THE MUSIC OF HUMAN HORMONES

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Abstract

In this study, the authors take on the challenge to translate biological form (science) into musical form (art). Through scientifically developed methodology, the authors link two aspects of human experience that influence human emotions: hormones, from the inside, and music, from the outside. The authors develop an original algorithm, which they use to represent the properties and effects of the "Love Hormone" Oxytocin in a musical composition. The authors performed a neurological test to verify the accuracy of the musical interpretation and investigated the parallel neurological impacts of the hormone's biological and musical form. This article describes the preliminary results of the study.

As described in this article, we have developed an innovative methodology that effectively bridges art and science across the following disciplines: genetics, molecular interactions, human physiology, neurology and neuroaesthetics, which we will apply to the specific sets of hormones defining human emotions, in a project called *Symphony of Emotions*.

1. The Music of DNA

Douglas Richard Hofstadter notably proposed a connection between proteins and music [1]. Susumu Ohno further explored the relationship between DNA genetic sequences and music, translating the malignant SARC oncogene, first discovered in chickens, into music [2]. He found that the more evolved an organism is, the more complicated the resulting music. Ohno first directly translated the DNA code into notes, then based the music on only four notes corresponding to the four nucleotide bases: adenine (A), cytosine (C), guanine (G) and thymine (T). Ohno found that even when two or three consecutive bases define a note, the resulting music has no recognizable theme or musical depth as a composition.

An alternative approach, developed by P. Gena and C. Strom, uses the physical properties of nucleotides and the corresponding mathematical apparatus of their description to derive a set of equations to translate the DNA into musical notes [3,4]. Another method, explored by several researchers in the 1990s and 2000s, uses the primary structure of the proteins, assigning a musical note to each amino acid [5-8], creating a range spanning two, even two and a half octaves, leading to big jumps in consecutive tones and a consequent lack of musicality. A nine-note scale---with each note being mapped to more than one amino acid was also proposed [9] but without taking into account the differences between amino acids assigned to the same note. To date, many algorithmic arts applications have been developed---based on these approaches and others that convert raw genetic data online into music [10-12]. One project transforms three-dimensional (3D) protein structures into complex and three-dimensional music.

Some researchers have proposed an opposite approach---translating music into DNA code. Of particular note is Z.W. Geem's metaheuristic harmony search for a mathematical algorithm [13]. The resulting algorithm, inspired by jazz music, was applied to the prediction of the RNA secondary structure [14] in therapeutic medical physics [15] and other applications.

These methodologies for translating DNA sequences into music are logically constructive, but in our opinion none captures all the properties of the biological structures they represent. We propose a translation algorithm that integrates the physical properties of amino acids (such as hydrophilicity, hydrophobicity and charge along its 3D structures) and the processes of the biological activity of a protein's expression in the cell.

1.1.Protein Synthesis:

Within our cells' DNA, genes contain the instructions for making proteins. The complex path from DNA sequence to protein sequence has two major steps: first, transcription from DNA nucleic acid language to RNA nucleic acid language and second, translation from RNA nucleic acid language to protein amino acid language.

When a gene is switched on, an enzyme called RNA polymerase attaches to the start codon [the first codon of a mRNA transcript translated by a ribosome. It is always "Met" (AUG). Please, see fig.3.] of the gene. It moves along the DNA, making a strand of messenger RNA (mRNA) out of free bases in the nucleus. The DNA code determines the order in which the free bases are added to the mRNA. This process is called transcription (Fig. 1A). Before the mRNA can be used as a template for the production of proteins, it needs to be processed---this involves removing and adding sections of RNA. The mRNA then moves out of the nucleus into the cytoplasm. Protein factories in the cytoplasm, called ribosomes, bind to the mRNA. The ribosome reads the code in the mRNA to produce a chain made up of amino acids. There are 20 different types of amino acids. Transfer RNA (tRNA) molecules carry the amino acids to the ribosome. The mRNA reads three bases at a time. As each triplet is read, a tRNA molecule delivers the corresponding amino acid. This is added to the growing chain of amino acids. This process is called translation (Fig. 1B). Once the last amino acid is added, the chain folds into a complex 3D shape to form the protein.
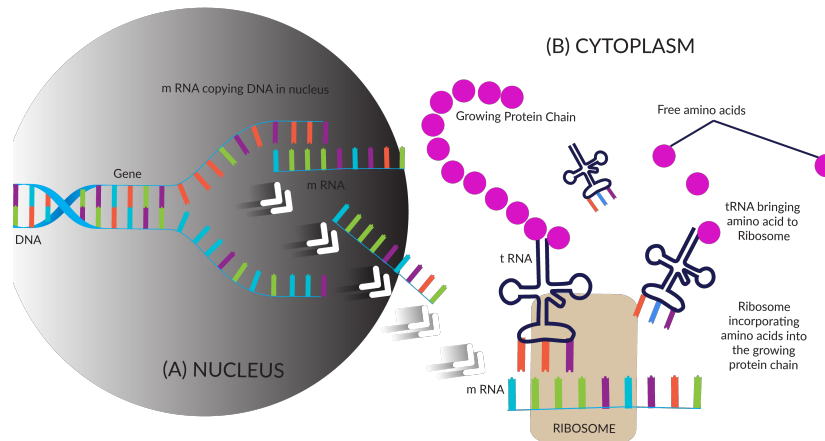

