

Daniel Lobo

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Education

- 2015 **Postdoc. Developmental, Regenerative, and Cancer Biology** *Tufts University, MA*
- 2010 **Ph.D. Computer Science** *University of Malaga, Spain*
Thesis distinguished Summa Cum Laude, Doctor Europeus
- 2007 **M.S. Computer Science and Artificial Intelligence** *University of Malaga, Spain*
Thesis distinguished with highest honors
- 2005 **B.S. Computer Science and Computer Engineering** *University of Seville, Spain*
Thesis distinguished with highest honors

Academic & Professional Experience

- Aug 2015 – Present **Assistant Professor** *University of Maryland, Baltimore County, MD*
Department of Biological Sciences
- Sep 2017 – Present **Full Member** *Marlene and Stewart Greenebaum Cancer Center, MD*
Program in Oncology
- Apr 2011 – Jul 2015 **Postdoctoral Research Associate** *Tufts University, MA*
Department of Biology
- Oct 2005 – Mar 2011 **Research Assistant** *University of Malaga, Spain*
Department of Computer Science
- Oct 2009 – Dec 2009 **Visiting Research Scholar** *Otto-Von-Guericke University, Germany*
Department of Computer Science
- Dec 2007 – Jun 2008 **Visiting Research Scholar** *Cornell University, NY*
Departments of Computer Science & Mechanical Engineering
- Oct 2003 – Sep 2005 **Software Engineer** *Isotrol Inc, Spain*
Control Systems Division

Honors & Awards

- 2020 **Outstanding Investigator Award (R35)**, National Institutes of Health
- 2017 **Research Starter Award**, PhRMA Foundation
- 2014 **Annual Postdoc Poster Competition for Travel Fellowships**, 1st place, Tufts University
- 2013 **Research Visualization Awards**, Software, 2nd place, Tufts University
- 2012 **Research Visualization Awards**, Illustration, 2nd place, Tufts University

- 2011 **Elected Full Member**, Sigma Xi, The Scientific Research Society
- 2009 **Research Stay Fellowship at Otto-Von-Guericke University**, Education Ministry of Spain
- 2009 **Spin-off Award**, University of Malaga
- 2008 **Fastest Prototyping Team Award**, The ICRA Robot Challenge, Pasadena, CA
- 2007 **Visiting Fellowship at Cornell University**, Cornell University Graduate School
- 2005 **Doctoral Fellowship at University of Malaga**, Education Ministry of Spain
- 2003 **Travel Scholarship at The University of Edinburgh**, Education Ministry of Spain
- 2000 **Undergraduate Scholarship at University of Seville**, Education Ministry of Spain

Research Support

- 09/2020 – 06/2025 **National Institutes of Health**, award #R35GM137953
D. Lobo. *Systems Biology of Shape and Size Regulation*.
Role: Principal Investigator
Total funds: \$1,894,361
- 10/2019 – 09/2022 **National Science Foundation**, award #1920079
H. Pirsiavash, N. Karimi, C. Matuszek, D. Doyle, F. Ferraro. *MRI: Acquisition of a Heterogeneous GPU Cluster to Facilitate Deep Learning Research at UMBC*.
Role: Senior Personnel
Total funds: \$300,000
- 10/2018 – 05/2019 **UMBC**, Office of Vice President for Research
D. Lobo. Supplement for Undergraduate Research Experiences.
Role: Principal Investigator
Total funds: \$1,500
- 10/2017 – 05/2018 **UMBC**, Office of Vice President for Research
D. Lobo. Supplement for Undergraduate Research Experiences.
Role: Principal Investigator
Total funds: \$1,500
- 09/2017 – 08/2020 **National Science Foundation**, award #1726023
M.K. Gobbert, D. Lobo, M. Olano, J. Wang, M. Yu. *MRI: Acquisition of Cutting-Edge GPU and Phi Nodes for the Interdisciplinary UMBC High Performance Computing Facility*.
Role: Co-Principal Investigator
Total funds: \$552,353
- 06/2017 – 08/2017 **UMBC**, Office of Vice President for Research
D. Lobo. *Automated design and optimization of engineered regulatory-metabolic networks for multi-microbe biofuel production*.
Role: Principal Investigator
Total funds: \$6,000
- 02/2017 – 07/2018 **PhRMA Foundation**, Research Starter Grant in Informatics
D. Lobo. *Automated inference of human intra-tumor interaction networks for discovering optimal treatments*.
Role: Principal Investigator
Total funds: \$100,000

- 08/2016 **NVIDIA Corporation**
D. Lobo. *Inferring predictive dynamic regulatory mechanisms from biological experimental data.*
Role: Principal Investigator
Total funds: equipment valued at \$6,000
- 06/2016 – 08/2016 **UMBC**, Office of Vice President for Research
D. Lobo. *Reverse-engineering of integrated regulatory-metabolic networks in bacterial systems.*
Role: Principal Investigator
Total funds: \$6,000
- 04/2016 – 08/2019 **National Science Foundation**, award #1566077
D. Lobo. *CRII: III: Automated discovery of predictive regulatory models from morphogenetic experimental data.*
Role: Principal Investigator
Total funds: \$191,000
- 01/2015 – 06/2016 **National Science Foundation**, Extreme Science and Engineering Discovery Environment, award #CDA130008 (renewal)
D. Lobo, M. Levin. *Automatic discovery of regulatory networks for growth and form.*
Role: Principal Investigator
Total funds: computational resources valued at \$32,893
- 07/2013 – 12/2014 **National Science Foundation**, Extreme Science and Engineering Discovery Environment, award #CDA130008
D. Lobo, M. Levin. *Automated synthesis of biological models from experiment-phenotype data.*
Role: Principal Investigator
Total funds: computational resources valued at \$51,118
- 03/2013 **Silicon Mechanics Inc.**, 2nd Annual Research Cluster Grant
M. Levin, D. Lobo, M. Scheutz, D. Kaplan, C. Börgers
Role: Co-Principal Investigator
Total funds: high-performance computer cluster valued at \$80,000
- 11/2012 – 10/2013 **National Science Foundation**, Extreme Science and Engineering Discovery Environment, award #CDA130001
D. Lobo. *Automated discovery of algorithmic patterning models from biological experimental data.*
Role: Principal Investigator
Total funds: computational resources valued at \$6,922
- 09/2011 – 08/2015 **National Science Foundation**, award #1124651
M. Levin. *Collaborative Research: CDI Type-1: A Computer Framework for Modeling Complex Pattern Formation.*
Role: Other Personnel – Postdoctoral Associate
Total funds: \$380,000
- 02/2010 – 03/2014 **Andalusian Regional Ministry of Economy, Innovation, and Science**, award #P09-TIC-5123
F.J. Vico. *GENEX: Novel computational intelligence techniques for modeling genetic regulatory networks controlling embryonic development.*
Role: Other Personnel – Graduate Student

