On the DNA resonance code

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Most basic experiments on biological fields involve two samples such as cell culture aliquotes in sealed quartz cuvettes separated by optical filters. When one of the aliquotes is perturbed, the second one may catch the signal that is transferred non-chemically and is blocked by light impermeable filters. Such effects are often referred to as "non-chemical cell-cell communication" and are reviewed in refs [1–4]. Original experimental reports include communication between cell culture aliquotes via polystyrene petri dish [5,6] and between plant roots through the air [7].

Among such models, simplest and most robust seems a model of Burlakov [8] that uses fish embryos. Compared to cell culture and adult organisms, embryos are more sensitive, produce stronger biological fields and their developmental abnormalities are easier to observe. In Burlakov's model, 50 fish embryos are placed in each of two quartz cuvettes stacked on top of each other and incubated for several days in a metal box. It was observed that older embryos inhibit the development of the younger ones. A Germanium mirror accelerates the development when a single cuvette is placed on it, and a quartz retroreflector prism represses the development and causes developmental abnormalities.[8] Burlakov's lab has published great many papers using this model [8–18] and is continuing the tradition of the scientific school of Alexander Gurwitsch.

Alexander Gurwitsch (1874-1954) developed experimental models for the measurement non-chemical communication between biological objects 96 years ago. He postulated the existence of the morphogenic field [19] responsible for creation of the shape of the body in 1922, proved the existence of such a field [20–25] and characterized its spectral properties [26] . His results were reproduced by Anna Gurwitch [27,28] Burlakov [8] and over 100 works of others, reviewed in ref. [29,30] and his scientific school is continuing after an 8-year interruption in 1948-1956 [23]. Alexander Gurwitsch was nominated for Nobel Prize 11 times.

A typical Gurwitsch's experiment used a growing onion root as a source of biologically active waves which he called mitogenic radiation since it accelerated mitosis [26]. Another growing onion root or a petri dish with yeast culture was used as a receiving object. The sending and receiving objects were separated by a quartz prism allowing for spectral mapping of mitogenic irradiation. The further experiments of Burlakov with retroreflector prisms proved that such an irradiation is not only capable of accelerating mitosis but also of producing developmental abnormalities thus confirming the concept of morphogenic properties of the field.[31,32]

The concept of morphogenic field is a response to the need to explain biological development: how is the shape of the body, organs and tissues formed from a single fertilized egg cell. Current chemical explanations of development are correct but insufficient. Understanding the fundamental mechanisms of development has an immediate practical application: controlling the shape of the body would help curing obesity, growing new organs, bones, limbs, teeth, remodeling scarred wounds and rejuvenating aged joints.

The idea that the morphogenic field is holographic and created by the genomic DNA was first published by Richard Miller and Burt Webb.[33] Luc Montagnier [34] continuing the work of Jacques Benveniste [35] demonstrated that DNA sequences produce biologically active electromagnetic fields. Konstantin Meyl [36] proposed that biological electromagnetic waves produced by DNA have unusual field structure allowing them to transmit through tissues without loss.

Even though the background ideas for explaining the role of DNA in morphogenesis through morphogenic field has been laid by Gurwitsch, Miller, Burlakov, Montagnier, Meyl and others, the specific mechanism for morphogenic field is not discovered yet. Here we outline specific approaches for discovery of this mechanism.

Let us determine "DNA resonance" as a wave interaction between identical DNA sequences or DNA sequences that are not identical, but have similar oscillatory properties. An example of wave resonance is in music, when a sound made by one instrument causes a string in another instrument vibrate if the second string is tuned to this exact tone. Similarly, a tuning dial in an analogue radio receiver changes the frequency of reception by adjusting the capacitance in a resonant circuit thus allowing us to tune into a specific radio station. Similarly, we propose that specific DNA sequences or DNA-protein complexes of chromatin that have similar oscillatory patterns would resonate allowing synchronisation and signaling from one sequence to another.

Although the idea that morphogenic field is holographic and is produced by the genomic sequence has been around since 1973 [33], and expanded by Peter Gariayev [37,38], and Marco BIschof [39], there has been no published attempts to actually decipher the algorithm of the conversion of DNA sequence into the wave patterns. Here we name this algorithm as "DNA resonance code" and define it as an algorithm which describes the conversion of genomic DNA sequence into the structure of the morphogenic field and ultimately to the shape of the body. For example, although the initial sequence of the human genome has been completed in 2001 [40,41], and of the mouse genome in 2002 [42] , now, 16 years later it is impossible to tell how these genomes make the shape of their respective owners. Even more, the science lacks the algorytm by which the sequence of the genome defines the shape of any species. Currently there is no way for a computational genomics to reconstruct the shape of a warm, a fly, a dog or a human from their genomic sequence. This is because the genomics studies only molecular interactions and ignores the resonance language of the DNA. Since a large fraction of the genome remains chemically passive, it was referred as "junk DNA" even though a large portion of so called "junk DNA" bears a sign of functional significance: the proportion of sequenced conserved between species is approximately equal among transcribed and non-transcribed parts of the genome [40]. We propose that both transcribed and non-transcribed parts of the genome are involved into important work of creating and sustaining the shape of the body, organs and tissues, guidance of the biochemical factory of the cell and ultimately in the work of the mind. Speaking of the DNA resonance code, we believe that it is not only the algorithm of reading from DNA structure into the wave structure, but that the process is two-directional - the genome receives the information via wave resonance and converts it into the structural information of the DNA by epigenetically condensing and condensing chromatin, modifying chromatin's chemistry and thus recording

the received wave signals into the chemical structure.

The periodic nature of the DNA's double helix inspired many researchers to model its mechanical oscillations. [38,43,44] Since DNA is highly charged, bound by water and by proteins of chromatin and transcription factors, we doubt it can sustain mechanical oscillations independently of the surrounding water and proteins, although it should be able to vibrate together with them. Since we are looking for sustained oscillations which are defined by the DNA sequence, we favor not mechanical (submolecular) oscillations but the oscillations of collective delocalized pi-electron resonance clouds of the base stack and similarly collective delocalized proton clouds of hydrogen bonds of DNA. We have suggested [45,46] that it is more likely that these are the electron and proton cloud oscillations in the base stack of DNA responsible for DNA resonance and morphogenic field, since the base stack is hydrophobic inside and its core is separated from the water, proteins and any other molecules of the surrounding milieu thus making it an insulated wire and a linear (double-helical) crystal. This should allow electron and proton charges oscillate in the base stack without disturbing the other atoms and therefore without much dissipation of energy.

