

Lawrence E. Hunter, PhD

Personal History

Current Positions:

University of Colorado, Professor, 2008 to present:
School of Medicine, Department of Pharmacology
School of Public Health, Department of Biometrics
Arts & Sciences (Boulder), Department of Computer Science
Arts & Sciences (Denver), Department of Biology
Computational Bioscience Program (Director)
Biomolecular Structure Program
Cardiovascular Institute
Cancer Center
Human Medical Genetics Program
IQ Biology / BioFrontiers Program (Boulder)

Professional Address:

University of Colorado School of Medicine
Mailstop 8303
Aurora, CO 80045-0511
Phone: 303-724-3574
Fax: 303-724-3648
Email: Larry.Hunter@uchsc.edu

Education

- B.A. in Psychology, 1982, Yale University, *cum laude*.
- M.S. and M.Phil. in Computer Science, 1987, Yale University.
- Ph.D. in Computer Science, 1989, Yale University.
- Thesis: *Knowledge Acquisition Planning: Gaining Expertise Through Experience*, advised by Roger Schank.

Academic Appointments

Teaching Assistant, Yale University, Computer Science Department 1983-1988.
Adjunct Assistant Professor, George Mason University, Computational Science and Informatics, 1991-1997
Adjunct Associate Professor, George Mason University, Computational Science and Informatics, 1997-2000
Fellow, Krasnow Institute of Advanced Study in Cognition, 1995-2000.
Associate Professor, University of Colorado School of Medicine, 2000-2008.
Professor, University of Colorado School of Medicine, 2008-

Other Professional Positions

Government Positions

Board of Scientific Counselors, Environmental Protection Agency, Office of Research and Development / Computational Toxicology Subcommittee 2009-2012

Chief of Section, National Cancer Institute (NIH), Section on Molecular Statistics and Bioinformatics, 1999-2000.

Computer Scientist, National Library of Medicine (NIH), Lister Hill Center, 1989-1999.

National Science Foundation Scientific Database Network Project, Board of Directors, 1992-1996;

Corporate Positions

Consultant, SomaLogic, Inc., 2014-

Consultant, Cycorp, Inc. 2010-11

Founder & Member of the Board of Directors, Molecular Mining Corporation, 1997-2003

Cooperative Research and Development Agreement (CRADA) with VIPS Systems, Inc. 1998-2000

Consultant, Medical Scientists, Inc. (1998-2005)

Consultant, SmithKlein Beecham, Inc. (1996-2000)

Honors, Special Recognition, and Awards

Daniel T. Richards Prize, Medical Library Association, 2016

Outstanding Service Award, International Society for Computational Biology, 2015

Senior member, American Association for Artificial Intelligence, 2014-

Fellow, International Society for Computational Biology, 2010-

Fellow, American College of Medical Informatics, 2002-

Excellence in Research Award, UC Denver Pharmacology Department, 2007

Excellence in Teaching Award, Preventive Medicine and Biometrics Department, 2004

Engelmore Prize for Innovative Applications of Artificial Intelligence, 2003 (presented by the American Association for Artificial Intelligence)

Regent's Award for Scholarship and Technical Achievement, (the highest honor granted by the National Library of Medicine), 1994.

Meritorious Service Award, National Library of Medicine, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998

Winner, student paper competition, Knowledge Acquisition for Knowledge Based Systems Workshop, 1988.

Patents

A System for Synergistic Combination of Multiple Automatic Induction Methods and Re-Representations of Data. US Patent 6,449,603, issued September 10, 2002. Licensed to firms in healthcare, insurance and the pharmaceutical industry.

A Machine Learning Method for Predicting Rare but Significant Events. US Patent 6,917,926 issued July 12, 2005. Coinventors Hung-Han Chen, Harry Poteat and Kristin Kendall.

Membership in professional organizations

International Society for Computational Biology, 1996-. Founder, 1996; President 1996-2000; Awards Committee Chair, 2003-2005; Finance Committee Chair 2005-2007; member of the Board of Directors, 1996-2007

American Association for Artificial Intelligence, 1984-

American Medical Informatics Association, 1990-, Publications Committee (1990-1993)

International Biomatrix Society, Board of Directors, 1991-1996;

Major Committee and Service Responsibilities

Departmental

Curriculum Committee, 2000-2004

Faculty Search Committee, 2002-2003

Space Planning Committee, 2003-2009

Graduate Training Committee, 2007

Promotion and Tenure Committee, 2009-2012, 2014-

School of Medicine

Strategic Plan Committee, 2002-2003

Research Advisory Committee, 2003-2005

Computational Bioscience Program, 2004- (Director)

D2V, 2016- (Training Program co-director)

UCD AMC

Search Committee, Director of the Dennison Library, (2006-2007)

Faculty Promotions Committee 2012-2014

CU Boulder

Faculty Search Committee, Computer Science Department (2005)

Molecular Biotechnology Initiative (2005-2006)

CU Denver

Steering Committee, CU Denver Center for Computational Biology (2001-2006)

Faculty Search Committee, Biology Department, 2012

CU System

University Without Walls (2002-2004)

Genomics Taskforce (2001-2005)

National / International Scientific Advisory Boards

University of Pittsburgh Biomedical Informatics Training Program 2016-

ELIXIR Scientific Advisory Board (European Union) 2016-

RD-Connect Scientific Advisory Board, (UK) 2012-

BioMedNet Scientific Advisory Board (European Commission), 2012-2016

Multidisciplinary Research Partnership on Bioinformatics (Ghent, Belgium), Scientific Advisory Board, 2012-2016

Dartmouth Medical School Quantitative Biology Program, 2015

European Bioinformatics Institute, Literature Services Advisory Board, 2011-2015

Rat Genome Database, Scientific Advisory Board, 2007-2012

Gene Ontology Consortium, Scientific Advisory Board 2004-2009

Columbia University Department of Biomedical Informatics, External Reviewer 2004

University of Michigan Computational Biology Program, External Reviewer 2003

National / International Conference Organizing

Founder, International Conference on Intelligent Systems for Molecular Biology 1993 (Co-chair, 1993; Organizing committee 1994-1996). Still the most successful academic conference in bioinformatics

Founder and Co-chair, Pacific Symposium on Biocomputing (1996-)

Founder and Program Chair, Rocky Mountain Regional Conference on Computational Biology (2004-)

Founder and Steering Committee Member, VizBi conference on computational visualization in biology, 2010-

Steering Committee, IEEE Conference on Biological Visualization, 2011-

Program chair, Biotechnology Computing Track, Hawaiian International Conference on System Sciences, 1993, 1994, 1995.

Program chair, Biotechnology Computing Minitrack, Hawaiian International Conference on System Sciences, 1991, 1992

Area Chair for Machine Learning, National Conference on Artificial Intelligence, 1992, 1993.

Program committee, AAAI-91 Workshop on Pattern Recognition and Inference in Molecular Biology, 1991

Program chair, AAAI Spring Symposium on Artificial Intelligence and Molecular Biology, 1990.

Program committee, International Conference on the Biomatrix, 1990

Review and referee work

Service on Editorial Boards

Associate Editor, *Journal of Biomedical Informatics*, 2002-2012
Associate Editor, *BMC Bioinformatics*, 2009-2014
Associate Editor, *PLoS Computational Biology*, 2010-
Associate Editor, *Bioinformatics*, 2010-
Editorial Board, *Journal of Machine Learning Research*, 1999-2004
Special editor, *IEEE Expert*, track on Molecular Biology Applications, 1996.
Associate Editor, *Journal of Artificial Intelligence Research*, 1993-1997
Editorial board, *Artificial Intelligence and Medicine*, 1993-1995
Editorial board, *Journal of Computational Molecular Cell Biology*, 1993-1998

Grant Study Sections and Ad Hoc Grant Reviews

Ad Hoc Reviewer for BD2K 2016/05 ZRG1-PSE-K-50
Ad Hoc reviewer at NCATS, 2016/10 ZTR1-CI-9-01
Ad Hoc reviewer at NHLBI 2017/01 ZHL1-CSR-Q-F1
Chair, NIH Office of the Director Transformative Research Award Review ZRG1 BCMB-A (50) R 2015-2016
Chair, NIAID Special Emphasis Panel ZAI1 MP-I (S4), 2008
Biomedical Library and Informatics Review Committee, National Library of Medicine study section, 2004-2008
Ad hoc reviewer, NIH Office of the Director, Big Data to Knowledge Research Center awards, 2014
Ad hoc reviewer, NIH Office of the Director, Pioneer awards, 2014, 2015
Ad hoc reviewer, NIH Office of the Director, Transformational Science Awards, 2012, 2013, 2014, 2015
Ad hoc reviewer, NCRRT / CTSA reviews, 2010
Ad hoc reviewer, National Library of Medicine, 2009
Ad hoc reviewer, National Library of Medicine, 1999-2004
Ad hoc reviewer, NIH Roadmap U54 Interdisciplinary Research Consortia, 2007
Ad hoc reviewer, National Institute of General Medical Sciences, 2004
Ad hoc reviewer, National Academy of Sciences, 2003
Genome Canada Research Review Panel, 2001, 2003
Ad hoc reviewer, National Institute for Mental Health, 2000
Human Brain Project (trans-NIH review section), 1997-1999
Ad hoc reviewer, National Institute for Mental Health (Research Contracts), 1998

Invited lectures and presentations (highlights)

The Challenges of Biological Information Visualization, Keynote at ISMB Biomedical Information Visualization SIG, 2015

Ontologically Grounded Knowledge Representation for Semantic Data Integration and Natural Language Processing Keynote at ISMB BioOntologies SIG, 2015

Knowledge Representation in and about Text. Keynote at Biological Linked Annotation Hackathon 2015

Translational Analytics: Semantic Computing at Genomic Scale. Translational Bioinformatics Conference keynote 2014

A Mind for Life: Why Watson isn't AI-Complete, and How Molecular Biomedicine Might Make It So. Invited address to IBM Deep Q/A Research Team, 2012

