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Role of Locally Synthesised Protein in Long Term Memory - An Analytical Approach

Brajagopal Majumder

Former Chairman, State Resource Centre-Tripura, Melarmath Agartala, India

Abstract Permanent alteration in the structure and number of synapses involves new protein synthesis and assemblage of new memory circuits resulting changes in electrical activity of specific regions of the brain due to different learning experiences. Injections of protein inhibitor in the temporal lobe of mice led to the fact that learning is effective in long-term memory (LTM). Studies of long term potentiation (LTP) and long term depression (LTD) in mammalian brains resulted in two distinct phases- the early one (typically lasting 1-3 hours) is independent of new protein synthesis and the late one (typically lasting more than 8 hours) depends on new protein synthesis. This paper focuses on developing an Analytical Approach for mathematical analysis of these experimental findings basing on the role of protein vibrations in learning and memory with the assumption that dissociation or association of the number of amino acid molecules are required for synthesis of new protein responsible for LTM.

Keywords Protein vibration, Long term potentiation, Local protein, Units of time, Association, Dissociation, Amino acids

1. Introduction

It is now an established fact that memory has considered as the combined process of perception, conception and consciousness. In addition, brain is the storehouse of these combined activities and their recall. Specific regions of the brain like hippocampus, amygdale, thalamus etc. become activate periodically in accordance with the sensation created by nerve impulses. For example, hippocampus is responsible for learning events and their recall, while amygdale responses to emotions of the individuals.

However, the process of memory storing and reproduction is not beyond controversy. Now stimulus response (S-R) hypothesis has viewed in the context of molecular biology and biochemistry. Recent physiological and biochemical investigations reveal that proteins in different forms like neurotransmitter, neuromodulator and neuroreceptor play vital role in different phases of learning and memory traces. Number of experimental models emerged out in the area of phosphorylation of protein centering on Caenorhabditis elegans, drosophila melanogaster and Aplysia californica following the first demonstration of protein **(C57B1/6J)** in mice, which results in instrumental aversive foot-shock conditioning [1].

In a recent paper [2] it has been established that the cAMP stimulates protein kinase **A(PK-A)** which phosphorylates the K+ channels on the membrane resulting in short term memory (STM) or cAMP response to element binding with protein in long-term memory (LTM). Long-term memory traces are usually associated with permanent alteration in the structure and number of synapses. Such an alternation involves new protein synthesis and assemblage of new memory circuits. This means that there occur changes in the electrical activity of specific regions of the brain due to different learning experiences. The process of learning gets disturbed if recruitment of synaptic vesicle or neurotransmitter interrupted.

In the same paper [2] it was held by the authors that vibrations created in different proteins due to either electrostatic force or continuous oscillations of electrical potentials with different amplitudes and frequencies are found to vary with respect to molecular weight of the protein. It has assumed that more the molecular weight of the protein, the more stable the memory is. It also holds that more the molecular weight of the protein molecule is, the less would be the magnitude of vibration frequency and more the frequency of vibration is less would be molecular weight of protein. This means there is frequent vibrations in case of proteins of less molecular weight where reverse may find in case of protein of higher molecular weight.

Protein synthesis inhibitors discovered in late 1950 by Yarmolinsky and **De La Haba.** [3]. Basing on this discovery, Louis and Josefa Flexner [4] in 1963 administrated injections of protein inhibitor puromycin in the temporal lobe of mice. They found that learning was effective from day **1** to **3** in

* Corresponding author:
bgmajumder@gmail.com (Brajagopal Majumder)
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blocking long-term memory in mice for the location where an electric shock received in a Y-shaped maze. They also noticed that the injection made later than 3 days after training did not result in consistent memory deficit. These findings are found to be in consistent with those found by Stanton & Survey [5] and Frey et al. [6]. Their studies of long-term potentiation (LTP) and Long-term depression (LTD) in mammalian brains resulted in two distinct phases. While in one phase (typically lasting 1-3 hours), these are independent of new protein synthesis, in a late phase (typically lasting more than 8 hours) these are dependent on new protein synthesis.

