

CURRICULUM VITAE

RYAN J. URBANOWICZ, Ph.D.

PERSONAL

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Twitter: www.twitter.com/DocUrbs

YouTube: www.youtube.com/c/ryanurbanowicz

Date and place of birth: January 28, 1982
New Milford, Connecticut, USA

EDUCATION

2005-2012 Dartmouth College Ph.D. in Genetics/Computational Biology
Hanover, New Hampshire
Mentor: Dr. Jason Moore, Department of Genetics

2004-2005 Cornell University M.Eng. in Biological and Environmental Eng.
Ithaca, New York
Mentor: Dr. Richard Durst, Department of Biological and Environmental Eng.

2000-2004 Cornell University B.S. in Biological and Environmental Engineering
Ithaca, New York
Mentor: Dr. Ruth Collins, Department of Molecular Medicine

POSTDOCTORAL TRAINING

2012-2015 Dartmouth College Postdoctoral Research Associate
Hanover, New Hampshire

Mentors: Dr. Jason H. Moore, Department of Genetics & Dr. Eugene Demidenko, Department of Biostatistics and Epidemiology

LICENSURE AND CERTIFICATION

none

ACADEMIC APPOINTMENTS

- 2015-present Research Associate with Dr. Jason Moore, Division of Informatics of the Department of Biostatistics, Epidemiology, and Informatics. University of Pennsylvania, Philadelphia, Pennsylvania
- 2012-2015 Postdoctoral Research Associate with Dr. Jason Moore, Department of Genetics and Dr. Eugene Demidenko, Department of Biostatistics and Epidemiology, Dartmouth College, Hanover, New Hampshire
- 2013 Faculty of the Citizen Science Program at Bard College, Annandale-on-Hudson, New York
- 2006-2012 Graduate Research Assistant with Dr. Jason Moore, Department of Genetics, Computational Biology Laboratory, Geisel School of Medicine, Hanover, New Hampshire
- 2004-2005 Graduate Research Assistant with Dr. Richard A. Durst and Dr. Antje J. Baeumner, Department of Biological and Environmental Engineering, Cornell University, Ithaca, New York
- 2004 Undergraduate Research Assistant with Dr. Ruth N. Collins, Department of Molecular Biology, Cornell University, College of Veterinary Medicine, Ithaca, New York
- 2003 Undergraduate Environmental Engineering Intern with Larry Marsicano and Joe Polulech (Engineer), Candlewood Lake Authority, Sherman, Connecticut
- 2000 High School Research Intern at Boehringer Ingleheim Pharmaceuticals, Ridgefield, Connecticut
- 1997-1999 High School Research Intern with Dr. Jacqueline Burns, Cytogenetics Laboratory, Danbury Hospital, Danbury, Connecticut

OTHER PROFESSIONAL POSITIONS

none

MAJOR COMMITTEE ASSIGNMENTS AND CONSULTATIONS

International, National and Regional

- 2015-present Cornell Alumni Admissions Ambassadors Network (CAAAN), Alumni Ambassador of the greater Philadelphia, Pennsylvania region.

- 2016 Lead-Organizer, International Workshop on Evolutionary Rule-Based Machine Learning at the Genetic and Evolutionary Computing Conference (GECCO'17), Berlin, Germany
- 2016 Co-Organizer, International Workshop on Evolutionary Rule-Based Machine Learning at the Genetic and Evolutionary Computing Conference (GECCO'16), Denver, Colorado
- 2015 Chair, Hot off the Press Session at the Genetic and Evolutionary Computing Conference (GECCO'15), Madrid, Spain
- 2014-2015 Co-Chair, Biological and Biomedical Applications Track at the Genetic and Evolutionary Computing Conference (GECCO'15), Madrid, Spain
- 2014-2015 Algorithm/Prediction Consultant, MedicFP, LLC
- 2010-2014 Co-Organizer, International Workshop on Learning Classifier Systems (IWLCS)
- 2013 Chair, Session on Genetics Based Machine Learning at the Genetic and Evolutionary Computing Conference (GECCO'12), Amsterdam, The Netherlands
- 2013 Co-Chair, International Workshop on Learning Classifier Systems (IWLCS) at the Genetic and Evolutionary Computing Conference (GECCO'13), Amsterdam, The Netherlands
- 2012 Chair, Session on Genetics Based Machine Learning at the Genetic and Evolutionary Computing Conference (GECCO'12), Philadelphia, Pennsylvania
- 2012 Co-Chair, International Workshop on Learning Classifier Systems (IWLCS) at the Genetic and Evolutionary Computing Conference (GECCO'12), Philadelphia, Pennsylvania
- 2011 Co-Chair, International Workshop on Learning Classifier Systems (IWLCS) at the Genetic and Evolutionary Computing Conference (GECCO'11), Dublin, Ireland
- 2009 Chair, Session on Session on Bioinformatics and Computational Biology at the Genetic and Evolutionary Computing Conference (GECCO'09), Montreal, Canada