Twenty years of the Intelligent Systems for Molecular Biology Conference. Keynote address, ISMB, 2012

Openness as a value in biomedical research, Invited address, Third Annual Research Ethics Conference, University of Colorado, 2012

Formal Knowledge Representation and Automated Reasoning for Explanation of Genome-Scale Data Keynote address, International Conference on Biomedical Ontology, 2012

The Role of Openness in Knowledge-based Systems for Biomedicine, invited presentation to the Biomedical Open Source Conference / ISMB SIG, 2011

Sense-making in Molecular Biology, invited presentation, IEEE conference on Visualization in Biology, 2011

Computational Bridges over Biomedical Chasms, invited presentation, Gold Lab Symposium, 2011

Building a Mind for Life, invited presentation to International Lisp Conference, 2010

Visualization in Biology, invited capstone panel presentation, IEEE VizWeek, Oct. 2009

Rethinking our goals for BioNLP and its evaluation, Keynote address, BioCreative II.5, October 2009

Innovative Training for Bioinformatics, Invited address, National Library of Medicine Board of Regents, September 2009

Tools for Scientific Insight, invited presentation, SRI International, October 2007

Twenty Years of Planning to Learn, keynote presentation, Planning to Learn workshop, European Conference on Machine Learning, September 2007

New ideas for secondary school biology education, Ewing Marion Kaufmann Foundation, May 2006

Bioinformatics: Putting Systems Biology Information in Context, lecture in UCHSC Systems Biology and Biomedical Research Symposium, Dec 2, 2005

Language, Knowledge and Molecular Biology, Invited presentation to Yale Bioinformatics Symposium, New Haven, CT, November 3, 2005

Biomedical Language Processing, Keynote address to Human Language Technology / Empirical Methods in Natural Language Processing conference, Vancouver, Canada, Oct. 6, 2005

Biognostic Systems, Keynote address to Italian Association for Artificial Intelligence conference, Milan, Italy Sept. 20, 2005

The Role of Community in Computational Biology, keynote address to the Rocky Mountain Regional Bioinformatics Meeting ("Rocky 1") in Aspen, Colorado, December 5-7, 2003.

The Era of Biognostic Machines, keynote address to Association for Computing Machinery Special Interest Group on Applied Computing (ACM-SAC) conference., 2003

Proteomic Bioinformatics, Center for Computational Pharmacology mini-symposium, 2003

Biognostic Machines for Cognitive Disability, invited address, Coleman Institute annual meeting, 2002

Bioinformatics and Human Health, UCHSC Chancellor's Luncheon Address, 2002

Data Mining for High Throughput Biomedicine, keynote address to the Research Society on Alcoholism conference, Denver, Colorado, June 2000

Edgar: Extraction of Drugs, Genes and Relations from the Biomedical Literature, Pacific Symposium on Biocomputing, January, 2000

The Role of Machine Learning and Natural Language Processing in Contemporary Drug Discovery, Pharmacology Grand Rounds, University of Colorado School of Medicine, October, 1999

Inductive Modeling: Power and Pitfalls, keynote address to MODEL-IT conference, Wageningen, the Netherlands, November 1998

Coevolution of Symbol Systems and Behavior, lecture and workshop, Simulations of Adaptive Behavior conference, Zurich, Switzerland, August 1998.

Machine Learning for Drug Discovery, invited address, SmithKline Beecham Data Mining Days, November 1997.

Computer Science : Biology :: Mathematics : Physics, MIT Media lab, April 1997

The Role of Computation in Cognitive Science, Krasnow Institute for Advanced Study of Cognition Seminar Series, November, 1996.

Coevolution Learning: Synergetic Evolution of Learning Agents and Problem Representations, Multistrategy Learning Workshop, June, 1996.

AI Models for Biology, and Biological Models for AI, Keynote address, Second International Conference on Intelligent Systems for Molecular Biology, July 1995.

Computers, Modelling , and Theoretical Biology, Invited address to the Keystone Center Scientist to Scientist Colloquium, August, 1994

The National Library of Medicine on the Internet: A Digital Library for Biomedicine. Invited address to the Computers and Chemistry Division of the American Chemical Society conference, Aug 1994

Planning to Discover in Molecular Biology, MIT AI Lab Revolving Seminar Series, April 1994

Molecular Biology for the Computer Scientist, Full day tutorial at the Hawaiian International Conference on System Sciences, January 1993. Repeated Jan 1994.

AI & Molecular Biology, Plenary address, National Conference on Artificial Intelligence, San Jose, CA, July 1992.

Megaclustering of Unsegmented Datastreams and Applications to Molecular Biology, Johns Hopkins Applied Physics Laboratory distinguished lecture series, October 1992.

Electronic Facilitation of Scientific Communication, Panel organizer and speaker, International Conference on the Biomatrix, George Mason University, July 1990

Knowledge Acquisition Planning for Inference from Large Datasets, Keynote address, 1990 Conference on AI Systems in Government, Washington, DC, May 1990

Machine Learning: Ready for Industrial Application, Invited address to Third Annual Artificial Intelligence Forum, Sanibel Island, FL, February, 1989

Artificial Neural Networks as Theories of Mind. International Neural Network Society, Boston MA, September, 1988

Machine Learning for Molecular Biology. Invited address to the Theoretical Biology and Biophysics Group, Los Alamos National Laboratory, June 1988

Indexing and Recognition. AI/BioMed: The First International Conference on Artificial Intelligence and its Impacts in Biology and Medicine, Montpellier, France, September 1986

Computers and Privacy. Guest lecture in Constitutional Law, University of Connecticut at Hartford Law School, Dec., 1985.

Teaching record

Courses taught

2010-present SoM CPBS 7712 *Research in Computational Biology* (course director 2010-12)

2009-present SoM CPBS 7711 *Introduction to Computational Biology* (course director, 2009-2012)

2008, 2011, 2013, 2015 SoM CPBS 7605 *Ethics and Values in Computational Biology*

2011-2012 SoM CPBS 7792 *Next Generation Human Phenotyping*

2004 BIOI 7791 *Readings in Computational Biology*

2003-2006 SoM BIOI 7713 (each year) *Research in Computational Biology*

2003, 2005, 2013, 2014 BIOI 7792 *Special Topics in Computational Biology*

2002-2007 SoM BIOI 7710, 7711 (each year) *Introduction to Computational Biology*

2002, 2003 University of Colorado, Denver, BIOL 5099 *Biology for Computer Scientists, Mathematicians and Engineers*

2001 PHCL 7611 *Advanced Statistics for Pharmacology*

2000 PHCL 6611 *Statistics for Pharmacology*

1991-1999 George Mason University *Graduate Computational Bioscience*

Lectures given in other courses

2003-2014 PHCL 7561 *Bioinformatics in Drug Discovery*

2004-2014 PHCL 7600 *Innovative Bioinformatics for Pharmacology*

2004-2009 Informatics Elective for Residents *Clinical Bioinformatics*

2001 PHRD 4450 *Ethical Issues in Pharmacy Informatics*

Courses Created

CPBS 7792 *Next generation human phenotyping.*

BIOI 7605 (now CPBS 7605) *Ethics and Values in Computational Biology*

BIOI 7710 *Survey of Bioinformatics Methods*

BIOI 7711 (now CPBS 7711) *Introduction to Computational Biology*

BIOI 7712 (now CPBS 7712) *Research in Computational Biology*

BIOI 7713 *Graduate Bioinformatics 3* (now included in 7712)

BIOI 7791 *Readings in Bioinformatics*

BIOI 7792 *Special Topics in Bioinformatics*

BIOL 5099 (CU Denver) *Molecular Biology for Computer Scientists, Mathematicians and Engineers*

Teaching Administration

Director, Computational Bioscience Training Program

Course Director, CPBS 7711

Course Director, CPBS 7712

Course Director, CPBS 7792

Course Director, CPBS 7605

Teaching Awards

Excellence in Teaching Award, Preventive Medicine and Biometrics Department, 2004.

Ph.D. Dissertations Directed

Jeffery L. Krichmar, *A Computational Model of Cerebellar of Saccadic Control*, GMU Computational Science and Informatics, 1997.

Judith E. Devany, *Equation Discovery Through Global Self-Referential Geometric Invariants and Machine Learning*, GMU Information Technology, 1997.

Imran Shah, *Predicting Enzyme Function from Sequence*, GMU Computational Science and Informatics, 1998

Barry Zeeberg, *Whole Genome Information Analysis and Processing*, GMU Computational Science and Informatics, 1999

Robert S. Erb, *Analysis and Modeling of Gene Expression Circuits*, GMU Computational Science and Informatics, 1999

Myriam Abramson, *Learning Coordination Strategies* GMU Information Technology, 2003.

Lorraine Tanabe, *Text mining the biomedical literature for genetic interactions* GMU Computational Science and Informatics, 2003

Ronald Taylor *Reconstruction of metabolic and genetic networks from gene expression perturbation data using a Boolean model: construction of a simulation testbed and an empirical exploration of some of the limits* GMU Computational Science and Informatics, 2003.

Min Hong, *Implicit constraint enforcement to control physically-based biomedical simulation* UCHSC Computational Bioscience 2005

Steve Russell, *Machine Learning and In-silico Modeling for Improved Identification of Peptides from Shotgun Proteomic MS/MS Spectra*. UCHSC Computational Bioscience 2005

Sonia Leach, *Informed Structural Priors for Bayesian Networks: Applications in Molecular Biology Using Heterogeneous Data Sources* Brown University Computer Science 2006

Zhiyong Lu, *Text Mining on GeneRIFs*, UCHSC Computational Bioscience 2007

Anis Karimpour-Fard, *Prediction of protein-protein interactions and function in bacteria* UCHSC Computational Bioscience 2008

Elizabeth White, *Pattern-Based Recovery of Argumentation from Scientific Text*, UC Boulder Computer Science, 2009

Philip V. Ogren, *Coordination resolution in biomedical texts*. UC Boulder Computer Science, 2011

Daniel C. McShan, *Computational Bioalchemistry: Optimal Search Algorithms for the Analysis and Synthesis of Metabolic Systems*. UC Denver Computational Bioscience, 2012

Ronald P. Schuyler, *Multi-component Genetic Associations*. UC Denver Computational Bioscience, 2012

Christopher Funk, *Ontological Concept Recognition and its Application for Biomedical Discovery*, UC Denver Computational Bioscience, 2015

William A. Baumgartner, Jr., *Enhancing Ontology Term Enrichment through Deductive Entailment*, UC Denver Computational Bioscience, 2015

Formal Junior Faculty Mentoring

Deborah Glueck, Department of Preventive Medicine and Biometrics

Debra Goldberg, Department of Computer Science (Boulder).