Total funds: €432,535

Publications

Refereed Journal Articles

- [1] J. Hwang, A. Hari, R. Cheng, J.G. Gardner, D. Lobo. 2020. *Kinetic modeling of microbial growth, enzyme activity, and gene deletions: an integrated model of β -glucosidase function in *Cellvibrio japonicus**. **Biotechnology and Bioengineering**, doi: 10.1002/bit.27544.
- [2] A. Hari, D. Lobo. 2020. *Fluxer: a web application to compute and visualize genome-scale metabolic flux networks*. **Nucleic Acids Research**, 48, pp. 427-435.
- [3] J. Roy, E. Cheung, J. Bhatti, A. Muneem, D. Lobo. 2020. *Curation and annotation of planarian gene expression patterns with segmented reference morphologies*. **Bioinformatics**, 36(9), pp. 2881-2887.
- [4] J.M. Ko, D. Lobo. 2019. *Continuous dynamic modeling of regulated cell adhesion: sorting, intercalation, and involution*. **Biophysical Journal**, 117(11), pp. 2166-2179.
- [5] S. Herath, D. Lobo. 2019. *Cross-inhibition of Turing patterns explains the self-organized regulatory mechanism of planarian fission*. **Journal of Theoretical Biology**, 485, 110042.
- [6] M. García-Quismondo, M. Levin, D. Lobo. 2017. *Modeling regenerative processes with Membrane Computing*. **Information Sciences** 381, pp. 229-249.
- [7] D. Lobo, M. Lobikin, M. Levin. 2017. *Discovering novel phenotypes with automatically inferred dynamic models: a partial melanocyte conversion in *Xenopus**. **Scientific Reports** 7, 41339.
- [8] D. Lobo, J. Morokuma, M. Levin. 2016. *Computational discovery and in vivo validation of *hnf4* as a regulatory gene in planarian regeneration*. **Bioinformatics** 32(17), pp. 2681-2685.
- [9] F. Durant, D. Lobo, J. Hammelman, M. Levin. 2016. *Physiological controls of large-scale patterning in planarian regeneration: A molecular and computational perspective on growth and form*. **Regeneration** 3(2), pp. 78-102. (Selected for the journal cover)
- [10] D. Lobo, J. Hammelman, M. Levin. 2016. *MoCha: molecular characterization of unknown pathways*. **Journal of Computational Biology** 23(4), pp. 291-297.
- [11] M. Emmons-Bell, F. Durant, J. Hammelman, N. Bessonov, V. Volpert, J. Morokuma, K. Pinet, D. Adams, A. Pietak, D. Lobo, M. Levin. 2015. *Gap junctional blockade stochastically induces different species-specific head anatomies in genetically wild-type *Girardia dorotocephala* flatworms*. **International Journal of Molecular Sciences** 16(11), pp. 27865-27896. (Selected for the journal cover)
- [12] B.P. Rubin, J. Brockes, B. Galliot, U. Grossniklaus, D. Lobo, M. Mainardi, M. Mirouze, A. Prochiantz, A. Steger. 2015. *A dynamic architecture of life*. **F1000Research** 4:1288.
- [13] M. Lobikin, D. Lobo, D.J. Blackiston, C.J. Martyniuk, E. Tkachenko, M. Levin. 2015. *Serotonergic regulation of melanocyte conversion: A bioelectrically regulated network for stochastic all-or-none hyperpigmentation*. **Science Signaling** 8(397), p. ra99. (Reviewed in a focus paper, **Science Signaling** 8(397), pp. fs17)
- [14] D. Lobo, M. Levin. 2015. *Inferring regulatory networks from experimental morphological phenotypes: a computational method reverse-engineers planarian regeneration*. **PLoS Computational Biology** 11(6): e1004295. (In the top-10 most-viewed research articles in the journal)

- [15] D. Lobo, E.B. Feldman, M. Shah, T.J. Malone, M. Levin. 2014. *Limbform: a functional ontology-based database of limb regeneration experiments*. **Bioinformatics** 30(24), pp. 3598-3600.
- [16] D. Lobo, E.B. Feldman, M. Shah, T.J. Malone, M. Levin. 2014. *A bioinformatics expert system linking functional data to anatomical outcomes in limb regeneration*. **Regeneration** 1(2), pp. 37-56.
- [17] M. Budnikova, J.W. Habig, D. Lobo, N. Cornia, M. Levin, T. Andersen. 2014. *Design of a flexible component gathering algorithm for converting cell-based models to graph representations for use in evolutionary search*. **BMC Bioinformatics** 15:178.
- [18] D. Lobo, M. Solano, G.A. Bubenik, M. Levin. 2014. *A linear-encoding model explains the variability of the target morphology in regeneration*. **Journal of the Royal Society Interface** 11(92):20130918. (Recommended by **F1000Prime**, Faculty of 1000, 718232471)
- [19] D. Lobo, T.J. Malone, M. Levin. 2013. *Planform: an application and database of graph-encoded planarian regenerative experiments*. **Bioinformatics** 29(8), pp. 1098-1100.
- [20] D. Lobo, T.J. Malone, M. Levin. 2013. *Towards a bioinformatics of patterning: a computational approach to understanding regulative morphogenesis*. **Biology Open** 2(2), pp. 156-169. (Selected for the journal cover)
- [21] M. Lobikin, B. Chernet, D. Lobo, M. Levin. 2012. *Resting potential, oncogene-induced tumorigenesis, and metastasis: the bioelectric basis of cancer in vivo*. **Physical Biology** 9(6): 065002. (Selected for the journal cover)
- [22] D. Lobo, W.S. Beane, M. Levin. 2012. *Modeling planarian regeneration: a primer for reverse-engineering the worm*. **PLoS Computational Biology** 8(4): e1002481. (Selected for the journal cover)
- [23] J.D. Fernández, D. Lobo, G.M. Martín, R. Doursat, F.J. Vico. 2012. *Emergent diversity in an open-ended evolving virtual community*. **Artificial Life** 18(2), pp. 199-222.
- [24] D. Lobo, F.J. Vico, J. Dassow. 2011. *Graph grammars with string-regulated rewriting*. **Theoretical Computer Science** 412(43), pp. 6101-6111. (Reviewed in **Mathematical Reviews**, American Mathematical Society, MR2883035)
- [25] D. Lobo, F.J. Vico. 2010. *Evolution of form and function in a model of differentiated multicellular organisms with gene regulatory networks*. **BioSystems** 102(2-3), pp. 112-123.
- [26] D. Lobo, F.J. Vico. 2010. *Evolutionary development of tensegrity structures*. **BioSystems** 101(3), pp. 167-176.
- [27] Y. Seamari, J.A. Narvaez, F.J. Vico, D. Lobo, M.V. Sanchez-Vives. 2007. *Robust off - and online separation of intracellularly recorded Up and Down cortical states*. **PLoS ONE** 2(9): e888.

