Action of Excited State Molecular Networks

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Abstract
Nanodomains are groups of water molecules held together by an electron in an excited state. We investigate the interaction of nanodomains with living matter through acceleration of an enzyme cycle. We formulate a mechanistic model with four enzyme forms in a cycle and three successive phases. In Phase 1 a slowly catalyzing reaction approaches steady state. In Phase 2 the enzyme forms convert to their excited states using nanodomain energy, and a new stationary state is reached. The high rate of excited state energy movement in living systems leads to rapid conversion to the excited state, and the excitation energy needs to be supplied for only a short period. The excited state produces a very fast cycle, which is stable for a much smaller enzyme concentration than needed for the slow cycle. In Phase 3 the excited states decay. These phases are simulated by solving differential equations numerically.

Keywords: Enzyme reaction; Excited states; Coherence domains; Nanodomains; Sub-cellular structures

Introduction
The original concept of ‘the memory of water’ (see for instance Chaplin [1]) was based on water clusters serving as information carriers. However, Cowan et al. [2] showed that hydrogen bonds in these clusters have too short a lifetime to hold information. To meet this objection Czerlinski and Ypma [3] proposed the existence of nanodomains in water, formed as a result of a mechano-chemical effect such as the vigorous shaking that is part of the homeopathic process. Such nanodomains may be produced by groups of synchronously vibrating bonds in water molecules losing their vibrational energy in the process of breaking an OH-bond. The bond breaking generates H- and OH-radicals, each containing a radical electron in the triplet excited state. Czerlinski and Ypma [4] exploited the suggestion of Nagl and Popp [5] that two triplet excited states participate in an energy transfer, with one triplet becoming a singlet excited state and the other returning to the ground state. Foerster [6] and Weller [7] showed that singlet excited states produce a large pKₐ-shift, and Smith [8] showed that pH-changes occur when storing electromagnetic energies in water. The electron in the singlet excited state is a bound electron delocalized in the nanodomains. Thus nanodomains can accept and store chemical characteristics of dissolved chemical agents, such as homeopathic substances, in the form of electromagnetic waves, when acting in coherent cooperation. The geomagnetic field promotes such cooperation. Coherent cooperation also vastly increases the lifetime of the nanodomains. Groups of nanodomains form micro domains (coherence domains) which may cooperate in organs or smaller units within a physiological network. Gather and Yun [9] recently showed that biological fluorophors, free or in live cells, can be made to act like lasers under classical conditions without damage to cells. This is relevant here, since we assume extensive coherence of waves in living systems. These domains and their electromagnetic spectra may interact with similar targets in the living system and thus be useful for medical purposes. A simplified mathematical description of the relevant kinetics together with a discussion of the associated magnetic fields was presented in Czerlinski and Ypma [10].

Czerlinski and Ypma [11] studied the interaction of aqueous nanodomains with living systems, using a model system with one enzyme catalyzed reaction. Free enzyme was assumed to be available in both active and inactive forms, with interconversion between them. The excited state energy of the aqueous nanodomains, functioning in coherent cooperation, was assumed to act on the inactive form, initiating the process of converting it to the active form via a short-lived excited state using the excitation energy derived from the fast moving nanodomains. In the present study, the excited state energy of the aqueous nanodomains is assumed to act on all the enzyme forms in a four-step catalytic cycle, converting all the enzyme components to an excited state. Although the two models differ significantly, both produce a very fast conversion, as shown here for the second model.

We study here an enzyme reaction with two catalytic cycles: a slow inner cycle involving relatively inactive enzyme forms, connected to a corresponding fast outer cycle involving their excited states. The main kinetic difference between the cycles is a pair of rate constants, which are much larger in the outer cycle than in the inner cycle. The cycles are connected by a rate constant, which is changed from zero to a large value to simulate activation of the outer cycle. Numerical simulation shows that the total enzyme concentration has to be much larger in the inner cycle than in the outer cycle in order to maintain stability in the substrate concentration values.