Institutional

- 2007-2008 Graduate Student Representative for the Molecular and Cellular Biology (MCB) Graduate Committee, Dartmouth College, Hanover, New Hampshire

MEMBERSHIPS IN PROFESSIONAL SOCIETIES

- 2012-present International Genetic Epidemiology Society (IGES)
- 2007-present Association for Computing Machinery (ACM)
- 2007-present American Society of Human Genetics (ASHG)
- 2006-present International Society of Computational Biology (ISCB)

EDITORIAL BOARDS

- 2012-2015 Guest Associate Editor for Evolutionary Intelligence, Special Issue on Advancements in Learning Classifier Systems

AWARDS AND HONORS

- 2016 Best Paper Award, (Co-Author) Genetic and Evolutionary Computation Conference (GECCO'16), Denver, Colorado
- 2016 Best Paper Award, (Co-Author) EvoBIO, Porto, Portugal
- 2012-2015 NIH R25 Post-Doctoral Training Grant CA134286
- 2012 Best Paper Award, (First Author) 2012 Translational Bioinformatics Conference, Jeju, South Korea
- 2010 Best Paper Award, (First Author) Genetic and Evolutionary Computation Conference (GECCO'10), Portland, Oregon
- 2009-2010 Graduate Research Fellowship from the William H. Neukom 1964 Institute for Computational Sciences at Dartmouth College
- 2008 Best Paper Nomination, (First Author) Genetic and Evolutionary Computation Conference (GECCO'18), Atlanta, Georgia
- 2007 PSB Department of Energy Travel Award, Pacific Symposium on Biocomputing, Maui, Hawaii
- 2004 New Horizons Summer Research Grant, Cornell University, Ithaca, New York
- 2004 Teaching Research Specialist Grant, Cornell University, Ithaca, New York
- 2000 Eagle Scout, Boy Scouts of America, Sherman, Connecticut

REFEREE ACTIVITIES

- 2011-present referee for Genetic and Evolutionary Computation Conference (GECCO), International Workshop on Learning Classifier Systems (IWLCS), and Pacific Symposium on Biocomputing (PSB), Evolutionary Intelligence (EI), Evolutionary Computation Journal (ECJ), International Journal of Molecular Sciences, American Journal of Human Genetics (AJHG), PeerJ Computer Science, Artificial Intelligence in Medicine (AIME), Translational Bioinformatics Conference (TBC), Evostar

MAJOR RESEARCH INTERESTS

Common human disease research has evolved into a largely complex and interdisciplinary pursuit. Modern epidemiological challenges such as the characterization of complex systems, the management of 'big data', or the integration of data for systems biology epitomize this trend. The early stages of biomedical research typically focus on connecting predictive factors, whether they be genetic, epigenetic or environmental, to increased or decreased common disease susceptibility. This attempt to detect patterns of association is likely complicated by non-linear phenomena such as complex gene-gene interactions, gene-environment interactions, genetic heterogeneity, and phenocopy. My primary research interests focus on the development, evaluation, and application of novel computational, statistical, and visualization methods to facilitate classification and data mining in the complex, noisy domain of biomedical research.

My thesis research focused on the adaptation of a learning classifier system (LCS) algorithm to the task of detecting, modeling, and characterizing epistatic and heterogeneous associations within single nucleotide polymorphism (SNP) association studies. The development and application of LCS algorithms has since become a particular area of specialization. My post-doctoral work expanded upon this successful LCS groundwork leading to the development of ExSTraCS, an Extended Supervised Tracking and Classifying System. This work epitomizes my interest in (1) developing strategies which limit the number of assumptions made about the data, and instead allows the data to speak for itself for detecting complex or heterogeneous patterns, (2) allowing for the integration of data types by offering an algorithmic framework which functions for all combinations of discrete/continuous, attributes/endpoints, and (3) promoting a user friendly, interpretable environment for knowledge discovery. My work with LCS algorithms has also led me to pursue visual and statistical strategies with which to guide and facilitate knowledge discovery. My interests have also branched off into the theory and practice of complex disease model and data simulation, which led to the development of the open source GAMETES software package. Also, my interest in tackling issues related to 'big data' have motivated me to explore, expand and develop new feature selection approaches (e.g. ReliefF, SURF, SURF*, MultiSURF*, and MultiSURF), for computational and algorithmic flexibility and efficiency. These algorithms offer critical preprocessing steps for feature selection and the generation and application of statistical, objective, and unbiased expert knowledge to more efficiently guide stochastic algorithm learning.