Figure 1: *DNA Transcription and Translation. (A) Transcription (Nucleus) - the process by which DNA is copied (transcribed) to mRNA, which carries the information needed for protein. (B) Translation (Cytoplasm) - process by which mRNA directs protein synthesis with the assistance of tRNA [13].*

1.2. Connections between DNA and Music

Any gene can be expressed as a sequence of **four letters** (Fig. 2A): A (adenine), C (cytosine), G (guanine) and T (thymine); **(**U (uracil) replaces T in RNA**)**. This set of nitrogenous bases is used in the construction of nucleotides, which in turn build up nucleic acids like DNA and RNA. The bases are crucial: their sequencing into DNA and RNA is the means by which the **genetic** information is stored. The nitrogenous bases of each nucleotide pair together through hydrogen bonds in specific combinations-adenine **(A)** is always paired with uracil**(U),** and guanine**(G)** is always paired with cytosine**(C)**. DNA's language uses three-letter words---formed by a four-letter alphabet---called codons (Fig. 2B); one codon encodes one amino acid. The ribosome reads and connects amino acids in series to form proteins. The reading is accomplished by connecting the codon from the mRNA with the complementary anticodon from the tRNA (Fig. 2C). This brings a particular amino acid into its proper position during translation.
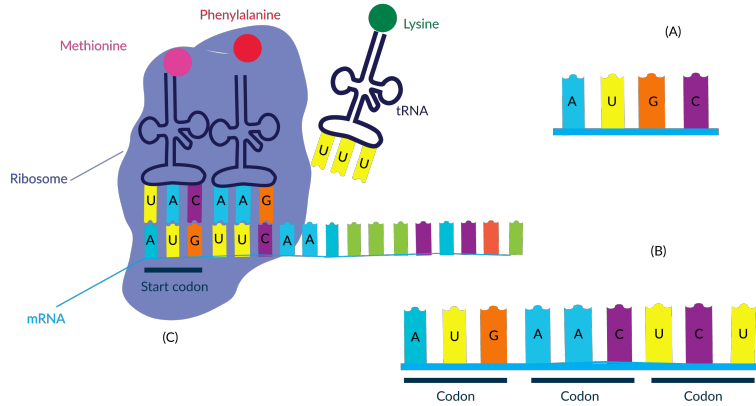
Phenylalanine

Lysine

Methionine

tRNA

Ribosome

U U U

U A C A A G

A U G U U C A A

mRNA

Start codon

(C)

(A)

A U G C

(B)

A U G A A C U C U

Codon   Codon   Codon

Figure 2: *mRNA Translation Process.* ***(A)*** *The nitrogenous bases – A, U, G, C.* ***(B)*** *Codons – AUG, AAC, UCU.* ***(C)*** *Translation – connecting Codon from mRNA with Anticodon from tRNA. [15].*

There are 64 codons in human DNA. Three of them are used to mark the end of the gene (stop codon) and one its beginning (start codon - AUG>Met amino acid). The remaining 61 codons code the 20 amino acids; one amino acid may be encoded by several codons. For a given amino acid, the first two letters are the same. The third letter is floating---this can mean either a different codon for the same amino acid or another amino acid (Fig. 3).

