

Quantum Algorithms and the Genetic Code

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Replication of DNA and synthesis of proteins are studied from the view-point of quantum database search. Identification of a base-pairing with a quantum query gives a natural (and first ever!) explanation of why living organisms have 4 nucleotide bases and 20 amino acids. It is amazing that these numbers arise as solutions to an optimisation problem. Components of the DNA structure which implement Grover’s algorithm are identified, and a physical scenario is presented for the execution of the quantum algorithm. It is proposed that enzymes play a crucial role in maintaining quantum coherence of the process. Experimental tests that can verify this scenario are pointed out.

I. GENETIC INFORMATION

I am going to talk about processes that form the basis of life and evolution. The hypothesis that living organisms have adapted to their environment, and have exploited the available material resources and the physical laws governing them to the best of their capability, is the legacy of Charles Darwin—survival of the fittest. This is an optimisation problem, but it is not easy to quantify it in mathematical terms. Often we can explain various observed features of living organisms [1]. The explanation becomes more and more believable, as more and more of its ingredients are verified experimentally [3]. Yet even when definite predictions exist, an explanation is an explanation and not a proof; there is no way we can ask evolution to repeat itself and observe it like many common scientific experiments.

With this attitude, let us look at life. Living organisms try to perpetuate themselves [4]. The disturbances from the environment, and the damage they cause, make it impossible for a particular structure to survive forever. So the perpetuation is carried out through the process of replication. One generation of organisms produces the next generation, which is essentially a copy of itself. The self-similarity is maintained by the hereditary information—the genetic code—that is passed on from one generation to the next. The long chains of DNA molecules residing in the nuclei of the cells form the repository of the genetic information. These DNA molecules control life in two ways: (1) their own highly faithful replication, which passes on the information to the next generation (each life begins as a single cell, and each cell in a complex living organism contains identical DNA molecules), and (2) the synthesis of proteins which govern all the processes of a living organism (haemoglobin, insulin, immunoglobulin etc. are well-known examples of proteins) [5].

Computation is nothing but processing of information. So we can study what DNA does from the view-point of computer science. In the process of designing and building modern computers, we have learnt the importance of various software and hardware features. Let us look at some of them.

The first is the process of digitisation. Instead of handling a single variable covering a large range, it is easier to handle several variables each spanning a smaller range. Any desired accuracy can be maintained by putting together as many as necessary of the smaller range variables, while the instruction set required to manipulate each variable is substantially simplified. This simplification means that only a limited number of processes have to be physically implemented, leading to high speed computation. Discretisation also makes it possible to correct small errors arising from local fluctuations. There are disadvantages of digitisation in terms of increase in the depth of calculation and power consumption, but the advantages are so great that digital computers have pushed away analogue computers to obscurity. Even before the discovery of DNA, Erwin Schrödinger had emphasised the fact that an aperiodic chain of building blocks carries information [6], just like our systems of writing numbers and sentences. The structure of DNA and protein reveals that life has indeed taken the route of digitising its information. DNA and RNA chains use an alphabet of 4 nucleotide bases, while proteins use an alphabet of 20 amino acids.

The second is the packing of the information. When there are repetitive structures or correlations amongst different sections of a message, that reduces its capacity to convey new information—part of the variables are wasted in repeating what is already conveyed. Claude Shannon showed that the information content of a fixed length message is maximised when all the correlations are eliminated and each of the variables is made as random as possible. Our languages are

not that efficient; we can immediately notice that consonants and vowels roughly alternate in their structure. When we easily compress our text files on a computer, we remove such correlations without losing information. Detailed analyses of DNA sequences have found little correlation amongst the letters of its alphabet, and we have to marvel at the fact that life has achieved the close to maximum entropy structure of coding its information.

The third is the selection of the letters of the alphabet. This clearly depends on the task to be accomplished and the choices available as symbols. A practical criterion for fast error-free information processing is that various symbols should be easily distinguishable from each-other. We use the decimal system of numbers because we, at least in India, learnt to count with our fingers. There is no way to prove this, but it is a better explanation than anything else. We can offer a better justification for why the computers we have designed use the binary system of numbers. 2 is the smallest base available for a number system, and that leads to maximal simplification of the elementary instruction set. (The difference is obvious when we compare the mathematical tables we learnt in primary schools to the corresponding operations in binary arithmetic.) 2 is also the maximum number of items that can be distinguished with a single yes/no question. (Detecting on/off in an electrical circuit is much easier than identifying more values of voltages and currents.) Thus it is worth investigating what life optimised in selecting the letters of its alphabet.

The computational task involved in DNA replication is ASSEMBLY. The desired components already exist (they are floating around in a random ensemble); they are just picked up one by one and arranged in the required order. To pick up the desired component, one must be able to identify it uniquely. This is a variant of the unsorted database search problem, unsorted because prior to their selection the components are not arranged in any particular order. (It is important to note that this replication is not a COPY process. COPY means writing a specific symbol in a blank location, and unlike ASSEMBLY, it is forbidden by the linearity of quantum mechanics.) The optimisation criterion for this task is now clear—one must distinguish the maximum number of items with a minimum number of identifying questions. I have already pointed out that in a classical search, a single yes/no question can distinguish two items. The interesting point is that a quantum search can do better.