Book Chapters

- [28] D. Lobo. 2021. *Computational systems biology of morphogenesis*. S. Cortassa, M.A. Aon (Eds.), Computational Systems Biology in Medicine and Biotechnology, Springer Nature, to appear.
- [29] D. Lobo. 2020. *Reverse engineering phenotypes of regeneration*. S. Blanchoud, B. Galliot (Eds.), Whole-body regeneration, Springer Nature, to appear.

- [30] D. Lobo, M. Levin. 2017. *Computing a worm: reverse-engineering planarian regeneration*. A. Adamatzky (Ed.), *Advances in Unconventional Computing: Emergence, Complexity and Computation*, Springer, pp. 637-654.
- [31] J. Hammelman, D. Lobo, M. Levin. 2016. *Artificial neural networks as models of robustness in development and regeneration: stability of memory during morphological remodeling*. S. Shanmuganathan, S. Samarasinghe (Eds.), *Artificial Neural Network Modelling*, Springer, pp. 45-65.
- [32] D. Lobo, J.D. Fernández, F.J. Vico. 2013. *Behavior finding: morphogenetic designs shaped by function*. R. Doursat, H. Sayama, O. Michel (Eds.), *Morphogenetic Engineering: Toward Programmable Complex Systems*, Springer-Verlag, pp. 441-472.

Refereed Conference Articles

- [33] D. Lobo, D.A. Hjelle, H. Lipson. 2009. *Reconfiguration algorithms for robotically manipulatable structures*. Proceedings of the ASME/IFTOMM International Conference on Reconfigurable Mechanisms and Robots, ReMAR2009, pp. 13-22, London, UK.
- [34] F.J. Vico, V. Canteli, D. Lobo, J.D. Fernández, C. Bandera, A. García-Linares, R. Rivas, M. Rosen, B. Schlegel. 2007. *Mobile Just-in-time training application for emergency healthcare services*. Proceedings of the IADIS International Conference on Mobile Learning, IADIS2007, pp. 209-213, Lisbon, Portugal.

Abstracts and Short Articles

- [35] A. Hari, D. Lobo. 2020. *A novel methodology and web application for computing, visualizing and analyzing genome-scale metabolic flux networks*. Annual Meeting of the Society for Mathematical Biology, virtual.
- [36] J. Ko, D. Lobo. 2020. *Regulated Cell Adhesion Dynamics in a Continuous Model: Sorting, Intercalation, and Involution*. Annual Meeting of the Society for Mathematical Biology, virtual.
- [37] D. Lobo. 2020. *A Turing system explains regeneration patterning and fission behavior in planaria*. Annual Meeting of the Society for Mathematical Biology, virtual.
- [38] A. Hari, D. Lobo. 2020. *Computing, analyzing and visualizing genome-scale metabolic flux networks with Fluxer*. 28th International Conference on Intelligent Systems for Molecular Biology, virtual
- [39] J. Ko, D. Lobo. 2020. *Modeling Sorting, Intercalation, and Involution Tissue Behaviors due to Regulated Cell Adhesion*. 28th International Conference on Intelligent Systems for Molecular Biology, virtual
- [40] D. Lobo. 2020. *Whole-body regeneration and size-dependent fission controlled by a self-regulated Turing system in planaria*. 28th International Conference on Intelligent Systems for Molecular Biology, virtual
- [41] K. Taguba, D. Lobo. 2020. *An Efficient Machine Learning Method For Building Atlases Of Gene Regulatory Networks*. 24th Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [42] H. Ramcharan, D. Lobo. 2020. *Identifying Spatial And Temporal Gene Expression Dynamics From Multiple Sequencing Data*. 24th Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.

