**REINHARD C. LAUBENBACHER, PH.D.**

*January 2022*

Reinhard C. Laubenbacher, Ph.D.

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Division of Pulmonary, Critical Care, and Sleep Medicine

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**ACADEME**

**Education**

Ph.D. Mathematics 1985 Northwestern University, Evanston IL

M.A. Mathematics 1978 Indiana University, Bloomington, IN

Vordiplom Mathematics 1975 University of Munich, Germany

**Employment and Academic Positions**

2020-present Dean’s Professor of Systems Medicine, Department of Medicine, University of Florida

2020-present Director, Laboratory for Systems Medicine, University of Florida Health

2013-2020 Professor of Computational Biology, Jackson Laboratory for Genomic Medicine, Farmington, CT

2013-2020 Member, Comprehensive Cancer Center, Jackson Laboratory, Bar Harbor, ME

2013-2020 Professor, Department of Cell Biology, School of Medicine, University of Connecticut, Farmington, CT

2013-2020 Director, Center for Quantitative Medicine, University of Connecticut Health, Farmington, CT

2013-2020 Adjunct Professor, Department of Mathematics, University of Connecticut, Storrs, CT

2013-2020 Adjunct Professor, Department of Computer Science and Engineering, University of Connecticut, Storrs, CT

2013-2020 Professor, Institute for Systems Genomics, University of Connecticut, Storrs, CT

2013-2020 Professor, Center for Cell Analysis and Modeling, University of Connecticut Health Center, Farmington, CT

2008-present Affiliate Faculty, Biomedical Engineering and Sciences (SBES), Virginia Polytechnic Institute and State University (Virginia Tech) - Wake Forest University

2005-present Adjunct Professor, Department of Cancer Biology, Wake Forest University School of Medicine, Winston-Salem, NC

2008-2013 Director of Education & Outreach, Virginia Bioinformatics Institute –Virginia Tech, Blacksburg, VA

2003-2013 Faculty, Interdepartmental Ph.D. program “Genetics, Bioinformatics, and Computational Biology,” Virginia Tech, Blacksburg, VA

2001-2013 Professor, Department of Mathematics, Virginia Tech, Blacksburg, VA

2001-2013 Professor, Virginia Bioinformatics Institute at Virginia Tech, Blacksburg, VA

2011-2012 Member, Mathematical Biosciences Institute, The Ohio State University, Columbus, OH

2008-2009 Member, Statistical and Applied Mathematical Sciences Institute, Durham, NC

Spring 2007 Member, Institute for Mathematics and its Applications, University of Minnesota, Minneapolis, MN

1999-2004 Visiting Faculty, Basic and Applied Simulation Science Group, Los Alamos National Laboratory, Los Alamos, NM

1996-2001 Professor, Department of Mathematical Sciences, New Mexico State University, Las Cruces, NM

Fall 1998 Member, Mathematical Sciences Research Institute, Berkeley, CA

1991-1996 Associate Professor, Department of Mathematical Sciences, New Mexico State University, Las Cruces, NM

1993-1994 Visiting Associate Professor, Department of Mathematics, Cornell University, Ithaca, NY

1990-1991 Visiting Associate Professor, Department of Mathematics, Cornell University, Ithaca, NY

1985-1991 Assistant Professor, Department of Mathematical Sciences, New Mexico State University, Las Cruces, NM

1983-1985 Lecturer, Department of Mathematics, Loyola University, Chicago, IL

**Academic Honors and Awards**

* Fellow of the American Association for the Advancement of Science (AAAS), 2015-present.
* Fellow of the Society for Mathematical Biology, 2017-present.
* Fellow of the American Mathematical Society, 2012-present.
* “Programs That Work” award for the Kids’ Tech University outreach program, Virginia Department of Education and Virginia Math and Science Coalition, 2012.
* Phi Delta Kappa Award for Excellence in Education, 1998.
* Patricia Christmore Teaching Award, New Mexico State University, 1990.
* Fulbright Scholarship, 1977-1978.

**RESEARCH**

**Interests**

Multiscale modeling, systems medicine, mathematical and computational biology, immunology, cancer systems biology, bioinformatics.

**Research Support**

**Current Extramural Research Support**

NIH 1 R011AI135128-01 (Multi-PI)

Role: Contact PI

7/1/2018-6/30/2023 $3,014,116

 *Multiscale modeling of the battle over iron in invasive lung infection*

NIH 1R01GM127909-01 (Multi-PI)

Role: Contact PI

04/01/2018 – 03/31/2022 $1,696,582

 *Control of heterogeneous microbial communities using model-based multi-objective optimization*

NIH 3 R01 GM127909-01S1 (Multi-PI)

Role: Contact PI $110,182

 *Equipment Supplement to* 1R01GM127909-01

NIH 1U01EB024501-01 (Multi-PI)

Role: Contact PI $2,722,086

9/20/2017-8/31/2021

 *Modular design of multiscale models, with an application to the innate immune response to fungal respiratory pathogens.*

NSF CBET-1750183

Role: PI

5/1/2018-4/30/2019 $90,000

 *EAGER: Modular Design of Multiscale Models, with an Application to the Innate Immune Response to Fungal Respiratory Pathogens*

Mayday Fund

Role: PI

3/15/2018-3/15/2019 $50,000

 *Connecticut Pain Consortium Planning Grant*

NIH 1RO1GM114949-01A1 (subcontract to Worcester Polytechnic Institute)

Role: Subcontract PI $90,000

9/1/2015-8/30/2019

*Copper homeostasis in bacteria: Systems analysis from detailed molecular interactions*

NIH 1R01CA188025-01 Torti (PI)

Role: Co-investigator

07/01/14-08/31/19 $1,847,628

*Iron addiction and the biology of ovarian cancer*

**Select Completed Research Support**

NSF CBET-1750183

Role: PI

5/1/2018-4/30/2019 $90,000

 *EAGER: Modular Design of Multiscale Models, with an Application to the Innate Immune Response to Fungal Respiratory Pathogens*

Mayday Fund

Role: PI

3/15/2018-3/15/2019 $50,000

 *Connecticut Pain Consortium Planning Grant*

NIH 1RO1GM114949-01A1 (subcontract to Worcester Polytechnic Institute)

Role: Subcontract PI $90,000

9/1/2015-8/30/2019

*Copper homeostasis in bacteria: Systems analysis from detailed molecular interactions*

NIH 1R01CA188025-01 Torti (PI)

Role: Co-investigator

07/01/14-08/31/19 $1,847,628

*Iron addiction and the biology of ovarian cancer*

NIH Chuang (PI)

Role: Co-investigator

9/30/2015-6/30/2018

*Big Genomic Data Skills Training for Professors*

UConn Research Excellence Program

Role: PI

6/1/2017-6/30/2018

*Understanding the progression of ovarian cancer through the use of 3D bioprinting and mathematical modeling*

NIH 3R01MH102854-03S1 (PI: Stevens)

Role: Subcontract PI

8/2017-9/2018

*Dynamic connectivity in neural networks engaged for emotion regulation*

NSF-DMS 1460967

Role: PI

05/01/15-04/30/18

*REU Site: Modeling and Simulation in Systems Biology*

NIH Chuang (PI)

Role: Co-investigator

08/01/2016-06/30/2017

 *Big Genomic Data Skills Training for Professors* (competitive supplement)

W911NF-14-1-0486 U.S. Army Research Office

Role: PI

08/01/14-07/31/17

*Biomathematics-Canalization: A fundamental design principle of gene regulatory networks*

NSF DBI-1146819

Role: PI

6/2012-5/2016 (1-year no cost extension)

*PlantSimLab: A simulation laboratory for plant biology*

(Subaward to J. Glazebrook, Univ. of Minnesota, $62,017)

NIAID-NIH 1R21AI101619-01

Role: PI

6/2012-5/2014

 *The systems biology of iron homeostasis and the immune response to Aspergillus*

NCI-NIH 1R21CA156133-01A1

Role: PI

8/2011-7/2013

 *A Systems Approach to Iron Metabolism in Cancer Cells*

U.S. Army Research Office W911NF0910538

Role: PI

8/2009-7/2013

*Computational Biomathematics: Toward Optimal Control of Complex Biological Systems*

NSF-CMMI-0908201

Role: PI

10/2009-9/2013

*Polynomial dynamical systems over finite fields: from structure to dynamics*

NSF-DMS-1062878

Role: PI

1/2011-1/2014

 *REU Site: Modeling and Simulation in Systems Biology*

USDA AFRI

PI: B. Tyler

Role: Co-PI

4/2011-3/2016

*Integrated management of oomycete diseases of soybean and other crop plants*

Wake Forest University Translational Science Institute (TSI)

V. Shulaev (PI)

Role: Co-PI

6/2008-5/2010

*Translational breast cancer metabolomics*

DMS-0755322-NSF – REU

Role: PI

5/2008 - 4/2011

*REU Site: Modeling and Simulation of Biological Networks.*

RO1CA120170-01A2 – NIH

V. Shulaev (PI)

Role: Co-PI

6/2007- 5/2010

*Molecular fingerprinting of breast cancer development*.

