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Satyavarapu Naga Parameswara Gupta (SNP Gupta)

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Nanobiotechnology is a wonderful multidisciplinary budding science have its roots in four main branches of science viz, Particle Physics, Nano Biology, and Micro chemistry and Engineering. We are working Nano particle Physics portion which is forming the basis of the Nanobiotechnology. Until today the behaviour of fluid particles in Brownian motion are explained using Single molecule theory. But many questions remain for the last 400 years or so, how this Brownian motion happens? Why collisions happen between the Molecules? How the momentum is generated in the starting place? What are the are the trajectories of individual particles or molecules? The Physics and the calculations behind the force and individual velocities of molecules with relevant theoretical analysis is proposed in this paper. For the Multi Molecule Theory (MMT) Subbarao Simulations (SSMMT) were developed in the last two months. Here we will discuss the basic theory, Excel implementation, simulation results of using, and four the attached Excel files which confirmed the proposition that the Gravitation is the binding force between molecules on different cases.

Keywords: nanobiotechnology, multi molecule theory, dynamic universe model, subbarao simulations, reynolds number, singularity_free cosmology, blue shifted galaxies, red shifted galaxies, grazing radiation frequency changes, formation of elements, nucleosynthesis.

Classification: FOR Code: 020105

Language: English

London Journals Press

LJP Copyright ID: 925663
Print ISSN: 2631-8490
Online ISSN: 2631-8504

London Journal of Research in Science: Natural and Formal

Volume 20 | Issue 10 | Compilation 1.0

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Nanobiotechnology is a wonderful multidisciplinary budding science have its roots in four main branches of science viz, Particle Physics, Nano Biology, and Micro chemistry and Engineering. We are working Nano particle Physics portion which is forming the basis of the Nanobiotechnology. Until today the behaviour of fluid particles in Brownian motion are explained using Single molecule theory. But many questions remain for the last 400 years or so, how this Brownian motion happens? Why collisions happen between the Molecules? How the momentum is generated in the starting place? What are the are the trajectories of individual particles or molecules? The Physics and the calculations behind the force and individual velocities of molecules with relevant theoretical analysis is proposed in this paper. For the Multi Molecule Theory (MMT) Subbarao Simulations (SSMMT) were developed in the last two months. Here we will discuss the basic theory, Excel implementation, simulation results of using, and four the attached Excel files which confirmed the proposition that the Gravitation is the binding force between molecules on different cases.

Earlier the concepts of this paper were published as five separate papers, here we present the whole work as a single paper so that referencing will be easy.

Keywords: nanobiotechnology, multi molecule theory, dynamic universe model, subbarao simulations, reynolds number, singularity-free cosmology, blue shifted galaxies, red shifted galaxies, grazing radiation frequency changes, formation of elements, nucleosynthesis.

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I. INTRODUCTION

Nanobiotechnology is a new budding branch of science. Here in this paper we try to attempt the explanation of Brownian Motion using the concepts of Dynamic Universe Model. We will try to modify SITA simulation software for using in this platform and call it as Subbarao Simulations. In section **4.1** the formation of excel-sheet was shown. And we will discuss salient formation points for of final Results. We did not assume any boundaries for molecules or nanoparticle movements.

We did 1500 iterations for two different types data files in these simulations as we discussed with same the staring data. In the second type earth gravity was also considered along with the gravity between individual molecules and we did 7000 iterations. In a third test we transferred all the data into another old Laptop and conducted 2015 iterations just to confirm the data and results with earth gravity.

For each simulation test of 500 iterations, the calculation time taken is approx. 4 to 5 hours.

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In the three cases Viscosity of the (muddy) water plus all the additives is increased from 1 to 4 times higher. that means intermolecular distances were reduced to 25% of original distances. Other two types are considered further at present.

We took a microsecond time step between iterations. Though this is 1000 times high observed movements of molecules (which are of about 10 nano seconds), we considered this to reduce the number of iterations to view faster results.

When we considered earth gravitation, we got better displacements.

Section 5.2.1. gives details about various Excel file attachments with this paper. Further details can be obtained the author.

1.1 Introduction: Brownian motion

Brownian motion is well known. This can be seen in Liquids, gases easily and can be seen in solids with high end electron microscopes. For example, lets observe a single colloid with an optical microscope. Observe a 2 μm latex particle, which will undergo a constant motion in water within seconds of placing it in water in all the three dimensions. This random motion is called Brownian Motion. The sizes of the particles have a key role to play, the same type of motion is observed for colloids of 1 nm in diameter as well. This length corresponds to the size of single molecules, biomolecules such as DNA, RNA, proteins. They should therefore experience this type of motions. See very good explanations in the paper 'Life at low Reynolds number' by Purcell [1]. Here in this paper we will try to develop some equations for molecular forces, Brownian motions, coefficient of diffusion etc., using this Multi Molecule Theory instead of the age old 'single Molecule theory'.

II. HISTORY

In 1959, Alder and Wainwright[4] used an IBM 704 computer to simulate perfectly elastic collisions between hard spheres. They said " this many-body problem" was solved numerically using simultaneous equations of motion. Numerical methods give raise to errors always. This method solves many problems in both equilibrium and nonequilibrium statistical mechanics [5]. Probably the first simulation of matter, Gibson et al. simulated radiation damage of solid copper by using a Born–Mayer type of repulsive interaction along with a cohesive surface force. In his paper " Correlations in the Motion of Atoms in Liquid Argon" in 1964, Rehman A., said "The pair-correlation function and the constant of self-diffusion are found to agree well with experiment; the latter is 15% lower than the experimental value. The spectrum of the velocity autocorrelation function shows a broad maximum in the frequency region $\omega=0.25(k_BT/\hbar)$". He used a system of 864 particles interacting with a Lennard-Jones potential and obeying classical equations of motion [6]. These are some of the N-body problem type solutions about 60 years back.

III. MATHEMATICAL BACKGROUND FOR MULTI MOLECULE THEORY OF NANOBIOTECHNOLOGY

Let us assume an inhomogeneous set of N Molecules as a Colloid. This colloid is mix of water molecules, Individual proteins, polymers of living matter such as DNA, RNA, actin or microtubules, molecular motors etc. Water is universal solvent, universally available, so we take water + colloid particles for this theory. These don't react with each other chemically. All these molecules behave like bouncing rubber balls, sizes are different All these set will have different masses in accordance with their type. This colloid will lead to have Brownian motions of the NanoBio-Particles due to mutual gravitation attraction forces between individual particles. We will consider the gravitation influence of

Earth, Sun, Moon etc., also on this colloid. Lets take total number of molecules to be 133, to use modified SITA calculations. We call these calculations as SUBBARAO Simulations or Multi Molecule Theory (Later we will call as 'SSMMT'). For a broader perspective, let us call this set of all the systems of point masses as an Ensemble. Let us further assume that there are many Ensembles each consisting of a different number of systems with different number of point masses. Similarly, let us further call a group of Ensembles as Aggregate. Let us further define a Conglomeration as a set of Aggregates and let a further higher system have a number of conglomerations and so on and so forth.

We will start with133 particles / molecules in a Micro-cubical cubical in a glass beaker. We will assume a Micro-Cubicle in this beaker with invisible elastic walls. We will use 3D Cartesian coordinates with some appropriate center of its axes in this beaker.

- All the boundaries are perfectly elastic. Any Nanobio-Particle which hits the boundary will return according to Newtons laws. We will take nano distances and pico-second times as appropriate. To this case. We assume all the molecules to be perfect elastic spheres. There will be bumping and collisions between particles, and each pair will move and trace their path back after the elastic collision between the two. We can detect collisions by SSMMT software by two bumping particles when the center to center distance is less than or equal to the sum of two molecular radii of these Bio-spheres.

So it is obvious that the distance between the two molecules will increase and their velocities reverses after each pair's collision.

In this paper we will not consider gravitational repulsion at very low distances, only the bumping will happen at that distance, later we will introduce this concept in a next paper….

Similarly, we will introduce the Viscosity forces in another forthcoming paper.

Initially, let us assume a set of N mutually gravitating point masses in a system under Newtonian Gravitation. All these Nanobio-particles will have some finite radii r_i which we will use for the calculation of bumping or collision in the SSMMT software.

Let the α^{th} ^point mass has mass m_α, and is in position x_α. In addition to the mutual gravitational force, there exists an external φ_{ext}, due to other systems, ensembles, aggregates, and conglomerations etc., which also influence the total force F_α acting on the point mass α. In this case, the φ_{ext} is not a constant universal Gravitational field but it is the total vectorial sum of fields at x_α due to all the external to its system bodies and with that configuration at that moment of time, external to its system of N point masses.

