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"Multi Molecule Theory" with Gravitation as Binding Force between Molecules Can Explain Brownian Motion-After Seeing Final Positive Results of SSMMT Simulation

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Abstract

Paper 4, Positive Simulation Results: Nano-biotechnology is a wonderful multidisciplinary budding science. Here in our persuasions to explore to explain the Physics portion which is forming the basis of the Nano-biotechnology, this paper is the FIFTH paper based of FINAL results of 4th paper, in this series of earlier four papers on Multi Molecule Theory (MMT) as listed below in this abstract.

What is the basis of Brownian motion and what its basic mechanism? We can safely and positively take Gravitation as the force field between Molecular pairs to explain Brownian Motions.

As we mentioned in the fourth paper, the number of iterations were done more than 7000, concluding about 'Gravitation' is the final force of attraction between molecules. In this paper we will discuss the positive theory behind MMT.

We can say that "Gravitation" as the force of attraction is not sufficient to give enough force between a single pair of Molecules. But the collective vectoral sum of these forces of multiple molecules in MMT, with sufficient number of iterations will explain the motions. Here we are talking about the Brownian motion and the Physics and the calculations behind the force and individual velocities of molecules with relevant theoretical analysis as proposed in the FIRST paper. For this theory of MMT EXCEL simulations were developed about month back.

1st Paper presented theory of MMT with the thinking Gravitation may not be sufficient to explain inter molecular forces.

2nd Paper gave details of implementation to excel where Gravitation as binding force.

3rd Paper present these simulation results of using Gravitation as binding force between molecules here different simulation of each 55 iterations were presented.

4th Paper gives the Final concluding simulations giving positive results Using Excel simulations.

5th Paper (This Paper) we are revising the earlier theory paper on MMT published and now we are incorporating the above 4th paper final results.

Keywords: Nano-biotechnology; 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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Introduction

BNanobiotechnology is a new branch of science combining cell biology, chemistry and particle Physics. 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.

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. 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. See wonderful explanations in the paper 'Life at low Reynolds number' by Purcell C [1]. Now 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' [2,3].

Materials and Methods

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 rise to errors always. This method solves many problems in both equilibrium and non-equilibrium 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 $\omega=0.25(kBT/\hbar)$ ". 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.

Mathematical Background for Multi Molecule Theory of Nano biotechnology

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 Nano Bio-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 with 133 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 Nano-bio-Particle which hits the boundary will return according to Newton's 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 force on the point mass α is F_α , Let $F_{\alpha\beta}$ is the gravitational force on the α^{th} point mass due to β^{th} point mass, Moment of inertia tensor (We will assume moment inertia is the dominating, but for theoretical calculations for this paper we will ignore Viscus forces) (Equations 1 and 2).

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

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

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. The full development of all equations up to equation 3 are the basis of dynamic universe model and are available in many published papers. This paper shows how to apply these equations of dynamic universe model to multi molecule theory (MMT) (Equation 3).

$$\Phi_{ext}(\alpha) = -\sum_{\substack{\beta=1 \\ \alpha \neq \beta}}^{N^T} \frac{Gm_{\beta}^{\gamma}}{|x^{\gamma\beta} - x^{\gamma\alpha}|} - \sum_{\substack{\beta=1 \\ \alpha \neq \beta}}^{N^{\delta\gamma}} \frac{Gm_{\beta}^{\delta\gamma}}{|x^{\delta\gamma\beta} - x^{\delta\gamma\alpha}|} \quad (3)$$

The Equation 3 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 way of calculations provides a solution of X, Y, Z values of coordinates, velocities and accelerations of each Molecule in the setup for that particular instant of time. 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 [7].

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 [8,9] 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. The second book in the series describes the SITA software in EXCEL emphasizing the singularity free portions. This book written in 2011 [10] 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. Some of the other papers published by the author are available at refs [11-14].

This Subbarao Software can be used in many places like presently unsolved applications of MMT, and we will discuss in our future papers. Here we have shown that this

'SSMMT using Gravitation between molecules' approach can be used positively in Nano Biology Technology.

Discussion and Conclusion

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

Till now this Nano-biotechnology used Single molecule theory and all the experiments in the Laboratory were conducted on the basis of the SMT only. This SSMMT opens a window to conducting lab experiments in a more elaborate broader and wider way. We feel that the Lab equipment also will be available in more cheaper and simpler equipment as we need not isolate to a single molecule level. Let's hope for the best this branch of science is very powerful and versatile.

We all know that Mathematics for 'single molecule' theories was fully developed. There are many problems and difficulties for isolating single molecule for observations via an optical microscope. 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

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