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1. Education

Ph.D. (2003)   Chemical Engineering, Purdue University, West Lafayette, IN 47907, USA
Thesis: Integrating Causal Models and Trend Analysis
                for Process Fault Diagnosis
Advisor: Prof. Venkat Venkatasubramanian
GPA: 3.83/4.00

M.E. (1999)   Chemical Engineering, The City College of the City University of New York, New York, NY, 10031, USA
Thesis: Process Identification and Controller Design
                for a Fluid Catalytic Cracking Unit
Advisors: Prof. Irven H. Rinard and Prof. Reuel Shinnar
GPA: 3.94/4.00

B. Tech (1998)   Chemical Engineering, Indian Institute of Technology, Bombay, Powai, Mumbai, 600036, India
Thesis: Application of Qualitative Analysis in
                Chemical Engineering
Advisor: Prof. Raghunathan Rengaswamy
GPA: 8.70/10.00

2. Research Experience

Oct 06 – Present   **Scientist** [with Prof. Shankar Subramaniam, University of California, San Diego]:

- **Identification of biomarkers using multi-omics data for Non-Alcoholic Fatty Liver Disease (NAFLD) [LIPIDMAPS Consortium], 2012-2015**
  – Analysis of RNA-Seq data from about 100 people.
  – Data-reduction and statistical analysis such as ANOVA, clustering, correlation analysis, and related biological interpretation.

- − Linear discriminant analysis of lipid and gene data to identify biomarkers among normal, steatosis, steatohepatitis and cirrhosis samples.
  − SNP/GWAS analysis to identify key SNPs such as PNPLA3.
  − Identification of microRNA biomarkers for NAFLD using statistical analysis and support vector machines.
- **Supervision and maintenance of a Linux server (NGOMICS) for lab use for Multi-Omics data analysis, 2012-current**
  − Environments/software: R, Python, LAMP stack, various bioinformatics tools for mapping, format conversion and analysis of sequence data.
  − Deployed/debugged/tested a software called DM-ChIP (A statistically robust method to compare ChIP-Seq data sets; available at http://ngomics.sdsc.edu/dmchip/, developed by Dr. Nassim Ajami in python/R using Django framework) using Apache/wsgi on NGOMICS server.
- **Temporal-data driven network reconstruction using optimization/parameter estimation (reverse engineering/DS), 2008-current**
  − Development of temporally evolving networks using LASSO-based approach and their application to RNA-Seq time-course data from mouse cell cycle.
  − Integrated various complementary methods for data-driven network causal inference/reconstruction and predictive modeling (DPLASSO).
  − Developed information-theory and Granger-causality-based approaches to study the dynamic changes in reconstructed data-driven networks.
  − Performed comparative analysis of several methods for network reconstruction.
  − Developed an algorithm to integrate partial-least squares-based input/output modeling and statistical-hypothesis testing to identify signaling protein interactions using phosphoprotein data in RAW 264.7 cells.
  − Developed a methodology for F-test in k-fold cross-validation for input/output modeling to avoid over-fitting of data.
- **Community detection in large-scale biological networks, 2017-current**
  − Carried out a comprehensive comparison of several methods for community detection (such as Louvain, COMBO and Spinglass) on human and yeast protein-protein interaction networks using topological and functional comparison of the communities.
  − Ongoing work on community-based analysis of temporally evolving large-scale biological networks and their implications for biological dynamics.

- **Development of a pharmacokinetic model for a Complement-3 inhibitor using large-scale temporal data in rhesus monkey under intravenous (IV) and subcutaneous (SQ) doses, 2014-2015** [with Prof. John Lambris (University of Pennsylvania)]

- – Estimation of parameters using Matlab/Simbiology in a complex three compartment pharmacokinetic model using temporal days/weeks long data at various IV and SQ doses.
  - – Sensitivity analysis and prediction to identify minimal effective dose.
  - – Computational toxicology: Prediction of high dose response.
- **Effect of shear stress on endothelial cells, 2014-current** [with Profs. Shu Chien and John Shyy]
  - – Analysis of next-gen sequencing-based mRNA and microRNA data.
  - – Dynamic data-integration for the development of systems level networks and their interpretation.
  - – Application to study the effect of oscillatory and pulsatile (blood flow) shear stress on endothelial cells, with focus on differentiation in HUVECs.
  - – Analysis of data on role of 25-hydroxy-cholesterol (25-OHC) in endothelial cells in mediating effect of shear-stress.
  - – Mapping of more than ten different data sets related to shear stress and role of LINC520 in vascular health.
  - – Application to study effect of different flow patterns in HAECs.
- **Role of complement system in priming phase of liver regeneration, 2013-2016** [with Prof. John Lambris (University of Pennsylvania)]
  - – Analysis of RNA-Seq data from C3-/- knockout mouse with partial hepatectomy or sham surgery.
  - – Functional interpretation and network analysis in a temporal context.
- **Modeling of kinesin/dynein attachment to APP vesicles in neurons, 2012-2016** [with Prof. Lawrence S. B. Goldstein]
  - – Development of a kinetic model for the association of kinesin/dynein to APP vesicles based on data on the fraction of APP vesicles in various bound states.
  - – Parametric sensitivity analysis and prediction of the system's response for the knockdown/overexpression of kinesin and dynein motors.
- **Analysis of biomedical data from "healthy" overweight and obese people, 2013-2014** [with Profs. Beatriz Y. Salazar-Vazquez and Marcos Intaglietta]
  - – Statistical analysis and modeling of metabolic-panel data and other parameters from currently 'healthy' young overweight and obese adults to identify risk-factors as potential biomarkers for future metabolic and cardiovascular diseases.
- **Lipid metabolism and transcriptomic analysis in macrophages, 2007-current**
  - – Performed integrative analysis of metabolomic and transcriptomic data from bone-marrow derived macrophages (BMDM) subject to inflammatory stimuli.
  - – Performed comprehensive analysis of data from BMDM treated with 25-hydroxy-cholesterol (25-OHC): ANOVA on lipid data and its interpretation, and

clustering analysis on the gene data to elucidate the feedback regulation of sterol pathway by 25-OHC via LXR and SREBP2.

- Developed a systems-level kinetic model of eicosanoid metabolism to understand the preferential coupling of cyclooxygenase (COX) 1 and 2 to terminal synthases producing prostaglandin D2 and E2 and Thromboxane B2.
- Re-developed the above model using a cybernetic modeling approach [with Prof. Doraiswami Ramkrishna].
- Developed and applied advanced approaches for statistical analysis of transcriptomic data on macrophages (RAW 264.7 and primary macrophages) using statistical significance-test, pathway enrichment and pathway-level gene-gene or joint lipid-gene correlation-based hierarchical clustering.
- Performed comparative analysis of the transcriptome of RAW 264.7 cells and Thioglycollate-elicited macrophages using Pearson- and distance-based-correlation and Kolmogorov-Smirnov test.
- Developed a kinetic model for the metabolism of Eicosanoids (Arachidonic acid and its COX-2 products) and Sphingolipids in RAW 264.7 macrophages. COX is a target for anti-inflammatory drugs.
- Carried out further analysis of 25-OHC data in BMDM cells from LIPID MAPS to explore integration of data from macrophages and endothelial cells from Dr. John Shyy lab at UCSD.

