THE BIOLOGICAL PHYSICIST

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In this Issue

This issue of THE BIOLOGICAL PHYSICIST invites reader participation in our TBP Reader Opinion Survey. We also take you on a visit to the biophysics laboratories at Drexel University for a conversation with Frank Ferrone, Brigita Urbanc, Luis Cruz Cruz, Jian-Min Yuan and Guoliang Yang about where interdisciplinary science is today, and where it's going in the future. And of course, all the usual suspects – PRE & PRL Highlights, job ads and DBP announcements.

– SB & CS

FEATURE

BIOPHYSICS AT DREXEL UNIVERSITY

Interview by S. Bahar

Drexel University has been expanding dramatically over recent years, engulfing more of Philadelphia and increasingly rivaling its neighbor, the University of Pennsylvania. Meanwhile, its biophysics program, based in the Department of Physics[1], has been building on its existing strengths and expanding into new areas. Says Department Head Prof. Michel Vallières, "Throughout the past years we have followed a strategic plan which calls for us to develop 4 areas of specialization: Astrophysics, Biophysics, Condensed Matter/Low Temperature Physics, and Neutrino Physics. In particular, Biophysics is well regarded on campus following the merging with [Hahnemann] Medical School. The presence of the Medical School has emphasized the importance of Bio-related Sciences on campus. These are now pursued in various departments from the Medical School and the Bioscience Department all the way through Biomedical Engineering and Physics."

THE BIOLOGICAL PHYSICIST visits with five Drexel biophysicists, Dr. Jian-Min Yuan, who has been at the university since 1978, Dr. Frank Ferrone, (since 1980), Dr. Guoliang Yang (since 2000) and Drs. Luis R. Cruz Cruz and Brigita Urbanc, who joined Drexel just last year, to talk about their current research and their take on the field as a whole.

[1] Full disclosure: your editor received her B.S. in Physics from Drexel in 1991. While she retains fond memories of her time there, she promises that all reporting in this article will be completely fair and balanced.

THE BIOLOGICAL PHYSICIST: **Describe how you became interested in biological physics? Did you begin as a "pure" physicist? What led you into a more interdisciplinary field?**

Frank Ferrone: I got into it by accident. I was post-qualifiers, looking for a project in solid state physics. Bob Shulman from Bell Labs was giving a graduate course in Biophysics, and almost everybody in the department was sitting in: faculty as well as students. My advisor asked in one of our meetings if that was something that interested me, since it seemed to him one could do a lot of the same types of measurements in biophysics as in solid state. And there it was.

Luis Cruz Cruz: As a student I started out in Condensed Matter. First, it was on optical properties of surfaces and later, for my graduate studies, in electrical and magnetic properties of polymers. The approach to both of these topics was mostly computational. It was not until I was doing my postdoc that I was faced with a choice of topics and I chose to work on biophysics, specifically in neurological diseases. The choice was natural for me since I grew up in a family of medical doctors in a health-oriented atmosphere and moreover the transition was neither lengthy nor painful since I kept applying concepts and experience in computation but now to another field of study.

I never thought of myself as belonging to either "pure" or "applied" physicists. Other than the distinction between experimentalists and not experimentalists, I always viewed myself in my work in biophysics as doing "applications of

statistical physics" to biology. But I did not feel allegiance to particular camps or subgroups and saw my interdisciplinary work as an "opportunity" to apply my knowledge to other fields.

Brigita Urbanc: I was raised as a typical physicist who got interested in astrophysics and quantum physics as a teenager but ended up as a theoretical physicist working on Landau-Ginsburg theory of ferroelectric liquid crystals at the University of Ljubljana, Slovenia. After graduation I came to Boston University as a post-doctoral fellow to work in the group of Dr. Gene Stanley. Consequently, I moved away from black-and-white, pen paper calculations into a colorful computational physics. Dr. Brad Hyman from Harvard Medical School knew of Gene's prior work on diffusion-limited aggregation models and suggested that we find a growth model of senile plaque relevant to Alzheimer's disease that would be able to account for a specific porous nature of senile plaques, Subsequently, this was resolved for the first time in his lab using state-of-the-art confocal microscopy. This was simultaneously challenging and rewarding work that got me into the Alzheimer's disease research [1].

Ever since I can recall, I was curious about different diseases and how the human body was affected by them. However, not until recently when my research focused on proteins associated with neurological disorders, their structure and function at atomic resolution, did I realize how profoundly protein structure, and, by implication, living organisms, are affected by basic principles of quantum mechanics.

Guoliang Yang: My Ph.D. research was in condensed matter physics. I got into the field of biophysics at the beginning of my postdoctoral work. As I was finishing my Ph.D. in the early 1990s, there seemed to be too many graduates in condensed matter physics and the prospect of the job market was discouraging. With my research advisor's suggestion, I was looking for opportunities in other areas, that were both interesting to me and compatible with my graduate research experience, for my postdoc training. During that time, Professor Carlos Bustamante (at the University of Oregon then) gave a seminar in our Department on his work of using AFM for studying biological macromolecules. I found the work very fascinating. I applied for, and was offered, a postdoctoral research position in his lab. It was difficult in the beginning since I had to learn the terminology and many basics of biology and biochemistry while carrying out experiments. After sometime, it became a rewarding experience, and I have been doing research in biophysics since then.

