

CURRICULUM VITAE

Robert F. Murphy

Ray and Stephanie Lane Professor of Computational Biology Emeritus

Carnegie Mellon University
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EDUCATION

Columbia University, New York, B.A., 1974, Biochemistry.
California Institute of Technology, Pasadena, CA, Ph.D., 1980, Biochemistry (Dr. James Bonner)

PROFESSIONAL EXPERIENCE

Ray and Stephanie Lane Professor of Computational Biology Emeritus, School of Computer Science, Carnegie Mellon U. 2021-

Ray and Stephanie Lane Professor of Computational Biology, Carnegie Mellon U., 2007-2021
Founding Head, Computational Biology Department (originally called the Lane Center for Computational Biology, which received department status in the School of Computer Science in September 2009; name changed to Computational Biology Department in January 2015), Carnegie Mellon University, 2007-2020

Professor of Machine Learning, Carnegie Mellon U., 2006-2021

Professor of Biological Sciences and Biomedical Engineering, Carnegie Mellon U., 2003-2021

Honorary Professor of Biology, Albert Ludwig University of Freiburg, 2011-

Founder and Board Member, Quantitative Medicine LLC, 2012-2020 (sold to Predictive Oncology, Inc.)

Senior Fellow, Allen Institute for Cell Science, 2015-2020

External Senior Fellow, Freiburg Institute for Advanced Studies, Freiburg, Germany 2008-2017

Founding Director, Joint CMU-Pitt Ph.D. Program in Computational Biology, 2005-2009

Founding Director, Center for Bioimage Informatics, Carnegie Mellon U., 2004-2008

Associate Professor of Biological Sciences, Carnegie Mellon University, 1989-2003

Associate Professor of Biomedical Engineering (by courtesy), 2002-2003

Voting Faculty Member, Center for Automated Learning and Discovery, 2002-2006

Director, Merck Computational Biology and Chemistry Program, 1999-2004

Director, Summer Undergraduate Research Program, Dept. Biological Sciences, 1996-2004

Member, University of Pittsburgh Cancer Institute, 1994-2021.

Faculty of Biomedical Engineering, Carnegie Mellon University, 1998-2002

Faculty Member and Program Leader for Undergraduate and Graduate Education, Center for Light Microscope Imaging and Biotechnology, 1991-2002.

Undergraduate Research Advisor, Dept. of Biological Sciences, Carnegie Mellon, 1996-2000

Director, Beckman Scholars Program at Carnegie Mellon University, 1998-1999

Visiting Associate Professor of Biology, Johns Hopkins University, 1994.

Associate Member, Pittsburgh Cancer Institute, 1986-1993.

Founding Member, Center for Fluorescence Research in Biomedical Sciences, 1983-1991

Assistant Professor of Biological Sciences, Carnegie Mellon University, 1983-1989

Consultant, Becton Dickinson Immunocytometry Systems, 1982-1992.

Postdoctoral Research Associate, Columbia University, Dr. Charles Cantor, Departments of Chemistry and Human Genetics, 1979-1983.

BUSINESS EXPERIENCE

CoFounder and Member of the Board of Directors, Quantitative Medicine LLC, 2012-2020
Company acquired by Predictive Oncology Inc (NASDAQ: POAI) on July 1, 2020
Scientific Advisory Board, Predictive Oncology, Inc., 2023-2024

HONORS

Alan J. Perlis Award for Imagination, School of Computer Science, Carnegie Mellon U., 2021
Fellow, IEEE, 2020
Senior Member, International Society for Computational Biology, 2018
Distinguished Service Award, International Society for Advancement of Cytometry, 2016
Honorary Professor of Biology, Albert Ludwig University of Freiburg, 2011
Alexander von Humboldt Foundation Research Award, 2008
Senior Member, IEEE, 2007
Fellow, American Institute of Medical and Biological Engineering, 2007
Presidential Young Investigator Award, 1984
Damon Runyon-Walter Winchell Cancer Foundation Fellowship, 1979
Earle C. Anthony Fellowship, Caltech, 1974

