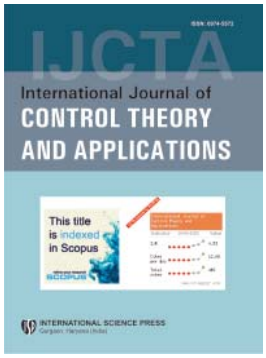

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Adaptive Energy Minimization Approach to Melanoma Cancer

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Abstract: Prediction of the minimum energy is of high importance in the field of molecular dynamics. Identifying the exact technique to find the optimal energy minimum is a difficult task. Our work aims at finding the energy minimum required by an amino acid to bind to each other to form a protein. This protein can be used as an indicator on the receptor of the cell membrane to find a better pathway to cure melanoma. This paper proposes an approach for finding minimum energy used by each protein to perform activities like cell growth division and cell proliferation. The energy minimization algorithm determines the energy given by the protein cells.

Keywords: *Energy minimum, amino acids, proteins, melanoma, molecular dynamics*

1. INTRODUCTION

Atoms are the fundamental parts of matter and they define the element structure. The atoms consists of neutrons, protons and electrons. An atom can gain a large quantity of electrons to raise their stable nature. An atom can interchange or donate electron to another atom in a molecule. The chemical bond is generated to clutch two or more than two atoms together to form a molecule.

The bond length is the measure of space from the nucleus of one atom to the nucleus of another atom bonded together. The bond angle is the measure of the angle of one atom to another. The bond length and the bond angle decide the form and figure of the molecule. The torsion angle is used as the conformations surrounding the movable bonds. It acts as a base of protein for the prediction of protein structure.

The nuclear motion helps to determine the construction and dynamism of a molecule. The molecular mechanics is dependent on three values which are the force fields, the parameters and the energy minimization algorithms.

The force fields represent the potential energy of a molecule through various constants and functions. The parameters are the various values like the mass of an atom, length of the bond between two atoms, angle between two atoms, torsion angle and various other measurements. The energy minimization algorithms are used to determine the new minimal energy for the atoms that bond together to form a molecule or the amino acids that bond together to form a protein.

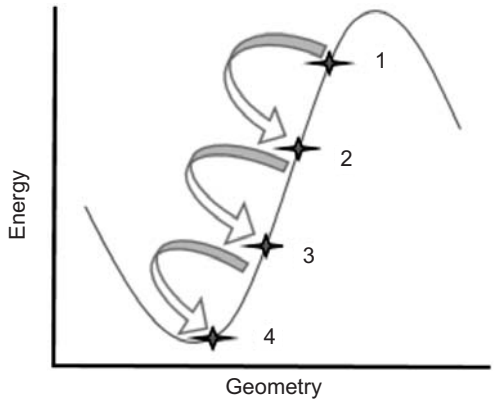

Figure 1: Energy minimization process changing the geometry of the molecule until a minimum is reached

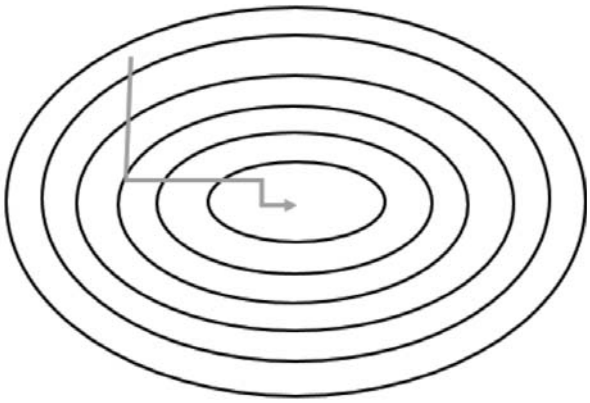

Figure 2: Steepest Descent energy minimization technique when two geometrical coordinates exist

The molecular mechanics is used to calculate the minimum energy required by a protein by using any of the algorithms like steepest descent technique, conjugate gradient technique and many more. The same process is iterative until it reaches the exact position for the amino acids to bond together to form a protein. The optimum minimum energy is conformed when a geometry is used to optimize the molecule.