The experimental findings of Flexner et al. [4] and a number of scholars like Agranoff et al. [7] and Davis & Squire [8] led to conduct similar experiments and they also held the view that protein synthesis is required for animals to form enduring memories. Recently, a number of scientists like Kelleher et al. [9] Costa Mattioli et al. [10] and Banko et al. [11] supported Flexner's findings in the context of genetic approaches. Although the volume of work goes on increasing day by day, there is lack of clear understanding of "why" protein synthesis is critically so important for controlling memory processing. Question also arises how this newly synthesized protein can alter the functional capabilities of synapse etc. particularly in respect of storing long-term information. These however open a new channel of dendrite protein synthesis, also its role in LTP (Long-term potentiation) and **LTD** (Long term depression) in mammalian brain.

The findings of different scholars regarding period of retentivity of learning events with respect to involvement of different proteins along with synthesis of new protein constitute the basis of our proposed paper. An attempt has taken here to develop an "Analytical Approach" to analyze mathematically the experimental findings demonstrated by different scholars. This has developed on basis of our hypothesis of the role of protein vibration in learning and memory (2) with the assumption that proteins of large molecular weight are responsible for stable memory while short tern memory is concerned with protein of small molecular weights.

2. Methodology

Frequencies of vibrations of certain protein generated due to electrostatic force and the subsequent vibration energy in terms of joules were computed **(2)** basing on the simple equation.

$$E_{vi} = (\nu + \tfrac{1}{2})\frac{h}{2\pi}\sqrt{\frac{K}{m}} \qquad (1)$$

Where, ν stands for different quantum level ($\nu = 0, 1, 2, 3\ldots$) and other quantities K, m stand for force constant & mass of the protein respectively. In addition, it analytically establishes that proteins of large molecular weight executing less number of vibrations are responsible for stable memory while the reverse is available in case of proteins of small molecular weight.

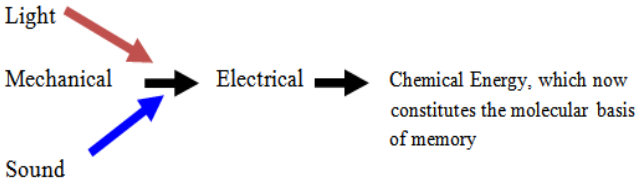
Basing on the above hypothesis, an attempt has is taken here to establish mathematically the experimental findings of the scholars as-

i) Leaning is effective from day 1 to 3 and are independent of protein synthesis.

ii) Leaning lasting for more than **8** (eight) units of time (hour or day) is dependent on new protein synthesis and there should be a critical period for new protein synthesis.

iii) Proteins constitute the molecular basis of memory.

In his proposed approach of electro- chemical correlates of learning and memory, the author **[12]** held the view that learning and memory are nothing but transformation of energy from one form to another viz.



There is no standard mathematical formula for measuring retentivity or the retained amount of learnt event. The classical psychological methodology of measuring retentivity $R=R_1-R_2$ (where $\mathbf{R_1}$ is the amount of retained event after first unit of time and $\mathbf{R_2}$ is that during experimental time) as used by Ebbinghaus and others are still being used by the scholars of the day in the context of macro approaches. However, learning and memory have now considered from the molecular point of view. Here also no universally accepted mathematical formulation for measuring the amount of retentivity or the amount of learnt event with respect to time is available.

Considering the experimental findings of the scholars and keeping in view our proposed hypothesis of protein vibrations, an attempt has been taken here to formulate a mathematical expression for crosschecking the experimental findings and hence to have a comparative study of the experimental findings. Following the standard expression of energy decay law, decay of vibration energy of certain membrane bound proteins has calculated from the Equation.

$$E_D = E_n e^{-\omega t} \qquad (2)$$

Where, $\mathbf{E_D}$ = Decay energy.