The existence of the collective delocalized electron clouds in the base stack has been reasonably established by the researchers of the DNA's electrical conductivity, typically called "DNA charge transfer". The base stack of DNA was observed to be a good electric conductor and a semiconductor able to transmit either excess electron or electron holes.[47] The unique properties of the electron clouds in the base stack are due to aromatic properties of the DNA bases and the fact that they are squished together by the sugar-phosphate backbone. Since the bases are hydrophobic, the water pushes them together aiming to minimize the contact with them, while the charges of the phosphates repel each other making the DNA as linear as possible. This combination of pulling and pushing is responsible for its perfect double helical structure and for the perfect structure of the base stack inside. The pi-electrons of the base stack are doubly delocalized into a collective cloud: first, they are dissociated from their host carbon and nitrogen atoms by the aromatic rings (well known from the hexagon nut of benzene), and second, these aromatic bases are stacked on top of each other into a double helical ladder, making their electron rings overlap in a periodic fashion. Note that the periodicity should also help oscillations in these distributed collective delocalized electron structures.

Importantly, the electrons in the base stack are distributed via Heisenberg's quantum uncertainty, which in chemistry is referred to as chemical resonance. This uncertainty in electron's location is illustrated by the popular Schrodinger's cat paradox. Until the electron is exported into a non-aromatic molecule, its location is uncertain and spread over long distance of the DNA which for the longest chromosome is 3 inches.

Richard Alan Miller wrote 45 years ago: "The formation of a certain type of chemical bond known as the resonance bond (which is most easily seen in the case of the Benzene molecule) leads to a peculiar situation in which certain electrons are freed from a local or particular location in the molecule. These are then free to travel around the entire molecule. This means that the electrons occupy an energy shell of the whole molecule as opposed to any particular atom in the molecule. The existence of molecular systems with mobile electrons has been found to be of profound significance in the phenomena of life." [48] "All the essential biochemical substances, which perform the fundamental functions of living matter, are composed completely or partially of such mobile electrons. Molecules which contain these electrons are known as conjugated systems [49]. The essential fluidity of life may correspond with the fluidity of the electronic cloud in conjugated molecules. Such systems may best be considered as both the cradle and the main backbone of life." [48] The importance of conjugation of pi-electrons of aromatic bases and amino acids was also highlighted by Stewart Hameroff who observed a revealing correlation between aromaticity of anesthetic compounds and their potency and connected this to the signal transduction via microtubules. [50]

To our knowledge the conjugation of the protons of the hydrogen bonds in DNA has not been yet proposed. It is known that these hydrogen-bond protons are also in the state of chemical resonance being

quantum-distributed between tautomeric states of the bases. We suggest that stacking of the bases should conjugate the hydrogen-bond protons between the base pairs of the stack into a continuous proton cloud spreading as far as the unbroken base stack spreads, possibly to the length of the chromosome up to 3 inches. Such conjugation of protons have not been shown for DNA but has been described as "proton conductivity" or "proton highways" in protein solutions. [51]

The idea that DNA can have magnetic properties goes back to the experimental works of Lev Blumenfeld in the 1959.[52] The dispute about these properties continues to this day [53–62]. All experiments on this topic are carried out in strong magnetic fields and using the purified DNA. We came to this question from another angle. We have noticed [45] that two DNA strands in biological reactions such as ligation, transcription, replication and formation of hairpins, behave very much like pairs of antiparallel magnets, Fig. [Ligation]. For example, in a ligation reaction of a plasmid vector, blunt ends find each other with high specificity. This is usually attributed to high efficiency of the ligase enzyme, but we suspect, that even in the absence of ligase, DNA ends could attract to each other as pairs of antiparallel magnets, Fig. [Ligation].

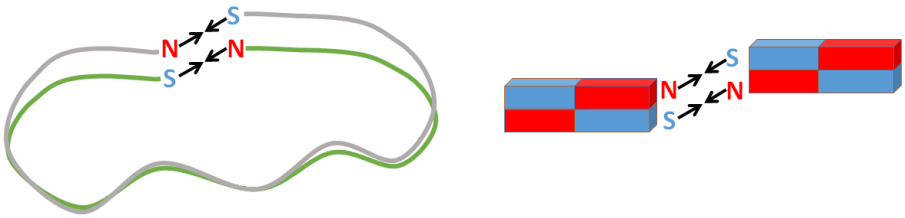

Fig. [Ligation] Two strands of natural DNA may be magnetized in antiparallel fashion. Blunt ends of a vector may be magnetically attracted to each other.

Note, that our hypothesis on antiparallel magnetisation of DNA strands did not come from experimental evidence but from DNA behavior in enzymatic reactions. We noticed that antiparallel magnetization of DNA strands would often greatly improve specificity of enzymatic reactions and explain some of observed specificity.

How could DNA strands be magnetic? The idea that ring currents [63–68] may be responsible [69] for magnetism in DNA is coming from nuclear resonance studies, NMR. It is a textbook knowledge that in a strong magnetic field, not only in aromatic rings of DNA but in any aromatic rings, a ring current is known to be induced which in turn, induces a secondary magnetic field directed in the opposite direction to the primary field. This secondary field is deshielding the adjacent protons observed as a shift of corresponding peaks in NMR. [70,71]

Typically NMR studies are done in solid substances, but in the solution, aromatic rings turn their axis perpendicular to the initial field thus disabling the induction of the ring current, Fig. [Ring Current, C1-C5]. [72,73] Same is true about the DNA: the DNA turns perpendicular to the initial magnetic field, Fig. [Ring Current, D1-D2]. [74–76]