Grant support:

<u>Active Grants (Principal Investigator)</u>	<u>Annual direct costs</u>
NIH 2R01LM009254 <i>Biomedical Language Processing Writ Large: Scaling to all of PubMedCentral</i>	9/2006-4/2019 \$404,767
NIH 2R01LM008111 <i>Technology Development for a Molecular Biology Knowledge-base</i>	10/2003-3/2018 \$401,329
NIH 5T15LM009451 <i>Computational Bioscience Program Training Grant</i>	7/2007-6/2017 \$472,566
<u>Pending Grants (Principle Investigator)</u>	<u>Annual direct costs</u>
NIH 1P01GM118485 <i>Automated Explanation and Hypothesis Generation at Genomic Scale</i>	9/2016 – 8/2021 \$998,405
<u>Prior Grants (Principal Investigator)</u>	<u>Annual direct costs</u>
NIH/Clinical Center Research Contract <i>Gene Expression Array Analysis for Investigation of Sepsis</i>	7/2000-6/2001 \$100,000
NIH 1U01 AA13524 <i>Neuroinformatics Core for the Integrated Neuroscience Initiative on Alcoholism</i>	9/2001-8/2006 \$500,000
Genetics Institute / Wyeth-Ayerst <i>Development of Biological Literature Text Mining Software</i>	9/2001-8/2003 \$113,650
NIH 5G08LM009639-02 <i>Construction of a Full Text Corpus for Biomedical Text Mining</i>	9/2007- 9/2010 \$142,851
NIH 3G08LM009639-02S1 <i>Supplement (additional annotators) to corpus construction grant</i>	7/2009-9/2010 \$66,015
NIH 5R01GM083649-02 <i>Ontologies and Biomedical Language Processing</i>	9/2007- 8/2011 \$631,600
NIH 3T15LM009451-04S1 <i>Supplement (curriculum development) to training grant</i>	9/2010-8/2011 \$199,259
NIH HHS-N276201000033C <i>Contract: Computational Thinking to Support Clinicians and Biomedical Scientists</i>	9/2010-8/2011 \$377,982
NIH 3T15LM009451-03S2 <i>Supplement (additional trainees) to training grant</i>	6/2010-6/2012 \$37,179
NIH 5R01LM010120-02 <i>Automated Literature Mining for Validation of High-Throughput Function Prediction</i> (Transferred from Verspoor in 2011)	7/2009-6/2012 \$577,291
NSF DBI-0965616 <i>GOSTRUCT: Modeling the Structure of the Gene Ontology for Accurate Protein</i>	7/2009-5/2014 \$49,680

Function Prediction
(Transferred from Verspoor in 2011)

Prior Grants (Co-investigator)

DARPA W911NF-14-C-0109 (Burstein, PI) 1/2015 – 1/2016 \$200,000

R3E: Reading, Reasoning, and Reporting

Role: Colorado Subcontract PI

NSF DBI - 0849977 (Burns, PI) 10/01/09 – 09/30/13

Text Mining Infrastructure for the Entire Biomedical Literature

(U. Colorado subcontract)

NIH 5R01 DE015191-02 (Richard Spritz, PI) 4/04-3/08

Gene Discovery for Craniofacial Disorders

NIH 5P50 CA058187-09 (Paul Bunn, PI) 9/92-4/08

SPORE Grant in Lung Cancer

Canine Health Foundation (Jamie Modiano, PI) 12/2005 – 11/2008

Spontaneous Canine Tumors as Models for Cancer Gene Discovery

NIH 5P01 HL68743 (Edward Abraham, PI) 9/2002-8/2007

Heterogeneous neutrophil responses in acute lung injury

NIH 1 R24 AA13162-01 (Boris Tabakoff, PI) 4/2001-3/2006

Gene Expression Array Technology Center for Alcohol Research

NIH 1M01 RR00051 (Robert Eckel, PI) 4/2002-3/2007

University of Colorado General Clinical Research Center.

NIH 5 P30 CA46934-15 (Paul Bunn, PI) 3/1988-1/2006

Cancer Center Support Grant.

NIH P01 HL67671-01 (Robert Mason, PI) 7/2001-6/2004

SCOR: Pathobiology of Fibrotic Lung Disease.

Cystic Fibrosis Foundation, (David Rodman, PI) 4/2001-3/2003

Effects of Pseudomonas aeruginosa on Inflammatory Gene Expression.

NIH 5R01HL072340-02 (Mark Geraci, PI) 10/2002-9/2005

Application of expression analysis to study disease pathogenesis

Philanthropic gifts received

Pfizer/Selventa, 2012: \$125,000 Fund for computational bioscience research

Larry Gold, 2011-present: \$5,000 each year to support scientific conference organizing effort

NEC America, 2011, \$5,000 to support conference organizing

IBM, 2005-present: \$10,000 each year to support scientific conference organizing

IBM, 2007: \$24,000 UIMA Innovation Award

Hibernia, Inc., 2006: \$500 Fund for computational bioscience recruiting

Oracle, 2005: CIT Innovation award (license, support & training for Oracle 10g, value \$2500)

Hitachi, 2005: CIT Innovation award (10TB RAID Array, value: \$50,000)

IBM, 2003 (p690 Supercomputer with 64GB of RAM, value \$990,000)

Bibliography

Peer Reviewed Publications

1. **Hunter, L.**, Schank, RC. Encapsulation and Expectation: A response to Fodor's Modularity of Mind. *Behavioral and Brain Sciences*, 8(1): 29-30, 1985.
2. **Hunter, L.** Indexing and Recognition: Metaknowledge for Organizing Information. *Proceedings of AI/BioMed: The First International Conference on Artificial Intelligence and its Impacts in Biology and Medicine*, Montpellier, France, September 1986, p.93-5
3. **Hunter, L.** Steps Toward building a Dynamic Memory. *Proceedings of the Third International Workshop in Machine Learning*, Skytop, PA, June 1986, p.70-74, Morgan Kaufmann Associates, San Mateo, CA
4. Collins, G., **Hunter, L.**, Schank, RC. Transcending Inductive Category Formation in Learning, *Behavioral and Brain Sciences*, 9(4):639-686, December 1986.
5. **Hunter, L.** and Silbert, J. Progress Report on IVY: A Learning System for Information Retrieval in Pathology, *Proceedings of the Artificial Intelligence and Medicine Workshop*, Seattle WA, 1987.
6. **Hunter, L.** Knowledge Acquisition Planning. *Third Knowledge Acquisition for Knowledge Based Systems Workshop*, Banff, Alberta, Canada, November, 1988 (Winner, best student paper prize)
7. **Hunter, L.** Artificial Neural Networks as Theories of Mind. *Proceedings of First Annual Conference of the International Neural Network Society*, Boston MA, September, 1988, IEEE Computer Society Press, Los Alamitos, CA.
8. **Hunter, L.** Explanation Based Discovery. *Proceedings of the AAAI Symposium on Explanation Based Learning*, Stanford, CA, March 1988, pp. 2-7.
9. **Hunter, L.**, Some Memory, but No Mind: A response to Smolensky's On the Proper Treatment of Connectionism. *Behavioral and Brain Sciences*, 11(1), March 1988
10. **Hunter, L.** Estimating Human Cognitive Capacities *Cognitive Science*, 12(2):257-261, April-June 1988
11. **Hunter, L.** Planning to Learn, *The Proceedings of The Twelfth Annual Conference of the Cognitive Science Society*, Boston, MA., July 1990, pp. 26-34, Lawrence Erlbaum Associates, Hillsdale, NJ.
12. **Hunter, L.** Knowledge Acquisition Planning for Inference from Large Datasets, *The Proceedings of The Twenty Third Annual Hawaii International Conference on System Sciences, Kona, HI. vol. 2, Software track*, pp. 35-44. IEEE Press, 1990.