$\mathbf{E_n}$ = Energy at n level of vibrations.

ω = Frequency of external stimuli (EEG rhythms)

t = Time of decay

$\mathbf{E_n}$ is the Vibration energy at n=6 quantum level of vibration.

The expression for the vibration frequency stands for

$$\nu_{vib} = \frac{1}{2\pi}\sqrt{\frac{k}{m}} \qquad (3)$$

Using Equation **(3)** vibration frequency $(\boldsymbol{m^{-1}})$ of some memory related proteins with molecular weights and the vibration energies at Zero-Level were calculated by the authors [2] and these are tabled in Table No-1 & Table No-2

Table 1. Vibration frequencies (m^{-1}) of some memory related Proteins with molecular weights

External electrical stimuli in microvolt	m = 16.9	m = 19.98	m = 24	m = 32	m = 42	m = 54	m = 250
20	0.17	0.67	0.60	0.52	0.46	0.40	0.18
25	0.81	0.74	0.68	0.58	0.51	0.45	0.25
50	1.14	1.05	0.96	0.83	0.72	0.63	0.29
100	1.60	1.49	1.34	1.16	1.01	0.90	0.41
150	1.93	1.83	1.63	1.42	1.24	1.06	0.50
250	2.23	2.37	2.15	1.86	1.62	1.43	0.66
350	3.03	2.67	2.55	2.20	1.92	1.69	0.79

Table 2. Vibration Energy of Proteins at Initial (n=0) Levels

Initial energy	Final energy x 10^{-22} J						
	m=16.9	m=19.98	m=24	m=32	m=42	M=54	m=250
(i) Initial energy due to 20 microvolt equaling to 11.0X10^{-22} joules	14.29	12.89	11.91	10.32	9.13	7.94	3.57
(ii) Initial energy due to 25 microvolt equaling to 13.75 X10^{-22} joules	16.08	15.06	13.50	11.51	10.12	8.93	4.17
(iii) Initial energy due to 50 microvolt equaling into 27.50 X10^{-22} joules	22.64	20.54	19.06	16.48	14.29	12.51	5.75
(iv) Initial energy due to 100 microvolt equaling to 55.00 X10^{-22} joule	31.77	29.66	26.61	23.03	20.05	17.87	8.14
(v) Initial energy due to 150 microvolt equal to 82.50 X10^{-22} joule	38.32	35.42	32.37	28.20	24.62	21.05	9.93
(vi) Initial energy due to 250 microvolt equal to 137.50 X10^{-22} joule	44.28	43.26	42.69	36.93	32.17	28.39	13.10
(vii) Initial energy due to 350 microvolt equal to 192.50 X10^{-22} joule	60.17	54.18	50.64	43.69	38.13	33.56	15.68

Table 3. Vibration Energy of Protein in the context of quantum Number

		Quantum Number						
Magnitude of external stimuli in Joules	Molecular mass of protein	n=0	n=1	n=2	n=3	n=4	n=5	n=6
20x10^{-22} Joules	m=19.98	12.89	19.33	32.22	45.12	58.00	70.89	83.78
	m=54	7.94	11.91	19.85	27.89	35.83	43.77	51.71
	m=250	3.57	5.35	8.92	12.49	16.06	19.63	23.20
25x10^{-22} Joules	m=19.98	15.06	22.59	40.20	56.28	72.36	88.44	104.52
	m=54	8.93	13.39	22.32	31.25	40.18	49.11	58.04
	m=250	4.17	6.25	10.42	14.59	18.76	22.93	27.10
27.50 x 10^{-22} Joules	m=19.98	20.54	30.81	51.35	71.89	92.43	112.97	133.51
	m=54	12.51	18.76	31.27	43.78	56.29	68.80	81.31
	m=250	5.75	8.62	14.37	20.13	25.87	31.62	37.37
55.00 x 10^{-22} Joules	m=19.98	29.66	44.49	74.15	103.81	133.47	163.13	192.79
	m=54	17.87	26.80	44.67	62.54	80.41	98.28	116.15
	m=250	8.14	12.21	20.35	28.49	36.63	44.77	52.91
82.50 x 10^{-22} Joules	m=19.98	35.42	53.13	88.55	123.97	159.39	194.81	230.23
	m=54	21.05	31.57	52.62	73.67	94.72	115.77	136.82
	m=250	9.93	14.89	24.82	34.75	44.68	54.61	64.54
137.50x10^{-22}J oules	m=19.98	43.26	64.89	108.15	151.41	194.67	237.94	281.19
	m=54	28.39	42.58	70.97	99.36	127.75	156.14	184.53
	m=250	13.10	19.65	32.75	45.85	58.95	72.05	85.15
192.50x10^{-22} Joules	m=19.98	54.18	81.27	135.45	189.63	243.81	297.99	352.17
	m=54	33.56	50.34	83.90	117.46	151.02	184.58	218.14
	m=250	15.68	23.52	39.20	54.88	70.56	86.24	101.92