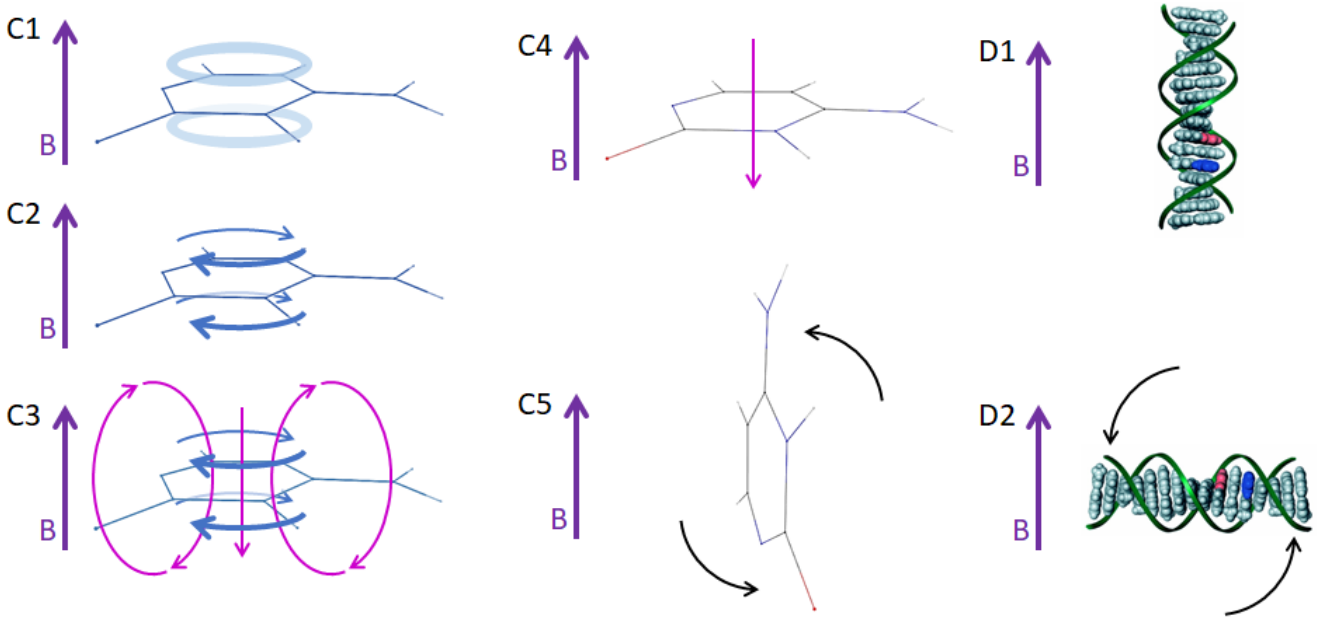

Fig. [Ring Current]. C1. Magnetic field is applied to cytosine. C2. The field induces ring current in cytosine. C3. The field turns cytosine perpendicular to the field. D1. DNA solution is placed in the magnetic field. D2. DNA double helices turn perpendicular to the field.

We proposed [45] that in the cell, in the absence of the strong magnetic field, ring currents may be induced by some of the enzymes using the energy of ATP. Specifically, we have noticed that many of the DNA-associated proteins are iron–sulfur proteins [77]. We suggested [45] that iron-sulphur clusters in these proteins are utilized to magnetise specific sequences and create static and dynamic patterns of magnetisation in DNA sequence. This idea is in line with the idea of Blumenfeld that DNA can function as a magnetic tape to record and, store and retrieve information in magnetic form. [78–80] Importantly, the DNA has an advantage over the magnetic tape that it has unique sequences which could be used as addresses for cataloguing the information, very much like on a formatted computer disk.

While ring currents in single ring molecules such as pyrimidines (C and T) have simple geometry, fused-ring molecules such as purines (A and G) are more complex. Although under a strong magnetic field the ring current in purines circles their perimeter, Fig. [Purines, a], we predicted [45] that in physiological weak magnetic conditions, the ring currents in purines would flip into an infinity ∞ shape, Fig. [Purines, b].

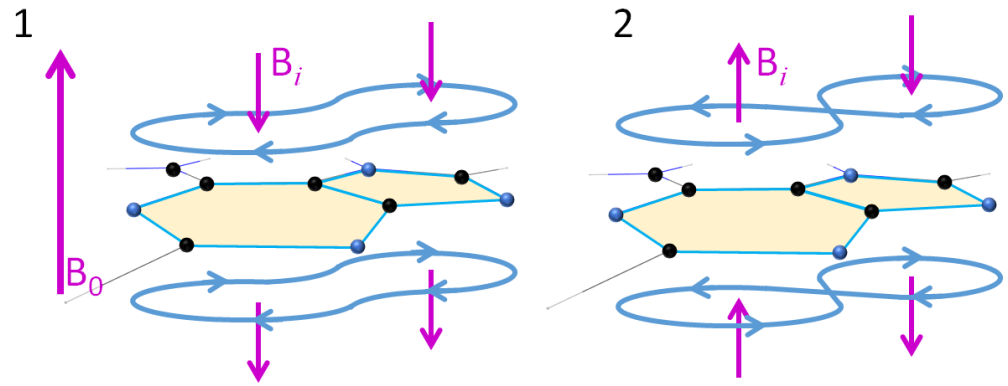

Fig. [Purines] 1. Ring current in a purine under a strong magnetic field circles the perimeter. 2. We predict that ring current in a purine under a natural magnetic field should take on an infinity shape.

The infinity shape of the ring current would be most optimal since it would create antiparallel magnetic vectors

within a purine canceling each other. When combined in a base stack, the magnetic vectors of the bases would combine creating patterns of magnetic lines as shown on Fig. [Patterns]. The stretches of purines would have double lines and the stretches of pyrimidines - single lines.