codon >> amino acid

	U	C	A	G
U	UUU >> Phe	UCU >> Ser	UAU >> Tyr	UGU >> Cys
	UUC >> Phe	UCC >> Ser	UAC >> Tyr	UGC >> Cys
	UUA >> Leu	UCA >> Ser	UAA >> Stop	UGA >> Stop
	UUG >> Leu	UCG >> Ser	UAG >> Stop	UGG >> Trp
C	CUU >> Leu	CCU >> Pro	CAU >> His	CGU >> Arg
	CUC >> Leu	CCC >> Pro	CAC >> His	CGC >> Arg
	CUA >> Leu	CCA >> Pro	CAA >> Gln	CGA >> Arg
	CUG >> Leu	CCG >> Pro	CAG >> Gln	CGG >> Arg
A	AUU >> Ile	ACU >> Thr	AAU >> Asn	AGU >> Ser
	AUC >> Ile	ACC >> Thr	AAC >> Asn	AGC >> Ser
	AUA >> Ile	ACA >> Thr	AAA >> Lys	AGA >> Arg
	AUG >> Met	ACG >> Thr	AAG >> Lys	AGG >> Arg
G	GUU >> Val	GCU >> Ala	GAU >> Asp	GGU >> Gly
	GUC >> Val	GCC >> Ala	GAC >> Asp	GGC >> Gly
	GUA >> Val	GCA >> Ala	GAA >> Glu	GGA >> Gly
	GUG >> Val	GCG >> Ala	GAG >> Glu	GGG >> Gly

Figure 3*: The Genetic Codon Chart. In* white *– non-charged amino acids and in* ***yellow*** *are shown hydrophobic amino acids. In* ***red*** *are shown (-) charged amino acids and in* ***blue*** *– (+) charged amino acids. In* ***green*** *is shown amino acid Cysteine.* ▢ *is translation Start codon and* ▢ *is translation Stop codon. [18].*

Three of the letter designations of the C major scale coincide with nitrogen bases in the nucleotides---C| (do) matches with C (cytosine) in the nucleotide, G| (sol) with G (guanine), and A| (la) with A (adenine). The simplest way to translate DNA into music is by replacing each nitrogenous base with its corresponding musical note. For the last base, T (thymine), we have the freedom to use any note, for example, B| (si). Nucleotides and amino acids are the structural units by which DNA, RNA and proteins are constructed, just as notes are the structural units of a melody. We can look at these structural blocks as monomers and DNA, RNA, proteins and melody as polymers. DNA is a sequence of bases and a melody is a sequence of notes, but only the sequence itself can carry information---genetic or musical. A simple sequence of amino acids cannot indicate the structure of the protein, just as a simple sequence of words cannot tell a story. Likewise, a sequence of notes cannot create a tune. To become music, it needs rhythm

and dynamics. We consider the tempo as a subset of dynamics - depending on the three-dimensional structure of the protein where the composer introduces variations in loudness.

2. Methodology of Translation

2.1. The Algorithm

We use one and a half octaves (Fig. 4A)-two tones from the small octave, the whole first octave and two tones from second octave, or a total of 12 white keys on a piano. In this way, the repetition of the same musical tone over the several beats is avoided.
We choose this range, influenced by the charge and physicochemical characteristics of the amino acids defined by their side chains. For example - C', E', G', C'' correspond to amino acids with:
- negative charge (C');
- positive charge (E');
- hydrophobic (G');
- hydrophilic (C'');

The other amino acids have been allocated to the remaining notes, again according to these characteristics. [Please, see the table from fig.4.]

The choice of octaves is according specific characteristics of amino acids (see Fig. 3 and Fig. 4B), defined by their side chains. These characteristics define the amino acids' roles in the protein structure: hydrophobicity (low propensity to be in contact with water) or hydrophilicity (energetically favorable contact with water) and charge (positive or negative).
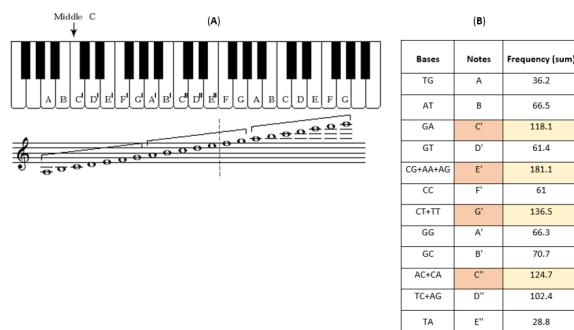

Bases	Notes	Frequency (sum)
TG	A	36.2
AT	B	66.5
GA	C'	118.1
GT	D'	61.4
CG+AA+AG	E'	181.1
CC	F'	61
CT+TT	G'	136.5
GG	A'	66.3
GC	B'	70.7
AC+CA	C''	124.7
TC+AG	D''	102.4
TA	E''	28.8

Figure 4: Choice of range from piano keyboard and musical notes. (A) Range of tones from octaves: from A in small octave to E$^{\|}$ in second octave. A-B – small octave, C$^{|}$-B$^{|}$ - first octave (middle C), C$^{\|}$-E$^{\|}$ - second octave. (B) Choice of musical notes.