II. UNSORTED DATABASE SEARCH

Let the database contain N distinct objects arranged in a random order. A certain object has to be located in the database by asking a set of questions. Each query is a yes/no question based on a property of the desired object (e.g. is this the object that I want or not?). In the search process, the same query is repeated using different input states until the desired object is found. Let Q be the number of queries required to locate the desired object in the database.

Using classical probability analysis, it can be easily seen that (a) $\langle Q \rangle = N$ when all objects are available with equal probability for each query (i.e. each query has a success probability of $1/N$), and (b) $\langle Q \rangle = (N + 1)/2$ when the objects which have been rejected earlier in the search process are not picked up again for a query. Here the angular brackets represent the average expectation values. Option (b) is available only when the system possesses memory to recognise what has already been tried before. In the random cellular environment, the rejected object is thrown back into the database, and only option (a) is available to a classical ASSEMBLY operation.

Lov Grover discovered a quantum database search algorithm that locates the desired object using fewer queries [7]. Quantum algorithms work with amplitudes, which evolve in time by unitary transformations. At any stage, the observation probability of a state is the absolute value square of the corresponding amplitude. The quantum database is represented as an N -dimensional Hilbert space, with the N distinct objects as its orthonormal basis vectors. The quantum query can be applied not only to the basis vectors, but also to their all possible superpositions (i.e. to any state in the Hilbert space). Let $|b\rangle$ be the desired state and $|s\rangle$ be the symmetric superposition state [8].

$$|b\rangle = (0 \dots 010 \dots 0)^T, \quad |s\rangle = (1/\sqrt{N})(1 \dots 1)^T. \quad (1)$$

Let $U_b = 1 - 2|b\rangle\langle b|$ and $U_s = 1 - 2|s\rangle\langle s|$ be the reflection operators corresponding to these states [9]. The operator U_b distinguishes between the desired state and the rest. It flips the sign of the amplitude in the desired state, and is the query or the quantum oracle. The operator U_s treats all objects on an equal footing. It implements the reflection about the average operation. Grover's algorithm starts with the input state $|s\rangle$, and at each step applies the combination $-U_s U_b$ to it. Each step just rotates the state vector by a fixed angle (determined by $|\langle b|s\rangle| = 1/\sqrt{N}$) in the plane formed by $|b\rangle$ and $|s\rangle$. Q applications of $-U_s U_b$ rotate the state vector all the way to $|b\rangle$, at which stage the desired state is located and the algorithm is terminated.

$$(-U_s U_b)^Q |s\rangle = |b\rangle. \quad (2)$$

This relation is readily solved, since the state vector rotates at a constant rate, giving

$$(2Q + 1) \sin^{-1}(1/\sqrt{N}) = \pi/2. \quad (3)$$

Over the last few years, this algorithm has been studied in detail. I just summarise some of the important features:

- For a given N , the solution for Q satisfying Eq.(3) may not be an integer. This means that the algorithm will have to stop without the final state being exactly $|b\rangle$ on the r.h.s. of Eq.(2). There will remain a small admixture of other states in the output, implying an error in the search process. The size of this admixture is determined by how close one can get to $\pi/2$ on the r.h.s. of Eq.(3). Apart from this, the algorithm is fully deterministic.
- The algorithm is known to be optimal [10], going from $|s\rangle$ to $|b\rangle$ along a geodesic. No other algorithm, classical or quantum, can locate the desired object in an unsorted database with a fewer number of queries.
- The iterative steps of the algorithm can be viewed as the discretised evolution of the state vector in the Hilbert space, governed by a Hamiltonian containing two terms, $|b\rangle\langle b|$ and $|s\rangle\langle s|$. The former represents a potential energy attracting the state towards $|b\rangle$, while the latter represents a kinetic energy diffusing the state throughout the Hilbert space. The alteration between U_b and U_s in the discretised steps is reminiscent of Trotter's formula used in construction of the transfer matrix from a discretised Feynman's path integral [11].
- Asymptotically, $Q = \pi\sqrt{N}/4$. The best that the classical algorithms can do is to random walk through all the possibilities, and that produces $Q = O(N)$ as mentioned above. With the use of superposition of all possibilities at the start, the quantum algorithm performs a directed walk to the final result and achieves the square-root speed-up.
- The result in Eq.(3) depends only on $|\langle b|s\rangle|$; the phases of various components of $|s\rangle$ can be arbitrary, i.e. they can have the symmetry of bosons, fermions or even anyons.

To come back to the genetic code, let us look at two of the solutions of Eq.(3) for small Q . The only exact integral solution is $Q = 1$, $N = 4$. Base-pairing during DNA replication can be looked upon as a yes/no query, either the pairing takes place through molecular bond formations or it does not, and its task is to distinguish between 4 possibilities. The other interesting solution is $Q = 3$, $N = 20.2$. The well-known triplet code of DNA has 3 consecutive nucleotide bases carrying 21 signals [12], 20 for the amino acids plus a STOP [13]. 3 base-pairings between t-RNA and m-RNA transfer this code to the amino acid chain [5].