EEC-0609225- NSF

R. Davalos (PI)

Role: Co-PI

8/2006-8/2010

*BBSI: Summer Institute for Quantitative and Integrative Bioengineering.*

DMS-051144 – NSF

Role: PI

9/2005-8/2008

*Mathematical algorithms for computer simulation.*

RO1 GM068947-01 - NIH

Role: PI

5/2003-4/2008

*A new mathematical modeling approach to biochemical networks, with an application to oxidative stress in yeast.*

*Computer simulations of Epstein-Barr Virus infection.* NIH (subcontract), 2005-2006

*A mathematical foundation for computer simulation.* Los Alamos National Laboratory (PI), 2003-04.

*Algebraic algorithms for cell complexes*. NSF (PI), 2002-04.

*Biocomplexity-incubation activity: The mathematics of network dynamics in biological, social, and economic networks.* NSF (PI), 2002-03.

*Mathematical foundation of computer simulation.* Los Alamos National Laboratory (PI), 1999-2002.

*Decision related structures.* U.S. Department of Defense (senior personnel), 1999-2002.

*Cryptography as a teaching tool in secondary education.* Los Alamos Nat.Laboratory (PI), 1999-2002.

*A capstone course: learning mathematics through original sources*. NSF (co-PI), 1997-1999.

*Southwest Regional Institute in the mathematical sciences.* NSF (subcontract), 1996-99.

*Combinatorial dynamics.* Defense Intelligence Systems Agency (senior personnel), 1996-98.

*Noncommutative Gröbner bases and rewriting systems.* NSA (co-PI), 1996-97.

*Teaching with original sources.*  NSF (co-PI), 1995-96.

*Using original sources in mathematics teacher education.*  Eisenhower Foundation (co-PI), 1995.

*Computational algebraic geometry.* NSA (PI), 1994-95.

*Computational algebraic geometry.* NSF (PI), 1994-95.

*Teaching with original sources.* NSF (co-PI), 1994-95.

*Great problems of mathematics: summer workshop for high school students.* NSF (co-PI), 1992-93.