13. **Hunter, L.** & Ram, A. The Use of Explicit Goals for Knowledge to Guide Inference and Learning, *Proceedings of the Eighth International Workshop on Machine Learning*, Chicago, IL, June 1991, pp. 265-269, Morgan Kaufmann, San Mateo, CA.
14. **Hunter, L.** Applying Bayesian Classification to Protein Structure, *Proceedings of the Seventh Conference on Artificial Intelligence Applications*, vol. 1. Los Alamitos, CA: IEEE Computer Society Press. Feb. 1991; 10-16.
15. **Hunter, L.** Artificial Intelligence and Molecular Biology, *AI Magazine* 11(5):27-36, 1991 Supplement.
16. **Hunter, L.** Bayesian Classification of Protein Structure Fragments, *The Proceedings of The Twenty Fourth Annual Hawaii International Conference on System Sciences; vol. 1.* Los Alamitos, CA: IEEE Computer Society Press. Jan. 1991; 595-604
17. **Hunter, L.**, Harris, N. & States, DJ. Megaclassification: Discovering Motifs in Massive Datastreams, *Proceedings of the Tenth National Conference on Artificial Intelligence*, pp. 837-842, 1992, AAAI Press, Menlo Park, CA.
18. **Hunter, L.**, Harris, N. & States, DJ. Efficient Classification of Massive, Unsegmented Datastreams, *Proceedings of the Ninth International Workshop on Machine Learning*, pp. 224-233, 1992, Morgan Kaufmann Associates, San Mateo, CA.
19. **Hunter, L.** & States, DJ., Bayesian Classification of Protein Structure, *IEEE Expert*, 7(4):67-75, 1992.
20. **Hunter, L.** Knowledge Acquisition Planning: Using Multiple Sources of Knowledge to Answer Questions in Biomedicine, *Mathematical and Computer Modeling*, 16(6/7):79-91, 1992.
21. **Hunter, L.** & Ram, A., Goals for Learning and Understanding. *Journal of Applied Intelligence*. 2(1):47-73, 1992.
22. **Hunter, L.** AI and Grand Challenges in Biotechnology Computing, *Proceedings of the 13th International Joint Conference on Artificial Intelligence*, Morgan Kaufman, San Mateo, CA, Vol. 2, pp. 1677-1683, 1993.
23. Harris, N., **Hunter, L.** & States, DJ. ClassX: A Tool for Browsing Protein Sequence Megaclassifications, *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, vol. 1, Los Alamitos, CA: IEEE Computer Society Press, Jan 1993; pp 554-563.
24. **Hunter, L.** & Klein, T. Finding Relevant Biomolecular Features, in Hunter, et al., (eds). *Proceedings of the First International Conference on Intelligent Systems for Molecular Biology*, AAAI Press, Menlo Park CA, 1993, pp. 190-197.
25. States, DJ, Harris, N., **Hunter, L.** Computationally Efficient Cluster Representation in Molecular Sequence Megaclassification, in Hunter, et al (eds). *Proceedings of the First International Conference on Intelligent Systems for Molecular Biology*, AAAI Press, Menlo Park CA, 1993, pp. 387-394.

26. Dowe, D., Allison, L., Dix, T., **Hunter, L.**, Wallace, CS., & Edgoose, T., Circular Clustering of Protein Dihedral Angles by Minimum Message Length, *Pacific Symposium on Biocomputing* (1):242-255. World Scientific Press, 1996.
27. **Hunter, L.** Coevolution Learning: Synergistic Evolution of Learning Agents and Problem Representations, *Proceedings of 1996 Multistrategy Learning Conference*, pp. 85-94, Menlo Park, CA: AAAI Press, 1996.
28. Abramson. M. Z. and **Hunter, L.** Classification using Cultural Coevolution and Genetic Programming. *Genetic Programming: Proc. of the First Annual Conf.* 1996, pp. 249-254, MIT Press, 1996
29. Krichmar, JL, Olds, JL. & **Hunter, L.** Qualitative Neurobiology, *Proceedings of the 1997 Workshop on Qualitative Reasoning*, pp. 265-276, 1997
30. Krichmar, JL, Ascoli, G.A., Olds, J.L. and **Hunter, L.** A model of cerebellar saccadic motor learning using qualitative reasoning, *Biological and Artificial Computation: From Neuroscience to Technology* 1240: 133-145 (1997)
31. Shah, I. & **Hunter, L.** Functional Classification of Enzymes by Sequence Alignment, *Intelligent Systems for Molecular Biology*, 5:276-83 , Menlo Park, CA: AAAI Press 1997
32. Zeeberg, B.R. & **Hunter, L.** A Hidden Markov Model Whose Alphabet Is Nucleic Acid Triplet Codons and its Use to Discover Chimerism in Protein Families, *Intelligent Systems for Molecular Biology* 5:153-156 , Menlo Park, CA: AAAI Press, 1997
33. Zeeberg, B.R. & **Hunter, L.** Characterization of a Family of Chimeric Proteins, the Amino Acyl tRNA Synthetases, by Determining Differential Codon Usage using One and Two State HMMs. *Mathematical Modeling and Scientific Computation*, 9(1):58-67, 1998.
34. Shah, I. & **Hunter, L.** Visualization Based on the Enzyme Commission Nomenclature. *Pacific Symposium on Biocomputing* 3:142-152 (1998).
35. Shah, I. & **Hunter, L.** Identification of divergent functions in homologous proteins by induction over conserved modules. *Intelligent Systems for Molecular Biology* 6:157-64 (1998)
36. Tanabe L, Scherf U, Smith LH, Lee JK, **Hunter L**, Weinstein JN., MedMiner: an Internet text-mining tool for biomedical information, with application to gene expression profiling. *Biotechniques*. 1999 Dec;27(6):1210-4, 1216-7.
37. Tanabe, L., Rindflesch, T.C., Weinstein, J.N., **Hunter, L.**, Edgar: Extraction of Drugs, Genes and Relations from the Biomedical Literature, *Pacific Symposium on Biocomputing*, 5:514-525, 2000
38. Shah, I. & **Hunter, L.** Visual Management of Large Scale Data Mining Projects., *Pacific Symp. on Biocomputing*, 5:275-287, 2000
39. **Hunter, L.**, Taylor, R., Leach, S., & Simon, R., GEST: A Gene Expression Search Tool Based on a Novel Bayesian Similarity Metric, *Bioinformatics*. 2001 Jun;17 Suppl 1:S115-S122.

40. Edgerton, ME, Taylor, R., Powell, JI., **Hunter, L.**, Simon, R., and Liu, E., A Bioinformatics Tool to Mine Sequences for Microarray Studies of Mouse Models of Oncogenesis, *Bioinformatics*, 18(5):774-775. 2002
41. Cohen, K.B., Dolbey, A., Acquaaah-Mensah, G. and **Hunter, L.** Contrast and variability in gene names *Proceedings of the Workshop on Natural Language Processing in the Biomedical Domain*, Philadelphia, July 2002, pp. 14-20 Association for Computational Linguistics.
42. **Hunter, L.** Ontologies for Programs, Not People. *Genome Biology* 2002, 3(6):interactions1002.1-1002
43. Phang, T.L, Neville, M.C., Rudolph, M. and **Hunter, L.** Trajectory clustering: A non-parametric method for grouping gene expression time courses, with applications to mammary development., *Pacific Symposium on Biocomputing* 2003, 8:351-362.
44. Brown, E.B., Dolbey, A., **Hunter, L.** IBM Research and the University of Colorado TREC 2003 Genomics Track. *Proceedings of the Twelfth Text Retrieval Conference (TREC 2003)*:pp. 268-275, National Institute of Standards and Technology.
45. Shenkar, R., Elliott, J.P., Diener, K., Gault, J., Hu, L.J., Cohrs, R.J., Phang, T., **Hunter, L.**, Breeze, R.E., and Awad, I.A., Gene Expression in Human Cerebral Vascular Malformations, *Neurosurgery*, 52(2):465-478 2003
46. Witzmann, F., Li, J., Strother, W. McBride, W., **Hunter, L.**, Crabb, D., Lumeng, L., Li, T.K. Innate Differences in Protein Expression in the Nucleus Accumbens and Hippocampus of Inbred Alcohol-Preferring and -Nonpreferring Rats. *Proteomics* 2003 Jul;3(7):1335-44.
47. Rudolph, M., McManaman, J., **Hunter, L.**, Phang, T, Neville, M Initiation of Lactation in the Murine Mammary Gland: Temporal analysis of a complex biological switch with expression profiling and trajectory clustering. *J Mammary Gland Biol Neoplasia*. 2003 Jul;8(3):287-307
48. Ogren, P.V., Cohen, K.B. , Acquaaah-Mensah, G.K., Eberlein, J. **Hunter, L.** The Compositional Structure of Gene Ontology Terms *Pacific Symposium on Biocomputing* 2004, 9:214-225
49. **Hunter, L.** Life and Its Molecules: A Brief Introduction, *AI Magazine*, 25(1): 9-22, Spring 2004
50. Hong, M., Kairmpour-Fard, A., Russell, S. and **Hunter, L.**, Integrated Term Weighting, Visualization, and User Interface Development for Bioinformation Retrieval. *AI, Simulation and Planning in Highly Autonomous Systems Conference (AIS 2004)*. Reprinted in *Springer-Verlag Lecture Notes in Computer Science* 3397: 673-682 (2005)
51. Russell, S.A., Old, W., Resing, K.A.. and **Hunter, L.** Proteomic Informatics, *International Review of Neurobiology*, 61:129-157, 2004
52. Lu, Z. and **Hunter, L.** GO Molecular Function Terms are Predictive of Subcellular Localization, *Pacific Symposium on Biocomputing* 2005 10:151-161