These solutions are highly provocative. This is the first time they have come out of an algorithm that performs the actual task accomplished by DNA. It is fascinating that they are the optimal solutions [14]. Indeed it is imperative to investigate whether DNA has the quantum hardware necessary to implement the quantum search algorithm.

III. MOLECULAR BIOLOGY AND THE STRUCTURE OF DNA

Over the last fifty years, molecular biologists have learnt a lot about the structure and function of DNA by careful experiments (they have also been rewarded with many Nobel prizes). Let us quickly go through some of the facts they have unravelled [12,15,16].

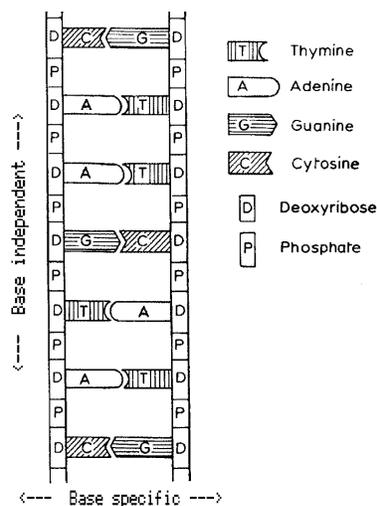


FIG. 1. A schematic representation of the DNA double helix, depicting base-specific and base-independent molecular bonds. The exact match between bases joins two complementary strands of DNA.

- DNA has the structure of a double helix. It can be schematically represented as a ladder, as in Fig.1. The sides of the ladder have a periodic structure with alternating sugar and phosphate groups. The nucleotide base pairs form the rungs of the ladder, and the genetic information is encoded in the order of these base pairs.
- DNA contains 4 nucleotide bases—A, T, C, G—which are closely related to each-other in chemical structure [17]. The bases are always paired as A-T and C-G along the rungs of the ladder by Hydrogen bonds. This base-pairing makes the two DNA strands complementary in character.
- The sugar and phosphate groups along the side of the ladder are held together by covalent bonds. Their bonding is completely insensitive to the bases attached to them, and takes place in the presence of DNA polymerase enzymes.
- During replication, the helicase enzyme separates the two strands of DNA by breaking the Hydrogen bonds, much like opening a zipper. The unpaired bases along each of the separated strands find their partners from the surrounding molecules, producing two copies of the original DNA.
- The sides of the ladder have asymmetric ends. The replication process is directed, always proceeding from the 5' end to the 3' end (these numbers label the position of the carbon atoms in the sugar rings) of the strand being constructed. The DNA polymerase enzyme slides along the intact strand, adding one base at a time to the growing strand. During this process, base-pairing and sugar-phosphate bonding alternate.
- RNA molecules carry the nucleotide bases—A, U, C, G—with U very similar in chemical structure to T. A-U pairing is as strong as A-T pairing. Messenger RNA (m-RNA) has a single strand structure. In the first step of protein synthesis, the RNA polymerase enzyme separates the paired DNA strands and constructs an m-RNA strand on the DNA template by base-pairing (the process is the same as in DNA replication). The m-RNA strand grows as the RNA polymerase enzyme slides along the DNA from the promoter to the terminator base sequence. Finally the RNA polymerase enzyme detaches itself from the DNA, the fully constructed m-RNA strand floats away to the ribosomes in the cytoplasm of the cell, and the separated DNA strands pair up again.
- Transfer RNA (t-RNA) molecules have 3 RNA bases at one end and an amino acid at the other, with a many-to-one mapping between the two. Inside cellular structures called ribosomes, 3 t-RNA bases line up against the matching bases of m-RNA, aligning the amino acids at the other end. The aligned amino acids then split off from the t-RNA molecules and bind themselves into a chain. The process again proceeds monotonically from the 5' end to the 3' end of the m-RNA. After the amino acids split off, the remnant t-RNA molecules are recycled. This completes the transfer of the genetic code from DNA to proteins.
- Enzymes play a crucial role in many of the above steps. In addition to facilitating various processes by their catalytic action, they store energy needed for various processes, ensure that DNA keeps out U and RNA keeps out T, and perform error correction by their 3' → 5' exonuclease action (i.e. reversing the assembly process to remove a mismatched base pair).
- Hereditary DNA is accurately assembled, with an error rate of 10^{-7} per base pair, after the proof-reading exonuclease action. Proteins are assembled less accurately, with an error rate of 10^{-4} per amino acid [14].

Let us also recollect some useful facts about various chemical bonds.

- Ionic bonds are strong, can form at any angle, and can be explained in terms of electrostatic forces. Ions often separate in solutions.
- Covalent bonds are strong, form at specific angles, and can be explained in terms of Coulomb forces between electrons and nuclei and the exclusion principle.
- Van der Waals bonds are weak, not very angle dependent, and explainable in terms of interactions between virtual electric dipoles. They play an important role in transitions between solid, liquid and gas phases, as well as in folding and linking of polymers.
- Hydrogen bonds are weak, highly angle dependent, and explainable in terms of a proton (H^+) tunneling between two attractive energy minima. The situation is a genuine illustration of a particle in a double well potential, e.g. $O - H \cdots : N \rightleftharpoons O^- : \cdots H - N^+$. High sensitivity of the tunneling amplitude to the shape of the energy barrier make Hydrogen bonds extremely sensitive to the distances and angles involved. They are the most quantum of all bonds; water is a well-known example.
- Delocalisation of electrons and protons over distances of the order of a few angstroms greatly helps in molecular bond formation. It is important to note that these distances are much bigger than the Compton wavelengths of the particles, yet delocalisation is common and maintains quantum coherence. In case of electrons, the phenomena are called resonance and hybridisation, e.g. the benzene ring. In case of protons, the different configurations are called tautomers, e.g. amino \rightleftharpoons imino and keto \rightleftharpoons enol fluctuations of the nucleotide bases.