Materials and Methods
Since micro domains are formed by many nanodomains, many enzyme molecules are involved. These enzymes are in reactive compartments, where they occur at much higher concentration than observed in a bulk analysis (Czerlinski and Ypma [12]). The fluid volume of a cell might be such a reactive compartment. If this volume might be present. To describe the chemical kinetics involved we consider individual molecules at their respective molar concentrations and numerically simulate the system. Our focus is on the mathematical modeling of these molecular kinetics.

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We study an isolated enzyme reaction in the simple metabolic system of Figure 1. Component 1 represents the food source; components 2 to 5 are metabolites (substrates). Components 6 to 9 are active but electronically unexcited enzyme forms in an inner catalytic cycle, whose concentrations depend on the amount of enzyme supplied and the adjacent substrate concentrations. Components 10 to 13 are the corresponding enzyme forms changed from their ground states to singlet excited states, in an outer catalytic cycle. The rate constant $k_{21}$ connects every enzyme form in the first cycle to its equivalent in the second cycle. Most of the rate constants corresponding to each other in these two cycles have the same value, except that $k_{23}$ (related to $k_7$) and $k_{25}$ (related to $k_9$) are larger by a factor of 10. This increase results in a much more rapid turnover in the outer enzyme cycle.

The reaction is modeled as three successive phases. Phase 1 denotes the approach to a stationary state with the initial free enzyme concentration $c_i^0$ set to a nonzero value and only the inner cycle active ($k_{21}=0$). In Phase 2 the outer cycle is activated by setting $k_{21}$ to a large concentration $c_6$, much more rapid turnover in the outer enzyme cycle.

2 with $k_{21}$ reset to zero; the small backward rate constants $k_{23}$ to $k_{26}$ are coherence, have a limited lifetime. Phase 3 is the continuation of Phase 2. There we denote by $c_i$ the concentration of component $i$; $c_i^0$ represents the concentrations of components 6 and 15 respectively. With the lowest values for $c_5$ and $c_8$ at about $10^{-6}$ M we get $1/\tau=0.452x10^9$ s$^{-1}$ for the larger $a_D$. Since $1/\tau$ is much larger than $k_{21}$ (10$^5$ s$^{-1}$, Table 2), the step with $k_{21}$ controls the timing of the two-step sequence and is the only one considered further.

Similar two-step reactions start from components 7, 8 and 9 to produce components 11, 12 and 13, respectively. In each case a very fast step with component 15 is followed by a much slower step controlled by $k_{21}$. As above, the fast first step may be dropped from further mechanistic consideration.

The differential equations describing the system of Figure 1 are listed in Table 1, and values for the associated constants are in Table 2. We denote by $c_i$ the concentration of component $i$; $c_i^0$ denotes its concentration at time $t=0$. The values in Table 2 satisfy the following conditions. The food source supplies a large excess of nutrients; thus $c_i^0=10^0$ M, resulting in $c_i^0=0$ for $i=2$ to 5. In the inner cycle there are two equilibration paths from component 6 to 8. This implies the interdependence of some rate constants, namely $k_i/k_j$.

The system of differential equations in Table 1 was solved

\begin{align*}
dc_1/dt &= k_2 c_3 - k_1 c_1 \\
dc_2/dt &= k_3 c_4 - k_2 c_2 \\
dc_3/dt &= k_4 c_5 - k_3 c_3 - k_7 c_4 c_5 + k_9 c_6 - k_8 c_5 c_9 + k_{10} c_8 - k_{11} c_7 + k_{21} c_7 + k_{23} c_{10} - k_{24} c_{11} - k_{18} c_{12} + k_{19} c_{10} + k_{17} c_{11} - k_{16} c_{13} - k_{15} c_{12} - k_{14} c_{11} + k_{20} c_{13} - k_{26} c_{12} + k_{25} c_{11} - k_{24} c_{12} + k_{22} c_{13} - k_{21} c_{12} + k_{22}^0 - k_{22} N_A a_D (D_1 + D_2) \phi_D,
\end{align*}