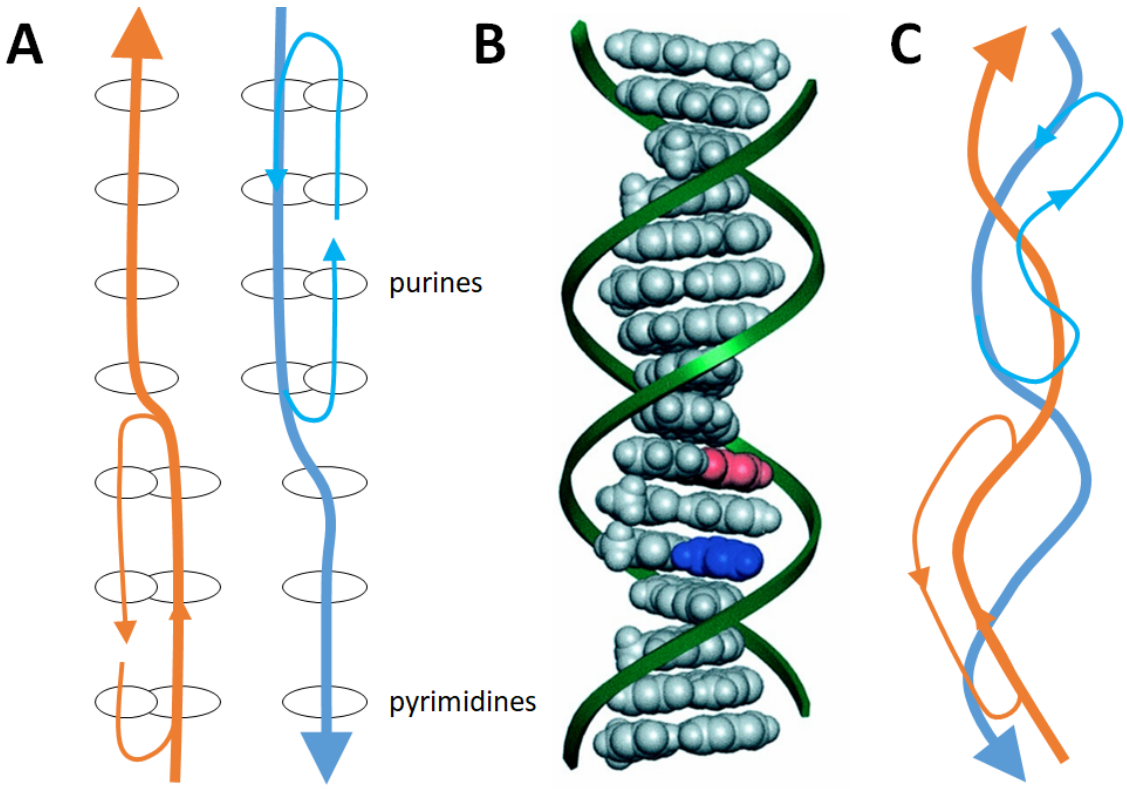

Fig. [Patterns] a. Hypothetical patterns of magnetic lines in the base stack, a flattened view. b. The 3D shape of the base stack. c. Hypothetical patterns of magnetic lines in a double-helical base stack, a helical view.

Note that the magnetic field of the magnetized base stack would spill over outside of the double helix and should be readable by possible field sensing molecules from outside. For example, the binding of B-zip transcription factors to the major groove of the double helix would depend on the sequence of the DNA and on the magnetization of the DNA in the binding site. Therefore the sequence will indeed act as a magnetic tape and the DNA sequence will be converted to the field pattern outside of the molecule. This fits our definition of the DNA resonance code: the algorithm of conversion of DNA sequence to the field structure. Yet, this is only a part of the answer, since there is still a need to figure out how these local fields combine to create the shape of the body.

Another thing is uncertain about the proposed ring circuit magnetisation of DNA: whether it is static or oscillating in living cells? The possibilities are vast: some chromatin structures might support the static magnetization, other chromatin structures might support oscillating ring currents that change their direction with a certain frequency. The sulphur iron containing enzymes may be providing energy to these oscillations while drawing the energy from splitting ATP. DNA, in turn, would serve as a resonator and provide structure to these oscillations. Note that reactions of transcription and translation which also utilize triphosphates might energise magnetic oscillations in DNA as a side product of their chemical activity.

What are the sizes of DNA oscillators? The smallest would be stretches of single nucleotide repeats. Higher genomes are rich in these stretches. Also frequent are di- tri- tetra and penta-nucleotide repeats. These are called microsatellites and were used in genotyping since they are prone to length variation. The abundance of microsatellites is roughly highest for single-nucleotide repeats and fades with the length of the repeating unit.

Among the simple repeats the telomeric repeat stands out. In vertebrae, many of the plant taxa and yeast the telomeric repeat is 6 bases long: GGGTTA. In some plant taxa it is 7 base long GGGTTTA and in many taxa of insects it is 5 bases long GGTTA.[81] The length of our telomeres is around 2500 repeats each.[81] We suggest that the telomeric repeat is one of the most essential resonators in the genome and may provide the basic carrying frequency for the cell and the body. Since this frequency is common between many forms of life surrounding us, it is one of the major frequencies of life, including us, and our food.

What are the other abundant repeats in the human genome? Alu repeat has the highest number of copies in our genome. It is an interspersed repeat, meaning that it is distributed throughout the genome without a perceivable order. The length of Alu is near 300 bp and it has about 1.1 million copies in our genome. The molecular functions of the genomic copies of Alu repeat are of high potential significance - it strongly binds nucleosomes, and often serves as a crystallisation point for chromatin condensation: the condensation (heterochromatization) of chromatin starts with Alu and spreads along the sequence in both directions. Yet, Alu repeats are frequent and conserved in gene promoters pointing at possible regulatory function of genomic Alu. Moreover, the variations within Alu sequence in a gene promoter correlate with transcriptional activity of that gene. [82–84] In addition to its function as chromatin condensation regulator and regulator of genes, Alu is a gene coding an untranslated RNA. Normally the million of the Alu repeats in the genome are silent, but in some cell types they are transcriptionally active. Their transcription is also activated by cellular stress. It is likely that abnormally high transcription of Alus is used by the cell as an indicator that something went wrong somewhere in the genome and that it is time for apoptosis.[85] Since Alu is unique to primates, it is likely that it is responsible for our unique brain functions. Therefore, we have proposed that Alu plays an important role in the brain.[85] Essentially, it is the genomic element and the gene that makes us humans. Since it is a very high copy gene and comprises 11% of our genome, we suggest that it is the main DNA sequence that makes us humans.