- [43] O. Ogunsan, D. Lobo. 2020. *Automatically Generated Phase Portraits For Understanding Biological Systems*. 24th Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [44] S. Hu, D. Lobo. 2020. *Automated Registration Of Planarian Gene Expression Patterns*. 24th Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [45] A. Rizvi, N. Shaikh, T. deCarvalho, D. Lobo. 2019. *Planarian fission behavior is modulated by population density and body length*. 22nd Undergraduate Research Symposium in the Chemical and Biological Sciences, UMBC, Baltimore, MD.
- [46] A. Rizvi, N. Shaikh, T. deCarvalho, D. Lobo. 2019. *Planarian fission behavior is modulated by population density and body length*. Annual Summer Undergraduate Research Fest, UMBC, Baltimore, MD.
- [47] J. Ko, D. Lobo. 2019. *Dynamic regulation of cell adhesion molecules in a continuous mathematical model*. Proceedings of the 2019 Mid-Atlantic Regional Meeting of the Society for Developmental Biology, p. 32, University Park, PA.
- [48] E. Cheung, J. Roy, D. Lobo. 2019. *Semi-automatic Ontology Curation Methods for a Planarian Gene Expression Pattern Database*. 23rd Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [49] C. Larkin, K.T. Pickford, D. Lobo. 2019. *An Evolutionary Algorithm to Reverse-Engineer Tumor Sub-Clonal Dynamics and Predict Optimal Treatment Targets*. 23rd Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [50] J. Ko, D. Lobo. 2019. *Dynamic regulation of cell adhesion molecules for tissue patterning*. 35th Annual GABS Symposium, UMBC, Baltimore, MD.
- [51] P. H. Ng, J. Wolf, T. deCarvalho, D. Lobo. 2019. *Molecular validation of a model-driven hypothesis on planarian fission*. 35th Annual GABS Symposium, UMBC, Baltimore, MD.
- [52] A. Hari, J. Hwang, D. Lobo. 2019. *Kinetic and Stoichiometric Analyses to Reverse Engineer Metabolic and Genetic Networks in *Cellvibrio japonicus**. 35th Annual GABS Symposium, UMBC, Baltimore, MD.
- [53] S. Herath, D. Lobo. 2019. *Cross-inhibited Turing patterns explain the self-organized signaling of planarian fission*. 7th Annual Winter Q-Bio Conference, Oahu, HI.
- [54] J. Roy, J. Bhatti, D. Lobo. 2018. *A Software Tool for the Curation of Planarian Gene Expression Patterns*. Annual Summer Undergraduate Research Fest, UMBC, Baltimore, MD.
- [55] E. Cheung, A. Muneem, J. Bhatti, J. Roy, D. Lobo. 2018. *A Centralized Database and Website of Planarian Gene Expression Patterns*. Annual Summer Undergraduate Research Fest, UMBC, Baltimore, MD.
- [56] C. Larkin, K.T. Pickford, D. Lobo. 2018. *Inferring Dynamic Models of Tumor Sub-Clonal Interactions to Predict Optimal Treatment Targets*. 26th Conference on Intelligent Systems for Molecular Biology, Chicago, IL.
- [57] S. Hu, D. Lobo. 2018. *Correcting differences in experimental protocols with dynamic time warping*. 22nd Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [58] J. Bhatti, J. Roy, D. Lobo. 2018. *A Software Tool for the Curation of Planarian Gene Expression Patterns*. 22nd Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.

- [59] E. Cheung, A. Muneem, J. Bhatti, J. Roy, D. Lobo. 2018. *A Centralized Database and Website of Planarian Gene Expression Patterns*. 22nd Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [60] C. Larkin, K.T. Pickford, D. Lobo. 2018. *Inferring Mathematical Dynamic Models of Tumor Sub-Clonal Interactions to Predict Optimal Treatment Targets*. 22nd Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [61] J. Ko, S. Herath, D. Lobo. 2018. *Simulating Cell Sorting by Differential Adhesion Using Continuous Mathematical Models*. 34th Annual GABS Symposium, UMBC, Baltimore, MD.
- [62] C. Larkin, K.T. Pickford, D. Lobo. 2018. *An Evolutionary Algorithm to Reverse-Engineer Tumor Sub-Clonal Dynamics and Predict Optimal Treatment Targets*. 6th Annual Winter Q-Bio Meeting, p. 92, Maui, HI.
- [63] J. Bhatti, J. Roy, L. Roth, D. Lobo. 2017. *Centralizing planarian regenerative experiments and their gene expression patterns with mathematical databases*. 20th Annual Undergraduate Research Symposium in the Chemical and Biological Sciences, p. 153, UMBC, Baltimore, MD.
- [64] C. Larkin, K.T. Pickford, D. Lobo. 2017. *A systems biology approach for inferring tumor sub-clonal dynamics and predicting prime therapeutic targets*. 20th Annual Undergraduate Research Symposium in the Chemical and Biological Sciences, p. 71, UMBC, Baltimore, MD.
- [65] C. Larkin, K. Pickford, D. Lobo. 2017. *A Computational Framework to Reverse-Engineer Intratumor Sub-Clonal Dynamic Models and Predict Optimal Treatment Targets*. Annual Summer Undergraduate Research Fest, UMBC, Baltimore, MD.
- [66] J. Bhatti, D. Lobo. 2017. *Paving the way for regenerative medicine: curating planarian experiments in a centralized mathematical database*. Annual Summer Undergraduate Research Fest, UMBC, Baltimore, MD.
- [67] S. Herath, M. Ebeid, D. Lobo. 2017. *Automatic Inference of Dynamic Regulatory Networks Controlling Shape And Form*. 18th International Conference on Systems Biology, Blacksburg, VA.
- [68] S. Herath, D. Lobo. 2017. *A continuous mathematical framework for biological shapes formation*. Mid-Atlantic Meeting of the Society for Developmental Biology, Baltimore, MD.
- [69] J. Hwang, M. Plungis, M. Avadhani, D. Lobo. 2017. *Constraining Automated Metabolic and Regulatory Inference Algorithms with Predicted Enzymatic Reactions*. 21st Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [70] S. Herath, D. Lobo. 2017. *A continuous mathematical framework for biological shapes formation*. 21st Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [71] J. Bhatti, A. Muneem, D. Lobo. 2017. *Paving the way for regenerative medicine: curating planarian experiments in a centralized mathematical database*. 21st Annual Undergraduate Research and Creative Achievement Day, UMBC, Baltimore, MD.
- [72] J. Hwang, M. Plungis, M. Avadhani, D. Lobo. 2017. *Constraining Automated Metabolic and Regulatory Inference Algorithms with Predicted Enzymatic Reactions*. Annual Graduate Association of Biological Sciences Symposium, UMBC, Baltimore, MD.
- [73] C. Larkin, D. Lobo. 2016. *Understanding Tumor Sub-Clonal Dynamics Using a Computational Framework*. Annual Biomedical Research Conference for Minority Students, Tampa, FL.