Total Mass of system = $$M = \sum_{\alpha=1}^{N} m_\alpha \quad (1)$$

Total force on the point massα is Fα, Let $F_{\alpha\beta}$ is the gravitational force on the α^{th}point mass due to β^{th}point mass.

$$F_\alpha = \sum_{\substack{\alpha=1 \\ \alpha\neq\beta}}^{N} F_{\alpha\beta} - m_\alpha \nabla_\alpha \Phi_{ext}(\alpha) \quad (2)$$

Moment of inertia tensor (We will assume moment inertia is the dominating , but for theoretical calculations for this paper we will ignore Viscus forces)

Consider a system of N point masses with mass m_α, at positions X_α, α=1, 2,…N; The moment of inertia tensor is in external back ground field φ_{ext}.

$$I_{jk} = \sum_{\alpha=1}^{N} m_\alpha x_j^\alpha x_k^\alpha \tag{3}$$

Its second derivative is

$$\frac{d^2 I_{jk}}{dt^2} = \sum_{\alpha=1}^{N} m_\alpha \left(\overset{\circ\circ}{x}_j^\alpha \, x_k^\alpha + \overset{\circ}{x}_j^\alpha \, \overset{\circ}{x}_k^\alpha + x_j^\alpha \, \overset{\circ\circ}{x}_k^\alpha \right) \tag{4}$$

The total force acting on the point massα is and $\hat{F}$ is the unit vector of force at that place of that component.

$$F_j^\alpha = m_\alpha \overset{\circ\circ}{x}_j^\alpha = \sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N} \frac{G m_\alpha m_\beta \left(x_j^\beta - x_j^\alpha\right)\hat{F}}{\left|x^\beta - x^\alpha\right|^3} - \nabla\Phi_{ext,j} m_\alpha \tag{5}$$

Writing a similar formula for F^α_k

$$F_k^\alpha = m_\alpha \overset{\circ\circ}{x}_k^\alpha = \sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N} \frac{G m_\alpha m_\beta \left(x_k^\beta - x_k^\alpha\right)\hat{F}}{\left|x^\beta - x^\alpha\right|^3} - \nabla\Phi_{ext,k} m_\alpha \tag{6}$$

$$\overset{\circ\circ}{x}_j^\alpha = \sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N} \frac{G m_\beta \left(x_j^\beta - x_j^\alpha\right)\hat{F}}{\left|x^\beta - x^\alpha\right|^3} - \nabla\Phi_{ext} \tag{7}$$

OR =>

$$\overset{\circ\circ}{x}_k^\alpha = \sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N} \frac{G m_\beta \left(x_k^\beta - x_k^\alpha\right)}{\left|x^\beta - x^\alpha\right|^3} - \nabla\Phi_{ext} \tag{8}$$

And =>

Lets define Energy tensor (in the external field φ_{ext})

$$\frac{d^2 I_{jk}}{dt^2} = 2\sum_{\alpha=1}^{N} m_\alpha \left(\overset{\circ}{x}_j^\alpha \, \overset{\circ}{x}_k^\alpha \right) + \sum_{\substack{\alpha=1 \\ \alpha\neq\beta}}^{N} \sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N} \frac{G m_\alpha m_\beta \left\{ \left(x_k^\beta - x_k^\alpha\right)x_j^\alpha + \left(x_j^\beta - x_j^\alpha\right)x_k^\alpha \right\}}{\left|x^\beta - x^\alpha\right|^3}$$

$$- \sum_{\alpha=1}^{N} \nabla\Phi_{ext} m_\alpha x_j^\alpha - \sum_{\alpha=1}^{N} \nabla\Phi_{ext} m_\alpha x_k^\alpha \tag{9}$$

Lets denote Potential energy tensor = Wjk =

$$\sum_{\substack{\alpha=1\\ \alpha\neq\beta}}^{N}\ \sum_{\substack{\beta=1\\ \alpha\neq\beta}}^{N}\frac{Gm_\alpha m_\beta\left\{\left(x_k^\beta-x_k^\alpha\right)x_j^\alpha+\left(x_j^\beta-x_j^\alpha\right)x_k^\alpha\right\}}{\left|x^\beta-x^\alpha\right|^3} \tag{10}$$

$$\text{Lets denote Kinetic energy tensor} = 2\,K_{jk} = 2\sum_{\alpha=1}^{N} m_\alpha\left(\ \overset{\circ}{x}_j^\alpha\ \overset{\circ}{x}_k^\alpha\ \right) \tag{11}$$

Lets denote External potential energy tensor = $2\,\Phi_{jk}$

$$= \sum_{\alpha=1}^{N}\nabla\Phi_{ext}m_\alpha x_j^\alpha+\sum_{\alpha=1}^{N}\nabla\Phi_{ext}m_\alpha x_k^\alpha \tag{12}$$

$$\text{Hence}\quad \frac{d^2I_{jk}}{dt^2} = W_{jk}+2K_{jk}-2\Phi_{jk} \tag{13}$$

Here in this case

$$F(\alpha)=\sum_{\substack{\beta=1\\ \alpha\neq\beta}}^{N}F_{\alpha\beta}-\nabla_\alpha\Phi_{ext}(\alpha)m_\alpha$$
$$=\sum_{\substack{\beta=1\\ \alpha\neq\beta}}^{N}\frac{Gm_\alpha m_\beta\left(x^\beta-x^\alpha\right)}{\left|x^\beta-x^\alpha\right|^3}-\nabla\Phi_{ext}m_\alpha \tag{14}$$

$$= \left\{\overset{\circ\circ}{x}{}^{\alpha}(\text{int})-\nabla_\alpha\Phi_{ext}(\alpha)\right\}m_\alpha \tag{15}$$

$$\overset{\circ\circ}{x}(\alpha)=\sum_{\substack{\beta=1\\ \alpha\neq\beta}}^{N}\frac{Gm_\beta\left(x^\beta-x^\alpha\right)}{\left|x^\beta-x^\alpha\right|^3}-\nabla\Phi_{ext} \tag{16}$$

We know that the total force at $x(\alpha)=F_{tot}(\alpha)=-\nabla_\alpha\Phi_{tot}(\alpha)m_\alpha$

Total PE at $\alpha=m_\alpha\Phi_{tot}(\alpha)=-\int F_{tot}(\alpha)dx$

$$=-\int\left\{\sum_{\substack{\beta=1\\ \alpha\neq\beta}}^{N}\overset{\circ\circ}{x}{}^{\alpha}_{\text{int}}m_\alpha-\nabla_\alpha\Phi_{ext}(\alpha)m_\alpha-\right\}dx$$

$$= \int \sum_{\substack{\beta=1 \\ \alpha \neq \beta}}^{N} \frac{Gm_\beta m_\alpha \left(x^\beta - x^\alpha\right)}{\left|x^\beta - x^\alpha\right|^3} dx - \int \nabla \Phi_{ext} m_\alpha dx \tag{17}$$

Therefore total Gravitational potential $\varphi_{tot}(\alpha)$ at x (α) per unit mass

$$\Phi_{tot}(\alpha) = \Phi_{ext} - \sum_{\substack{\beta=1 \\ \alpha \neq \beta}}^{N} \frac{Gm_\beta}{\left|x^\beta - x^\alpha\right|} \tag{18-s}$$

Lets discuss the properties of φ_{ext} *:-*

φ_{ext} can be subdivided into 3 parts mainly
φ_{ext} due to higher level system, φ_{ext} -due to lower level system, φ_{ext} due to present level. [Level : when we are considering point masses in the same system (Galaxy), they are at the same level, a higher level for a cluster of galaxies, and a lower level is for planets & asteroids].

φ_{ext} is due to lower levels : If the lower level is existing, at the lower level of the system under consideration, then its own level was considered by system equations. If this lower level exists anywhere outside of the system, the center of (mass) gravity outside systems (Galaxies) will act as (unit) its own internal lower level, practically will be considered into calculations. Hence separate consideration of any lower level is not necessary.

System – Ensemble:

Until now we have considered the system level equations and the meaning of $\varphi_{ext.}$ Now let's consider an ENSEMBLE of system consisting of N_1, N_2 ... Njpoint masses in each. These systems are moving in the ensemble due to mutual gravitation between them. For example, each system is a Galaxy, and then ensemble represents a local group. Suppose number of Galaxies is j, Galaxies are systems with point masses N1, N2 ....NJ, we will consider φ_{ext} as discussed above. That is we will consider the effect of only higher level system like external Galaxies as a whole, or external local groups as a whole.
Ensemble Equations (Ensemble consists of many systems)

$$\frac{d^2 I^\gamma{}_{jk}}{dt^2} = W^\gamma_{jk} + 2K^\gamma_{jk} - 2\Phi^\gamma_{jk} \tag{18-E}$$

Here $^\gamma$ denotes Ensemble.

This $\Phi^\gamma jk$ is the external field produced at system level. And for system

$$\frac{d^2 I_{jk}}{dt^2} = W_{jk} + 2K_{jk} - 2\Phi_{jk} \tag{13}$$

Assume ensemble in a isolated place. Gravitational potential $\varphi_{ext}(\alpha)$produced at system level is produced by Ensemble and $\varphi^\gamma{}_{ext}(\alpha) = 0$ as ensemble is in a isolated place.

$$\Phi^{\gamma}_{tot}(\alpha) = \Phi^{\gamma}_{ext} - \sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N^{\gamma}} \frac{Gm^{\gamma}_{\beta}}{\left| x^{\gamma\beta} - x^{\gamma\alpha} \right|} \tag{19}$$

As Ensemble situated in an isolated place, Gravitational potential $\varphi^{\gamma}_{ext}(\alpha) = 0$
Therefore

$$\Phi^{\gamma}_{tot} = \Phi_{ext}(\alpha) = -\sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N^{\gamma}} \frac{Gm^{\gamma}_{\beta}}{\left| x^{\gamma\beta} - x^{\gamma\alpha} \right|} \tag{20}$$

And $$2\Phi_{jk} = -\frac{d^2 I_{jk}}{dt^2} + W_{jk} + 2K_{jk} \tag{13}$$

$$= \sum_{\alpha=1}^{N} \nabla\Phi_{ext} m_{\alpha} x^{\alpha}_{j} + \sum_{\alpha=1}^{N} \nabla\Phi_{ext} m_{\alpha} x^{\alpha}_{k} \tag{21}$$

AGGREGATE Equations(Aggregate consists of many Ensembles)

$$\frac{d^2 I^{\delta\gamma}_{jk}}{dt^2} = W^{\delta\gamma}_{jk} + 2K^{\delta\gamma}_{jk} - 2\Phi^{\delta\gamma}_{jk} \tag{18-A}$$

Here $^{\delta}$ denotes Aggregate.