Once the optimal minimum energy is found then we can find the approach to determine the best pathway to cure the melanoma. Melanoma is one of the cancer, which affects the skin of a human body, which is developed from the cells pigments called melanocytes. Mitogen-activated protein kinases (MAPK) pathway are series of proteins in the cells that interacts by inputting indications from the receptor on to the cell membrane. The sign i.e. signals activates when the indicating molecules impasses to the receptor on the cell membrane and stops when the DNA in the nucleus couriers a protein and gives modification to the cell, like cell divisions. This indicating molecule is formed by the bonds between various atoms by using the optimal minimum energy concept.

2. LITERATURE REVIEW

Jay W. Ponder et.al [1] represents a computational technique for the energy minimization of the molecules. The important idea is to optimize the protein structure using the minimum energy. The energy minimization of the macromolecules uses non-linear conjugate gradient technique in which energy converges after very large number of iterations. Many tests are required to find the combination of various optimization techniques. The Newton techniques are very similar to conjugate gradient techniques in terms of the iterations required. This work is suitable for less molecules and greater used for huge structures.

Michael J. Dudek et.al [2] constructs an energy surface for the proteins and its twists are validated using the global energy minimum. The neighbouring torsion angles 2D Fourier transforms are added. The protein structure is predicted through the use of global energy minimum and their crystal structures. This work produces finely detached energy conformations. The search is not always far-reaching and it discovers the energy conformations with additionally established side chain positions.

Michael J. ROTHMAN et.al [3] explains about conversion state search using energy minimum technique. The work also expands the several energy minimum examining methods and their evaluations. The work does not require a prior information regarding the purposes of the pathway responses. The work had a drawback that the pathway on the surface be continuous only along some segment comprising an extreme and extreme happens merely at saddle point.

Ron Unger et.al [4] generates an outline of how genetic algorithms can be used for structure approximation. The genetic algorithms are used to solve the basics in issues related to optimization but there is no assurance that the genetic algorithms will always find the optimal solution. Foreseeing the three dimensional arrangement of a protein from its direct series is one of the important trials in molecular biology.

Craig E. Kundrot et.al [5] develops a numerical technique for predicting the size of a macromolecule. It is used to calculate the first derivative and second derivative of atomic values using its function. The changes noticed in the structures were alike the X-ray crystallographic changes. The work can be extended by defining the arcs perfectly.

G. Kresse et.al [6] creates an approach for to calculate the ground state of the metal arrangements. The iterative diagonalization of enormous mediums and scaling of the optimization of plane wave basis set is developed. The total energy is designed. The energy and the force touches the precise ground state.

Michael Levitt et.al [7] generates the energy minimization with respect to the atom's torsion angles and atomic ranges. The low energy conformations are alike the X-ray arrangements. The prediction of folded energy conformation for bonding of amino acids to form a protein molecule is the task. This approach consumed huge CPU processing time for the low energy conformation.

Michael Levitt et.al [8] grants a quick improvement process accomplished of developing the steady conformation of a macromolecule by investigational model co-ordinates. All the gradations of freedom of the molecule are permitted to differ and all portions of the arrangement are enhanced concurrently in a common energy ground. . The work has been defined and analysis had been completed on myoglobin and lyzozyme. The work had been prepared by the steepest descent rehearsals in releasing the lysozymes with unbound forces of energy. The work had a weakness that it was not quadratically convergent when distant from the minimum and non-bonded forces were not recycled in the enhancement.

M S Pallavi et.al [9] has proposed a work on spam detection using support vector machine algorithm. The support vector machine algorithm determines the results fast and provide exact results for the problem. This algorithm can be used to find a quick and optimal solution for any kind of related works of optimization.

Sabitha Mangalathillam et.al [10] has proposed a work on curcumin loaded chitin nanogels to cure melanoma. The drug scatters in water and is less toxic. There is active transdermal penetration where occurs a vigorous elements transported through the skin for complete dissemination.