- [74] J. Bhatti, A. Muneem, D. Lobo. 2016. *Paving the way for regenerative medicine: curating planarian experiments in a centralized mathematical database*. 19th Annual Undergraduate Research Symposium in the Chemical and Biological Sciences, p. 221, UMBC, Baltimore, MD.
- [75] C. Larkin, D. Lobo. 2016. *Understanding Tumor Sub-Clonal Dynamics Using a Computational Framework*. 19th Annual Undergraduate Research Symposium in the Chemical and Biological Sciences, p. 198, UMBC, Baltimore, MD.
- [76] C. Larkin, D. Lobo. 2016. *Understanding Tumor Sub-Clonal Dynamics Using a Computational Framework*. SACNAS National Diversity in STEM Conference, Long Beach, CA.
- [77] M. Avadhani, Y. Jampana, S. Amin, M. Ebeid, S. Herath, C. Larkin, J. Bhatti, A. Muneem, M. Plungis, D. Lobo. 2016. *Reverse-Engineering Dynamic and Stochastic Regulatory Networks from Morphological Experimental Data*. 17th International Conference on Systems Biology, Barcelona, Spain.
- [78] M. Plungis, M. Avadhani, D. Lobo. 2016. *A Machine Learning Method for Deriving Metabolic and Regulatory Models in Bacterial Systems*. Annual Summer Undergraduate Research Fest, UMBC, Baltimore, MD.
- [79] J. Bhatti, A. Muneem, D. Lobo. 2016. *Paving the way for regenerative medicine: curating planarian experiments in a centralized mathematical database*. Annual Summer Undergraduate Research Fest, UMBC, Baltimore, MD.
- [80] S. Herath, M. Ebeid, D. Lobo. 2016. *A Mathematical and Computational Framework for Discovering Models of Shape and Form Regeneration*. Annual Summer Undergraduate Research Fest, UMBC, Baltimore, MD.
- [81] C. Larkin, D. Lobo. 2016. *A Computational Method for Inferring Mathematical Models and Optimal Treatments of Tumor Sub-Clonal Dynamics*. Annual Summer Undergraduate Research Fest, UMBC, Baltimore, MD.
- [82] D. Lobo. 2015. *Reverse engineering dynamic regulatory networks of planarian regeneration from experimental resultant phenotypes*, Third North American Planarian Meeting, Chicago, IL.
- [83] D. Lobo, M. Levin. 2014. *Automatic discovery of regulatory networks from morphological experimental data*. Proceedings of the 12th ISCB Rocky Mountain Bioinformatics Conference, pp. 14, 64-65, Aspen, CO.
- [84] D. Lobo, M. Levin. 2012. *A new bioinformatics of shape for regenerative science*. Proceedings of the American Association for the Advancement of Science, Pacific Division, 31(1), pp. 63-64, Boise, ID.
- [85] F.J. Vico, D. Lobo, A. Gómez, S. Burrezo, J.D. Fernández, L. Duloquin, B. Maury, N. Peyrieras. 2009. *LTMaker: a tool for semiautomatic reconstruction of the embryonic lineage tree from 4D-microscopy*. Proceedings of the RNS/ISC PIF International Conference on Morphogenesis in Living Systems, MLS2009, pp. 59-60, Paris, France.
- [86] Y. Seamari, J.A. Narvaez, F.J. Vico, D. Lobo, M.V. Sanchez-Vives. 2007. *Separación automática off - y online de estados corticales de activación en registros intracelulares*, Proceedings of the Spanish Society of Neuroscience, XII, p. 101, Valencia, Spain.
- [87] F.J. Vico, V. Canteli, D. Lobo, J.D. Fernández, C. Bandera, A. García-Linares, R. Rivas, M. Rosen, B. Schlegel. 2007. *Just-in-time etraining applied to emergency medical services*. Proceedings of the International Conference on Computational Intelligence in Medicine and Healthcare, CIMED2007, p. 45, Plymouth, UK.

Seminars & Talks

- 2020 **Annual Meeting of the Society for Mathematical Biology**, virtual. *A Turing system explains regeneration patterning and fission behavior in planaria*
- 2020 **28th International Conference on Intelligent Systems for Molecular Biology**, virtual. *Whole-body regeneration and size-dependent fission controlled by a self-regulated Turing system in planaria*
- 2019 **Hematology/Oncology Grand Rounds**, University of Maryland Medical Center, Baltimore, MD. *Computational Systems Biology of Cancer Dynamics.*
- 2019 **119th International Titisee Conference**, Titisee, Germany. *Dynamic modeling and reverse engineering of pattern and shape regulation. (Funded by the Boehringer Ingelheim Fonds research foundation)*
- 2019 **7th Annual Winter Q-Bio Conference**, Oahu, HI. *Cross-inhibited Turing patterns explain the self-organized signaling of planarian fission.*
- 2018 **Meyerhoff Summer Bridge Program**, UMBC, Baltimore, MD. *Computational Systems Biology.*
- 2018 **University of Maryland, Baltimore**, Baltimore, MD. *Computational discovery of cancer signaling, sub-clonal interactions, and optimal treatments.*
- 2018 **Institute of Marine and Environmental Technology**, Baltimore, MD. *Reverse engineering the dynamic regulation of development, cancer, and metabolism.*
- 2017 **Computational Medicine and Bioinformatics Seminar Series**, University of Michigan, Ann Arbor, MI. *Reverse engineering the molecular mechanisms of developmental, cancer, and synthetic biology for predicting novel genes, phenotypes and optimal treatments.*
- 2017 **18th International Conference on Systems Biology**, Virginia Tech, Blacksburg, VA. *Automatic Inference of Dynamic Regulatory Networks Controlling Shape and Form.*
- 2017 **Precision Biosciences**, Durham, NC. *Automated discovery of biological dynamic mechanisms from phenotypic data.*
- 2017 **Collegiate Success Institute**, UMBC, Baltimore, MD. *Computational & Systems Biology: discovering biological mechanisms with AI.*
- 2017 **KeyGene at Institute for Bioscience and Biotechnology Research**, Rockville, MD. *Reverse engineering the dynamic mechanisms of biological regulation, signaling, and metabolism.*
- 2016 **Mid-Atlantic meeting of the Society for Developmental Biology**, Howard University, Washington, DC. *Inferring developmental and regenerative dynamic regulatory networks from morphological phenotypes.*
- 2016 **Dept. of Computer Science and Electrical Engineering**, UMBC, Baltimore, MD. *Reverse Engineering of Dynamic Regulatory Networks from Morphological Experimental Data*
- 2016 **Simons Center for Quantitative Biology**, Cold Spring Harbor Laboratory, NY. *Computational discovery of dynamic regulatory networks from experimental phenotypes.*
- 2015 **Third North American Planarian Meeting**, Chicago, IL. *Reverse engineering dynamic regulatory networks of planarian regeneration from experimental resultant phenotypes*
- 2015 **Novartis Institutes for Biomedical Research**, Cambridge, MA. *Inferring regulatory networks from experimental morphological phenotypes*

