskeletal protein interaction.

We could boldly generalize that if the QBD predicted coherence of water dipoles is not in vivo realizable option, no any Q-mind model will be realizable too! Thus if water molecules manifest dynamical order induced by their interaction with the quantized EM field then the evanescent photons are the only biologically vivid option for Bose-Einstein condensation in brain and associated with the condensation long-range coherent informational (energy and momentum) transfer.

Where is mind? – The hard problem

NAGEL (1974) successfully argued that experience is *the hard problem* that makes *the mind-body problem* intractable. Functionalist's theories of consciousness, in general, are not able to explain why performing of given function must be associated with any experience. In the materialistic school the current paradigm claims that the *sentient brain* emerges at critical level of complexity from *insentient matter*. However because the chemical atoms are essentially identical both for the *sentient brain* and the *insentient matter* we can start 'recipe' for building up a sentient brain from insentient matter and we must have answer when our product will '*start to feel*'. If we follow such recipe for building up a sentient brain we will come to a situation in which adding or removing a single atom will '*give*' or '*take*' the mind of the system - conclusion quite intolerable for the ordinary logic. Thus we came to the conclusion that experience must be fundamental

ingredient of the Universe we live in, that there is no insentient matter at all, and that we must '*construct*' sentient brain from sentient matter. Elsewhere in the literature is conjectured that the quantum theory provides physical picture in which consciousness (experience, mind) could be fundamental ingredient governing the behavior of quantum systems. There were successful analogies between the wave function and mind of a given quantum particle, which however are still issue of rigorous debates. Since this paper is presenting the mathematical formalism used to describe the unique interaction between cytoskeletal proteins, hydration shells and the local EM field it does not aim to speculate on the experiential nature of mind, no matter that QBD per se establishes a form of panprotopsyism (the matter is sentient). What we have shown is that mind could be linked to the quantum coherent dynamics of cytoskeletal proteins interacting with the surrounding water and the local electromagnetic field inside the brain cortical neurons.

Outline

Let us summarize in several brief paragraphs the novel ideas presented and/or used in the paper compared to older suggestions that were found to contain some defects or were eventually disproved.

- i. It was suggested that *mind operates at picosecond timescale* and not millisecond one. We have supposed that mind is linked to quantum processes taking part in the cytoskeleton, so the picosecond timescale is the only logical one since proteins operate in 10-15 ps. The reduced dynamic timescale increases the brain mass undergoing objective reduction with 8 orders of magnitude (compared to the experimentally disproved (!) 40Hz conjecture) and allows for areas from the whole brain cortex to be involved in realization of coherent conscious activities.
- ii. The *protein dynamics utilizes protein breathing* (the protein thermal fluctuations) *in promoting catalysis*, so the possibility for quantum mind to escape thermalization is unavailable option. This rules out formerly suggested superradiant models realized in brain microtubules.
- iii. The *vibrationally assisted tunnelling in mind catalytic action* is novel idea and no alternative is available. In exocytosis is expected mixed multidimensional tunnelling that is temperature dependent.
- iv. The *Bose-Einstein condensation is shown to be dependent on boson mass*. Thus an evanescent photon has 10^5 less mass than a Cooper pair in a protein and therefore the critical temperature for condensation is above the body temperature.
- v. Mind is suggested to be a quantum wave instead of a neural network composed from neuronal switches (on/off bits). If *consciousness is described by complex quantum wave* then it is an agent operating in Hilbert space and is essentially outside the 4D Minkowski space-time continuum. Mind is interactively engaged in making decisions. It is not result from the quantum wave collapse; instead the noncomputability of the collapse describes a fundamental free will.
- vi. The model stresses upon protein <-> water <-> EM field interaction in the brain cortex and requires multidisciplinary approach.

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