With all this information, the quantum search algorithmic requirements from the DNA structure are clear. It is convenient to take the distinct nucleotide bases as the quantum basis states in the Hilbert space. Then (1) The quantum query transformation U_b must be found in the base-pairing with Hydrogen bonds. (2) The symmetric transformation U_s must be found in the base-independent processes occurring along the sides of the ladder. (3) An environment with good quantum coherence must exist. Thermal noise is inevitable at $T \approx 300^\circ K$ inside the cells, so the transformations must be stable against such fluctuations. Figuratively, the best that can be achieved is

$$\text{Actual evolution} = \lim_{\text{decoherence} \rightarrow 0} [\text{Quantum evolution}] . \quad (4)$$

Thus we need quantum features that smoothly cross over to the classical regime, i.e. features that are reasonably stable against small decoherent fluctuations. Examples are: (a) geometric and topological phases, and (b) projection/measurement operators.

IV. BASE-PAIRING AS THE QUANTUM ORACLE

During DNA replication, the intact strand of DNA acts as a template on which the growing strand is assembled. At each step, the base on the intact strand decides which one of the four possible bases can pair with it. This is exactly the yes/no query (also called the oracle) used in the database search algorithm. To connect this oracle to the quantum transformation U_b , we have to look at how molecular bond formations transform a quantum state.

The generic quantum evolution operator is $\exp(-iHt)$, with H being the total Hamiltonian of the system. Global conservation of energy means that the overall phase $\exp(-iEt)$ will completely factor out of the evolution and will not affect the final probabilities. What matters is only the relative phase between pairing and non-pairing bases. During the pairing process, the bases come together in an initial scattering state, discover that there is a lower energy binding state available, and decay to that state releasing the extra energy as a quantum [18]. The interaction Hamiltonian for the bond formation process can be represented as

$$H_{int} \propto (a^\dagger b + b^\dagger a) , \quad (5)$$

where a, a^\dagger are the transition operators between the excited and ground states of the reactants, and b, b^\dagger are the transition operators between zero and one quantum states of energy released. Both the terms in Eq.(5) are necessary for the Hamiltonian to be Hermitian. The phase change φ during the bond formation satisfies

$$\exp(-iH_{int}t_b)|e\rangle|0\rangle = \varphi|g\rangle|1\rangle . \quad (6)$$

With only two states involved, Eq.(6) is easily solved by diagonalising H_{int} . In the two dimensional space, let

$$H_{int} = \Delta E_H \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix} , \quad \text{eigenvectors} : \frac{1}{\sqrt{2}} \begin{pmatrix} 1 \\ \pm 1 \end{pmatrix} , \quad (7)$$

and eigenvalues $\pm\Delta E_H$. Eq.(6) then reduces to

$$\exp(-i\Delta E_H t_b) = \varphi = -\exp(i\Delta E_H t_b) , \quad (8)$$

with the solution $\varphi = \sqrt{-1}$.

This is the geometric phase well-known in quantum optics. A complete Rabi cycle in a two-level system gives a phase change of -1 , and the transition process corresponds to half the cycle. The phase φ does not depend on specific values of ΔE_H or t_b , but only on the fact that the transition takes place. Quantum mechanics does not specify how φ will be divided between the bound state and the released energy quantum. In quantum optics, this break-up is determined by the phase of the laser. Here I assume that the process of decoherence is such that the energy quantum does not carry away any phase information.

At this stage, we discover a pleasant surprise that the base-pairing takes place not with a single Hydrogen bond but with multiple Hydrogen bonds (two for A-T and A-U, and three for C-G), as shown in Fig.2 [19]. Multiple Hydrogen bonds are necessary for the mechanical stability of the helix. But they are also of different length, making it likely that they form asynchronously. Assuming a two-step deexcitation process during base-pairing, the geometric phase change becomes $\varphi^2 = -1$, just what is needed to implement U_b .

The energy of a single Hydrogen bond is $\Delta E_H \approx 7kT$, giving $\exp(-\Delta E_H/kT) \sim 10^{-3}$. This roughly explains the observed error rate in DNA replication. The tunneling amplitude for bond formation is related to both ΔE_H and t_b , which determines the time scale of the base-pairing,

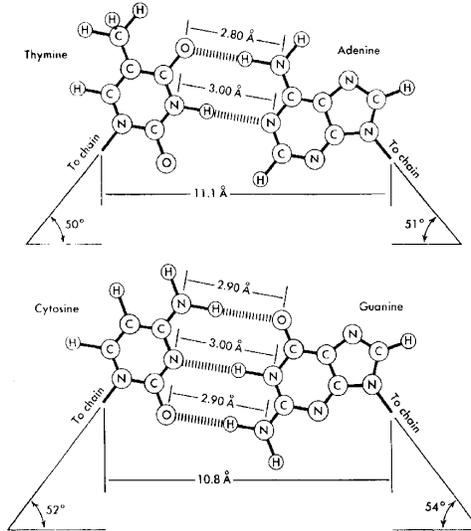


FIG. 2. The base-pairing in DNA with Hydrogen bonds. The figure is taken from Ref.[12].