53. Ogren, P., Cohen, K.B. and **Hunter, L.** Implications of compositionality in the gene ontology for its curation and usage, *Pacific Symposium on Biocomputing* 2005, 10:174-185
54. Kinoshita, S., Cohen K.B., Ogren, P.V., **Hunter, L.** BioCreAtIvE Task1A: Entity Identification with a Stochastic Tagger. *BMC Bioinformatics* 2005, 6(Suppl 1):S4 (24 May 2005).
55. Coors, ME. **Hunter, L.** Evaluation of Genetic Enhancement: Will Human Wisdom Properly Acknowledge the Value of Evolution? *American Journal of Bioethics*, 2005 Summer;5(3):21-2; discussion W4-9.
56. Cohen, KB, Fox, LM, Ogren, PV & **Hunter, L.** Corpus design for biomedical natural language processing. *Proc. Of the ACL-ISMB workshop Linking Biological Literature, Ontologies and Databases: Mining Biological Semantics* pp. 38-45, Association for Computational Linguistics. June 2005
57. Hu, X., Friedman, D., Hill, S., Caprioli, R., Kobilka, B, **Hunter, L.**, Limbird, L. Proteomic Exploration of Pancreatic Islets in Mice Null for the a2A adrenergic receptor. *J. Mol. Endocrin*, 2005 Aug 35(1):73-88.
58. Cohen, KB, Fox, LM., Ogren PV, **Hunter, L.** Empirical data on corpus design and usage in biomedical natural language processing, *Proc. Am. Medical Informatics Assoc.* Pp. 156-160, 2005
59. Caporaso, JG, Baumgartner WA., Cohen KB, Johnson, HL, Paquette J., and **Hunter, L.** Concept recognition and the TREC Genomics tasks. In: *The Fourteenth Text REtrieval Conference Proceedings*, 2005.
60. Lu, Z. Cohen, KB, **Hunter L.** Finding GeneRIFs via Gene Ontology Annotations, *Pacific Symposium on Biocomputing* 2006 11:52-63
61. Johnson, HL, Cohen, KB, Baumgartner, WA, Lu, Z, Bada, M, Kester, T, Kim, H, **Hunter L.** Evaluation of Lexical Methods for Detecting Relationships Between Concepts from Multiple Ontologies, *Pacific Symposium on Biocomputing* 2006 11:28-39
62. Johnson, HL, Baumgartner WA., Krallinger, M, Cohen KB, **Hunter L.** Refactoring Corpora *Proceedings of the HLT-NAACL BioNLP Workshop on Linking Natural Language and Biology* June 2006, pp. 116-117 <http://www.aclweb.org/anthology/W/W06/W06-1720>
63. **Hunter, L.** Cohen, KB Biomedical Language Processing: What's Beyond PubMed? *Molecular Cell* 21(5):589-594 March 3, 2006.
64. Lowes BD, Zolty R, Minobe WA, Robertson AD, Leach S, **Hunter L.** Bristow MR . Serial gene expression profiling in the intact human heart, *Journal Of Heart And Lung Transplantation* 25 (5): 579-588 May 2006
65. Bada, M and **Hunter, L.** Enrichment of OBO Ontologies. *Journal of Biomedical Informatics* Informatics 2006 Jul 26; 40(3):300-15
66. Cohen, KB and **Hunter, L.** A critical review of PASBio's argument structures for biomedical verbs *BMC Bioinformatics* 2006, 7(Suppl 3):S5

67. Guzelian J, Barwick JL, **Hunter L**, Phang TL, Quattrochi LC, Guzelian PS. Identification of genes controlled by the pregnane X receptor by microarray analysis of mRNAs from pregnenolone 16alpha-carbonitrile-treated rats. *Toxicol Sci.* 2006 Dec;94(2):379-87.
68. Lu, Z, Cohen, KB and **Hunter, L**. Generif Quality Assurance As Summary Revision *Pacific Symposuim on Biocomputing 2007*: 269-280
69. Leach, SM, Gabow, A, **Hunter, L** and Goldberg, D. Assessing And Combining Reliability Of Protein Interaction Sources. *Pacific Symposuim on Biocomputing*, 2007: 433-444
70. Johnson, HL, Cohen KB and **Hunter, L**. A Fault Model For Ontology Alignment And Mapping Systems. *Pacific Symposuim on Biocomputing 2007*: 233-244
71. Serkova, NJ, Zhang Y, Coatney JL, **Hunter L**, Wachs ME, Niemann CU, Mandell MS. Early Detection of Graft Failure Using the Blood Metabolic Profile of a Liver Recipient. *Transplantation* 2007 Feb 27;83(4):517-21.
72. Baumgartner WA Jr., Lu, Z., Johnson, HL., Caporaso, JG., Paquette, J, Lindemann, A., White, EK., Medvedeva, O., Cohen, KB., **Hunter, L.**, An integrated approach to concept recognition in biomedical text, *Proceedings of the BioCreative II Challenge Workshop*, April 2007
73. Baumgartner WA Jr, Cohen KB, Fox LM, Acquaah-Mensah G, **Hunter L**. Manual curation is not sufficient for annotation of genomic databases. *Bioinformatics.* 2007 Jul 1;23(13):i41-8. [Reprinted in the International Medical Informatics Association's *Yearbook of Medical Informatics* 2008.]
74. Caporaso JG, Baumgartner WA Jr, Randolph DA, Cohen KB, **Hunter L**. MutationFinder: a high-performance system for extracting point mutation mentions from text. *Bioinformatics.* 2007 Jul 15;23(14):1862-5
75. Bhave SV, Hornbaker C, Phang TL, Saba L, Lapadat R, Kechris K, Gaydos J, McGoldrick D, Dolbey A, Leach S, Soriano B, Ellington A, Ellington E, Jones K, Mangion J, Belknap JK, Williams RW, **Hunter LE**, Hoffman PL, Tabakoff B. The PhenoGen Informatics website: tools for analyses of complex traits. *BMC Genet.* 2007 Aug 30;8(1):59 <http://www.biomedcentral.com/1471-2156/8/59>
76. Johnson, HL, Baumgartner, WA. Jr., Krallinger, M., Cohen, KB, **Hunter, L.**, Corpus Refactoring: A Feasibility Study. *Journal of Biomedical Discovery and Collaboration* 2007, 2:4 (13 September 2007). <http://www.j-biomed-discovery.com/content/2/1/4>
77. Karimpour-Fard, A., Detweiler, CS., Erickson, KD, **Hunter, L.**, Gill, RT., Cross-Species Cluster Co-Conservation: A new method for generating protein interaction networks. *Genome Biology* 8(9):R185 (September 2007)
78. Karimpour-Fard A, **Hunter L**, Gill RT. Investigation of factors affecting prediction of protein-protein interaction networks by phylogenetic profiling. *BMC Genomics.* 2007 Oct 29;8(1):393
79. Caporaso, JG, Baumgartner, WA Jr., Randolph, DA, Cohen, KB, **Hunter, L.** Rapid Pattern Development for Concept Recognition Systems: Applications to Point

- Mutations, *Journal of Bioinformatics and Computational Biology*. 2007
Dec;5(6):1233-59
80. Glueck, D, Muller, KE, Karimpour-Fard, A, **Hunter, L.**, Expected Power for the False Discovery Rate with Independence. *Communications in Statistics - Theory and Methods*, Volume 37, Issue 12 January 2008 , pages 1855 - 1866.
 81. Baumgartner WA Jr., Cohen, KB and **Hunter, L.** An open-source framework for large-scale, flexible evaluation of biomedical text mining systems. *Journal of Biomedical Discovery and Collaboration*. 2008, 3:1 doi:10.1186/1747-5333-3-1
 82. Cohen, KB & **Hunter, L.** Getting started in text mining, *PLoS Computational Biology*, 2008 4(1): e20. doi:10.1371/journal.pcbi.0040020.
 83. Caporaso, JG, Deshpande, N, Fink, JL, Bourne, PE, Kohen, KB, **Hunter, L.** Intrinsic evaluation of text mining tools may not predict performance on realistic tasks. *Pacific Symposium on Biocomputing*, 13:640-651(2008)
 84. Baumgartner WA Jr., Lu, Z., Johnson, HL., Caporaso, JG., Paquette, J, Lindemann, A., White, EK., Medvedeva, O., Cohen, KB., **Hunter, L.**, Concept Recognition for Extracting Protein Interactions from Biomedical Text, *Genome Biology*, 2008, 9 (Suppl 2):S9
 85. Leitner, F, Krallinger, M, Rodriguez-Penagos, C., Hakenberg, J., Plake, C., Kuo, C-J., Hsu, C-N, Tsai, R.T-H., Hung, H-C., Lau, W.W., Johnson, C.A., Saetre, R., Yoshida, K., Chen, Y.H., Kim, S., Shin, S-Y., Zhang, B-T., Baumgartner, W.A. Jr., **Hunter, L.** Haddow, B., Matthews, M., Wang, X., Ruch, P., Ehrler, F., Ozgur, Z., Erkan, G., Radev, D.R., Krauthammer, M., Luong, T.B., Hoffman, R., Sander, C., Valencia, A., Introducing Meta-Services for Biomedical Information Extraction. *Genome Biology*, 2008, 9(Suppl 2):S6.
 86. **Hunter, L.**, Lu, Z., Firby, J., Baumgartner, WA. Jr., Johnson, HL, Ogren, PV, Cohen, KB, OpenDMAP: An open-source, ontology-driven concept analysis engine, with applications to capturing knowledge regarding protein transport, protein interactions and cell-specific gene expression. *BMC Bioinformatics*, 2008 Jan 31;9(1):78.
 87. Harvell DM, Spoelstra NS, Singh M, McManaman JL, Finlayson C, Phang T, Trapp S, **Hunter L**, Dye WW, Borges VF, Elias A, Horwitz KB, Richer JK. Molecular signatures of neoadjuvant endocrine therapy for breast cancer: characteristics of response or intrinsic resistance. *Breast Cancer Res Treat*. 2008 Dec;112(3):475-88.
 88. Gabow, AP, Leach SM, Baumgartner, WA Jr., **Hunter, L.**, Goldberg, DS. Improving Protein Function Prediction methods with Integrated Literature Data. *BMC Bioinformatics*, 2008 9:198.
 89. Bethard, S., Lu, Z., Martin, JH., **Hunter L.** Semantic Role Labeling for Protein Transport Predicates. *BMC Bioinformatics*, 2008, 9:277.
 90. Bada, M., **Hunter, L.**, Identification of OBO Nonalignments and Its Implications for OBO Enrichment, *Bioinformatics*, 2008 24(12):1448-1455.