**PUBLICATIONS**

**Peer-Reviewed Articles and Chapters**

1. L. Archambault, S. Koshy-Chenthittayil, A. Thompson, A. Dongari-Bagtzoglou, **R. Laubenbacher**, and P. Mendes, Understanding Lactobacillus paracasei and Streptococcus oralis biofilm interactions through agent-based modeling, *mSphere* **6**(6):e0087521, 2021.
2. L. Sordo Vieira and **R. Laubenbacher**, Computational models in systems biology: standards, dissemination, and best practices, *Current Opinion in Biotechnology,* under revision, 2021.
3. S. Koshy-Chenthittayil, P. Mendes, and **R. Laubenbacher**, Optimization of agent-based models through coarse-graining: A case study in microbial ecology, *Letters in Biomath.,* **8**(1), 167-178, 2021.
4. NC Atuegwu, MD Litt, S. Krishna-Sarin, **R. Laubenbacher**, MF Perez, EM Mortensen, E-cigarette use in young adult never cigarette smokers with disabilities: Results from the behavioral risk factor surveillance system survey, *Int. J. Environmental Res. and Public Health,* **18**, 5476, 2021.
5. Masison, J., J. Beezley, Y. Mei, H. a. L. Ribeiro, A. C. Knapp, L. Sordo Vieira, B. Adhikari, Y. Scindia, M. Grauer, B. Helba, W. Schroeder, B. Mehrad, **R. Laubenbacher**, A Modular Computational Framework for Medical Digital Twins, *Proceedings of the National Academy of Sciences* 118, no. 20, 2021. <https://doi.org/10.1073/pnas.2024287118>.
6. **R. Laubenbacher**, J.P. Sluka, J.A. Glazier, Using digital twins in viral infection, *Science,* **371**(6534), 1105-1106, DOI: 10.1126/science.abf3370, 2021.
7. S. Koshy-Chenthittayil, L. Archambault, D. Senthilkumar, **R. Laubenbacher**, P. Mendes, A. Dongari-Bagtzoglou, Agent based models of polymicrobial biofilms and the microbiome – A Review, *Microorganisms*, **9**(2), 417, 2021.
8. C. Kadelka, B. Keilty, **R. Laubenbacher**, Collectively canalizing Boolean functions, <http://arxiv.org/abs/2008.13741>, 2020.
9. Atuegwu NC, Oncken C, **Laubenbacher RC**, Perez MF, Mortensen EM, Factors associated with e-cigarette use in U.S. young adult never smokers of conventional cigarettes, *International Journal of Environmental Research and Public Health,* **17**(19), 7271, <https://doi.org/10.3390/ijerph17197271>, 2020.
10. Aguilar, Boris, Pan Fang, Reinhard Laubenbacher, and David Murrugarra, “A Near-Optimal Control Method for Stochastic Boolean Networks”. *Letters in Biomathematics* 7 (1), 67–80, 2020.
11. A. Konstorum, L. Tesfay, B.T. Paul, F.M. Torti; **R.C. Laubenbacher**, S.V. Torti, Systems biology of ferroptosis:  A modeling approach, *J. Theor. Biol.,* **493**, 2020.
12. C. Brunson, T. Agresta, and **R. Laubenbacher,** Sensitivity of comorbidity network analysis, *J. Amer. Med. Inform. Assoc. Open,* **3**(1) 94-103, <https://doi.org/10.1093/jamiaopen/ooz067>, 2020.
13. E. Paul, G. Pogudin, W. Qin and **R. Laubenbacher**, The dynamics of canalizing Boolean networks, *Complexity,* <https://doi.org/10.1155/2020/3687961>, 2020.
14. L. Sordo Vieira, **R. Laubenbacher**, and D. Murrugarra, Control of Intracellular Molecular Networks Using Algebraic Methods, *Bull. Math. Biol.,* **82**(2), 2019.
15. R. Posner and **R. Laubenbacher**, The contribution of microRNA-mediated regulation to short- and long-term gene expression predictability, *J. Theor. Biol.* **486**, doi: 10.1016/j.jtbi.2019.110055, 2019.
16. S. Ha; E. Dimitrova; S. Hoops; D. Altarawy; M. Ansariola; D. Deb; J. Glazebrook; R. Hillmer; H. Shahin; F. Katagiri; J. McDowell; M. McGraw; J. Setubal; B.M. Tyler; **R. Laubenbacher**, PlantSimLab - A Modeling and Simulation Web Tool for Plant Biologists, *BMC Bioinformatics,*20(1) 508, doi: 10.1186/s12859-019-3094-9, 2019.
17. R. Posner and **R. Laubenbacher**, Connecting the molecular function of microRNAs to cell differentiation dynamics, *J. Royal Soc. Interface,* **16** (158), 2019.
18. A. Konstorum, T. Vella, A. Adler, **R. Laubenbacher**,A mathematical model of combined CD8 T cell costimulation by 4-1BB (CD137) and OX40 (CD134) receptors, *Scientific Reports* **9**, Art. 10862, 2019.
19. Zhan YA, Wray CG, Namburi S, Glantz ST, **Laubenbacher R**, Chuang JH, Fostering bioinformatics education through skill development of professors: Big Genomic Data Skills Training for Professors. PLoS Comput Biol 15(6): e1007026, 2019. <https://doi.org/10.1371/journal.pcbi.1007026>
20. A. Veliz-Cuba and **R. Laubenbacher**, Dynamics of semilattice networks with strongly connected dependency graph, *Automatica,* 99:167-174, 2019.
21. J.H. Parmar, J. Quintana, D. Ramirez, **R. Laubenbacher**, J. Arguello, P. Mendes, An important role for periplasmic storage in Pseudomonas aeruginosa copper homeostasis revealed by a combined experimental and computational modeling study, *Molecular Microbiology,* 110:357–369, 2018.
22. Konstorum, A., Lynch, M.L., Torti, S.V., Torti, F.M., **Laubenbacher, R.**, A systems biology approach to understanding the pathophysiology of high grade serous ovarian cancer: focus on iron and fatty acid metabolism, *OMICS: A Journal of Integrative Biology*, 22(7):502-513, 2018.
23. E. Dimitrova, L. Carmine, **R. Laubenbacher\*** and L. Shapiro\* (\*joint last authors), The innate immune response to ischemic injury: a multiscale modeling perspective, *BMC Systems Biology,* 12:50, [https://rdcu.be/K5TZ](https://urldefense.proofpoint.com/v2/url?u=http-3A__em.rdcu.be_wf_click-3Fupn-3DlMZy1lernSJ7apc5DgYM8dxSRaDP7dFXQWA0XJ77CfU-2D3D-5Fyn5nOvQt-2D2B-2D2FmFo-2D2BY6cPIkw0-2D2Bpa-2D2FeJzaPVqcEWGQfVzITKycMT0829oqa5L1sOxJZ-2D2FMViVA-2D2BfAd9h2YnokAeVmyvnFRl8odeC03DX6J81ofgGxao2S6NT71ya760O6P7nhAotbA2rjXQQqs4nT-2D2FseyvWDY06IAfHPWBTxNPC9wM-2D2ByIika2XLmoqQPYySQ33m3ddhO6K2RR0ZYKrvGWrvI24mH78YrtP4DaOMeWooX7zUy-2D2FBS8owa2riiG-2D2Feu50UwJEvWnIj5yVINYhVZklSJpNfQ-2D3D-2D3D&d=DwMFaQ&c=EZxp_D7cDnouwj5YEFHgXuSKoUq2zVQZ_7Fw9yfotck&r=dN2VyO2xvnkzC6bvLkZrykjbsqixsZyrGUrEfMI-4lI&m=oZ-GNdQIAbdqMROIsd5MPWdy0-wzwVjX6hr99p5O8nc&s=7WacIjx1JqnsZ6-QWe3JD9ZEqs1_kWMnW5J4Xrf82Ow&e=), 2018.
24. C. Brunson and **R. Laubenbacher**, Applications of network analysis to routinely collected health care data: A systematic review, *J. Amer. Med. Inform. Assoc*., **25**(2), 2018.
25. A. Konstorum, A. Adler, T. Vella, and **R. Laubenbacher**, Addressing current challenges in cancer immunotherapy with mathematical and computational modeling, *J. Royal Soc. Interface,* **14**(131), DOI: 10.1098/rsif.2017.0240, 2017.
26. C. Kadelka, J. Kuipers, and **R. Laubenbacher**, The influence of canalization on the robustness of Boolean networks, *Physica D,* **353-354**, 39-47, 2017.
27. C. Brunson, X. Wang, **R. Laubenbacher**, Effects of research complexity and competition on the incidence and growth of coauthorship in biomedicine, *PLoS One,* 12(3):e0173444, 2017*.*
28. C. Kadelka, Y. Li, J. Kuipers, J.O. Adeyeye, **R. Laubenbacher**, Multistate nested canalizing functions and their networks, *J. Theor. Comp. Sci.,* 675,2017.
29. J. Chifman, S. Arat, Z. Deng, E. Lemler, J.C. Pino, L.A. Harris, M.A. Kochen, C.F. Lopez, S.A. Akman, F.M. Torti, S.V. Torti, **R. Laubenbacher**, Activated oncogenic pathway modifies iron network in breast epithelial cells: A dynamic modeling perspective, *PLoS Computational Biology* 13(2)*,* 2017.
30. G. An, B.G. Fitzpatrick, S. Christley, P. Federico, A. Kanarek, R. Miller Neilan, M. Oremland, R. Salinas, **R. Laubenbacher**, S. Lenhart, Optimization and control of agent-based models in biology: a perspective, *Bull. Math. Biol.,* 79(1), 2017.
31. D. Murrugarra, A. Veliz-Cuba, B. Aguilar, **R. Laubenbacher**, Identification of control targets in molecular Boolean network models via computational algebra, *BMC Syst. Biol.,* 2016, Sep 23;10(1):94.
32. M. Oremland, K.R. Michels, A.M. Bettina, C. Lawrence, B. Mehrad, **R. Laubenbacher**,A computational model of invasive aspergillosis in the lung and the role of iron, *BMC Systems Biology* **10**:34, doi: 10.1186/s12918-016-0275-2, 2016.
33. A. Ibrahim, P. Vera-Licona, **R. Laubenbacher**,T. Favre, AlgoRun, a Docker-based packaging system for platform-agnostic implemented algorithms, *Bioinformatics,* doi:10.1093/bioinformatics/btw120, 2016.
34. J.L. Cervantes, S.J. Benjamin, Y. Chang, J. Luo, C.J. La Vake, K.L. Hawley, M. Caimano, P. Vera-Licona, **R. Laubenbacher**, Y. Ruan, J. Radolph, J.C. Salazar, The phagosome: Meeting point of the Myddosome, NLRs, and degraded *Borrelia burgdorferi, J. Immunology* 196 (1 Supplement) 131.2, May 1, 2016.
35. Tsurutani N, Mittal P, St Rose MC, Ngoi SM, Svedova J, Menoret A, Treadway FB, **Laubenbacher R**, Suárez-Ramírez JE, Cauley LS, Adler AJ, Vella AT, Costimulation Endows Immunotherapeutic CD8 T Cells with IL-36 Responsiveness during Aerobic Glycolysis, *J Immunol*., 196(1):124-34, 2016.
36. M.G. Brandon, B.A. Howard, C.B. Lawrence, **R. Laubenbacher**, Iron acquisition and oxidative stress response in Aspergillus fumigatus, *BMC Systems Biology,* **9** (19),2015, doi: 10.1186/s12918-015-0163-1.
37. S. Arat, J. Bullerjahn, **R. Laubenbacher**,A network biology approach to denitrification in *Pseudomonas aeruginosa, PLoS One* **10** (2), 2015.
38. A. Veliz-Cuba, B. Aguilar, **R. Laubenbacher**, Dimension reduction of large sparse AND-NOT network models, *Electronic Notes in Theorical Computer Science* **316**, 83-95*,* 2015.
39. M. Oremland and **R. Laubenbacher,** Optimal harvesting for a predator-prey agent-based model using difference equations, *Bull. Math. Biol.,* **77** (3), 434-459, 2015.
40. A. Veliz-Cuba, B. Aguilar, F. Hinkelmann, **R. Laubenbacher**, Steady state analysis of Boolean molecular network models via model reduction and computational algebra, *BMC Bioinformatics,* **15**:221,2014.
41. A.S. Jarrah, F. Castiglione, N.P. Evans, R.W. Grange, and **R. Laubenbacher**, A mathematical model of skeletal muscle disease and immune response in the mdx mouse, *BioMed Research International*, http://dx.doi.org/10.1155/2014/871810, 2014.
42. P. Vera-Licona, A.S. Jarrah, L.D. Garcia-Puente, J. McGee, **R. Laubenbacher,** An algebra-based method for inferring gene regulatory networks, *BMC Systems Biology* **8:37**, doi:10.1186/1752-0509-8-37, 2014 (chosen as one of “Editor’s Picks”).
43. M. Oremland and **R. Laubenbacher**, Using difference equations to find optimal tax structures on the SugarScape, *J. Economic Interaction and Coordination* **9** (2), 233-253, 2014.
44. M. Oremland and **R. Laubenbacher,** Optimization of agent-based models: scaling methods and heuristic algorithms, *J. Artificial Societies and Social Simulation* **17** (2) 6, 2014.
45. **R. Laubenbacher**, F. Hinkelmann, D. Murrugarra, and A. Veliz-Cuba, Algebraic models and their use in systems biology, in *Discrete and Topological Models in Molecular Biology,* N. Jonoska and M. Saito (eds.), Springer Verlag, NY, 2014.
46. J.C. Brunson, S. Fassino, A. McInnes, M. Narayan, B. Richardson, C. Frank, P. Ion, and **R. Laubenbacher,** Evolutionary events in a mathematical sciences research collaboration network, *Scientometrics,* **99** (3), 973-998, 2013.
47. A. Veliz-Cuba, D. Murrugarra, and **R. Laubenbacher,** Structure and dynamics of acyclic networks, *Discrete Event Dynamic Systems,* DOI 10.1007/s10626-013-0174-2, 2013.
48. W. Sha, A. Martins, **R. Laubenbacher,** P. Mendes, and V. Shulaev, The genome-wide early temporal response of Saccaromyces cerevisiae to oxidative stress induced by cumene hydroperoxide, *PLoS One*, **8**, 2013, doi: 10.1371/journal.pone.0074939.
49. Y. Li, D. Murrugarra, J.O. Adeyeye, and **R. Laubenbacher,** The number of canalyzing functions over any finite set, *Open J. of Discrete Math.,* **3** (3), 130-136, 2013.
50. C. Kadelka, D. Murrugarra, and **R. Laubenbacher**,Stabilizing gene regulatory networks through feedforward loops, *Chaos,* **23** (2), DOI: 10.1063/1.4808248, 2013.
51. Y. Li, J.O. Adeyeye, D. Murrugarra, B. Aguilar, **R. Laubenbacher**, Boolean nested canalizing functions: a comprehensive analysis, *J. Theor. Comp. Sci.,* **481,** 24-36, 2013.
52. A. Veliz-Cuba, K. Buschur, R. Hamerschock, A. Kniss, E. Wolff, **R.** Laubenbacher, AND-NOT logic framework for steady state analysis of Boolean network models, *Appl. Math. Inf. Sci.,* **7** (4), 2013.
53. J.O. Adeyeye, Y. Li, I.J. Williams, J.D. Green, and **R. Laubenbacher**, Monomial dynamical systems over Fq with bidirectional cycle dependency graph, *Far East Journal of Dynamical Systems,* **20** (2) 77-93, 2012.
54. **R. Laubenbacher,** F. Hinkelmann, and M. Oremland, Agent-based models and optimal control in biology: a discrete approach, in R. Robeva and T. L. Hodge (eds.), *Mathematical Concepts and Methods in Modern Biology,* Elsevier, Jan 2013.
55. F. Hinkelmann and **R. Laubenbacher**, Finite Fields in Biology, in G. Mullen and D. Panario (Eds.), *Handbook of Finite Fields,* CRC Press, Boca Raton, FL, 2013.
56. D. Murrugarra, A. Veliz-Cuba, B. Aguilar, S. Arat, and **R. Laubenbacher**, Modeling stochasticity and variability in gene regulatory networks, *EURASIP J. Bioinf. and Sys. Biol.*, 2012:5.
57. D. Murrugarra and **R. Laubenbacher**, The Number of Multistate Nested Canalyzing Functions, *Physica D,* **241***,* 929-938, 2012.
58. J. Chifman, A. Kniss, P. Neupane, I. Williams, B. Leung, P. Mendes, V. Hower, F.M. Torti, S.A. Akman, S.V. Torti, and **R. Laubenbacher**, The core control system of intracellular iron homeostasis: a mathematical model, *J. Theor. Biol.,* **300**, 91-99, 2012.
59. A. Veliz-Cuba and **R. Laubenbacher**, On the computation of fixed points in Boolean networks, *J. Appl. Math. Comp.* **39** (1-2), 145-153, 2012.
60. D. Murrugarra and **R. Laubenbacher**, Regulatory patterns in molecular interaction networks, *J. Theor. Biol.,* **288**, 66-72, 2011.
61. F. Hinkelmann, M. Brandon, B. Guang, R. McNeill, G. Blekherman, A. Veliz-Cuba, and **R. Laubenbacher**, ADAM: Analysis of the Dynamics of Algebraic Models of Biological Systems using Computer Algebra, *BMC Bioinformatics,* 12:295, 2011.
62. **R. Laubenbacher**, A systems biology approach to cancer drug discovery; in Dubitzky W., Wolkenhauer, O., Cho K.-H., Yokota H. (Eds), *Encyclopedia of Systems Biology,* Springer Verlag, New York, 2011.
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64. G. Blekherman, **R. Laubenbacher**, D. Cortes, P. Mendes, F. Torti, S. Akman, S. Torti, and V. Shulaev, Bioinformatics tools for cancer metabolomics, *Metabolomics,* **7** (3) 329-243, 2011 (featured on journal cover).
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72. R. Robeva and **R. Laubenbacher,** Mathematical biology education: beyond calculus, *Science* **325***,* No. 5940, pp. 542-543, July 31, 2009.
73. **R. Laubenbacher** and A. Jarrah, Algebraic models in systems biology, *Methods in Enzymology*, **467**, 163-196, 2009.
74. **R. Laubenbacher,** V. Hower, A. Jarrah, S. V. Torti, V. Shulaev, P. Mendes, F. M. Torti, and S. Akman, A systems biology view of cancer, *Biochim Biophys Acta,* 2009, 1796(2):129-39.
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**Book Chapters and Other Publications**