Moreover we have suggested that the main function of Alu is vibrational. We propose that Alu is responsible for the creation of the uniquely human morphogenic field and that is the key resonating component of our mind and consciousness. Consider that if there is a DNA resonance process converting molecular signals to the dynamic field structures and vise versa, this process has to be mediated by special molecular structures, let's call them Main Resonators. Also since our genome is our program, these Main Resonators should be informationally connected to the genome sequence. And ultimately, for the system to have high fidelity and a high quality factor (low loss of energy), there should be many Main Resonators per cell. Also, the structure of the Main Resonator has to be sophisticated enough to support the oscillations and to transform the molecular signals to the field and vise versa. We believe that Alu is the best candidate for such a structure. Its 300 bases make it complex enough to be uniquely structured, its chromatin structure is well defined by the strong binding to a paif of nucleosomes, there are 1.1 million of Alus in the genome allowing for high qualify factor of resonation and Alus are enriched and conserved in gene promoters positioning them well to influence the function of the cell. We believe that Alus are creating the main part of the field in the nucleus and while interacting with the field they make the major contribution in the control of which genes are transcribed and when.

It is often the case that the same genes serve very different functions in somatic cells and in the brain. We believe that this is the case for Alu as well. As Stuart Hameroff explains [86], one of the problems with explaining the human consciousness via the mechanisms of action potential, synaptic connections and neuronal plasticity is that there is not enough neurons in the brain to program for the complexity of our mind and not enough synapses to account for the vast memory capacity of our brain. Hameroff offers neuronal microtubules as the main structure performing the function of information processing and memory storage via wave resonance mechanisms. While accepting the function of microtubules located in the cytoplasm, we propose Alu elements located in the nuclei of neurons and glia should be also playing an important role in information processing and memory storage via wave resonance. The importance of Alus in information processing may be highlighted due to their chromatin structure potentially allowing for complex oscillation patterns, their incorporation in the

genome allowing for communication with other DNA sequences and the fact that each Alu element is surrounded by unique sequences allowing them to have unique addresses in the genomic program. Thus an Alu represents a combination of the universal part performing a universal function of resonance communication and the unique flanking sequence address allowing it to serve as a local unique role as well. Similarly, various Alus within the genome have minor variations in their sequence allowing to assign them to different subclasses, thus potentially allowing broadcasting specific messages to subclasses.

We propose that Alus also serve as memory units in our brain. Each Alu is clearly capable of storing information epigenetically. Short term memory can be reversibly stored in Alu chromatin by changing its structure and binding of DNA binding factors. Thus field resonances could be recorded,stored and retrieved into, from Alu chromatin structures. Long term memory could also be stored in the Alu DNA via methylation. Alu sequences harbor many CpG pairs and CpG islands which are especially useful for storing epigenetic information long term. We will address the electromagnetic connection between Alu elements in the nucleus, microtubules in the axons and the action potential in the axons is discussed later in the article.

The idea that repetitive elements are regulatory elements controlling the activity of genes is older than genomic sequencing, older than the discovery of the double helix, and was made back in the time when the overwhelming majority of scientists rejected the idea that DNA is of any importance for genes. It was Barbara McClintock who discovered the repetitive (transposable) elements and called them control elements, proving that they are universal genetic elements controlling nearby genes.[87–89] In 1951, 67 years ago she described the "[repetitive] elements in the heterochromatin .. concerned with differential control of the times at which certain genes may become reactive."[87] We suggest that in humans, these are Alu elements and that these elements not only control expression of nearby genes, but also are resonators communicating electromagnetically with the morphogenic field which they help to create.

The literature on Alus is strongly dominated by the research of their transposition properties. While respecting the importance of transposition in the evolutionary past, we have emphasized [85,90] that the proposed function of Alus doesn't have to be related to transposition in any way. The transposition rate of the majority of the 1.1 million copies of genomic Alus is extremely low, possibly one transposition per generation. It may be somewhat higher in the brain, but overall, we have proposed that at the present, Alu has important resonance, gene regulation and memory functions unrelated to its transposability. [85,90] To illustrate this point with a cultural example, consider the population say, of Australia. Although, in the past, some two centuries ago, Australia was populated as a penal colony for British convicts, currently it wouldn't be productive to explain the function of Australian economy on the basis of its distant past. Same is true for Alus: their current function should be explored without heavy weight of their past. Even the fact, that they they selfishly occupied 11 percent of our genome may be redeemed by their proposed contribution to our morphogenic field and consciousness.

What could be the molecular structure of the Alu resonator? Since each Alu strongly binds two nucleosomes, and since Alu sequences are typically compacted (heterochromatinized), it is likely that Alu resonators include nucleosomes. Since the base stack behaves as an insulated conductor,[91] we proposed that nucleosomes serve as induction coils in such a resonator.[45] The way nucleosomes are organized in living cells has been uncertain for many years. Solenoid and two-start zigzag packaging was obtained in vitro using periodic DNA templates.[92–95] Recently, mapping nucleosomal packaging in living cells showed the irregular nature of nucleosomal packaging.[96–98] Most likely, since the genomic sequence is aperiodic, the nucleosomes in living cells are packaged in irregular structures [96–99]. Among these irregular structures, frequent are mono-, di- and tetranucleosomes.[99] We proposed that these structures may serve as a resonant circuits.[46] For example, we proposed an oscillation model for a tetranucleosome, Fig. [Tetranucleosome].[46]

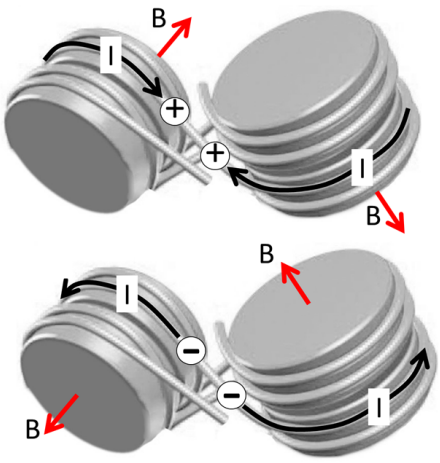

Fig. [Tetranucleosome] One of possible models of a tetranucleosomal oscillator. I – current, B – magnetic field. Top – the first phase, bottom – the second phase of the oscillation period.