- 2014 **12th Annual Rocky Mountain Bioinformatics Conference**, Aspen, CO. *Automatic discovery of regulatory networks from morphological experimental data.*
- 2014 **Second Annual Boston Data Festival**, Boston, MA. *Mining living organisms: inferring biological models from wet-lab experiments.*
- 2014 **Molecular Joint Meeting Seminar Series**, Tufts University, Medford, MA. *Artificial intelligence for understanding the algorithms of planarian regeneration.*
- 2014 **‘A Dynamic Architecture of Life?’ Workshop**, Academia Nazionale dei Lincei, Rome, Italy. *The encoding and processing of shape information during embryogenesis and regeneration*
- 2014 **Second Biologically Inspired Information Processing Conference**, Medford, MA. *Automated discovery of models of pattern regeneration.*
- 2014 **Boston Data Mining Group**, Cambridge, MA. *Mining the wet lab: automated discovery of models of biological pattern formation.*
- 2013 **Molecular Joint Meeting Seminar Series**, Tufts University, Medford, MA. *Automated discovery of models of pattern formation.*
- 2013 **Second North American Planarian Meeting**, Stowers Institute for Medical Research, Kansas City, MO. *A new bioinformatics of shape: facilitating constructive models of planarian regeneration.*
- 2012 **93rd Annual Meeting of the American Association for the Advancement of Science**, Pacific Division, Boise, ID. *A new bioinformatics of shape for regenerative science.*
- 2011 **Center for Regenerative and Developmental Biology**, Tufts University, Medford, MA. *Evolutionary development based on genetic regulatory models.*
- 2010 **Computer Science Department**, University of Malaga, Spain. *Evolutionary development based on genetic regulatory models for behavior-finding.*
- 2009 **Theoretical Computer Science Seminar Series**, Otto-Von-Guericke University, Magdeburg, Germany. *Formal and evolutionary properties in models of multicellular organisms.*
- 2008 **Cornell Computational Synthesis Laboratory**, Cornell University, Ithaca, NY. *Machine metabolism for structure reconfiguration.*
- 2008 **Distributed Robotics Laboratory**, Massachusetts Institute of Technology, Cambridge, MA. *Machine metabolism.*

Mentoring

Graduate student researchers

- 2020-Present **Reza Mousavi**, Ph.D. student in Biological Sciences - Computational Biology, Bioinformatics, and Systems Biology, UMBC.
- 2018-Present **Archana Hari**, Ph.D. student in Biological Sciences - Computational Biology, Bioinformatics, and Systems Biology, UMBC.
- 2017-Present **Jason Ko**, Ph.D. student in Biological Sciences - Computational Biology, Bioinformatics, and Systems Biology, UMBC.
- 2016-2019 **Jeanice Hwang**, M.S. student in Applied Molecular Biology, UMBC. Moved to West Virginia School of Osteopathic Medicine as a D.O. student.

- 2018-2019 **Paak Ng**, M.S. student in Applied Molecular Biology, UMBC.
- 2017 **Vikramaditya Battina**, M.S. student in Computer Science, UMBC.
- 2016 **Yogendra Jampana**, M.S. student in Information Systems, UMBC. Moved to IQLogg as a Technical Recruiter.
- 2016 **Terri Hobbs**, lab rotation, Ph.D. student in Biological Sciences - Computational Biology, Bioinformatics, and Systems Biology, UMBC.
- 2015-2016 **Arjun Kumar**, M.S. student in Computer Science, UMBC. Moved to the Institute for Genome Sciences at University of Maryland, School of Medicine as a Software Engineer.

Research associates and assistants

- 2017-2018 **Sri Harsha Konuru**, research associate, UMBC. Moved to AgricxLab as a Software Developer.
- 2017-2018 **Kyle Pickford**, research assistant, UMBC. Moved to Concepts NREC as a Software Engineer.
- 2016 **Neil Agarwal**, research associate, UMBC. Moved to the Department of Energy as an Operations Research Analyst.

Undergraduate student researchers

- 2020-Present **Biniam Teferedegn**, U-RISE Scholar, B.S. student in Bioinformatics and Computational Biology, UMBC.
- 2020-Present **Waverly Reginato**, FWS student, B.S. student in Biological Sciences, UMBC.
- 2019-Present **Hannah Ramcharan**, MARC U*STAR Scholar, B.S. student in Bioinformatics and Computational Biology, UMBC.
- 2019-Present **Alizay Rizvi**, URA Scholar, B.S. student in Biological Sciences, UMBC.
- 2019-Present **Noor Shaikh**, URA Scholar, B.S. student in Biological Sciences, UMBC.
- 2018-Present **Teni Ogunsan**, MARC U*STAR Scholar, Meyerhoff Scholar, B.S. student in Bioinformatics and Computational Biology, UMBC.
- 2017-Present **Eric Cheung**, URA Scholar, B.S. student in Biochemistry and Molecular Biology, UMBC.
- 2017-Present **Joy Roy**, URA Scholar, Maryland Delegate Scholar, B.S. student in Bioinformatics and Computational Biology, UMBC.
- 2017-Present **Sophia Hu**, URA Scholar, B.S. student in Bioinformatics and Computational Biology, UMBC.
- 2018-2020 **Kent Taguba**, URA Scholar, B.S. student in Biological Sciences and Computer Science, UMBC. Moved to Raytheon Technologies as a software engineer.
- 2016-2019 **Caroline Larkin**, URA Scholar, MARC U*STAR Scholar, Meyerhoff Scholar, B.S. student in Bioinformatics and Computational Biology, UMBC. Moved to Carnegie Mellon University as a Ph.D. student.
- 2016-2019 **Samantha Herath**, UBM Scholar, Sherman Scholar, B.S. student in Mathematics, UMBC. Moved as a member of the corps of Teach for America and then NASA.

