

# Understanding the complexities of life education essay

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My schooling and college was really of import factor in determining my calling. Excellent classes in board scrutinies, 83 % in 10th class and 82 % in 12th class, ever kept me in top 5 % of the school. Excellent module, which ever focused on the basics, motivated me to analyze harder and with complete apprehension of the topic. In my college, I became peculiarly interested in the field of Biology as I was ever amazed by the diverseness and complexness of life around me ; I chose to analyze biological science in more item. I chose Biotechnology as my major for my bachelor's A grade ( B. Sc. ) along with chemical science and fauna as bush leagues. Biotechnology helped me understand applied biological science in great inside informations. I besides attended an on occupation developing under Annual Biotechnology Training plan at Haffkin Institute, Mumbai where I got more exposure to practical biotechnology, different biophysical techniques and instrumentality. Parallel to all this, I was besides interested in computing machines right from my school yearss. A class on programming in C, gave me an chance to larn computing machine scheduling and its applications. Having heard of bioinformatics as a combination of biological science and computing machines, I applied for and got selected through big figure of applications to go to a workshop on bioinformatics at Indian Institute of Technology( IIT ) , Mumbai. Here, I was introduced to power of computing machines to reply inquiries in biological science. My apprehension of biological science, love towards computing machines and penetration into the universe of bioinformatics and its applications through my course of study and the workshop worked as a strong motive for me to take the specialisation for my maestro 's grade. I determined to prosecute my farther surveies in the field

of bioinformatics and computational biological science with an purpose of utilizing potencies of computing machine systems and of recent promotions in the field of information engineering in order to analyze biological science with more easiness and at accelerated rate.

I was selected to prosecute my Maestro of Science ( MSc ) in bioinformatics at Bioinformatics Centre, University of Pune, India, through a countrywide entryway scrutiny. I was ranked 8th from around 1000 appliers who appeared for the trial. My systematically good public presentation in entryway trial and in subsequent semesters made me eligible for Prof G. N. Ramchandranfamilyand Dept. of Biotechnology, Govt. of Indiascholarshipto prosecute my maestro 's degree instruction. Bioinformatics Centre is one of the Prime Minister institutes in India which is renowned for its part in the bioinformatics research and in developing good bioinformatics human resource. Two old ages of strict preparation in bioinformatics taught me a batch about this astonishing merger of biological scientific disciplines and information scientific disciplines. I was introduced to different computing machine scheduling linguistic communications and resources for application development in bioinformatics. Classs in biological science, computing machines and accent on their appropriate integrating made me believe of biological science in a really different and unconventional mode. In our 2nd semester, we had a capable Structural Biology and Molecular Modeling ( SBMM ) , where we were introduced to bio-macromolecular constructions with a computational and biophysical position. With the survey for this peculiar class, I became more focussed on my country of involvement.

Surveies of structural biological science of proteins were truly an interesting

portion of my course of study. Eminent scientists from different national research institutes gave us penetrations into the structural biological science of different biomolecules. I can not travel without adverting names of some of my instructors, Prof Ashok Kolaskar ( adviser, OHSL, USA and adviser, Internet2 ) , Dr. Dhananjay Bhattacharyya ( Saha Institute of Nuclear Physics ) , Dr. Raja Banerjee ( West Bengal University of Technology ) , Dr. Uddhavesb Sonawane ( C-DAC ) , Prof P. V. Balaji ( IIT, Mumbai ) to call a few.

My first research experience in the field of Bioinformatics was my maestro 's degree research undertaking under the counsel Dr. Pramod Wangikar in his Bio-systems Engineering Lab at Chemical Engineering section of Indian Institute of Technology ( IIT ) , Mumbai. Though it was non straight connected to my country of involvement, it gave me insights into how research methodological analysis works for computational biological science. Here I worked with analysis of regulative elements of cyanobacteria- Synechocystis as a little portion of big systems biological science undertaking traveling on in his lab. This undertaking, as a whole, was taking towards constructing a systemic theoretical account of Synechocystis. My part was to use microarray informations for cistron look of all Synechocystis cistrons and written text factor adhering site analysis in order to footnote some of the cistrons. I could foretell the map of two cistrons which found to be related to photosynthetic tract but were unknown boulder clay day of the month. I got familiar with the existent life applications of different tools and techniques that I had studied earlier. From here, I determined to prosecute my calling in the research field and contribute as per my capablenesss to the scientific community.