where $N_A$ is Avogadro’s Number ($6 \times 10^{23}$ molecules per mole), $a_D$ is the radius of interaction (see below), $D_1$ and $D_2$ are the diffusion constants of the relevant components (6 and 15 in this case) and $\phi_D$ is an ionic factor whose value is 1 when (as here) the charge of at least one of the components is zero. Here $D_2$, referring to enzymes, is in the range of $10^4$ dm$^2$ s$^{-1}$, but $D_1$ is potentially much larger. We must estimate a value for the diffusion constant of energy quanta along a chain of nanodomains. For heat diffusion in liquids a typical value is $10^{-5}$ cm$^2$ s$^{-1}$ [15]. Based on the time range for forming a nanodomain (Czerlinski and Ypma [4]) and for the onset of chemical activities (Cowen et al. [2]) we estimate the energy quanta diffusion constant to be at least 100 times faster than the heat diffusion constant, thus $10^4$ cm$^2$ s$^{-1}$.

For heat diffusion in liquids a typical value is $10^{-3}$ cm$^2$ s$^{-1}$ [15]. Based on the work of v. Smoluchowski [14] on the aggregation of spherical colloids with parameters expressed in terms of moles, liters and dm (1 liter=1 dm$^3$),

$$k_{22}=\pi N_A a_D (D_1 + D_2) \phi_D,$$
numerically by the Matlab (Mathworks, [16]) routine ode23s (Shampine and Reichelt [17]). This is an implementation of a variable steplength second order modified Rosenbrock method. The results of the simulations are shown in Table 3 and Figures 2 to 5 for Phase 1 and in Table 4 and Figures 6 to 9 for Phase 2; Figure 10 shows the results for Phase 3.

| Description | Symbol | Value | Units | Note |
|-------------|--------|-------|-------|------|
| rate constant | $k_1$ | 0.001 | s$^{-1}$ | |
| rate constants | $k_2 = k_3 = k_4$ | 0.1 | s$^{-1}$ | |
| complex 7 formation rate | $k_5$ | $10^6$ | M$^{-1}$ s$^{-1}$ | |
| complex 7 dissociation rate | $k_6$ | $10^6$ | s$^{-1}$ | |
| complex 8 formation rate | $k_7$ | $10^6$ | M$^{-1}$ s$^{-1}$ | |
| complex 8 dissociation rate | $k_8$ | $10^4$ | s$^{-1}$ | |
| forward isomerisation rate | $k_9$ | $10^2$ | s$^{-1}$ | |
| reverse isomerisation rate | $k_{10}$ | $10^2$ | s$^{-1}$ | |
| component 9 formation rate | $k_{11}$ | $10^5$ | M$^{-1}$ s$^{-1}$ | |
| component 9 dissociation rate | $k_{12}$ | $10^4$ | s$^{-1}$ | |
| complex 11 formation rate | $k_{13}$ | $10^6$ | M$^{-1}$ s$^{-1}$ | |
| complex 11 dissociation rate | $k_{14}$ | $10^4$ | s$^{-1}$ | |
| complex 12 formation rate | $k_{15}$ | $10^6$ | M$^{-1}$ s$^{-1}$ | |
| complex 12 dissociation rate | $k_{16}$ | $10^4$ | s$^{-1}$ | |
| forward to 12 isomer. rate | $k_{17}$ | $10^3$ | s$^{-1}$ | |
| reverse to 11 isomer. rate | $k_{18}$ | $10^2$ | s$^{-1}$ | |
| initial substrate concentration | $c_{10}$ | $1.0$ | M | |
| initial enzyme concentration | $c_{60}$ | $10^{-6}$ to $10^{-5}$ M | see Tables 3-5 | |
| other initial concentrations | $c_{i0}$ | $0$ | M | |

Note 1: Set to the value of $k_{12}$ of Table 2 of (Czerlinski and Ypma [3]).