R I Ramachandran et.al [11] explains the basics of computational chemistry and molecular modelling which is the fast evolving zone used for modelling and simulation to determine the behaviour of biological systems at molecular level.

3. PROPOSED METHODOLOGY

3.1. Energy minimization

Energy minimization is done to know the stable conformers for a molecule to allow the understanding of the qualities and behaviours depending on their structural features. It can also be called as geometry optimization.

Energy minimization is used to calculate the minimum on the surface of potential energy from a starting structure of higher or maximum potential energy.

Energy minimization methods are calculated by finding the slope and energy of the function at first point. Based on that the results can be analysed as coordinates are too large when it is positive slope or coordinates are too small when it is negative slope. Then accordingly the coordinates are adjusted. The value of the coordinates is reduced when there are positive slopes and energy and slopes are found again at second point and it is repeated. When a minimum energy is reached, it means the slope is zero.

There are many ways for calculating the minimum energy such as Steepest Descent Method, Conjugate Gradient Method and Newton Raphson Method. The energy of the protein can be calculated using any of the above methods which differs based on the number of steps and the total CPU time required for energy minimization.

The Steepest Descent method provides the position of the geometry which is being minimal first is in the position where there is larger gradient and continues until it reaches the desired tolerance.

3.2. Energy minimization algorithm

Input: Bond distance, slope

Output: Energy minimized or not

Step 1: Load the values to the application

Step 2: Validate inputs $x0$, $f0$, $fc0$, $x1$, slope, ae, maxitrn

Step 3: for $i = 1$ to maxitrn

Step 4: do

Step 5: $f0 = f(x0)$

Step 6: $fc0 = fc(x0)$

Step 7: if $fc0 <= slope$

Step 8: then go to step 16

Step 9: $x1 = x0-(f0/fc0)$

Step 10: if $(x1-x0)/x1 < ae$

Step 11: then go to step 18

Step 12: $x0 = x1$

Step 13: end for loop

Step 14: write "energy not minimized in maxitrn iterations"

Step 15: stop

Step 16: write "slope is too small", $x0$, $x1$, $f0$, $fc0$, i

Step 17: stop

Step 18: write "energy minimized in maxitrn iterations", x, i

Step 19: stop

4. EXPERIMENTAL RESULTS

The energy minimization algorithm used to find the energy minimum during the bonding of amino acids to form a protein structure is developed. A compound mutable function is defined. The sample bond distance and the slope initially is given along with the maximum number of iterations required to find the energy minimum and the results are found accordingly.