In this resonant circuit, the current circles the nucleosomes back and forth and the stacked pairs of the nucleosomes change their magnetic polarity from one phase of the cycle to another. [46] SInce the length of the linker DNA sequences connecting the stacked nucleosome pairs will depend on the sequence, the geometry of the tetranucleosomes will vary accordingly, thus the frequency and the geometry of the generated electromagnetic waves will change as well. This is in agreement with the above idea that various sequences will have various resonation properties and similar sequences will resonate. Moreover, this model is permissive to sequence variations: the resonance between two sequences will occur as long as the overall geometry remains similar. This illustrates a certain redundancy of the resonance code and suggests ways for its experimental discovery.

Although Alu elements are distributed through our genome seemingly at random, there is one exception: there are frequent pairs of Alus, structured as inverted repeats, where the Alu sequence is followed by its complement.[100,101] Usually, the there is a high similarity between the halves of the inverted Alu repeat. Notably, between the two Alu sequences in the inverted repeat, there usually is a short unique bridge sequence, which we think may be used by nature as a sequence tag to tag each inverted Alu repeat. Since each Alu binds two nucleosomes, the inverted Alu repeat should form a tetranucleosomal structure, which we suggest is a special type of resonator. Since there are many inverted Alu repeats in the genome, these special resonators may resonate with each other. The length of the bridge sequence should then fine tune resonant frequency and shape of the wave for specific groups of these inverted Alu resonators.

We believe that classical methods of genomics will be sufficient for decoding the resonance code of DNA: genetic engineering with subsequent measurement of spectral properties and full-genome mapping of the influence of waves on the openness and transcription of DNA. Toward that goal, we have shown the effect of red light on the expression of candidate genes in murine epidermis.[102]

What could be the frequency of natural DNA resonators? The frequency would depend on the size of the resonator and the mode of oscillation. The frequencies of short repeats such as telomeric repeats should be high. The physical length of the telomeric repeat GGGTTA is 1.8nm, depending on the mode of oscillation in these repeats, the frequency could be very high, possibly in the UV range. Coincidentally, UV range was identified by Gurwitch [103] and Burlakov [12,14] as the range of mitogenic radiation and morphogenic field in plants and fish embryos, Fig. [Spectrum]

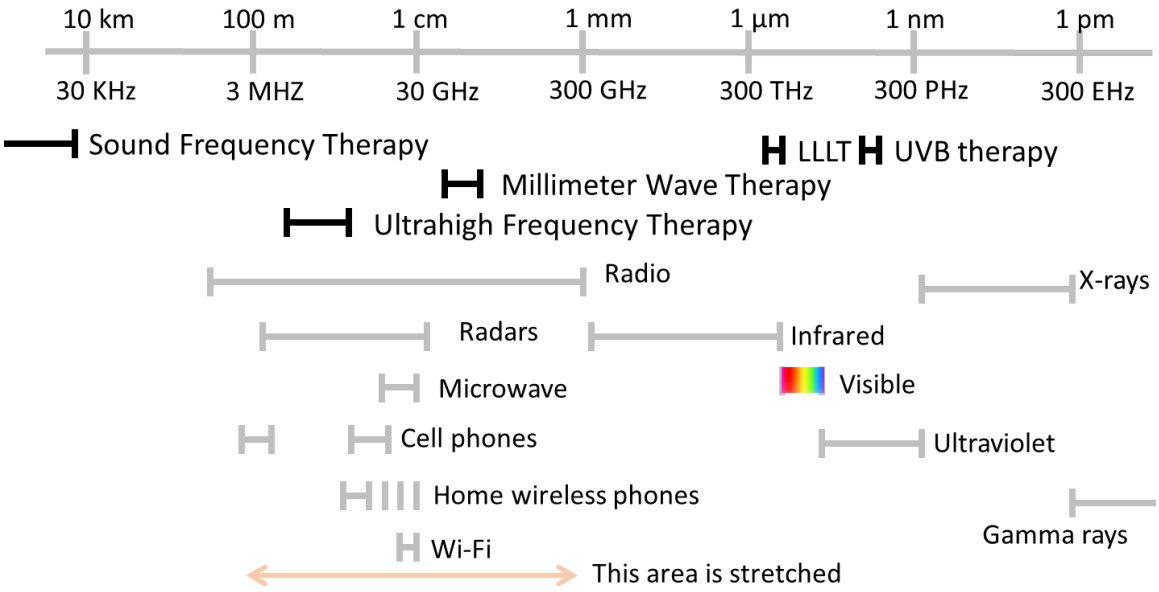

Fig. [Spectrum] Wavelength and frequency ranges of major types of electromagnetic therapy. LLLT – low level light therapy.

The size range of potential resonating structures in DNA is large, ranging from 0.3 nm for single bp in mono-nucleotide repeats to 8.2 cm of the largest chromosome. We believe whole chromosomes should be also included among possible resonators since DNA is known to be a good conductor and transmit the charge to large distances without loss. Therefore the range of candidate DNA resonator sizes covers 8.4 orders of magnitude, Table [Resonator lengths].

Table [Resonator lengths]

	Repeat length		Repeat length		
Mononucleotide repeat	1	bp	0.3	nm	
Telomeric repeat	6	bp	2	nm	
Alu repeat	300	bp	100	nm	
LINE1 repeat	6,000	bp	2,000	nm	
Chromosome 21	48,000,000	bp	16,000,000	nm	1.6 cm
Chromosome 1	249,000,000	bp	82,000,000	nm	8.2 cm

The ideal tool for testing sequence-dependent DNA oscillations would be experimental genomics. So far, very little is published in this area. Some clues might be inferred from electromagnetic therapy practice. Electromagnetic therapy in the West is usually limited to transcutaneous electrical nerve stimulation (TENS), and red - near infrared light therapy (low level light therapy, LLLT). Other forms of electromagnetic therapy are used in Eastern Europe, Russia and Asia including ultraviolet light, millimeter waves, ultrahigh frequency, and sound frequency electromagnetic waves, Fig. [Spectrum]. These waves have a capacity of being effective at very low doses, suggesting that they tap into existing signaling of the body, i.e. they influence the morphogenic field. We suggest that live chromatin may support oscillations at at every one of these frequencies: smaller DNA resonators would resonate at higher and larger at lower frequencies.

