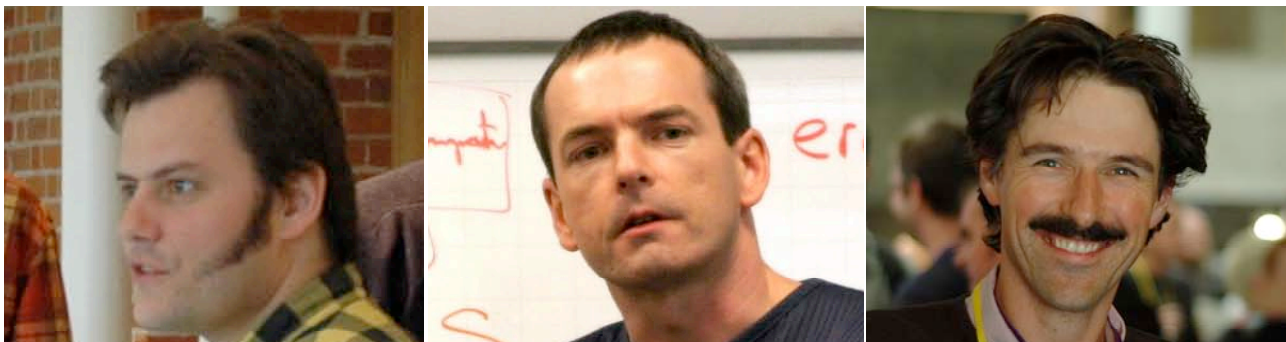




Joint Press release

For immediate release

European Bioinformatics Institute of the European Molecular Biology Laboratory (EMBL-EBI) and the SBML Team



Left to right, Nicolas Le Novère (EMBL-EBI), Michael Hucka (California Institute of Technology, USA) and Andrew Finney (University of Hertfordshire, UK).

A new way to share models of biological systems

Hinxton/Pasadena, Monday, April 11 – Today sees the launch of BioModels, the world's first database of annotated biological models. BioModels is the result of a collaboration led by the European Bioinformatics Institute (UK) and the SBML Team, an international group that develops open-source standards to describe biological systems. Other contributors include the Keck Graduate Institute (USA), the Systems Biology Institute (Japan) and Stellenbosch University (South Africa).

Even the simplest living organisms perform a mind-boggling array of different processes, which are interconnected in complex ways to ensure that the organism responds appropriately to its environment. One of the best ways of ensuring that we really understand how these processes fit together is to build computer models of them. If a computer model behaves differently than the real organism, we know that we've neglected an important component of the system. Quantitative models can also reveal previously unappreciated properties of complex systems, paving the way towards new drug treatments. This approach, known as 'computational systems biology,' is becoming increasingly popular now that scientists are accumulating detailed parts lists for many organisms, thanks to genome sequencing projects and other efforts to comprehensively document the components of living entities.

"Until now, computer modellers had no defined way of exchanging descriptions of biological systems, and there was no accepted place to deposit and share new models when they were developed," explains the EBI's Nicolas Le Novère. "The BioModels database aims to address these issues."

The first step was to develop a standard way of describing such models. The Systems Biology Markup Language (SBML), an open-source computer language developed by the SBML Team, is now widely accepted and is supported by over 75 different software systems worldwide. This allows computational systems biologists to write models using the tool of their choice, and then to share them so that others can build on their work.

Michael Hucka of the California Institute of Technology continues: "The next logical step was to build a community resource that would allow anyone to submit, download and reuse the models. That's the purpose of the BioModels database. BioModels provides access to published, peer-reviewed, quantitative models of biochemical and cell-biological systems."

Some of these systems are very simple, containing just a few processes or reactions; others contain hundreds. The models are checked to verify that they correspond to the reference publication. Human curators annotate and cross-link components of the models to other relevant data resources. This allows users to identify precisely the components of models, and helps them to retrieve appropriate models, which they can then visualize and build upon using any SBML-compatible software.

"Ultimately," says Le Novère, "we hope that publishers will encourage any author who plans to publish a new model to submit it to the BioModels database; this will ensure that all the models in the public domain are freely available for everyone to make the most of them."

The BioModels database is freely available at www.ebi.ac.uk/biomodels.

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About EMBL:

The European Molecular Biology Laboratory is a basic research institute funded by public research monies from 18 member states (Austria, Belgium, Denmark, Finland, France, Germany, Greece, Iceland, Ireland, Israel, Italy, the Netherlands, Norway, Portugal, Spain, Sweden, Switzerland and the United Kingdom). Research at EMBL is conducted by approximately 80 independent groups covering the spectrum of molecular biology. The Laboratory has five units: the main Laboratory in Heidelberg, and Outstations in Hinxton (the European Bioinformatics Institute), Grenoble, Hamburg, and Monterotondo near Rome. The cornerstones of EMBL's mission are: to perform basic research in molecular biology; to train scientists, students and visitors at all levels; to offer vital services to scientists in the member states; and to develop new instruments and methods in the life sciences. EMBL's International PhD Programme has a student body of about 170. The Laboratory also sponsors an active Science and Society programme. Visitors from the press and public are welcome.

About the EBI:

The European Bioinformatics Institute (EBI) is part of the European Molecular Biology Laboratory (EMBL) and is located on the Wellcome Trust Genome Campus in Hinxton near Cambridge (UK). The EBI grew out of EMBL's pioneering work in providing public biological databases to the research community. It hosts some of the world's most important collections of biological data, including DNA sequences (EMBL-Bank), protein sequences (UniProt), animal genomes (Ensembl), three-dimensional structures (the Macromolecular Structure Database) and data from microarray experiments (ArrayExpress). The EBI hosts several research groups and its scientists continually develop new tools for the biocomputing community. BioModels has been developed by the team of Nicolas Le Novère with the help of Marco Donizelli.

About the SBML Team:

The SBML Team is an international research team currently headed by Michael Hucka and Andrew Finney and distributed at institutions around the world. Its focus is on research and software development for systems biology. The group developed Systems Biology Markup Language (SBML), a free and open computer language for describing biological systems. SBML was initially funded by a generous grant from the JST ERATO Kitano Symbiotic Systems (Japan). Since then, the projects have also received funding from the BBSRC (UK), NEDO (Japan), NHGRI (USA), DARPA IPTO (USA), and AFOSR (USA). Additional support has been provided by California Institute of Technology (USA), the University of Hertfordshire (UK), the Molecular Sciences Institute (USA), and the Systems Biology Institute (Japan).

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