PROFESSIONAL SERVICE

Editorial

Guest Editor (with Gaudenz Danuser and Erik Meijering), Special Issue on Molecular and Cellular Bioimaging, IEEE Transactions on Image Processing, September 2005
Guest Editor (with Jelena Kovacevic), Special Issue on Molecular and Cellular Bioimaging, IEEE Signal Processing Magazine, May 2006
Member, Editorial Advisory Board, *Journal of Proteome Research*, January 2006-December 2008
Member, Editorial Board, *Cytometry Part A*, May 2007-June 2019
Software Section Editor, *PLOS Computational Biology*, March 2009-March 2015
Associate Editor, *BMC Bioinformatics*, May 2011-May 2016
Associate Editor, *Bioinformatics*, January 2014-December 2019
Member, Editorial Board, *Scientific Data*, January 2014-May 2023
Guest Editor (with Thilo Figge), Special Issue on Image-Based Systems Biology, *Cytometry Part A*, June 2015

Committee and Society Positions

Member, Data Standards Committee, International Soc. Analytical Cytology, Jan. 1990-March 2003 (Chair, Jan. 1998-March 2003)
Member, Publications Committee, International Society for Computational Biology, January 2004-2014
Councillor, International Society for Analytical Cytology, May 2004-May 2006
Chair, Scientific Communications Committee, International Society for Analytical Cytology, May 2004-May 2006
Member, International Society for Analytical Cytology Management Task Force, March 2005-September 2006
President-elect, International Society for Advancement of Cytometry, May 2006-May 2008

President, International Society for Advancement of Cytometry, May 2008-May 2010
Immediate Past-President, International Society for Advancement of Cytometry, May 2010-2012
Member, Steering Committee, Bioimage Informatics Conferences, November 2011-2014

Advisory Panels

Member, American Heart Association Western Pa. Peer Review Committee, March 1987-1991
Member, National Science Foundation Cell Biology Review Panel B, October 1989-March 1992
NIH, Special Study Section A (Biomedical Instrumentation), September 1990, June 1991
NIH, Biological Sciences 2 Study Section (Special Reviewer), July 1991, November 1991
NIH, Reviewers Reserve, December 1991-June 1993
Member, NIH Biological Sciences 2 Study Section, July 1993-June 1997
Chair, Carnegie Mellon University Faculty Development Fund, July 1996-June 1997
Member, NSF Research Experience for Undergraduates Review Panel, November 1996-1998
Member, NIH, ZRG2 CBY-1, March 1997, June 1997
Member, NIH, ZRG2 CBY-2, July, Dec. 1998 (Chair), March, July, Nov. 1999, March, June 2000
Member, NSF Research Experience for Undergraduates Review Panel, November 2000
Member, NSF Graduate Research Fellowship Panel, February 2001, February 2002
Member, Visiting Review Committee, Biological and Medical Informatics Program, University of California, San Francisco, March 28-29, 2002
Member, Scientific Advisory Board, Sequel Genetics, 2002-2003
Member, NIH SSS-U (Instrumentation), August 2002
Member, NIH SSS-H (Computational Biology), June 2002, November 2002, February 2003, June 2003, November 2003
Member, Visiting Review Committee, Image Analysis Laboratory, National Cancer Institute, Frederick, MD, January 2004
Member, NIH BDMA Study Section, March 2004
Chair, NIH BDMA Study Section, June 2004-June 2006
Member, NIH ZGM1 BRT-9 (KR) Study Section, August 2006
Member, NIH ZRG1 CB-B (40) Study Section, November 2006
Member, NIH ZRG1 BST-R (30) Study Section, October 2007
Member, NIH NIGMS Advisory Council, January 2009-December 2012
Member, Advisory Board, Caribbean Computing Center for Excellence, September 2010-2014
Member, NIH Council of Councils, November 2011-October 2014
Member, Review Panel, NSF-NIH BIGDATA initiative, October-November, 2012
Member, X02 Review Working Group, NIGMS, February 2013
Member, External Advisor Board, Bioinformatics Core Facility, University of Texas Southwestern Medical Center, January 15-
Member, Fellowship Selection Committee, Freiburg Institute for Advanced Studies, February 2015
Chair, External Advisory Board, MEP-LINCS program, Oregon Health & Science University, April 11-12, 2016 & November 28-29, 2016
Member, CTSA Collaborative Innovation Award Application (U01) Special Emphasis Panel ZTR1 CI-9 (01), National Center For Advancing Translational Sciences, May 11-12, 2016
Member, Special Emphasis Panel, ZCA1 RTRB-R J2 R on Research Centers for Cancer Systems Biology, November 9-10, 2016
Ad Hoc Member, National Institute of Allergy and Infectious Diseases Division of Intramural Research Board of Scientific Counselors, December 9-10, 2016