1. Y. Skaf and **R. Laubenbacher**, Student-centric graduate training: Challenges and opportunities, *SIAM News* **54**(09), Nov. 2021.
2. Y. Skaf and **R. Laubenbacher**, Toward student-centric graduate training, *SIAM News,* **54**(08), Oct. 2021.
3. **R. Laubenbacher**,The why and how of manuscript review: What goes around comes around, *SIAM News,* Sept. 2021.
4. **R. Laubenbacher** and E. Dimitrova, Boolean models in immunology, in *Systems Immunology: An Introduction to Modeling Methods for Scientists,* J. Das and C. Jayaprakash (eds.), Taylor&Francis Group, Abingdon, UK, 2019.
5. **R. Laubenbacher,** Algebraic and Discrete Mathematical Methods for Modern Biology (R. Robeva, ed.), book review, *SIAM Review* **58** (2), 367-369, 2016.
6. **R. Laubenbacher,** You can do anything with a math degree, invited blog post on the *Blog On Teaching and Learning Mathematics,* American Mathematical Society, January 2015, http://blogs.ams.org/matheducation/
7. J. Chifman, **R. Laubenbacher**, and S. Torti, A systems biology approach to iron metabolism, in *A Systems Biology Approach to Blood,* S.J. Corey and M. Kimmels (eds.), Springer Verlag, NY, 2014, in press.
8. A. Martins, P. Vera-Licona, **R. Laubenbacher**, Computational systems biology: discrete models of gene regulatory networks, in *Undergraduate Mathematics for the Life Sciences: Processes, Models, and Directions,* T. Comar, J. Carpenter, and G. Ledder (eds.), Mathematical Association of America, Washington, D.C., 2013.
9. **R. Laubenbacher**, Cancer drug discovery: a systems biology approach, in W. Dubitzky, O. Wolkenhauer, K.-H. Cho, H. Yokata (Eds.), Encylopedia of Systems Biology, Springer Verlag, New York, 2012.
10. **R. Laubenbacher**, Algebraic methods in mathematical biology (editorial), *Bull. Math. Biol.* **73** (4) 701, 2011.
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12. **R. Laubenbacher**, D. Murragarra, and A. Veliz-Cuba, Structure and dynamics of polynomial dynamical systems, NSF Engineering Research and Innovation Conference, Atlanta, January 2011.

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**Books**

**R. Laubenbacher** (ed.), *Modeling and simulation of biological networks*, Symposia in Pure and Applied Mathematics, Providence, RI: Amer. Math. Soc., 2007.

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**R. Laubenbacher** and B. Sturmfels (eds.), *Theory of Algebraic Invariants* by D. Hilbert, translated from the German by R. Laubenbacher. Cambridge University Press, New York, 1993.

**SELECTED PRESENTATIONS**

**2021**

* *A modular computational framework for medical digital twins,* NIH Working Group on Multiscale Modeling and Viral Pandemics, July 22.
* *Mathematics and medicine: toward a roadmap,* Annual Meeting of the Soc. Math. Biol. (virtual), June 17.
* *The role of mathematics in 21st century medicine,* Grand Rounds presentation, Department of Medicine, University of Florida, May 27.
* *Metabolic homeostasis in health and disease,* Scientific Symposium on “The Mathematics of Health and Disease,” AAAS Annual Meeting, February 9.

**2020**

* *Calibration of hybrid multi-scale simulation models with heterogeneous biological data,* SIAM Conference on Mathematics of Data Science, June 15.
* *Ask not what algebra can do for biology, ask what biology can do for algebra, Workshop on Model Theory of Differential Equations, Algebraic Geometry, and their Applications to Modeling,* Banff International Research Station, Banff, Canada, June 5.
* *Boolean networks and their dynamics,* International Workshop on Boolean Networks, University of Concepcion, Concepcion, Chile, January 8.
* *A multiscale mathematical model of the innate immune response to respiratory fungal infections,* American University, Sharjah, Sharjah, UAE, February 3.

**2019**

* *The dynamics of Boolean networks,* George Mason University, Fairfax, VA, November 6.
* *Multiscale computational models of disease,* Pfizer, Groton, CT, November 5.
* *A multiscale mathematical model of the innate immune response to respiratory fungal infections,* Annual Meeting Society for Mathematical Biology, Montreal, CA, July 26.
* *Multiscale models of disease,* University of Florida, Gainesville, FL, May 6.
* *Multiscale models of disease,* University of Virginia, Charlottesville, VA, March 29.
* *Iron metabolism and its role in breast cancer,* Moffitt Cancer Center, Tampa, FL, January 31.
* *Dynamic connectivity of functional brain networks for emotion regulation,* Joint Mathematics Meetings, Baltimore, MD, January 17.
* *Mathematics and medicine,* Joint Mathematics Meetings, Baltimore, MD, January 17.
* *From free-range advising to life coaching,* Joint Mathematics Meetings, Baltimore, MD, January 18.

**2018**

* *The role of iron metabolism in breast cancer,* Institut Curie, Paris, France, December 17.
* *Multi-scale models of disease,* Institut de Recherche et Interdisciplinarite, Paris, France, December 14.
* *Multi-scale modeling of disease,* University of Illinois, Urbana-Champaign, IL, October 23.
* *Dynamic connectivity of functional brain networks for emotion regulation,* SIAM Life Sciences Meeting, Minneapolis, MN, August 6.
* *The role of iron in tumor progression: a multiscale modeling approach,* Annual Meeting, Soc. Math. Biol., Syndey, July 11.
* *From data to knowledge: The power of computational models,* Virginia Military Institute, Lexington, VA, March 14.

**2017**

* *Multiscale modeling of disease,* Yale University, New Haven, CT, December 6.
* *Discrete Dynamic Networks,* CUNY-NYU Joint Symbolic-Numeric Computing Seminar, New York, NY, November 9.
* *Turing, a software package for discrete modeling,* 2017 SIAM Conf. on Appl. Alg. Geom., Atlanta, August 1.
* *Modular design of multiscale models,* Da Vinci Convergence Symposium, Univ. Southern California, March 9.
* *Inference of molecular networks in systems biology,* University of Cincinnati School of Medicine, March 31.
* *Iron metabolism and its role in breast cancer,* plenary lecture, Annual Conference on Computational Biology, Center for Genome Research and Biocomputing, Oregon State University, April 7.
* *The role of mathematical models in the study and control of disease: a case study in breast cancer,* Bristol-Myers Squibb, NJ, September 18.
* *The “battle over iron” as part of the innate immune response to fungal infections in the lung,* Bristol-Myers Squibb, NJ, September 18.

**2016**

* *Computational Systems Biology,* Director’s Forum, Jackson Laboratory for Genomic Medicine, Farmington, CT, January 27.
* *Algebraic methods in computational biology,* University of Kentucky, Lexington, KY, February 4.
* *Algebraic methods in systems biology,* Texas Tech University, Lubbock, TX, April 14.
* *Mathematics: A Driver of Precision Medicine,* Texas Tech University, Lubbock, TX, April 13.
* *Algebraic Methods in Systems Biology,* Workshop onContemporary Mathematical Challenges in the Life Sciences, Texas A&M University, May 16.
* *Algebraic Models in Systems Biology,* University of Buenos Aires, Buenos Aires, Argentina, August 3.
* *Quantitative Medicine Across Scales,* InCHIP, University of Connecticut, Storrs, September 29.
* *Quantitative Medicine,* Amherst College, November 3.