This $\Phi^{\delta\gamma}jk$ is the external field produced at Ensemble level. And for Ensemble

$$\frac{d^2 I^{\gamma}{}_{jk}}{dt^2} = W^{\gamma}_{jk} + 2K^{\gamma}_{jk} - 2\Phi^{\gamma}_{jk} \tag{18-E}$$

Assume Aggregate in an isolated place. Gravitational potential $\varphi_{ext}(\alpha)$ produced at Ensemble level is produced by Aggregate and $\varphi^{\delta\gamma}_{ext}(\alpha) = 0$ as Aggregate is in a isolated place.

$$\Phi^{\delta\gamma}_{tot}(\alpha) = \Phi^{\delta\gamma}_{ext} - \sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N^{\delta\gamma}} \frac{Gm^{\delta\gamma}_{\beta}}{\left| x^{\delta\gamma\beta} - x^{\delta\gamma\alpha} \right|} \tag{22}$$

$$\Phi^{\delta\gamma}_{tot}(Aggregate) = \Phi^{\gamma}_{ext}(\alpha)(Ensemble) = -\sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N^{\delta\gamma}} \frac{Gm^{\delta\gamma}_{\beta}}{\left| x^{\delta\gamma\beta} - x^{\delta\gamma\alpha} \right|} \tag{23}$$

Therefore

And
$$\Phi^{\gamma}_{jk} = \sum_{\alpha=1}^{N^{\gamma}} \nabla\Phi^{\delta}_{ext}\, m_{\alpha} x_{j}^{\delta\alpha} + \sum_{\alpha=1}^{N} \nabla\Phi^{\delta}_{ext}\, m_{\alpha} x_{k}^{\delta\alpha} \tag{24}$$

Total AGGREGATE Equations :(Aggregate consists of many Ensembles and systems)

Assuming these forces are conservative, we can find the resultant force by adding separate forces vectorially from equations (20) and (23).

$$\Phi_{ext}(\alpha) = -\sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N^{\gamma}} \frac{Gm_{\beta}^{\gamma}}{\left|x^{\gamma\beta} - x^{\gamma\alpha}\right|} - \sum_{\substack{\beta=1 \\ \alpha\neq\beta}}^{N^{\delta\gamma}} \frac{Gm_{\beta}^{\delta\gamma}}{\left|x^{\delta\gamma\beta} - x^{\delta\gamma\alpha}\right|} \tag{25}$$

This concept can be extended to still higher levels in a similar way.

Corollary 1:

$$\frac{d^2 I_{jk}}{dt^2} = W_{jk} + 2K_{jk} - 2\Phi_{jk} \tag{13}$$

The above equation becomes a scalar Virial theorem in the absence of an external field, that is φ=0 and is in a "steady state,"

$$\text{i.e.} \quad \frac{d^2 I_{jk}}{dt^2} = 0 \tag{27}$$

$$2K + W = 0 \tag{28}$$

But when the N-bodies are moving under the influence of mutual gravitation without external field then only the above equation (28) is applicable.

Corollary 2:
Ensemble achieved a steady state,

$$\text{i.e.} \quad \frac{d^2 I^{\gamma}_{jk}}{dt^2} = 0 \tag{29}$$

$$W^{\gamma}_{jk} + 2K^{\gamma}_{jk} = 2\Phi^{\gamma}_{jk} \tag{30}$$

This Φjk external field produced at system level. Ensemble achieved a steady state; means system also reached steady state.

$$\text{i.e.} \quad \frac{d^2 I_{jk}}{dt^2} = 0 \tag{27}$$

$$W_{jk} + 2K_{jk} = 2\Phi^{\gamma}_{jk} \tag{31}$$

Equation (20) gives $\varphi^{\gamma}_{tot}(\alpha)$, that is external potential field present at the system level . Combining Eqn (31) and eqn (9).

$$2\Phi_{ext}jk = \sum_{\alpha=1}^{N} \nabla\Phi_{ext} m_{\alpha} x_j^{\alpha} + \sum_{\alpha=1}^{N} \nabla\Phi_{ext} m_{\alpha} x_k^{\alpha} \tag{31-A}$$

The Equation 25 is the main powerful equation, which gives many results that are not possible otherwise today. This tensor can be subdivided into 21000 small equations without any differential equations or integral equations. Hence, this set up gives a unique solution of Cartesian X, Y, Z components of coordinates, velocities and accelerations of each point mass in the setup for that particular instant of time. instant of time. A point to be noted here is that the Dynamic Universe Model never reduces to General relativity on any condition. It uses a different type of mathematics based on Newtonian physics. This mathematics used here is relatively simple and straightforward. For all the mathematics, and the Excel based software, details are explained in the three books published by the author [14, 15, 16]

A point to be noted here is that the Dynamic Universe Model never reduces to General relativity on any condition. It uses a different type of mathematics based on Newtonian physics. This mathematics used here is simple and straightforward. As there are no differential equations present in Dynamic Universe Model, the set of equations give single solution in x y z Cartesian coordinates for every point mass for every time step. All the mathematics and the Excel based software details are explained in the three books published by the author[14, 15, 16] In the first book, the solution to N-body problem-called Dynamic Universe Model (SITA) is presented; which is singularity-free, inter-body collision free and dynamically stable. The Basic Theory of Dynamic Universe Model published in 2010 [14]. The second book in the series describes the SITA software in EXCEL emphasizing the singularity free portions. This book written in 2011 [15] explains more than 21,000 different equations. The third book describes the SITA software in EXCEL in the accompanying CD / DVD emphasizing mainly HANDS ON usage of a simplified version in an easy way. The third book is a simplified version and contains explanation for 3000 equations instead of earlier 21000 and this book also was written in 2011[16]. Some of the other papers published by the author are available at refs. [3, 5, 8, 9, 10, 11, 17, 19].

SITA solution can be used in many places like presently unsolved applications like Pioneer anomaly at the Solar system level, Missing mass due to Star circular velocities and Galaxy disk formation at Galaxy level etc. Here we are using it for prediction of blue shifted Galaxies.

To Simulate **...**

Lets Assume a muddy mix of 100 water molecules, 7 Individual proteins, 7 polymers of living matter such as DNA, RNA, 7 actin or microtubules, 7 molecular motors . 5 Latex Particles , Calculate Gravitation force between molecules = F= (G . M1 . M2) / (R .R)

In the example above the standard atomic weight of carbon is 12.011 g/mol, not 12.00 g/mol. This is because naturally occurring carbon is a mixture of the isotopes **^{12}C, ^{13}C and ^{14}C** which have masses of 12 Da, 13.003355 Da, and 14.003242 Da respectively. Moreover, the proportion of the isotopes varies between samples, so 12.011 g/mol is an average value across different places on earth. By contrast, there is less variation in naturally occurring hydrogen so the standard atomic weight has less variance.

The precision of the molar mass is limited by the highest variance standard atomic weight, in this example that of carbon.

Simulate Masses of Molecules

To simulate masses of various molecules we collected data from various papers published. We gave appropriate reference for all these data collection These data are shown below in various tables.

