MICHAEL HUCKA

PROFESSIONAL PREPARATION

University of Utah	Computer Science	B.S. Honors, June 1986
University of Utah	Electrical Engineering	B.S. Honors, June 1987
University of Michigan	Computer Science and Electrical Engineering	M.S.E. June 1991
University of Michigan	Computer Science and Electrical Engineering	Ph.D. June 1998
California Institute of Technology	Biology	Postdoc (1998-2000)

APPOINTMENTS

2009–present	Staff Scientist, Control and Dynamical Systems, Caltech
2005–2011	Senior Research Fellow, Control and Dynamical Systems, Caltech
2005–2009	Co-Director, Biological Network Modeling Center, Caltech
2001–2005	Staff Research Programmer, Control and Dynamical Systems, Caltech
1998–2000	Postdoctoral Scholar, Division of Biology, Caltech
1995–1998	Staff Programmer Analyst, Computer Science and Engineering, Univ. of Michigan
1992–1994	Staff Programmer, Computer Science and Engineering, Univ. of Michigan
1988–1992	Research Assistant, Computer Science and Engineering, Univ. of Michigan

PRODUCTS

1. 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.
2. D. Waltemath, R. Adams, F.T. Bergmann, **M. Hucka**, F. Kolpakov, A. Miller, I.I. Moraru, D. Nickerson, J. Snoep, N. Le Novère. Reproducible computational biology experiments with SED-ML—The Simulation Experiment Description Markup Language. *BMC Systems Biology* 5:198, 2011.
3. M. Courtot, N. Juty, C. Knüpfer, D. Waltemath, A. Zhukova, A. Dräger, M. Dumontier, A. Finney, M. Golebiewski, J. Hastings, S. Hoops, S. Keating, D. Kell, S. Kerrien, J. Lawson., A. Lister, J. Lu, R. Machne, P. Mendes, M. Pocock, N. Rodriguez, A. Villeger, D. Wilkinson, S. Wimalaratne, C. Laibe, **M. Hucka**, N. Le Novère. Controlled vocabularies and semantics in Systems Biology. *Molecular Systems Biology*, 7, 2011.
4. N. Le Novère, A. Finney, **M. Hucka**, U.S. Bhalla, F. Campagne, J. Collado-Vides, E.J. Crampin, M. Halstead, E. Klipp, P. Mendes, P. Nielsen, H. Sauro, B. Shapiro, J.L. Snoep, H.D. Spence, and B.L. Wanner, Minimum information requested in the annotation of biochemical models (MIRIAM), *Nature Biotechnology* 23(12):1509–1515, 2005.
5. **M. Hucka**, A. Finney, H. Sauro, H. Bolouri, J.C. Doyle, H. Kitano, A.P. Arkin, BJ. Bornstein, D. Bray, A. Cornish-Bowden, A.A. Cuellar, S. Dronov, E.D. Gilles, M. Ginkel, V. Gor, I.I. Goryanin, W.J. Hedley, T.C. Hodgman, J.-H. Hofmeyr, P. Hunter, N.S. Juty, J. Kasberger, A. Kremling, U. Kummer, N. Le Novère, L. Loew, D. Lucio, P. Mendes, E. Minch, E.D. Mjolsness, Y. Nakayama, M.R. Nelson, P.F. Nielsen, T. Sakurada, J.C. Schaff, B. Shapiro, T. Shimizu, H. Spence, J. Stelling, K. Takahashi, M. Tomita, J. Wagner, J. Wang, "The Systems Biology Markup Language (SBML): A Medium for Representation and Exchange of Biochemical Network Models", *Bioinformatics* 19(4):524-531, 2003.

OTHER SELECTED PRODUCTS

1. 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.
2. Dräger, N. Rodriguez, M. Dumousseau, A. Dörr, C. Wrzodek, N. Le Novère, A. Zell, and **M. Hucka**. JSBML: a flexible Java library for working with SBML. *Bioinformatics*, 27(15):2167–2168, 2011.
3. Li, M. Donizelli, N. Rodriguez, H. Dharuri, L. Endler, V. Chelliah, L. Li, C. He, A. Henry, M.I. Stefan, J.L. Snoep, **M. Hucka**, N. Le Novère, and C. Laibe, BioModels Database: An enhanced, curated and annotated resource for published quantitative kinetic models. *BMC Systems Biology*, 4(92), 2010.
4. B.J. Bornstein, S.M. Keating, A. Jouraku, and M. Hucka, LibSBML: an API Library for SBML. Bioinformatics, 24(6):880–881, 2008.

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

SYNERGISTIC ACTIVITIES

SBML. The Systems Biology Markup Language (SBML) is a machine-readable exchange language for computational models in systems biology. Hucka, with Andrew Finney, Hamid Bolouri, Herbert Sauro, John Doyle and Hiroaki Kitano, developed the first version in 2000. He continues to lead the international SBML effort. SBML is supported by 250+ software tools worldwide (open-source and commercial).