- 2016-2019 **Abraar Muneem**, B.A. student in Biology, UMBC. Moved to the Penn State College of Medicine as an M.D. student.
- 2016-2019 **Junaid Bhatti**, B.A. student in Biology, UMBC. Moved to the University of Maryland, School of Medicine as an M.D. student.
- 2018 **David Williams**, Meyerhoff Scholar, B.S. student in Computer Science, UMBC.
- 2017 **Laura Roth**, B.S. student in Bioinformatics and Computational Biology, UMBC. Moved to Personal Genome Diagnostics as a bioinformatician.
- 2016-2017 **Mark Ebeid**, UBM Scholar, B.S. student in Bioinformatics and Computational Biology, UMBC. Moved to Northrop Grumman as a Systems Analyst, then to Carnegie Mellon University as a Ph.D. student.
- 2016-2017 **Mikhail Plungis**, B.S. student in Bioinformatics and Computational Biology, UMBC.
- 2016 **Saqlain Amin**, B.S. student in Bioinformatics and Computational Biology, UMBC.
- 2015 **Elizabeth Cardosa**, B.S. student in Biological Sciences, UMBC.
- 2014-2015 **Jennifer Hammelman**, B.S. student in Biology and Computer Science, Tufts University. Moved to MIT as a Ph.D. student.
- 2014 **Erica B. Feldman**, B.S. student in Biology, Tufts University. Moved to the University of Miami, Miller School of Medicine as a MD/MPH student.
- 2013 **Michelle Shah**, B.S. student in Biology, Tufts University.
- 2012-2013 **Taylor J. Malone**, B.S. student in Biology, Tufts University. Moved to Yale University as a Ph.D. student.
- 2012 **Hayley A. Weiss**, B.S. student in Computer Science and Biology, Tufts University. Moved to Vecna as a Software Engineer.
- 2012 **Emma M. Marshall**, B.S. student in Biology, Tufts University.
- 2008 **Richard X. Yu**, B.S. student in Computer Science, Cornell University. Moved to Columbia University as a graduate student.
- 2007 **Antonio Gómez**, B.S. student in Computer Science, University of Malaga. Moved to Indra as a Software Engineer.

Graduate students as committee member

- 2019-Present **Christopher Mayer-Bacon**, Ph.D. student in Molecular & Cell Biology, UMBC.
- 2019-Present **Alin Voskanian-Kordi**, Ph.D. student in Biological Sciences - Computational Biology, Bioinformatics, and Systems Biology, UMBC.
- 2017-Present **Shuaishuai Liu**, Ph.D. student in Biological Sciences - Cell Biology, Developmental Biology, and Neurobiology, UMBC.
- 2017-Present **Terri Hobbs**, Ph.D. student in Biological Sciences - Computational Biology, Bioinformatics, and Systems Biology, UMBC.
- 2016-Present **Samuel Hulse**, Ph.D. student in Biological Sciences - Evolution, Ecology, and Behavior, UMBC.

- 2015-2016 **Patrick O'Neill**, Ph.D. student in Biological Sciences - Computational Biology, Bioinformatics, and Systems Biology, UMBC. Moved to Tyche Analytics Company as director of science.
- 2015-2016 **Sefa Kilic**, Ph.D. student in Biological Sciences - Computational Biology, Bioinformatics, and Systems Biology, UMBC. Moved to Google as a research software engineer.
- 2015-2016 **Thomas Peterson**, Ph.D. student in Biological Sciences - Computational Biology, Bioinformatics, and Systems Biology, UMBC. Moved to the University of California, San Francisco as a postdoc.

Other mentoring

- 2018-2020 **Alida Hartwell**, Hill-Lopes/CNMS Scholar mentee, B.S. student in Bioinformatics and Computational Biology, UMBC. Moved to Latvia with a Fulbright Award.

Teaching

University of Maryland, Baltimore County, Dept. of Biological Sciences

- 2020 Fall **Biol 426/626 - Approaches to Molecular Biology**, Guest lecturer
- 2020 Fall **Biol 737 - Research Seminar in Bioinformatics and Computational Biology**, Instructor
- 2020 Spring **Biol 316L - Phage Genome Analysis**, Guest lecturer
- 2020 Spring **Biol 495/695 - Seminar in Bioinformatics**, Guest lecturer
- 2020 Spring **Biol 303L - Cell Biology Laboratory**, Guest lecturer
- 2020 Spring **Biol 737 - Research Seminar in Bioinformatics and Computational Biology**, Instructor
- 2020 Spring **Biol 313 - Introduction to Bioinformatics and Computational Biology**, Instructor
- 2020 Spring **Biol 615 - Systems Biology**, Instructor
- 2020 Spring **Biol 415 - Systems Biology**, Instructor
- 2019 Fall **Biol 737 - Research Seminar in Bioinformatics and Computational Biology**, Instructor
- 2019 Spring **Biol 316L - Phage Genome Analysis**, Guest lecturer
- 2019 Spring **Biol 737 - Research Seminar in Bioinformatics and Computational Biology**, Instructor
- 2019 Spring **Biol 313 - Introduction to Bioinformatics and Computational Biology**, Instructor
- 2019 Spring **Biol 615 - Systems Biology**, Instructor
- 2019 Spring **Biol 415 - Systems Biology**, Instructor
- 2018 Spring **Biol 495/695 - Seminar in Bioinformatics**, Guest lecturer
- 2018 Spring **Biol 313 - Introduction to Bioinformatics and Computational Biology**, Guest lecturer
- 2018 Spring **Biol 316L - Phage Genome Analysis**, Guest lecturer

