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podcast summary
Download the September JBC podcast to hear an interview with David Graham, a professor of Chemistry and Biochemistry at the Institute for Cellular and Molecular Biology at the University of Texas, Austin, about his work with biosynthetic pathways in an extremophile. For this and other ASBMB AudioPhiles podcasts go to: www.asbmb.org/audio.aspx
Entering the World of Biomolecules

Physical Models Give Way to Holistic Approaches for Teaching Structure/Function Relationships

BY DUANE SEARS

The 2008 Proteins in Active Learning Models (PALM) Workshop was hosted this past spring in the newly situated Center for BioMolecular Modeling (CBM) at the Milwaukee School of Engineering (MSOE). About 25 science educators from a variety of professions—including secondary schoolteachers, university and community college professors and lecturers, a post-doctoral fellow, a textbook writer, and a professional biomolecular artist and writer—convened for an intense 3-day exposure to the educational resources and physical learning models that the CBM has developed over the years for the purpose of helping students learn about the nature and nuances of biomolecular structures and their functions.

Tim Herman, a biomolecular guru of sorts with unabounded raw energy and pure enthusiasm, is the brain-child behind the CBM. For about half of the workshop, he and his associates guided attendees through the myriad of tactile models and ancillary learning activities that the CBM has created for educators. The physical models can be obtained on loan from the MSOE Model Lending Library for just the cost of return shipping, or the models and other resources can be purchased with modest pricing. The models themselves range from simple water kits containing several geometrically accurate space-filled water molecules with embedded magnets for simulating the H-bonding properties of H₂O; to semi-flexible foam-covered wire “Tubers” for modeling protein and polynucleotide backbone structures; to hand-sized, molecularly accurate three-dimensional molecular models of literally hundreds of structures, only a scant few of which are actually displayed on the CBM model gallery website.

The latter models deserve special mention because Herman was among the first to realize that a widely used engineering method called rapid prototyping, which is used to produce physical mockups of computer-generated images, can be adapted to produce accurate three-dimensional (3-D) physical models of biomolecules based on their atomic coordinates. In the simplest of explanations, the rapid prototyping machine effectively “photocopies” a 3-D image by depositing a plaster powder in a series of thin two-dimensional (2-D) layers (from bottom to top) with spot applications of glue at any point where a structure is contiguous between adjacent 2-D planes. The end product is a rectangular 3-D block that, after being subjected to an air blower (to whisk away any unglued plaster powder), leaves behind a rigidly connected 3-D model accurately representing the computer image from which it was generated.

Herman and his colleagues, including the very talented Mark Hoelzer who is the lead designer at CBM, have introduced many useful modifications to this technique so the resulting models are light and resilient. They have also found ways to automatically introduce custom colors into specific portions of the model during the prototyping process, thereby eliminating any need to “paint” specific features on the models after they are produced. These models look every bit like the Jmol or Chime 3-D images we are accustomed to seeing on the computer screen, but they can be manipulated by hand, thereby lending a tangible dimension to a student’s understanding of molecular structure. This effect is greatly enhanced by the modularity of some of the models where different segments are held precisely in place by magnets so that the segments can easily be separated for closer inspection of the underlying features. The CBM has created hundreds of models in this way.

What eventually became apparent during the workshop is that the CBM is actively evolving toward a more comprehensive and rigorous educational approach where structural models are only one part of a broader educational package. This holistic shift in approach is spearheaded in large part by Margret Franzen, who recently became a permanent CBM staff member and who has won both local and national recognition for her teaching innovations. One particularly novel innovation is her NSF-funded guide for instructors that was developed to help students learn about the relationship between the evolutionary resistance of mosquitoes to insecticides and the evolutionary alterations in mosquito acetylcholinesterase, the target of some insecticides. Various exercises employ a modular 3-D model of the enzyme active site, which is available from the MSOE Model Lending Library, where wild-type and mutant enzyme structures are easily interconverted so as to illustrate the resulting effects on the binding of removable substrate and inhibitor molecules that are included with the model.

This is but one of several CBM projects aimed at placing biomolecular structure/function teaching activities under the microscope and converting them into a series of activities aimed at different educational levels. This, of course, dovetails with the need for such models to be used as educational tools in the primary and secondary schools and even at the pre-college level, where students are often first exposed to molecular biology and chemistry. With this in mind, Herman and his colleagues are working on a “model kit” for the classroom, with the goal of providing entry-level students with a “taste” of what is available from the CBM. The goal is to provide this kit to students in the secondary grades where they can get a taste of what biological models look like and how they might be used.

The new kit will include a variety of models, ranging from simple representations of the structure of biological molecules to more advanced models that provide a more in-depth look at the structural features of specific molecules. The kit will also include a manual that describes how to use the models and how they can be incorporated into classroom activities. This will allow teachers to use the models in a variety of ways, from simple demonstrations to more complex experiments. The kit will be available to schools that meet certain criteria, such as having a science program that includes biomolecular modeling and a commitment to using the models in classroom activities.
the larger umbrella of bioinformatics. Such efforts have produced yet another highly innovative instructional aid and learning activity, the Bioinformatics Map of the β-Globin Gene, which is also available from the CBM. In a nutshell, the entire β-globin gene sequence is laid out on an ≈5-inch x 15-foot laminated sheet (that is easily rolled up for storage) with three potential translated reading frames running below the sequence. As described by those at the meeting who had already used this remarkably simple learning tool, it is an effective guide for deepening and integrating students' understanding of a host of related biological concepts that cross over between genetics, gene structure, transcription, RNA processing, translation, protein structure, etc.

To help the CBM enter this new phase of developing teaching activities that meld biological structures with the larger knowledge base of bioinformatics, meeting participants were asked to share their teaching experiences with existing CBM resources, or other types of visual and tactile learning aids. Participants worked together in small groups on various "assignments" that were set up to spur discussion. Ultimately, these activities led to brainstorming sessions about future directions and new projects that the CBM might undertake. No project, however ambitious and seemingly complex, appears to be off limits as long as the educational payoff merits the effort. One such project that perfectly fits this bill is the structure and function of the nuclear pore complex as described at the workshop by Jody Franke from The Rockefeller University, who brought attendees up to date on what is currently known about this structure and the nature of the supporting experimental evidence. As a seemingly perfect gesture to what might eventually be a grand undertaking by the CBM, meeting participants, while waiting for their conference dinners to be served, spontaneously assembled into a nuclear pore complex-like structure under the high foyer ceiling of the Grohmann Museum of the MSOE.

Confessing that I had only been vaguely aware of the CBM and its educational mission prior to attending this workshop, I came away a convert to the power of the approaches being undertaken for rigorous science education. The extreme versatility of the types of models and resources that are already available was illustrated again and again by the diversity of approaches and applications described by the participants. The CBM is a fabulous teaching resource, and biochemists and biologists alike are bound to find unique teaching tools here that students will find interesting, relevant, and even exciting. The future looks bright for the CBM, and I look forward to what emerges from this unique educational center in the years to come.

Duane Sears is a professor in the Department of Molecular, Cellular, and Developmental Biology at the University of California, Santa Barbara. He can be reached at sears@lifesci.ucsb.edu.

REFERENCE