Table 2: Parameter values.

| $m$ | $c_1$ | $c_2$ | $c_3$ | $c_4$ | $c_5$ | $t_{\text{max}}$ | $c_5$ at $t_{\text{max}}$ |
|-----|-------|-------|-------|-------|-------|-----------------|------------------|
| 15  | 1.0092| 0.0101| 0.0101| 0.0005 | 0.0101 | 20.6538         | 0.0131           |
| 11.7| 1.0079| 0.0101| 0.0101| 0.0019 | 0.0101 | 34.2768         | 0.0108           |
| 10.708| 1.0000| 0.0100| 0.0100| 0.0100 | 0.0100 | 11.1038         | 0.0078           |
| 9.7 | 0.9231| 0.0092| 0.0092| 0.0892 | 0.0092 | 6.2038          | 0.0028           |
| 5   | 0.4808| 0.0048| 0.0048| 0.5448 | 0.0048 | 1.7258          | 0.0028           |
| 2   | 0.1934| 0.0019| 0.0019| 0.8408 | 0.0019 | 101.8591        | 0.0028           |
| 1.241| 0.1202| 0.0012| 0.0012| 0.9162 | 0.0012 | 109.9006        | 0.0110           |
| 1   | 0.0969| 0.0010| 0.0010| 0.9402 | 0.0010 | 112.7197        | 0.0010           |
| $c_{i0}$ | 1.0000| 0.0100| 0.0100| 0.0100 | 0.0100 | 112.7197        | 0.0010           |

Table 3: Phase 1 simulations. Stationary state concentrations at $t=10^4$ s for initial free enzyme concentration $c_{60}=m \times 10^{-6}$ M, the time $t_{\text{max}}$ at which $c_5$ has a maximum (if any), and that maximum value of $c_5$.

| $m$ | $c_1$ | $c_2$ | $c_3$ | $c_4$ | $c_5$ | $t_{\text{max}}$ | $c_5$ at $t_{\text{max}}$ |
|-----|-------|-------|-------|-------|-------|-----------------|------------------|
| 15  | 1.0096| 0.0101| 0.0101| 0.0001| 0.0101| 0.4508         | 0.0105           |
| 11.7| 1.0096| 0.0101| 0.0101| 0.0001| 0.0101| 0.7112         | 0.0118           |
| 10.708| 1.0096| 0.0101| 0.0101| 0.0001| 0.0101| 1.7258         | 0.0188           |
| 9.7 | 1.0096| 0.0101| 0.0101| 0.0001| 0.0101| 12.1339        | 0.0583           |
| 5   | 1.0094| 0.0101| 0.0101| 0.0003| 0.0101| 75.1623        | 0.0427           |
| 2   | 1.0085| 0.0101| 0.0101| 0.0013| 0.0101| 101.8591       | 0.0175           |
| 1.241| 1.0000| 0.0100| 0.0100| 0.0100| 0.0100| 109.9006       | 0.0110           |
| 1   | 0.8788| 0.0088| 0.0088| 0.1348| 0.0088| 112.7197       | 0.0068           |
| $c_{i0}$ | 1.0000| 0.0100| 0.0100| 0.0100| 0.0100| 112.7197       | 0.0010           |

Table 4: Phase 2 simulations. Stationary state concentrations at $t=10^4$ s for initial free enzyme concentration $c_{60}=m \times 10^{-6}$ M, the time $t_{\text{max}}$ at which $c_5$ has a maximum (if any), and that maximum value of $c_5$. 

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Results and Discussion

Kinetics

Ideally the steady state concentrations of $c_i$ to $c_6$ match their initial values. To reach this ideal state for a particular set of rate constants in the enzyme cycle one has to select the appropriate value of the initial enzyme concentration $c_6^0$. We tested several values of $c_6$ for Phase 1. We denote by $c_i$ the stationary state concentrations whose values are listed in Table 3. There is a unique value $c_6=10.708 \times 10^{-6}$ M for which $c_i=c_i^0$ for i=1 to 5 and the stationary state concentration of all the substrates is the same. We call this the ‘ideal’ case.

Figure 2 shows the concentrations of the enzymes in Phase 1 when the initial concentration of component 6 is $c_6=15 \times 10^{-5}$ M. Due to the high concentration of component 4, $c_4$ decreases rapidly to form $c_7$.

However, the full enzyme cycle is not operational until the time range of the isomerization of component 7 to 8 is reached. Figure 3 shows the concentrations of the substrates for the same situation. The changes in components 1 and 4 essentially mirror one another, as they do in all subsequent figures. The concentrations of components 3 and 5 increase briefly.