Chair, External Advisory Board, National Resource for Imaging Mass Spectrometry, Vanderbilt University, January 13, 2017

Member, Scientific Advisory Board, Morgridge Institute for Research, June 2017-

Chair, CTSA Program Data to Health Coordinating Center (U24) Special Emphasis Panel, ZTR1 CI-9 (01), National Center For Advancing Translational Sciences, May 17, 2017

Member, National Science Foundation Signal Transduction panel, February 21-23, 2018

Member, CTSA review Special Emphasis Panel ZTR1 CI-9 (01), June 14, 2018

Member, Special Emphasis Panel, ZRG1 BST-J (50) R, Tissue Mapping Centers for the Human BioMolecular Atlas Program (U54), June 28, 2018

Member, External Advisory Board, National Resource for Imaging Mass Spectrometry, Vanderbilt University, August 9, 2018

Member, Data Science Working Group, National Institutes of Health HubMAP Program, December 2018-present

Member, Schmidt Science Fellows Review Panel, December 2018-January 2019

Member, NIH Director's Transformative Research Award Editorial Board, November 2018-April 3, 2019

Member, CTSA review Special Emphasis Panel ZTR1 CI-9 (01), September 11-12, 2019

Member, Schmidt Science Fellows Review Panel, December 2019-January 2020

Final Selection Panel, Schmidt Science Fellows Program, March 2020

Member, NIH Director's Transformative Research Award Editorial Board, December 2019-April 7, 2020

Member, NIH INCLUDE Transformative R01 Study section, July 19, 2020

Member, AIMBE Review Committee on Biomedical Imaging and Instrumentation, August-September 2020

Member, NCI Subcommittee F study section, February 24, 2021

Final Selection Panel, Schmidt Science Fellows Program, March 2021

Member, NIH Director's Transformative Research Award Editorial Board, November 2020-April 3, 2021

Member, NIH Director's Pioneer Award Stage 2 Panel, April 12-14, 2021

Chair, NIH Cellular Senescence Network: Tissue Mapping Centers Panel, June 21-22, 2021

Member, AIMBE Review Committee of Computational Bioengineering, Systems Biology, and Bioinformatics, August-September 2021

Final Selection Panel, Schmidt Science Fellows Program, February 2022

Member, AIMBE Systems Biology Review Committee, August 2022

Chair, Final Selection Panel, Schmidt Science Fellows Program, February 2023

Member, National Center for Advancing Translational Sciences CTSA UM1 Review Special Emphasis Panel, June 4, 2024

Member, NSF Panel Innovation: Bioinformatics 2, March 10-11, 2025

Conference Organization and Program Committees

Chair, Cytometry Development Workshop, November 1998-October 2006

Scientific and Medical Advisory Board, Pittsburgh Bone Symposium, August 2003

Member, Program Committee, IEEE International Workshop on Neural Networks in Signal Processing, September 2003

Finance Chair, IEEE International Symposium on Biomedical Imaging, April 2006

Member, Organizing Committee, International Society for Analytical Cytology XXIII Congress, May 2006

Member, Program Committee, MICCAI Workshop on Microscopic Image Analysis with Applications in Biology, October 1, 2006

Member, Program Committee, International Conference on Bioinformatics Research and Development (BIRD), March 2007

Special Sessions Chair, IEEE International Symposium on Biomedical Imaging, April 2007

Member, Program Committee, Second International Workshop on Microscopic Image Analysis with Applications in Biology, September 21, 2007

Topic Chair, Bioengineering and Imaging Research Opportunities Workshop, January 2008

General Chair, International Society for Analytical Cytology XXIII Congress, May 2008

General Chair, International Conference on Bioinformatics Research and Development (BIRD), July 2008

Workshop Co-Organizer, “Automated Interpretation and Modeling of Cell Images,” International Conference on Machine Learning (ICML), June 2009

Area Chair for Bioimaging (with Eugene Myers), Intelligent Systems for Molecular Biology, July 11-13, 2010

Member, Organizing Committee, Bioimage Informatics 2010, Carnegie Mellon University, September 17-19, 2010

Organizer (with Anne Carpenter), Special Session, International Symposium on Biomedical Imaging, Chicago, Illinois, April 1, 2011

Member, Steering Committee, Great Lakes Bioinformatics Conference 2011, May 2-4, 2011