Jian-Min Yuan: As an undergraduate I did take courses in biochemistry, organic chemistry, and even botany. After working in the fields of molecular reaction dynamics, radiation-molecule interactions, and nonlinear physics for years, I became interested in biological physics, mainly because problems in biological physics are not only important because of their fundamental nature and also because of their strong connections to medicine. I was also encouraged by the fact that a more rigorous and quantitative approach to biology is in demand.

Describe your current research, and where you see your work going over the next decade.

Frank Ferrone: I see broadening of my research work on self assembly that has been honed on sickle cell disease. We have the best description of the kinetics of an assembly reaction anywhere: a single parameter theory that accurately describes reactions over 12 orders of magnitude is not too shabby! And accurately includes molecular crowding kinetics too. I'm looking forward to adapting this to other assembly diseases. In addition I see us becoming more involved in cellular level therapies for sickle cell disease.

Luis Cruz Cruz: My current research involves mainly applications to two branches of neuroscience. First, I am studying the loss of spatial

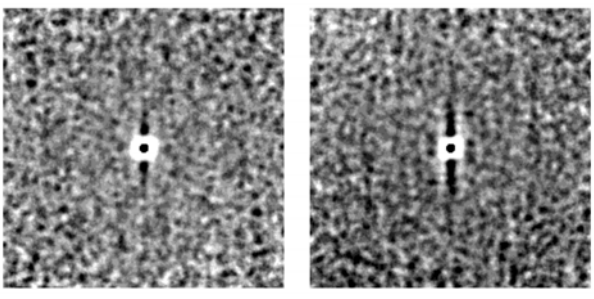

Figure 1. Density maps of cortical microcolumns.

organization of neurons in the aged brain using density maps, and in the other I am studying the folding of the Alzheimer amyloid β-protein using all-atom molecular dynamics.

More specifically, in the first topic I am interested in studying the correlations between the spatial organization of neuronal cells and cognitive decline in normal aging. In the late 1980s the prevalent theory for cognitive decline in normal aging was the loss of neurons in the brain. However, this theory has been unsubstantiated, leaving us with the challenge of finding a mechanism that while maintaining a constant number of neurons with age, can predict a cause for the cognitive decline. My current working hypothesis is that loss of organization in the spatial locations of neurons is

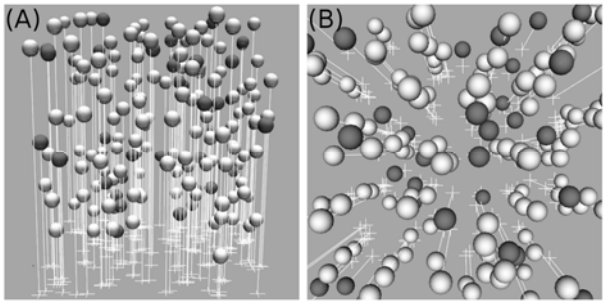

Figure 2. Model of microcolumnar configuration.

linked to the loss of cognitive abilities, and that studying the nature of this decay in organization will lead to the real culprit in the cognitive decline.

In addressing this hypothesis, one of the early studies in which I was involved indicated that neurons that once formed strong microcolumns ("vertical" organizations of neurons grouped into columnar arrangements that span all cortical layers and may act as a unit) do not form such a well-defined structure in Alzheimer's disease [2]. This was determined by using a novel approach called the density map method. I was involved in the initial developments in [2] and later expansions of this method in [3].

My colleagues and I have quantified microcolumns in the cortex of rhesus monkeys using brain samples provided by the Boston University School of Medicine and the Yerkes National Primate Research Center at Emory University in Atlanta. We showed that specific microcolumns can be characterized by quantities that we defined as "measures of microcolumnarity" [3]. These measures quantify, for example, the most apparent difference between the two density maps of cortical tissue shown in Figure 1, that the length of the central ridge is shorter for area 46 than for area TE (two important areas in higher order cognition), thus accurately indicating that microcolumns themselves have a longer effective length. Related to Alzheimer's disease in humans, this particular property of microcolumns, their length, was shown by our group to be the one that was mostly impaired in Alzheimer patients [2]. In more recent work [4] we found that, unlike in Alzheimer's disease, not the length, but rather the *strength* of microcolumnarity, one of the measures of microcolumnarity that quantifies the number of neurons belonging to a microcolumn relative to the average neuronal density, changes in the rhesus monkey brain during normal aging. In this same work we proposed a mechanism for the observed decrease in microcolumnar strength. Specifically, we proposed that neurons in rhesus monkey brains that lined up in orderly fashion, one above the other in these microcolumns, slightly fall out of place (subtle displacements) as the animals age. In addition, the amount of this "disorganization" correlates with experimental results on declining cognitive performance on rhesus monkeys [5]. Our work has shown that displacements of as little as one neuronal diameter (about 10 microns) are enough to completely disrupt the microcolumn's vertical organization [3]. This hypothesis was formulated using computer simulations (first developed in [6]) where neuronal positions from real tissue were slightly randomized and the strength of microcolumnarity was obtained as a function of total neuronal displacement.