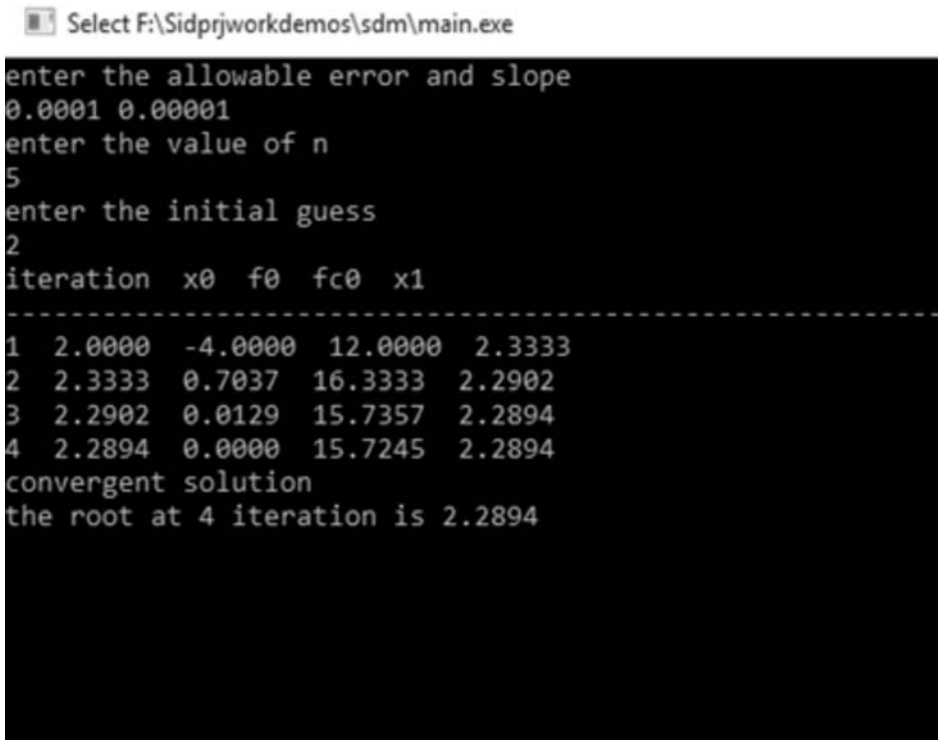

Figure 3: Energy minimum calculation when angle converge

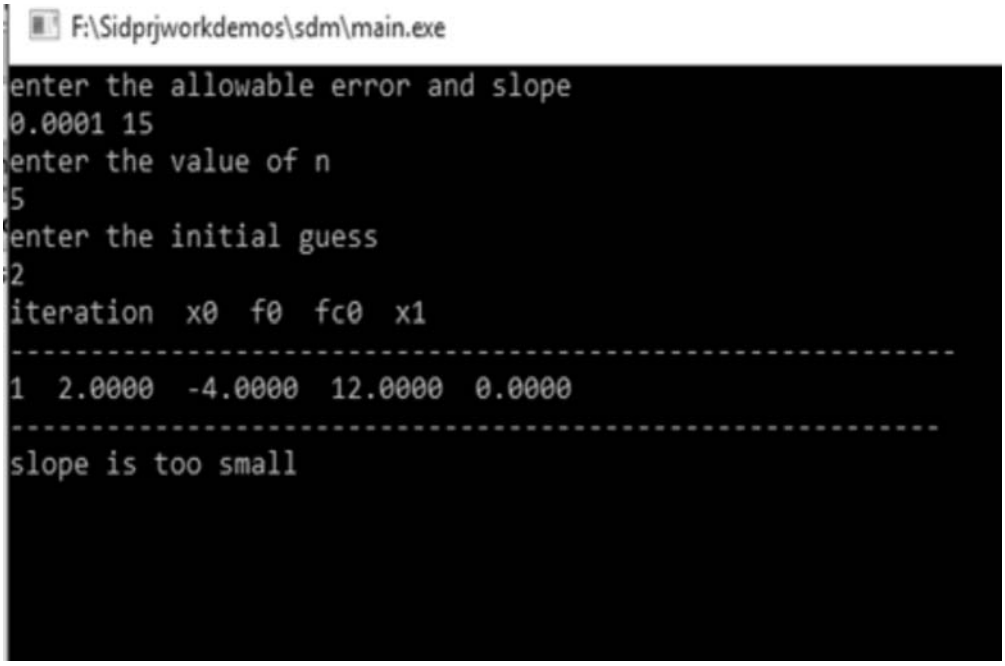

Figure 4: Energy minimum calculation when slope is too small

Fig. 3 shows the calculation of the minimum energy by providing the sample bond distance and the slope along with the allowable error and maximum number of iterations to calculate when the energy converges and minimizes whereas Fig. 4 shows the calculation of minimum energy by providing the sample bond distance and the slope but the slope becomes too small and the minimum energy cannot be determined.