In summary, my research interests lie at the intersection of genetics, genomics, biostatistics, epidemiology, machine learning, and computer science. I have adopted a quantitative biomedical research strategy that embraces, rather than ignores, the complexity of the relationship between predictive factors and disease endpoints.

RESEARCH FUNDING

(dollar amounts are annual direct costs)

2016-2020	NIH R01 HL134015 (P.I. – Pack and Robishaw)
	\$460,940 1.2 cal
	Approaches to Genetic Heterogeneity of Obstructive Sleep Apnea
	Role: Co-I to develop multi-phenotype methodology and assist with
	bioinformatics analysis.

TEACHING EXPERIENCE/CURRENT TEACHING RESPONSIBILITIES

The Perelman School of Medicine at the University of Pennsylvania (UPenn)

Courses and Lectures

2018	Module Director for Nature-Inspired Computing in Special Topics in Biomedical and Health Informatics (BMIN 504), UPenn (Scheduled for spring semester)
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- 2015-2017 Teaching Assistant and Lecturer for Blanca Himes, PhD, Graduate Data Science Course (EPID600), UPenn
2017 Recorded Online Lecture modules on topic of 'Data Science' for Nursing 165: Nursing Informatics, UPenn

Undergraduate Students Mentored

- 2017-present James Xue, UPenn (Wharton) – Economics/Statistics, Philadelphia, PA
2017-present Riley Wong, UPenn – Computer Science, Philadelphia, PA
2017-present Siddharth Verma, University of Delhi - Computer Engineering, Delhi
2016 Tuan A. Nguyen, Swarthmore College – Mathematics, Swarthmore, PA
2016-2017 Ben Yang, UPenn – Computational Biology, Philadelphia, PA
2016-present Christopher Lo, UPenn – Bioengineering, Philadelphia, PA
2017 Melissa Meeker, Ursinus College - Mathematics, Collegeville, PA

Masters Students Mentored

- 2016 Ted Fujimoto, UPenn – Computer Science, Philadelphia, PA
2016 Vishal Murali, UPenn - Mechanical Engineering, Philadelphia, PA

The Geisel School of Medicine at Dartmouth

Courses and Lectures

- 2013 Bioinformatics E-Learning Module Development: Hypothesis Testing
2008 Teaching Assistant, Undergraduate Biology (BIOL 11), Dartmouth College
2007 Center for the Advancement of Learning – Teaching Series, Dartmouth College

High School Students Mentored

- 2010-2015 Ambrose Granizo-MacKenzie, Hanover High School, Hanover, NH
2008-2009 Delaney Granizo-MacKenzie, Hanover High School, Hanover, NH (highlight: attended Princeton University).

Undergraduate Students Mentored

- 2014-2015 Niranjan Ramanand, class of 2017, Dartmouth College (highlight: student awarded Dartmouth Sophomore Science Scholarship)
2013 Dzung Pham, class of 2014 Saint Anselm College, NH, and class of 2015 University of Notre Dame, IN
2013 Ryan Amos, class of 2016, Dartmouth College
2013-2014 Gediminas Bertasius, class of 2014, Dartmouth College
2009-2013 Delaney Granizo-MacKenzie, Princeton University, NJ
2009-2012 Nicholas Sinnott-Armstrong, Brown University, RI
2012 Christine Cuddemi, SURF student, Emmanuelle College, MA

2010 Tyler Perry, class of 2012, Dartmouth College

Graduate Rotation Students Mentored

2014 Elizabeth Piette, Quantitative Biomedical Sciences (QBS), Dartmouth College

2013 Jie Tan, Molecular and Cellular Biology (MCB), Dartmouth College

2012-2013 James Rudd, Quantitative Biomedical Sciences (QBS), Dartmouth College

Masters Students Mentored

2009 Tamra Heberling, Mathematics, Montana State University

Bard College

Courses and Lectures

2013 Course Developer and Lecturer for “Citizen Science” (Required Freshman Course Teaching a Universal Scientific Skill Set - 4.5 Lecture Hours/Day for Three Weeks), Bard College, Annandale-on-Hudson, New York