$$\Delta E_{Ht_b} \approx \hbar \implies t_b \approx 4 \times 10^{-15} \text{ sec.} \quad (9)$$

V. A QUANTUM SEARCH SCENARIO

The next step is to look for the transformation U_s in the processes occurring along the sides of the DNA-ladder. During these processes, quantum evolution produces various phases as molecular bonds get formed and broken. But these bonds treat all the nucleotide bases in the same manner, so the phases completely factor out and have no effect on the final probabilities. Thus I leave the phases out.

Suppose that $|s\rangle$ is the equilibrium state of the physical system, favoured by the processes that occur along the sides of the DNA-ladder. This means that any other initial state will gradually relax towards $|s\rangle$, with the damping provided by the environment. Let t_r be the time scale for this relaxation process. Now $|s\rangle$ is a superposition state of nucleotide bases, and it can be created only if the cellular environment provides transition matrix elements between its various components. (In free space, transition matrix elements between nucleotide bases of different chemical composition vanish.) The magnitude of these transition matrix elements decides how quickly $|s\rangle$ cycles through its various components. Let t_{osc} be the time scale for these oscillations. Now let us look at the DNA replication process, when the above defined time scales satisfy the hierarchy

$$t_b \ll t_{osc} \ll t_r . \quad (10)$$

- (1) In the initial stage, the randomly floating around nucleotide bases come into contact with the growing DNA strand, and relax to the state $|s\rangle = (1/\sqrt{N}) \sum_i |i\rangle$.
- (2) When the nucleotide base finds its proper orientation, Hydrogen bond formation suddenly takes place, changing the state to $U_b|s\rangle$. This state is entangled between the nucleotide bases and the energy quanta, $U_b|s\rangle = (1/\sqrt{N})[\sum_{i \neq b} |i\rangle|0\rangle - |b\rangle|2\rangle]$.
- (3) After this sudden change, the relaxation process again tries to bring the system back to the state $|s\rangle$. With the time scales obeying Eq.(10), this relaxation occurs as damped oscillations, much like what happens when one gives a sudden jerk to a damped pendulum.
- (4) The opposite end of the damped oscillation is $(2|s\rangle\langle s| - 1)U_b|s\rangle = -U_s U_b|s\rangle$. When the system evolves to this opposite end, it discovers that it is no longer entangled between the nucleotide bases and the energy quanta, $-U_s U_b|s\rangle|0\rangle = |b\rangle|2\rangle$ for $N = 4$. At this point, the energy quanta are free to wander off with minimal disturbance to the quantum coherence. The departure of the energy quanta confirms the base-pairing, providing a projective measurement of the system. (I take the measurement time scale to be much smaller than t_{osc} .)
- (5) The energy quanta that have wandered off are unlikely to return, making the process irreversible. The replication then continues to add the next base onto the growing strand.

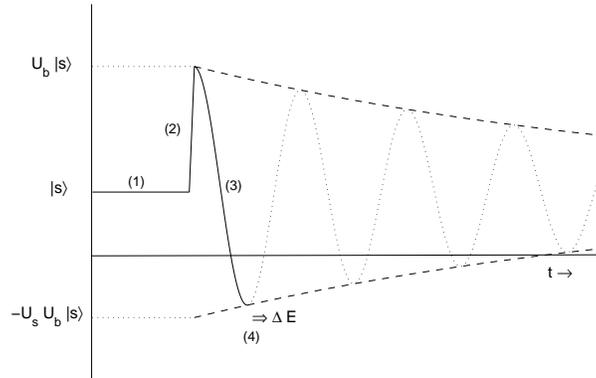


FIG. 3. A time evolution picture of the DNA replication algorithm. Numerical labels refer to the steps described in the text.

These steps are schematically shown in Fig.3. They provide a highly tuned yet a robust algorithm. There are no fine-tuned parameters; the hierarchy of Eq.(10) has enough room to take care of substantial variation in individual time scales. Life couldn't be simpler!

To illustrate the possibility that processes with time scales obeying the hierarchy of Eq.(10) do physically occur, let us look at a quantum example. Consider the processes involved in the functioning of the NH_3 maser. NH_3 is a molecule with two equivalent configurations, corresponding to the Nitrogen atom being above or below the triangle of Hydrogen atoms. These two configurations can be distinguished by the direction of their electric dipole moments. Quantum tunneling of the Nitrogen atom through the triangle of Hydrogen atoms mixes these two configurations, and the ground state is the symmetric superposition of the two. In NH_3 gas, any initial state decays towards this equilibrium ground state (molecular collisions help in this relaxation). If a electric field is applied to the gas for a short duration, it favours one of the two configurations and kicks the molecules out of their equilibrium state. After the removal of the electric field, the kicked molecules oscillate from one configuration to the other, till the oscillations are damped out by the decay process. Shining the molecules with a radio-frequency pulse resonant with t_{osc} removes the extra energy quickly by stimulated emission and produces a coherent maser.