SBML.org website (multiple generations). Hucka 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 continues to maintain the site and its infrastructure.

BioModels.net. In collaboration with Nicolas Le Novère of the European Bioinformatics Institute (EBI) in the UK, Hucka created *BioModels.net* for organizing several collateral efforts related to SBML and interoperability. The partnership includes *BioModels Database*, the subject of this proposal, as well as related efforts on standards for curation (MIRIAM) and the Systems Biology Ontology (SBO).

Other activities. Hucka performs outreach activities, including seminars at summer courses such as the Computational Cell Biology course at Cold Spring Harbor Labs, tutorials on SBML at conferences, and others. He co-organized two international conferences, the *2nd International Conference on Systems Biology* (ICSB 2001) the *8th International Conference on Systems Biology* (ICSB 2007). He is on the advisory committees of several community resources, such as Identifiers.org.

COLLABORATORS/CO-EDITORS/CO-AUTHORS DURING LAST 48 MONTHS

G.D. Bader (U. Toronto, Canada), D. Bérenguier (Institut de Mathématiques, France), F.T. Bergmann (U. Heidelberg, Germany), E. Birney (EMBL-EBI, UK), M. Blinov (UCHC), F. Büchel (ZBIT, Germany), L. Calzone (Institut Curie, France), C. Chaouiya (Instituto Gulbenkian de Ciência, Portugal), J. Cooper (U. Oxford, UK), M. Courtot (Terry Fox Laboratory, Canada), K. Dahlquist (Loyola Marymount University), H. de Jong (INRIA Grenoble, France), E. Demir (MSKCC Center, NYC), P. D'Eustachio (NYU School of Medicine), P. Dobson (U. Manchester, UK), A. Dörr (U. Tübingen, Germany), A. Dräger (U. Tübingen, Germany), M. Dumontier (Stanford), M. Dumousseau (EMBL-EBI, UK), L. Endler (EMBL-EBI, UK), W. Fontana (Harvard Med), A. Funahashi (Keio University, Japan), A. Garny (U. Oxford, UK), M. Golebiewski (HITS gGmbH, Germany), T. Helikar (U. Nebraska), M.J. Herrgård (UCSD), W. Hlavacek (LANL), S. Hoops (VBI), P. Hunter (U. Auckland, New Zealand), P.D. Karp (SRI International), S.M. Keating (EMBL-EBI, UK), D.B. Kell (U. Manchester, UK), S. Klamt (Max Planck Institute, Germany), H. Kitano (SBI, Japan), E. Klipp (Humboldt Universität, Germany), K. Kohn (NCI), C. Laibe (EMBL-EBI, UK), N. Le Novère (EMBL-EBI, UK), P. Li U. Manchester, UK, W. Liebermeister (Max-Planck-Institut, Germany), A. Luna (NIH), P. Mendes (U. Manchester, UK), H. Mi (SRI International), M. Mo (UCSD), S. Moodie (U. Edinburgh, UK), I.I. Moraru (UCHC), W. Müller (EML Research, Germany), P. Murray-Rust (U. Cambridge, UK), A. Naldi (U. Lausanne, Switzerland), D. Nickerson (U. Auckland, New Zealand), J. Nielsen (Technical U. of Denmark, Denmark), P. Nielsen (U. Auckland, New Zealand), S.G. Oliver (U. Manchester, UK), B. Ø. Pallson (UCSD), S. Pettifer (U. Manchester, UK), H. Planatscher (U. Tübingen, Germany), R.G. Posner (Translational Genomics, Phoenix), , N. Rodriguez (EMBL-EBI, UK), J. Saez-Rodriguez (EMBL-EBI, UK), S. Sahle (U. Heidelberg, Germany), C. Sander (MSKCC, NYC), H.M. Sauro (U. Washington), J. Schaff (UCHC), F. Schreiber (Leibniz Institute, Germany), I. Shah (EPA), N. Shah (Stanford), K. Smallbone (U. Manchester, UK), L.P. Smith (U. Washington), A. Sorokin (U. Edinburgh, UK), A. Splendiani (Université Rennes, France), M.I. Stefan (EMBL-EBI, UK), N. Swainston (U. Manchester, UK), I. Thiele (U. Iceland, Iceland), D. Thieffry (IBENS, France), P. Thomas (SRI International), M. van Iersel (Maastricht University, The Netherlands), A. Villéger (U. Manchester, UK), D. Waltemath (U. Rostock, Germany), H.V. Westerhoff (U. Manchester, UK), D. Wilkinson (Newcastle U., UK), S. Wimalaratne (EMBL-EBI, UK), O. Wolkenhauer (U. Rostock, Germany), C. Wrzodek (U. Tübingen, Germany), A. Zell (U. Tübingen, Germany.

GRADUATE AND POSTGRADUATE ADVISORS

Graduate advisors: Professors John E. Laird and Stephen Kaplan, University of Michigan.
Postgraduate advisors: Professor James Bower, Caltech, Pasadena.
Thesis Advisor and Postgraduate-Scholar Sponsor: none.