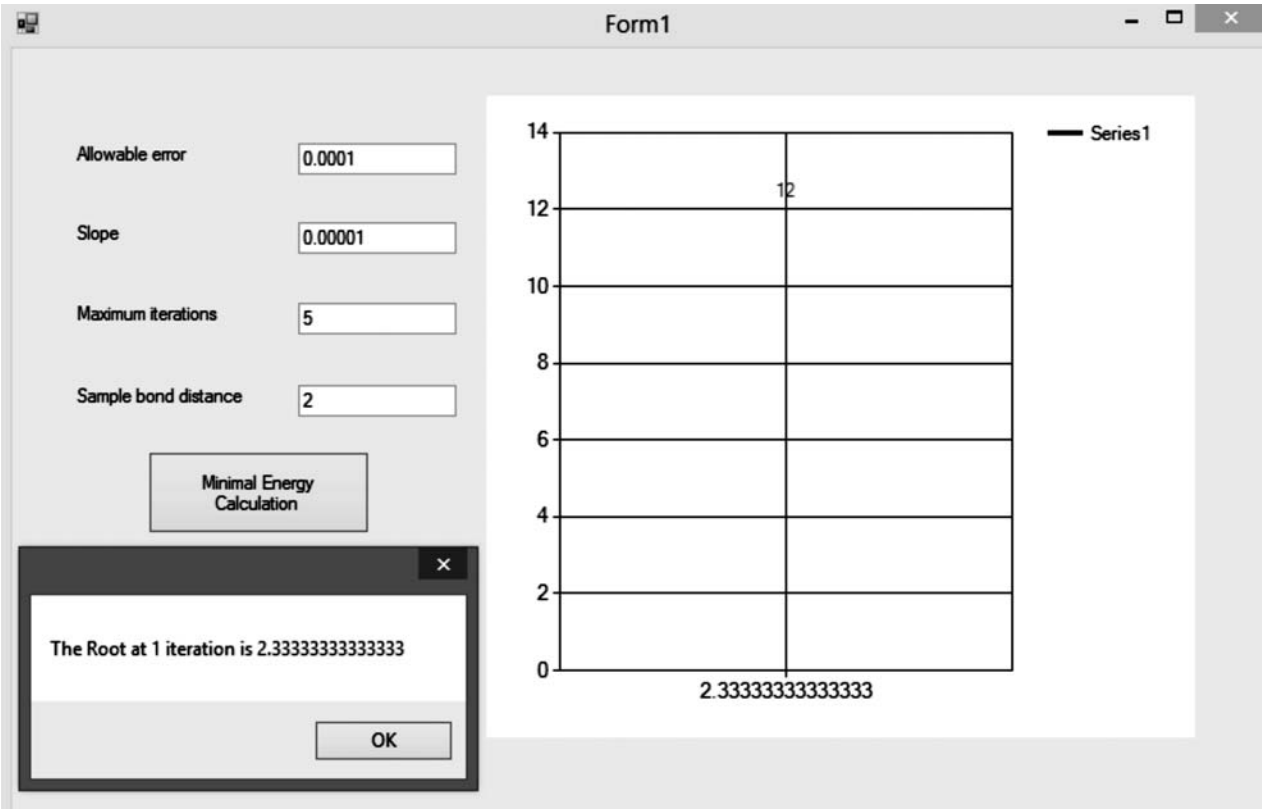

Figure 5: Energy minimum graph (Iteration 1)