The relaxation time scale t_r depends on temperature as well as on various molecular concentrations, and governs the overall replication rate. Under normal circumstances, DNA replication is observed to occur at the rate of 1000 base-pairings/sec, constraining t_r to be smaller than $O(10^{-3})$ sec. Without any knowledge of the transition matrix elements, I do not have any estimate of t_{osc} .

Strictly speaking, I should not talk about quantum states in processes that involve damping; the proper mathematical formulation must be in the language of density matrices. But when the damping is small, as is the case here, it is easier to talk about states. The steps above can be easily transcribed in the language of density matrices, without changing their outcomes.

Now we can proceed to the remaining pieces needed to complete the scenario: a mechanism that favours the state $|s\rangle$ as the equilibrium state, and an environment that permits an almost coherent quantum evolution. For that I have to appeal to the ingredients ignored so far—the enzymes.

VI. THE ROLE OF THE ENZYMES

Enzymes play a very important role in many biochemical reactions, and some of the things they do were mentioned in section III. The rates of various biochemical reactions, when estimated with the standard thermodynamical analysis (probability distributions, diffusion processes, kinetic theory, etc.), fall too short of the observed rates, often by orders of magnitudes. One is left with no choice but to admit that these reactions are catalysed.

Enzymes are the objects which catalyse biochemical reactions. They are large complicated molecules, much larger than the reactants they help, made of several peptide chains. Their shapes play an important part in catalysis, and often they completely surround the reaction region. They do not bind to either the reactants or the products, just help them along the way. The standard explanation is that enzymes lower reaction barriers. Just how this lowering of reaction barriers occurs is not clearly understood, and is an active area of research (for example, enzymes can form weak bonds with the transition state or suck out solvent molecules from in between the reactants). Ultimately it must be explained in terms of some underlying physical laws.

I put forward two specific hypotheses about what enzymes accomplish in the processing of genetic information.

- *Enzymes provide a shielded environment where quantum coherence of the reactants is maintained.* This is a rather passive task, consistent with the properties of enzymes mentioned above, and it is also plausible. For instance, diamagnetic electrons do an extraordinarily good job of shielding the nuclear spins from the environment—the coherence time observed in NMR is $O(10)$ sec, much longer than the thermal environment relaxation time ($\hbar/kT \sim O(10^{-14})$ sec) and the molecular collision time ($O(10^{-11})$ sec), and still neighbouring nuclear spins couple through the electron cloud. A few orders of magnitude increase in coherence time is sufficient in many reactions for faster quantum algorithms to take over from their classical counterparts, and provide the catalytic speed-up.
- *Enzymes are able to create superposed states of chemically distinct molecules.* This is an active task. Various nucleotide bases differ from each other only in terms of small chemical groups, containing less than 10 atoms, at their Hydrogen bonding end. To convert one base into another, enzymes have to be repositories of these chemical groups which differentiate between various nucleotide bases. Enzymes are known to do cut-and-paste jobs with such chemical groups (e.g. one of the simplest substitution processes is methylation, replacing $-H$ by $-CH_3$, which converts U to T). Given such transition matrix elements, quantum dynamics automatically produces a superposition state as the lowest energy equilibrium state. (Note that the cut-and-paste job in a classical environment would produce a mixture, but in a quantum environment it produces superposition.) It is mandatory that the enzymes do the cut-and-paste job only on the growing strand and not on the intact strand. Perhaps this is ensured by other molecular bonds.

These hypotheses are powerful enough to explain many observed properties of enzymes from a new perspective. For example,

- It is obvious why DNA replication always takes place in the presence of enzymes. If base-pairing were to occur by chance collisions, it would occur anywhere along the exposed unpaired strand.
- Since enzymes control the transition matrix elements, they can keep U out of DNA and T out of RNA.
- Quantum processes can tunnel through the reaction barriers, instead of climbing over them.
- As long as quantum coherence is maintained, the replication process is reversible. This can easily explain the error-correcting exonuclease action of the polymerase enzymes.

More importantly, these hypotheses are experimentally testable, provided one can observe the replication process at its intermediate stages. That is within the grasp of modern techniques such as X-ray diffraction analysis, electron microscopy, NMR spectroscopy, radioactive tagging of atoms in chemical reactions, and femtosecond photography.

VII. SUMMARY AND FUTURE

I have proposed a quantum algorithmic mechanism for DNA replication and protein synthesis. This genetic information processing takes place at the molecular level, where quantum physics is indeed the dominant dynamics (classical physics effects appear as decoherence and are subdominant). It is reasonable to expect that if there was something to be gained from quantum computation, life would have taken advantage of that at this physical scale [20]. For DNA replication, the quantum search algorithm provides a factor of two speed-up over classical search, but it is still an advantage. Quantum algorithms can provide a bigger advantage for more complicated processes involving many steps.