- **Multiscale simulation, 2009-2014** [with Prof. Daniel M. Tartakovsky (UCSD, now at Stanford University)]
  - Developed a methodology for efficient stochastic simulation of reaction-diffusion systems using operator-splitting.
  - Developed and applied algorithms for multiscale hybrid stochastic simulation of biochemical pathways. Tested on calcium dynamics in RAW 264.7 cells.
  - Developed an advanced algorithm for time-scale decomposition of ordinary-differential equations-based models.

- **Gene-regulatory networks in cardiac development, 2006-current**
  - Development of microRNA-target-protein-interaction networks for cardiomyogenesis [with Dr. Mark Mercola (Sanford Burnham Prebys Medical Discovery Institute, now at Stanford University)].
  - Reconstruction of signaling and gene-regulatory networks active during cardiomyogenesis in development using microRNA screening data [with Dr. Mark Mercola].
  - Analysis of data related to role of Hippo Pathway in mediating effect of miRNAs that Induce Human Cardiomyocyte Proliferation.

Oct 03 – Sep 06   Postdoctoral Researcher [with Prof. Shankar Subramaniam]:
- **Data/model reduction**
  – Developed a multi-parametric variability analysis-based approach for model reduction and applied it to GTPase cycle module in G-protein signaling.
  – Developed a mixed-integer nonlinear-optimization-based approach for model reduction.
- **Data mining, machine learning and network reconstruction**
  – Developed a framework to reduce the number of false positives using Principal Component Regression and model-size minimization, developed a predictive network model for cytokine release in RAW 264.7 cells. Identified the regulators of gene-expression of TNF-alpha, a target for rheumatoid arthritis.
  – Designed a Partial Least-Squares-based algorithm to decipher gene-regulatory networks using temporal transcriptional data.
- **Systems-level kinetic modeling and parameter estimation for predictive models**
  – Developed a parallelized computer program using MPI for kinetic parameter estimation using genetic algorithms.
  – Developed a prototype kinetic modeling software in MATLAB to model biochemical reaction systems, which can use knockdown data with subpopulational variation.
  – Developed a model for calcium dynamics in RAW 264.7 cells using knockdown data with subpopulational variation.

March 03 – Sep 03   Non-thesis Work during Ph.D.:
- Developed a reduced-order model for the Mitogen-Activated Protein Kinase (MAPK) pathway in mouse NIH-3T3 cells.

Aug 99 – Sep 03   Ph.D. Thesis Work:
- **Signed digraph (SDG)-based modeling**
  – Designed and rigorously proved the methodologies for the development and analysis of SDG models.
  – Implemented a constraint satisfaction framework for SDG-based qualitative simulation and fault diagnosis of chemical process flow-sheets with feedback loops.
  – Designed an algorithm for SDG-based diagnosis of control loops.
- **Qualitative trend analysis (QTA) and Principal component analysis (PCA)**
  – Signal processing: Developed a methodology to extract qualitative shapes/trends in time-series data which extensively used t-test and F-test along with convex/quadratic constrained optimization.
  – Designed and implemented a prototype in Matlab for QTA-based on-line process diagnosis.

- **Integration of QTA with other methods**
  - Integrated principal component analysis (PCA) into the QTA-based diagnostic system to reduce the overall computation time due to dimensionality reduction.
  - Integrated QTA with SDG-based fault diagnosis to utilize topological information in diagnosing novel faults.

3. **Research Interests**

- Bioinformatics and Computational Systems Biology
- Big Data and Parallel Computing
- Multi-Omics and Clinical Data Integration, Machine Learning and Biostatistics
- Mechanisms and Biomarker Discovery and Diagnostic/Clinical Applications
- Modeling, Simulation and Optimization
- Applications of Graph Theory and Artificial Intelligence (AI)

4. **Teaching Experience**

CHE 450   Design and Analysis of Processing Systems, Undergraduate level, Purdue University, Spring 2002 (Head Teaching Assistant)

CHE 557   Intelligent Systems in Process Engineering, Graduate level, Purdue University, Fall 2000, 2001 (Teaching Assistant)

CHE 456   Process Dynamics and Control, Undergraduate level, Purdue University, Fall 2000 (Teaching Assistant)

5. **Advanced Course Work**

Process Control/Optimization   Advanced Process Control, Linear Programming, Non-Linear Programming, Discrete Optimization

Computer Science/AI   Pattern Recognition, Intelligent Systems, Neural Networks, Neural Fuzzy Systems, Artificial Intelligence

Core Chemical Engineering   Thermodynamics, Advanced Transport Phenomena, Reaction Engineering, Advanced Engineering Mathematics

6. Honors and Awards

1. International Federation of Automatic Control (IFAC) 2002 – 2005 paper prize for a paper in the journal *Engineering Applications of Artificial Intelligence* (2004) in the category "application-oriented paper on symbolic AI approaches"

2. Graduate Research Assistantship, Purdue University, 1999-2003

3. Graduate Fellowship, City University of New York, 1998 – 1999

4. Undergraduate Merit-cum-Means scholarship, IIT Bombay, 1994 – 1998

7. Memberships

American Institute of Chemical Engineers (1999-2008), American Chemical Society (2007-2008), American Association for the Advancement of Science (2007-2008), Sigma Xi, The Scientific Research Society (2007-2008)

8. Grants

1. NIH/NLM 1R01LM012595-01A1, Reconstruction and Modeling of Dynamical Molecular Networks, **Co-Investigator** (PI: Shankar Subramaniam, UCSD), 07/01/2018 – 06/30/2022, $1,348,953, **funded**.

2. NIH/NHLBI 5R01HL108735, Systems Biology Analyses for Hemodynamic Regulation of Vascular Homeostasis, Investigator/Senior Person (PIs: Shu Chien, Shankar Subramaniam, John Shyy, UCSD), 07/01/2017 – 06/30/2021, **funded, I wrote the Systems Biology Aim of the proposal**.

3. NIH/NHLBI, 2R01HL106579, Nucleolin Regulation of miRome by Shear Stress, Senior person (PIs: Shu Chien, John Shyy, Shankar Subramaniam, UCSD), 12/2018 – 11/2022, **funded, I wrote the Computational Systems Biology part of the proposal**.

4. NSF 1356594, ABI Development: The BioSystems Workbench, Co-PI (PI: Shankar Subramaniam, UCSD), 6/2014 - 5/2018, $2,036,672, not funded.

5. NIH/NHLBI, 1 R01 HL108735, Systems Biology Analyses for Hemodynamic Regulation of Vascular Homeostasis, PI(s): Shu Chien, Shankar Subramaniam, John Shyy (UCSD), 02/01/12-01/31/17, My role: **Senior Investigator**, **funded**.

6. UCSD-LANL Fees Research Program, Multiscale Modeling of Biological Systems, PI: Shankar Subramaniam; CoPIs: Daniel M Tartakovsky, **Mano R Maurya**, Gaurav Arya, Goutam Gupta (LANL), 07/2012-06/2015, $1,500,000, not funded.

7. UCSD-LANL Fees Research Program, Reconstruction of networks from data in biological systems, PI: Daniel M Tartakovsky; CoPIs: Shankar Subramaniam, **Mano R Maurya**, Brendt Wohlberg (LANL), 07/2012-06/2015, $1,500,000, not funded.

8. NIH/NIBIB, R21 EB015603-01A1, Coarse-Graining and Reduced-Order Modeling of Biochemical Reaction Systems, PI: **Mano R Maurya**, 04/01/2013-03/31/2015, $275,000 direct cost, not funded.