91. Glueck, DH., Mandel, J., Karimpour-Fard, A., **Hunter, L.**, Muller, KE. Exact Calculations of Average Power for the Benjamini-Hochberg Procedure, *The International Journal of Biostatistics*, 2008 4(1):11.
92. Glueck, DH., Karimpour-Fard, A., Mandel, J., **Hunter, L.**, Muller, KE. Fast computation by block permanents of cumulative distribution functions of order statistics from several populations. *Communications in Statistics - Theory and Methods*, 37(18):2815-2824 January 2008.
93. Karimpour-Fard, A., Leach, SM, **Hunter, L.**, Gill, R. The topology of the bacterial co-conserved protein network and its implications for predicting protein function, *BMC Genomics*, 2008, 9:313.
94. Cohen KB, Palmer M, **Hunter L** Nominalization and Alternations in Biomedical Language. *PLoS ONE* 2008 3(9): e3158 doi:10.1371/journal.pone.0003158
95. Karimpour-Fard, A., Leach, S.M., Gill, R.T., **Hunter, L.** Predicting Protein Linkages in Bacteria: Which Method is Best Depends on Task. *BMC Bioinformatics* 2008, 9:397 doi:10.1186/1471-2105-9-397
96. Baumgartner WA Jr, Lu Z, Johnson HL, Caporaso JG, Paquette J, Lindemann A, White EK, Medvedeva O, Cohen KB, **Hunter L.** Concept recognition for extracting protein interaction relations from biomedical text. *Genome Biol.* 2008;9 Suppl 2:S9. Epub 2008 Sep 1.
97. Yen CY, Meyer-Arendt K, Eichelberger B, Sun S, Houel S, Old WM, Knight R, Ahn NG, **Hunter LE**, Resing KA. A simulated MS/MS library for spectrum-to-spectrum searching in large-scale identification of proteins. *Mol Cell Proteomics.* 2008 Dec 22.
98. Caporaso, JG, Smit, S., Easton, BC, **Hunter, L.**, Huttley, GA., Knight, R. Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. *BMC Evolutionary Biology*, 2008 Dec 3;8(1):327.
99. Tipney, HJ, Leach, SM, Feng, W., Spritz, R., Williams, T., **Hunter, L.** Leveraging existing biological knowledge in the identification of candidate genes for facial dysmorphology. *BMC Bioinformatics* 2009, 10(Suppl 2):S12
100. Leach, SM, Tipney, H, Feng, W., Baumgartner, W Jr., Kasliwal, P., Schuyler, R., Williams, T, Spritz, R., **Hunter, L.** Biomedical Discovery Acceleration, with Applications to Craniofacial Development. *PLoS Computational Biology*, 5(3): e1000215. 2009
101. Tamburini, BA, Trapp, S, Phang, TL, Schappa, JT, **Hunter, L.**, Modiano, JF. Gene Expression Profiles of Sporadic Canine Hemangiosarcomas are Uniquely Associated with Breed. *PLoS One* 4(5): e5549. 2009
102. Verspoor, K., Dvorkin D., Cohen, KB., **Hunter, L.** Ontology Quality Assurance through analysis of term transformations. *Bioinformatics* 2009 June 15; 25(12):177-84
103. Kano, Y., Baumgartner, WA Jr., McCrohon, L, Ananiadou, S., Cohen, KB, **Hunter, L.**, Tsujii, J. U-Compare: share and compare text mining tools with UIMA. *Bioinformatics*, 2009 Aug 1 25(15):1997-8

104. Cohen, KB., Verspoor, K., Johnson, HL., Roeder, C., Ogren, PV., Baumgartner, WA. Jr., White, E., Tipney, H., **Hunter, L.** High-precision biological event extraction with a concept recognizer. *Proceedings of the Workshop on BioNLP: Shared Task*, pp 50-58, Association for Computational Linguistics.
<http://aclweb.org/anthology-new/W/W09/W09-1407.pdf>
105. Verspoor, K., Baumgartner, W., Roeder, C., **Hunter, L.** Abstracting the Types away from a UIMA Type System. *Proceedings of the 2009 German Society for Computational Linguistics and Language Technology Conference*. Reprinted in Chiarcos, C., Eckhart de Castilho, Stede, M. (eds), *Von der Form zur Bedeutung: Text automatisch verarbeiten / From Form to Meaning: Processing Texts Automatically*. Tuebingen: Narr, 2009, p. 249-256.
106. Verspoor, K., Cohen, KB., Hunter, L. Textual characteristics of traditional and Open Access scientific journals are similar, *BMC Bioinformatics* 2009, 10:183.
107. Coulet A, Shah N, **Hunter L**, Barral C, Altman RB. Extraction of genotype-phenotype-drug relationships from text: from entity recognition to bioinformatics application. *Pac Symp Biocomput.* 2010:485-7.
108. Cohen, K.B., Roeder, C., Baumgartner Jr., W.A., **Hunter, L.** and Verspoor, K. Test suite design for biomedical ontology concept recognition systems. *Proceedings of the Seventh conference on International Language Resources and Evaluation (LREC'10)* pp. 441-446, May 2010
109. Roeder C, Jonquet C, Shah NH, Baumgartner WA Jr, Verspoor K, **Hunter L.** A UIMA wrapper for the NCBO annotator. *Bioinformatics.* 2010 Jul 15;26(14):1800-1. Epub 2010 May 26.
110. Verspoor, K., Roeder, C., Johnson, H., Cohen, K.B., Baumgartner, W.A., **Hunter, L.** Exploring species-based strategies for gene normalization. *IEEE Transactions on Computational Biology and Bioinformatics.* 7(3):462-471 July-September 2010
111. Karimpour-Fard, A., Dumas, L., Phang, T., Sikela, JM, **Hunter, L.** A Survey of analysis software for array-comparative genomic hybridization studies to detect copy number variation. *Human Genomics* 4(6) 421-7, August 2010
112. Cohen KB., Johnson HL., Verspoor K., Roeder C., **Hunter L.** The structural and content aspects of abstracts versus bodies of full text journal articles are different. *BMC Bioinformatics*, 11:492 September 2010.
113. Tamburini, BA., Phang, TL., Fosmire, SP., Scott, MC., Trapp, SC., Duckett, MM., Robinson, SR., Slansky, JE., Sharkey, LC., Cutter, GR., Wojcieszyn, JW., Bellgrau, D., Gemmill, RM., **Hunter, LE.**, Modiano, JF. Gene expression profiling identifies inflammation and angiogenesis as distinguishing features of canine hemangiosarcoma. *BMC Cancer* 2010 10:619 doi:10.1186/1471-2407-10-619
114. Galligan JJ, Fritz KS, Tipney H, Smathers RL, Roede JR, Shearn CT, **Hunter LE**, Petersen DR. Profiling Impaired Hepatic Endoplasmic Reticulum Glycosylation as a Consequence of Ethanol Ingestion. *J. Proteome Research*, 10(4):1837-1847 Apr 2011

115. Epperson LE, Karimpour-Fard A, **Hunter LE**, Martin SL. Metabolic Cycles in a Circannual Hibernator. *Physiol Genomics*. 2011 May 3.
116. Scott MC, Sarver AL, Gavin KJ, Thayanithy V, Getzy DM, Newman RA, Cutter GR, Lindblad-Toh K, Kisseberth WC, **Hunter LE**, Subramanian S, Breen M, Modiano JF. Molecular subtypes of osteosarcoma identified by reducing tumor heterogeneity through an interspecies comparative approach. *Bone*. 2011 May 15
117. Kano, Y., Miwa, M., Cohen, KB., **Hunter, L.**, Ananiadou, S., Tsujii, J. U-Compare: a modular NLP workflow construction and evaluation system. *IBM Journal of Research and Development* 55 (3) 11:1-11:10, May-June 2011.
118. Cohen, K.B.; Verspoor, K.; Johnson, H.L.; Roeder, C.; Ogren, P.V.; Baumgartner Jr., W.A.; White, E.; Tipney, H.; and **Hunter, L.E.** High-precision biological event extraction: Effects of system and data. *Computational Intelligence* 27(4):681-701. Nov 2011
119. Hindle AG, Karimpour-Far A, Epperson LE, **Hunter LE**, Martin SL. Skeletal muscle proteomics: carbohydrate metabolism oscillates with seasonal and torpor-arousal physiology of hibernation. *Am J Physiol Regul Integr Comp Physiol*. 2011 Nov; 301(5):R1440-52
120. Grabek KR, Karimpour-Fard A, Epperson LE, Hindle A, **Hunter LE**, Martin SL. Multistate proteomics analysis reveals novel strategies used by a hibernator to precondition the heart and conserve ATP for winter heterothermy. *Physiol Genomics*. 2011 Nov 21; 43(22):1263-75.
121. Kano Y, Björne J, Ginter F, Salakoski T, Buyko E, Hahn U, Cohen KB, Verspoor K, Roeder C, **Hunter LE**, Kilicoglu H, Bergler S, Van Landeghem S, Van Parys T, Van de Peer Y, Miwa M, Ananiadou S, Neves M, Pascual-Montano A, Özgür A, Radev DR, Riedel S, Sætre R, Chun HW, Kim JD, Pyysalo S, Ohta T, Tsujii J. U-Compare bio-event meta-service: compatible BioNLP event extraction services. *BMC Bioinformatics*. 2011 Dec 18; 12:481
122. Cohen KB, Christiansen T, Hunter LE. Parenthetically speaking: classifying the contents of parentheses for text mining. *AMIA Annu Symp Proc*. 2011; 2011:267-72.
123. Galligan JJ, Smathers RL, Fritz KS, Epperson LE, **Hunter LE**, Petersen DR. Protein carbonylation in a murine model for early alcoholic liver disease. *Chem Res Toxicol*. 2012 May 21 ;25(5):1012-21.
124. Rehrer CW, Karimpour-Fard A, Hernandez TL, Law CK, Stob NR, **Hunter LE**, Eckel RH. Regional Differences in Subcutaneous Adipose Tissue Gene Expression. *Obesity* (Silver Spring). 2012 May 4
125. Kulikowski CA, Shortliffe EH, Currie LM, Elkin PL, **Hunter LE**, Johnson TR, Kalet IJ, Lenert LA, Musen MA, Ozbolt JG, Smith JW, Tarczy-Hornoch PZ, Williamson JJ. AMIA Board white paper: definition of biomedical informatics and specification of core competencies for graduate education in the discipline. *J Am Med Inform Assoc*. 2012 Jun 21.
126. Jani A, Orlicky DJ, Karimpour-Fard A, Epperson LE, Russell RL, **Hunter LE**, Martin SL. Kidney proteome changes provide evidence for a dynamic metabolism