For example, individual aromatic rings of DNA bases are well known to resonate at 260 nm (1.2 PHz) of UV range. These are small structures, 0.3-0.7 nm size. On the other hand chromatin is known also to oscillate at very slow rate 1 oscillation every 40 minutes (1.5 cycles per hour, 0.0004 Hz).[104,105] The frequency difference between these two oscillations (1.2 PHz of UV absorption and 0.0004 Hz of chromatin oscillations) is 61 orders of magnitude. How could chromosomes be involved in such a wide range of oscillations? In addition to size difference between the oscillators, consider the mass and the geometry of the oscillator. Above we mentioned 3 types of oscillations in the DNA - oscillation of the parts of the DNA molecule (mechanical oscillations),

oscillations of the delocalized electron cloud of the base stack (electron oscillations) and oscillations of the delocalized hydrogen bond protons of the base stack (proton oscillations). Proton is nearly 1900 times heavier than electron and a basepair of DNA is 640 times heavier than proton. Consider also that DNA molecule is heavily hydrated and bound to chromatin which makes its mass much bigger. The geometry of oscillations would also strongly affect the frequency. Swinging oscillations would be much slower than stretching oscillations. Thus, we conclude that the variation in size of oscillators within the chromosome, nature of oscillating fields (electron, proton, molecule) and geometry of oscillations should allow DNA to support a very wide range of frequencies.

In addition to classical electromagnetic waves, alternative electromagnetic wave geometries have been proposed by Konstantin Meyl [36,106]. These proposed electromagnetic waves are helical, longitudinal and characterized by an unusual phase shift between electric and magnetic vectors. Meyl proposes that these waves are produced by DNA, making the biofield and that these waves have special properties allowing them to work in the irregular milieu of biological tissues.

This brings us to the question of dissipation of electromagnetic waves in the biological tissues. Dissipation is the strongest argument against the morphogenic field. For example, among the therapeutic frequencies, UV is strongly absorbed by DNA, red and near infrared light are not absorbed by DNA but likely somewhat absorbed by chromatin and DNA binding proteins, and millimeter waves are strongly absorbed by water. How could morphogenic field function and organize biological structures which are so complex, malleable and irregular?

One answer could be that the nature of waves is unusual, such as in special waves of Meyl. Another possibility is that much of biomolecular events happen at the microscopic and nanoscale level where neither macroscopic laws nor quantum chemistry laws are applicable and new quantum biology laws are working. In addition to above possibilities, we propose that some of the signal scattering problems are solved by nature by using waveguides. Specifically, consider the problem of signal scattering for the DNA which is located in the nucleus and has to communicate across nuclear, cellular and organelle membranes to the DNA in other nuclei. Since the cellular milieu contains many organelle membranes and uneven shapes, scattering of light in the cells and in the biological tissue is high and should challenge the electromagnetic communication between the nuclei. A similar problem is to be solved for explaining the possible role of genomic resonance in the works of mind and consciousness. The problem is that the main sensory, movement and thinking activities are mediated by the movement of action potential along the axons of neurons but the DNA is located in the nucleus being insulated and spatially removed from these action potentials. For example, the nuclei of dorsal ganglia of touch sensing cells are located in our spine, while their nerve endings are located in the skin. Thus the length of axon for the foot is around 2.5 feet. How could the electromagnetic communication take place at such large distances?

We suggest that it is microtubules which serve as waveguides to transfer the electromagnetic signal from the nucleus through the cytoplasm. The theory of microtubular signal transmission have been developed by Stuart Hameroff and coauthors for the last 30 years.[107–110] Hameroff proposed that microtubules in neurons contribute to creation of consciousness by transmitting, computing and storing information. He proposed that it is delocalized electrons of aromatic amino acids that are oscillating in microtubules. Stuart Hameroff and Anirban Bandyopadhyay proposed that oscillating are electron spins. We have noticed that microtubules radiating from the nucleus to cell periphery come close to the nucleus and to the cell wall and therefore we proposed that microtubules serve as waveguides connecting all the nuclei of the body and that they communicate electromagnetically across the cell wall with the DNA and across the cell membrane in cell junctions with the microtubules of the adjacent cells, Fig. [Microtubules].[111,112]

We propose that the microtubules and DNA communicate resonantly through the nuclear membrane, and that the microtubules of neighboring cells communicate resonantly through the contact points of the cell membranes, thereby integrating all the body nuclei by the waveguides. From this it follows that resonant vibrations of DNA propagate not by chance, but are guided by waveguides of microtubules. We propose that

the nervous system and connective tissue are primarily responsible for uniting the organism into one resonating system.