Figure 4 shows the concentrations of the substrates for $c_6=1.241 \times 10^{-6}$ M, which was the ‘ideal’ value in the sense defined above. The changes are much smaller than in Figure 3. Here $c_4$ essentially reverts to its original value after its initial decrease, as do $c_3$ and $c_5$, while compensating changes in $c_1$ and $c_2$ appear only at the end.

Figure 5 shows the concentrations of most of the substrates for $c_6=1.241 \times 10^{-6}$ M, which was the ‘ideal’ value in the sense defined above in our earlier model (Czerlinski and Ypma [3]). Interestingly, $c_4$ changes later than $c_2$ due to compensating effects of the other concentrations.

We see from Figures 3-5 and Table 3 that the results for Phase 1 are...
very different depending on whether $c_6^0$ is above or below the 'ideal' value $c_6^0=10.708\times10^{-6}$ M. In the first case the enzyme cycle is too fast, reducing $c_4$; in the second case the enzyme cycle is too slow, leading to an accumulation of $c_4$. Any $c_6^0>10.708\times10^{-6}$ M eventually leads to concentrations for components 2, 3 and 5 not deviating much from that for $c_6^0=10.708\times10^{-6}$ M. However, $c_6^0 < 10.708\times10^{-6}$ M leads to major changes in these concentrations, hampering the performance of the system.

The initial concentrations for Phase 2 are the steady state concentrations at the end of Phase 1. Table 4 shows the values of all steady state substrate concentrations for Phase 2. Table 4 shows that for Phase 2 the 'ideal' value of $c_6^0$ (that is, the value of $c_6^0$ at the start of Phase 1 for which the substrate concentrations at the stationary state for Phase 2 are the same as at the beginning of Phase 1) is $c_6^0=1.2413\times10^{-6}$ M. This is the same 'ideal' value as in our prior study since identical values for the rate constants are used, but is much lower than the 'ideal' value for Phase 1 above.

![Figure 6: Phase 2 enzyme concentrations for highest initial total enzyme concentration used. Phase 2 with $c_6^0=15\times10^6$ M, showing the concentration of components 6 and 10 through 13.](image)

![Figure 7: Phase 2 substrate concentrations for highest initial total enzyme concentration used. The concentration of components 2, 3, 4 and 5 are shown under the conditions of Figure 6. Three subgraphs are needed to show all the changes.](image)

![Figure 8: Phase 2 substrate concentrations for a lower initial total enzyme concentration. As Figure 7 with $c_6^0=10.708\times10^6$ M. Two subgraphs suffice.](image)

![Figure 9: Phase 2 substrate concentrations for a very low initial total enzyme concentration. As Figure 8 with $c_6^0=1.241\times10^6$ M](image)

![Figure 10: Phase 3 substrate concentrations; two cases. The concentration of components 1, 2, 3, 4 and 5 with $c_6^0=10.708\times10^6$ M. Only $c_1$ and $c_4$ differ significantly between the two cases.](image)
transients in c3 and c5 displacing the timing between components 1 and 2. At 0.916 M, far above its ideal value of 0.01 M. Most of this is provided by the pulsed change in c5. Concentrations at the beginning of a phase. For c6, Figure 9 shows the same concentrations but with c6 appearing next and reacting quickly with substrate 4 to add to component 11. Table 3 shows that in Phase 1 c5 only has a transient maximum for c6 above 1.2413x10^-6 M. Table 4 similarly shows that for enzyme forms in the ground state (S0). Figure 10 shows a pair of cooperating polymers (nanodomains) can exhibit coherent interaction upon proper orientation by the geometric field. The steps of this cyclic interaction are shown from top to bottom; fs-scale. The profile of the nanodomain-reflected is shown as an ellipse, though the actual geometric structure has yet to be determined. A dot near the bottom of the ellipse indicates that the delocalized electron is in its ground state (S0); a dot near the top indicates that the electron is in its (first) excited state (S1). The distances a and b are discussed in the text.