- and regional redistribution of plasma proteins during torpor-arousal cycles of hibernation. *Physiol Genomics*. 2012 Jul 15;44(14):717-27
127. Verspoor, K.M.; Cohen, K.B.; Lanfranchi, A.; Warner, C.; Johnson, H.L.; Roeder, C.; Choi, J.D.; Funk, C.; Malenkiy, Y.; Eckert, M.; Xue, N.; Baumgartner Jr, W.A.; Bada, M.; Palmer, M.; **Hunter, L.E.** A corpus of full-text journal articles is a robust evaluation tool for revealing differences in performance of biomedical natural language processing tools. *BMC Bioinformatics*, 2012 Aug 17;13(1):207.
 128. Bada, M., Eckert, M., Evans, D., Garcia, K., Shipley, K., Sitnikov, D., Baumgartner Jr., W.A., Cohen, K.B., Verspoor, K.M., Blake, J., **Hunter, L.E.** Concept Annotation in the CRAFT Corpus. *BMC Bioinformatics*, 2012 Jul 9;13:161.
 129. Cohen, KB., **Hunter, LE.**, Palmer, M. Assessment of software testing and quality assurance in natural language processing applications and a linguistically inspired approach to improving it. *Joint workshops on Intelligent Methods for Software System Engineering* Aug 2012
 130. **Hunter LE**, Hopfer C, Terry SF, Coors ME. Reporting actionable research results: shared secrets can save lives. *Sci Transl Med*. 2012 Jul 18; 4(143):143cm8
 131. Sarkar SA, Lee CE, Tipney H, Karimpour-Fard A, Dinella JD, Juhl K, Walters JA, Hutton JC, **Hunter LE** Synergizing Genomic Analysis with Biological Knowledge to Identify Novel Genes in Pancreatic Development. *Pancreas*. 2012 Aug;41(6):962-9.
 132. **Hunter L.** Computational challenges of mass phenotyping. *Pac Symp Biocomput*. 2013:454-5.
 133. Frantz AM, Sarver AL, Ito D, Phang TL, Karimpour-Fard A, Scott MC, Valli VE, Lindblad-Toh K, Burgess KE, Husbands BD, Henson MS, Borgatti A, Kisseberth WC, **Hunter LE**, Breen M, O'Brien TD, Modiano JF. Molecular Profiling Reveals Prognostically Significant Subtypes of Canine Lymphoma. *Vet Pathol*. 2013 Feb 22. DOI: 10.1177/0300985812465325
 134. Liu H, **Hunter LE**, Kešelj V, Verspoor K. Approximate subgraph matching-based literature mining for biomedical events and relations. *PLoS One*. 2013 Apr 17;8(4):e60954.
 135. Yarborough, M., **Hunter, LE.** Teaching Research Ethics Better: Focus on Excellent Science, Not Bad Scientists. *Clinical and Translational Science* 6(3):201-203 June 2013
 136. Livingston KM, Bada M, **Hunter LE**, Verspoor K. Representing annotation compositionality and provenance for the Semantic Web. *J Biomed Semantics*. 2013 Nov 22;4:38. doi: 10.1186/2041-1480-4-38. PMC4129183
 137. Funk CS, **Hunter LE**, Cohen KB. Combining heterogeneous data for prediction of disease related and pharmacogenes. *Pac Symp Biocomput*. 2014:328-39. PMC3910248
 138. Funk C, Baumgartner W Jr, Garcia B, Roeder C, Bada M, Cohen KB, **Hunter LE**, Verspoor K. Large-scale biomedical concept recognition: an evaluation of

- current automatic annotators and their parameters. *BMC Bioinformatics*. 2014 Feb 26;15(1):59.
139. LM Fox, LA Williams, **L Hunter**, C Roeder (2014) Negotiating a Text Mining License for Faculty Researchers *Information Technology and Libraries* 33(3)5-21
 140. Hinterberg MA, Kao DP, Bristow MR, **Hunter LE**, Port JD, Görg C. Peax: interactive visual analysis and exploration of complex clinical phenotype and gene expression association. *Pac Symp Biocomput*. 2015;20:419-30.
 141. Pattin KA, Greene AC, Altman RB, Cohen KB, Wethington E, Görg C, **Hunter LE**, Muse SV, Radivojac P, Moore JH. Training the next generation of quantitative biologists in the era of big data. *Pac Symp Biocomput*. 2015;20:488-92
 142. Vehlow C, Kao DP, Bristow MR, **Hunter LE**, Weiskopf D, Görg C. Visual analysis of biological data-knowledge networks. *BMC Bioinformatics*. 2015 Apr 29;16:135.
 143. Livingston KM, Bada M, Baumgartner WA Jr, **Hunter LE**. KaBOB: ontology-based semantic integration of biomedical databases. *BMC Bioinformatics*. 2015 Apr 23;16:126.
 144. Karimpour-Fard A, Epperson LE, **Hunter LE**. A survey of computational tools for downstream analysis of proteomic and other omic datasets. *Hum Genomics*. 2015 Oct 28;9:28. doi: 10.1186/s40246-015-0050-2. Review. PMID: 26510531
 145. Moore JH, Jennings SF, Greene CS, **Hunter LE**, Perkins AD, Williams-Devane C, Wunsch DC, Zhao Z, Huang X. NO-BOUNDARY THINKING IN BIOINFORMATICS. *Pac Symp Biocomput*. 2016;22:646-648. PubMed PMID: 27897015
 146. Eberlein J, Davenport B, Nguyen T, Victorino F, Haist K, Jhun K, Karimpour-Fard A, **Hunter L**, Kedl R, Clambey ET, Homann D. Aging promotes acquisition of naive-like CD8 memory T cell traits and enhanced functionalities. *J Clin Invest*. 2016 Oct 3;126(10):3942-3960. PubMed PMID: 27617858
 147. Funk CS, Cohen KB, Hunter LE, Verspoor KM. Gene Ontology synonym generation rules lead to increased performance in biomedical concept recognition. *J Biomed Semantics*. 2016 Sep 9;7:52. PubMed PMID: 27613112

Books

148. Editor, *Artificial Intelligence and Molecular Biology*, AAAI/MIT Press, 1993. Now available free online <http://www.aaai.org/AITopics/classic/hunter.html>
149. *The Processes of Life*, MIT Press, 2009.

Proceedings Volumes Edited:

150. **Hunter, L.**, Mudge, T., Milutinovic, V. (eds) *Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences*, vol. 1: Computer Architecture and Biotechnology Computing, Los Alamitos, CA: IEEE Computer Society Press, Jan 1993

151. **Hunter, L.**, Shavlik, J. & Searls, DB (eds) *Proceedings of the First International Conference on Intelligent Systems for Molecular Biology*, Menlo Park, CA: AAAI Press, July 1993
152. **Hunter, L.**, (ed) *Twenty-Seventh Annual Hawaii International Conference on System Sciences*, vol. 5: Biotechnology Computing, Los Alamitos, CA: IEEE Computer Society Press, Jan 1994
153. Rawlings, C., Clark, D., Altman, RB, **Hunter, L.**, Lengauer, T., Wodak, S., (eds) *Proceedings of the Third International Conference on Intelligent Systems for Molecular Biology*, Menlo Park, CA: AAAI Press, July 1995
154. States, DJ, Agarwal, P., Gaasterland, T. **Hunter, L.**, Smith, R. (eds) *Proceedings of the Fourth International Conference on Intelligent Systems for Molecular Biology*, Menlo Park, CA: AAAI Press, July 1996
155. **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '96*, Singapore: World Scientific Press, January 1996.
156. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '97*, Singapore: World Scientific Press, January 1997.
157. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '98*, Singapore: World Scientific Press, January 1998.
158. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '99*, Singapore: World Scientific Press, January 1999.
159. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '00*, Singapore: World Scientific Press, January 2000
160. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '01*, Singapore: World Scientific Press, January 2001
161. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '02*, Singapore: World Scientific Press, January 2002
162. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '03*, Singapore: World Scientific Press, January 2003
163. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '04*, Singapore: World Scientific Press, January 2004
164. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '05*, Singapore: World Scientific Press, January 2005
165. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '06*, Singapore: World Scientific Press, January 2006
166. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '07*, Singapore: World Scientific Press, January 2007
167. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '08*, Singapore: World Scientific Press, January 2008
168. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '09*, Singapore: World Scientific Press, January 2009

169. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '10*, Singapore: World Scientific Press, January 2010
170. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '11*, Singapore: World Scientific Press, January 2011
171. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '12*, Singapore: World Scientific Press, January 2012
172. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '13*, Singapore: World Scientific Press, January 2013
173. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '14*, Singapore: World Scientific Press, January 2014
174. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '15*, Singapore: World Scientific Press, January 2015
175. Altman, RB, Dunker AK, **Hunter, L.**, Klein TE, (eds) *Pacific Symposium on Biocomputing '16*, Singapore: World Scientific Press, January 2016

Book Chapters:

176. **Hunter, L.** An Introduction to Molecular Biology for the Computer Scientist, in *Artificial Intelligence and Molecular Biology*, L. Hunter, ed., AAAI Press, 1993.
177. **Hunter, L.** Planning to Learn About Protein Structure, in *Artificial Intelligence and Molecular Biology*, L. Hunter, ed., AAAI Press, 1993.
178. **Hunter, L.** Classifying for Prediction: A Multistrategy Approach to Predicting Protein Structure, in *Machine Learning IV*, ed. by R. Michalski & G. Tegucci, Morgan Kaufmann, 1994.
179. **Hunter, L.**, Ram, A., The Use of Explicit Goals for Knowledge to Guide Inference and Learning, in *Goal-Driven Learning*, ed. by Ashwin Ram and David B. Leake, MIT Press, 1995.
180. **Hunter, L.**, Planning to Learn, in *Goal-Driven Learning*, ed. by Ashwin Ram and David B. Leake, MIT Press, 1995.
181. Krichmar, JL, Ascoli, GA, **Hunter, L.**, Olds, JL. The Qualitative Reasoning Neuron: A New Approach to Modeling in Computational Neuroscience, in *Computational Neuroscience*, James Bower (ed), Plenum Press, NY. 1998
182. **Hunter, L.** & Rule, JB. A New Personal Right for the Information Age, in *Visions for Privacy*, Collin Bennett and Rebecca Grant (eds.) University of Toronto Press, 1999.
183. **Hunter, L.** & Cohen, K.B. Natural Language Processing for Systems Biology, in *Artificial Intelligence Methods and Tools for Systems Biology* W. Dubitzky & F. Azuaje (eds). Springer 2004
184. Russell, S., Old, W., Resing, K. & **Hunter, L.** Proteomic Informatics, in *Human Brain Proteomics*, L. Neuhold (ed). Elsevier, 2004.
185. Kim, H, Kechris, KJ, **Hunter, L.** Mining Discriminative Distance Context of Transcription Factor Binding Sites on ChIP Enriched Regions in *Bioinformatics*

