live cell. "The gratifying thing is that not only does it make a ring, but it makes it in 10 minutes—which is actually a big constraint," Pollard says.

"It's fascinating work," comments **Alex Mogilner, PhD**, professor of neurobiology, physiology and behavior and of mathematics at the University of California, Davis. "I think there will be more surprises in the future," he says, "but they nailed the essence of what's going on."

—By Kristin Sainani, PhD

Modeling the Deformable Body

August 2007 saw a surge of new open-source software for simulating musculoskeletal movement. In addition to OpenSim 1.0 (described in the Fall 2007 issue of this magazine), FEBio arrived on the scene. While OpenSim uses rigid body mechanics—simulating the body moving essentially as a series of segments attached at joints—FEBio (Finite Elements for Biomechanics) addresses the other part of the problem. It can simulate how movement deforms and places stresses upon solid parts of the body such as muscles, tendons, ligaments, cartilage and bone.

Created by **Jeff Weiss, PhD**, associate professor of bioengineering at the University of Utah, and his colleagues, FEBio already has 200 to 250 users. "Initially we developed FEBio for our use in-house," says Weiss, "but we saw the potential for it to be a really popular tool in the research community and decided to make it available to everyone."

Before now, biomechanics researchers studying the solid mechanics of soft tissue have relied upon costly general-purpose finite-element programs such as Abaqus or LS-DYNA. But because these programs are proprietary, it's hard to add new features to the code. "We saw that as a major shortcoming in our field," says Weiss. So he and his colleagues tailored FEBio to address the kinds of problems that come up in biomechanics.

In addition to FEBio itself, Weiss and his colleagues also released programs that allow users to prepare their models in advance of using FEBio (PreView) and to analyze and visualize the results of an FEBio simulation (PostView). "That's one of the advantages of FEBio," says **Steve Maas**, a software developer who works with Weiss. "You can do your model creation and post-processing on your own computer and use a high performance computer only for the FEBio step."

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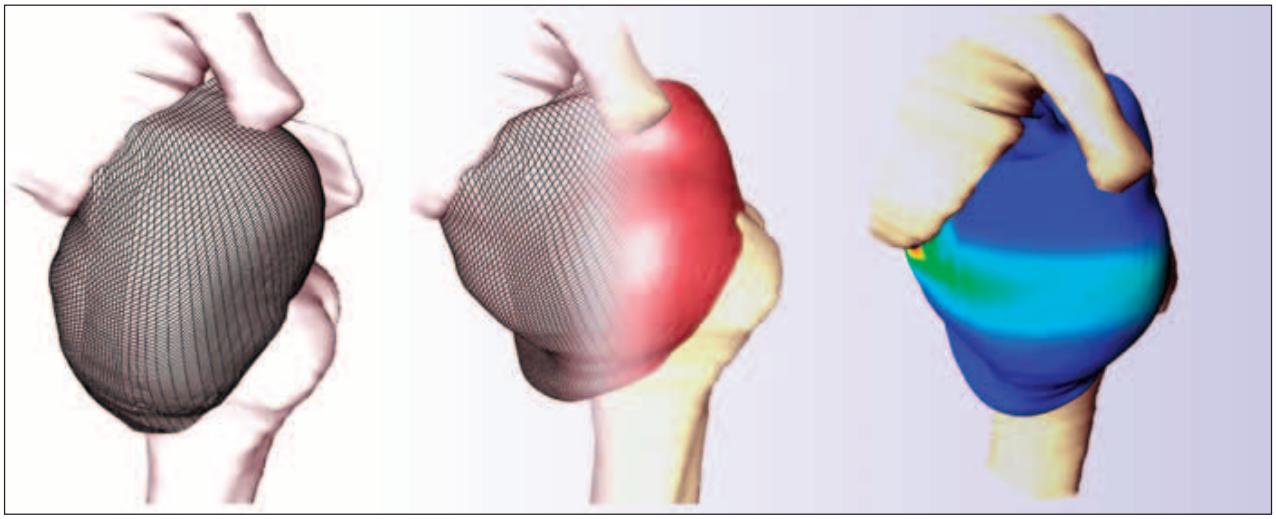
FEBio's users come from many different disciplines including orthopedics, ophthalmology and cardiovascular mechanics. Weiss himself has used FEBio for a variety of research projects including a study of hip stresses in



In this FEBio model of a shoulder capsule—the soft-tissue envelope that surrounds the shoulder joint—the upper arm bone (the humerus) is moved upward and then rotated around its axis. The left image shows the initial undeformed mesh, the middle image shows an intermediate state, and the rightmost image shows the stresses on the capsule in the final deformed state (blue means low stress, red means high stress). During a shoulder examination, clinicians typically move the shoulder in various ways in an attempt to determine the source of a problem. Models of this kind could eventually help clinicians better understand the results of such tests. Courtesy of Jeff Weiss and Steve Maas.

people with displasia and a study of the shoulder capsule. He and his colleagues are also continuing to add new features to FEBio.