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After MSc, I worked under the counsel of Prof Valadi Jayaraman from Center for Development of Advanced Computing ( C-DAC ) , India. I worked with Prof Jayaraman on short term undertaking titled Prediction of RNA adhering proteins utilizing random woods. His first-class counsel and my difficult work contributed to my apprehension of machine acquisition applications in biological science and utilizing information from biological constructions for better apprehension of the biological procedures. The undertaking involved extraction of of import characteristics from the RNA adhering sphere of many RNA binding proteins and developing the random forest classifier to do accurate anticipations about RNA adhering belongings of unknown proteins. This once more provided me with a really utile technique of machine acquisition for work outing jobs in biological science and besides enhanced my accomplishments of computing machine programming for existent life applications.

Parallel to this work with Prof Jayaraman, I besides worked in an industry, Persistent Systems Limited, Pune as Domain Analyst, where I learnt a batch about industrial position of bioinformatics and recent IT advancements assisting bioinformatics grow. It gave me an chance to form my ideas, represent myself professionally and to larn clip and resource direction. I worked on supplying preparation and support to many of US universities, our clients, for caTissue clinical information sciences application. But my passion and finding for making research prepared my head to go forth industry and carry out research.

I applied for the position of Research Associate at Bioinformatics Centre, University of Pune. I got selected after strict interview procedure by an elegant panel under the Centre of Excellence ( CoE ) grant of Dept. of Biotechnology ( DBT ) , Govt. of India. Here I started working on some of the authorities funded undertakings. I worked on `` Understanding the mechanism of anisomycin induced activation of p38 MAP kinase utilizing computational attack '' under the high counsel of Dr. Sangeeta Sawant. Anisomycin is an antibiotic, which besides activates p38 MAP kinase, an of import constituent of signal transduction. But no information is available on how precisely it binds to and activates p38 MAP kinase. I attempted to execute molecular docking surveys and molecular kinetics simulation experiments. This work resulted in happening out putative binding site for anisomycin on p38 MAPK and in understanding different molecular interactions taking topographic point at the interface of these two molecules. I learnt a batch about structural belongings of proteins and power of MD Simulations to research mechanisms underlying cellular procedures. I used Amber molecular kinetics simulation bundle extensively to transport out the simulations. Another undertaking was `` Analyzing the comparative stableness of conformational antigenic determinants: a instance survey of muramidase '' , which was carried out under the counsel of Dr. Sangeeta Sawant and Dr. Urmila Kulkarni-Kale. This survey was carried out to understand the comparative stableness of single antigenic determinants and happening out antigenic determinants which might retain their stableness during their processing. We could back up the hypothesis that such antigenic determinants do be and can be identified. Possible application

of this survey would be in placing possible drug/vaccine marks. We used blossoming simulation technique to analyze the phenomenon. I am happy to province that a portion of this work was presented with batch of grasp at International Conference on Biomolecular Forms and Functions, held at Indian Institute of Science, Bangalore and complete work is in concluding phases of its entry for publication. Both these undertakings equipped me with a needed attitude to transport out research and believe in a logical and rational manner to come to a solution. It made my foundations about structural biological science, biophysical chemical science and computing machine simulations stronger than they were. Currently I am keeping the same place and seeking to take my work to a logical terminal.

Presently, I am besides involved in the development of Chemical Reaction Optimization ( CRO ) based cistron choice algorithm under the counsel of Prof Valadi Jayaraman of C-DAC, Pune. This undertaking work, which had merely started, is using my scheduling and bioinformatics accomplishments to plan and implement cistron choice algorithm utilizing CRO, a late proposed optimisation technique.

I besides served as a sing module of bioinformatics for biotechnology pupils at Ruia College, Mumbai, which prepared me for my sphere capable with more duties. It helped me to go more confident and responsible to do others understand bioinformatics in a elusive mode. Teaching microarray informations analysis at University of Pune, Pune and Patkar College, Mumbai besides helped my instruction accomplishments grow. I besides organized and conducted a four twenty-four hours workshop on bioinformatics for life

scientists at Ruia College. Success of this workshop and positive response from the participant made me confident about my organisational accomplishments. I have attended big figure of conferences and workshops, have presented my work at national degree conferences therefore have had changeless updates about new kingdom of biological research. I besides appeared for BioInformatics National Certification ( BINC ) scrutiny, conducted by Dept. of Biotechnology ( DBT ) , Govt. of India, to prove the ability of bioinformatics human resource and certify and congratulate really few of them who deserve to be good bioinformaticians. This test is of import in manner that it holds three documents, two usual aim and theory inquiries which test your capable cognition and one practical session which examines your ability to compose computing machine plans for bioinformatics. I was awarded BINC enfranchisement with All India Rank ( AIR ) 14 and besides a family to prosecute farther research in the field. BINC enfranchisement boosted my assurance about my cognition of bioinformatics. I besides have received grasp from module for good computing machine scheduling and presently I am involved in development of a plan suit for incorporating phyletic analysis package tools to fix an machine-controlled grapevine.