The first two letters of the codon define the musical note. There are 16 possible combinations. Eight of the combinations each encode a single amino acid and correspond to a single note in middle C (the first octave). The remaining eight combinations define either an amino acid or a start/stop codon (the third letter in the codon dictates which) or two amino acids that have similar physical properties. To keep the total number of notes to 12 (to avoid big jumps in tones), we form these remaining eight combinations into four groups such that in each group amino acids with similar physical properties are present.

The choice of musical note in this octave and a half is defined by the frequency at which a specific two-letter code occurs in the human genetic code (Fig. 4B) [16]. The most common codons in the human body correspond to the three basic tones in the tonality C major: C (do), E (mi) and G (sol). The combination **UG** (green), encoding the AA(amino acid) Cys + 1 stop codon (red box) + Trp (blue)- hydrophobic AA, correspond to note A (la) in small octave on the piano keyboard. The second note in pitch B (si) is juxtaposed with the hydrophobic AA Isoleucine(Ile), encoded by **AU** (blue) + start codon Met (green). After the small octave follows the first octave and middle C' (do), which corresponds to **GA** (red) and the negatively charged AA - aspartic acid (Asp) and glutamic acid (Glu).
GU (blue) - encoding Val (hydrophobic AA) correspond to note D' (re) in first octave. **CG + AA + AG** (yellow)- encoding (Arg) + (Lys) + (Arg) - positive charged AA (yellow) correspond to note E' (mi) in first octave.
The codons **GG** (blue) and **GC** (blue) encode the hydrophobic amino acids glycine (Gly) and alanine (Ala) and match with the tones A' (la) and B' (si). **AC + CA** (white) which encode the non-charged AA threonine (Thr), histidine (His) and glutamine (Gln), are juxtaposed with the musical note C'' (do) in the second octave. **UC+AG** (white) encode the

non-charged hydrophilic AA Serine (Ser) and is assigned to D" (re) in second octave. The last tone is E"(mi) in second octave, which corresponds to the codon **UA** (white), which encodes the hydrophilic AA tyrosine (Tyr) + 2 stop codons (red box). **CC** (blue)- encoding Pro (hydrophobic AA) correspond to note F' (fa) in first octave. **CU** + **UU** (blue)- encoding Leu (hydrophobic AA) correspond to note G' (sol) in first octave.

To make a melody, we need to construct a rhythm for the music. We do so by using biological form characteristics to assign durations to the individual tones. As discussed above, one amino acid can be encoded by several codons. The first two letters of these codons determine the amino acid and the third defines the type of tRNA that is supposed to transport the corresponding amino acid to the ribosome. The concentration of the different tRNA transporting the same amino acid varies significantly. The higher the concentration of a given tRNA (thus the probability of finding it) in the cell, the faster the corresponding amino acid will be delivered to the ribosome. Therefore the third letter in the codon effectively defines the time needed by the ribosome to add the next amino acid to the protein chain. In Fig. 5, the frequency of occurrence of a given tRNA is matched with a corresponding time value for a note. The frequency scale is divided into four ranges. The range with the frequency higher than 25 corresponds to a whole note (see, fig. 5). For example, in a 4/4, a whole note is held for four counts, or four beats. Frequencies in the interval 25 to 17 are correspond to a half note, corresponding to two counts in 4/4. Frequencies from 17 to eight correspond to a quarter note (one beat or count). For frequencies from zero to eight, we choose the eighth note (one half of a beat). The majority of the codons fall within this diapason, and this mapping produces more rhythmic and dynamic music**.**