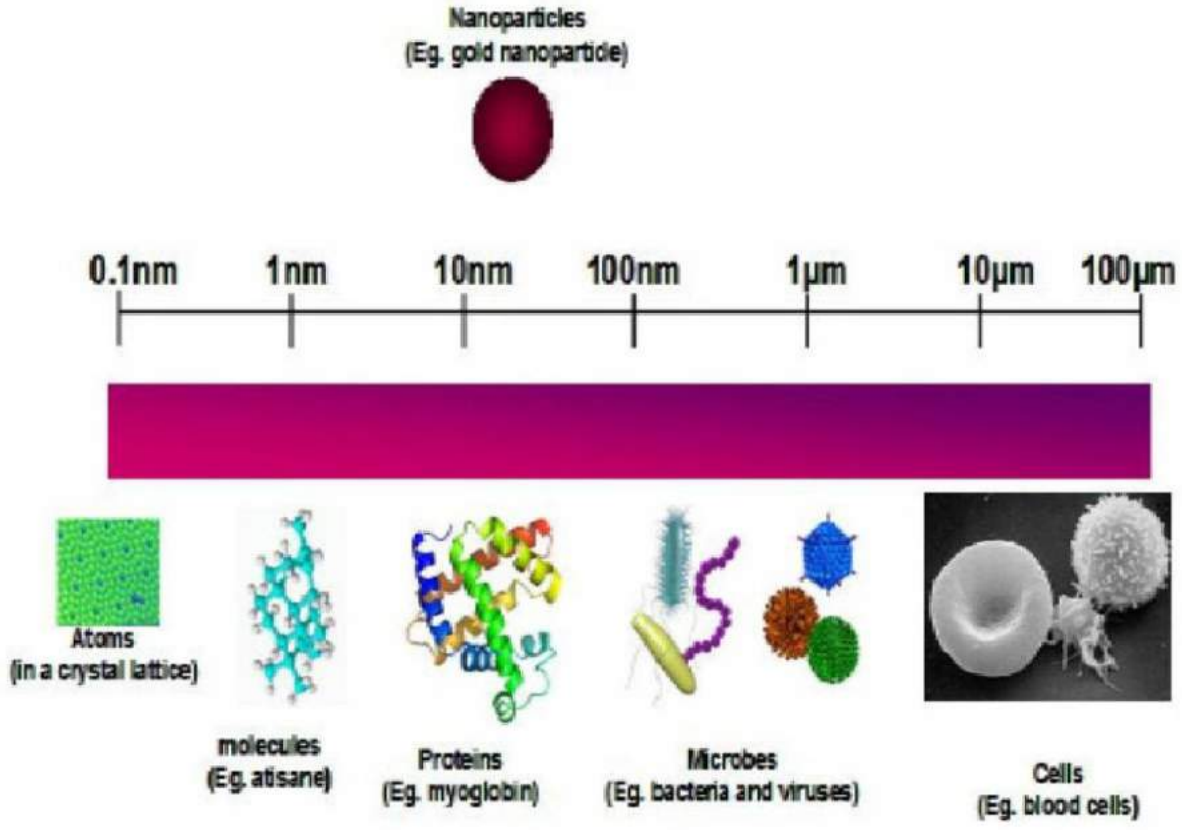

Fig.1: This pic from wikipedia give a visula glimpse of various sizes of mloecules.

For Latex : rubber biosynthesis -from T. koksaghyz latex. Photon correlation spectroscopy and transmission electron microscopy revealed an average particle size of 320 nm, and 13C nuclear magnetic resonance (NMR) spectroscopy confirmed that isolated rubber particles contain poly(cis-1,4-isoprene) with a purity >95%. Size exclusion chromatography indicated that the weight average molecular mass (M w)..... See ref [7] and [8]

Natural Rubber Latex(1):				
Latex particles	Mass (Min)=	M = See above ref	4000	kDa
Latex particles	Size =	R =	3.200000000E-07	Meters (320 Nanometers)
Latex particles	Distance =	D =	3.200000000E-07	Meters (320 Nanometers)
Latex particles	Number In this Simulation =		5	
Natural Rubber Latex (2):				
Latex particles	Mass =	M = See above ref	5000	kDa
Latex particles	Size =	R =	2.000000000E-06	Meters (2 Micrometers)
Latex particles	Distance =	D =	2.000000000E-06	Meters (2 Micrometers)

Latex particles	Number In this Simulation =		5	
Natural Rubber Latex(3):				
Latex particles	Mass (Min)=	M = See above ref	4000	kDa
Latex particles	Size =	R =	2.000000000E-06	Meters (2 Micrometers)
Latex particles	Distance =	D =	2.000000000E-06	Meters (2 Micrometers)
Latex particles	Number In this Simulation =		5	
Natural Rubber Latex (4):				
Latex particles	Mass =	M = See above ref	5000	kDa
Latex particles	Size =	R =	3.200000000E-07	Meters (320 Nanometers)
Latex particles	Distance =	D =	3.200000000E-07	Meters (320 Nanometers)
Latex particles	Number In this Simulation =		5	
Polimemars(1 kb DNA)particle See ref [9]				
Polimemars(1 kb DNA)particle	Mass =	M =	37	37 kDa protein
Polimemars(1 kb DNA)particle	Size =	R =	9.00E-08	Meters (90 Nanometer approx)
Polimemars(1 kb DNA)particle	Distance =	D =	9.00E-08	Meters (90 Nanometer approx)
Polimemars(1 kbDNA)particle	Number In this Simulation =		7	

Length/M.W. of Common Nucleic Acids.(Nucleic Acid = lambda DNA; Number of Nucleotides= 48,502(dsDNA);) See ref [10] and Note 1					
Length/M.W. of Common Nucleic Acids.(Nucleic Acid = lambda DNA; Number of Nucleotides= 48,502(dsDNA);)	Mass =	M =	3.20E+07	Da	
Length/M.W. of Common Nucleic Acids.(Nucleic Acid = lambda DNA; Number of Nucleotides= 48,502(dsDNA);)	Size =	R =	200	nanometers	AFM images
Length/M.W. of Common Nucleic Acids.(Nucleic Acid = lambda DNA; Number of Nucleotides= 48,502(dsDNA);)	Distance =	D =	200	nanometers	of poly(A) show both short bent lumpy molecules with
Length/M.W. of Common Nucleic Acids.(Nucleic Acid = lambda DNA; Number of Nucleotides= 48,502(dsDNA);)	Number In this Simulation =		7		an apparent persistence length of 40 nm and long
					straight molecules with an apparent persistence

					length of 600 nm.
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide [Ref 11 & 9]			200	kDa	
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	Mass =	M (Min)=	40	nanometers	PAM particles with average particle sizes
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	Size =	R =	40	nanometers	generally smaller than 200 nm in diameter and particle size distribution in the range of
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	Distance =	D =	7		50-400 nm and viscosity-average molecular weights as high as 8×106 g.mol-1 were
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	Number In this Simulation =				obtained.
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide[9 & 11]					
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	Mass =	M (Max)=	200	kDa	
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	Size =	R =	200	nanometers	PAM particles with average particle sizes
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	Distance =	D =	200	nanometers	generally smaller than 200 nm in diameter and particle size distribution
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	Number In this Simulation =		7		50-400 nm and viscosity-average molecular weights as high as 8×106 g.mol-1 were obtained
Water Molecules Ref wiki					
Water Molecules	Mass =	M =	18.0153	daltons	
Water Molecules	Size =	R =	3.00E-10	Meters (3 angstrom)	
Water Molecules	Distance =	D =	3.00E-10	Meters (3 angstrom)	
Water Molecules	Number In this Simulation =		100		
Total					

Note 1. of poly(A) show both short bent lumpy molecules with an apparent persistence length of 40 nm and long straight molecules with an apparent persistence length of 600 nm.

Table 1: Various data collected for doing Simulation

Molecular Forces,Diffusion coefficients				
		Latex Particle Size =	2.000000000E-06	Meters (2 Micrometers)
		Colloid (DNA, RNA)particle size=	1.000000000E-09	Meters (1 Nanometers)
		Both the above types experience sme motion		
in Eqn.(1) $F \propto k_B T / a$	In ' F propo kBT/ a' , a=	colloid of a typical length 'a'=	4.000000000E-09	Meters (4 Nanometers)

in Eqn.(1)	In ' F propo kBT/ a' , kB=	k_B is the Boltzmann constant =	4.000000000E-21	J
		T the temperature = Room Temp		
in Eqn.(1)	In ' F propo kBT/ a', F expected=	Force	1.000000000E-12	Newtons (1 picoNewtons)
in Eqn.(2) $D = k_BT / 6\pi\eta a$	*in' D* = k_BT / 6πηa' D=	coefficient of diffusion D	4.000000000E-09	Meters (4 Nanometers)
in Eqn.(2)	*in' D* = k_BT / 6πηa', η =	η is the viscosity of the solvent.	1.000000000E-03	Pa.s (Pascal .Seconds) for water
		Re = Reynolds number = *inertial forces / viscous forces*		
in Eqn.(3) Re = *inertial forces / viscous forces* = ρav / η	*in' Re*= = ρav / η' , ρ=	Density of water =	1.000000000E+03	Kg / Meter Cube (1000)
in Eqn.(3)	*in' Re*= = ρav / η' , a=	colloid of a typical length 'a'=	4.000000000E-09	Meters (4 Nanometers)
in Eqn.(3)	*in' Re*= = ρav / η' ,	η = is the viscosity of the solvent.	1.000000000E-03	Pa.s (Pascal .Seconds) for water
in Eqn.(4) $v = F / 6\pi\eta a$ with F≈1 pN.	*in' v* = F / 6πηa' v=	v the speed associated to typical forces	4.000000000E-09	Meters (4 Nanometers)
in Eqn.(4)	*With ' F approx* ='	with F≈1 pN.	1.000000000E-12	Newtons (1 picoNewtons)
in Eqn.(5) Re ~ 10^{-4} << 1	Re ~ 10^{-4} << 1	Re ~ 10^{-4} << 1	1.000000000E-04	Dimension less number

This motion will be anywhere in the cell though, in contrast to molecular motors that will transport proteins/lipids to specific locations within the cell in a targeted manner.

When a ball is being kicked in a soccer game, the ball continues its trajectory when it has left the foot. In the same manner, the colloid would undergo a sustained motion because of the shocks provided by the molecules of the solvent.

D as the ratio of the energy associated with Brownian motion over the friction with the solvent. We get 5 μm2/ms for the estimate, again consistent with measurements performed with various techniques.