Cornell University

Courses and Lectures

2005 Teaching Assistant, Personal Finance (HADM 3200), Cornell University

2004 Teaching Assistant, Physiological Engineering (BEE 4540), Cornell University

Other Teaching Experience

2000-2016 Adult Leader and Merit Badge Counselor for Troop 48 of the Boy Scouts of America (Engineering, Fire Safety, Emergency Preparedness, Reading, Scholarship, and Astronomy), Sherman, Connecticut

2016 Created Educational YouTube Video: ‘Learning Classifier Systems in a Nutshell’
https://www.youtube.com/watch?v=CRge_cZ2cJc

2008-2015 Science Educator for the “Camp-in at the Museum” Program, Astronomy/Star-Lab and Chemistry Stations, Montshire Children’s Museum of Science, Norwich, Vermont

2008-2009 Science Mentor for the Montshire-Rivendell-Dartmouth Howard Hughes Medical Institute Science Camp, Norwich, Vermont

2002-2005 Substitute Teacher and Teaching Assistant for the Sherman Elementary School (K-8), Sherman, Connecticut

INVITED PRESENTATIONS

International, National and Regional

- 2017 “Avoiding Common Machine Learning Mistakes”, DataPhilly Meetup, Philadelphia, PA, November 7. (<https://www.meetup.com/DataPhilly/events/244140696/>)
- 2017 Tutorial: “Introducing Rule-Based Machine Learning: Capturing Complexity”, Genetic and Evolutionary Computing Conference (GECCO’17). Berlin, Germany, July 15.
- 2017 “Co-evolving Genetic Programming Trees and Rules in a Learning Classifier System for Problem Driven Machine Learning” Genetic Programming Theory and Practice (GPTP). Ann Arbor, Michigan, May 18.
- 2017 Webinar - “An Introduction to Bioinformatics” for multi-site T32 on genetics of sleep and sleep disorders (John Hopkins, University of Michigan, and Stanford), Philadelphia, PA, April 24.
- 2017 “An Introduction to Data Science”, invited lecturer, Nursing Informatics 651, UPenn, Philadelphia, PA, April 3.
- 2017 “Feature Selection with REBATE”, invited speaker, Epistasis Discovery in Genetics and Epidemiology (EDGE) workshop, Key West, Florida, February 9. (Host: Marylyn Ritchie).
- 2016 “Pareto-Inspired Multi-Objective Rule Fitness for Adaptive Rule-Based Machine Learning”, International Workshop on Evolutionary Machine Learning at the Genetic and Evolutionary Computing Conference (GECCO’16). Denver, Colorado, July 20.
- 2016 Tutorial: “Introducing Rule-Based Machine Learning: Capturing Complexity”, Genetic and Evolutionary Computing Conference (GECCO’16). Denver, Colorado, July 20.
- 2016 “A New ‘Front’ in Rule-Based Machine Learning”, invited speaker, Epistasis Discovery in Genetics and Epidemiology (EDGE) workshop, Key West, Florida, February 4. (Host: Marylyn Ritchie).
- 2015 “ExSTraCS 2.0: Description and Evaluation of a Scalable Learning Classifier System” Hot Off The Press Selection at the Genetic and Evolutionary Computing Conference (GECCO’15). Madrid, Spain, July 13.
- 2015 “Continuous Endpoint Data Mining with ExSTraCS: A Supervised Learning Classifier System”, International Workshop on Evolutionary Machine Learning at the Genetic and Evolutionary Computing Conference (GECCO’15). Madrid, Spain, July 12.
- 2015 Tutorial: “Introducing Rule-Based Machine Learning: A Practical Guide” Co-presented with Will Browne PhD, Genetic and Evolutionary Computing Conference (GECCO’15). Madrid, Spain, July 11.
- 2015 “Modeling Complex Disease Associations with ExSTraCS: A Study of Scalability”, invited speaker, Epistasis Discovery in Genetics and Epidemiology (EDGE) workshop, Key West, Florida, February 5. (Host: Marylyn Ritchie).
- 2014 “An Introduction to Learning Classifier Systems”, invited speaker for Evolutionary Computation Course, University of Vermont, October 23. (Host: Margaret J. Eppstein).
- 2014 “The Role of Genetic Heterogeneity and Epistasis in Bladder Cancer Susceptibility and Outcome: A Learning Classifier System Approach” Hot Off The Press Selection at the Genetic and Evolutionary Computing Conference (GECCO’14). Vancouver BC, Canada, July 15.
- 2014 “ExSTraCS: An Extended Michigan-Style Learning Classifier System for Flexible Supervised Learning Classification and Data Mining”, International Workshop on Learning Classifier Systems at the Genetic and Evolutionary Computing Conference