Figure 6 shows the concentration of enzyme components 10 through 13 for Phase 2, with c6=1.5x10^-6 M used for Phase 1. Their concentrations start at zero but increase quickly as components 6 and 7 decrease. Component 10 appears next and reacts quickly with substrate 4 to add to component 11. The stationary state values of c5 and c6 in Phase 2 are quite different from those of the corresponding c5 and c6 in Phase 1.

Figure 7 shows c6 to c11 under the conditions of Figure 6. The changes in c6 and c7 are displaced by the timing of the pulsed change in c6.

Figure 8 shows the same components as Figure 7 but with c6=10.708x10^-6 M (the ‘ideal’ c6 for enzyme forms in the ground state). The steady state concentrations are distinctly different in these two figures. Both figures show a strong decrease in c5, with opposing transients in c6 and c7 displacing the timing between components 1 and 4. Figure 9 shows the same concentrations but with c6=1.241x10^-6 M (the ‘ideal’ c6 for enzyme forms in the excited state). Figure 9 shows a strong decrease in c6 from its earlier high value but the timing is visibly off due to c5 and c7 increasing. Evidently the conditions for Phase 2 result in a more efficient enzyme cycle, requiring much less original enzyme concentration.

Tables 3 and 4 also show the coordinates of intermediate maxima (if any) for the concentration of component 5. These maxima decrease and shift to later times with decreasing initial enzyme concentration. Table 3 shows that in Phase 1 c6 only has a transient maximum for c6 above the ideal value of c6=1.708x10^-4 M. Table 4 similarly shows that c6 only has significant transient values for c6 above 1.241x10^-6 M. Thus, the presence of transients depends on the initial value of key concentrations at the beginning of a phase. For c6=1.241x10^-6 M in Phase 1, c5 starts at 1 M but has end value for Phase 1 (and hence start value for Phase 2) of 0.12 M, far below its ideal level, while c6 starts Phase 2 at 0.916 M, far above its ideal value of 0.01 M. Most of this increase in c5 occurs at the expense of c6.

We examined two cases for Phase 3, as reflected in alternative sets of values for the rate constants k6 to k9 listed in Table 2. In Case A all four rate constants have the same value, while in Case B one of the four rate constants is much larger than the other three. In each case a stationary state with the same stationary state values as those found in Phase 1 is reached. As shown in Figure 10, c6 changes from a very small value to its stationary state value, but more slowly in Case B than Case A. For c6, c7, and c8, the differences are very small.

Physics

Czerlinski and Ypma [10]. Figure 4, introduced groups of nanodomains as ‘polymers’; these are identical to the coherent domains of Arami et al. [18] and Del Giudice and Preparata [19]. The latter computed the radius of a coherence domain (CD) as RCD=1µm=10^-5 dm. Assuming a spherical volume this gives VCD=4.18x10^-15 dm^3 per CD. Its reciprocal gives the molecular concentration as 0.239x10^-9 CDs per liter. Dividing this number by Avogadro’s Number gives the concentration cCD=3.98x10^-10 M. Assumingly maximally 1000 imprints of frequencies per CD, as obtained by Smith [20], and one frequency per nanodomain (ND), one obtains 0.239x10^-10 CDs per liter or, with Avogadro’s Number, cCD=3.98x10^-7 M. The amount of tightly-packed spherical CD-volumes may be unrealistic; cubes with spherically rounded corners may be more realistic. For cubes VCD=8x10^-15 dm^3 per CD or 0.125x10^-15 CDs per liter, giving cCD=2.08x10^-10 M and cND=2.08x10^-7 M. These values of cCD are not far below our early estimate of 10^-6 M (Czerlinski and Ypma [4]), where we did not distinguish between bound and free radicals (bound radicals will most likely decay via free radicals).