The tempo in our algorithm is defined by the three-dimensional structure of the protein. This 3D structure comes in three variations: alpha-helices, beta-sheets and unstructured in the space (see Fig. 6). For a peptide with alpha-helical regions, we use allegro; for a peptide with beta-sheets regions, we use moderato; and for a peptide with unstructured regions, we use lento.
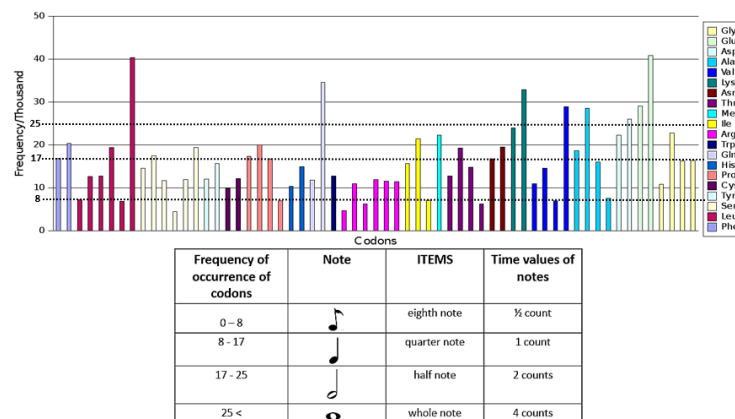

Frequency of occurrence of codons	Note	ITEMS	Time values of notes
0 – 8		eighth note	½ count
8 – 17		quarter note	1 count
17 – 25		half note	2 counts
25 <		whole note	4 counts

Figure 5: *Frequency of occurrence of codons in human genome and relevant time values of the musical notes.*

The above algorithm of DNA translation into music was implemented made into **[QA: change to "made into"?]** [A: OK] a computer code. The input is the DNA sequence and the output is a MIDI file and PDF with a note sequence. For the realization of a complete musical work, the developed algorithm is used in combination with a music engraving program LilyPond 2.18.2 [12] It brings the aesthetics of traditionally engraved music to computer printouts.

2.2 The Love Hormone

Oxytocin the *"love hormone"* has a peptide structure that acts both on the peripheral tissues as a hormone and as a neurotransmitter in the brain. It plays an important role in the control of uterine contractions during labor and in the secretion of milk and a key role in the socialization process, creating the biological conditions for interpersonal bonding [18]. Oxytocin is synthesized from neurons located in the hypothalamus and is transported by axons of the hypothalamic-pituitary tract as a prohormone (bound to the protein neurophysin; see Fig. 6A). It accumulates in the posterior pituitary, where it is secreted into the bloodstream in response to various stimuli [19]. Oxytocin accomplishes its functions via interaction with specific oxytocin receptors (belonging to the rhodopsin-type [class I] group of G-protein-coupled receptors [GPCRs]) embedded in the cell membrane (Fig. 6B and C). The hormone binds to the transmembrane portion of the receptor and thus activates it, causing the start of various intracellular signaling pathways. A gene encodes the oxytocin receptor (OXTR) and the neurophysin (Fig. 7). The 3D structure of the

receptor is not known. In order to construct it, we perform homology modeling using the program Modeller [20]. The resulting 3D structure determines the tempo. The visualization of the neurophysin and oxytocin can be seen in a video available as a supplemental file.[see "Oxytocin and Neurophisin.avi" on www.refoundation.net/projects/ Music of Human Hormones]
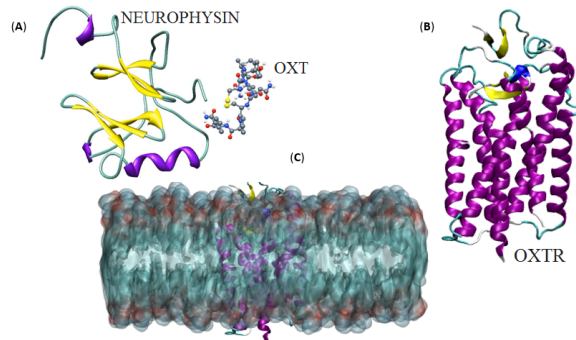

Figure 6: *Neurophysin and Oxytocin (**A**), Oxytocin receptor (**B**) and Oxytocin receptor embedded in membrane (**C**). The 3D structures are download from Protein Data Bank [16] and visualized through the program Visual Molecular Dynamics (VMD).*

Figure 7: *Genes for Oxytocin (OXT), Oxytocin Receptor (OXTR) and Neurophysin [11].*

3. The Music of Oxytocin

Using the proposed algorithm, we have created PDFs with notes *(which are the music tones of each ingredient (aminoacid sequence) that are interacting with each other and this interaction is recreated by the composer)* for the oxytocin (see Fig. 8), its cell receptor and the neurophysin in the corresponding supplemental files (see OXT.png, OXTR.pdf and NEUROPHYSIN.pdf at www.refoundation.net/projects/Music_of_Human_Hormones). MIDI audio files are available as well (oxy.midi, neuro-new.midi and OXTR.full.midi). These audio files can be played directly or used as an input for electronic music. For audio and video of performance of the music of oxytocin, see the file OXT-music_and_3Dstructure.mp4.