Implementation of quantum database search does not require a general purpose quantum computer. A system that can implement the quantum oracle and quantum state reflections is sufficient. I have described the physical analogues of these operations in genetic information processing, and it is not unusual for living organisms to find the correct ingredients without bothering about generalities. In fact various pieces of the scenario have fitted together so nicely (database search paradigm, optimal (Q, N) values—(1, 4) and (3, 20.2), quantum transformations implementing U_b and U_s), that with the courage of conviction, I have made bold hypotheses to fill the remaining gaps. The role that enzymes play, as described in section VI, is both plausible and experimentally verifiable. The other assumptions I have made (i.e. two-step cascade deexcitation in base-pairing, energy quanta not carrying away any phase information, energy quanta departing only when they cause minimal decoherence to the system) concern how decoherence modifies pure quantum evolution, and are also experimentally testable. Such experimental tests would decide the future of this proposal.

It is clear that if experiments verify the quantum scenario for genetic information processing presented here, there will be a significant overhaul of conventional molecular biology. There is nothing inappropriate in that—the subject of molecular biology was born out of quantum physics, and quantum physics has not yet had its last word on it.

I also want to acknowledge that molecular biology is a far more complicated subject than the simplest features I have explored in this work. If quantum physics provides better explanations for other more complex phenomena of life, it would be a wonderful development.

APPENDIX: SOME QUESTIONS AND ANSWERS

I am grateful to the audience for their many comments and questions. I summarise below some of the important concepts they brought out.

Q: Are there any examples of genetic codes which use other values of Q , say $Q = 2$?

A: I do not know of any such examples. May be some day we shall become clever enough to synthesise such instances in the laboratory.

Q: Parallel processing can also speed-up algorithms. Why is that not used in the case of genetic code?

A: In case of DNA replication, enzymes separate only a limited region of paired strands as they slide along replicating the information. Complete separation of the strands would break too many Hydrogen bonds and cost too much in energy. Thus the replication remains a local process. In case of protein synthesis, random pairing of t-RNA and m-RNA at several different locations would lead to a lot of mismatches and errors, since the triplet code needs precise starting and ending points. Parallel processing does take place though: several ribosomes work simultaneously on a single m-RNA strand, each one traversing the full length of m-RNA from one end to the other and constructing identical amino acid chains.

Q: Three nucleotide bases can form 64 distinct codes. Why do you still say that 20 is the optimal number for the triplet code?

A: When the DNA assembly takes place, with each base as a separate unit, the number of possibilities explored is indeed 4^Q . But this is not what happens in the matching between t-RNA and m-RNA. The three bases come as a single group, without any possibility of their rearrangement. The whole group has to be accepted or rejected as a single entity. In such a situation, the number of objects that can be distinguished is smaller, as given by Eq.(3).

Q: Do you have any understanding of degeneracy of the triplet code?

A: With only 21 signals embedded amongst 64 possibilities, the amino acid code is indeed degenerate. Moreover, all the amino acids are not present in living organisms with equal frequency, quite unlike the nucleotide bases. Ribosomes are also much bigger and more complicated molecules than the polymerase enzymes, and so capable of carrying out more complex tasks. All this makes protein synthesis a more difficult process to study than DNA replication. I have not analysed it in detail, and I am unable to provide any understanding of the degeneracy of the triplet code.

Q: The energy quanta do not have to be released exactly at the opposite end of the oscillation. Oscillations spend more time near their extrema anyway, and so even random emission will give high probability for correct base-pairing.

A: I agree. But a smaller success probability means that more trials will be necessary to achieve the correct base-pairing. That would diminish the advantage of the quantum algorithm.

Q: Enzymes are also proteins which have to be synthesised by the DNA. How are they synthesised in the first place?

A: Classical algorithms can do everything that quantum algorithms do, albeit slower. In the absence of enzymes, various steps will take place only by random chance, and so the start-up will be slow. But once processes get going, as in a living cell, enzymes will be manufactured along the way and there will be no turning back to slower algorithms.

Q: If polymerase enzymes have to keep on supplying various chemical groups to nucleotide bases, they would run out of their stock at some stage. What happens then?

A: In my proposal, the polymerase enzymes substitute one chemical group for another. With the DNA base sequence being random, the chemical groups are recycled with high probability. So with a reasonable initial stock an enzyme can perform its task for a long time. Of course if an enzyme runs out of its stock, it has no choice but to quit and replenish its stock.

Q: How essential is the environment of a living cell in DNA replication? Are there any other molecules besides enzymes involved?

A: DNA replication can take place without cellular environment. With proper enzymes in the solution, the polymerase chain reaction can rapidly multiply DNA. This is used in DNA fingerprinting from dead cells.

Q: Many inorganic reactions can be speeded up by appropriate catalysts. Are they quantum reactions too?

A: In my view, catalysts convert random walk processes into directed walks, providing a \sqrt{N} speed-up in the number of steps. Quantum superposition is one way to achieve this, but it does not have to be the only way. There may be even classical mechanisms which can do the same job.

Q: Living organisms are known to emit radiation, which is coherent and not thermal (black-body). Is there any connection between these biophotons and your proposal?

A: This is the first time I have heard about biophotons. If they are related to some quantum processes going on inside living cells, that would be great.

Q: Are there any applications of your proposal?

A: Understanding the basic processes of life will always lead to new applications. For example, molecular biologists have been working on accelerating synthesis of desired proteins and inhibiting growth of cancer and harmful viruses. I am not inclined to speculate more on this issue right now.