- Research and Applications*, Pan, Y, Narasimhan G, Lu, S, Harrison, RW (eds). Springer 2007
186. Saba, L.M., Hoffman, P.L., **Hunter, L.** and Tabakoff, B. The Marriage of Phenomics and Genetical/Genomics: A Systems Approach to Complex Trait Analysis, in *Systems Biology and Psychiatry: New frontiers in psychobiological understanding of mental disorders*. Tretter, F., Gebicke-Haerter, P.J., Winterer, G., Mendoza, E. (eds). Wiley, 2010
187. Cohen, KB, **Hunter, LE.** Text Mining for Translational Bioinformatics. *PLoS Computational Biology* 2013 May;9(5):e1003076.

Invited or Unreviewed Publications:

188. **Hunter, L.**, Schank, RC, The Quest to Understand Thinking. *Byte*, 10(4):143-155, April 1985.
189. **Hunter, L.**, Review of Stewart Brand's *The Media Lab*. in *The New York Times Book Review*, Sept. 27, 1987, p. 38
190. **Hunter, L.**, AI Attitudes and Techniques in Computer Supported Collaborative Work. *New Science: AI Research*, Aug. 15, 1988, p. 765
191. **Hunter, L.**, AI Techniques: Temporal Reasoning. *New Science: AI Research*, July 4, 1988, p. 719.
192. **Hunter, L.**, Review of Winograd and Flores *Understanding Computers and Cognition*. in *Technology Review*, July 1988
193. **Hunter, L.**, AI Techniques: Analogical Reasoning. *New Science: AI Research*, June 20, 1988, p.709.
194. **Hunter, L.** *Industrial Applications of Machine Learning*, New Science AI Industry Report, June 1989
195. **Hunter, L.**, ARRIS: Searching for Drugs With AI Software *New Science: AI Research*, June 18, 1990, p. 1464
196. **Hunter, L.** Artificial Intelligence and Molecular Biology: Extended abstract of invited address, *Proceedings of the Tenth National Conference on Artificial Intelligence*, pp. 866-868, 1992, AAAI Press, Menlo Park, CA.
197. **Hunter, L.** Review of Steven Levy's *Artificial Life* in *IEEE Spectrum* May 1993, 30(5):11-12.
198. B. Grosz, R. Davis, R. Bajcsy, P. Bonisone, B. Bullock, S. Minton, T. Mitchell, R. Perrault, T. Lozano-Perez, **L. Hunter**, M. Pollack, P. Rosenbloom, S. Shieber, H. Strobe D. Weld, A Report to ARPA on Twenty-First Century Intelligent Systems, AAAI Press, Menlo Park, 1994
199. **Hunter, L.** Public Image: Privacy in the Information Age. *Whole Earth Review*, 44:32-37, January 1985. Reprinted in *Social Issues Resource Services: Privacy, Volume 3*, 1986. Also reprinted in *The Borzoi College Reader*, eds. Charles Muscatine & Marlene Griffith, 7th edition, McGraw Hill, NY, 1992. Also

- reprinted in *Computers, Ethics and Social Values*, Deborah Johnson & Helen Nissenbaum, Prentice Hall, 1995.
200. **Hunter, L.**, Shavlik, J, Searls, DB. Conference Report: The First International Conference on Intelligent Systems for Molecular Biology, *AI Magazine* 15(1):12-13, 1994
 201. **Hunter, L.**, Shavlik, J, Searls, DB. Introduction to the Special Issue on Molecular Biology Applications, *Machine Learning*, 21: (1-2) 5-9 Oct-Nov 1995
 202. **Hunter, L.**, The State of Biotechnology Computing, 1994, *Proceedings of the Hawaiian International Conference on System Sciences* IEEE Computer Science Press, vol. 5, pp vi-viii, 1995
 203. **Hunter, L.**, Review of *Computer: A History of the Information Machine* by Martin Campbell-Kelly and William Aspray. in *The New York Times Book Review*, Nov. 17, 1996
 204. **Hunter, L.**, Rule, JB. Privacy Wrongs, with James Rule. *The Washington Monthly*, November 1996.
 205. **Hunter, L.**, Review of *Trapped in the Net* by Gene Rochlin, in *The New York Times Book Review*, Sept. 7, 1997.
 206. **Hunter, L.**, Rawlings, CJ., Creating a Professional Society for Bioinformatics - The International Society for Computational Biology (ISCB), *Bioinformatics* 14: (6) 471-471 1998
 207. **Hunter, L.**, Review of *Howard Aiken: Portrait of a Computer Pioneer* by I. Bernard Cohen, in *The New York Times Book Review*, September 12, 1999.
 208. **Hunter, L.**, Lathrop, R.H. Computer science and biology: an unlikely pair [Guest Editorial Introduction] *IEEE Intelligent Systems* Mar/Apr 2002 17(2):8- 10
 209. **Hunter, L.**, Brown, E., Dolbey, A. *IBM Research and the University of Colorado TREC 2003 Genomics Track Report*. IBM technical report RC23056, 2004.
 210. **Hunter L**, Altman RB, Bourne PE. The international society for computational biology 10th anniversary. *PLoS Comput Biol*. 2007 Jun 29;3(6):e135.
 211. Smith L, *et al.*, Overview of BioCreative II gene mention recognition. *Genome Biol*. 2008;9 Suppl 2:S2. Epub 2008 Sep 1.
 212. Karp PD, Sherlock G, Gerlt JA, Sim I, Paulsen I, Babbitt PC, Laderoute K, **Hunter L**, Sternberg P, Wooley J, Bourne PE. Changes to NIH grant system may backfire. *Science*. 2008 Nov 21;322(5905):1187-8.
 213. Shortliffe, EH., Califano, A., **Hunter, L.** New JBI emphasis on translational bioinformatics. *J. Biomedical Informatics*, 42(2):199-200, April 2009
 214. Tipney, H, **Hunter, L.**, An introduction to effective use of enrichment analysis software. *Human Genomics* 2010 Feb;4(3):202-6.
 215. Lussier YA, Butte AJ, **Hunter L.** Current methodologies for translational bioinformatics. *J Biomed Inform*. 2010 Jun;43(3):355-7. Epub 2010 May 12

216. **Hunter, L.** Computational Challenges of Mass Phenotyping. *Pacific Symposium on Biocomputing* 2013:454-5
217. **Hunter, L.** Rocky Mountain Conference on Bioinformatics Celebrates 10 Years. *PLoS Computational Biology* 2013: 9(5): e1003076.
doi:10.1371/journal.pcbi.1003076
218. Hewett D, Whirl-Carrillo M, **Hunter LE**, Altman RB, Klein TE. A twentieth anniversary tribute to PSB. *Pac Symp Biocomput.* 2015:1-7.

Software Systems and Databases

219. *Hanalyzer*: The Hanalyzer is a data integration and visualization system designed to help biologists analyze results observed in genome-scale experiments. It combines information extraction techniques, semantic data integration, with reasoning and network visualization. Available as open source: <http://hanalyzer.sourceforge.net/>
220. *OpenDMAP*: OpenDMAP is an ontology-driven, rule-based concept analysis and information extraction system. It had the best performance in protein-protein interaction task in BioCreative II global competition. Available as open source: <http://opendmap.sourceforge.net/>
221. *Knowtator*: Knowtator is a general-purpose text annotation tool that is integrated with the Protégé knowledge representation system. In use by several academic annotation projects. Available as open source: <http://knowtator.sourceforge.net/>
222. *Bio-UIMA component repository* The BioNLP Unstructured Information Management Architecture (UIMA) Component Repository provides UIMA wrappers for novel and well-known 3rd-party NLP tools used in biomedical text processing, such as tokenizers, parsers, named entity taggers, and tools for evaluation. Available as open source: <http://bionlp-uima.sourceforge.net/>
223. *MutationFinder*: an information extraction system for extracting descriptions of point mutations from free text. . Available as open source: <http://mutationfinder.sourceforge.net/>
224. *CL-Statistics* Common Lisp code for a variety of statistical calculations. Available as open source: <http://compbio.uchsc.edu/hunter/cl-statistics.lisp>
225. *COEV: A system for co-evolving learning agents and problem representations.* Common Lisp and C code that implements a form of cultural co-evolution for synergistic multistrategy machine learning. Patented and licensed by several major US corporations.
226. *Audio Knowledge Acquisition Tool*, with Chuck McMath. A Macintosh application for the management of large amounts of audio protocol data. Distributed by the US National Technical Information Service; used by knowledge engineers, psychologists, anthropologists and oral historians. No longer maintained.
227. *Amino Acid Representation Package.* Common Lisp code for implementing a wide variety of representations for amino acids, including the novel Atoms-Orbitals-Hydrogens (AOH) representation. Used by machine learning researchers for protein structure prediction and other tasks. No longer maintained.

228. *AI & Molecular Biology Researchers Database*. Database of names, contact information and research interests of more than 150 researchers worldwide. In 1995, the second most frequently accessed file in the European Molecular Biology Laboratory WAIS-server, widely used by students, academics and commercial organizations. No longer maintained.