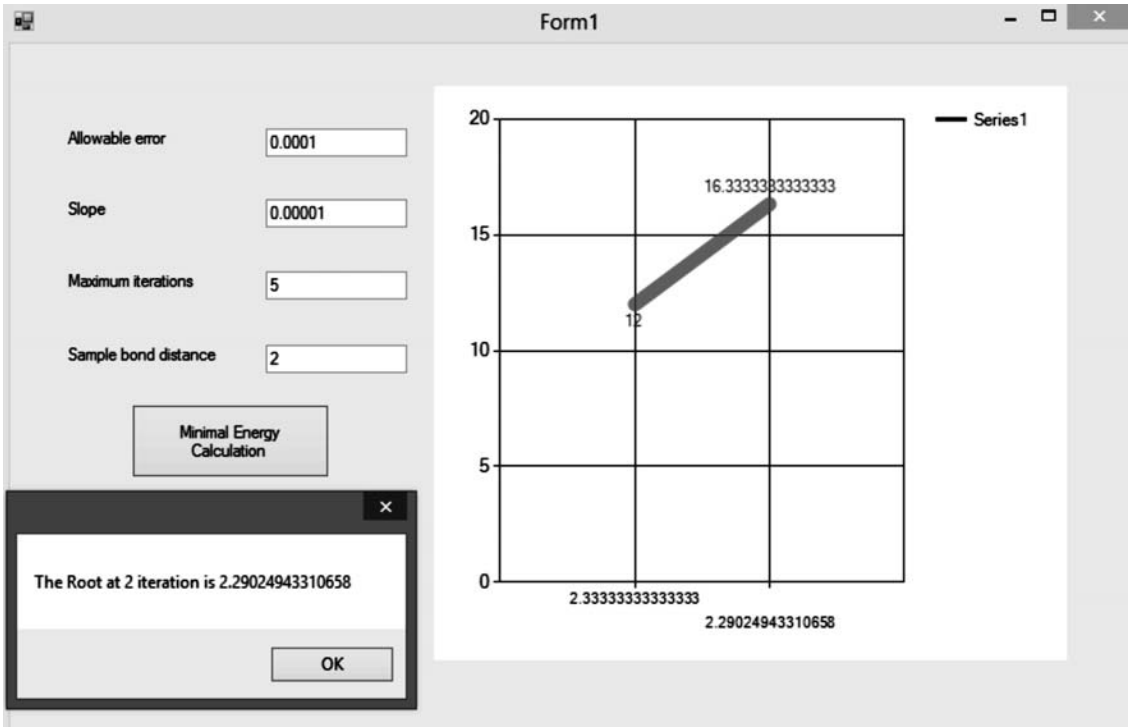

Figure 6: Energy minimum graph (Iteration 2)