- (GECCO'14). Vancouver BC, Canada, July 12.
- 2013 "An Introduction to Learning Classifier Systems", invited speaker for Evolutionary Computation Course, University of Vermont, October 24. (Host: Margaret J. Eppstein).
- 2013 "A Simple Multi-Core Parallelization Strategy for Learning Classifier System Evaluations", International Workshop on Learning Classifier Systems at the Genetic and Evolutionary Computing Conference (GECCO'13). Amsterdam, The Netherlands, July 6.
- 2013 "ExSTraCS: A Genetics-Based Supervised Machine Learning Tool for Epidemiological Data Mining", International Workshop on Learning Classifier Systems at the Genetic and Evolutionary Computing Conference (GECCO'13). Amsterdam, The Netherlands, July 6.
- 2013 Tutorial: "Introduction to Learning Classifier Systems" Co-presented with Will Browne PhD, Genetic and Evolutionary Computing Conference (GECCO'13). Amsterdam, The Netherlands, July 6.
- 2013 "Classification and Data Mining in Genetic Epidemiology: A Learning Classifier System Approach", invited speaker for Bioinformatics course, University of Southern Maine, April 11. (Host: Clare B. Congdon).
- 2013 "GAMETES: Complex Genetic Model Simulation", invited speaker, Epistasis Discovery in Genetics and Epidemiology (EDGE) workshop, Key West, Florida, January 31. (Host: Jason Moore).
- 2013 "Tackling Complexity in Common Human Disease Research: Machine Learning Disease Risk", Invited Faculty Lecture, Bard College, Annandale-on-Hudson, New York, January 22. (Host: Amy Savage)
- 2012 "The Role of Genetic Heterogeneity and Epistasis in Bladder Cancer Susceptibility and Outcome: A Learning Classifier System Approach", Translational Bioinformatics Conference, Jeju, South Korea, Oct 13-16.
- 2012 "Instance-Linked Attribute Tracking and Feedback for Michigan-Style Supervised Learning Classifier Systems", Genetic and Evolutionary Computing Conference (GECCO'12), Genetics Based Machine Learning Track, Philadelphia, Pennsylvania, July 7-11.
- 2012 "An Analysis Pipeline with Visualization-Guided Knowledge Discovery for Michigan Style Learning Classifier Systems: Interpreting the Black Box", International Workshop on Learning Classifier Systems at the Genetic and Evolutionary Computing Conference (GECCO'12), Philadelphia, Pennsylvania, July 7-11.
- 2011 "Random Artificial Incorporation or Noise in a Learning Classifier System Environment", International Workshop on Learning Classifier Systems: Genetic and Evolutionary Computing Conference (GECCO'11), Dublin, Ireland, July 12-16.
- 2010 "The Application of Michigan-Style Learning Classifier Systems to Address Genetic Heterogeneity and Epistasis in Association Studies", Genetic and Evolutionary Computing Conference (GECCO'10), Bioinformatics Track. Portland, Oregon, July 7-11.
- 2008 "Mask Functions for the Symbolic Modeling of Epistasis Using Genetic Programming", Genetic and Evolutionary Computing Conference (GECCO'08), Bioinformatics Track. Atlanta, GA, July 12-16.

Institutional

- 2017 "Evolutionary Algorithms and Rule-Based Machine Learning" Guest Lecture for Data Science (EPID600) at UPenn (Host: Blanca Himes PhD), November 16 [upcoming].