The studies described above can be very good indicators of what are the real causative anatomical changes that are reflected in the loss of neuronal organization, such as atrophy of synapses and dendrites. To this end, I am currently designing computer models that reconstruct the three-dimensional positions of neurons in the brain using as input previously published microcolumnar measures available from our density map calculations. An example configuration is shown in Figure 2, where a model was built using only the

x,y experimentally-determined positions of neurons from Nissl thin sections from [3]. The method to build this three-dimensional reconstruction is presented in [7].

One of my immediate goals is to apply this three-dimensional model to understand changes in neuronal organization from control and aged brains. Comparison between these two age groups can lead to hypothesis formulation on the effects of normal aging on microcolumns in the brain. To this end, I have started computer simulations where the neurons in the model are the simple components of this complex system that can undergo simple "random walk" displacements and interact between each other as hard balls [8]. The experimental goal of this part of the project is that my results will be mapped from the computer model to real anatomical changes available from my collaborators using filled cells and sequential tangential sections from thick block sections of brain samples. Preliminary results show that age-related neuronal displacements parallel to the surface of the brain, rather than parallel to the microcolumnar axis, are consistent with the microcolumnar disruptions observed in our previous work. When applied to real brain anatomy, these results postulate the hypothesis that peripheral dendrites, rather than apical ones, are more likely to undergo atrophy or retraction as a function of age.

Another important goal in this project is to use the three-dimensional model to understand neuronal organization in brains of patients with neurological disorders. The flexibility of the model allows for studies of changes in the 3D locations of neurons in the brain as a function of the pathological variables, such as plaque burden and severity of disease in Alzheimer's disease.

In the second topic, I am interested in understanding the initial stages of folding of the amyloid β-protein. The importance of this research lies in the evidence provided by experiments that the folding and aggregation of the amyloid β-protein into oligomers is a key pathogenic event in Alzheimer's disease. Understanding how the folding happens at an early stage may be crucial to inhibiting the pathologic forms of the aggregated amyloid β and could be effective in the prevention and treatment of Alzheimer's disease [9-10].

Using all-atom molecular dynamics simulations in various types of explicit solvent, I studied the dynamics of folding of a decapeptide segment of the amyloid β (from amino acid 21 to 30 only) [11]. This decapeptide has been shown experimentally to nucleate the folding process of the larger amyloid β. I also studied the decapeptide with an amino acid substitution linked to a hereditary type (Dutch) of Alzheimer's disease. The solvents I used were pure water at normal density, pure water at reduced density, and normal water with salt ions.

The results of this study show that hydrophobic interactions and internal salt bridges between some of the amino acids drive the formation of a loop configuration--also present in experiments. In Figure 3, I show a snapshot from a simulation where the hydrophobic collapse between the Val and Lys amino acids is being assisted by a salt bridge between amino acids Asp and Lys. A similar situation occurs where a salt bridge between amino acids Glu and Lys forms and assists the hydrophobic collapse. Although these two salt bridges occur with less frequency than the hydrophobic collapse, they assist in the overall formation of the loop of this decapeptide. In the figure we can see that there is a very well defined loop between amino acids Val and Lys while both ends of the chain are able to move more freely, although not enough to destabilize the loop.

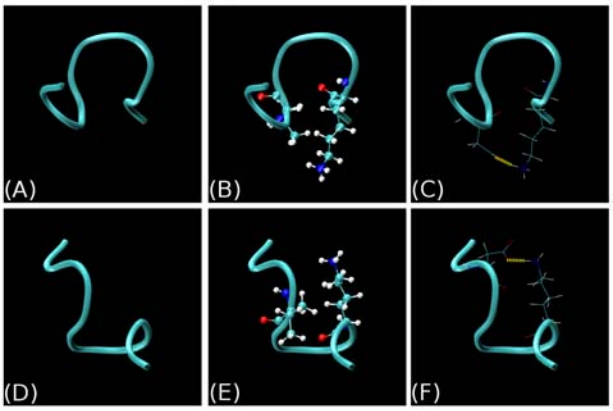

Figure 3. Simulation of hydrophobic collapse.

In addition, these simulations show that salt ions dissolved in the solvent water enhance the stability of the loop, while solvent water with a reduced density (negative pressure system) induces the

formation of a helix, as may be expected from environments with less water, such as cell membranes, plasma, and cerebrospinal fluid. Also, simulations of the peptide with the Dutch mutation in water, in contrast to the wild-type peptide, fail to form a long-lived Val-Lys (hydrophobic) loop, suggesting that loop stability is a critical factor in determining whether Aβ folds into pathologic structures.