Using Equation (1) numerical values of energy at n=6 level of some membrane bound proteins having molecular weight m=19.98, m=54 and m=250 KD are calculated and these are also tabled in Table No-3

The decayed vibration energies of the aforesaid proteins have been calculated by using Equation No.(2) for different frequencies of the External stimuli in the form of EEG rhythms from 0.5cps to 30cps and of amplitudes in the range of 20 to 350 micro volts. For example, only 3 tables (No. 4-6) are cited here for protein of masses m=19.98, m=54 & m=250 KD for Zero level energies viz. ($\mathbf{E_0}$ = 29.66, $\mathbf{E_0}$ = 17.87 and $\mathbf{E_0 = 8.14) \times 10^{-22}}$ Joules with respect to external stimuli of 100 microvolt equaling to 55.00 $\mathbf{\times 10^{-22}}$ Joules. Depending on these amount of decayed energies with respect to proteins of higher (m=250), middle range mass (m=54) and lower masses (m=19.98), retentivity of learnt events with respect to time is analyzed mathematically.

Table 4. Vibration Energy of Proteins with respect to time and frequencies Weight/mass of protein=19.98 KD

Magnitudes of external stimuli in Joules	Energy attained by proteins at Zero Level (n=o)	Energy attained by protein in quantum level (n=6)	Time	ω = External frequencies. D = Amount of Decayed energy					
				ω = 0.5 cps	ω = 3.5 cps	ω = 4 cps	ω = 8 cps	ω = 13 cps	ω = 30 cps
				D	D	D	D	D	D
			1	191.82	186.23	185.27	177.94	169.26	142.85
			2	190.86	179.68	179.94	164.25	148.64	105.84
			3	189.89	174.47	171.00	151.72	130.51	78.27
			4	188.93	167.53	164.25	139.96	114.51	58.02
$55x10^{-22}$J	**29.66J**	**192.79 J**	5	187.97	162.71	157.89	129.16	100.63	42.99
			6	187.00	156.35	151.72	119.33	88.29	31.81
			8	185.07	145.74	139.96	101.60	68.05	17.54
			9	184.30	141.31	134.56	93.88	59.76	12.91
			10	183.34	135.91	129.16	86.56	52.05	9.44
			15	182.18	114.51	105.84	58.02	27.37	2.12
			20	174.47	95.62	86.56	38.94	14.26	0.38
			30	165.49	67.28	58.02	17.54	3.85	-

Table 5. Vibration Energy of Proteins with respect to time and frequencies Weight/mass of protein=54 KD

