Michael Hucka

Control and Dynamical Systems
California Institute of Technology
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EDUCATION

Ph.D., Computer Science and Engineering, University of Michigan, Ann Arbor, MI 1998
Major subject areas: cognitive science, computational neuroscience. Dissertation: *Texture-Based Segmentation and Form Estimation Combined in a Model of Approximate Spatial Layout Processing in the Visual System*.

M.S.E., Computer Science and Engineering, University of Michigan, Ann Arbor, MI 1991

B.S. with honors, Electrical Engineering, University of Utah, Salt Lake City, UT 1987

B.S. with honors, Computer Science, University of Utah, Salt Lake City, UT 1986

EMPLOYMENT HISTORY

Member of the Professional Staff, Control and Dynamical Systems, Caltech 2011-present

Principal Investigator and leader of the international Systems Biology Markup Language (SBML) development project. SBML is the de facto standard today for representing computational models in systems biology, and is supported by over 250 software tools worldwide as well as journals such as Nature and others. Activities include obtaining and managing multiple grants from national and international agencies, coordinating the development of new extensions to SBML and the maintenance of existing SBML versions, writing new versions of the SBML specification documents, writing, documenting and maintaining software libraries for SBML, maintaining the SBML.org website and associated servers and software, organizing and running biannual international workshops, coordinating with other related efforts in systems biology, and managing staff members. Instrumental in organizing the development of BioModels Database (a free public database of curated computational models in biology), including obtaining NIH funding for its early development, and currently a member of its advisory board. Co-developer of the first version of the Systems Biology Graphical Notation (SBGN), a standard graphical notation for network diagrams in biology. Co-developer of related standards such as MIRIAM ("Minimum Information Requested in the Annotation of biochemical Models"), and the Systems Biology Ontology (SBO). Liaison to related efforts such as BioPAX and MIASE ("Minimal Information About a Simulation Experiment"). Co-creator and leader of a new community organization, COMBINE ("Computational Modeling in Biology Network"), which has the goal of coordinating and better integrating all of the different related standardization efforts today.

Senior Research Fellow, Control and Dynamical Systems, Caltech 2005–2011

Same activities as those listed under *Member of the Professional Staff* above.

Co-director, Beckman Institute Biological Network Modeling Center (BNMC) 2005–2009

The BNMC's aim is to foster collaboration between biologists, bioengineers, mathematicians, and computer scientists to develop and apply computational tools for modeling and analyzing complex biological phenomena. The BNMC provides a home for numerous activities focused on this aim, including obtaining grants for software and theory development, organizing workshops and seminars on topics of interest to the Caltech biological modeling community, giving tutorials to Caltech students, providing web resources, and (in 2007) co-organizing the premiere conference in systems biology, the *Eighth International Conference on Systems Biology (ICSB 2007)*, held at the Long Beach Convention Center and attended by 640 researchers from academia and industry. Co-developed the initial BNMC concept, co-wrote the grant proposal to the Beckman Institute, and then co-directed the BNMC for its first four years while it was funded as a Beckman Institute Director's Initiative. My responsibilities involved all aspects and functions of the BNMC.

Staff Research Programmer, Control and Dynamical Systems, Caltech **2001–2004**

Co-designed and co-developed an open-source software framework, the Systems Biology Workbench (SBW), and co-created the Systems Biology Markup Language (SBML), in Dr. John Doyle's group.

Postdoctoral Scholar, Division of Biology, Caltech **1998–2000**

Maintained the GENESIS software system for neurophysiological simulations, as well as designed new software systems and standards including the NeuroML markup language. Laid the groundwork for the development of the Systems Biology Workbench (SBW) and the Systems Biology Markup Language (SBML).

Programmer Analyst, EECS, University of Michigan **1995–1998**

Performed systems support for a medium-sized departmental network of Unix computers (primarily Solaris-based Sun workstations and servers). Involved in all facets of support, from configuring new computers, to installing and maintaining software, to interacting with users. Also served as the primary Usenet server administrator for the Electrical Engineering and Computer Science (EECS) department.

Programmer, EECS, University of Michigan **1992–1994**

Developed software for the Soar research project under the direction of Dr. John Laird. (Soar is an adaptive rule-based software system meant to imitate human reasoning in various tasks.)

Research Assistant, EECS, University of Michigan **1988–1992**

Performed research and developed applications of the Soar system to robotic control, under the direction of Dr. John Laird.

Systems Programmer, College of Engineering, University of Michigan **1987–1988**

Performed systems administration and support for the College of Engineering's network of several hundred Unix workstations (primarily Apollo DOMAIN, DEC and Sun systems).

Research Programmer, Computer Science, University of Utah **1986–1987**

Ported an implementation of Common Lisp to different Unix-based platforms.

FUNDING AWARDED

Current grants

NIH NIGMS R01, $1,544,636 total cost (3 years), Hucka (PI), *"Continued Support of Essential SBML Software and Community Resources",* 2013-2016.

Subcontract from Mount Sinai School of Medicine, New York, on their NIH R01 award titled "Modeling Immunity in for Biodefense" (PI: S. Sealfon), to develop a translator from MATLAB to SBML. $113,044 total cost (2 years), 2014-2015.

Past/completed

NIH NIGMS R01, $2,151,057 total cost (3 years). Hucka (PI), "Continued Development and Support of Essential SBML Infrastructure Software", 2010–2013.

NIH NIGMS R01, $1,654,403 total cost (3 years). Hucka (PI), "Continued Support and Development of SBML and Essential SBML Infrastructure", 2007–2010.