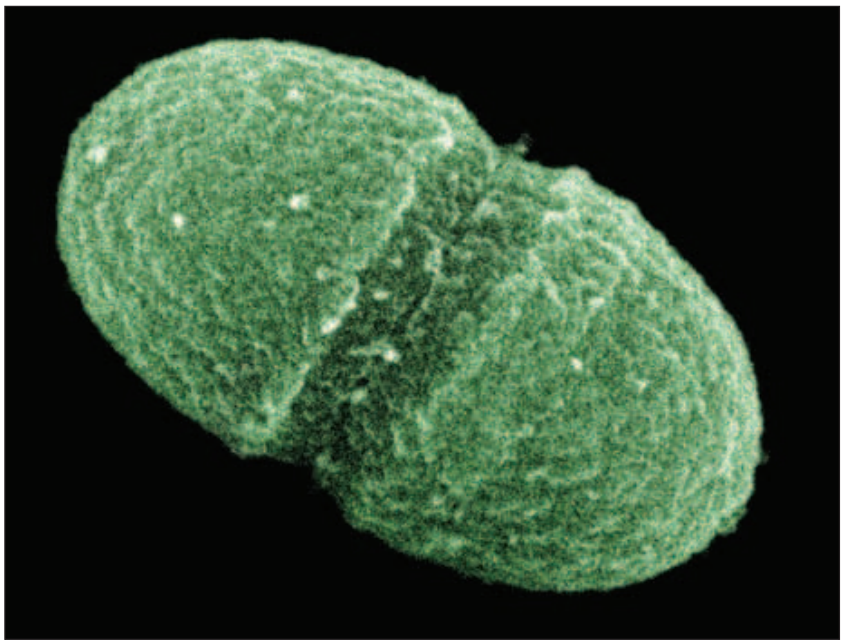
Weiss and one of the OpenSim creators **Scott Delp, PhD**, a professor of bioengineering at Stanford University, have begun a collaboration to link the two programs to address problems that can't be handled by either program alone. Although Delp's group has combined dynamics with finite element approaches in previous work (for example in a study of knee pain), "development of advanced methods in biomechanics would be accelerated if one could use two open-source programs connected in a straightforward way. I'm looking forward to that day," Delp says.
—By Katharine Miller

Discovering The Bugs Within

We are crawling with bugs. It might even be better to say that we are bugs. For every human cell in our bodies there may be ten or even a hundred other cells that aren't human at all. Yet many of these microbes are entirely unknown to science. To change that, the National Institutes of Health has just begun a five-year, $115 million Roadmap initiative called the Human Microbiome Project. It aims to find out what these bacteria, viruses, archaea and fungi are, how they function, and the ways they can keep us healthy or make us sick.

"There have been some tantalizing findings that gut flora influence things like obesity and irritable bowel disorder," says **Jane Peterson, PhD**, associate director of the Division of Extramural Research at the National Human Genome Research Institute and a program director for the project. "Ultimately, what we really want to understand is health as well as disease. What makes us healthy? Our microbes are a part of that."

But learning about these bugs has seemed like an overwhelming undertaking. Part of the problem is simply numbers: thousands of different species of microbes swarm on and in our bodies.



A human gut microbe. This bacterium,* Entercoccus faecalis*, which lives in the human gut, is just one type of microbe that will be studied as part of NIH's Human Microbiome Project. Courtesy: United States Department of Agriculture

The most obvious way to find out what they are is to understand their genomes. Unfortunately, sequencing these microbes is even harder than sequencing our own genome because most of the microbes have an obstreperous unwillingness to grow in isolation in a lab. They will only grow in the particular conditions of, say, our teeth, where they commune with a particular group of other microbes that create an agreeable environment.

Sequencing technology has been improving rapidly, however, bringing the task within reach now. "Metagenomic" techniques have been developed to study the genomes of many different microbes simultaneously, making it unnecessary to culture the microbes in the lab. In addition, modern sequencing machines can now produce millions of sequences in a day, compared to a few thousand in the past, and they do it less expensively.

The Human Microbiome Project has already awarded $8.2 million to research groups around the country in 2007, and they currently have six requests for proposals out, due between February and May.

Analyzing the data from all these far-flung groups will require the development of new computational techniques. Genomic analysis already produces such

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