1058-Pos Board B844
Far Field Fluorescence and AFM Superposition with 10nm Special Resolution
Jeffery Hodges, Anil Ghimire, Jordan Gerton, Saveez Saffarian.
University of Utah, Salt Lake City, UT, USA.
We have developed a technique which allows us to determine the location of a fluorescent signal to within 10nm accuracy within a topological scan created by AFM. Imaging topological markers that are both fluorescent and resolvable in an AFM scan, we can triangulate the fluorescence of these markers in conjunction with the fluorescence and topology of a sample to within 10nm accuracy. Here we show data from this method in air as well as wet buffers which are ideal for biological sample measurements. This technique will facilitate localization of fluorescent molecules within asymmetric diffraction limited biological samples.

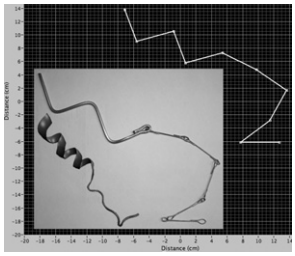
1059-Pos Board B845
Quantitative Imaging of Electron Transfer Flavoprotein Autofluorescence Reveals Lipid Partitioning Dynamics in Pancreatic Islets
Alan K. Lam[1,2], Svetlana M. Altamentova[2], Jonathan V. Rocheleau[1,2].
[1]IBBME, University of Toronto, Toronto, ON, Canada, [2]TGRI, University Health Network, Toronto, ON, Canada.
Pancreatic islet beta-cells are sensitive to plasma nutrients in the body. Excess levels of glucose and fatty acids lead to glucolipotoxicity, resulting in declined beta-cell function and survival - a major component of type 2 diabetes mellitus (T2DM). Despite significant knowledge of glucose-stimulated insulin secretion, the effect of fatty acids remains uncertain. Here we show a novel way to measure a response from fatty acids in *ex vivo* pancreatic islets using quantitative autofluorescence imaging of a Complex II flavin, electron transfer flavoprotein (ETF). Together with two-photon imaging of NAD(P)H and our previously reported lipoamide dehydrogenase (LipDH) autofluorescence, we found that the electron transport chain is nutrient supply-driven and dominated by Complex I rather than Complex II. These data are consistent with beta-cells being predominantly glucose responsive. Furthermore, we found an oxidized ETF redox response in the presence of excess glucose-stimulation, suggesting a shift in lipid partitioning from fatty acid oxidization to synthesis above 10 mM glucose. Our results demonstrate that ETF autofluorescence can in part be used as readout of islet response to fat. Overall, we anticipate our ETF imaging platform to be a starting point for more sophisticated biological studies that will explore mechanisms of mitochondrial dysfunction in T2DM.

Biophysics Education

1060-Pos Board B846
Membranes, Ions, and Signals: An Integrated, Multimedia, Biophysics Module for First-Year Medical Students
Daniel Gardner, Olaf S. Andersen, Lonny R. Levin.
Weill Cornell Medical College, New York, NY, USA.
First-year medical students, unlike typical graduate students, include many non-science majors with varying prior exposure to mathematics or physical sciences. To provide a common substrate for medical education that acknowledged these disparate backgrounds, an introductory Molecules to Cells course was designed in 1996 by D.G., O.S.A., and colleagues. Now Molecules, Genes, and Cells (MGC), this spans protein structure, lipids, cellular genetics, metabolic biochemistry, cell division, and more.
We now report design and implementation of a Membranes, Ions, and Signals (MIS) module for MGC, covering cellular biophysics, physiology, and pharmacology. Building on membrane lipid structure and function, MIS incorporates:
• plasma membrane and compartments
• properties of those compartments important to electrochemistry, signaling, and biophysics,
• structure and function of membrane channels, transporters and receptors
• electrophysiology of excitable tissue
• signals and information: synaptic, cellular, cytoplasmic, and nuclear
• signals in disease contexts
• signals into actions: structure and function of skeletal and smooth muscle
This material is both essential and conceptually difficult, and MIS is designed to offer students an optimal sequence, schedule, and presentation forms and formats to aid understanding. As an integrated module, MIS relates these topics and makes them relevant to contemporary work and translational promise. Staffing is interdepartmental, via Physiology & Biophysics, Pharmacology, Biochemistry, and Cardiology. MD-PhD students take the course and module in their first year, then participate as journal club instructors. A signals-and-channels computer lab incorporates material from Richardson and Richardson (1992), Brandon and Tooze (1999), and R. Bookman (U.Miami) for in-class instruction utilizing 40 workstations for ~100 students.
Introduced in Fall, 2010, student evaluation of the material and integration was highly positive; currently (Fall 2011) textual and graphic material is being delivered to students via iPad.