NIH EB R01, $1,966,613 total cost (3 years). Written by Hucka but formulated for M. Stalzer as PI, "An Open and Scalable Stochastic Simulation Library for Biology", 2007–2010.

Beckman Institute Director's Initiative, $330,000 direct cost portion to Hucka (4 years). J. Doyle (co-PI) and E. Meyerowitz (co-PI), "Biological Network Modeling Center (BNMC)", 2006–2009.

NIH NIGMS R01, $605,370 total cost (2 years). Hucka (PI), "Comprehensive Test Suite for SBML", 2006–2008.

NEDO (New Energy and Industrial Technology Development Organization, Japan), $148,473 total cost portion to Hucka (3 years). H. Kitano (co-PI), M. Hucka (co-PI), N. Le Novère (co-PI), A. Funahashi (co-PI), "International Standard for Graphical Notation of Biological Networks", 2006–2008.

NIH NIGMS R13, $10,000 total cost (1 year). Hucka (PI), "Eighth International Conference on Systems Biology (ICSB 2007)", 2007.

NSF MCB, $10,000 total cost (1 year). Hucka (PI), "Conference: Eighth International Conference on Systems Biology (ICSB 2007) to be held October 1–6, 2007 in Long Beach, CA", 2007.

NIH NIGMS R01 supplement, $451,870 total cost portion to Hucka (2 years). J. Doyle (PI), "Continued Development and Maintenance of Bioinformatics and Computational Biology Software", 2005–2007.

NIH NIGMS R01 supplement, $23,895 total cost (1 year). Hucka (PI), meeting support for "Continued Support and Development of SBML", 2005.

DARPA Bio-SPICE, $149,204 total cost (1 year). Hucka (PI), "Continued Enhancement of SBML and libSBML", 2005.

NEDO (New Energy and Industrial Technology Development Organization, Japan), $31,000 total cost portion to Hucka (2 years). H. Kitano (PI), original title in Japanese, 2003–2004.

NIH NIGMS R13, $5,000 total cost portion to Hucka (1 year). J. Doyle (PI), "SBML Forum Meeting October 2004", 2004.

NIH NIGMS R01, $829,154 total cost (3 years). J. Doyle original PI but later transitioned to Hucka. "Continued Support and Development of SBML", 2004–2007.

PEER-REVIEWED JOURNAL PUBLICATIONS

C. Chaouiya, D. Bérenguier, S.M. Keating, A. Naldi, M.P. van Iersel, N. Rodriguez, A. Dräger, F. Büchel, T. Cokelaer, B. Kowal, B. Wicks, E. Gonçalves, J. Dorier, M. Page, P.T. Monteiro, A. von Kamp, I. Xenarios, H. de Jong, M. Hucka, S. Klamt, D. Thieffry, N. Le Novère, J. Saez-Rodriguez, and T. Helikar. SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. *BMC Systems Biology* 7:135, 2013.

F. Büchel, N. Rodriguez, N. Swainston, C. Wzrodek, T. Czauderna, R. Keller, F. Mittag, M. Schubert, M. Glont, M. Golebiewski, M. van Iersel, S. Keating, M. Rall, M. Wybrow, H. Hermjakob, M. Hucka, D.B. Kell, W. Müller, P. Mendes, A. Zell, C. Chaouiya, J. Saez-Rodriguez, F. Schreiber, C. Laibe, A. Dräger, N. Le Novère. Path2Models: large-scale generation of computational models from biochemical pathway maps. *BMC Systems Biology* 7:116, 2013

I. Thiele, N. Swainston, R.M.T. Fleming, A. Hoppe, S. Sahoo, M.K. Aurich, H. Haraldsdottir, M.L. Mo, O. Rolfsson, M.D. Stobbe, S.G. Thorleifsson, R. Agren, C. Bölling, S. Bordel, A.K. Chavali, P.

Dobson, W.B. Dunn, L. Endler, D. Hala, M. Hucka, D. Hull, D. Jameson, N. Jamshidi, J.J. Jonsson, N. Juty, S.M. Keating, I. Nookaew, N. Le Novère, N. Malys, A. Mazein, J.A. Papin, N.D. Price, E. Selkov Sr, M.I. Sigurdsson, E. Simeonidis, N. Sonnenschein, K. Smallbone, A. Sorokin, J. HGM van Beek, D. Weichart, I. Goryanin, J. Nielsen, H.V. Westerhoff, D.B. Kell, P. Mendes, B.Ø. Palsson. A community-driven global reconstruction of human metabolism. *Nature Biotechnology* 31(5):419–425, 2013.

Waltemath, D., Adams, R., Bergmann, F.T., Hucka, M., Kolpakov, F., Miller, A., Moraru, I.I., Nickerson, D., Snoep, J., Le Novère, N. Reproducible computational biology experiments with SED-ML—The Simulation Experiment Description Markup Language. *BMC Systems Biology* 5:198, 2011.

Courtot, M., Juty, N., Knüpfer, C., Waltemath, D., Zhukova, A., Dräger, A., Dumontier, M., Finney, A., Golebiewski, M., Hastings, J., Hoops, S., Keating, S., Kell, D.B., Kerrien, S., Lawson, J., Lister, A., Lu, J., Machne, R., Mendes, P., Pocock, M., Rodriguez, N., Villeger, A., Wilkinson, D.J., Wimalaratne, S., Laibe, C., Hucka, M., Le Novère, N. Controlled vocabularies and semantics in Systems Biology. *Molecular Systems Biology*, 7:543, 2011.