The melody, on which is based the further development of the music of oxytocin, can be seen in Fig. 8. We experiment with the basic melody of oxytocin in three different styles: an electronic version that combines the melody of the hormone with the beat of the human heart, triggering deep emotions in the listener; a classical canon; and a crab canon. These three variations on the melody of the oxytocin can be heard in the audio files oxy_canon.midi, crab_canon.midi and oxytocin.wav.

The canon is the strictest musical form. In this form, individual parts imitate a tune at regular intervals (starting at different times). The initial melody is called the leader, while the imitative melody, which is played in a different voice, is called the follower [21]. While in a classical canon the follower must imitate the leader, either exactly replicating its rhythms and intervals or some transformation thereof, in a crab canon the follower accompanies the leader backward [22]. The crab canon is one of the most exotic forms of the canon, as it involves playing the melody forward and backward at the same time---each melody is read once from left to right (forward) and then from right to left (backward). A well-known example is found in J.S. Bach's *Musical Offering*.

So far, all the wondrous musical workings of oxytocin obey the same law **[canon].**The resulting forms of the music of oxytocin are intriguing, but we do not consider these as works of art. The role of human creativity in developing the overall musical structure is crucial. The action of oxytocin involves three different proteins, interacting in a complex way to trigger the final reaction (emotion) in the human body. The translation of the DNA code into music would not be complete without the composer's use of the note material of the oxytocin, neurophysin and oxytocin receptor to present the process of interrelation of these three biological structures as a documentary "fairy-tale" narrative in its integrity.*(note: The ordinary translation can translate the single biological structure into the single simple melody, but in real life there is a harmonic correlation between the different structures and here is the important role of composer - to turn the three simple melodies (of the above three biological single structures) into a complete musical work, recreating the connections and interactions between the various structures, by the overall musical arrangement.)* The musical interpretation of the oxytocin and its story of birth, transportation and, finally, connection with its receptor can be found in the supplemental file *the Music of the Love Hormone_Oxytocin.wav* by the composer Mihai Iosifov.

Figure 8: *Output from algorithm and LilyPond software for Oxytocin.*
Semiquavers are appear because the algorithm is written so that it splits automatically last note to fill four times in tact.

4. Neurophysiological Test
To test the accuracy of the translation of oxytocin from biological into musical form, we conduct a neurophysiological testing experiment. We compare physiological reactions to natural oxytocin and to the musical translation of oxytocin, measuring cerebral function (via a quantitative electroencephalogram [QEEG]) and heart rate variability (HRV).

A QEEG measures cerebral function---electrical activity at the surface of the brain [23], represented in waveforms of varying frequency and amplitude measured in microvolts. The most familiar classification is that of alpha, beta, theta and delta waves**.** Each site of the skull has a letter to identify the lobe and a number to identify the hemisphere location. The letters F and C in Fig. 9 stand for the frontal and central lobes, respectively; "z" refers to an electrode placed on the midline between hemispheres. Alpha rhythms are derived from the white matter of the brain. This is the main rhythm throughout mindful life. The characteristic states and emotions linked with these brainwaves are tranquil but conscious. Theta waves are connected with creativity, intuition, daydreaming and fantasizing and are a repository for memories, emotions and sensations [24], reflecting the state between wakefulness and sleep and relating to the subconscious. The last brain wave measured by the QEEG is the sensorimotor rhythm (SMR), an oscillatory idle rhythm of synchronized electric brain activity produced when the sensorimotor areas are idle---during states of immobility and refers to empathy, contemplation, meditation.
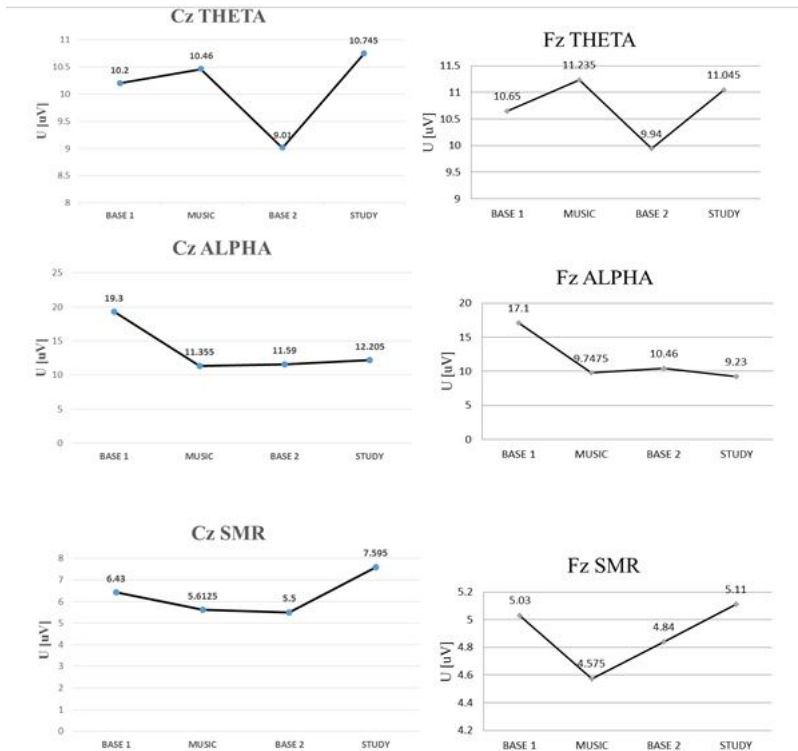
Figure 9*: Average Results from QEEC.*
Base 1 and 2 are neutral state. Study is state of injection of the chemical structure of Oxytocin.

