what the nucleosome core would look like." Schlick says.

Regardless of which of the four folding models they started their simulation with, they found that their virtual chromatin always folded into an irregular zig-zag conformation after enough computational steps. They also pinpointed the key electrostatic attractions and repulsions that drive chromatin folding and unfolding.

"This is not the first attempt to model the chromatin fiber, but this one makes the fewest artificial assumptions," says Sergei Grigoryev, PhD, assistant professor of biochemistry and molecular biology at Penn State University College of Medicine.

Their findings agree with the experimental data he has collected on chromatin folding using electron microscopy.

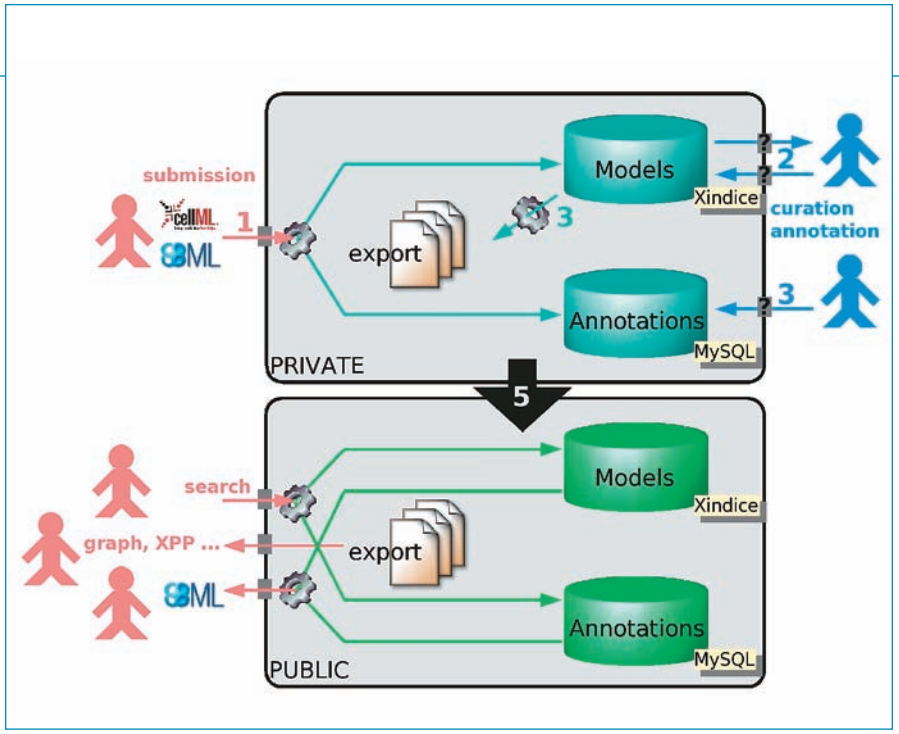
"I really admire their paper," he says. "For the first time it produced a nucleosome array model that really matches biological observations."

Reliable Models Now Available

As systems biologists develop models that attempt to simulate life, they need a good way to make them accessible to others as well as a good way to access other people's models—and to know they can be trusted to work. An international collaboration known as BioModels intends to provide just that; in April they released an initial set of fully annotated models for public use.

"We are storing quantitative, peer-reviewed models so that people can use them," says Nicolas Le Novere, PhD, a computational neurobiologist with the European Bioinformatics Institute (EBI) in the United Kingdom. "We want it to be a kind of golden resource." BioModels is the result of a collaboration led by EBI and the SBML Team, an international group that develops open-source standards to describe biological systems.

The project staff only accepts models that have been published in peer-reviewed literature. Curators then check to make sure that, when downloaded and run in the appropriate simulation software, the model will do what it's supposed to do. Next, annotators add model descriptions and cross-links to related models and papers. At that point, the model is released for public use.



A graphical depiction of the private BioModels submission (1), checking (2), and annotation (3) steps (above) and the public access steps (below). Courtesy of Nicolas Le Novere.

The systems biology community is wagering that this collection of models will prove extremely valuable. According to an editorial in *Nature*, "It is hoped that BioModels will form the basis of a universally accepted repository that can do for systems biology what GenBank and the Protein Data Bank have done for genetics and structural biology." *Nature* 435, 1 (5 May 2005)

> "We want it to be a kind of golden resource," says Philip La Novere of the BioModels project.

The majority of early submissions to the database deal with signaling pathways or metabolic networks, but they are quantitative and dynamic models—not just pathways. "You can import these models into a simulator, click 'run,' and see things happen, see values updated," says Le Novere.

Formalized, realistic models of subcellular parts or even muscles can also be stored in BioModels. And although models of that type haven't arrived yet, Le Novere says the project already has a backlog of submissions. "We have so many good models arriving that we have to prioritize."

BioModels' initial users are primarily the people who've created the models, says Le Novere, but he anticipates that will soon change. The site should prove extremely valuable to experimental biologists who want to have an idea of how a system works before designing an experiment. And pharmaceutical companies could turn to it as well, in order to test the likely effect of enhancing or inhibiting a molecule or doing things that affect several parts of a network at the same time.

For more information, visit http://www.ebi.ac.uk/biomodels/ □