As a way to determine whether this inertia is also at play at the scale of the colloid, a simple dimensionless parameter can be calculated, the Reynolds number Re. It is written as:

It is interesting to note that the typical distance performed by a free protein will be of the order of about 10 milliseconds, that is

$$(Dt)^{0.5} = 10\ \mu\ M$$

So the viscous forces are much larger than the forces associated with inertia (see Eq. 3). In effect, the colloids are moving but after the shocks from the molecules of the solvent, they are very shortly stopped; the motion proceeds in a given direction or in another, because other shocks from other molecules arise.

The consequences of this framework at the scale of single molecules are important: instead of having acceleration compensated by forces, velocities are equilibrated by forces. In other words, a force has always to be applied on single objects to trigger its motion.

Vak 24 June 20 Bhilai :

Nanobiotechnology Simulations : In Nano Scales

Take arbitrary coordinates (0,0,0) in glass os water
Viscocity factor= μ= 1
Convert Dalton to Kilogram 1.66E-27

4.1 Excel simulations Initial data

Here we are using the Excel for all the numerical calculations as it is simple and any person who had just fundamental knowledge of using a PC can understand these excel worksheets. So, anyone who has little further interest can very easily verify the calculations of this SSMMT. We have already seen in the earlier paper 2 '"Multi Molecule Theory" by Dynamic Universe Model with Gravitation as Force Field between molecules: Excel Implementation for Nanobiotechnology.'

We started with this initial data as shown in Table 1

	Sl.no	Da Daltons	Mass:KG	xsimu: Mtr	Ysimu: Mtr	Zsimu: Mtr	Mtrs
λ DNA Nucleic Acid= Number of Nucleotides= 48,502(dsDNA)	1	3.20E+07	5.31E-20	1.28E-06	1.31E-06	4.94E-08	2.00E-07
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	2	200000	3.32E-22	9.54E-07	1.35E-06	1.55E-06	2.00E-07
Water Molecules	3	18.0153	2.99E-26	1.97E-09	9.34E-09	2.61E-09	3.00E-10
Water Molecules	4	18.0153	2.99E-26	2.3E-09	1.88E-09	1.28E-09	3E-10
1Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	5	200000	3.32E-22	7E-09	2.98E-08	2.09E-07	4E-08
1Natural Rubber Latex(1):	6	4000000	6.64E-21	1.56E-06	1.33E-06	1.37E-07	3.2E-07
2Natural Rubber Latex(1):	7	5000000	8.3E-21	1.12E-09	2.43E-09	1.26E-08	2E-09
3Natural Rubber Latex(1):	8	4000000	6.64E-21	9.11E-09	1.51E-08	1.61E-08	2E-09
4Natural Rubber Latex(1):	9	5000000	8.3E-21	7.75E-07	2.54E-06	1.24E-06	3.2E-07
1 kb DNA-Polimemars particle	10	37000	6.14E-23	7.67E-07	8.24E-07	7.26E-07	9E-08
Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	11	200000	3.32E-22	8.76E-07	9.62E-08	1.08E-06	2E-07
1Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide	12	200000	3.32E-22	3.26E-07	3.53E-08	1.69E-07	4E-08

1Natural Rubber Latex(1):	13	4000000	6.64E-21	2.13E-06	8.43E-07	3.2E-06	3.2E-07
2Natural Rubber Latex(1):	14	5000000	8.3E-21	1.84E-08	1.23E-08	3.14E-09	2E-09
3Natural Rubber Latex(1):	15	4000000	6.64E-21	1.32E-08	8.88E-09	1.06E-08	2E-09
4Natural Rubber Latex(1):	16	5000000	8.3E-21	1.98E-06	3.09E-06	3.04E-06	3.2E-07
1Natural Rubber Latex(1):	17	4000000	6.64E-21	1.22E-06	1.02E-06	3.01E-06	3.2E-07
2Natural Rubber Latex(1):	18	5000000	8.3E-21	1.06E-08	1.36E-08	1.7E-08	2E-09
3Natural Rubber Latex(1):	19	4000000	6.64E-21	1.8E-09	3.7E-09	2.97E-09	2E-09
4Natural Rubber Latex(1):	20	5000000	8.3E-21	2.22E-06	1.9E-06	7.05E-07	3.2E-07
1 kb DNA-Polimemars particle	21	37000	6.14E-23	6.58E-07	1.35E-07	1.82E-07	9E-08
1 kb DNA-Polimemars particle	22	37000	6.14E-23	6.12E-07	3.34E-07	2.34E-07	9E-08
Water Molecules	23	18.0153	2.99E-26	1.23E-09	2.56E-09	1.03E-09	3E-10
Water Molecules	24	18.0153	2.99E-26	1.85E-09	2.69E-09	2.93E-09	3E-10
Water Molecules	25	18.0153	2.99E-26	1.98E-09	1.13E-09	9.67E-09	3E-10
Water Molecules	26	18.0153	2.99E-26	2.45E-09	1.39E-09	1.99E-09	3E-10
Water Molecules	27	18.0153	2.99E-26	2.3E-09	2.29E-09	2.07E-09	3E-10
Water Molecules	28	18.0153	2.99E-26	7.40E-09	2.44E-09	7.29E-09	3E-10
Water Molecules	29	18.0153	2.99E-26	2.01E-09	2.75E-09	2.68E-09	3E-10
Water Molecules	30	18.0153	2.99E-26	2.96E-09	1.61E-09	3.77E-09	3E-10
Water Molecules	31	18.0153	2.99E-26	2.82E-09	1.4E-09	2.7E-09	3E-10
Water Molecules	32	18.0153	2.99E-26	1.12E-09	1.39E-09	3.77E-09	3E-10
Water Molecules	33	18.0153	2.99E-26	2.95E-09	1.86E-09	2.33E-09	3E-10
Water Molecules	34	18.0153	2.99E-26	2.59E-09	1.09E-09	6.33E-09	3E-10
Water Molecules	35	18.0153	2.99E-26	2.66E-09	2.08E-09	6.90E-09	3E-10
Water Molecules	36	18.0153	2.99E-26	1.46E-09	1.5E-09	1.44E-09	3E-10
Water Molecules	37	18.0153	2.99E-26	1.95E-09	1.79E-09	2.12E-09	3E-10
Water Molecules	38	18.0153	2.99E-26	6.68E-09	1.83E-09	1.24E-09	3E-10
Water Molecules	39	18.0153	2.99E-26	1.58E-09	1.37E-09	2.54E-09	3E-10
Water Molecules	40	18.0153	2.99E-26	2.88E-09	2.22E-09	1.29E-09	3E-10
Water Molecules	41	18.0153	2.99E-26	1.65E-09	9.87E-09	2.17E-09	3E-10
Water Molecules	42	18.0153	2.99E-26	2.24E-09	2.73E-09	2.85E-09	3E-10
Water Molecules	43	18.0153	2.99E-26	6.55E-09	2.7E-09	1.3E-09	3E-10
Water Molecules	44	18.0153	2.99E-26	2.26E-09	2.52E-09	8.34E-09	3E-10
Water Molecules	45	18.0153	2.99E-26	2.81E-09	1.62E-09	2.1E-09	3E-10
Water Molecules	46	18.0153	2.99E-26	3.34E-09	2.98E-09	2.66E-09	3E-10
Water Molecules	47	18.0153	2.99E-26	1.77E-09	4.92E-09	2.90E-09	3E-10
Water Molecules	48	18.0153	2.99E-26	1.7E-09	5.57E-09	1.36E-09	3E-10
Water Molecules	49	18.0153	2.99E-26	2.23E-09	9.10E-09	4.41E-09	3E-10
Water Molecules	50	18.0153	2.99E-26	2.59E-09	2.96E-09	2.07E-09	3E-10
Water Molecules	51	18.0153	2.99E-26	1.23E-09	1.98E-09	7.98E-09	3E-10
Water Molecules	52	18.0153	2.99E-26	5.17E-09	1.73E-09	2.31E-09	3E-10
Water Molecules	53	18.0153	2.99E-26	2.09E-09	4.10E-09	1.16E-09	3E-10
Water Molecules	54	18.0153	2.99E-26	1.22E-09	4.45E-09	2.77E-09	3E-10
Water Molecules	55	18.0153	2.99E-26	1.13E-09	1.46E-09	1.69E-09	3E-10
Water Molecules	56	18.0153	2.99E-26	2.98E-09	1.85E-09	3.31E-09	3E-10
Water Molecules	57	18.0153	2.99E-26	1.85E-09	3.99E-09	1.77E-09	3E-10
Water Molecules	58	18.0153	2.99E-26	2.15E-09	2.32E-09	1.52E-09	3E-10
Water Molecules	59	18.0153	2.99E-26	2.00E-09	1.62E-09	2.74E-09	3E-10
Water Molecules	60	18.0153	2.99E-26	1.79E-09	6.95E-09	1.1E-09	3E-10
Water Molecules	61	18.0153	2.99E-26	2.01E-09	6.48E-09	2.16E-09	3E-10
Water Molecules	62	18.0153	2.99E-26	2.43E-09	1.35E-09	2.78E-09	3E-10
Water Molecules	63	18.0153	2.99E-26	1.94E-09	4.00E-09	7.68E-09	3E-10
Water Molecules	64	18.0153	2.99E-26	1.09E-09	7.40E-09	2.28E-09	3E-10