Heart rate variability (HRV) is measured by variations in the beat-to-beat interval and is related to emotional arousal. High-frequency (HF) activity has been found to decrease under conditions of acute time pressure and emotional strain [25] and during elevated states of anxiety [26], presumably related to a narrowed focus of attention and motor inhibition.

We designed the experiment to compare the impacts of the musical and chemical forms of oxytocin (with the chemical form being introduced as a nasal spray to act upon the oxytocin receptors as they are the olfactory ones). The baseline study involves 14 volunteer participants. We measure the cerebral function and HRV of the participants during the following three stages of the experiment: Stage 1, the neutral condition; Stage 2, while listening to the music (oxytocin audible structure)**,** and Stage 3, after nasal injection with the spray (oxytocin chemical structure). The music of oxytocin used in this neurophysiological study can be heard in the file *The Music of the Love Hormone_Oxytocin*. The individual results show similar responses in HRV and in QEEG theta divisions. The main information in this study comes from theta and SMR waves in QEEG. An increase of theta waves when listening to the music of oxytocin leads to increased serotonin in the brain. Simultaneously, the SMR waves decrease (see Fig. 10). Average results show similar trends in neurophysiological responses to the musical composition and after nasal injection. A correlation of brain reactions to the action of oxytocin in both biological and musical forms is observed. However, more definitive conclusions will require further testing for sufficient data.

Bases 1 and 2 in Fig. 9 are the neutral states. "Study" is the state at the time of the injection of the chemical structure of oxytocin.

Parameter	Basic Level	Music	Oxytocin
Average heart rate beats per minute	76,6	75,7	73,9
Energy expense ratio and energy recovery processes (Sympathetically: parasympathetics) rate of 1.5 - 2	0,95	1,57	1,2
Centralization of the management of heart rhythm *	3,39	1,02	1,01

Figure 10: *Average results from HRV.*
The values: ***> 1*** *means optimal regulated only by the AHC (amygdalo–hippocampal complex).* ***<1*** *means that the regulation of the heartbeat becomes under energized and with duplicated control - from the AHC and hormonal (may be an indication of anxiety);*

Conclusions

Our basic idea in the design of the algorithm was to follow as closely as possible the coding, production and functioning processes of proteins in the human body. A formal correspondence of DNA-coding nucleotides to musical notes had already been established in the majority of existing algorithms. We also included information about the production process of the protein in the ribosome and its final 3D structure parameters. The result is a sequence of musical tones (notes) reflecting the structure of the corresponding protein and following the production and molecular interaction processes.

A complete translation of the action of a given protein should include not only the protein under consideration but also the other proteins taking part in its expression. In terms of music, this means that the DNA code of the other players should be translated into notes as well, and a full musical piece should be composed out of the note material of all participants in the process. Enter music theory and human interpretation: The composer Mihail Iosifov, uses the note material to tell the story of the protein actions. The artistic interpretation of the translation can be developed in different musical styles.