Because the loop conformation found in my studies, as well as the one also found in the full length amyloid β, are implicated in the initial stages of folding, my studies indicate the detrimental importance of mutations, while factors such as changing the solvent environment may prove to be of importance in preventing the pathologic folding from occurring in the first place.

My current goal in this project is to analyze the stable configuration of this decapeptide using other force fields. Up to now I have used the CHARMM-27 force field with the facilities of the NAMD 2.0 program and now I am extending these calculations to use the OPLS/AA force field with the GROMACS package. Preliminary results indicate that the decapeptide using the OPLS/AA force field, in contrast to the CHARMM force field, can develop a metastable β-hairpin conformation. This is an important result because the development of secondary structure such as this would reduce the exposure of the decapeptide to water, thus precluding the formation of larger sized conglomerates of many peptides known to be detrimental to neurons in tissue.

In future studies, I will consider additional genetic mutations of this decapeptide (Arctic and Iowa) which are also linked to stronger and/or earlier versions of Alzheimer's disease. By studying these mutations, the complex behavior of this system can systematically be characterized, and the behavior of the folding understood in the hopes of finding agents that may prevent or alter the ultimate pathological folding of the amyloid β-protein.

Brigita Urbanc: I am currently interested in folding and early assembly of proteins associated with Alzheimer's and Parkinson's diseases. The core method of my current research is discrete molecular dynamics combined with a hierarchy of protein models of various complexities [12] that are able to capture biologically significant processes and yield structural information [13-15] beyond the current experimental reach [10]. Aβ normally exists in the human body in two alloforms, Aβ40 and Aβ42. Even though the difference in the amino acid sequence is only 2 amino acids (only 5% difference in the sequence), the longer alloform, Aβ42, is more associated with significantly higher toxicity and is genetically implicated in the disease. Currently, substantial *in vitro* and *in vivo* evidence demonstrates that small Aβ42 assemblies are the initial triggers of the disease. Fig. 4 demonstrates a degree of structural resolution exposed by the discrete molecular dynamics approach by showing an *in silico* assembly of 5 Aβ42 chains, which is presumably associated with the highest toxicity in the Alzheimer's disease brain.

Misfolding and self-assembly of proteins into nanoassemblies of different sizes and morphologies is a common theme unifying a number of human pathologies termed protein misfolding diseases. These include Alzheimer's, Parkinson's, Huntington's, Creutzfeld-Jacob disease, amyotrophic lateral sclerosis, and others. Alzheimer's disease happens to be the most prevalent form of dementia in the elderly and it is not (despite popular belief) a normal part of aging, but rather a

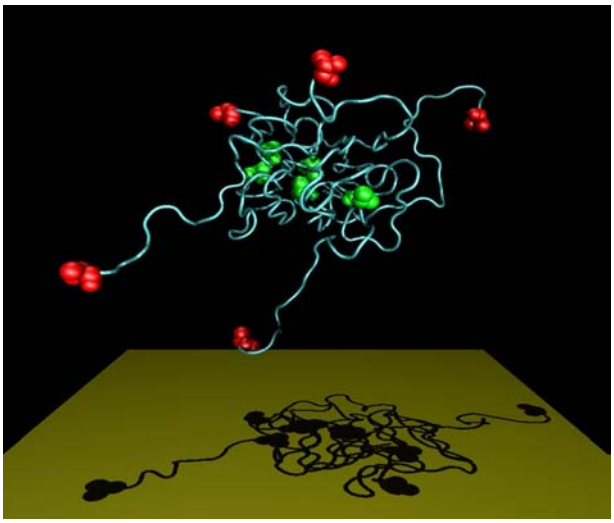

Figure 4. A pentamer of Aβ42 obtained by discrete molecular dynamics simulations. The red sphere mark the N-terminal amino acids (D1) and the green spheres represent the most hydrophobic C-terminal amino acids (I41) which are within the core of the assembly.

progressive and fatal disease (the seventh leading cause of death in the USA) without any existing cure.

The question of where my research will end up in the next decade is the most challenging of all your questions. Research may be predictable on a time scale of a year or two. However, beyond a couple of years from now, the research orientation strongly depends on the breakthroughs of my and other groups working on similar problems. The best thing about research is the fact that it is unpredictable and thus exciting. My short-term goals are to: (A) evolve and spread the computational methodology I am applying to other labs; (B) evolve the computational approach to a level at which we can simulate not only proteins but also the cell membrane and other components present *in vivo* and thereby move towards more disease-relevant conditions; (C) explore experimental methods such as photo-induced cross-linking of unmodified proteins that was brought into Aβ research by Gal Bitan and David B. Teplow [16], my collaborators from UCLA, and that gives *in vitro* information directly comparable to computer-generated results.