Magnitudes of external stimuli in Joules	Energy attained by proteins at Zero Level (n=o)	Energy attained by protein in quantum level (n=6)	Time	ω = External frequencies. D = Amount of Decayed energy					
				ω = 0.5 cps	ω = 3.5 cps	ω = 4 cps	ω = 8 cps	ω = 13 cps	ω = 30 cps
				D	D	D	D	D	D
			1	115.56	112.20	111.62	107.20	101.97	86.06
			2	114.98	108.25	107.20	98.95	89.55	63.76
			3	114.40	105.11	103.02	91.41	78.63	47.15
			4	113.82	100.93	95.95	84.32	68.99	34.96
55.00x 10^{-22}J	**17.87J**	**116.15 J**	5	113.24	98.03	95.12	77.82	60.63	25.90
			6	112.66	94.19	91.41	71.89	53.19	19.16
			8	111.50	87.80	84.32	61.21	41.00	10.56
			9	111.03	85.13	81.07	56.56	36.00	7.78
			10	110.45	81.88	77.82	52.15	31.36	5.69
			15	109.76	68.99	63.76	34.96	16.49	1.27
			20	105.11	57.61	52.15	23.46	8.59	0.23
			30	100.00	40.53	34.96	10.56	2.32	-

Table 6. Vibration Energy of Proteins with respect to time and frequencies Weight/mass of protein=250 KD

Magnitudes of external stimuli in Joules	Energy attained by proteins at Zero Level (n=o)	Energy attained by protein in quantum level (n=6)	Time	ω = External frequencies. D = Amount of Decayed energy					
				ω = 0.5 cps	ω = 3.5 cps	ω = 4 cps	ω = 8 cps	ω = 13 cps	ω = 30 cps
				D	D	D	D	D	D
			1	51.45	49.95	49.69	47.72	45.40	38.31
			2	51.19	48.18	47.72	44.05	39.86	28.38
			3	50.93	46.79	45.86	40.69	35.00	20.99
			4	50.67	44.93	44.05	37.54	30.71	15.56
$55.00x10^{-22}$J	**8.14J**	**52.91 J**	5	50.41	43.64	42.37	34.64	26.99	11.53
			6	50.15	41.93	40.69	32.00	23.68	8.53
			8	49.64	39.09	37.54	27.25	18.25	4.70
			9	49.43	37.90	36.09	25.18	16.03	3.46
			10	49.17	36.45	34.64	23.21	13.96	2.53
			15	48.16	30.71	28.38	15.56	7.34	0.56
			20	46.79	25.64	23.21	10.44	3.82	0.10
			30	44.52	18.04	15.56	4.70	1.03	-

These represented graphically. From the graphical presentations, sudden fall of decayed energy, which means sudden decrease in learning amount, is observed particularly with respect to more than with 8 (hours/day) units of time, while the nature of graph follows almost straight line up to (3-6) units of time with certain amount of variations with respect to higher molecular weight of proteins.

An attempt has taken to examine these findings and to establish the fact that the **2^{nd}** objective i.e. new synthesis of protein is required for learning lasting more than **8** units of time (hour/day etc.).Here we like to recall to the fact when an electric signal gets to a neuron, the structure of the membrane lipid is changed and they pass into a new state with intensifying RNA activity and its constituent protein synthesis. At this stage, the lipid structure gets restructure, the nature of the synthesis of the constituent protein becomes different and the entire synthesis process of the cell passes into a new state. The re-oriented proteins enter the lipids and stabilize their new structure [12].

The re-oriented or newly synthesized protein requires association or dissociation of amino-acid molecule and hence it is clear that molecular weight of protein depends on the no. of amino- acid residues-attached or detached.

If **N** be the amino-acid molecule and the probability of transition be X, the probability of transition in a short interval of time **dt** would be **X dt**. If N be kept as unchanged molecule, there results the relation $\frac{dN}{dt}$**= - X dt** which on integration yields to

$$\ln \frac{N}{No} = -\,xt \tag{4}$$

Where No is the initial number of amino-acid molecules for t = 0 and t is the total time elapsed. The probability of transversal per unit time is independent of the size of the small region given by $\frac{KT}{h}$.

Where, **K** is the Boltzmann constant, **T** is the temperature in absolute scale and **h** is the Plank constant.