Dräger, A., Rodriguez, N., Dumousseau, M., Dörr, A., Wrzodek, C., Le Novère, N., Zell, A., and Hucka, M. JSBML: a flexible Java library for working with SBML. *Bioinformatics,* doi:10.1093/bioinformatics/btr361, 2011.

Waltemath, D., Adams, R., Beard, D. A., Bergmann, F. T., Bhalla, U. S, Britten, R., Chelliah, V., Cooling, M. T., Cooper, J., Crampin, E., Garny, A., Hoops, S., Hucka, M., Hunter, P., Klipp, E., Laibe, C., Miller, A., Moraru, I., Nickerson, D., Nielsen, P., Nikolski, M., Sahle, S., Sauro, H., Schmidt, H., Snoep, J. L., Tolle, D., Wolkenhauer, O., and Le Novère, N. Minimum Information About a Simulation Experiment (MIASE). *PLoS Computational Biology*, 7(4):e1001122. doi:10.1371/journal.pcbi.1001122, 2011.

Demir, E., Cary, M. P., Paley, S., Fukuda, K., Lemer, C., Vastrik, I., Wu, G. N., D'Eustachio, P., Schaefer, C., Luciano, J., Schacherer, F., Martinez-Flores, I., Hu, Z. J., Jimenez-Jacinto, V., Joshi-Tope, G., Kandasamy, K., Lopez-Fuentes, A. C., Mi, H. Y., Pichler, E., Rodchenkov, I., Splendiani, A., Tkachev, S., Zucker, J., Gopinath, G., Rajasimha, H., Ramakrishnan, R., Shah, I., Syed, M., Anwar, N., Babur, O., Blinov, M., Brauner, E., Corwin, D., Donaldson, S., Gibbons, F., Goldberg, R., Hornbeck, P., Luna, A., Murray-Rust, P., Neumann, E., Reubenacker, O., Samwald, M., van Iersel, M., Wimalaratne, S., Allen, K., Braun, B., Whirl-Carrillo, M., Cheung, K. H., Dahlquist, K., Finney, A., Gillespie, M., Glass, E., Gong, L., Haw, R., Honig, M., Hubaut, O., Kane, D., Krupa, S., Kutmon, M., Leonard, J., Marks, D., Merberg, D., Petri, V., Pico, A., Ravenscroft, D., Ren, L. Y., Shah, N., Sunshine, M., Tang, R., Whaley, R., Letovksy, S., Buetow, K. H., Rzhetsky, A., Schachter, V., Sobral, B. S., Dogrusoz, U., McWeeney, S., Aladjem, M., Birney, E., Collado-Vides, J., Goto, S., Hucka, M., Le Novere, N., Maltsev, N., Pandey, A., Thomas, P., Wingender, E., Karp, P. D., Sander, C., and Bader, G. D., The BioPAX community standard for pathway data sharing. *Nature Biotechnology,* 28(9):935–942, 2010.

Li, C., Donizelli, M., Rodriguez, N., Dharuri, H., Endler, L., Chelliah, V., Li, L., He, C. U., Henry, A., Stefan, M. I., Snoep, J. L., Hucka, M., Le Novère, N., and Laibe, C., BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. *BMC Systems Biology*, 4(92), 2010.

Le Novère, N., Hucka, M., Mi, H. Y., Moodie, S., Schreiber, F., Sorokin, A., Demir, E., Wegner, K., Aladjem, M. I., Wimalaratne, S. M., Bergman, F. T., Gauges, R., Ghazal, P., Kawaji, H., Li, L., Matsuoka, Y., Courtot, M., Dogrusoz, U., Freeman, T. C., Funahashi, A., Ghosh, S., Jouraku, A., Kim, S., Kolpakov, F., Luna, A., Sahle, S., Schmidt, E., Watterson, S., Wu., G. M., Goryanin, I., Kell, D. B., Sander, C., Sauro, H., Snoep, J. L., Kohn, K., and Kitano, H., The Systems Biology Graphical Notation. *Nature Biotechnology*, 27(8):735–741, 2009.

Dräger, A., Planatscher, H., Wouamba, D. M., Schröder, A., Hucka, M., Endler, L., Golebiewski, M., Müller, W., and Zell, A., SBML2LaTeX: Conversion of SBML files into human-readable reports. *Bioinformatics*, 2009.

Herrgård, M. J., Swainston, N., Dobson, P., Dunn, W. B., Arga, K. Y., Arvas, M., Blüthgen, N., Border, S., Costenoble, R., Heinemann, M., Hucka, M., Li, P., Liebermeister, W., Mo, M. L., Oliveira, A. P., Petranovic, D., Pettifer, S., Simeonidis, E., Smallbone, K., Spasic, I., Weichart, D., Brent, R., Broomhead, D. S., Westerhoff, H. V., Kırdar, B., Penttilä, M., Klipp, E., Palsson, B. Ø., Sauer, U., Oliver, S. G., Mendes, P., Nielsen, J., and Kell, D. B., A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. *Nature Biotechnology,* 26(10): 1155–1160, 2008.

Bornstein, B. J., Keating, S. M., Jouraku, A., and Hucka, M., LibSBML: an API Library for SBML. *Bioinformatics*, 24(6):880–881, 2008.

Hlavacek, W. S., Faeder, J. R., Blinov, M. L., Posner, R. G., Hucka, M., and Fontana, W., Rules for modeling signal-transduction systems. *Science STKE*, 344, July 18, 2006.

Keating, S. M., Bornstein, B. J., Finney, A., and Hucka, M., SBMLToolbox: an SBML Toolbox for MATLAB users. *Bioinformatics*, 22:1275–1277, 2006.