Figure 11 shows a pair of nanodomains interacting within a CD. The thickness depends on the number of water molecules participating in the polymerization to a nanodomain; assuming at least 4 water molecules the minimum thickness is about 1 nm. Previously we estimated the distance a ‘between nanodomains as being at least 100 nm, based on the requirement that for resonance to occur the distance of resonators has to be considerably above the Foerster energy transfer distance (around 10 nm). Alternatively, note that coherence of electromagnetic waves extends from 200 nm to 800 nm. If half the wavelength is the minimum distance for resonance between fully aligned nanodomains, then ‘a’ has a minimum of 100 nm, while the longest wavelength gives a maximum value of 400 nm.

With n=1000 nanodomains per CD, CDs then range in size (side length of cubes) from 1 µm to 4 µm (computed as a x 10^n). Since the spectrum of radio waves carried by nanodomains in a CD often has more than 1000 data points (Smith [20]), with one nanodomain per wavelength, CDs could be considerably larger than 4 µm.

Now consider the lifetimes associated with these spatial dimensions. Using the vacuum speed of light, c=3x10^8 m/s, its travel time over the above minimum distance is s=ct/c=10^-7/(3x10^8)=0.33x10^-15 s=0.33 fs (assuming classical physics). The duration of the excited state is probably much longer than that of the wave state, at least a/(a(max)/a(min))=64 times longer. Rise time and fall time for the singlet excited state are the propagation time of one wavelength each. The rapid switching between wave state and excited state extends the lifetime of the excited state, which normally is around 1 ns or less (Foerster [6]).

Biology and coherence

Nanodomains cooperating in CDs store electromagnetic frequencies in the UV and visible range, as in a resonator cavity, with each nanodomain in a CD storing the same frequency. For frequencies to characterize biochemical compounds a whole spectrum
of frequencies in the radiofrequency range must be stored in one CD. Storage of different radiofrequencies in different nanodomains is assured by the Pauli principle, applied to the frequencies (as hν) stored in a cooperating CD. CDs can thus carry the characteristic spectrum of an agent to a target in a living system [21].

Czerlinski and Ypma [11] considered living systems in which nanodomains contain DNA. Kim [22] observed linear arrays of DNA in acupuncture meridian systems, suggesting that CDs in the meridian system are linear. Then 1000 nanodomains would lead to a CD length of 0.1 to 0.4 mm, considerably larger than ordinary cells. If the nanodomains of a cooperating pair are at each end of such a coherence domain, the travel time in the wave state could be as long as 0.4×10^3 m/(3×10^8 m/s) = 0.133×10^-3 or s=1.33 fs.

Czerlinski and Ypma [4] discuss possible metal-like behavior of nanodomains, possibly corresponding to the mirrors postulated by Gariaev et al. [23] for activity in living systems. In such a metal-like reflector system there should be no absorption characteristic of radicals or similar compounds. This is exactly what Ruth and Popp [24] as well as Quickenden and Hee [25] observed.

So far only OH-systems have been considered as forming nanodomains. The H component could be replaced by C, as in ethanol or various sugars. In a biological environment, aromatic ring systems could supply the excited state and the electron in the excited state producing the metal-like environment. The principal contenders for excited state entities in proteins are tryptophan (360 nm [26]) and tyrosine (305 nm [27]). They are the only amino acids with photon absorption above the vacuum UV region (the wavelength of their emission spectrum maximum is indicated above). In a physiological system these amino-acid residues are probably aligned for coherent cooperation and form nanodomains, as aromatic amino-acid residues would do in proteins. Udenfriend and Saltzman [28] showed that fluorescence of aromatic rings in DNA only becomes apparent in hydrolysates. Their maximum fluorescence emissions are in the range of 200 to 400 nm, where these residues could replace part of nanodomains or act as energy gates to and from nanodomains in CDs. Aromatic rings could thus act as modulators, assisting in switching spectra in and out of CDs. Such modulators may be active in low level laser treatment [29].

CDs (coherence over visible and UV-light waves) are related to the radio wave spectra mentioned earlier and the holographic waves (those around 30 s⁻¹) described by Gariaev et al. [23]. Usually the frequency ranges and details of the spectra are controlled by the temperature of the environment. However, in nanodomains they are linked to the frequencies in coherence, which means that the excited states carry their energy quanta. In other words, lower frequency bands are protected from the effects of the thermodynamic heat barrier.