- 2017 “Functional Annotation and Enrichment Analysis” Guest Lecture for Data Science (EPID600) at UPenn (Host: Blanca Himes PhD), November 14 *[upcoming]*.
- 2017 “A New Paradigm for Data Mining in Bioinformatics: Embracing Genetic Heterogeneity” Invited candidate faculty seminar, UPenn (Host: John H. Holmes PhD), June 1.
- 2016 “Functional Annotation and Enrichment Analysis” Guest Lecture for Data Science (EPID600) at UPenn (Host: Blanca Himes PhD), November 17.
- 2016 “An Introduction to Rule-Based Machine Learning”, Lunch and Learn Series, UPenn, October 31.
- 2016 “Evolutionary Algorithms and Rule-Based Machine Learning” Guest Lecture for Data Science (EPID600) at UPenn (Host: Blanca Himes PhD), October 27.
- 2016 “Simulation Studies: Model/Dataset Generation and Study Design” Lunch and Learn Series, UPenn, June 13
- 2016 “Relief-Based Algorithms”, Lunch and Learn Series, UPenn, April 25.
- 2016 “An Introduction to Machine Learning: Practical Guidelines and Algorithm Selection”, Lunch and Learn Series, UPenn, January 11.
- 2015 “Functional Annotation and Enrichment Analysis” Guest Lecture for Data Science (EPID600) at UPenn (Host: Blanca Himes PhD), November 12.
- 2014 “Modeling Complex Disease Associations with ExSTraCS: A Study of Scalability”, Pizza Talk Series, Dartmouth College, December 12.
- 2014 “The Rise of Machine Learning: Advancing Epidemiological Data Mining, Prediction, and Knowledge Discovery”, Invited Faculty Interview Talk, Dartmouth College, April 8.
- 2013 “GAMETES: Software for Simulating Complex Epistatic Models and Heterogeneous Datasets for the Advancement of Algorithm Development”, Pizza Talk Series, Dartmouth College, December 13.
- 2013 “ExSTraCS: The Development of a Genetics Based Supervised Machine Learning Tool for Epidemiological Data Mining”, Pizza Talk Series, Dartmouth College, February 22.
- 2012 “The Detection and Characterization of Epistasis and Heterogeneity: A Learning Classifier System Approach”, Thesis Defense, Dartmouth College. Feb. 20.
- 2011 “The Detection, Characterization, and Modeling of Genetic Heterogeneity and Epistasis: A Learning Classifier System Approach”, MCB Research in Progress, Dartmouth College. Sept. 28.
- 2010 “The Detection, Characterization, and Modeling of Genetic Heterogeneity and Epistasis: A Learning Classifier System Approach”, Pizza Talk Series, Dartmouth College, February 11.
- 2010 “The Detection, Characterization, and Modeling of Genetic Heterogeneity and Epistasis: A Learning Classifier System Approach”, Institute for Quantitative Biomedical Sciences Applicant, Dartmouth College, December 20.
- 2010 “The Detection, Characterization, and Modeling of Genetic Heterogeneity and Epistasis: A Learning Classifier System Approach”, MCB Research in Progress, Dartmouth College, November, 10.
- 2010 “The Detection, Characterization, and Modeling of Genetic Heterogeneity and Epistasis: A Learning Classifier System Approach”, MCB Research in Progress, Dartmouth College. February, 17.
- 2009 “The Detection, Characterization, and Modeling of Genetic Heterogeneity and Epistasis”, MCB Research in Progress, Dartmouth College. February, 11.

- 2008 "The Detection, Characterization, and Modeling of Genetic Heterogeneity and Epistasis", MCB Research in Progress, Dartmouth College. April, 9.
- 2007 "Mask Functions for Symbolic Modeling of Epistasis", MCB Research in Progress, Dartmouth College. May 23.