Water Molecules	65	18.0153	2.99E-26	2.42E-09	9.73E-09	1.86E-09	3E-10
Water Molecules	66	18.0153	2.99E-26	2.43E-09	1.03E-09	2.9E-09	3E-10
Water Molecules	67	18.0153	2.99E-26	2E-09	2.89E-09	4.26E-09	3E-10
Water Molecules	68	18.0153	2.99E-26	9.89E-09	1.86E-09	7.12E-09	3E-10
Water Molecules	69	18.0153	2.99E-26	4.13E-09	1.53E-09	6.52E-09	3E-10
Water Molecules	70	18.0153	2.99E-26	1.42E-09	5.92E-09	2.42E-09	3E-10
Water Molecules	71	18.0153	2.99E-26	5.46E-09	4.13E-09	2.58E-09	3E-10
Water Molecules	72	18.0153	2.99E-26	2.01E-09	2.74E-09	1.88E-09	3E-10
Water Molecules	73	18.0153	2.99E-26	1.67E-09	9.70E-09	2.97E-09	3E-10
Water Molecules	74	18.0153	2.99E-26	1.9E-09	2.01E-09	1.4E-09	3E-10
Water Molecules	75	18.0153	2.99E-26	1.6E-09	2.74E-09	1.53E-09	3E-10
Water Molecules	76	18.0153	2.99E-26	2.63E-09	1.77E-09	2.23E-09	3E-10
Water Molecules	77	18.0153	2.99E-26	2.88E-09	1.57E-09	2.71E-09	3E-10
Water Molecules	78	18.0153	2.99E-26	1.62E-09	1.64E-09	8.46E-09	3E-10
Water Molecules	79	18.0153	2.99E-26	1.96E-09	1.79E-09	1.94E-09	3E-10
Water Molecules	80	18.0153	2.99E-26	6.84E-09	1.51E-09	1.11E-09	3E-10
Water Molecules	81	18.0153	2.99E-26	2.94E-09	1.63E-09	5.11E-09	3E-10
Water Molecules	82	18.0153	2.99E-26	4.02E-09	1.31E-09	2.9E-09	3E-10
Water Molecules	83	18.0153	2.99E-26	2.94E-09	2.79E-09	1.32E-09	3E-10
Water Molecules	84	18.0153	2.99E-26	9.68E-09	5.36E-09	1.8E-09	3E-10
Water Molecules	85	18.0153	2.99E-26	2.62E-09	7.73E-09	9.19E-09	3E-10
Water Molecules	86	18.0153	2.99E-26	1.67E-09	2.84E-09	2.06E-09	3E-10
Water Molecules	87	18.0153	2.99E-26	2.08E-09	2.3E-09	1.6E-09	3E-10
Water Molecules	88	18.0153	2.99E-26	2.43E-09	2.86E-09	4.31E-09	3E-10
Water Molecules	89	18.0153	2.99E-26	1.67E-09	2.5E-09	1.24E-09	3E-10
Water Molecules	90	18.0153	2.99E-26	1.65E-09	1.09E-09	8.64E-09	3E-10
Water Molecules	91	18.0153	2.99E-26	2.66E-09	2.21E-09	2.87E-09	3E-10
Water Molecules	92	18.0153	2.99E-26	2.07E-09	2.15E-09	2.16E-09	3E-10
Water Molecules	93	18.0153	2.99E-26	2.3E-09	1.2E-09	2.27E-09	3E-10
Water Molecules	94	18.0153	2.99E-26	2.17E-09	6.46E-09	4.40E-09	3E-10
Water Molecules	95	18.0153	2.99E-26	9.06E-09	1.23E-09	7.45E-09	3E-10
Water Molecules	96	18.0153	2.99E-26	1.91E-09	2.92E-09	7.25E-09	3E-10
Water Molecules	97	18.0153	2.99E-26	1.38E-09	1.08E-09	3.63E-09	3E-10
Water Molecules	98	18.0153	2.99E-26	1.88E-09	1.23E-09	1.6E-09	3E-10
Water Molecules	99	18.0153	2.99E-26	7.51E-09	5.23E-09	1.72E-09	3E-10
Water Molecules	100	18.0153	2.99E-26	5.88E-09	8.30E-09	1.23E-09	3E-10
Water Molecules	101	18.0153	2.99E-26	2.89E-09	2.5E-09	1.17E-09	3E-10
Water Molecules	102	18.0153	2.99E-26	1.3E-09	1.41E-09	7.74E-09	3E-10
Water Molecules	103	18.0153	2.99E-26	2.25E-09	1.92E-09	9.70E-09	3E-10
Water Molecules	104	18.0153	2.99E-26	7.87E-09	1.27E-09	1.57E-09	3E-10
Water Molecules	105	18.0153	2.99E-26	2.17E-09	6.15E-09	2.21E-09	3E-10
Water Molecules	106	18.0153	2.99E-26	9.96E-09	3.27E-09	2.3E-09	3E-10
Water Molecules	107	18.0153	2.99E-26	8.05E-09	1.39E-09	2.88E-09	3E-10
Water Molecules	108	18.0153	2.99E-26	1.47E-09	5.09E-09	1.42E-09	3E-10
Water Molecules	109	18.0153	2.99E-26	1.13E-09	2.00E-09	5.53E-09	3E-10
Water Molecules	110	18.0153	2.99E-26	2.81E-09	2.09E-09	1.37E-09	3E-10
Water Molecules	111	18.0153	2.99E-26	2.23E-09	7.70E-09	1.37E-09	3E-10
Water Molecules	112	18.0153	2.99E-26	4.25E-09	1.58E-09	2.6E-09	3E-10
Water Molecules	113	18.0153	2.99E-26	6.97E-09	2.92E-09	6.89E-09	3E-10
Water Molecules	114	18.0153	2.99E-26	8.91E-09	1.3E-09	6.67E-09	3E-10
Water Molecules	115	18.0153	2.99E-26	2.6E-09	5.42E-09	1.33E-09	3E-10
Water Molecules	116	18.0153	2.99E-26	2.6E-09	5.14E-09	1.74E-09	3E-10

Water Molecules	117	18.0153	2.99E-26	1.75E-09	5.00E-09	1.59E-09	3E-10
Water Molecules	118	18.0153	2.99E-26	7.37E-09	2.03E-09	2.46E-09	3E-10
Water Molecules	119	18.0153	2.99E-26	8.20E-09	6.38E-09	2.71E-09	3E-10
Water Molecules	120	18.0153	2.99E-26	1.54E-09	3.98E-09	2.59E-09	3E-10
Water Molecules	121	18.0153	2.99E-26	2.82E-09	6.34E-09	5.45E-09	3E-10
Water Molecules	122	18.0153	2.99E-26	1.3E-09	2.05E-09	1.32E-09	3E-10
Water Molecules	123	18.0153	2.99E-26	2.87E-09	2.11E-09	2.73E-09	3E-10
Water Molecules	124	18.0153	2.99E-26	2.07E-09	1.05E-09	2.74E-09	3E-10
Water Molecules	125	18.0153	2.99E-26	1.04E-08	6.46E-09	7.82E-09	3E-10
Water Molecules	126	18.0153	2.99E-26	5.19E-09	2.79E-09	2.73E-09	3E-10
Water Molecules	127	18.0153	2.99E-26	5.20E-09	5.45E-09	2.98E-09	3E-10
Water Molecules	128	18.0153	2.99E-26	7.43E-09	4.79E-09	2.79E-09	3E-10
Water Molecules	129	18.0153	2.99E-26	1.2E-09	2.06E-09	2.24E-09	3E-10
Water Molecules	130	18.0153	2.99E-26	1E-09	7.61E-09	8.25E-09	3E-10
Water Molecules	131	18.0153	2.99E-26	1.54E-09	2.26E-09	1.16E-09	3E-10
Water Molecules	132	18.0153	2.99E-26	1.71E-09	2.57E-09	1.31E-09	3E-10
Water Molecules	133	18.0153	2.99E-26	1.80E-09	1.8E-09	1.28E-09	3E-10

Table 1: This Table gives the initial data that was compiled in in paper 2. All the calculations were done based on this data

4.1. Excel simulations Initial data

Here we are using the Excel for all the numerical calculations as it is simple and any person who had just fundamental knowledge of using a PC can understand these excel worksheets. So, anyone who has little further interest can very easily verify the calculations of this SSMMT. We have already seen in the earlier paper 3 '"Multi Molecule Theory" by Dynamic Universe Model with Gravitation as Force Field between molecules: Simulation Results Using Excel Implementation for Nanobiotechnology.'

We continued with same initial data as shown in Table 1 in that paper. All the calculations were done based on the same data.