Schilstra, M. J., Li, L., Matthews, J., Finney, A., Hucka, M., and Le Novère, N., CellML2SBML: Conversion of CellML into SBML. *Bioinformatics*, 22:1018–1020, 2006.

Le Novère, N., Finney, A., Hucka, M., Bhalla, U. S., Campagne, F., Collado-Vides, J., Crampin, E. J., Halstead, M., Klipp, E., Mendes, P., Nielsen, P., Sauro, H., Shapiro, B., Snoep, J. L., Spence, H. D., and Wanner, B. L., Minimum information requested in the annotation of biochemical models (MIRIAM). *Nature Biotechnology*, 23(12):1509–1515, 2005.

Le Novère, N., Bornstein, B., Broicher, A., Courtot, M., Donizelli, M., Dharuri, H., Li, L., Sauro, M., Schilstra, M., Shapiro, B., Snoep, J. L., and Hucka, M., BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems. *Nucleic Acids Research*, 34, Database issue, D689–D691, 2006.

Hucka, M., Finney, A., Bornstein, B. J., Keating, S. M., Shapiro, B. E., Matthews, J., Kovitz, B. L., Schilstra, M. J., Funahashi, A., Doyle, J. C., and Kitano, H., Evolving a Lingua Franca and Associated Software Infrastructure for Computational Systems Biology: The Systems Biology Markup Language (SBML) Project. *Systems Biology*, 1(1):41–53, 2004.

Sauro, H. M., Hucka, M., Finney, A., Wellock, C., Bolouri, H., Doyle, J., and Kitano, M., Next Generation Simulation Tools: The Systems Biology Workbench and BioSPICE Integration. *OMICS: A Journal of Integrative Biology*, 7(4):355–372, 2004.

Shapiro, B., Hucka, M., Finney, A., and Doyle, J. C, MathSBML: A Package for Manipulating SBML-Based Biological Models. *Bioinformatics*, 20(16):2829–2831, 2004.

Finney, A., and Hucka, M., Systems Biology Markup Language: Level 2 and Beyond. *Biochem. Soc. Trans.*, 32:1472–1473, 2003.

Hucka, M., Finney, A., Sauro, H. M., Bolouri, H., Doyle, J. C., Kitano, H., Arkin, A. P., Bornstein, B. J., Bray, D., Cornish-Bowden, A., Cuellar, A. A., Dronov, S., Gilles, E. D., Ginkel, M., Gor, V., Goryanin, I. I., Hedley, W. J., Hodgman, T. C., Hofmeyr, J.-H., Hunter, P. J., Juty, N. S., Kasberger, J. L., Kremling, A., Kummer, U., Le Novère, N., Loew, L. M. , Lucio, D., Mendes, P., Minch, E., Mjolsness, E. D., Nakayama, Y., Nelson, M. R., Nielsen, P. F., Sakurada, T., Schaff, J. C., Shapiro, B. E., Shimizu, T. S., Spence, H. D., Stelling, J., Takahashi, K., Tomita, M., Wagner, J., and Wang, J., The Systems Biology Markup Language (SBML): A Medium for Representation and Exchange of Biochemical Network Models, *Bioinformatics*, 9(4):524–531, 2003.

Goddard, N. H., Beeman, D., Cannon, R., Cornelis, H., Gewaltig, M. O., Hood, G., Howell, F., Rogister, P., De Schutter, E., Shankar, K., and Hucka, M., NeuroML for Plug and Play Neuronal Modeling. *Neurocomputing*, 44:1077–1081, 2002.

Goddard, N. H., Hucka, M., Howell, F., Cornelis, H., Shankar, K., and Beeman, D., Towards NeuroML: Model Description Methods for Collaborative Modelling in Neuroscience. *Philosophical Transactions of the Royal Society of London B*, 356(1412):1209–1228, 2001.

Hucka, M., Weaver, M., and Kaplan, S., Hebb's Accomplishments Misunderstood. *Behavioral and Brain Sciences*, 18(4):635–636, 1995.

Laird, J. E., Yager, E. S., Hucka, M., and Tuck, C. M., Robo-Soar: An Integration of External Interaction, Planning, and Learning Using Soar. *Robotics and Autonomous Systems*, 8:113–129, 1991.

BOOK CHAPTERS

Hucka, M., and Schaff, J. Trends and Tools for Modeling in Modern Biology. In *Photosynthesis in silico: Understanding Complexity from Molecules to Ecosystems*, ed. Laisk, A., Nedbal, L., and Govindjee, Springer Science+Business Media B.V., 2009.

Shapiro, B. E., Finney, A., Hucka, M., Bornstein, B. J., Funahashi, A., Jouraku, A., and Keating, S. M., SBML Models and MathSBML. In *Introduction to Systems Biology*, ed. Choi, S., Humana Press, 2007.

Finney, A., Hucka, M., Bornstein, B. J., Keating, S. M., Shapiro, B. E., Matthews, M., Kovitz, B. L., Schilstra, M. J., Funahashi, A., Doyle, J., and Kitano, H., Software Infrastructure for Effective Communication and Reuse of Computational Models. In *System Modeling in Cellular Biology: From Concepts to Nuts and Bolts*, eds. Szallasi, Z., Stelling, J., and Periwal, V., MIT Press, 2006.

Wanner, B. L., Finney, A., and Hucka, M., Modeling the *E. coli* cell: The need for computing, cooperation, and consortia. In *Systems Biology: Definitions and Perspectives*, eds. Alberghina, L., and Westerhoff, H., Springer, 2005.