The rate of association of amino-acid molecule may represent by

$$X_1 = \frac{KT}{h} e^{-Er_1/KT} \tag{5}$$

Similarly, the rate of dissociation of amino-acid molecule may represent by

$$X_2 = \frac{KT}{h} e^{-Er_2/KT} \tag{6}$$

Which means X varies as

$$e^{-Er/KT} \tag{7}$$

Where, E_r stands for the energy value in **r** level.

It has suggested by the author [12] that the action potential accelerates the probability of transversal of amino acid through membrane whatever may be its size. As a result, the rate of association would accelerate and it would be proportional to $\frac{dv}{dx}$, the measure of action potential. Therefore, **X** stands as.

$$X \propto \frac{dv}{dx} \tag{8}$$

Hence, combining Equations (7) & (8), X can is written as

$$X = F\frac{dv}{dx}\ \frac{KT}{h}\ e^{\frac{-Er}{KT}} \tag{9}$$

Where, F is the Faraday constant. The unit for X is per second. Substituting these into Eqn. (4) we get

$$\ln \frac{N}{No} = -F\frac{dv}{dx} \cdot \frac{KT}{h}\ e^{-Er/KT} \cdot t \tag{10}$$

This will give the number of amino acids associated or dissociated during synthesis or degradation of particular proteins.

With a view to make the translation probability per unit time, the right hand side of the **Equation (10)** has made dimensionless with appropriate quantity for energy/mol. It is

also to be noted here that the vibration energy as calculated by following Eqn.(1) and used in Eqns.(2) and (10) in exponential form have been standardized up to decimal one to three for the sake of avoiding complexity of numerical calculation.

With the application of Eqn.(10), the approximate number of amino acids associated or dissociated for a protein of small weight (m=19.98) and a protein of higher weight (m=250) have been evaluated for energies of magnitudes 29.66 X 10^{-22} ***joules*** and 8.14 x 10^{-22} ***joules*** generated due to external stimuli of amplitudes 100 microvolt of EEG rhythms as

N = 138(approx), where N_O = Initial number of amino acid = 182 for protein of molecular weight=19.98 KD.

N = 468(approx), where N_O = Initial number of amino acid=1852 for protein of molecular weight=250 KD

This number of amino acids are predicted to be dissociated when erasing of memory happens and associated when the synthesis of local protein occurs after t>8 units of time and hence memory gets stable.

However, once the newly synthesized protein detected, the amino acid sequences may be determined knowing the molecular weight of the same.

3. Resulted and Discussion

From the tables no significant losses of vibration energy from **n=6** quantum level for protein of small, middle and large masses (m=19.98,54,250 KD) are observed for frequencies of 0.5 cps to 8 cps with respect to **t ≥3** units of time, but for **t >8** units of time, energy losses are found to occur rapidly in inconsistent manner. Basing on the role of protein vibration energy in learning and memory it held that loss of vibration energy means loss of memory. From our mathematical analysis, it has held that learning events initially remain almost constant with respect to **t ≥ 3** units of time for frequencies of **0.5** cps to **8** cps of external stimuli irrespective of molecular weights of proteins. However, for **t >8** units of time, reverse found to occur rapidly for **ω ≥.3.5** cps with respect to small and middle molecular weights of proteins but in case of protein of large molecular weights, loss of vibration energy is less and hence memory loss is also less. However, in case of lower vibration frequency =0.5 cps of the external stimuli, loss of vibration energy occurs in a consistent rate for **t>** 8 units of time irrespective of weights of proteins. It has also found to be relevant from the graphical representation of Data. The graphs (Fig-1, Fig-2, and Fig-3) are in decay nature and it found to be compatible with those observed by Ebbinghaus with respect to the amount of retention of learning of unorganized (nonsense) events. The graphs were plotted with decay energy with respect to time for protein of masses m=19.98, 54,250 KD for external stimuli of 100 microvolt in the form of EEG rhythms for frequency ω =0.5 to 30 cps. It has also noted that learning with respect to mice may be concerned with one single point but not for multiple issues (organized learning) which are usually concerned with human beings.