- 2018 Spring **Biol 615 - Systems Biology**, Instructor
- 2018 Spring **Biol 415 - Systems Biology**, Instructor
- 2017 Fall **Biol 700 - Introduction to the graduate experience**, Guest lecturer
- 2017 Spring **Biol 313 - Introduction to Bioinformatics and Computational Biology**, Guest lecturer
- 2017 Spring **Biol 316L - Phage Genome Analysis**, Guest lecturer
- 2017 Spring **Biol 615 - Systems Biology**, New course design and instructor
- 2017 Spring **Biol 415 - Systems Biology**, New course design and instructor
- 2016 Fall **Biol 700 - Introduction to the graduate experience**, Guest lecturer
- 2016 Spring **Biol 313 - Introduction to Bioinformatics and Computational Biology**, Guest lecturer (two lectures)
- 2016 Spring **Biol 316L - Phage Genome Analysis**, Guest lecturer
- 2015 Fall **Biol 410 - Modeling in the Life Sciences**, Guest lecturer

Tufts University, Dept. of Computer Science

- 2015 Spring **Comp 167 - Introduction to Computational Biology**, Guest lecturer (two lectures)
- 2014 Spring **Comp 167 - Introduction to Computational Biology**, Guest lecturer (two lectures)
- 2013 Spring **Comp 167 - Introduction to Computational Biology**, Guest lecturer (five lectures)

Service

Department Service

- 2015-Present Member, **Graduate Committee**, Dept. Biological Sciences, UMBC
- 2015-Present Member, **Webpage & Marketing Committee**, Dept. Biological Sciences, UMBC
- 2019-2020 Member, **Pre-Faculty Search Committee**, Dept. Biological Sciences, UMBC
- 2017-2019 Member, **Executive Committee**, Dept. Biological Sciences, UMBC

University Service

- 2019-Present Member, **Governance Committee**, High Performance Computing Facility, UMBC
- 2018-Present Member, **Executive Committee**, Latino and Hispanic Faculty Association, UMBC
- 2015-Present Member, **Latino and Hispanic Faculty Association**, UMBC
- 2015-2016 CNMS representative, **Race, Equity, and Justice Working Group**, UMBC

Conference Committees

- 2020 Program Committee Member, **6th International Conference on Machine Learning, Optimization, and Data Science (LOD)**, Certosa di Pontignano, Italy
- 2020 Program Committee Member, **29th Genetic and Evolutionary Computation Conference (GECCO)**, Cancun, Mexico

- 2019 Program Committee Member, **5th International Conference on Machine Learning, Optimization, and Data Science (LOD)**, Certosa di Pontignano, Italy
- 2019 Program Committee Member, **2019 Conference on Artificial Life (ALIFE)**, Newcastle upon Tyne, United Kingdom
- 2019 Program Committee Member, **28th Genetic and Evolutionary Computation Conference (GECCO)**, Prague, Czech Republic
- 2018 Program Committee Member, **4th International Conference on Machine Learning, Optimization, and Data Science (LOD)**, Volterra, Italy
- 2018 Program Committee Member, **2018 Conference on Artificial Life (ALIFE)**, Tokyo, Japan
- 2018 Program Committee Member, **27th Genetic and Evolutionary Computation Conference (GECCO)**, Kyoto, Japan
- 2017 Program Committee Member, **3rd International Conference on Machine Learning, Optimization, and Big Data (MOD)**, Volterra, Italy
- 2017 Program Committee Member, **14th European Conference on Artificial Life (ECAL)**, Lyon, France
- 2017 Co-Organizer, **2017 Mid-Atlantic Regional Meeting of the Society for Developmental Biology**, Baltimore, MD
- 2017 Program Committee Member, **26th Genetic and Evolutionary Computation Conference (GECCO)**, Berlin, Germany
- 2016 Program Committee Member, **25th Genetic and Evolutionary Computation Conference (GECCO)**, Denver, CO
- 2016 Program Committee Member, **15th International Conference on the Simulation & Synthesis of Living Systems (ALIFE)**, Cancun, Mexico
- 2015 Program Committee Member, **24th Genetic and Evolutionary Computation Conference (GECCO)**, Madrid, Spain
- 2015 Program Committee Member, **13th European Conference on Artificial Life (ECAL)**, York, United Kingdom
- 2014 Program Committee Member, **23rd Genetic and Evolutionary Computation Conference (GECCO)**, Vancouver, Canada
- 2014 Program Committee Member, **14th International Conference on the Simulation & Synthesis of Living Systems (ALIFE)**, New York, NY
- 2013 Program Committee Member, **22nd Genetic and Evolutionary Computation Conference (GECCO)**, Amsterdam, The Netherlands
- 2013 Program Committee Member, **12th European Conference on Artificial Life (ECAL)**, Taormina, Italy
- 2012 Awards Committee Member, **93rd Meeting of the American Association for the Advancement of Science**, Pacific Division (AAASPC), Boise, ID
- 2012 Program Committee Member, **21st Genetic and Evolutionary Computation Conference (GECCO)**, Philadelphia, PA
- 2011 Program Committee Member, **11th European Conference on Artificial Life (ECAL)**, Paris, France

Grant Proposal Reviewer

- 2018 Panelist, **National Science Foundation**, Computer & Information Science & Engineering
2018 Ad hoc reviewer, **National Science Foundation**, Biological Sciences
2017 Panelist, **National Science Foundation**, Computer & Information Science & Engineering

Journal Article Reviewer

- Since 2020 Computer Methods and Programs in Biomedicine
Since 2020 Biotechnology & Bioengineering
Since 2019 Complexity
Since 2019 Seminars in Cell & Developmental Biology
Since 2017 ACM Computing Surveys
Since 2017 Science
Since 2017 Physical Review E
Since 2017 Bioinformatics
Since 2016 Journal of the Royal Society Interface
Since 2015 PLoS Computational Biology
Since 2015 Scientific Reports
Since 2014 Communicative & Integrative Biology
Since 2014 Nature Communications
Since 2012 Artificial Life
Since 2011 BioSystems
Since 2010 Applied Mathematical Modelling
Since 2010 PLoS ONE