Bower, J. M., Beeman, D., and Hucka, M., The GENESIS Simulation System. In *The Handbook of Brain Theory and Neural Networks*: *Second Edition*, ed. Arbib, M., MIT Press, 2003.

Hucka, M., Shankar, K., Beeman, D., and Bower, J., The Modeler's Workspace: Making model-based studies of the nervous system more accessible. In *Computational Neuroanatomy: Principles and Methods*, ed. Ascoli, G., Humana Press, 2002.

Hucka, M., Finney, A., Sauro, H., Bolouri, H., Doyle, J., and Kitano, H, The ERATO Systems Biology Workbench: An Integrated Environment for Multiscale and Multitheoretic Simulations in Systems Biology. In *Foundations of Systems Biology*, ed. Kitano, H., MIT Press, 2001.

Morohashi, M., Hucka, M., Sauro, H., Finney, A., Bolouri, H., Doyle, J., and Kitano, H., Systems Biology Workbench. In *Development of Systems Biology*, ed. Kitano, H., Springer-Verlag Tokyo, 2001.

Laird, J. E., Yager, E. S., Hucka, M., and Tuck, C. M., Robo-Soar: An Integration of External Interaction, Planning, and Learning Using Soar. In *Towards Learning Robots*, ed. Van de Velde, W., MIT Press, 1993.

OTHER PUBLICATIONS (PEER-REVIEWED CONFERENCE PAPERS, EDITORIALS, NON-PEER-REVIEWED OTHER)

Le Novère, N., Hucka, M., Anwar, N., Bader, G., Demir, E., Moodie, S., Sorokin, A. Meeting report from the first meetings of the Computational Modelling in Biology Network (COMBINE), *SIGS* 5(2): 577, 2011.

Hucka, M., Bergmann, F. T., Keating, S. M., and Smith, L., A profile of today's SBML-compatible software. *IEEE e-Science 2011 Workshop on Interoperability in Scientific Computing*, 2011.

Hucka, M. and Le Novère, N., Software that goes with the flow in systems biology. *BMC Bioinformatics*, 8:140, doi:10.1186/1741-7007-8-140, 2010.

Hucka, M., Bergmann, F. T., Hoops, S., Keating, S. M., Sahle, S., Schaff, J. C., Smith, L. P., and Wilkinson, D. J., The Systems Biology Markup Language (SBML): Language Specification for Level 3 Version 1 Core. *Nature Precedings*, http://dx.doi.org/10.1038/npre.2010.4959.1, 2010.

Hucka, M., An Overview of Several Standardization Efforts for Systems Biology. *Journal of Physiological Sciences*, 59 (Suppl.):102, 2009.

Hucka, M., Hoops S., Keating S., Le Novère N., Sahle S., Wilkinson D.J. Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. *Nature Precedings*, doi: 10.1038/npre.2008.2715.1, 2008. [This is SBML Level 2 Version 4.]

Le Novère, N., Moodie, S., Sorokin, A., Hucka, M., Schreiber, F., Demir, E., Mi, H., Matsuoka, Y, Wegner, K., and Kitano, H. Systems Biology Graphical Notation: Process Diagram Level 1. *Nature Precedings*, DOI:10101/npre.2008.2320.1, 2008.

Hucka, M., Finney, A., Hoops, S., Keating, S., and Le Novère, N., Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. *Nature Precedings*, doi:10101/npre.2007.58.1, 2007. [This is SBML Level 2 Version 3.]

Sauro, H. M., Harel, D., Uhrmacher, A. M., Hucka, M., Kwiatkowska, M., Shaffer, C. A., Mendes, P., Strömbäck, L., Tyson, J. J. Challenges for modeling and simulation methods in systems biology. In *Proceedings of the 2006 Winter Simulation Conference*, IEEE Press, 2006.

Hucka M., Finney A., and Le Novère N., Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. http://sbml.org/Documents/Specifications/, 2006. [This is Level 2 Version 2.]

Hucka, M., and Finney, A., Escalating model sizes and complexities call for standardized forms of representation. *Molecular Systems Biology*, doi:10.1038/msb4100015, 25 May 2005.

Hucka M., and Finney A., Systems Biology Markup Language (SBML) Level 2: Structures and Facilities for Model Definitions. http://sbml.org/Documents/Specifications/, 2003. [This is Level 2 Version 1.]

Hucka M., Finney A., Sauro, H., and Bolouri, H., Systems Biology Markup Language (SBML) Level 1: Structures and Facilities for Basic Model Definitions. http://sbml.org/Documents/Specifications/, 2003. [This is Level 1 Version 2.]

Hucka, M., Sauro, H., Finney, A., Bolouri, H., Doyle, J., and Kitano, H., The ERATO Systems Biology Workbench: Enabling Interaction and Exchange Between Software Tools for Computational Biology. In *Biocomputing 2002*, ed. Altman, R., et al., 2002.

Hucka, M., Finney, A., Sauro, H. M., Bolouri, H., Doyle, J., and Kitano, H., The ERATO Systems Biology Workbench: Architectural Evolution. In *Proceedings of the Second International Conference on Systems Biology*, eds. Yi, T.-M., Hucka, M., Morohashi, M. and Kitano, H., Omnipress, Inc., 2001.

Finney, A. F., Hucka, M., Sauro, H. M., Bolouri, H., Doyle, J., and Kitano, H., An Overview of the ERATO Systems Biology Workbench Project. In *Proceedings of the 2nd Workshop on Computation of Biochemical Pathways and Genetic Networks*, eds. Gauges, R., van Gend, C., and Kummer, U., Logos-Verlag, 2001.