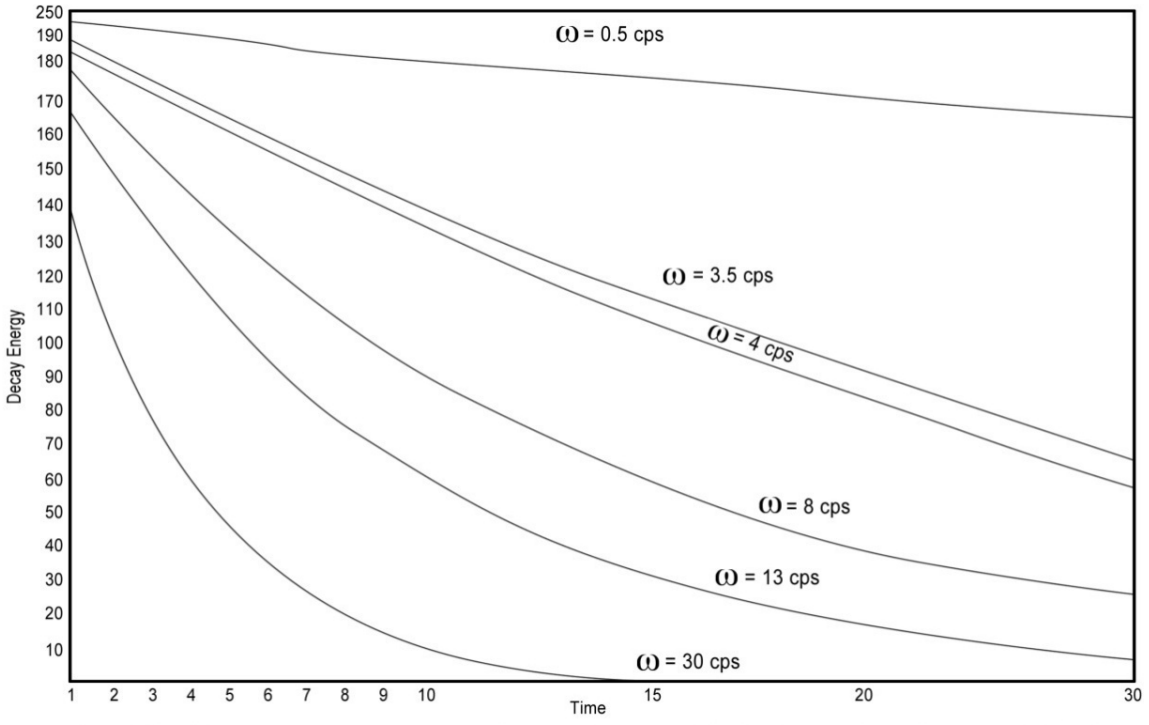


Figure 2. Graphical representation of Decay Energy with respect to time for protein of mass = 19.98KD