9. NSF 1062563, ABI Development: The BioSystems Workbench, Co-PI (PI: Shankar Subramaniam, UCSD), 6/2011 - 5/2016, $2,647,954, not funded.

10. NSF 0965713, The Biochemical Modeling Workbench: Models, Algorithms and Web Interfaces, Co-PI (PI: Shankar Subramaniam), 6/2010 – 5/2014, not funded.

11. NIH/NIGMS glue grant, U54 GM069338, LIPID MAPS ("Lipid Metabolite and Pathway Strategy") Consortium. **Coordinator for Bridge A** ("Networks") under Dr. Shankar Subramaniam (Co-P.I.; P.I.: Edward A. Dennis, UCSD), 09/2008 – 08/2013 (Bridge A: ~$200,000/year), Wrote Research Design & Methods, **Funded**.

12. NIH/NHLBI (1 R33 HL087375-01A1), Reconstruction and Modeling of Networks involved in Cardiomyogenesis, Shankar Subramaniam (P.I.), Mark Mercola (Co-P.I., The Burnham Institute) and Juan Carlos Izpisúa Belmonte (Co-P.I., Salk Institute for Biological Studies), 07/01/07 – 06/30/10 (SS portion: $235,364/year), Wrote the computational part of Research Design and Methods, **Funded**.

9. Publications

a. Journal Papers:

a.1. Chemical Process Systems Engineering

1. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "A Systematic Framework for the Development and Analysis of Signed Digraphs for Chemical Processes. 1. Algorithms and Analysis", *Ind. Eng. Chem. Res.,* **42**(20), 4789-4810, 2003.

2. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "A Systematic Framework for the Development and Analysis of Signed Digraphs for Chemical Processes. 2. Control Loops and Flowsheet Analysis", *Ind. Eng. Chem. Res.,* **42**(20), 4811-4827, 2003.

3. Dash, S., **M. R. Maurya**, R. Rengaswamy and V. Venkatasubramanian, "A Novel Interval-halving Framework for Automated Identification of Process Trends", *AIChEJ*, **50**(1), 149-162, 2004.

4. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Application of Signed Digraphs-Based Analysis for Fault Diagnosis of Chemical Process Flowsheets", *Engineering Applications of Artificial Intelligence*, **17**(5), 501-518, 2004 (**won IFAC 2002 – 2005 paper prize**).

5. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Fault Diagnosis by Qualitative Trend Analysis of the Principal Components", *Chemical Engineering Research and Design*, **83**(A9), 1122-1132, 2005.

6. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "A Signed Directed Graph-based Systematic Framework for Steady-State Malfunction Diagnosis inside Control Loops", *Chemical Engineering Science*, **61**(6), 1790-1810, 2006.

7. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Fault Diagnosis Using Dynamic Trend Analysis: A Review and Recent Developments", *Engineering Applications of Artificial Intelligence*, **20**(2), 133-146, 2007.

8. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "A Signed Directed Graph and Qualitative Trend Analysis-Based Framework for Incipient Fault Diagnosis", *Chemical Engineering Research and Design*, **85**(A10), 1407-1422, 2007.

9. **Maurya, M. R.**, P. K. Paritosh, R. Rengaswamy and V. Venkatasubramanian, "A Framework for On-Line Trend Extraction and Fault Diagnosis", *Engineering Applications of Artificial Intelligence*, **23**(6), 950-960, 2010.

a.2. Systems Biology (equal effort*)

10. Bornheimer, S. J., **M. R. Maurya**, M. G. Farquhar and S. Subramaniam, "Computational Modeling Reveals How Interplay between Components of the GTPase Cycle Regulates Signal Transduction", *Proc. Natl. Acad. Sci. USA*, **101**(45), 15899-15904, 2004.

11. **Maurya, M. R.**, S. J. Bornheimer, V. Venkatasubramanian and S. Subramaniam, "Reduced-Order Modeling of Biochemical Networks: Application to the GTPase-Cycle Signaling Module", *IEE Proc. - Systems Biology*, **152**(4), 229-242, 2005.

12. **Maurya, M. R.**, S. R. Katare, P. R. Patkar, A. Rundell and V. Venkatasubramanian, "A Systematic Framework for the Design of Reduced-Order Models for Signal

Transduction Pathways from a Control Theoretic Perspective", *Computers and Chemical Engineering*, **30**(3), 437-452, 2006.

13. Pradervand*, S., **M. R. Maurya*** and S. Subramaniam, "Identification of Signaling Components Required for the Prediction of Cytokine Release in RAW 264.7 Macrophages", *Genome Biology*, **7**(2), R11, 2006.

14. **Maurya, M. R.** and S. Subramaniam, "A Kinetic Model for Calcium Dynamics in RAW 264.7 Cells: 1. Mechanisms, Parameters and Sub-populational Variability", *Biophysical Journal*, **93**(3), 709-728, 2007.

15. **Maurya, M. R.** and S. Subramaniam, "A Kinetic Model for Calcium Dynamics in RAW 264.7 Cells: 2. Knockdown Response and Long-Term Response", *Biophysical Journal*, **93**(3), 729-740, 2007.

16. **Maurya, M. R.**, S. J. Bornheimer, V. Venkatasubramanian and S. Subramaniam, "A Mixed-Integer Nonlinear Optimization Approach to Coarse-Graining Biochemical Networks", *IET – Systems Biology*, **3**(1), 24-39, 2009.

17. Gupta, S., **M. R. Maurya**, D. L. Stephens, E. A. Dennis and S. Subramaniam, "An Integrated Model of Eicosanoid Metabolism and Signaling Based on Lipidomics Flux Analysis", *Biophysical Journal*, **96**(11):4542-51, 2009.

18. Gupta, S., **M. R. Maurya** and S. Subramaniam, "Identification of Crosstalk between Phosphoprotein Signaling Pathways in RAW 264.7 Macrophage Cells", *PLoS Comput Biol.*, **6**(1), e1000654, 2010.

19. Choi*, T. J., **M. R. Maurya***, D. M. Tartakovsky and S. Subramaniam, "Stochastic Hybrid Modeling of Intracellular Calcium Dynamics", *J. Chem. Phys.*, **133**(16), 165101, 2010.

20. Dennis, E. A., R. A. Deems, R. Harkewicz, O. Quehenberger, H. A. Brown, S. B. Milne, D. S. Myers, C. K. Glass, G. Hardiman, D. Reichart, A. H. Merrill, M. C. Sullards, E. Wang, R. C. Murphy, C. R. H. Raetz, T. Garrett, Z. Guan, A. C. Ryan, D. W. Russell, J. G. McDonald, B. M. Thompson, W. A. Shaw, M. Sud, Y. Zhao, S. Gupta, **M. R. Maurya**, E. Fahy and S. Subramaniam, "A Mouse Macrophage Lipidome", *Journal of Biological Chemistry*, **285**(51), 39976-85, 2010.

21. Gupta, S., **M. R. Maurya**, A. H. Merrill, Jr., C. K. Glass and S. Subramaniam, "Integration of Lipidomics and Transcriptomics Data Towards a Systems Biology Model of Sphingolipid Metabolism", BMC Systems Biology, **5**, 26, 2011.

