STATEMENT OF RESEARCH

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Studying in computer science has helped me developing my analytical power over the problems in a systematic fashion. A systematic analysis approach visualizes all the phenomena as a network of interrelated bodies in a defined scale set that would interact with each other in defined and possibly not completely understood protocols. These protocols, interacting bodies and consequently the whole ensemble become highly sophisticated when this vision is projected to the life science domain.

Post genomic era with all data and technological novelties has brought about such a complicated network yet remained to be elucidated. Massive amount of data from wet lab experiments, complicated biophysical models, sophisticated mathematical formulization along with high processing and communicating capacity of twenty first century are now on board the human civilization. Much of the intelligence to the deadly and chronic disease pathways and their therapeutic solutions is encrypted in the already available data. To decipher these intelligence all the on-hand resources need to be properly integrated and utilized. Researchers with an interdisciplinary knowledge, whom can understand biology, make the mathematical formalization understandable by biologist and have the skill-set to employ the high processing capacities can interface for such knowledge integration. This could be perceived as a marriage between biology and computer science, where one can anticipate promising in-silico hypothesis testing tools in its horizon. I believe, during my PhD program I have gained such a capacity by expanding the domain of my knowledge to life science while extending my mathematical modeling and computational skills.

Research Background

I started my research with CReWMAN research center which is among the largest networking research centers in Texas. Here we have different research disciplines on networking, ranging from Core networks to biological networks. During my Masters I had been a member of Core networking and Systems (CoNS) research group where we would apply the concepts from algorithms and graph theory along with optimization techniques to develop novel algorithms and protocols for scheduling, data transport, QoS management, and etc. for different network technologies. I have been the lead participant of a team that proposed "COCoNet" a new core optical network technology for Terabit data transport networks. I have also proposed an efficient algorithm for multimedia data transport over multi data-rate wireless mobile networks. At the end of my master degree I did a gearshift and joined the newly established Biological Networking (BioNet) research group. After joining BioNet, I started working on a few topics in bioinformatics domain including: gene finding algorithm using Hidden Markov Models (HMM), design of Distributed Annotation Servers (Das) and application of Boolean Network in Gene Regulatory Networks. In mid 2005 the “iSimBioSys” project was defined for our group which established the base of my PhD research in computational systems biology. “iSimBioSys” is a simulation platform for studying the dynamics of a prokaryotic cell at the system level.

Current Research

My current research focus is in the interdisciplinary field of computational systems biology. More specifically, on building computational models to capture physicochemical behavior of biological processes, then further integrating these models to study the dynamics of an objective complex biological system. During my PhD program I have been affiliated with different projects where the most important is “eukaSimBioSys”. This project is the predecessor of “iSimBioSys” where we are striving to develop a platform for conducting in-silico hypothesis testing experiments for a eukaryotic cell at molecular level. Such platform abstracts a pathway as a network of stochastic events and evolves through the execution of individual events in a discrete time domain. Each network might cross-talk to the other networks or positively/negatively feeds back to itself. With an in-silico version of a pathway we can perceive the effect of external and internal signals on that pathway. We also can predicate the behavior of a cellular function or pathway under certain condition that otherwise would not be empirically possible due to verity of limitations.

The are two major differences between the “eukaSimBioSys” and most of the available hypothesis testing tools: Firstly, the current tool captures the dynamics of a cellular function at the system level. Secondly, it’s stochastic discrete event based characteristic and its unique architectural design significantly boots the scalability and efficiency of the platform compared to its counter parts, e.g. StockSim and Gillespie. In “eukaSimBioSys” an external or internal signal initiates a cellular function. A cellular function is composed of one or more pathways which span across three networks, i.e., Transcription Regulatory Network, Signal Transduction Network, and Metabolic Network of a cell. Current tool abstracts these pathways by capturing the interaction among these networks through event entities. Each event represents a bioprocess, e.g. phosphorelytion, transcription, splicing, ligand-receptor docking, etc. Once a complex network of such events is identified, it is stored in the database along with required molecular resources entities to be utilized by the engine. Each event is associated with a biomodel which captures the temporal behavior of the target bioprocess. A biomodel captures the physicochemical behavior of a bioprocess and generates a stochastic holding time (execution time) for the associated event along with the changes to molecular resources that are being affected by this event. Each biomodel is based on a qualitative model from biology and/or biochemistry which has been supported by empirical data from wet lab experiments. I have been actively participating in modeling different bioprocesses, designing the database, and development of this project for past three years. For my dissertation I am employing “eukaSimBioSys” to conduct the in-silico experiment to identify the effect of insulin on the switch between energy sources in a human myocardial cell.

My other works include computational modeling of chromatin remodeling, the effect of genetic code on nucleosome occupancy across an organisms genome, and molecular dynamic simulation of protein-protein interactions using NAMD tool. Also, I allot a small portion of my time to collaborate with some wireless networking projects.

Research Agenda

Keeping up an inquisitive and explorative attitude, I believe, leads to a constant learning process. This approach adds to the already immense potential for innovation that exists in research. In my long-term career plan I am willing to continue practicing research in this interdisciplinary field. I would like to extend the breath of my research across network biology while getting more in-depth experience in modeling and simulation of biological systems. Engaging in the projects that involve in-silico approach for discovering new pathways, which could ultimately be applied in the drug discovery and/or lead to new therapeutic solution for the chronic disease, are to the keen of my interest. Also, along with my future projects, I would like to continue my collaboration with BioNet and further improve and extend the "eukaSimBioSys" project.

I am very interested and open to novel ideas and with the experience from my PhD I can easily adapt to an object research paradigm. As my career goal I would like to join a research laboratory with systems biology and/or computation biology discipline. I believe such collaboration not only gives me the opportunity to extend my scientific view but also enables me to share my knowledge and ideas with new colleagues whom possibly have different schools of thoughts. I enjoy teamwork and can be very productive in a collaborative effort. During my graduate studies I have always been member of different research teams where we published original results and high quality articles.

Along with research I am also enthusiastic in teaching and have the experience of teaching as instructor for two semesters and as teaching assistant for two years at UTA. I view teaching as an opportunity to remain acquainted with diverse topics in systems biology and bioinformatics.

I look into this Post Doctoral fellowship as an excellent opportunity for me to devote myself to excel in the research pursued by your lab where I can exploit my talent and skills in conducting novel research and publishing in prominent scientific journals.