4.2 Excel files enclosed

We are enclosing the following files for further reference to the reader.
4.2.1. vvtc 1500 itr Diff new-start vis 0.25 REF SSMMT BioNanoTech.xls
4.2.2. vvtc 7000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
4.2.3. vvtc1 itr2015 1microS TIME REF Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
4.2.4. Vvtc diff 5-7000 compile.xls

V. EXCEL SIMULATIONS RESULTS

We present the results here from the above files in simple words……

5.2.1. vvtc 1500 itr Diff new-start vis 0.25 REF SSMMT BioNanoTech.xls

The staring data as give in the attachment in 2nd paper. Earth gravity not considered. Viscosity is increased from 1 to 4 times higher. Intermolecular distances were reduced to 25% of original distances

5.2.2. vvtc 7000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls

Here earth gravity was also considered along with the gravity of individual molecules. Here in this simulation set the conditions are same as mentioned in the above section **5.2.1.**

5.2.3. vvtc1 itr2015 1microS TIME REF Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls

These simulations were conducted on a old laptop. Here also Viscosity is increased from 1 to 4 times higher. Intermolecular distances were reduced to 25% of original distances. Here earth gravity was also considered along with the gravity of individual molecules. Here in this simulation set the conditions are same as mentioned in the above section **5.2.1.**

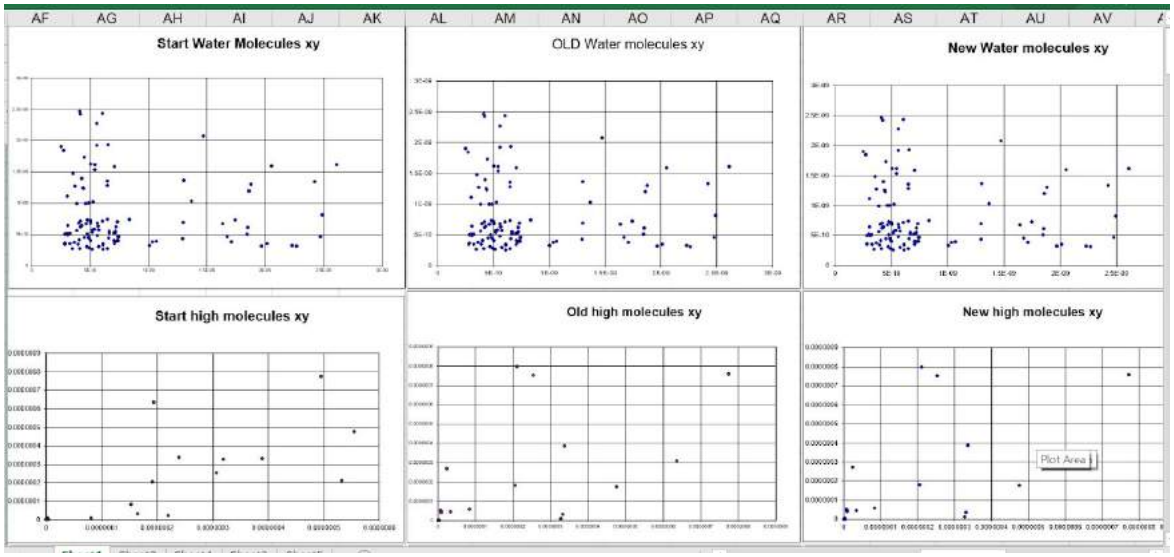

Fig.1: The compiled picture of data which shows the XY projections of coordinates. All the data is having XYZ coordinates. Here picture shows status after

5.4 Iterations With Out Earth Gravitation

This picture is taken from the file
vvtc visco 0.25 REF SSMMT START BioNanoTech.xls

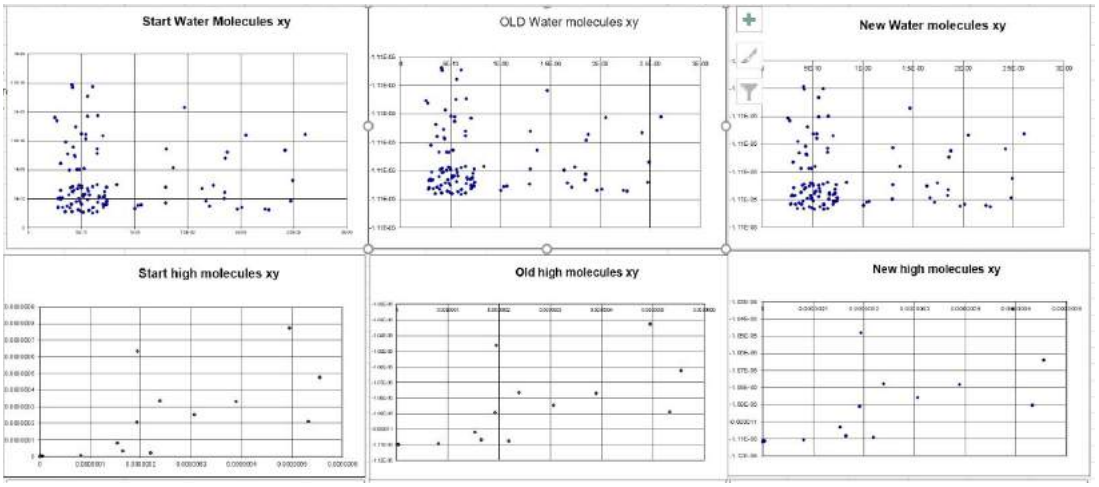

Fig.2: This is the compiled picture of data which shows the XY projections of coordinates. All the data is having XYZ coordinates. This is similar picture as above after 1500 iterations WITH EARTH GRAVITATION, one can observe the change in scales, though the picture is looking similar.

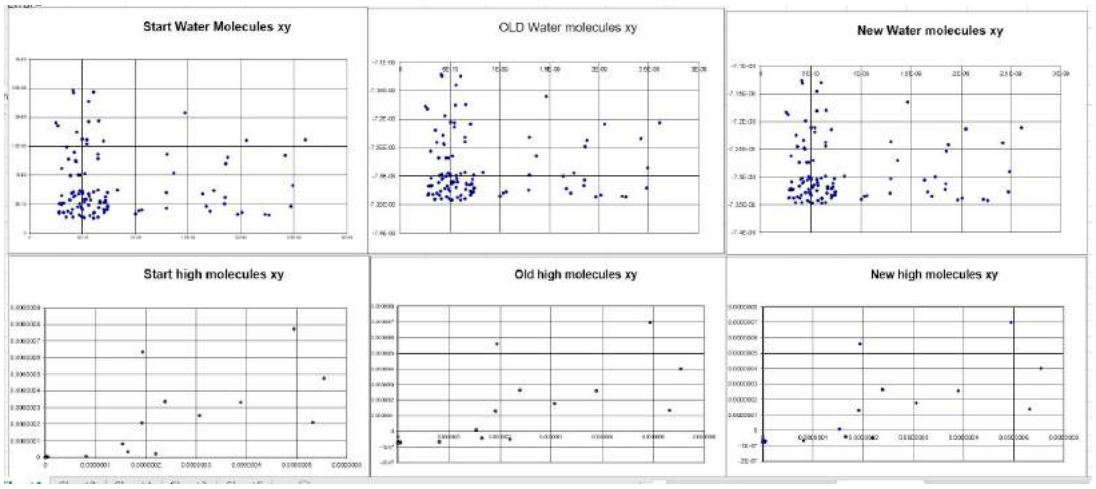

Fig. 3: The compiled picture of data which shows the XY projections of coordinates. All the data is having XYZ coordinates. Here picture shows status after 1500 iterations WITH OUT EARTH GRAVITATION.

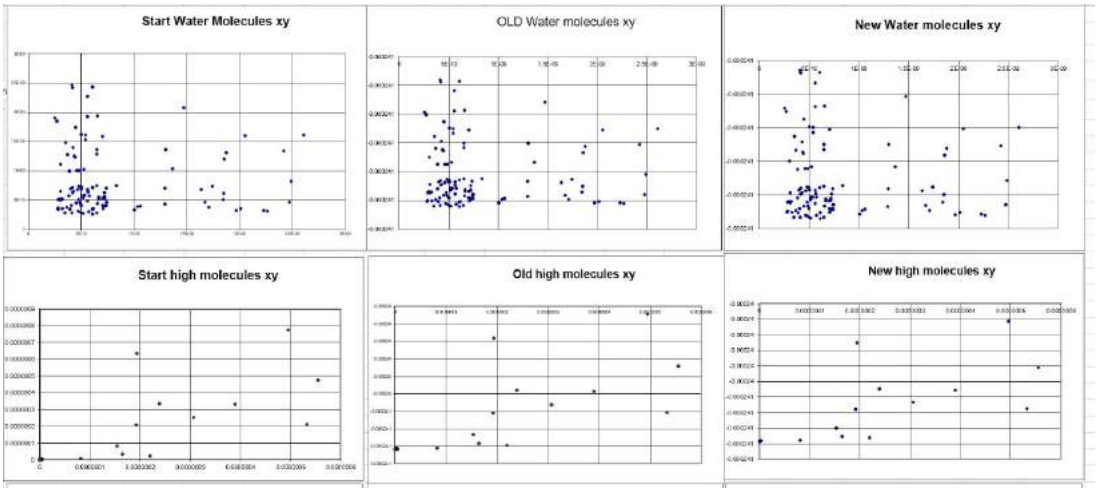

Fig.4: This is the compiled picture of data which shows the XY projections of coordinates. All the data is having XYZ coordinates. This is similar picture as above after 7000 iterations WITH EARTH GRAVITATION, one can observe the change in scales, though the picture is looking similar.