22. Subramaniam , S., E. Fahy, S. Gupta, M. Sud, R. W. Byrnes, D. R. Cotter, A. R. Dinasarapu and **M. R. Maurya**, "Bioinformatics and the Systems Biology of the Lipidome", *Chemical Reviews*, **111**(10), 6452-6490, 2011 (invited, review paper).

23. DeAngelis, R.A., M. M. Markiewski, I. Kourtzelis, S. Rafail, **M. R. Maurya**, S. Gupta, S. Subramaniam and J. D. Lambris, "A complement-IL-4 regulatory circuit controls liver regeneration", *Journal of Immunology*, **188**(2), 641-648, 2012.

24. Asadi*, B., **M. R. Maurya***, D. M. Tartakovsky and S. Subramaniam, "Comparison of Statistical and Optimization-Based Methods for Data-Driven Network Reconstruction of Biochemical Systems", *IET Systems Biology*, **6**(5), 155-163, 2012.

25. Choi*, T. J., **M. R. Maurya***, D. M. Tartakovsky and S. Subramaniam, "Stochastic Operator-Splitting Method for Reaction-Diffusion Systems", *J. Chem. Phys.*, **137**(18), 184102, 2012.

26. **Maurya, M. R.**, S. Gupta, X. Li, E. Fahy, A. R. Dinasarapu, M. Sud, H. A. Brown, C. K. Glass, R. C. Murphy, D. W. Russell, E. A. Dennis and S. Subramaniam, "Analysis of Inflammatory and Lipid Metabolic Networks across RAW264.7 and Thioglycolate-elicited Macrophages", *Journal of Lipid Research*, **54**(9), 2525-2542, 2013.

27. Dinasarapu, A. R., S. Gupta, **M. R. Maurya**, E. Fahy, J. Min, M. Sud, M. J. Gersten, C. K. Glass and S. Subramaniam, "A Combined Omics Study on Activated Macrophages – Enhanced role of STATs in Apoptosis, Immunity and Lipid Metabolism", *Bioinformatics*, **29**(12), 2735-2743, 2013.

28. Lemons, D., **M. R. Maurya**, S. Subramaniam and M. Mercola, "Developing microRNA Screening as a Functional Genomics Tool for Disease Research", *Frontiers in Computational Physiology and Medicine*, **4**, Ar223.1-11, 2013 (invited, review paper).

29. Shibata, N., A. F. Carlin, N. J. Spann, K. Saijo, C. S. Morello, J. G. McDonald, C. Romanoski, **M. R. Maurya**, M. Kaikkonen, M. Lam, A. Crotti, D. Reichart, J. N. Fox, O. Quehenberger, C. R. Raetz, M. C. Sullards, R. C. Murphy, A. H. Merrill, Jr., H. A. Brown, E. A. Dennis, E. Fahy, S. Subramaniam, D.R. Cavener, D.H. Spector, D.W. Russell, C.K. Glass, "25-hydroxycholesterol activates the Integrated Stress Response to reprogram transcription and translation in macrophages", *Journal of Biological Chemistry*, **288**(50), 35812-23, 2013.

30. Kihara*, Y., S. Gupta*, **M. R. Maurya**, O. Quehenberger, A. Armando, C. K. Glass, E. A. Dennis and S. Subramaniam, "Modeling of Eicosanoid Fluxes in Macrophages

Reveals Functional Coupling between Cyclooxygenases and Terminal synthases", *Biophysical Journal*, **106**(4), 966-975, 2014.

31. Masnadi-Shirazi*, M., **M. R. Maurya*** and S. Subramaniam, "Time-Varying Causal Inference from Phosphoproteomic Measurements in Macrophage Cells", *IEEE Trans. Biomed. Circuits Syst.*, **8**(1), 74-86, 2014.

32. Farhangmehr*, F., **M. R. Maurya***, D. M. Tartakovsky and S. Subramaniam, "Information Theoretic Approach to Complex Biological Network Reconstruction: Application to Cytokine Release in RAW 264.7 Macrophages", *BMC Systems Biology*, **8**(1), 77, 2014.

33. Rojas-Muñoz*, A., **M. R. Maurya***, F. Lo and E. Willems, "Integrating Omics into the Cardiac Differentiation of Human Pluripotent Stem Cells", *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, **6**(4), 311-328, 2014 (review paper).

34. Gorden, D. L., D. S. Myers, P. T. Ivanova, E. Fahy, **M. R. Maurya**, S. Gupta, J. Min, N. J. Spann, J. G. McDonald, S. L. Kelly, J. Duan, M. C. Sullards, T. J. Leiker, R. M. Barkley, O. Quehenberger, A. M. Armando, S. B. Milne, T. P. Mathews, M. D. Armstrong, C. Li, W. V. Melvin, R. H. Clements, M. K. Washington, A. M. Mendonsa, J. L. Witztum, Z. Guan, C. K. Glass, R. C. Murphy, E. A. Dennis, A. H. Merrill, Jr., D. W. Russell, S. Subramaniam and H. A. Brown, "Biomarkers of NAFLD Progression: A Lipidomics Approach to an Epidemic", *Journal of Lipid Research*, **56**(3), 722-736, 2015.

35. Zarrinpar, A., S. Gupta, **M. R. Maurya**, S. Subramaniam and R. Loomba, "Serum microRNAs Explain Discordance of Non-Alcoholic Fatty Liver Disease in Monozygotic and Dizygotic Twins: A Prospective Study", *Gut*, 65(9), 1546-54, 2016.

36. Gupta, S., Y. Kihara, **M. R. Maurya**, P. C. Norris, E. A. Dennis and S. Subramaniam S., "Computational Modeling of Competitive Metabolism between omega-3- and omega-6-Polyunsaturated Fatty Acids in Inflammatory Macrophages", *Journal of Physical Chemistry B*, **120**(33), 8346-8353, 2016.

37. Min, J. S., R. A. DeAngelis, E. S. Reis, S. Gupta, **M. R. Maurya**, C. Evans, A. Das, C. Burant, J. D. Lambris and S. Subramaniam. "Systems Analysis of the Complement-Induced Priming Phase of Liver Regeneration", *Journal of Immunology*, **197**(6), 2500-2508, 2016.

38. Asadi*, B., **M. R. Maurya***, D. M. Tartakovsky and S. Subramaniam, "Doubly Penalized LASSO for Reconstruction of Biological Networks", *Special Issue,*

Proceedings of the IEEE "-Foundations & Applications of Science of Information", **105**(2), 319-329, 2017.

39. Ajami, N. E., S. Gupta, **M. R. Maurya**, P. Nguyen, J. Y. Li, J. Y-J. Shyy, Z. Chen, S. Chien and S. Subramaniam, "Systems Biology Analysis of Longitudinal Functional Response of Endothelial Cells to Shear Stress", *Proc. Natl. Acad. Sci. USA*, 2017, **114**(41), 10990-10995.

40. Li, Z., M. Martin, J. Zhang, H. Y. Huang, L. Bai, J. Kang, M. He, J. Li, **M. R. Maurya**, S. Gupta, G. Zhou, P. Sangwung, Y. J. Xu, T. Lei, H. D. Huang, M. Jain, M. K. Jain, S. Subramaniam, and J. Y. Shyy, "Kruppel-Like Factor 4 Regulation of Cholesterol-25-Hydroxylase and Liver X Receptor Mitigates Atherosclerosis Susceptibility", *Circulation*, 2017, **136**(14), 1315-1330.