Hucka M., Finney A., Sauro, H., and Bolouri, H., Systems Biology Markup Language (SBML) Level 1: Structures and Facilities for Basic Model Definitions. http://sbml.org/Documents/Specifications/, 2001. [This is Level 1 Version 1.]

Hucka, M., and Kaplan, S., Texture-Based Processing in Early Vision and a Proposed Role for Coarse-Scale Segmentation. *Online Proceedings of the 1996 Midwest Artificial Intelligence and Cognitive Science Conference*, ed. Gasser, M., 1996.

Hucka, M., Ritter, F. E., and McGinnis, T. F., *Soar-mode Manual*. Technical Report CMU-CS-92-205. School of Computer Science, Carnegie Mellon University, Pittsburgh, 1992.

Laird, J. E., Hucka, M., Huffman, S., and Rosenbloom, P., An Analysis of Soar as an Integrated Architecture. *ACM SIGART Bulletin Special Section on Integrated Cognitive Architectures*, 1991.

Laird, J. E., Hucka, M., Yager, E. S., and Tuck, C. M., Correcting and Extending Domain Knowledge Using Outside Guidance. In *Proceedings of the Seventh International Conference on Machine Learning*, Morgan Kaufmann, 1990.

Laird, J. E., Yager, E. S., Tuck, C. M., and Hucka, M., Learning in Tele-autonomous Systems using Soar. *1989 NASA Conference on Space Telerobotics*, 1989.

INVITED AND PLENARY LECTURES

"How SBML and other tools are transforming computer models of life", invited lecture, *Victorian Systems Biology Symposium*, Melbourne, Australia, August, 2013.

"A summary of SBML and other COMBINE standardization and integration activities", invited lecture, *International Symposium on Integrative Bioinformatics 2013*, Gatersleben, Germany, March, 2013.

"SBML and related resources and standardization efforts", invited lecture, *The 4th Global COE International Symposium on Physiome and Systems Biology for Integrated Life Sciences and Predictive Medicine*, Osaka, Japan, November, 2011.

"SBML (the Systems Biology Markup Language)", invited virtual lecture, NCI *caBIG IGR seminar series*, July, 2011.

"Possibly relevant efforts in SBML Level 3", invited lecture, *Multicellular Modeling Workshop*, Nottingham, UK, May 2011.

"MIRIAM Resources", invited lecture, *NeuroML Development Workshop*, London, UK, March, 2011.

"Finding common ground between modelers and simulation software in systems biology", keynote lecture, *Merging Knowledge: From Programming Languages to Personalised Healthcare*, Trento, Italy, 2010.

"SBML fly-by", invited lecture, *Cell Behavior Ontology and Standards for Multicellular Modeling Workshop*, Edinburgh, Scotland, 2010.

"A brief summary of SBML (the Systems Biology Markup Language)", invited lecture, *Second NeuroML Development Workshop*, Tempe, Arizona, 2010.

"Sharing computational models: SBML and related standardization efforts for systems biology", invited lecture, *Winter School on Computational Modeling in Biology*, Okinawa, Japan, 2009.

"An overview of several standardization efforts for systems biology", invited lecture, *Building the Virtual Physiological Human Community Satellite Symposium of IUPS 2009*, Kyoto, Japan, 2009.

“The Systems Biology Markup Language (SBML) and related standardization efforts”, invited lecture, NIH *National Technology Centers for Networks and Pathways Annual All Hands Meeting*, Bethesda, Maryland, 2009.

“SBML, SBGN, and more: An overview of several standardization efforts for computational systems biology”, invited lecture, 3rd MEI International Symposium on *Physiome and Systems Biology for Integrated Life Sciences and Predictive Medicine*, San Francisco, California, 2008.

“An overview of several standardization efforts for computational systems biology”, invited seminar, *Center for Computational and Systems Biology (CoSBi)*, Trento, Italy, 2008.

“SBML: present status and extensions to support the representation of molecular states and complexes”, invited lecture, *Genomes to Systems 2008*, Manchester, UK, 2008.

“The SBML experience of developing a popular format”, invited lecture, *Workshop on Standards and Specifications in Synthetic Biology*, Seattle, Washington, 2008.

“Modular models in SBML Level 3: Update on progress”, invited lecture, *Workshop on Standards and Specifications in Synthetic Biology*, Seattle, Washington, 2008.

“Standardization efforts for the representation and exchange of computational models”, invited lecture, *International Workshop on Future Challenges for Systems Biology*, Tokyo, Japan, 2008.

“SBML, BioModels Database, MIRIAM, and SBO: Infrastructure Projects for Computational Systems Biology”, plenary lecture, *AusBiotech Bioinformatics Australia 2007*, Brisbane, Australia, 2007.

“Share what you know: SBML and BioModels.net”, invited lecture, *Computational Cell Biology IV*, Cold Spring Harbor Laboratory, NY, 2007.

“SBML and Related Efforts in Standardization for Computational Systems Biology”, invited seminar, University of Rostock, Germany, 2007.

“The Systems Biology Markup Language (SBML): Where It's Been and Where It's Going”, invited lecture, *Seventh International Conference on Systems Biology (ICSB 2006)*, Yokohama, Japan, 2006.

“SBML, SBGN and BioModels.net”, invited lecture, PRIME *Pathway Databases and Modeling Tools Workshop*, 2006.

“Evolving Standards and Infrastructure for Systems Biology: SBML, SBGN, and BioModels.net”, invited lecture, *Third IECA Conference on Systems Biology of E. coli*, Jeju Island, Korea, 2006.