Statistical thermodynamics, especially a description of rotational and translational degrees of freedom, helps to understand multiple frequency bands. The quanta of translation are much smaller than those of rotation, which are those of the radiofrequencies discussed earlier. Bandwidths for the latter two ranges cannot be given, since we do not know the cellular compartment sizes involved. Spectral details could be detected on turning off the geomagnetic field and measuring released radiation. Meyl [30] describes the importance of radio waves for intercellular communication. Meyl [31] emphasizes that classical electrodynamic theory should not be applied, if events extend over less time than a single sinc-wave takes. Experiments regarding the non-validity of classical electrodynamic could start with the correlation between the distance of pairs of nanodomains in coherence and the concentration of these nanodomains, \( c_{CD} \).

**Verification**

The analysis of Endler et al. [32] on the climbing speed of frogs as a function of low-level thyroxin concentration in their water showed that (i) succession (vigorously shaking) of the hormone solution after each dilution is required for any effect, (ii) the effect is maximal even if only a few drops of a sample are added to the water, with the drops diluted in thyroxin to much less than 1 molecule per liter, supporting the action of homeopathic dilutions, (iii) if a solution sample is sealed in a glass ampoule and placed into the bowl with the frogs, the frogs are almost as active as without the ampoule encasement of the hormone, suggesting that electromagnetic radiation is involved. We lack details of the electromagnetic spectra emitted from these vials. Nevertheless these and other data led Czerkinski and Ypma [3] to their molecular description of high-dilution homeopathy, where succession produces water radicals, with some bound in small polymers carrying the electromagnetic information.

How this information is carried was elucidated by the pH-experiments of Scott-Morley [33] and Smith [8]. The former placed homeopathic solutions in ampoules in front of a wideband radio wave amplifier, collecting the amplified radiation in (pretreated) water, and then measured the pH-change, which was significantly above noise level. The latter simulated the storage action of homeopathic solutions by using a radio wave generator, stepping one frequency at a time. He found that at pH 8 he could only saturate the water with close to 400 frequencies, producing a distinct pH-change of 0.04 units. When the geomagnetic field was reduced to 1/100 of its initial value, the pH-change reversed, indicating the loss of photons. Unfortunately neither author calibrated their pH-change by adding a known amount of HCl or NaOH. Nevertheless these experiments show that singlet excited states are involved in storing electromagnetic energy in nanodomains. Since pH-changes are based on the absorption of electromagnetic radiation, the spectra of such radiation should contain information on the origin of the radiation. Such changes arise from the difference in the pKₐ of ordinary water compared to when H₂O is bound in the nanodomain with the radical electron in the excited state. Since the excited state derives from photon absorption, these photons could be observed from the output of a wideband amplifier with input restricted to a specific area of the living system. Variation of the magnetic field strength may be useful.

The rate of diffusion of excited state energy quanta is difficult to measure since it involves fast optical transfer of energy. The concentration of excited state energy quanta might be measured by rapidly moving a mu-metal box over samples, thereby reducing the effect of the earth’s magnetic field to near zero, and observing the emitted photons and the time course of the emission. The distance between nanodomains with excited state energies could possibly be determined by photoflash luminescence using lasers, thus verifying these distances independent of volume estimates and obtaining a better value for nanodomain concentrations.

Another approach to measuring the concentration of nanodomains is to observe free and bound radicals directly. Zafrirou et al. [34] previously used NO and NO-derivatives to measure radicals. Different NO-derivatives may form different complexes, thus revealing differentiating spectral characteristics including those of radical electrons bound within nanodomains.
Conclusions

We described an enzyme activation process which may occur throughout a living system: classical enzyme reactions are energized by converting enzyme components to their excited state, which in turn increases values of rate constants and speeds up turnover. Since nanodomains cooperate coherently in coherence domains they are long-lived, with the electromagnetic spectrum of the coherence domains controlling the action of the stored energies. These domains may interact with similarly designed targets in living systems. These domains may thus be medically useful, as may the electromagnetic spectra themselves. Considering nanodomains as electromagnetic energy storage elements also introduces the notion of photon communication within living systems.

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