Proteins, indispensable biomolecules, are the workhorses of all the cellular maps. Their features and maps are chiefly attributed to their third construction. Always amazed by the manner this machinery works ; I am interested to work on structural bioinformatics of proteins and their interactions with other molecules. My primary research involvements continue to be in the development of fresh methodological analysiss to understand mechanisms underlying cellular procedures. There are many

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other research countries in structural biological science which involvement me like molecular mold and molecular kineticss simulation, algorithm development and executions, protein construction development, understanding the protein-protein interactions, anticipation of protein construction all of which are interlinked in a manner or other.

I have been introduced to protein construction by high panel of scientists working in this country, and that has elevated my involvements to a greater tallness and inspired me to prosecute research in the same. My twelvemonth long research experience in the field of molecular kineticss simulations and molecular moorage, in order to understand the mechanisms of biological procedures and for easing vaccinum development hold given me needed experience. Besides, it introduced me to some of the restrictions and demands of bing methods of protein construction analysis. One of my research involvements is to come up with a newer representation of protein construction for usage in molecular kineticss simulation. Currently available methods require truly thorough calculation power as it involves tremendous computations on each and every atom of the system. It takes immense sum of clip on simple machines to run a molecular kineticss simulation. While working with assorted simulations, I have observed that inexplicit solvent theoretical accounts can be good mark to accomplish this end. There is a demand to better these theoretical accounts in such a manner that they will come close expressed solvent simulations in a better manner. One of the ways in which it might work is deducing forms of interactions from expressed solvent systems and integrating them in inexplicit dissolver theoretical accounts. Current inexplicit dissolver theoretical accounts include theoretical

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consequence of solvent molecules but we could better these theoretical accounts by presenting non merely distance dependance, but besides clip dependent solvent interactions. It means that we could present consequence of existent dissolver system at specific clip intervals by adding some solvent molecules and redefine the theoretical account after each interval therefore propagating the alterations brought approximately by solvent molecules.

Another research country which entreaties me most is protein construction anticipation. Looking back in the history of bioinformatics, tremendous attempts have been taken to understand and foretell protein construction, which in bend imparts map to the protein. Our limited success even after such tremendous attempts illustrates why protein construction anticipation is known as Holy Grail of bioinformatics. Though I have had no experience in the country, I find it really interesting country to work upon and use my cognition of protein chemical science, machine acquisition and computing machine scheduling and algorithms to lend to the field.

As we look at the of import mileposts in the history of computing machine scientific discipline, we can see distinguishable markers in the development of unreal intelligence. On one manus, biological science is researching expertness from assorted subjects to be utilized in biological research and on the other manus, techniques in computing machine scientific discipline have of all time since widened their pertinence sphere. With this, my profound involvement in computing machines and my passion for biological science has widened my research ends to applications of machine larning techniques in bioinformatics and computational biological science. I have strong

experience in utilizing support vector machines and random forest classifiers for working out simple biological jobs and I wish to travel farther and assist with much more complex jobs utilizing machine learning. Currently I am involved in the development of a chemical reaction optimization (CRO) based genetic algorithm. My primary involvement in this country is predicting accurate ligand binding sites on a protein structure. Current ligand binding site prediction algorithms work on rather generalized rules like geometry based, energy based etc. I strongly think that protein binding site prediction for proper ligand binding should be based on more empirical rules and information should be brought in from a large number of known protein binding sites and ligands. Categorization of proteins and ligands into several categories and qualifying each category on certain characteristics seems indispensable to me before using any generalized ligand binding site prediction algorithm.

Another facet that I would wish to research is protein folding and kinetics. Most of the attempts we have made to understand an indispensable procedure of protein folding property is to the built-in characteristics of proteins, but many of the experimental consequences have shown that many other factors in the cell contribute to the protein folding procedure. Chaperons, microenvironment, different ions besides play a function. I would wish to travel a measure further and seek to gather all these factors together in a computational paradigm and seek to understand folding in a better mode. Folding of a protein, which is an important measure in finding its structure and interactions, will assist in developing new drug targets and interventions for various diseases.

These are some of the jobs I would wish to work upon. My long clip calling ends are to set up myself as a research worker in the field of protein scientific discipline and contribute as per my capablenesss to the society. I besides want to be invariably indulged in learning biological science, as I truly bask learning and sharing my cognition. Besides it makes me more confident with the topic I teach.

With my preparation and experiences, and my research and calling ends, I need a suited topographic point where I can use my cognition and experience to develop my thoughts further and set them to people 's usage. While seeking for suchenvironment, I was peculiarly attracted by a really fresh plan in Mathematical, Computational and Systems Biology at University of California, Irvine. Amazing blend of first-class research workers from assorted subjects would certainly do a difference. That 's why I decided to use at UCI. I am peculiarly interested in the work of Ray Luo.