BIBLIOGRAPHY

Refereed Publications

1. **Urbanowicz, R.J.**, White, B.C., Barney, N., Moore, J.H. Mask functions for the symbolic modeling of epistasis using genetic programming. Proceedings of the Genetic and Evolutionary Computing Conference. ACM Press, pp. 339-346 (2008). (Highlight: nominated for Best Paper Award, Bioinformatics and Computational Biology Track).
2. **Urbanowicz, R.J.**, Moore, J.H. Learning classifier systems: A complete introduction, review and roadmap. Journal of Artificial Evolution and Applications 2009, 1-25 (2009). (Highlight: cited 70 times as of November 2013)
3. **Urbanowicz, R.J.**, Moore, J.H. The application of Michigan-style learning classifier systems to address genetic heterogeneity and epistasis in association studies. Proceedings of the Genetic and Evolutionary Computing Conference. ACM Press, pp. 195-202 (2010). (Highlight: won best paper award at GECCO'10).
4. **Urbanowicz, R.J.**, Moore, J.H. The application of Pittsburgh-style learning classifier systems to address genetic heterogeneity and epistasis in association studies. Lecture Notes in Computer Science pp. 195-202 (2010).
5. **Urbanowicz, R.J.**, Sinnott-Armstrong, N., Moore, J.H. Random artificial incorporation of noise in a learning classifier system environment. Proceedings of the Genetic and Evolutionary Computing Conference. ACM Press, pp. 369-374 (2011).
6. **Urbanowicz, R.J.**, Granizo-Mackenzie, A., Moore, J.H. An analysis pipeline with statistical and visualization-guided knowledge discovery for Michigan-style learning classifier systems. Computational Intelligence Magazine 7, 35-45 (2012).
7. **Urbanowicz, R.J.**, Granizo-Mackenzie, A., Moore, J.H. Instance-linked attribute tracking and feedback for Michigan-style supervised learning classifier systems. Proceedings of the Genetic and Evolutionary Computing Conference. ACM Press, pp. 927-934 (2012).
8. **Urbanowicz, R.J.**, Granizo-Mackenzie, A., Moore, J.H. Using expert knowledge to guide covering and mutation in a Michigan-style learning classifier system to detect epistasis and heterogeneity. Lecture Notes in Computer Science 7491, 266-275 (2012).
9. **Urbanowicz, R.J.**, Kiralis, J., Sinnott-Armstrong, N.A., Heberling, T., Fisher, J.M., Moore, J.H. GAMETES: A fast, direct algorithm for generating pure, strict, epistatic models with random architectures. BioData Mining 5, 16 (2012).
10. **Urbanowicz, R.J.**, Kiralis, J., Fisher, J.M., Moore, J.H. Predicting the difficulty of pure, strict, epistatic models: Metrics for simulated model selection. BioData Mining 5, 15 (2012).
11. **Urbanowicz, R.J.**, Andrew, A.S., Karagas, M.R., Moore, J.H. The role of genetic heterogeneity and epistasis in bladder cancer susceptibility and outcome: A learning

- classifier system approach. Journal of the American Medical Informatics Association, 20(4), 603-612 (2013). (Highlight: Won a best paper award at the 2013 Translational Bioinformatics Conference, South Korea)
12. Rudd, J., Moore, J.H., **Urbanowicz, R.J.** A simple multi-core parallelization strategy for learning classifier system evaluations. Proceedings of the Genetic and Evolutionary Computing Conference. ACM Press, 1259-1266 (2013).
 13. Tan, J., Moore, J.H., **Urbanowicz, R.J.** Rapid rule compaction for knowledge discovery in a supervised learning classifier system. Advances in Artificial Life, ECAL, 12. 110-117 (2013).
 14. Rudd, J., Moore, J.H., **Urbanowicz, R.J.** A multi-core parallelization strategy for statistical significance testing in learning classifier systems. Evolutionary Intelligence. 6(2), 127-134 (2013).
 15. **Urbanowicz, R.J.**, Granizo-Mackenzie, A., Kiralis, J., Moore, J.H. A classification and characterization of two-locus pure, strict epistatic models for simulation and detection. BioData Mining. 7(1), 8 (2014).
 16. **Urbanowicz, R.J.**, Bertasius, G., Moore, J.H. An extended michigan-style learning classifier system for flexible supervised learning, classification, and data mining. In Parallel Problem Solving From Nature (PPSN XIII). Springer International Publishing, 211-221 (2014).
 17. **Urbanowicz, R.J.**, Moore, J.H. ExSTraCS 2.0: Description and evaluation of a scalable learning classifier system. Evolutionary Intelligence. 8(2-3), 89-116 (2015). (Highlight: Solved the extremely complex 135-bit benchmark multiplexer problem directly for the first time reported in literature).
 18. **Urbanowicz, R.J.**, Ramanand, N., Moore, J.H., Continuous endpoint data mining with ExSTraCS. Proceedings of the Genetic and Evolutionary Computing Conference. ACM Press, 1029-1036 (2015).
 19. **Urbanowicz, R.J.**, Moore, J.H., Retooling fitness for noisy problems in a supervised Michigan-style learning classifier system. Proceedings of the Genetic and Evolutionary Computing Conference. ACM Press, 591-598 (2015).
 20. Olson, R.S, **Urbanowicz, R.J.**, Moore, J.H., Automating biomedical data science through tree-based pipeline optimization. In European Conference on the Applications of Evolutionary Computation. Springer International Publishing, 123-137 (2016). (Highlight: Won a best paper award in the EvoBIO track)
 21. **Urbanowicz, R.J.**, Olson, R.S, Moore, J.H., Pareto inspired multi-objective rule fitness for noise-adaptive rule-based machine learning. In International Conference on Parallel Problem Solving From Nature (PPSN XV). Springer International Publishing, 514-524 (2016).
 22. Olson, R.S, **Urbanowicz, R.J.**, Moore, J.H., Evaluation of a tree-based pipeline optimization tool for automating data science. Proceedings of the Genetic and Evolutionary Computing Conference. ACM Press, 485-492 (2016). (Highlight: Won a best paper award in the Evolutionary Machine Learning Track at GECCO'16)
 23. Olson, R.S., LaCava W., Orzechowski, P., **Urbanowicz, R.J.**, Moore, J.H. PMLB: A large benchmark suite for machine learning evaluation and comparison. BioData Mining. (In Press - 2017) (Preprint: <https://arxiv.org/abs/1703.00512>)