1061-Pos Board B847
Math Preparation of Undergraduates in General Chemistry, a Gatekeeper Course Required for Biophysicists
Cynthia A. Stanich, Colleen F. Craig, Sarah L. Keller.
University of Washington, Seattle, WA, USA.
Gatekeeper courses for undergraduates wishing to pursue careers in biophysics and other STEM fields include introductory chemistry, physics, and biology. At the University of Washington, as at many other peer institutions, a high level of math is required for enrollment in main sequence General Chemistry. Specifically, students must have fulfilled a calculus requirement or be co-enrolled in calculus. Moreover, the average high school GPA of freshmen entering directly from high school is 3.7. Nevertheless, we find that significant fractions of students enrolled in General Chemistry are unable to complete problems in which they are asked to manipulate exponents (~20%), logarithms (~40-50%), or probabilities (~40%). Researchers at University of Minnesota have documented similar results [Leopold and Edgar, 2008, Chemical Education Research 85:724]. We find that some math deficiencies among undergraduates persist into the senior year, at least for biochemistry majors. Here we track undergraduate math competencies through the first two academic terms of General Chemistry after introducing an intervention of a math quiz and feedback. We separately track competencies after student use of a program called ALEKS, which uses adaptive questioning to determine student competencies and then instruct on deficient topics.

1062-Pos Board B848
A Simple Model of Protein Folding: From Crystal Structure to the Living Cell
Maxim B. Prigozhin, Sharlene Denos.
Univesity of Illinois, Urbana, IL, USA.
Construction of simple models is an integral part of any scientific investigation, yet it almost never makes it even to the college science curriculum. We developed a series of 4 lessons that uses protein dynamics as a platform to introduce modeling to students at the high school and undergraduate levels. These lessons guide students from a textbook picture of a protein as a rigid crystal structure to a more realistic view: proteins are highly dynamic entities in the crowded environment inside the living cells. Methods of statistics and physical chemistry are employed along the way to investigate a flexible version of a protein that can sample various conformations within the folded ensemble and ultimately unfold into a random coil. Simple mechanical and computer models that evolve in their complexity are at the core of this lesson.



1063-Pos Board B849
A Ubiquitous Learning Environment For Molecular Biology
Eric Jakobsson.
University of Illinois, Urbana, IL, USA.
There is widespread agreement on the need to integrate education in physical, mathematical, and life sciences. It is now feasible to create a ubiquitous learning and inquiry environment for providing a comprehensive introduction for biology to physical and mathematical scientists, which can be accessed from everywhere using a networked laptop. This paper proposes such an environment. The didactic portion is organized according to the flow of information among biomolecular systems, starting with the genome and continuing with the processes of transcription, translation, and post-translational modification, and the interaction of gene products to give rise to the cellular phenome and to interactions among cells. Reverse information flow via influence of the environment on the cell completes the information loop, with dynamic responses ranging in time scales from fractions of a second for an emergency response to thousands or millions of years for evolutionary change. The textbook level of understanding can be assembled from the NCBI bookshelf. The ability of students to dig deeper in all subjects is achieved through training in the use of Google Scholar and PubMed to assemble functional bibliographies beginning with seminal papers (early papers with many citations) leading up to the most recent advances, punctuated with review papers. Hands-on interaction with the concepts can be introduced with the use of bioinformatics and molecular modeling tools accessible online, leading to an early experience in computational research and in framing meaningful problems to be attacked