Besides these major topics, I am also involved in research on aging in collaboration with Dr. Luis Cruz, where we use image analysis including automated neuron recognition to map all the neurons in specific cortical areas relevant to aging and quantify spatial correlations between neuronal positions [17]. This methodology, I hope, will evolve within the next decade to include not only neurons but also glial cells and their spatial relationship to neurons.

Guoliang Yang: My lab is focused on the study of mechanical force-induced protein unfolding and refolding using AFM-based single molecule manipulation methods. We characterize the properties of the free energy landscape of protein molecules and investigate their mechanical stability and functions. In addition, we also make efforts to improve the single molecule technique in broadening the scope of measurements and optimizing data acquisition and analysis. In the next decade, I would like to see that several types of proteins, representative of different folds, sizes and functions, will be characterized by the single molecule technique. Such results will be complementary to bulk measurements and provide new insights into the protein folding mechanisms, as well as help to establish the single molecule approach as a widely accepted method for protein folding and other macromolecular studies.

Jian-Min Yuan: We are working on several fundamental problems related to the structure changes and aggregation properties of proteins, stimulated by their relation to neurodegenerative diseases. In one project, statistical mechanical methods, such as partition functions, transfer matrices, and master equations, are being applied to study phase transitions in proteins. Here, conformational changes, such as helix-sheet transitions in proteins, are treated using methodology of phase transitions. In another project, we study the aggregation properties of intrinsically disordered peptides, for example, (AAKA)4, experimentally investigated in the lab of Reinhard Schweitzer-Stenner of the Chemistry Department at Drexel. We are also interested in the effects of macromolecular crowding on protein stability and aggregation. Numerical simulations are being done in parallel to the experimental work of Guoliang Yang's lab in our department. Using atomic force microscopy, they measure directly the force required to unfold a protein as a function of the crowder concentration. On the other hand, we have also studied the systems dynamical behavior of signaling pathways related to cancer and diabetes using non-equilibrium thermodynamics, control strategy, and sensitivity analysis. The latter, for example, can be used to rank the kinases and phosphatases in the pathways for their potentials to be drug targets.

At the present time, we are far from understanding clearly the mechanisms of aggregation and different aspects of crowding effects. As these fields progress in the next decade, we expect to gain better understanding of these processes using both experimental and theoretical means.

How long has there been a biological physics (biophysics?) program at Drexel? How did the program of interdisciplinary research at Drexel originate? Describe how the program has evolved and changed over the years.

Frank Ferrone: Drexel has had biophysics faculty since the mid 70s, which makes it one of the older traditions in the country, I'd wager. This history has made it more the norm than a hybrid discipline. Is astrophysics an amalgam of astronomy and physics? Is solid state physics a merger of materials science and physics? Once it is accepted, the course structure can be adapted around it. So we offer our first and second years survey courses in all our topical disciplines. Additional learning can occur later, but that is again not limited to biophysics. In short, it's mainstream here.

Are there interdisciplinary courses now offered for grad students or undergraduates, or do most students do their interdisciplinary learning "on the job"?

Brigita Urbanc: There are currently two courses, Biophysics and Computational Biophysics, which are geared towards both undergraduate and graduate students. These are interdisciplinary courses because they involve knowledge of physics, biology, chemistry, and computer science.

Guoliang Yang: In addition to the biophysics and computational biophysics courses, I have been teaching a course "Single Molecule Methods in Biophysics", for graduate and upper level undergraduate students. The course covers the instrumentation, physical principles and the biophysical applications of the most commonly used single molecule techniques, including atomic force microscopy, laser tweezers and single molecule fluorescent spectroscopy.

Drexel has expanded so dramatically over the past few years, acquiring a medical school (Hahnemann) among other new developments. Has the expansion of Drexel significantly changed the research atmosphere for you? Is there much collaboration between your groups and clinicians at Hahnemann?

Frank Ferrone: The expanded atmosphere has been great, but ironically, it is the engineering college rather than medical school that is making the most direct impact. There are people we now collaborate with, or plan to, in Mechanical Engineering and Mechanics, Biomed, and Materials Science and Engineering. There are people in Chemical and Biological Engineering doing molecular dynamics simulations of biomolecules! Thus, in addition to the folks in the College of Medicine, who have added immensely, we find a young talented core of engineers who also find the bio realm to be easily within the scope of their endeavors.

What do you see as the most dramatic changes in interdisciplinary science over the past few years? What do you see as major new trends?

Frank Ferrone: Interdisciplinary science has become mainstream, and that is tremendously healthy. In the old days, if I gave a talk to a physics audience I'd either have to start with some apology (or joke about a spherical chicken, or something) as to why physicists should be listening to this, followed by a few well-worn slides on what a protein was. Today it's expected that one hears the talks, and knows the background. The newest "practical" frontier is the the use of physics ideas in finance. But the most dramatic change is perhaps in the mindset of modern scientists: there is no "attitude" about the purity of the science, or appropriateness of the area. Students have a chance to take lots of courses in a broad variety of subjects today. Moreover, so far as biophysics is concerned, look at any modern "standard" biology book: it's all molecular.