**2015**

* *Using algebra to infer gene regulatory networks,* University of California, Berkeley, February 9.
* *Multiscale modeling of the innate immune to Aspergillus fumigatus in the lung*, Pennsylvania State University, February 24.
* *Iron metabolism,* Center for Cell Analysis and Modeling, UConn Health, March 30.
* *Algebraic models in systems biology,* International Conference on Mathematical Sciences, University of Sharjah, Sharjah, United Arab Emirates, April 4.
* *The battle over iron: the innate immune response to Aspergillus fumigatus in the lung,* International Workshop on Modeling Metabolic Health, Cambridge, UK, October 6.

**2014**

* *Algebraic models in systems biology,* University of Wisconsin, Milwaukee, April 18.
* *A systems biology approach to iron metabolism*, Worcester Polytechnic Institute, Worcester, MA, March 26.
* *Steady analysis of Boolean network models through model reduction and computational algebra,* European Conf. on Comp. Biol. Workshop on the Logical Modelling and Analysis of Cellular Networks, September 8.
* *Dimension reduction of large sparse networks,* The Fifth International Workshop on Static Analysis and Systems Biology, September 10.
* *Attractors, Stochasticity, and Spatial Considerations in Mitochondrial Information Transfer,* National Cancer Institute Workshop on Mitochondrial Information Transfer, NIH, September 23.

**2013**

* *The battle for iron: A multiscale in silico model of Aspergillus fumigatus in the airway,* Q-Bio Winter Meeting, Honolulu, HI, February 18.
* *PlantSimLab: a simulation laboratory for plant biology,* Keystone Symposia Conference on Plant Immunity: Pathways and Translation, Big Sky, Montana, April 9.
* *Dynamical systems over finite fields in systems biology,* Workshop on “The Art of Iterating Rational Functions Over Finite Fields,” Banff International Research Station, Banff Centre, Banff, Canada, May 8.
* *Iron regulation in health and disease: two case studies,* Jackson Laboratory for Genomic Medicine, Farmington, CT, May 20.
* *Iron regulation in health and disease: two case studies,* Jackson Laboratory, Bar Harbor, ME, May 22.
* *PlantSimLab: a simulation laboratory for plant biology,* Center for Cell Analysis and Signaling, UConn Health Center, Farmington, CT, June 13.
* *The battle for iron: a multiscale in silico model of Aspergillus fumigatus in the airway,* Annual Meeting of the Soc. for Industrial and Applied Math., San Diego, CA, July 11.

**2012**

* *Algebraic geometry in systems biology,* Dept. of Mathematics and Statistics, Bowling Green State University, Bowling Green, OH, January 20.
* *Patterns are everywhere: how and why?,* Kids’ Tech University at Bowling Green State University, Bowling Green, OH, January 21.
* *Cancer Systems Biology,* Bioinformatics and Computational Biology Program, Iowa State University, February 1.
* *Algebraic models in systems biology,* Department of Mathematics, Mississippi State University, Mississippi State, MS, February 16.
* *Algebraic geometry for large networks,* DARPA Summit Meeting on Mathematics, Lake Tahoe, NV, February 21.
* *Algebraic models in systems biology,* Workshop on Discrete and Topological Models in Molecular Biology, Tampa, FL, March 13.
* *Steady state analysis of Boolean network models via a universal class of models,* Special Session on Dynamics of Complex Networks, AMS meeting, Washington, DC, March 18.
* *Wnt sigaling in melanoma cells,* Special Session on Mathematical Methods in Disease Modeling, AMS meeting, Washington, DC, March 18.
* *Algebraic models in systems biology,* Dept. of Mathematics, University of Delaware, Newark, DE, April 2.
* *Algebraic models in systems biology,* Department of Mathematics, University of Nebraska, Lincoln, NE, April 19.
* *Cancer systems biology,* Department of Mathematics, University of Nebraska, Lincoln, NE, April 20.
* *Algebraic methods is systems and evolutionary biology,* Mathematical Biosciences Institute, Columbus, OH, May 11.
* *Iron metabolism,* Mathematical Biosciences Institute, Columbus, OH, May 18.
* *Science and the fight against cancer,* keynote address, American Cancer Society, Relay for Life, Tazewell, VA, May 31.
* *The role of SIAM as an advocate for the mathematical sciences community,* SIAM Annual Meeting, Minneapolis, MN, July 12.
* *Downregulation of LRP6 inhibits growth of melanoma cells,* SIAM Annual Meeting, Minneapolis, MN, July 13.
* *Algebraic models in systems biology,* Department of Mathematics, University of Connecticut, Storrs, September 6.
* *Algebraic models in systems biology,* Department of Mathematics, Virginia Tech, September 21.
* *Algebraic models in systems biology,* Oregon State University, October 8.
* *Iron metabolism and the innate immune response to Aspergillus fumigatus,* Oregon State University, October 9.
* *Patterns are everywhere. Why and How?,* Kids’ Tech University, Southwest Virginia Higher Education Center, Abingdon, VA.
* *Scientific posters: the good, the bad, and the ugly,* Virginia Tech SIAM Student Chapter, November 13.

**2011**

*Algebraic geometry in systems biology,* Workshop on “Algebraic geometry in the sciences,” University of Oslo, Norway, January 11.

*Patterns are everywhere: how and why?,* Kids’ Tech University at Virginia Tech, January 29.

*A systems biology view of cancer,* Workshop at the Wake Forest University School of Medicine Cancer Biology Department, Winston-Salem, NC, March 25.

*A systems biology view of cancer,* School of Pharmacy, Xavier University, New Orleans, March 28.

*A systems biology view of cancer,* School of Medicine, Marshall University, Huntington, WV, April 4.

*Cancer Systems Biology,* GBCB Seminar, Virginia Tech, Blacksburg, VA, April 21.

*Trends in Modern Mathematical Biology,* keynote address, MAA PREP Workshop on “Mathematical Biology: Beyond Calculus.” Sweet Briar College, Sweet Briar, VA, June 13.

*A mathematical framework for agent based models of complex biological networks,* MAA PREP Workshop on “Mathematical Biology: Beyond Calculus.” Sweet Briar College, Sweet Briar, VA, June 13.

*Trends in symbolic computation development and applications,* panelist, 17th International Conference on Applications of Computer Algebra (ACA), Houston, TX, June 28.

*Algebraic computation in bioinformatics and systems biology*, plenary address, 17th International Conference on Applications of Computer Algebra (ACA-2011), Houston, TX, June 29.

*The relationship between iron metabolism and breast cancer,* Roche Pharma, Nutley, NJ, August 21.

*Cancer Systems Biology,* New Mexico Center for Spatiotemporal Modeling of Cell Signaling, University of New Mexico, September 8.

*Algebraic models in systems biology,* SIAM Conference on Applied Algebraic Geometry, Raleigh, NC, October 7.

*Patterns are everywhere: how and why?,* Kids’ Tech University at Virginia State University, October 22.

*Algebraic computation in bioinformatics and systems biology,* plenary address, Conference on Technological Applications of Symbolic Computation, Granada, Spain, November 18.

**2010**

*Nested canalyzing polynomial dynamical systems,* Special Session on Applications of Algebraic Geometry, Amer. Math. Soc. Joint Mathematics Meetings 2010, San Francisco, CA, January 17.

*The relationship between structure and dynamics in biological networks,* Western Michigan University, Kalamazoo, MI, March 25.

*Mathematics-aided medicine,* Café Scientifique, Blacksburg, VA, March 29.

*Cancer Systems Biology,* Jackson State University, Jackson, MS, April 29.

*Mathematical Biology Education: Beyond Calculus,* Keynote Address, Math. Assoc. Amer. Workshop on Mathematical Biology, Sweet Briar College, Sweet Briar, VA, June 14.

*Algebraic models in systems biology,* Plenary Lecture, Workshop for Young Researchers in Mathematical Biology,Mathematical Biosciences Institute, Columbus, OH, September 1.

*Mathematics and the public in the U.S.A.,* Workshop on “Raising Public Awareness of Mathematics,” Obidos, Portugal, September 27.

*Mathematics and the Systems Biology of Cancer,* Minicourse, Annual meeting of the Society for the Advancement of Chicanos and Native Americans in Science, Anaheim, CA, September 30.

*Toward a predictive model of iron metabolism,* Marie Curie Cancer Center, Paris, France, October 15.

*Training in Cancer Systems Biology,* Annual Meeting of the Cancer Biology Training Consortium, Tuscon, AZ, November 5.

*Algebraic models in systems biology,* University of Kentucky, November 18.

*Algebraic models in systems biology,* Arizona State University, November 29.

*Kids’ Tech University,* Arizona State University, November 30.

*A systems biology approach to iron metabolism in aging and cancer,* Conference on the Systems Biology of Human Aging, Philadelphia, December 7.

*Toward a predictive model of intracellular iron homeostasis,* Glaxo-Smith-Kline, Philadelphia, December 9.

*A systems biology approach to iron metabolism and cancer,* Workshop on Nanotechnology, Proteogenomics, and Visual Analytic Applications for Shistosomiasis Control, Abuja, Nigeria, December 15.

**2009**

Dynamical systems over graphs: the relationship between graph topology and dynamics, Special Session on Applications of Topology, Amer. Mathematical Society, Joint Mathematics Meetings 2009, Washington, D.C., January 5.

*Introduction to Systems Biology,* Department of Cancer Biology,Wake Forest University, Winston-Salem, NC, January 20.