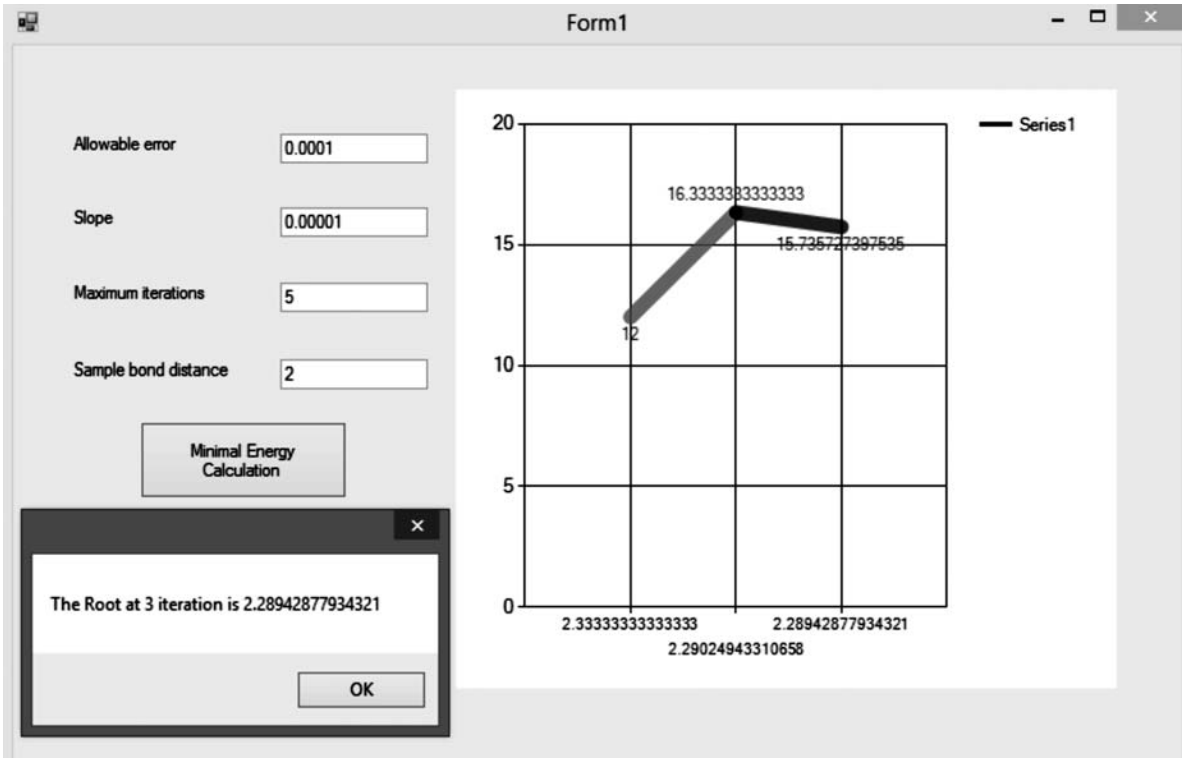

Figure 7: Energy minimum graph (Iteration 3)

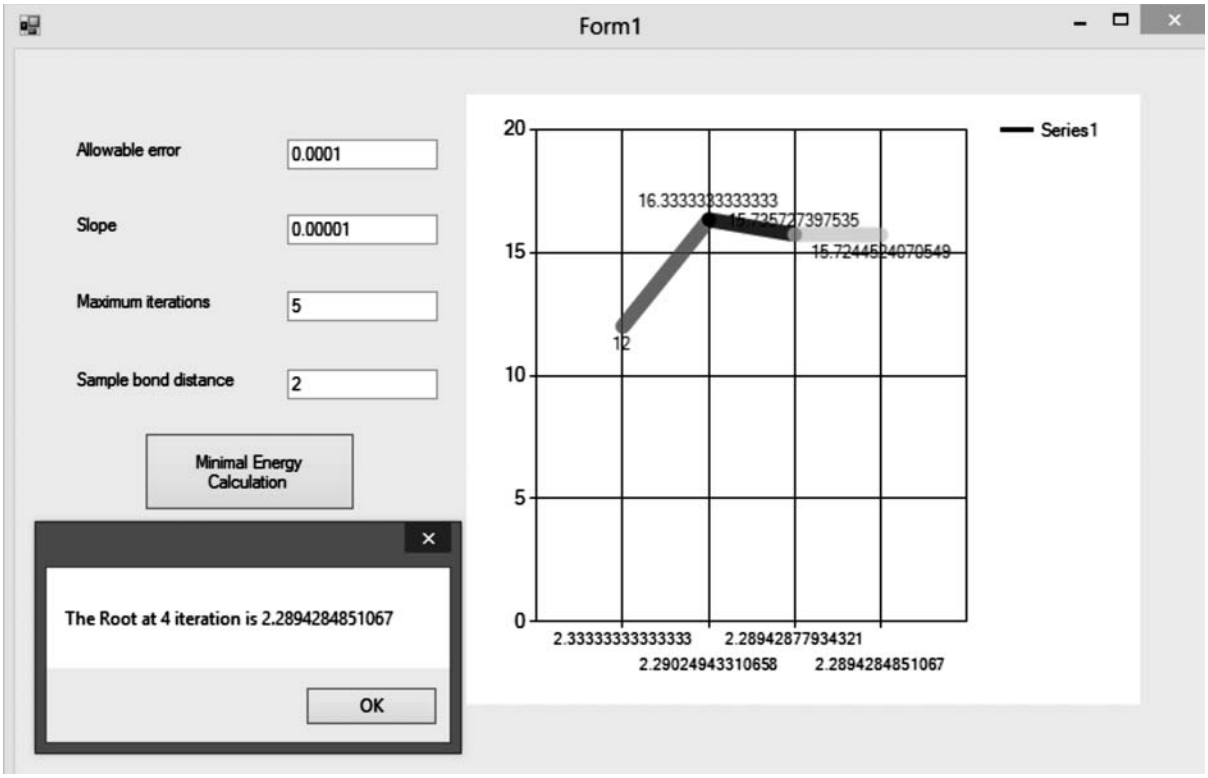

Figure 8: Energy minimum graph (Iteration 4)