41. Miao, Y., N. E. Ajami, T.-S. Huang, F.-M. Lin, C.-H. Lou, Y.-T. Wang, S. Li, J. Kang, H. Munkacsi, **M. R. Maurya**, S. Gupta, S. Chien, S. Subramaniam and Z. Chen, "Enhancer-associated long non-coding RNA LEENE regulates endothelial nitric oxide synthase and endothelial function", *Nature Communications*, 2018, **9**(1), 292.

42. Diez-Cuñado, M., K. Wei, P. J. Bushway, **M. R. Maurya**, R. Perera, S. Subramaniam, P. Ruiz-Lozano and M. Mercola, "MiRNAs that Induce Human Cardiomyocyte Proliferation Converge on the Hippo Pathway", *Cell Reports*, 2018, **23**(7), 2168–2174.

43. Aboulmouna, L., S. Gupta, M. R. Maurya, F. T. DeVilbiss, S. Subramaniam and D. Ramkrishna, "A Cybernetic Approach to Modeling Lipid Metabolism in Mammalian Cells", *Processes*, 2018, 6(8), 126.

44. Rahiminejad, S., **M. R. Maurya** and S. Subramaniam, "Topological and Functional Comparison of Community Detection Algorithms in Biological Networks", *BMC Bioinformatics*, 2019, Accepted.

45. Masnadi-Shirazi, M., **M. R. Maurya**, G. Pao, E. Ke, I. M. Verma, S. Subramaniam, "Time Varying Causal Network Reconstruction of a Mouse Cell Cycle", *BMC Systems Biology*, 2019, Accepted (being transferred to *BMC Bioinformatics*).

a.3. Submitted

46. Ajami, N. E., **M. R. Maurya**, S. Gupta and S. Subramaniam, "DM-ChIP: An accessible online suite for the comparison of broad-peaked ChIP-seq data sets", BMC Bioinformatics, 2018, Submitted.

47. Zarrinpar*, A., S. Gupta*, **M. R. Maurya***, M. Downes, M. Valasek, D. A. Brenner, R. M. Evans, S. Subramaniam and R. Loomba, "Novel Association between Serum

MicroRNA Profiling and Fibrosis in NAFLD: A Prospective Study", Hepatology Letters, 2017, Submitted.

b. Book chapters:

1. **Maurya, M. R.**, C. Benner, S. Pradervand, C. Glass and S. Subramaniam, "Systems Biology of Macrophages", Chapter 6 in *Current Topics in Innate Immunity*, Series: *Advances in Experimental Medicine and Biology*, Volume: 598, Editor: John D. Lambris, Publisher: Springer Science + Business Media, New York, ISBN-13: 978-0387717654, pp 62-79, 2007 (Invited).

2. **Maurya, M. R.** and S. Subramaniam, "Computational Challenges in Systems Biology", Chapter 8 in *Systems Biomedicine: Concepts and Perspectives*, Editors: E. T. Liu and D. A. Lauffenburger, Publisher: Academic Press, San Diego, CA, USA, ISBN-13: 978-0123725509, pp 177-223, 2009 (Invited).

3. Gupta*, S., A. R. Dinasarapu*, M. J. Gersten*, **M. R. Maurya*** and S. Subramaniam, "Omics Approaches to Macrophage Biology", Chapter 29 in *Macrophages: Biology and Role in the Pathology of Diseases*, Editors: Subhra K. Biswas and Alberto Mantovani, Publisher: Springer-Verlag, New York, NY, USA, ISBN-13: 978-1-4939-1310-7, pp 587-615, 2014 (Invited).

c. <u>Refereed</u> Publications in Conference Proceedings (speaker*):

1. **Maurya, M. R.**, R. Rengaswamy* and V. Venkatasubramanian, "Systematic Development and Application of Digraphs for Process Diagnosis and Hazards Analysis", In the proceedings of the *4th IFAC Workshop on On-Line Fault Detection & Supervision in the Chemical Process Industries (CHEMFAS-4), Korea, June 7-8*, pp 327-332, 2001.

2. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Incipient Fault Diagnosis of Tennessee Eastman Flowsheet using Signed Directed Graph and Trend Analysis", In the supplementary proceedings of the *12th European Symposium on Computer Aided Process Engineering (ESCAPE-12), The Hague, The Netherlands, May 26-29*, 2002 [G. V. Reklaitis*], Paper No. 461.

3. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Qualitative Trend Analysis of the Principal Components: Application to Fault Diagnosis", In the proceedings of the *8th International Symposium on Process Systems Engineering (PSE-2003), P.R. China, January 5-10*, pp 968-973, 2004.

4. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Consistent Malfunction Diagnosis inside Control Loops using Signed Directed Graphs", In the proceedings of the *13th European Symposium on Computer Aided Process Engineering (ESCAPE-13), Lappeenranta, Finland, June 1-4*, pp 473-478, 2003 [S. R. Katare*].

5. **Maurya, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "A Framework for On-line Trend Extraction and Fault Diagnosis", In the preprints of the *International Symposium on Advanced Control of Chemical Processes (ADChEM-2003), Hong Kong, January 11-14*, pp 423-428, 2004.

6. **Maurya*, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Fault Diagnosis by Qualitative Trend Analysis of the Principal Components: Prospects and some new Results", In the proceedings of the *5th IFAC symposium on Fault Detection, Supervision and Safety of Technical Processes (SAFEPROCESS-2003), Washington D.C., USA, June 9-11*, pp 861-866, 2003.

7. **Maurya, M. R.**, S. J. Bornheimer*, V. Venkatasubramanian and S. Subramaniam, "Reduced-Order Modeling of Biochemical Networks by Simultaneous Determination of Network Topology and Parameters", In the proceedings of the *Foundations of Systems Biology in Engineering (FOSBE 2005), University of California, Santa Barbara, August 7-10*, pp 281-284, 2005.

8. Srinivasan, R., **M. R. Maurya** and R. Rengaswamy, "Root Cause Analysis of Oscillating Control Loops", In the proceedings of the *International Symposium on Advanced Control of Chemical Processes (ADChEM-2006), Gramado, Brazil, April 2-5*, pp 1151-1156, 2006.

9. Asadi*§, B., **M. R. Maurya**§, D. M. Tartakovsky and S. Subramaniam, "Comparison of Statistical and Optimization-based Methods for Data-Driven Network Reconstruction of Biochemical Systems", In the proceedings of the *IASTED International Conference (CompBio 2010), Cambridge, MA, USA, Nov. 1-3*, pp 587-592, 2010 [§: equal effort].

10. Asadi*, B., **M. R. Maurya**, D. M. Tartakovsky and S. Subramaniam, "Doubly Penalized LASSO for Reconstruction of Biological Networks", In the proceedings of the *IEEE Second International Conference on Healthcare Informatics, Imaging and Systems Biology (HISB), San Diego, CA, Sept. 27-28*, pp.129, 2012.

d. Posters and Papers Presented at Conferences and Meetings (speaker*, §: equal effort):

1. **Maurya*, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Systematic Development of Digraphs and Application in Process Operations", In *AIChE Annual Meeting, 267b, Reno, NV, Nov. 4-9*, 2001 [poster].**Maurya*, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Signed Directed Graph and Trend Analysis-Based Framework for Incipient Fault Diagnosis- Application to Tennessee Eastman Case Study", In *AIChE Annual Meeting, 263h, Indianapolis, IN, Nov. 3-8*, 2002.