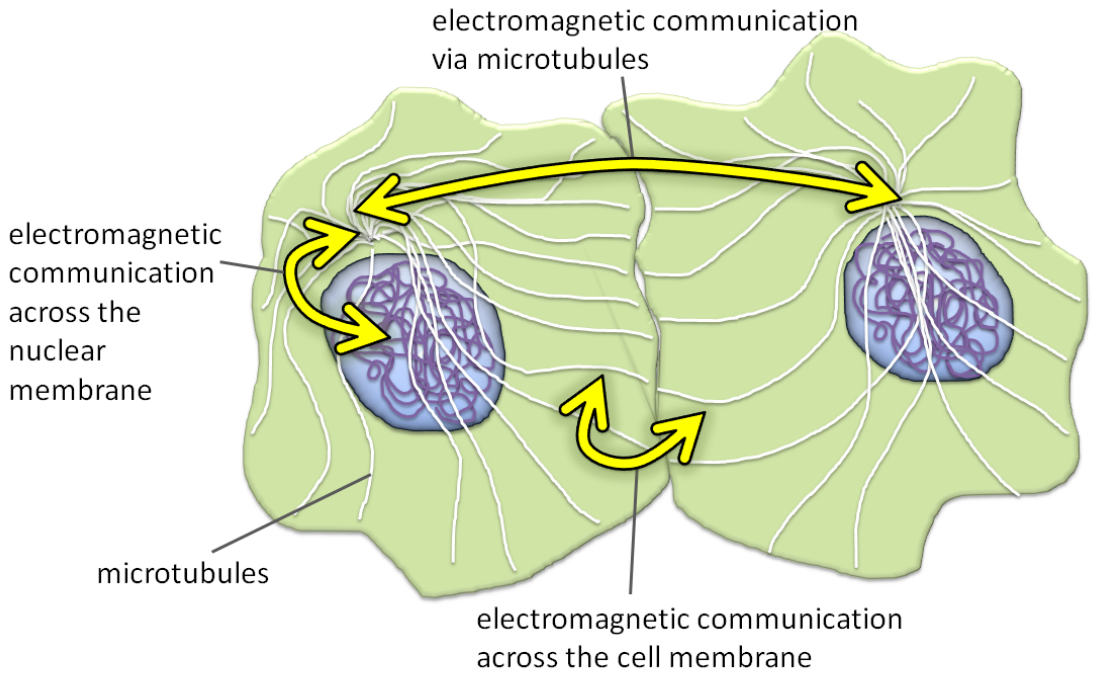

Fig. [Microtubules] We propose that the electromagnetic oscillations in DNA within the nucleus and microtubules in cytoplasm are synchronized across the nuclear membrane and that the oscillations between microtubule networks of adjacent cells are synchronized across cellular membranes thus uniting all nuclei of the body in one oscillation network via waveguides of microtubules.

We propose that in neurons, the propagation of action potential across the axons is the process of reading and writing of information into and from microtubules and that this propagation of action potential is electromagnetically connected via the microtubules with the DNA in the nucleus thus allowing the participation of DNA in the work of mind and memory, Fig. [Action potential].

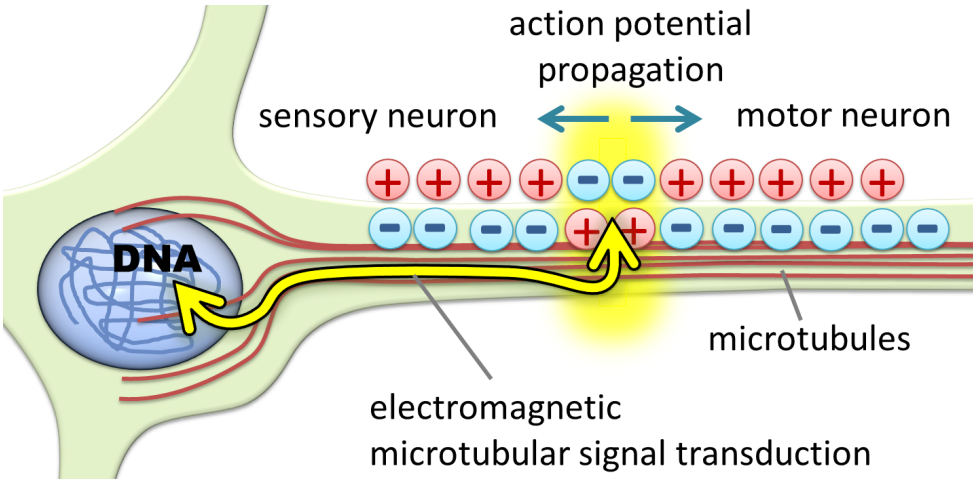

Fig. [Action potential] We propose that in neurons, action potential propagation is electromagnetically linked to DNA via microtubules and via the nuclear membein, allowing the genome to sense and control action potential propagation and thus actively participate in perception, movement control, memory, and other aspects of mind and consciousness.

To our knowledge although the holographic model of genome-generated morphogenic field was proposed 45 years ago, very little has been done so far experimentally to decipher the code. We believe that standard approaches of modern science should be sufficient for cracking and deciphering it. Consider a couple examples of cracking unknown codes from the past: the key to the decipherment of Egyptian hieroglyphs was the Rosetta stone which contained parallel inscriptions in Egyptian and two known languages. Comparing these three texts allowed Jean-François Champollion and Thomas Young to decipher the code some 200 years ago. In the case of DNA resonance code, we suggest that the code can be deciphered by the combining quantum chemical molecular modeling, biophysical experiments, genome-wide chromatin accessibility and transcriptional activity mapping in response to electromagnetic waves, spectral analysis of synthetic DNA and gene-modified live tissue and linguistic computational analysis.

Another historical example is the decipherment of the amino acid-coding genetic code by Marshall Nirenberg and others 57 years ago. The approach he used was to feed a synthetic nucleic sequence into a cellular extract and analyzing the molecular outcome. We suggest that the same approach could be employed for the discovery of the DNA resonance code - by inserting a sequence into a cell, allowing the cells to transfer the message via waves to another batch of cells and using genome-wide analysis to map the resulting chromatin changes. In the case of Nirenberg, once the first letter of the code (UUU coding for Ala) was discovered, it took a very short time for the world community to crack the rest of the code. Note, that for DNA resonance code we already proposed a set of candidate sequences including Alu and LINE1.

Once the code is cracked, the potential applications will stem from the two major roles which were proposed by us and others: the role of DNA in creation and interaction with the morphogenic field and with the mind.

Since the proposed role of the morphogenic field is to drive biological development of tissues, organs and body structure, understanding its code will allow us to control the body shape, reverse obesity, induce the growth of tissues, organs, limbs and new teeth. We argue that the slow progress in organ engineering achieved by science so far is because of the lack of DNA resonance code and its deciphering will enable effective organ engineering.

We also proposed that DNA resonance is linked to the work of the mind via resonance patterns and that deciphering the DNA resonance code will greatly facilitate the deciphering of electrophysiological patterns of the brain. In short, we propose that the brain code and DNA resonance codes are linked and speak the same

language. The deciphering of the brain code will allow the development of brain-computer and of brain-technology-brain interface also known as synthetic telepathy. We suggest that the path to the brain code via DNA (although counterintuitive) may be the shortest path since DNA is digital, and the methods for genetic engineering and genome wide analysis are exceptionally efficient.

The implications of the decipherment of the DNA resonance code should also affect the self-image of humanity since it will clearly demonstrate that all of us are linked via DNA resonance vibrations to each other and to all life on the planet and that should help our unity and ecology.

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