We use this approach to represent the properties and the impact of an essential human hormone. We apply our algorithm to this process and create three musical sequences. A composer then presents the story of the three proteins.

To verify the translation, we perform a neurophysiological test on 14 volunteers. The brain and heart reactions to chemical oxytocin (introduced as nasal spray) and its musical interpretation are compared. Evidence of correlation in the reactions is observed. We plan to conduct a follow-up investigation on a larger scale to draw conclusions about the effects of the music of Oxytocin along the other human hormones responsible for human emotions.

The next stage of project development is applying and expanding this knowledge onto the specific sets of hormones defining human emotions---a project called *Symphony of Emotions*.

Acknowledgments

List of Abbreviations

DNA - DeoxyriboNucleic acid
RNA - RiboNucleic acid
mRNA - messenger RNA
tRNA - transfer RNA
AA – Amino Acid
A – Adenine
C - Cytosine
G – Guanine
T – Thymine
U – Uracil
Tyr - Tyrosine
C do
D re
E mi
F fa
G sol
A la
B si
Cys – Cysteine
Trp – Tryptophan
Ile – Isoleucine
Met – Methionine
Asp - Aspartic
Glu - Glutamic
Val - Valine
Arg - Arginine
Lys - Lysine
Asp - Asparagine
Pro - Proline
Leu – Leucine
Gly – Glycine
Ala – Alanine
Thr - Threonine
His - Histidine
Gln – Glutamine
Ser – Serine
Tyr – Tyrosine
OXT – OXyTocin
OXTR – OXyTocin Receptor
VMD – Visual Molecular Dynamics
GPCRs - G-Protein Coupled Receptors
QEEG - Quantitative ElectroEncephaloGraphy
HRV - HeaRt Variability;
F- Frontal
C - Central
z- zero
SMR - SensoriMotor Rhythm
HF – High-Frequency
AHC - Amygdalo–Hippocampal Complex

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Fig. 1.
DNA transcription and translation. (A) Transcription (nucleus)---the process by which DNA is copied (transcribed) to mRNA, which carries the information needed for the protein. (B) Translation (cytoplasm)---the process by which the mRNA directs protein synthesis with the assistance of the tRNA [27]. (<c> Cv. Ivanova**,** L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)

Fig. 2.
The mRNA translation process. (A) The nitrogenous bases: A, U, G, C. (B) Codons: AUG, AAC, UCU. (C) Translation: connecting the codon from mRNA with the anticodon from the tRNA [28]. (<c> Cv. Ivanova, L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)

Fig. 3.
The genetic codon chart. Noncharged amino acids are shown in white, and hydrophobic amino acids are shown in gray. Charged amino acids are represented by diagonal lines (\) and charged amino acids are represented by dots (·). The amino acid cysteine is shown in black is the translation stop codon and AUG>>Met is the translation start codon [29]. (<c> Cv. Ivanova, L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)

Fig. 4.
Choice of Piano keyboard range and musical notes (A) Range of tones from octaves: from A in the small octave to E|| in the second octave. A--B, small octave; C|--B|, first octave (middle C); C||--E||, second octave. (B) Choice of musical notes. (<c> Cv. Ivanova, L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)

Fig. 5.
Frequency of occurrence of tRNA matched to a given codon in human cells and the relevant time values of the corresponding musical notes. (<c> Cv. Ivanova, L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)

Fig. 6.
Neurophysin and oxytocin (A), oxytocin receptor (B) and oxytocin receptor embedded in membrane (C). The 3D structures are downloaded from the Protein Data Bank [30] and visualized through the program Visual Molecular Dynamics (VMD). (<c> Cv. Ivanova, L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)

Fig. 7.

Genes for oxytocin (OXT), oxytocin receptor (OXTR) and neurophysin [31]. (<c> Cv. Ivanova, L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)

Fig. 8.
Output from algorithm and LilyPond software for oxytocin. Semiquavers are present because the algorithm is written so that it automatically splits the last note to fill four times in beat (<c> Cv. Ivanova, L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)

Fig. 9.
Average results from the QEEG. (<c> Cv. Ivanova, L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)

Fig. 10.
Average results from the HRV test. >1 is optimal, regulated only by the AHC (amygdalo–hippocampal complex). <1 means that the regulation of the heartbeat is under energized, with duplicated control by the AHC and hormones (may be an indication of anxiety). (<c> Cv. Ivanova, L. Litov, R. Marinova, T. Ivanov, M. Yossifov and A. Dejnowicz-Velitchkov)