Luis Cruz Cruz: I have seen a large influx from researchers working in the more "traditional" fields to biology and health-related fields. This could possibly be because of the trend that funding has followed in the last decade or so, but also could be due to my biased sampling since I am more in contact with biophysics in general. But either way, this trend is strong and growing.

Brigita Urbanc: Interdisciplinarity came as a consequence of new research interest in the brain and its function. Due to its intrinsic complexity, studies of the brain started to involve researchers from very different backgrounds: mathematics, physics, biology, chemistry and engineering. Research on proteins associated with neurological diseases, such as Alzheimer's and Parkinson's disease, represents such an interdisciplinary scientific field. As the neurological diseases associated with protein misfolding and abnormal

assembly are triggered by age-induced mechanisms, and as the life expectancy in developed countries increases, the quality of life becomes more of an issue and the societal pressure to find a cure provides a positive feedback on the research.

Concurrent with the interest in brain functioning and the societal pressure to find cures for various age-induced diseases, there was a paradigm shift in the way young physicists were raised and in the way more mature physicists identified the key physics questions worth pursuing. I believe a critical mass of physicists moved away from the perception of pure physics being the only honorable topic that a "real" physicist should be concerned with. For example, 15 years ago I do not recall any other physicist working on Alzheimer's disease research. In fact, I heard a fellow physicist whom I respect (not for the following comment, to be clear) that no decent physicist would wish to dirty her/his hands with such a non-physics topic. I attended the Biophysical Society meeting in spring 2009, that is, 15 years later, and I could not believe the amount of physicists concerned with questions related to proteins, membranes, detection of early protein assemblies in the brain, etc. I hope we are moving towards a new research era, in which the only qualifier will be based on the quality of provided evidence resulting in either good or bad science. That is all that really matters.

Jian-Min Yuan: Many important and urgent problems of present days are interdisciplinary in nature. This has promoted collaborations among scientists of different disciplines and will certainly impact upon what students should learn and courses that we should offer.

Guoliang Yang: The research community has become much more enthusiastic about research projects spanning several scientific disciplines, owing to the realization that many scientific problems, especially in biology, are so complicated that solving these problems necessitates the concerted effort of researchers from all related fields. As knowledge is accumulated at an increasing pace and accessibility becomes easier, it is a challenging task for researchers with different backgrounds to comprehend each other efficiently. A major trend will be that researchers [from various disciplines] working on solving the same problems get more familiar with each other's language and techniques, such that information can be used more effectively to understand the complexity of a problem, and to develop novel strategies to solve the problem.

As interdisciplinary science has become more "popular" of the past couple of decades, have you seen a shift in the number of graduate students wanting to pursue studies in biophysics? In the number of undergraduates expressing interest?

Frank Ferrone: Hard to say. The swirling trends of overall graduate enrollment, international students, etc., makes for a very noisy baseline.

Luis Cruz Cruz: From a limited perspective, I have not seen a big shift in the number of students wanting to "migrate" to more interdisciplinary sciences. Many physics students want to work on the more traditional fields. However, there is a sense of "acceptance" among physicists that biophysics is important and growing, and that our skills and knowledge are required to pursue progress in other important fields. Perhaps the shift is happening in steps, with the first step being the growth of research that encompasses interdisciplinary science which in turn drives student migration towards next-generation, interdisciplinary research in these new topic areas.

Brigita Urbanc: I met a couple of graduate students who really wished to focus on biophysics of proteins and membranes, but these are still not that common. Overall, the students seem to be more flexible and open to pursue research in various areas of biophysics.

There has been some argument about whether there is a difference between biophysics and biological physics. Do you see a distinction, or do you see this debate as purely semantic?

Frank Ferrone: Is it condensed matter physics or solid state physics? Particle physics or high energy physics? The titles try to emphasize certain features, but the emphasis varies with the audience. "Biological physics" emphasizes the physics roots of the discipline, but most people prefer the short

form. Do we hear of astronomical physics? Hmm. Our department refers to the "astro" group or the "bio" group.

Luis Cruz Cruz: I do not see a real difference between these two classifiers. However, this could be because of my lack of sense of "belonging" to particular groups. Regardless of the label assigned to me at any particular time, I hope to apply my knowledge and experience to the scientific problem at hand.

Guoliang Yang: I do see making such a distinction as purely semantic. The application of well-known physics concepts, theories and experimental methods to solve a biological problem, and the establishment of a physical model to describe a particular biological system, are often interwoven.

Brigita Urbanc: If there is a difference, it is meaningless to me: the scientific knowledge should have no boundaries imposed by scientific disciplines or discipline names. If I am allowed to be a bit sarcastic, I believe that the distinction might have been made between physicists who perceived themselves to be brilliant enough to only spread their pure physics knowledge into biology (without any effort to understand what might be relevant to biology or not) and those who found that the knowledge of pure physics was insufficient, therefore they needed to expand their knowledge-base by learning biology, chemistry, neuroscience, and other "dirty" topics. Clearly belonging to the latter group, not to sound offensive to anyone, I would like to encourage the reader to look into the recent theory of why modern humans survived, while Neanderthals, who co-existed with modern humans and are believed to have been just as intelligent as modern humans, did not. Apparently, Neanderthals, as exclusive carnivores, ate only very specific foods that eventually were depleted, while modern humans were more flexible and ate whatever was available.