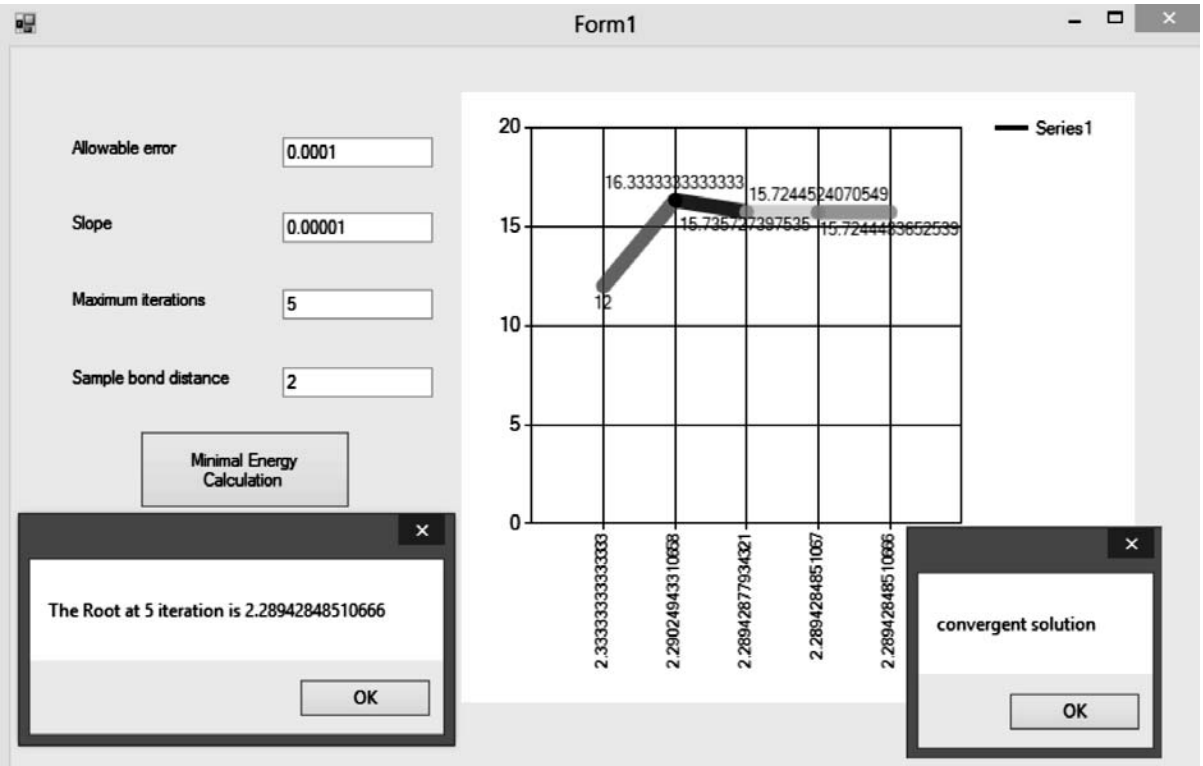

Figure 9: Energy minimum graph (Iteration 5)

Fig. 5-9 shows the graphical view of the energy being minimized by representing the mutable function at each iteration along Y-axis versus the energy minimized at each iteration along X-axis. It gives a convergent solution and the optimal minimum energy calculated.

5. CONCLUSION

In this work, we have dealt with the energy minimization concept in which we find the minimum energy utilized by each protein cells for cellular based activities. The energy minimization algorithm determines minimum energy utilized during bonding of amino acids, protein structures and other cellular activities. In our experiment the compound mutable function is defined and it is used to calculate the minimum energy at each iteration. We give a sample bond distance and the slope initially along with the maximum number of iterations required to find the energy minimum and the results of the energy minimization are found accordingly to the inputs we give to our system. This minimum energy is needed by the amino acids to form a protein which in turn acts as a ligand which binds to the receptor on the cell membrane to carry the signal to the nucleus through the pathway for curing melanoma by cell growth division and cell proliferation.

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