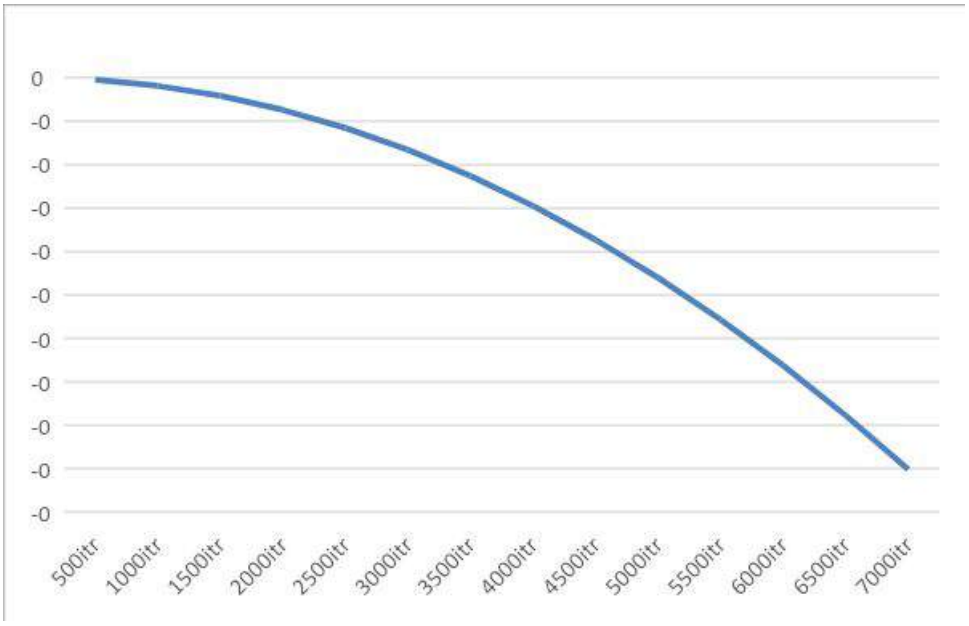

Fig.5: Maximum displacement was found in " Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide " whose atomic number is high. File name "Vvtc diff 5-7000 compile"

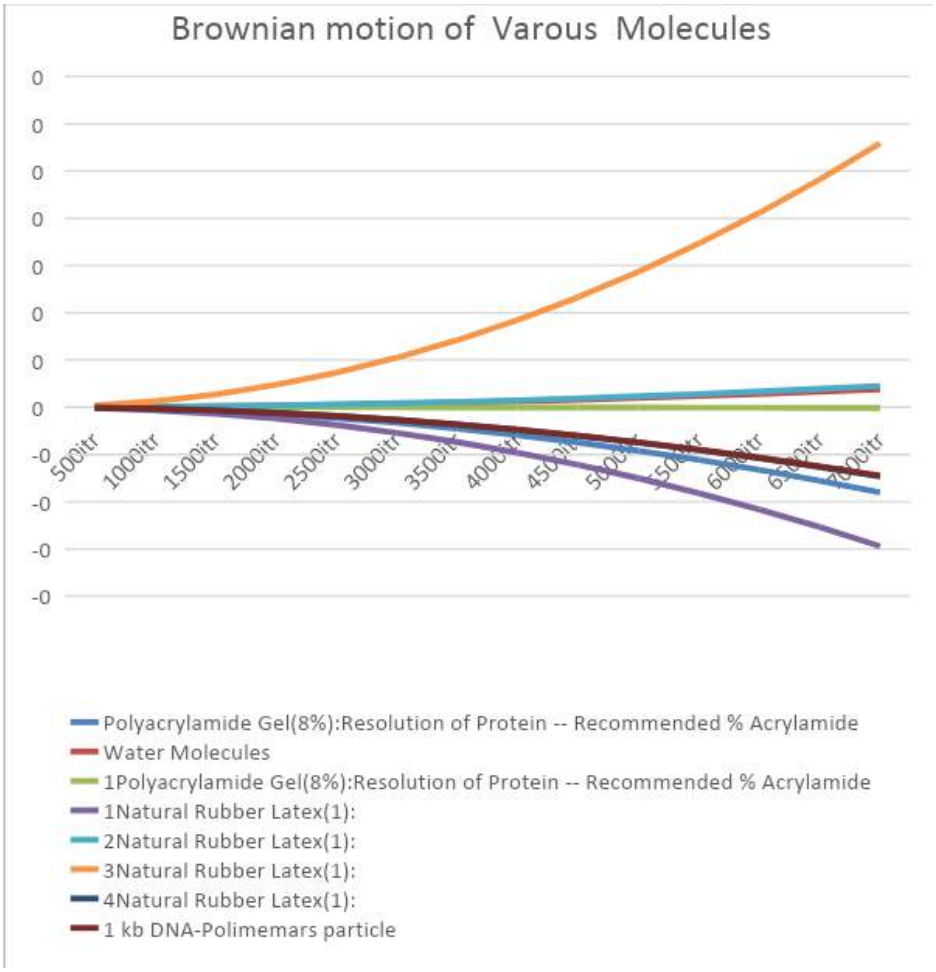

Fig. 6: Comparision of displacents in first eight molecules including "Polyacrylamide Gel(8%):Resolution of Protein -- Recommended % Acrylamide" but excluding earth. Water molecule was also added for comparision sake. File name " Vvtc diff 5-7000 compile"

Table 2. File name " Vvtc diff 5-7000 compile" gives actual differences found in the last iteration. Though these differences in position are significant, these can not be seen in the graph. All numbers are in meters. This data is taken from the files

vvtc 5 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 500 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 1000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 1500 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 2000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls6vvtc 2500 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls

vvtc 3000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 3500 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 4000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 4500 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 5000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 5500 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 6000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 6500 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 7000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 6500 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls
vvtc 7000 itr Diff new-start earth Gravty 1G visco 0.25 SSMMT BioNanoTech.xls

File name "Vvtc diff 5-7000 compile" gives Comparison table of difference and the graphs shown above. These graphs can be made for any row of the 133 molecules.
Such files can be prepared for the other sets of simulations also..... We did not prepare such graphs, as they will depict similar results....

5.5 Number of iterations done

500 itr 25Jul20 @11.24am IST	3000 itr 26Jul20 @7.45 am IST	5500 itr 27Jul20 @3.00 pm IST
1000 itr 25Jul20 @2.30pm IST	3500 itr 26Jul20 @10.35 am IST	6000 itr 27Jul20 5.40 pm IST
1500 itr 25Jul20 @5.18 pm IST	4000 itr 26Jul20 1.00 pm IST	6500 itr 28Jul20 @2.00 am IST
2000 itr 25Jul20 @8.30pm IST	4500 itr 26Jul20 @3.50 pm IST	7000 itr 28Jul20 @5.20 am IST
2500 itr 26Jul20 @5.00 am IST	5000 itr 26Jul20 6.40 pm IST	

This table gives the date and time of finishing every 500th iteration up to 7000th iteration when earth gravitation was considered.

500 itron 29th July 2020@6.45 pm
1000 itron 30th July 2020@01.35 am
1500 itr on 30th July 2020@07.55 am

This small supplementary table to above table gives the date and time of finishing every 500th iteration up to 1500th iteration when earth gravitation was **NOT** considered. All the times are IST, the Indian standard time.

IV. CONCLUSION AND DISCUSSION

Finally, Dynamic Universe Model entered the new era and new subject of NANOBIOTECHNOLOGY, which is a budding science and is a conglomeration of four main branches of science viz, Physics, Biology, and chemistry and Engineering.

Assembly of molecules in test tubes usually hinder the behaviours of single molecules. The ensemble averages out the behaviour of single molecules. Now with the help of this SSMMT we don't have to do

elaborate methods to Isolate single molecule, to do variety of EXPERIMENTS with SIMPLER and CHEAPER LAB equipment. Simple experimental Fluctuations NEED NOT be screened out. As usual the observation of moliecular events can be done with single molecule theories.
This branch of science is very powerful and versatile.

Mathematics for 'single molecule' theories were fully developed. There are many for problems and difficulties for isolating single molecule for observations via an optical micro scope. With SSMMT such problems will be reduced.

A humble attempt is made to develop mathematical background for the Subbarao Simulation of Multi Molecule theory for an oral presentation in the upcoming conference Nanobiotech 2020

I could not do any simulation for more than 7000 iterations because I felt they are sufficient to conclude that Gravitation is the binding force between the molecules in water. Though it is weak force, but the nano movements of molecules of the order of 10^{-20} meters in every nano second are added together with multiple innumerable number of molecules acting gravitationally increases these movements heavily.

In these simulations 133 particles were considered. Higher number gives higher accuracies in simulations. Each set of 500 iterations simulation took an average of 5 hours of continuous calculations on this Laptop. Another important factor to be noted is gravitation is a weak force, but the gravitation action of Multiple molecules and number of iterations gave enough movement to cause the Brownian motions in fluids, which is evident from the attached graphs.

All these simulations and papers were done in just one month of time

More iterations are required to the tune of millions to see displacements to see fully.

Here with sets of simulations we can safely conclude that Gravitation is the binding attraction force, which we could not conclude in the third earlier paper . Maybe I will do bigger simulation on a bigger computer if I can get some resources.

A humble attempt is made to develop mathematical background for the Subbarao Simulation of Multi Molecule theory for an oral presentation in the upcoming conference Nanobiotech 2020

ACKNOWLEDGEMENTS

I thank Maa Vak for giving me continuous Guidance on this new work. I also thank Prof Caroline Kelly, Program Director, Nanobiotech 2020, for asking me to deliver a lecture on NANOBIOTECHNOLOGY, which is a perfectly new subject for me. And she inspired me to do this work for the upcoming online Conference during Aug 3-4, 2020.

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