*Careers in computational biology,* Hampton University, Hampton, VA, January 22.

Algebraic models in systems biology, Mathematics Department, Clemson University, January 26.

Biology + Math= Biology, Oakwood University, Huntsville, AL, February 5.

*Algebraic Methods in Systems Biology*, Amer. Mathematical Society, Plenary Address - Spring Southeastern Sectional Meeting, North Carolina State University, Raleigh, NC, April 4.

*Experience in developing collaborations with MSI (particularly HBCUs) with VBI*, Achieving Inclusive Excellence in Grant Proposals Workshop, Virginia Tech, May 6.

*Reverse-engineering in systems biology (short course),* Instituto Gulbenkian de Ciencia (IGC), Lisbon, Portugal, May 18-21.

*Algebraic models in systems biology*, Mathematical Applications Seminar series, George Washington University, Washington, D.C., May 28.

*Discrete models of gene regulation networks,* Plenary address, 15th International Conference on DNA Computing and Molecular Programming, University of Arkansas, Fayetteville, AR, June 10.

*Parameter estimation for algebraic models*, Emerging Modelling Methodologies in Medicine and Biology, International Centre for Mathematical Sciences, Edinburgh, Scotland, July 21.

*Experimental design and biochemical network inference,* Annual Meeting of the American Statistical Society, Washington, D.C., August 3.

*The relationship between dynamics and structure of biological networks,* 47th IEEE Allerton Conference on Communication, Control, and Computing, Urbana-Champaign, IL, Sept. 30.

*The relationship between dynamics and structure of biological networks,* Southern Methodist University, Dallas, TX, Oct 14.

*Cancer systems biology,* National Conference of the Society for the Advancement of Chicanos and Native Americans in Science (SACNAS), Dallas, TX, Oct 16.

*Careers in computational biology,* Norfolk State University, Norfolk, VA, Nov. 18.

*A predictive model for the regulation of mammalian iron metabolism,* Harvard Medical School, Boston, MA, December 4.

**2008**

*Metabolic fingerprinting of breast cancer*, Department of Biostatistics, Bioinformatics and Biomathematics, Georgetown University Medical School, Washington, DC.

*Design of experiments and biochemical network inference*, Department of Statistics, University of Kentucky, Lexington, KY.

*Algebraic Methods in Systems Biology,* University of Marburg, Germany.

*An introduction to systems biology,* Statistical and Applied Mathematical Sciences Institute (SAMSI), Durham, NC.

*Algebraic Methods in Systems Biology*, Department of Mathematics, Georgia Tech, Atlanta, GA.

*Computer Algebra Methods for the Inference of Biochemical Networks,* Department of Mathematics, NC State University, Raleigh, NC.

*The Dynamics of Conjunctive Boolean Networks*, Discrete Models of Biological Networks Workshop, Institut de Mathématiques de Luminy, Marseille, France.

*Algebraic Methods in Systems Biology*, Institut des Hautes Études Scientifiques (IHÉS), Paris, France.

* Undergraduate Research Panel, Blackwell-Tapia Conference, SAMSI, Research Triangle Park, NC.

*Data analysis for molecular fingerprinting of breast cancer*, American Mathematical Society (AMS) Joint International Meeting, Fudan University, Shanghai, China.

*Algebraic Models in Systems Biology*, Shanghai Jiao Tong University, China.

**2007**

*Parametric Inference of Biochemical Network Models,* SIAM Minisymposium on Mathematical Modeling of Complex Systems in Biology, Annual Joint Meetings of the AMS-MAA-SIAM, New Orleans, LA.

*Parametric Inference of Biochemical Network Models,* Keynote lecture,2nd Bioinformatics Research Symposium, Clemson University, Clemson, SC.

*Polynomial dynamical systems over finite fields, with applications to modeling and simulation of biological networks,* IMA Workshop on Applications of Algebraic Geometry to Biology, Dynamics, and Statistics, University of Minnesota, Minneapolis, MN.

*Biochemical network inference*, FLAD Computational Biology Collaboratorium (FCBC) at the Instituto Gulbenkian de Ciencia (IGC), Lisbon, Portugal.

*Algebraic Methods in Systems Biology,* Applied Mathematical Sciences Summer Institute (AMSSI) **California State Polytechnic University, Pomona, CA.**

*The Role of Mathematics in Systems Biology,* Second Argentinian Summer School in Biomathematics (BIOMAT), Córdoba, Argentina.

*Discrete Models of Biochemical Networks: The Toric Variety of Nested Canalyzing Functions.* Algebraic Biology 2007, Research Institute for Symbolic Computation (RISC), Linz, Austria.

*A mathematical formalism for agent-based modeling,* Discrete Mathematics and Algorithms Conference, Clemson University, Clemson, SC.

*Complexity in biological systems,* Cyber-Enabled Discovery and Innovation (CDI) Workshop, Statistical and Applied Mathematical Sciences Institute (SAMSI), Research Triangle Park, NC.

*Graduate studies in computational biology,* The Institute for Math Biology Education and Research (TIMBER), Appalachian State University, Boone, NC.

**2006**

*A Computational Algebra Approach to the Reverse-engineering of Biochemical Networks,* Chinese Academy of Sciences, Shanghai, China.

*Algebraic Models in Systems Biology,* Rutgers University, New Brunswick, NJ.

*Discrete Models in Epidemiology,* Summer School - Mathematical Modeling in Epidemiology, San Salvador, El Salvador.

*Finite Dynamical Systems,* Clemson University, Clemson, SC.

*Mathematical Methods in Computational Biology,* Annual Meeting of the Soc. for the Advancement of Native Americans and Chicanos in Science (SACNAS).

*A Computational Algebra Approach to Yeast Systems Biology,* Center for Genomics, Cuernavaca, Mexico.

**2005**

[*A Computational Algebra Approach to the Reverse Engineering of Gene Regulatory Networks*](http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6WMD-4CNJ934-2&_user=10&_handle=V-WA-A-W-AB-MsSAYZW-UUW-U-AAWAZAZWDY-AAAEAEDUDY-ADYAVECUV-AB-U&_fmt=summary&_coverDate=08%2F21%2F2004&_rdoc=7&_orig=browse&_srch=%23toc%236932%232004%23997709995%23510256%21&_cdi=6932&view=c&_acct=C000050221&_version=1&_urlVersion=0&_userid=10&md5=c359dc454d395648b615145cbc419b28)*,* Eastern Michigan University, Ypsilanti, MI.

*System identification of biochemical networks,* Summer School on Nanoscience and Systems Biology, University of Munich, Germany.

*System identification of biochemical networks using discrete models,* Fourth Workshop on the Computation of Biochemical Pathways and Genetic Networks, European Media Lab, Heidelberg, Germany.

*Algebraic Models in Systems Biology,* 1st Intl. Conference on Algebraic Biology, Tokyo, Japan.

*Algebraic Models in Systems Biology,* Academia Sinica, Taiwan, Taipeh.

*Mathematical Methods in Computational Biology,* First Argentinian Summer School in Biomathematics (BIOMAT), Cordoba, Argentina.

*A Computational Algebra Approach to Reverse-engineering of Biochemical Networks,* IMPA, Rio de Janeiro, Brazil.

**2004**

*Mathematical Models of Biochemical Networks: a case study,* Bioinformatics Colloquium, Ludwig-Maximilians University, Munich, Germany.

*Mathematics Methods in Bioinformatics,* Society for Advancement of Chicanos and Native Americans in Science (SACNAS) conference, Austin, TX.

*An Optimal Control Problem for* in vitro *Virus Competition,* 43rd IEEE Conference on Decision and Control, Bahamas.

*Discrete Models of Biochemical Networks,* Free University Amsterdam, Netherlands.

*Finite Dynamical Systems: A Mathematical Foundation for Simulation Science,* Univ. Western Ontario, Canada.

*Finite Dynamical Systems: Theory and Practice,* 16th Intl. Symposium on Mathematical Theory of Networks and Systems, Leuven, Belgium.

**2003**

*A Computational Algebra Approach to the Modeling of Biochemical Systems,* Univ. Buenos Aires, Argentina.

*A Computational Algebra Approach to the Modeling of Biochemical Systems,* Univ. of Cordoba, Argentina.

*A Computer Algebra Approach to the Modeling of Biochemical Systems,* Plenary address, International Symposium on Symbolic and Algebraic Computation (ISSAC), Drexel University, Philadelphia, PA.

*Modeling of Biochemical Networks,* ISSAC, Drexel University, Philadelphia

*The Need for Data to Fit Models,* NIEHS Workshop on Systems Biology, Research Triangle Park, NC.

*Polynomial Models of Finite Dynamical Systems,* Institute for Mathematics and its Applications, Minneapolis, MN.

*Open Problems in Algebraic Statistics,* American Institute for Mathematics, Palo Alto, CA.

*Mathematics in the Age of Networks,* Virginia Tech, Blacksburg, VA.

*Finite Dynamical Systems: theory and practice,* Stanford University, Palo Alto, CA.

*A Mathematical Foundation for PathSim: a rule-based spatial model of immune response to viral pathogens,* Ohio State University, Columbus, OH.

*Symbolic Computation Methods in Computational Biology,*  Technical University, Munich, Germany.

*Computer Simulation and Biological Systems,* Plenary address, Mathematics Conference of the Puerto Rican Math Society, Ponce, Puerto Rico.