Non-Refereed Letters and Invited Publications

24. Loiacono, D., Orriols-Puig, A., **Urbanowicz, R.J.** Special issue on advances in learning classifier systems. Evolutionary Intelligence, 1-2 (2012).
25. Shafi, K., **Urbanowicz, R.J.**, Iqbal, M. Special issue on advances in learning classifier systems. Evolutionary Intelligence, 1-2 (2013).
26. **Urbanowicz, R.J.** ExSTraCS: Rule Based Machine Learning, Classification and Knowledge Discovery for Complex Problems. SIGEVolution Newsletter of the ACM Special Interest Group on Genetic and Evolutionary Computation. 8(1) <http://www.sigevolution.org/> (2014)

Book Chapters

27. **Urbanowicz, R.J.**, Moore, J.H. Learning classifier systems: The rise of genetics-based machine learning in biomedical data mining. In. Sarkar, N., (Eds.) Methods in Biomedical Informatics, 1st Edition, Elsevier. (2014).

Books and Edited Proceedings

28. **Urbanowicz, R.J.** Reassessment of a ganglioside-liposome biosensor for the detection of biological toxins. Durst, R.A, Baeumner, A.J. (Eds.) Masters Dissertation, Cornell University. (2005).
29. **Urbanowicz, R.J.** The detection and characterization of epistasis and heterogeneity: a learning classifier system approach. Moore, J.H., Whitfield, M.L., Eppstein M.J., Gross, R.H., Thornton-Wells, T.A. (Eds.) Genetics PhD Thesis, Dartmouth College. (2012).
30. **Urbanowicz, R.J.**, Browne, W. Book: Introduction to learning classifier systems. Springer, New York, NY (2017). (Available on amazon.com)

Other Non-Refereed Publications

31. **Urbanowicz, R.J.**, Kiralis, J., Fisher, J.M., Moore, J.H. GAMETES User's Guide. BioData Mining Supplemental Materials (2012).
32. **Urbanowicz, R.J.**, Bertasius, G., Moore, J.H. ExSTraCS 1.0 User's Guide. <http://sourceforge.net/projects/exstracs/> (2014).
33. **Urbanowicz, R.J.**, Moore, J.H. ExSTraCS 2.0 User's Guide. <http://sourceforge.net/projects/exstracs/> (2014).

Submitted Publications

34. **Urbanowicz, R.J.**, Meeker, M., LaCava, W., Olson, R.S., Moore, J.H. Relief-based feature selection: Introduction and review. Submitted to Journal of Machine Learning Research. (Preprint: <https://arxiv.org/abs/1711.08421>)
35. **Urbanowicz, R.J.**, Olson, R.S., Schmitt, P., Meeker, M., Moore, J.H. Benchmarking Relief-based feature selection methods. Submitted to Journal of Machine Learning Research. (Preprint: <https://arxiv.org/abs/1711.08477>)

36. Verma, S.S., Lucas, A., Zhang, X., Veturi, Y., Dudek, S., Li, B., Li, R., **Urbanowicz, R.J.**, Moore, J.H., Kim, D., Ritchie, M.D. Collective feature selection to identify crucial epistatic variants. Submitted to BioData Mining.
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Publications in Preparation

41. **Urbanowicz, R.J.**, Lo, C., Moore, J.H. Improved heterogeneity characterization using attribute tracking with time recency weighting (In preparation)
42. **Urbanowicz, R.J.**, Andrews, P., Moore, J.H. GAMETES 2.0: software for simulating complex epistatic models and heterogeneous datasets. (In preparation)
43. Madan, E., Nagane, M., Arias-Pulido, H., Qualls, C., Marotti, J., Costa, C., **Urbanowicz, R.J.**, Kaufman, P., Hamilton, J., Chaher, N., Royce, M., Bakkar, R., Martinez, C., Kuppusamy, P., Moreno, E., Gogna, R. Stromal p53 predicts metastasis and poor survival in breast cancer patients. (On Hold – delayed due to first author’s medical leave)
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