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ELECTIONS IN OCTOBER!

DBP elections will be held in October. Nominations for Members at Large and Vice Chair can be sent to James Glazier, Chair, Nominating Committee at glazier@indiana.edu

DBP ANNOUNCEMENT

New 2009 American Physical Society/Division of Biological Physics Award for Outstanding Doctoral Thesis Research in Biological Physics

Description: Biological Physics is one of the most rapidly growing, exciting and interdisciplinary branches of contemporary physics. To encourage the healthy development of this field, the Division of Biological Physics has established an annual award for Outstanding Doctoral Thesis Research in any area of experimental, computational, engineering, or theoretical Biological Physics. The award consists of $1,500, a certificate citing the contribution made by the Awardee, and a travel allowance and fee waiver to attend the subsequent March meeting and to present an invited talk. The two runners-up will receive certificates of merit.

Rules & Eligibility: Doctoral students at any university in the USA or abroad who have passed their thesis defense for the Ph.D. in any areas of experimental, computational, engineering, or theoretical Biological Physics, broadly construed, any time from October 1st 2008-September 30th 2009 are eligible. The applicant, advisor and degree awarded may be in any appropriate related area, including, Physics, Biomedical Engineering, Applied Mathematics, Applied Physics or Biological Physics, Biophysics, Biology, Mathematics, Biochemistry, Chemistry or Chemical Engineering.

Nomination: Nominations by the thesis advisor or supervisor must be received by the Chair of the 2009 Biological Physics Thesis Award prior to **October 5th, 2009**. Nominations **must** be submitted as a single PDF file to the Chair of the Selection Committee in an e-mail attachment.

The nomination package consists of the following materials:

1. A letter from the thesis advisor citing the specific contributions of the nominee and the significance of those contributions.
2. A letter from the department chair and/or relevant program director certifying the date of the thesis defense.
3. Two letters seconding the nomination.
4. A manuscript prepared by the nominee describing the thesis research; the manuscript may not exceed 1,500 words (excluding figures and references).
5. An abstract prepared by the nominee suitable for publication in the Bulletin of the American Physical Society; the abstract may not exceed 1,300 characters. The name of the thesis supervisor and the institution should be indicated in a footnote.
6. A full curriculum vitae of the nominee including a publication list.

Nominators and seconding letter-writers may only submit one letter per year.

Send Nominations to: Prof. James A. Glazier, Indiana University, Biocomplexity Institute and Department of Physics. **E-mail: glazier@indiana.edu**.
Visit http://www.aps.org/programs/honors/dissertation/biological.cfm for more information.

DBP ANNOUNCEMENT

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JOB AD

Postdoctoral Fellowship

at the

University of California San Diego &
University of Chicago
in

Computational and Experimental Neuroscience

Professors Henry Abarbanel at UCSD/CTBP and Daniel Margoliash at the University of Chicago seek to hire two postdoctoral fellows in computational and experimental neuroscience for three year terms beginning in Fall, 2009/Winter, 2010.

One position will be located primarily at the University of Chicago within the Margoliash laboratory. The principal effort will be to describe the dynamics of different classes of neurons recorded in brain slice and in vivo in the avian song system. Prior experience conducting intracellular recordings is essential. The postdoctoral fellow located at Chicago will make regular visits to UCSD to work with other members of the collaboration on the development and use of advanced nonlinear dynamical approaches for the analysis of these data. She/he will also participate in "lab meetings" across the two campuses on a frequent basis.

The other position will be primarily located at UCSD within the Center for Theoretical Biological Physics/Institute for Nonlinear Science and will involve the development, numerical exploration, and use of advanced nonlinear dynamical approaches for the analysis of the data collected in Chicago. The postdoctoral fellow located at UCSD will make regular visits to Chicago to work with other members of the collaboration. She/he will also participate in "lab meetings" across the two campuses on a frequent basis.

A goal of the collaborative effort is to identify from experiment and nonlinear dynamical analysis realistic models of neurons in the avian song system, in particular in the adult song production pathway (HVC and RA and brainstem nuclei). Modeling will initially be in software, but transition to hardware implementations is possible. Computations, especially on models of the functional networks of these birdsong nuclei, will be done on local Linux clusters as well as massively parallel machines at the Argonne National Laboratory. There is significant opportunity, then, for advanced scientific computing skills as well.

Please apply directly to:

habarbanel@ucsd.edu OR dan@bigbird.uchicago.edu

Include a statement of your research interests, two letters of recommendation and a CV with bibliography.