*Computer Simulation of Immune Response to EBV Infection,* NIAID workshop, National Institutes of Health, Bethesda, MD.

*Reverse Engineering of Gene Regulatory Networks,* University of Munich, Germany

*Reverse-Engineering of Biological Networks,* Virginia Tech, Blacksburg, VA.

**2002**

*A New Combinatorial Homotopy Theory of Graphs,* University of Western Ontario, New London, Canada.

*Oh What a Tangled Web We Weave: The Age of Networks*, Biever Lecture, Loyola University, New Orleans, LA.

*Polynomial Methods for Reverse-Engineering of Biochemical Networks,* University of California, Berkeley, CA.

*Polynomial Methods in Mathematical Biology,* Virginia Tech, Blacksburg, VA.

*A Categorical Framework for Sequential Dynamical Systems,* SIAM Conf. on Discrete Mathematics, San Diego, CA.

**SERVICE TO THE PROFESSION**

**Offices Held**

* Member, Publications Committee, Society for Mathematical Biology, 2021-2024
* Founding Director, Connecticut Pain Consortium, 2018-2020
* Secretary, AAAS Section A (Mathematics) 2018-2022
* Member, Amer. Math. Soc. Liaison Committee to AAAS, 2017-present
* Vice President for Science Policy, Society for Industrial and Applied Mathematics, 2009-2013
* Chair, Committee on Science Policy, Society for Industrial and Applied Mathematics, 2009-2013
* Member, Committee on Science Policy, Society for Industrial and Applied Mathematics, 2009-2019
* Member, Society for Industrial and Applied Mathematics, Committee on Committees, 2008-2009

**Editorial Boards/Advisory Boards**

* Editor-in-Chief, *Bulletin of Mathematical Biology,* 2016-present
* Member, Editorial Board, *BMC Systems Biology,* 2013-present
* Member, Editorial Board, *Journal of Algebra,* 2008-2018
* Member, Editorial Board, *Bulletin of Mathematical Biology, 2008-2016*
* Member, Editorial Board, *Journal of Symbolic Computation,* 2003-present
* Member, Editorial Board, *Applied Mathematical Sciences* book series, Springer Verlag

Member, Editorial Board, *Mathematical Modelling: Theory and Applications* book series, Springer Verlag

* Member, Advisory Board, “Multiscale Immune System Simulator for the Onset of Type 2 Diabetes, European Framework 7 project coordinated by Consiglio Nazionale della Ricerche, Italy, 2013-2017
* Member, Host-Pathogen Working Group, Malaria Host-Pathogen Interaction Center, Emory University, 2013-2017
* Member, Steering Committee, Visual Analytics in Biology Curriculum Network, Jackson State University, Jackson, MS, NSF funded, 2011-2013.
* Member, Scientific Advisory Committee, Mathematical Biosciences Institute, Ohio State University, 2011-2013
* Member, Steering Committee for Activity Group in Algebraic Geometry, Society for Industrial and Applied Mathematics (SIAM)
* Editor, Special issue, *Bull. Math. Biol.* **73**, 2011, Algebraic Methods in Mathematical Biology.
* Co-editor, Special issue on “Biomathematics: Newly developed applied mathematics and new mathematics arising from biosciences,” *Discrete and Continuous Dynamical Systems,* Dec.2011.
* Member, Minority Serving Institutions Advisory Council, Virginia Tech, 2008-2009
* Member, Systems Biology Working Group, NIAID Advisory Panel to five Pathosystems Biology Centers, 2009-2013.
* Member, External Advisory Committee, Alliance for the Advancement of Biomedical Research Excellence in Puerto Rico (AABRE-PR) 2005-present
* Member, Steering Committee, Interdepartmental Ph.D. Program “Genetics, Bioinformatics, and Computational Biology,” Virginia Tech, 2003-2013
* Member, External advisory committee to the NIH-funded *Biomedical Research Infrastructure Network, University of Puerto Rico,* 2003-2006

**Other Selected Professional Service**

* Ad hoc member, NIH Study Section on Mathematical Analysis of Biological Systems, February 2021.
* Co-founder and co-lead, NIH IMAG/MSM Working Group on Multiscale Modeling and Viral Pandemics, 2020-present.
* Course Director, *Computational Biology and Bioinformatics,* Special topics course, UConn School of Medicine, Fall 2017, Spring 2019, Spring 2020.
* Member, MIRA Study Section, NIGMS, 2016.
* Co-Instructor, Topics in Scientific Computation, Special topics course, University of Connecticut, Storrs, 2015, 2019
* Seminar leader, NSF REU Summer Institute in Mathematics for Undergraduates, Uconn Health, summer 2015-2017.
* Member, Study Section on Multiscale Modeling, NIBIB, 2014, 2016, 2018, 2019.
* Ad hoc member, NIH “Modeling and Analysis of Biological Systems (MABS)” Study Section, 2013-2019.
* Ad hoc member, NIAID Study Section, Omics Technologies for Predictive Modeling of Infectious Diseases, February 2013.
* Ad Hoc Member, Study Section on Cancer Genetics, National Cancer Institute, October 2010.
* Expert witness at Congressional Hearing on 21st Century Biology, Subcommittee on Research and Education of the House Committee on Science and Technology, June 29, 2010.
* Member, Study Section on Biological Data Management and Analysis, National Institute for General Medical Sciences, 2010.
* Founder and President of Kids’ Tech University (<http://kidstechuniversity.org>), 2009-present.
* Member, Study Section on Molecular Oncology, National Cancer Institute, 2009.
* Seminar leader, NSF REU Summer Institute in Mathematics for Undergraduates, Virginia Tech, summer 2008-2013.
* Reviewer for National Science Foundation, National Institutes of Health, and National Academy of Sciences.
* Reviewer for various mathematical and scientific journals.
* Seminar leader, NSF REU Summer Institute in Mathematics for Undergraduates, University of Puerto Rico, summer 2000, 2001.
* Co-teacher of MAA minicourse at 1995 National Meetings of AMS/MAA on “Teaching with Original Sources”.

**Program & Conference Organization**

* Moderator, Panel Discussion on *Mathematics and Medicine,* 2021 Annual Meeting of the Society for Mathematical Biology.
* Member, Scientific Committee, 2021 Annual Meeting of the Society for Mathematical Biology, 2021.
* Member, Program Committee, International Conference on Systems Biology, Hartford, 2020
* Member, Foundations of Computational Mathematics 2020 (FoCM2020), Organizing Committee for Workshop on *Computational Mathematical Biology with Emphasis on the Genome,* Vancouver, 2020
* Member, Scientific Committee, Workshop on Qualitative Computational Modeling of Biological Networks, International Conference on Systems Biology, Okinawa, 2019
* Member, Organizing and Scientific Committees, 2020 International Conference on Systems Biology
* Member, International Advisory Board, Third International Conference on Mathematics and Statistics, American University of Sharjah, UAE, 2020
* Member, Organizing Committee, Workshop on Computational Mathematical Biology With Emphasis on the Genome, Foundations of Computational Mathematics (FoCM2020), Vancouver, 2020
* Organizer (together with M. Alber), Scientific Symposium, “Mathematical modeling of diseases: Translational approaches.” AAAS Annual Meeting, Washington, DC, February 15, 2019
* Chair, Organizing Committee, Symposium on “A Precision Medicine Approach to Pain,” Jackson Laboratory for Genomic Medicine, November 30, 2017.
* Member, Program Committee, 15th Conference on Computational Methods for Systems Biology, Sept. 27-29, 2017, Darmstadt, Germany.
* Member, Program Committee, 12th International Conference on Computational Methods in Systems Biology, University of Manchester, Manchester, England, 2014.
* Member, Program Committee, 5th International Workshop on Static Analysis and Systems Biology, Munich, Germany, 2014.
* Co-chair, International Conference on Cell Biology, Virginia Tech, 2013.
* Member, Program Committee, 2012 RECOMB Conference on Regulatory and Systems Genomics, with DREAM Challenges, San Francisco.
* Member, Program Committee, SIAM Conference on Applications of Algebraic Geometry, Colorado State U., 2013.
* Co-organizer, Working Group on Optimal Control of Agent-based Models, National Institute for Mathematical and Biological Synthesis (NIMBioS), University of Tennessee, 2011-2013.
* Member, Program Committee, 21st International Conference on Database and Expert System Applications, 2010.
* Member, Organizing Committee, workshop on “Bootcamp on Cancer Modeling,” Mathematical Biosciences Institute, Ohio State University, September 2010.
* Member, Organizing Committee, workshop on “Mathematical Developments Arising from Biology,” Mathematical Biosciences Institute, Ohio State University, Nov. 2009.
* Member, Organizing Committee, 2011-2012 program on “Stochastics in Biological Systems,” Mathematical Biosciences Institute, Ohio State University.
* Member, Organizing Committee, workshop on “Optimal Control and Optimization for Individual-based and Agent-based Models,” National Institute for Mathematical and Biological Synthesis, University of Tennessee (NIMBioS), Dec. 2009.
* Program Leader, Program on Algebraic Methods in Systems Biology and Statistics, Statistical and Applied Mathematical Sciences Institute, Research Triangle Park, NC, 2008-2009.
* Co-organizer, Special Session on “Combinatorics and Discrete Dynamical Systems,” 1st Joint Intl. Meeting of AMS and Shanghai Mathematical Soc., Shanghai, China, 2008.
* Co-organizer, Special Session on “Biomathematics: Newly Developed Applied Mathematics and New Mathematics Arising from Biosciences,” 1st Joint Intl. Meeting of AMS and Shanghai Mathematical Soc., Shanghai, China, 2008.
* Member, Program Committee, 2nd International Conference on Bioinformatics Research and Development (BIRD), Vienna, Austria, 2008.
* Member, Program Committee, Mathematical Theory of Networks and Systems (MTNS), 2008.
* Member, Program Committee, RECOMB Systems Biology, 2007-present
* Co-organizer, 1st Canadian Discrete & Algorithmic Mathematics Conf. (CanaDAM), Alberta, Canada, 2007.
* Co-organizer, Atlantic Coast Conf. on Mathematics in the Life & Biological Sciences, Virginia Tech, 2007.
* Member, Program Committee, 9th Annual Computational Genomics Conference, Baltimore, 2006.
* Organizer, AMS Short Course on Mathematical Methods in Computational Biology, AMS-MAA-SIAM Joint Meetings, San Antonio, 2006.
* Co-organizer and co-principal lecturer, MSRI Graduate Summer Workshop on Mathematical Methods in Computational Biology, 2006.
* Member, Program Committee, First International Conference on Algebraic Biology, Tokyo, 2005.
* Organizer, session on genetic networks, International Symposium on the Mathematical Theory of Networks and Systems (MTNS), University of Notre Dame, 2002.
* Co-organizer, Joint U.S.-Canadian Conference on Symbolic Computational Algebra, Waterloo, Ontario, 2002.
* Member, Program Committee, International Symposium on Symbolic & Algebraic Computation(ISSAC) 2001.
* Co-organizer, AMS-SIAM summer conf. “Symbolic Computation and Polynomial System Solving,” 2000.
* Organizer, conference on “Cryptography as a Teaching Tool,” for NM high school teachers, 1998.
* Co-organizer of an AMS Special Session on Computational Algebraic Geometry, Joint Annual Meetings of the AMS/MAA/SIAM, San Diego, January 1997.
* Co-organizer of 22nd NMSU Holiday Symp. on “Rewriting techniques and Gröbner bases,” January 1996.
* Co-organizer of a contributed paper session on “Teaching with Original Sources” at the 1995 National Meetings of the AMS/MAA.
* Co-organizer of 21st NMSU Holiday Symposium on “Gröbner Bases and Convex Polytopes,” December 1994.