3. **Maurya*, M. R.**, R. Rengaswamy and V. Venkatasubramanian, "Computational Aspects of Trend-Extraction and Trend-Based Similarity Estimation", In *AIChE Annual Meeting, 448e, San Francisco, CA, Nov. 16-21*, 2003.

4. **Maurya*, M. R.**, S. R. Katare, P. R. Patkar, A. Rundell and V. Venkatasubramanian, "Control Theoretic Perspective of Mitogen Activated Protein Kinase Signaling Pathways", In *AIChE Annual Meeting, 463e, San Francisco, CA, Nov. 16-21*, 2003.

5. Shimada, Y., C. Zhao*, F. Mu, **M. R. Maurya** and V. Venkatasubramanian, "A Design Rationale Centered Integrated Environment for Batch Process Design", In *AIChE Annual Meeting, 422d, San Francisco, CA, Nov. 16-21*, 2003.

6. **Maurya, M. R.**, S. J. Bornheimer*, V. Venkatasubramanian and S. Subramaniam, "Reduced-Order Models of Biochemical Networks: GTPase Cycle as an Exemplar", In *Second RGS Protein Colloquium, Washington, D.C., April 17*, 2004 [poster].

7. **Maurya*, M. R.**, S. J. Bornheimer, V. Venkatasubramanian and S. Subramaniam, "A Multidimensional Sensitivity Analysis Approach to Reduced-Order Modeling: GTPase Cycle as an Exemplar", In *AIChE Annual Meeting, 426b, Austin, TX, Nov. 7-12*, 2004.

8. **Maurya*, M. R.**, "Computational Models for GTPase Cycle and Calcium Signaling", In *AIChE Annual Meeting, 293bd, Austin, TX, Nov. 7-12*, 2004 [poster].

9. **Maurya*, M. R.**, S. J. Bornheimer, V. Venkatasubramanian and S. Subramaniam, "Model-Reduction by Simultaneous Determination of Network Topology and Parameters: Application to Modules in Biochemical Networks", In *AIChE Annual Meeting, 381a, Cincinnati, OH, Oct. 31 – Nov. 4*, 2005.

10. Pradervand, S., **M. R. Maurya*** and S. Subramaniam, "Identification of Important Signaling Proteins and Stimulants for the Production of Cytokines in RAW 264.7 Macrophages", In *AIChE Annual Meeting, 304g, Cincinnati, OH, Oct. 31 – Nov. 4*, 2005.

11. **Maurya*, M. R.** and S. Subramaniam, "Modeling of Heterotrimeric G-Protein Mediated Calcium Response in RAW 264.7 Macrophage Cells", In *AIChE Annual Meeting, 506g, Cincinnati, OH, Oct. 31 – Nov. 4*, 2005.

12. **Maurya*, M. R.** and S. Subramaniam, "Optimization as a Tool for Predictive Modeling of Biological Systems and Mining of Large-Scale Data Sets", In *AIChE Annual Meeting, 4bl, Cincinnati, OH, Oct. 31 – Nov. 4*, 2005 [poster].

13. Lo*, F., S. Subramaniam, M. Mercola, R. Guzzo, A. Foley, **M. R. Maurya**, "Reconstruction of Pathways Leading to Cardiomyocyte Differentiation from ESCs", Presented by Frederick Lo. In *The Stem Cell Meeting on the Mesa, La Jolla, CA, Oct. 20*, 2006 [poster]**.**

14. Gupta*, S., **M. R. Maurya**, A. Maer and S. Subramaniam, "Integrated Modeling of Lipids Metabolism and Signaling Pathways", In *AIChE Annual Meeting, 242g, Salt Lake City, UT, Nov. 4 – 9*, 2007.

15. Gupta*, S., **M. R. Maurya** and S. Subramaniam, "Reconstruction of Phosphoproteins Signaling Network In Raw 264.7 Macrophages", In *AIChE Annual Meeting, 572u, Philadelphia, PA, Nov. 16 – 21*, 2008 [poster].

16. Choi*, T., **M. R. Maurya**, D. M. Tartakovsky and Shankar Subramaniam, "Stochastic Simulation of Cytosolic Calcium Dynamics", In *AIChE Annual Meeting, 151b, Nashville, TN, Nov. 8 – 13*, 2009.

17. Gupta*, S., **M. R. Maurya** and S. Subramaniam, "Modeling of Sphingolipids Metabolism in Mouse Macrophage RAW 264.7 Cells", In *AIChE Annual Meeting, 173f, Nashville, TN, Nov. 8 – 13*, 2009.

18. **Maurya*, M. R.** and S. Subramaniam, "Sensitivity Analysis of a Model of Calcium Dynamics Reveals Hot-Spots of Signaling", In *AIChE Annual Meeting, 636d, Nashville, TN, Nov. 8 – 13*, 2009.

19. Sud*, M., D. Cotter, E. Fahy*, R. Byrnes, S. Gupta, S. Li, **M. R. Maurya**, Y. Zhao, S. Subramaniam, H. A. Brown, C. K. Glass, A. H. Merrill, Jr., R. C. Murphy, C. R. H. Raetz, D. W. Russell, E. A. Dennis, "LIPID Metabolites And Pathways Strategy (LIPID MAPS)", In *LIPID MAPS Annual Meeting, Poster No. 18, La Jolla, CA, May 06 – 07*, 2009.

20. Sud*, M., E. Fahy, Y. Zhao, D. Cotter, R. Byrnes, S. Gupta, S. Li , **M. R. Maurya**, S. Subramaniam, H. A. Brown, C. K. Glass, A. H. Merrill, Jr., R. C. Murphy, C. R. H. Raetz, D. W. Russell, E. A. Dennis, "Integrated Lipids, Genes, and Pathways Data across Timecourse Experiments for RAW 264.7 Cells Treated with Kdo2-lipid A", In *LIPID MAPS Annual Meeting, Poster No. 19, La Jolla, CA, May 06 – 07*, 2009.

21. Byrnes*, R., D. Cotter, E. Fahy, S. Gupta, S. Li, **M. R. Maurya**, M. Sud*, S. Subramaniam, "LIPID MAPS Methodologies for Pathway Construction and Analysis", In *LIPID MAPS Annual Meeting, Poster No. 46, La Jolla, CA, May 03 – 04*, 2010.

22. DeAngelis*, R. A., M. M. Markiewski, **M. R. Maurya**, S. Gupta, S. Subramaniam, and J. D. Lambris, "A Complement-IL-4 Regulatory Circuit Controls Liver Regeneration", In XXIII International Complement Conference, New York, NY (Molecular Immunology, 47(13), 2227-2227 (Abstract No. 173)), Pergamon-Elsevier Science Ltd, Oxford, UK. Aug 1-5, 2010.

23. **Maurya*, M. R.** and S. Subramaniam, "On the Incorporation of Direction and Magnitude in Statistical Correlation: Application to Gene-Microarray Data", In *AIChE Annual Meeting, 693f, Salt lake City, UT, Nov. 7 – 12*, 2010.

24. **Maurya*, M. R.**, T. Choi, D. M. Tartakovsky and S. Subramaniam, "Timescale Analysis of Cytosolic Calcium Dynamics", In *AIChE Annual Meeting, 155d, Salt lake City, UT, Nov. 7 – 12*, 2010.