“The Systems Biology Markup Language (SBML)”, invited lecture, *BioPAX Symposium*, Tokyo, Japan, 2005.

“The Systems Biology Markup Language (SBML) Project”, invited seminar, Blueprint Initiative, Toronto, Canada, 2005.

“The Systems Biology Markup Language (SBML): Candidate Model Definition Language?”, invited lecture, DARPA *Workshop on Tool and Software Infrastructure for Systems Biology*, Washington, DC, 2005.

“Efforts Towards Spatial Representation for the Systems Biology Markup Language (SBML) Level 3”, invited lecture, *Workshop on Computational Methods for Spatially Realistic Cellular Simulations,* Pittsburgh, PA, 2004.

“Software Infrastructure for Enabling Greater Collaboration in Computational Modeling: The Systems Biology Markup Language (SBML) Project”, invited lecture, *International Conference on Molecular Systems Biology (ICMSB'04)*, Tahoe City, Nevada, 2004.

“A Roundup of Software Tools for SBML from SBML.org”, invited lecture, *2004 Biopathways Consortium* workshop, Glasgow, Scotland, 2004.

“Software in Systems Biology and the Systems Biology Markup Language (SBML)”, invited seminar, CHR Colloquium Series, CIIT, Research Triangle Park, NC, 2004.

“The Systems Biology Markup Language (SBML) and the Systems Biology Workbench (SBW)”, invited lecture, *ERATO Final Symposium*, Tokyo, Japan, 2003.

“Systems Biology Markup Language (SBML): Recent Progress and Current Directions”, invited lecture, *2003 Biopathways Consortium* workshop, Brisbane, Australia, 2003.

“Systems Biology Markup Language (SBML): Recent Progress and Current Directions”, invited lecture, *First IECA Conference on Systems Biology of E. coli, Tsuruoka, Japan, 2003*.

“Modeling and Simulation in Systems Biology”, invited seminar, Regenstrief Institute Medical Informatics Computational Molecular Biology Series, Indiana University School of Medicine, 2003.

“The Systems Biology Markup Language”, invited lecture, I3C 4th Quarter Technical Meeting, San Diego, CA, 2002.

TEACHING AND STUDENT SUPERVISION

Courses

Lecturer, Cold Spring Harbor Laboratory (CSHL) course *Computational Cell Biology*, 2008–2014.

Lecturer, *Winter School on Computational Modeling in Biology*, Okinawa, Japan, 2009.

Lecturer, *BioModels.net Training Camp*, EBML-EBI, Hinxton, UK, 2006–2007.

Lecturer (remote), *Introductory Course on Systems Biology*, National Autonomous University of Mexico, 2007.

Instructor, *Programming in Common Lisp* summer course (organized, developed and co-taught), Electrical Engineering and Computer Science department, University of Michigan, 1988.

Ph.D. student visitors

Joanna Murakami (2009), Enuo He (2007), Adrián López García de Lomana (2005).

Student competitions

Panel judge, *Doris S. Perpall Speaking Award* (presentations by Caltech undergraduates), 2008.

ADVISORY ACTIVITIES

Invited grant proposal reviews

NIH study sections: *Special Emphasis Panel for Continued Development and Maintenance of Software* (May 2010), *Challenge Grants in Health and Science Research* (June 2009), *Special Reviews in Bioengineering* (August 2008), *Modeling and Analysis of Biological Systems* (June 2008), *Special Emphasis Panel on Data Sharing & Collaboration Tools* (2004), *Modeling and Analysis of Biological Systems* (June and October, 2004).

BBSRC (UK) *Bioinformatics and Biological Resources Fund*, 2007 and 2008.

Japan Science and Technology *Exploratory Research for Advanced Technology* (ERATO), 2008.

Israel Science Foundation, 2007.

Invited advisory & program committee participation

15th International Conference on Systems Biology (ICSB 2014) Scientific Committee member, 2014.

13th International Conference on Systems Biology (ICSB 2012) Program Committee member, 2012.

Winter Simulation Conference 2012, Modeling Methodology Track, Program Committee member.

Identifiers.org Board of Trustees member, 2011–present.

Systems Biology Graphical Notation (SBGN) Scientific Committee member, 2010–present.

BioModels Database Scientific Advisory Board member, 2007–present.

Virtual Physiological Human (VPH) Network of Excellence (NoE) Scientific Advisory Board member, 2009–2011.

Microsoft Research – University of Trento Centre for Computational and Systems Biology (CoSBi) Scientific Advisory Board member, 2009–2011.

11th International Conference on Systems Biology (ICSB 2010) Scientific Committee member, 2010.

EcoCyc Steering Committee member, 2006–2010.

EcoliHub Steering Committee member, 2007–2009.

9th International Conference on Systems Biology (ICSB 2008) Program Committee member, 2008.

7th International Conference on Systems Biology (ICSB 2006) Program Committee member, 2006.

International Society for Systems Biology (ISSB) Founding member and Executive Board member, 2006–2008.

6th Annual CHI Beyond Genome Conference, Scientific advisor and session chair, 2004.

5th Annual CHI Beyond Genome Conference, Scientific advisor and session chair, 2003.

Invited panel participation

Society of Toxicology CCT "Building for Better Decisions: Multi-Scale Integration of Human Health and Environmental Data", May 2012.

NSF *US-European Commission Workshop on Infrastructure Needs of Systems Biology*, May 2007.

NSF workshop on *Facilitating Microbial Research Through Advanced Data Management*, 2003.

NARRC Working Group meeting on *Computational Infrastructure for Cell Biology*, 2002.