JOB AD

The Bruno H. Zimm Biological Physics Postdoctoral Fellowship

The Center for Theoretical Biological Physics (CTBP) at the University of California, San Diego invites applications for the Bruno H. Zimm Postdoctoral Fellowship

Applications are due October 15, 2009

For additional information and application instructions, visit:

http://ctbp.ucsd.edu/zimm_fellowship.html

CTBP is a consortium of researchers from UCSD, the Salk Institute for Biological Studies, and the University of Michigan, involved in research on fundamental problems at the interface between physics and biology. Research encompasses three synergy themes – ***Cellular Tectonics***, the dynamic mesoscale structure of the intracellular milieu; ***Computational Approaches to Intracellular and Intercellular Communication,*** chemical-based reaction-diffusion governed communication across complex spaces; and ***Gene Regulatory Networks***, genetic/signaling networks that exhibit specificity and robustness in the face of intrinsic stochasticity, and yet retain evolvability. The Zimm fellowship is for recent graduates who have demonstrated exceptional research aptitude and are interested in pursuing more independent, semi-autonomous research than is available in a traditional postdoctoral position. Zimm fellows will be expected to pursue intensive research in any area of biological physics related to the CTBP research synergies.

CTBP Faculty include:

Henry Abarbanel, Physics, UCSD
Olga Dudko, Physics, UCSD
Terence Hwa, Physics, UCSD
Bo Li, Mathematics, UCSD
José Onuchic, Physics, UCSD
Terence Sejnowski, Salk Institute
Wei Wang, Chemistry, UCSD
Charles L. Brooks, III, U Michigan
Michael Holst, Mathematics, UCSD
Herbert Levine, Physics, UCSD
J. Andrew McCammon, Chemistry, UCSD
Wouter-Jan Rappel, Physics, UCSD
Tatyana Sharpee, Salk Institute

For more information contact Christopher Smith, PhD., CTBP, Department of Physics, 9500 Gilman Drive, MC0374, University of California, San Diego, CA 92093, csmith@ctbp.ucsd.edu (858) 534-8370

CTBP** is a Physics Frontiers Center of the **National Science Foundation

JOB AD

Software Developer/Research Associate/Post Doctoral Fellow

The Indiana University Biocomplexity Institute seeks a Research Associate or Post Doctoral Fellow to participate in research on the development and improvement of the Tissue Simulation Environment (www.compucell3d.org). Rank is commensurate with experience. There is a possibility that two positions will be filled.

Preferred skills and abilities include extensive experience in C++, Python, user interface design and implementation. Candidate should be able to interact with users and help prepare training workshops, and should be able to work in a small team environment with limited supervision. Position will offer opportunities to collaborate on new research projects and participate in publications with Biocomplexity Institute scientists. Areas of interest include Monte Carlo methods, statistical mechanics, fluid dynamics, partial differential equations, mathematical modeling of biological systems, computer graphics visualization, and scientific software development.

Skills in numerical modeling and parallel programming are required. Graphics and visualization programming are a plus, as is having a strong (Masters or Ph.D.) scientific background. Technical writing and documentation experience also preferred. Review of applicants will begin immediately and continue until position is filled. Initial appointment will begin as early as September 1st, 2009, and is expected to last one year with extension possible, subject to satisfactory performance. Please send a CV and arrange to have 3 letters of recommendation sent to Prof. James Glazier (glazier@indiana.edu) with subject heading: CC3D JOB 09

Department of Physics
Biocomplexity Institute
Simon Hall MSB1, 047G
212 S. Hawthorne Drive

Indiana University is an equal opportunity / affirmative action employer.

JOB AD

Faculty Position in Computational Biophysics

Wake Forest University invites applications for a tenure track faculty position at the level of Assistant Professor with a joint appointment in the Departments of Computer Science and Physics to begin in the fall semester of 2010. Applicants should have completed a PhD in an appropriate field by the time of appointment. Wake Forest University is a highly ranked, private university with about 4500 undergraduates, 750 graduate students, and 1700 students in the professional schools of medicine, law, divinity and business. The Physics Department has a major concentration in biophysics with approximately one third of the departmental faculty working in that field. Several computer science faculty are actively engaged in scientific computing, computational systems biology, biological modeling and bioinformatics. Interdisciplinary research is highly valued and encouraged by the departments and University.

The successful candidate will have a strong research record in computational biophysics. The candidate should also have demonstrated ability to teach courses relating to topics in physics, biophysics, or computer science. The successful candidate will be expected to teach in both departments at the undergraduate and graduate levels. Excellence in research, teaching, and obtaining external funding will be expected.

Applicants should send a copy of their CV, statements regarding their research interests and teaching philosophy, and the names of three references to the

Computational Biophysics Search Committee,
Box 7507,
Wake Forest University, Winston-Salem,
NC 27109-7507.

Application materials can be sent electronically in the form of a single PDF document to physcscrecruit@lists.wfu.edu. Review of applications will begin November 1, 2009 and will continue through January 15, 2010.

Wake Forest University is an equal opportunity/affirmative action employer.