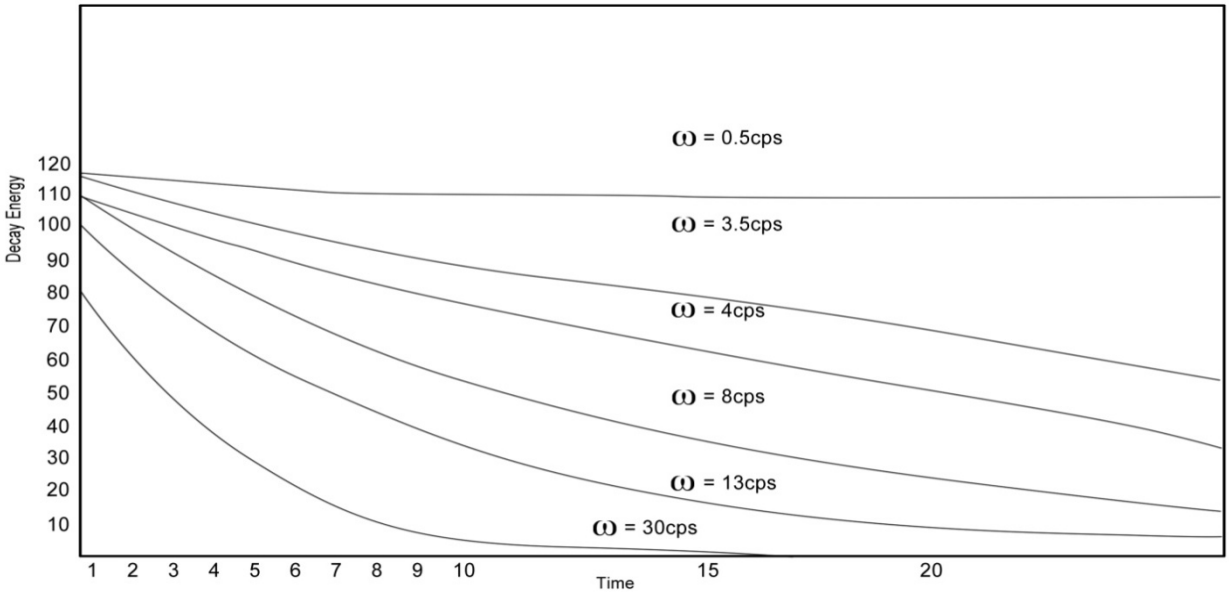


Figure 2. Graphical representation of Decay Energy with respect to time for protein of mass = 54KD

Thus, it held that our mathematical analyses are in parity with the experimental findings, which read as

i) Learning is effective for day **1** to **3** & is independent of further protein synthesis.

ii) There is a critical time for sustainable - learning.

iii) Learning lasting for more than **8** units of time is dependent of new protein synthesis.

iv) Number of amino acids associated or disassociated from the master protein may be evaluated approximately on the basis of our proposed expression cited in Eqn.(10).

V) These amino acid may take part in synthesizing new protein or the disassociated amino acid as a whole, may also act as newly synthesized derivative of the master one.

Basing on the experimental findings and remarks of the scholars that learning lasting for more than **8** units of time requires new protein synthesis. The proposed approach of dissociation or association of amino acid molecules compared to the "erasing and reforming mechanism" of memories with CaMKII protein suggested by Lismen et al. [13]. Here lies the significance of our analytical approach of locally synthesized protein responsible for LTM. Our mathematical analysis to protein synthesis and hence to evaluate the number of amino-acid molecules with the help of Eqn**. (10)** may open a new channel for characterization of newly synthesized protein. However, synthesis of protein responsible for learning and the memory traces is a complex biochemical phenomenon. Hence, practical initiatives can only establish our mathematical approaches.

4. Conclusions

It is observed from our analysis that the duration of learning events evaluated on the basis of protein vibration for 1-6 units of time for frequencies(3.5to 8) cps and of amplitudes 20-350 microvolt of external stimuli in the form of EEG rhythms are in responsible proximity with the experimental findings of **Flexner's et al..**

However, the learning events evaluated on the same basis of protein vibrations for time greater than **8** units suggest that the vibration energies of proteins decrease at these levels rapidly. It demands for orientation of new protein. These observations are also in reasonable proximity with those observed by the scholars.

Considerable analysis of our proposed mathematical approach also supports the experimental findings of **Michael A. Sutton** and **Erin M. Schuman** that the formation of long term memories requires a critical period (in our case, it is $t \geq 8$ units of time) for synthesis of protein. A mathematical approach for detecting the number of amino acids also suggested in this paper. This may open a new vista of knowledge if this approach supports the physical characteristic of newly synthesized proteins as suggested by the scholars. For example, it may be held that there is evidence of local protein synthesis in dendrite which can interact with synaptic growth mechanism as demonstrated in mammals by **Engart** and **Bonchoeffer** [14], Harris et al. [15], Matsuzaki et al. [16] and Zhou et al. [17].

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