**Professional Memberships**

* American Association for the Advancement of Science
* American Mathematical Society
* Society for Industrial and Applied Mathematics
* Association for Women in Mathematics
* Society for Mathematical Biology
* International Society for Systems Biology

**TRAINING**

**Graduate Students**

**Current**

**Name Grad. Program Institution**

Yara Skaf 2023 M.D./Ph.D. UConn Health/U Florida

Joseph Masison 2021 M.D./Ph.D. UConn Health

**Former**

**Name Grad. Current Position Institution**

Bandita Adhikari 2021 Postdoctoral Fellow Univ. Pennsylvania

Russell Posner 2019 M.D./Ph.D. UConn Health

Ulysses Andrews 2016 Internal Consultant Private Industry

Seda Arat 2015 Senior Scientist Pfizer

Claus Kadelka 2015 Assistant Professor Iowa state university

Shernita Lee 2014 Director Virginia Tech

Matt Oremland 2013 Staff Scientist Regeneron

Ariane Hofmann 2012 Ph.D. student Biosys. Sci., ETH Zuerich

David Murrugarra 2012 Professor University of Kentucky

Franziska Hinkelman 2011 Staff Scientist Google

Alan Veliz-Cuba 2010 Associate Professor University of Dayton, OH

Paola Vera-Licona 2007 Assistant Professor UConn Health

Elena Dimitrova 2006 Professor CalPoly, San Luis Obispo,

 Mathematical Sciences

Brandylin Stigler 2005 Professor Southern Methodist University,

 Department of Mathematics

Dustin Potter 2005 Real Estate Investor

Omar Colón-Reyes 2005 Associate Professor Univ. of Puerto Rico (Mayaguez),

 Department of Mathematics

Luis Garcia-Puente 2004 Professor Colorado College, Dept. of Mathematics

Abdul Jarrah 2002 Professor American University, Sharjah, UAE

Karen Schlauch 1998 Professor University Nevada–Reno,

 Department of Biochemistry & Molecular Biology

Xenia Kramer 1996 Senior Research Private Industry

 Scientist

Cynthia Woodburn 1994 Professor Pittsburg State University, Department of Mathematics

**Postdoctoral Fellows**

**Current**

**Name Current Position Dates of Training Institution**

Henrique de Assis Postdoctoral Fellow 2019-2022 UConn Health/U Florida

Melody Walker Postdoctoral Fellow 2021-2023 University of Florida

**Former**

**Name Current Position Dates of Training Institution**

Lokendra Poudel Postdoctoral 2019-2020 UConn Health

Sherli Chenthittayil Postdoctoral 2017-2020 UConn Health

Luis Sordo Vieira Postdoctoral 2018-2019 Jackson Laboratory

Cory Brunson Postdoctoral 2014-2019 UConn Health

Anna Konstorum Postdoctoral 2015-2019 Institute for Defense Analysis

Byoungkoo Lee Postdoctoral 2016-2017 Jackson Laboratory

Sook Ha Asst. Professor 2013-2016 Virginia Military Institute

Anael Verdugo Assoc. Professor 2012-2013 UC Fullerton

Greg Blekherman Assoc. Professor 2009-2010 Georgia Tech

Julia Chifman Asst. Professor 2009-2013 American University

 Washington DC

Valerie Hower Assoc. Professor 2008-2009 Miami University

**BUSINESS EXPERIENCE**

Co-founder and Chief Scientific Officer, 3RBiosystems, 10755 Scripps Poway Pkwy 456, San Diego, CA 92131.

The company was incorporated in 2012. Its focus is the development and application of a systems biology platform for diagnostics and prognostics related to cancer immunotherapy.

**MEDIA COVERAGE**

UF Health researcher plans for next big step in medicine – human digital twins, University of Florida Health press release, March 22, 2021

<https://ufhealth.org/news/2021/uf-health-researcher-plans-next-big-step-medicine-human-digital-twins>

Micro-RNAs keep stem cells from growing up too fast, UConn Today, December 19, 2019

[https://today.uconn.edu/2019/12/micro-rnas-keep-stem-cells-growing-fast/#](https://today.uconn.edu/2019/12/micro-rnas-keep-stem-cells-growing-fast/)

Using mathematical modeling to target infections, Jackson Laboratory for Genomic Medicine Press Release, September 4, 2018

<https://www.jax.org/news-and-insights/2018/september/using-mathematical-modeling-to-target-infections>

New $3M NIH Grant Targets Respiratory Infections With Mathematical Modeling, UConn Today, September 4, 2018

<https://today.uconn.edu/school-stories/new-3m-nih-grant-targets-respiratory-infection-mathematical-modeling/>

Ovarian cancer cells hoard iron to fuel growth, UConn Today, August 15, 2018

<https://today.uconn.edu/2018/08/ovarian-cancer-cells-hoard-iron-fuel-growth/>

CT scientists want pain research to finally get its due, and funding, Hartford Business Journal, July 16, 2018

<http://www.hartfordbusiness.com/article/20180716/PRINTEDITION/307129945/1004?utm_source=enews&utm_medium=HBJToday&utm_campaign=Monday>

UConn Health and Jackson Lab to Collaborate on Statewide Pain Consortium, Hartford Courant, July 12, 2018

[http://www.courant.com/education/hc-ct-pain-consortium-uconn-health-jackson-20180705-story.html](https://urldefense.proofpoint.com/v2/url?u=http-3A__www.courant.com_education_hc-2Dct-2Dpain-2Dconsortium-2Duconn-2Dhealth-2Djackson-2D20180705-2Dstory.html&d=DwMGaQ&c=EZxp_D7cDnouwj5YEFHgXuSKoUq2zVQZ_7Fw9yfotck&r=dN2VyO2xvnkzC6bvLkZrykjbsqixsZyrGUrEfMI-4lI&m=CoD8AxymIqQHOvGc9TGzf2rx-ulNJuruUkMfCHg0K-o&s=Q6Z59dNEo_Ehf20ISZIueQxi0GkRIp_Va3wlSZXEytY&e=)

First of its kind pain consortium, UConn press release, June 28, 2018

<https://health.uconn.edu/quantitative-medicine/2018/06/28/first-of-its-kind-pain-consortium/>

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[https://today.uconn.edu/school-stories/controlling-biofilms-predictive-mathematical-models/](https://urldefense.proofpoint.com/v2/url?u=https-3A__today.uconn.edu_school-2Dstories_controlling-2Dbiofilms-2Dpredictive-2Dmathematical-2Dmodels_&d=DwMFAg&c=EZxp_D7cDnouwj5YEFHgXuSKoUq2zVQZ_7Fw9yfotck&r=dN2VyO2xvnkzC6bvLkZrykjbsqixsZyrGUrEfMI-4lI&m=NshhR563QaWydc2U-UIqUo_OuNB1aoB6tjb0FfKWtqs&s=GkC1YFmwlvHiaUqECUrYXwkhTgckwCKYCMO9OjfrBTM&e=)

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