25. Gupta, S., **M. R. Maurya*** and S. Subramaniam, "Matrix and Optimization Approach to Kinetic Modeling of Lipid Pathways", In *AIChE Annual Meeting, 568o, Salt lake City, UT, Nov. 7 – 12*, 2010 [poster].

26. **Maurya*, M. R.**, S. Gupta and S. Subramaniam, "F-Test in k-Fold Cross Validation and Its Application to the Discovery of Biological Networks", In *AIChE Annual Meeting, 597b, Salt lake City, UT, Nov. 7 – 12*, 2010.

27. Choi*, T., **M. R. Maurya**, D. M. Tartakovsky and S. Subramaniam, "Stochastic Operator Splitting Method for Biological Systems", In *AIChE Annual Meeting, 243f, Minneapolis, Oct. 16 – 21*, 2011.

28. **Maurya*, M. R.**, S. Gupta, E. Fahy, A. R. Dinasarapu, X. Li, M. Sud and S. Subramaniam, "Comparative Analysis of Transcriptome and Lipidome of RAW 264.7 and Primary Macrophages", In *AIChE Annual Meeting, 306f, Minneapolis, Oct. 16 – 21*, 2011.

29. Asadi*, B., **M. R. Maurya**, D. M. Tartakovsky and S. Subramaniam, "Data-Driven Network Reconstruction of Biological Systems: Comparison of Statistical and Optimization-Based Methods", In *AIChE Annual Meeting, 764b, Minneapolis, Oct. 16 – 21*, 2011.

30. **Maurya*, M. R.**, S. Gupta, A. R. Dinasarapu, E. Fahy, M. Sud and S. Subramaniam, "Integrated Transcriptomic and Lipidomic Study of Macrophage Response to Liver

X Receptor Ligand 25-Hydroxy-Cholesterol", In *AIChE Annual Meeting, 760g, Pittsburgh, PA, Oct. 28 – Nov. 2*, 2012.

31. Asadi*§, B., **M. R. Maurya**§, D. M. Tartakovsky and S. Subramaniam, "Doubly Penalized Approach for Reconstructing Biological Networks", In *AIChE Annual Meeting, 497h, Pittsburgh, PA, Oct. 28 – Nov. 2*, 2012.

32. Gupta*, S., Y. Kihara, **M. R. Maurya**, O. Quehenberger, A. Armando, C. K. Glass, E. A. Dennis and S. Subramaniam, "Integration of Transcriptomic Data in Kinetic Modeling of Eicosanoids Fluxes Reveals Functional Coupling between Cyclooxygenases and Terminal Synthases", In *Biomedical Engineering Society Annual Meeting, P-Fri-B-10, Atlanta, GA, Oct. 24 – 27*, 2012.

33. **Maurya*§, M. R.**, A. R. Dinasarapu§, S. Gupta§, E. Fahy, M. Sud and S. Subramaniam, "An Integrated Transcriptomic and Lipidomic Study of Oxidized Lipid Activated RAW 264.7 Macrophages", In *BMES Annual Meeting, P-Fri-B-21 ("Genomics, Transcriptomics and Proteomics"), Seattle, WA, Sept 25-28*, 2013 [poster].

34. Gupta*, S., A. R. Dinasarapu, **M. R. Maurya**, E. Fahy, J. Min, M. Sud, M. J. Gersten, C. K. Glass and S. Subramaniam, "Intricate Interplay Between TLR4 and Purinergic Receptor Signaling in Activated Macrophages", In *BMES Annual Meeting, P-Fri-B-7 ("Genomics, Transcriptomics and Proteomics"), Seattle, WA, Sept 25-28*, 2013 [poster].

35. Asadi*, B., **M. R. Maurya**, D. M. Tartakovsky and S. Subramaniam, "Data-Driven Reconstruction of Biological Networks Using a Nonlinear Model Formulation", In *AIChE Annual Meeting, 680a, San Francisco, CA, Nov. 3 – Nov. 8*, 2013.

36. Masnadi-Shirazi, M., **M. R. Maurya*** and S. Subramaniam, "Causal Inference of Time-Varying Signaling Networks Using Dynamic Data", In *AIChE Annual Meeting, 601e, Atlanta, GA, Nov. 16 – Nov. 21*, 2014 [poster].

37. DeVilbiss*, F. T., D. Jayachandran, **M. R. Maurya**, S. Gupta, S. Subramaniam and D. Ramkrishna, "Predicting Gene Expression Data from Changes in Eicosanoid Metabolite Levels in RAW 264.7 Macrophages Using Cybernetic Variables", In *AIChE Annual Meeting, 332g, Atlanta, GA, Nov. 16 – Nov. 21*, 2014.

38. DeVilbiss*, F. T., **M. R. Maurya**, S. Gupta, A. Mandli, S. Subramaniam and D. Ramkrishna, "Prediction of Gene Expression Using Goal-Directed Metabolic Models", In AIChE Annual Meeting, 72e, Salt Lake City, UT, Nov. 8 – Nov. 13, 2015.

39. **Maurya*, M.R.**, L. Szpankowski, L. S. B. Goldstein and S. Subramaniam, "Dynamic Modeling of Molecular Motor Association with Axonal Amyloid Precursor Protein

Vesicles", In AIChE Annual Meeting, 72h, Salt Lake City, UT, Nov. 8 – Nov. 13, 2015.

40. Gupta*, S., Y. Kihara, **M. R. Maurya**, P. C. Norris, E. A. Dennis and S. Subramaniam, "A systems Biology Approach to Metabolic Antagonism Between Omega-3 and Omega-6 Fatty Acids During Macrophage Inflammatory Response", In Biomedical Engineering Society Annual Meeting, P-Th-109, Tampa, FL, Oct. 7-10, 2015.

41. **Maurya*, M. R.**, E. Fahy, S. Gupta, J. Min, S. Subramaniam and LIPID MAPS Consortium, "Lipidomic and Transcriptomic Biomarkers for Diagnosis of Nonalcoholic Fatty Liver Diseases", In AIChE Annual Meeting, 228dr, San Francisco, CA, Nov. 13 – Nov. 18, 2016 [poster].

42. DeVilbiss*, F. T., **M. R. Maurya**, S. Gupta, S. Subramaniam and D. Ramkrishna, "Deductive Determination of Dynamic Cellular Objectives from Biological Data", In AIChE Annual Meeting, 740g, San Francisco, CA, Nov. 13 – Nov. 18, 2016.

43. Masnadi-Shirazi, M., **M. R. Maurya**, G. Pao, E. Ke, I. M. Verma, S. Subramaniam, "Time Varying Causal Network Reconstruction of Mouse Cell Cycle using Temporal Gene Expression Data", In Biomedical Engineering Society Annual Meeting, 653, Phoenix, AZ, Oct. 11-14, 2017.

44. Aboulmouna, L., F. T. DeVilbiss, **M. R. Maurya**, S. Gupta, S. Subramaniam and D. Ramkrishna, "A Cybernetic Approach to Modeling Lipid Metabolism in Mammalian Cells", In AIChE Annual Meeting, 732c, Minneapolis, MN, Oct. 29 - Nov. 03, 2017.

45. Subramaniam, S. and **M. R. Maurya**, "Computational Challenges in Systems Biology", In AIChE Annual Meeting, 89c, Pittsburgh, PA, Oct. 28 - Nov. 02, 2018.