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- [1] I mention here the explanation of physical shapes of living organisms [2]. At microscopic level, the physical forces (e.g. diffusion, surface tension) are essentially isotropic. Consequently single free cells are found to be more or less spherical in shape (e.g. many bacteria, amoeba). At larger scales, the isotropy is explicitly broken by gravity. This leads to large stationary living organisms being axially symmetric about the vertical direction (e.g. plants, hydra). The symmetry is also broken spontaneously by the need of the organisms to move/grow in order to find food. For small enough organisms where the effects of gravity is not important, there arises an axial symmetry about the direction of movement (e.g. worms, some bacteria). For most animals, both gravity and movement are important, with gravity restricting the direction of movement to be horizontal. The surviving symmetry is then bilateral, i.e. mirror reflection in the plane formed by directions of gravity and movement. What is striking in this example is the simplicity of the logic, i.e. how far one can go with how little input once the ingredients are right. It is also obvious that there is a limit to how far simple logic can be pushed—to explain the structure in more depth, one would require more detailed physical data.
- [2] M. Gardner, *The New Ambidextrous Universe: Symmetry and Asymmetry, from Mirror Reflections to Superstrings*, Third Edition, W.H. Freeman (1991).
- [3] For the above explanation of shapes of living organisms, one can estimate the scale at which effects of gravity and motion would become important. The orders of magnitude estimates do come out right. On the other hand, many attempts have been made to link observed chirality of important molecules of life (sugars and amino acids) to the chirality of the weak interactions. But weak interactions are just too weak to produce any influence at the molecular scale, and no attempt has come anywhere close to convincing.
- [4] The same physical laws used by living organisms for self-perpetuation, also imply that the atoms making up the organisms will last forever. In that case, why the atoms should first organise themselves in complicated structures, and then try to perpetuate them, is something that I cannot answer.
- [5] Protein synthesis involves several steps. First the DNA synthesises messenger RNA molecules, much in the same manner that it replicates itself. These m-RNA molecules then travel from the nucleus of the cell to the ribosomes in its cytoplasm. There, with the help of transfer RNA molecules, they construct proteins from amino acids. The matching between m-RNA and t-RNA molecules follow the same rules as in DNA replication.
- [6] E. Schrödinger, *What is Life?*, Cambridge University Press (First published 1944).
- [7] L. Grover, *A Fast Quantum Mechanical Algorithm for Database Search*, Proceedings of the 28th Annual ACM Symposium on Theory of Computing, Philadelphia (1996), p.212, [quant-ph/9605043](#).
- [8] I am using the standard quantum mechanical notation introduced by Dirac. The suffix b is used, since that will correspond to the state which forms Hydrogen bonds in nucleotide base-pairing.
- [9] A projection operator $P = |x\rangle\langle x|$ satisfies $P^2 = P$. Then $(1 - P)$ is also a projection operator, $(1 - P)^2 = 1 - P$, and $(1 - 2P)$ is a reflection operator, $(1 - 2P)^2 = 1$.
- [10] C. Zalka, *Grover's quantum searching algorithm is optimal*, Phys. Rev. A60 (1999) 2746, [quant-ph/9711070](#).
- [11] L. Grover, these proceedings.
- [12] J.D. Watson, N.H. Hopkins, J.W. Roberts, J.A. Steitz and A.M. Weiner, *Molecular Biology of the Gene*, Fourth Edition, Benjamin/Cummings (1987).
- [13] The START signal for synthesis of an amino acid chain is somewhat complicated; it is represented by the code for the amino acid Methionine preceded by an arrangement of several bases. But the STOP signal for terminating the chain is encoded in the DNA base sequence in the same manner as the signals for specific amino acids.
- [14] DNA replication should be error-free to faithfully pass on the hereditary information to the next generation. Protein synthesis can tolerate more errors, since proteins are disposable items, made in large numbers and broken up into parts once their use is over. With $Q = 3$ and $N = 21$, the quantum search algorithm has an error rate of about 1 part in 1000.
- [15] L. Stryer, *Biochemistry*, Fourth Edition, W.H. Freeman (1995).
- [16] An informative book at popular level is: J. Gribbin, *In Search of the Double Helix: Quantum Physics and Life*, Penguin Books (1995).
- [17] It is easy to give the bases binary labels based on their chemical structure. The first bit can be a pyrimidine/purine label (i.e. a single or a double ring), and the second bit an amino/keto label (i.e. $-NH_2$ or = O group). Then pairing occurs amongst bases differing in both the bits.

- [18] In the cellular environment, it is far more likely that this binding energy is released as an inelastic collision or a phonon, than the radiation of a photon.
- [19] A different nucleotide base, I, appears sometimes in the wobble position of t-RNA. In the base-pairing between t-RNA and m-RNA at this position, the additional combinations, I-A, I-C, I-U and U-G, are held together by two Hydrogen bonds.
- [20] We can also look at a different example. Living organisms also carry out information processing using their nervous systems. This processing takes place at the cellular level, where classical physics dominates. Expectedly, neural communications use binary code—neurons communicate with each-other by firing electrical pulses, and a neuron fires or does not fire depending on whether its input potential is above or below certain threshold.