Standards editorial boards

Chair, Systems Biology Markup Language (SBML) Editors, 2003–present.

Systems Biology Graphical Notation (SBGN) Editor, 2005–2009.

PROFESSIONAL ACTIVITIES AND SERVICE

Conference organization

Co-organizer, *Eighth International Conference on Systems Biology (ICSB 2007)*, Long Beach, CA, October 1–6, 2007.

Co-organizer, *Second International Conference on Systems Biology (ICSB 2001)*, Pasadena, CA, November 4–7, 2001.

Workshop organization

Co-organizer*, COmputational Modeling in Biology NEtwork (COMBINE) series, 2010–present.*

Co-organizer*, HAckathon on Resources for MOdeliNg in biologY (HARMONY) series, 2011–present.*

Co-organizer, all international and national *SBML Forum* workshops (10 total), 2002–2009.

Co-organizer, all international and national *SBML Hackathon* workshops (7 total), 2003–2010.

Co-organizer, multiple international SBML focused workshops (4 total), 2007–2011.

Co-organizer, Caltech BNMC Workshops, Caltech, 2006–2009.

Co-organizer, *CellML-SBGN-SBO-BioPAX-MIASE Workshop,* Auckland, New Zealand, 2009.

Co-organizer, *Systems Biology Graphical Notation (SBGN)* workshops (5 total), 2006–2008.

Co-organizer, *Standards and Ontologies for Systems Biology* workshop, Okinawa, Japan, 2008.

Co-organizer, *Rule-Based Modeling of Biochemical Systems* workshop, Santa Fe Institute, 2007.

Co-organizer, NSF-European Commission Workshop on *Infrastructure Needs of Systems Biology*, Boston, Massachusetts, May 2007.

Co-organizer, *Workshop on Software Platforms for Systems Biology* series, 2001–2002 (3 total).

Institutional seminar series organization

Co-organizer, Caltech BNMC Seminars, 2006–2009.

Principal organizer, *Natural and Artificial Vision Systems* series (University of Michigan), 1996.

Principal organizer, *Neural Computing* seminar series (University of Michigan), 1993.

Journal reviews

Associate Editor, BMC Systems Biology.

Ad hoc reviewer for Bioinformatics, BMC Bioinformatics, BMC Biology, BMC Systems Biology, Computer Methods and Programs in Biomedicine (CMPB), IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB), Nature, Nature Biotechnology, PLoS Computational Biology, Science, Wiley Interdisciplinary Reviews—Systems Biology.

RESOURCE DEVELOPMENT

(The following is a selection of my more recent work on software and related resources.)

Co-developer, *SBML Test Suite*, 2008–present. The SBML Test Suite consists of several components. The standalone SBML Test Runner is written in Java and uses the SWT user interface toolkit, while the Online SBML Test Suite is written in Java, JavaScript, JSP and HTML, and runs in an Apache Tomcat server. Collectively, the Test Suite is a conformance-testing suite that allows users to test software against a collection of SBML test models and verify whether the simulation results match those expected for each test case. The standalone version is a desktop application that drives applications and plots the results, while the online version allows users to upload simulation results and compares the uploaded results to results expected for each test model, then produces graphs and other visualizations to show how the uploaded results differ from the expected values. Like all software developed by my team, the underlying software is available under LGPL terms from the SBML project area on SourceForge.net.

Co-developer, *libSBML*, 2003–present. LibSBML is a free, open-source, programming library that helps software application developers implement support for reading, writing, manipulating, translating, and validating SBML files and data streams. It is portable to Windows, Mac OS X, and Linux. It is written in C++ and C, and includes SWIG-based language interfaces to C#, Java, MATLAB, Octave, Perl, Python, and Ruby. It also includes extensive, high-quality API documentation. We release updated versions of libSBML roughly every two months, and the download statistics at SourceForge.net indicate that *each* release is downloaded an average of 2500 to 6000 times.

Principal developer and maintainer, *SBML.org* website (multiple generations), 2000–present. I single-handedly designed and implemented all aspects of the website, including custom MediaWiki skins, custom MediaWiki PHP and Javascript extensions, HTML & graphics content, site structure, back-end facilities, server operations, hardware configuration and management, Linux systems management, and backup system, and continue to maintain the site and its infrastructure. According to Google Analytics, the SBML.org website receives a *monthly* average of 2500 unique visitors and 11,000 page views, with 56% of visitors being new (based on averaging the monthly data from the period of November 1, 2013, to March 1, 2014).

Principal developer, Caltech BNMC website (original version, all aspects), 2006–2009.

Principal developer, *SBGN.org* website (layout and MediaWiki implementation), 2006–2009.

Principal developer, *BioModels.net* website (original version—no longer online), 2004–2009.

Co-developer, *Systems Biology Workbench* (SBW), 2000–2003. SBW is a software interoperability framework, similar to CORBA but lighter and simpler. It uses a broker-based architecture that enables applications (potentially running on separate machines) to discover and communicate with each other. The communications facilities allow heterogeneous software tools to be connected together using a custom remote procedure call mechanism, this mechanism uses a simple message-passing network protocol and allows both synchronous and asynchronous invocation. SBW includes interface libraries for C, C++, Delphi, Java, Perl and Python, runs on Windows, Linux and FreeBSD, and includes a number of SBW modules such as a stochastic simulator, a simple generic GUI for simulation control, a simple plotting module, and more. (Note: I stopped working on SBW in 2003. Another one of the original developers, H. Sauro, and his students continued to support and enhance it since that time, but apart from the network protocol and basic concept, very little in the current version of SBW resembles the original.)