46. Aboulmouna, L., S. Gupta, **M. R. Maurya**, F. T. DeVilbiss, S. Subramaniam and D. Ramkrishna, "Application of Cybernetic Control Variables in the Modeling of Lipid Metabolism in Mammalian Systems", In AIChE Annual Meeting, 188dk, Pittsburgh, PA, Oct. 28 - Nov. 02, 2018.

e. Invited Presentations:

1. **Maurya, M. R.**, "Computational Models for GTPase-Cycle Signaling and Calcium Signaling", At the *Joint Department of Biomedical Engineering, North Carolina State University, Raleigh, and University of North Carolina, Chapel Hill, March 21*, 2005.

2. **Maurya*, M. R.** and S. Subramaniam, "Computational Modeling of Cellular Signaling Networks", In *Third International Symposium of the Austrian Proteomics Platform, Seefeld, Tyrol, Austria, January 16-19*, 2006.

3. **Maurya, M. R.,** "Offline and Online Process Safety Analysis", At the *Artie McFerrin Department of Chemical Engineering, Texas A&M University, College Station, Texas, April 21*, 2006.

4. **Maurya, M. R.,** "A Model of Calcium Signaling in Non-Excitable Cells", At the *National Institute of Allergy and Infectious Diseases (NIAID) of the National Institutes of Health (NIH), Bethesda, Maryland, April 26*, 2007.

5. **Maurya, M. R.,** "Process Fault Diagnosis for Abnormal Event Management", At *ExxonMobil Research and Engineering Company, Annandale, New Jersey, May 23*, 2007.

6. **Maurya, M. R.,** "Systems Biology of Macrophages", At *School of Biomedical Engineering, Science and Health Systems, Drexel University, Philadelphia, Pennsylvania, April 24*, 2008.

7. **Maurya, M. R.,** "Systems Biology of Macrophages", At *Department of Chemical Engineering, University of Puerto Rico at Mayagüez, May 8*, 2008.

8. **Maurya*, M. R.** and S. Subramaniam, "Data Integration in the Life Sciences: From Data to Networks, Models and Phenotypes", In *7th World Congress on Alternatives and Animal Use in the Life Sciences, Rome, Italy, August 30 – September 3*, 2009.

9. **Maurya, M. R.,** "Activation of Macrophages during Immune Response: A Case Study in Systems Biology", At *University of Florida, Gainesville, October 28*, 2009.

10. **Maurya, M. R.,** "A Signaling, Transcriptomic and Lipidomic Perspective of Macrophage Activation during Immune Response", At *University at Buffalo, The State University of New York, Buffalo, New York, June 16*, 2011.

11. **Maurya, M. R.,** "Integrated Transcriptomic and Lipidomic Study of Macrophage Inflammatory Response", At *University of Rochester, Biostatistics & Computational Biology, Rochester, NY, April 5*, 2012.

10. Unofficial Supervision of Graduate/Postdoctoral Researchers

a. Graduate students

1. Scott J. Bornheimer, 2003-08, Ph.D. research-co-advisor/collaborator, Modeling of GTPase cycle module [UCSD].

2. Dr. Frederick Lo, 2005-11, Ph.D. research-co-advisor/collaborator, Kinetic modeling of biochemical pathways and network reconstruction in cardiomyogenesis [UCSD].

3. TaiJung Choi, 2009-2013, Ph.D. research-co-advisor (6th Member on thesis committee), Stochastic simulation of biochemical systems [UCSD].

4. Thomas F. Gallegos, 2009, Microarray data analysis [UCSD].

5. Jessica DeQuach, Ph.D. student, 2009-10, Interpretation of principal components [UCSD].

6. Tejaswini Narayanan, Ph.D. student, Command-line arguments in C/C++ programming in Unix [UCSD].

7. Behrang Asadi, 2010-2013, Ph.D. research co-advisor (6th Member on thesis committee), Data-driven integrated approaches for network reconstruction of biochemical systems [UCSD].

8. Farzaneh F. Mehr, 2011-2014, Ph.D. research co-advisor, Information theoretic approaches to data-driven network reconstruction [UCSD].

9. Maryam masnadi-Shirazi, 2012-2018, Ph.D co-advisor/collaborator, Data-driven approaches to the reconstruction of dynamic networks [UCSD].

10. Jun Min Sung, 2012-2017, Ph.D. research co-advisor/collaborator, Systems Biology approaches to study liver regeneration and diseases using next-gen sequencing (NGS) and other patient data [UCSD].

11. Thomas Atanasov, 2013-2014, Ph.D. research co-advisor/collaborator, Systems Biology approaches to study effect of shear stress on endothelial cells using NGS–based mRNA and microRNA data [UCSD].

12. Sindhu Raghunathan, 2013-2017, Ph.D. student, Systems Biology approaches to study mechanisms in liver diseases using NGS–based mRNA and mass-spec proteomic data [UCSD].

13. Nassim Ajami, 2015-2018, Ph.D. research co-advisor/collaborator, Systems Biology approaches to study effect of shear stress on endothelial cells using NGS–based mRNA and microRNA data [UCSD].

14. Shamim Mollah, 2016-current, Ph.D. student, Systems Biology and Bioinformatics approaches to study ovarian cancer in human using proteomic data [UCSD]; my role: initial advising on use of PLS for network reconstruction.

15. Sara Rahiminejad, 2016-current, Ph.D. student, co-advisor/collaborator, Modularity-based approaches to study dynamics of biological networks [UCSD].

b. Postdoctoral researchers

1. Shakti Gupta, 2006-09, co-researcher, Kinetic modeling of lipid signaling and metabolism and network reconstruction [UCSD].

2. Ankur Dnyanmote, 2007-08, Computational modeling of Organic Anion Transport system in Kidney [UCSD].

3. Sean Li, 2007-10, co-researcher, Advanced analysis of LIPID MAPS data [UCSD].

4. Ashok Reddy Dinasarapu, 2010-2013, co-researcher, Advanced analysis of LIPID MAPS data [UCSD].

11. Professional Activities

a. Reviewer
Chemical and Process Systems Engineering:
American Control Conference, Computers and Chemical Engineering, Chemical Engineering Science, Control Engineering Practice, Process Safety Progress, Industrial and Engineering Chemistry Research, IEEE Transactions on Control Systems Technology, IET - Control Theory & Applications, American Control Conference (2008), Conference on Control and Fault Tolerant Systems (2010, SYSTOL10), Proceedings of the Institution of Mechanical Engineers, Part E, Journal of Process Mechanical Engineering, Engineering Applications of Artificial Intelligence, Journal of Process Control.

Bioengieering/Bioinformatics:
IET – Systems Biology, Biophysical Journal, BMC Bioinformatics (unofficial), Journal of Theoretical Biology (unofficial), Bulletin of Mathematical Biology, Journal of Lipid Research.

b. Editorial Board Member
ISRN Biophysics (August 2011-).

c. Chair/Co-chair at Conferences and Meetings
Co-chair, AIChE Annual Meeting, 2014-2016, Division: Computing and Systems Technology (CAST), Sub-division: 10E (Advances in Data Analysis).

12. University Services

Committee member, Ad-hoc review for assistant project scientist applications, UCSD, Bioengineering
PhD thesis Committee member for graduate students, UCSD