Member, Organizing Committee, CYTO 2011, Baltimore, Maryland, May 21-25, 2011

Area Chair for Bioimaging and Visualization (with Eugene Myers and Sean O’Donoghue), Intelligent Systems for Molecular Biology, Vienna, Austria, July 15-19, 2011

Chair, “Image-based Models of Cell Organization and Function,” International Conference on Systems Biology, Heidelberg, Germany, August 28-September 1, 2011

Member, Program Committee, Microscopic Image Analysis with Applications in Biology, Mannheim, Germany, September 2, 2011

Member, Program Committee, International Symposium on Biomedical Imaging, Barcelona, Spain, May 2-5, 2012

Honorary Conference Chair and member of Organizing Committee, GLBIO 2012, Ann Arbor, Michigan, May 15-17, 2012

Member, Organizing Committee, CYTO 2012, Leipzig, Germany, June 22-27, 2012

Area Chair for Bioimaging and Visualization (with Sean O’Donoghue), Intelligent Systems for Molecular Biology, Long Beach, California, July 15-17, 2012

Track Chair for Bioimage Analysis, ACM Conference on Bioinformatics, Computational Biology and Biomedicine, Orlando, Florida, October 7-10, 2012

Special Sessions Chair, IEEE International Symposium on Biomedical Imaging, San Francisco, California, April 7-11, 2013

Steering Committee, GLBIO 2013, Pittsburgh, Pennsylvania, May 13-15, 2013

Member, Organizing Committee, CYTO 2013, San Diego, California, May 19-22, 2013

Track Chair for Bioimage Analysis, ACM Conference on Bioinformatics, Computational Biology and Biomedicine, Washington, DC, 2013

Member, Program Committee, 2nd International Workshop on Pattern Recognition in Proteomics, Structural Biology and Bioinformatics, Naples, Italy, September 10-11, 2013

Member, Organizing Committee, CYTO 2014, Ft. Lauderdale, Florida, May 17-21, 2014

Area Chair for Bioimaging and Visualization, Intelligent Systems for Molecular Biology, Boston, Massachusetts, July 11-15, 2014

Member, Organizing Committee, CYTO 2015, Glasgow, Scotland, June 26-30, 2015

Session Organizer and Chair, Machine-Learning Advances in the Life Sciences, Society for Laboratory Automation and Screening Annual Meeting, Washington, DC, February 9, 2015

Area Chair for Bioimaging and Visualization, Intelligent Systems for Molecular Biology, Dublin Ireland, July 11-15, 2015

Organizer (with James Faeder), National Institute for Mathematical and Biological Synthesis Working Group on “Spatial Cell Simulations, Knoxville, Tennessee, December 1-3, 2015

Associate Editor, IEEE International Symposium on Biomedical Imaging, Prague, Czech Republic, April 13-16, 2016

Member, Organizing Committee, CYTO 2016, Seattle, Washington, June 11-15, 2016

Area Chair for Bioimaging and Visualization, Intelligent Systems for Molecular Biology, Orlando, Florida, July 8-12, 2016

Organizing Committee member, Symposium on Clinical and Pharmaceutical Solutions through Analysis, 2016-2017

Member, Scientific Program Committee, 2018 Annual Meeting, American Association for Cancer Research, Chicago, Illinois, April 14-18, 2018

Member, Program Committee, Intelligent Systems for Molecular Biology, Chicago, Illinois, July 6-10, 2018

Associate Editor, IEEE International Symposium on Biomedical Imaging, Prague, Czech Republic, April 8-11, 2019

Member, Program Committee, Intelligent Systems for Molecular Biology, Basel, Switzerland, July 21-25, 2019

Member, Program Committee, Intelligent Systems for Molecular Biology, Montreal, Canada, July 12-16, 2020

Member, Program Committee, Intelligent Systems for Molecular Biology, Madison, Wisconsin, July 10-14, 2022

Co-Chair, Organizing Committee, 3rd Nobel Turing Challenge Initiative Workshop, Pittsburgh, Pennsylvania, July 11-12, 2023

Courses and Tutorials

Invited Tutorial “Signal and Image Processing Issues in Molecular and Cellular Imaging,” ICASSP 2005, Philadelphia, Pennsylvania, March 19, 2005

Invited Tutorial “Signal and Image Processing Issues in Molecular and Cellular Imaging” (with Christos Faloutsos), SIGMOD 2005, Baltimore, Maryland, June 14, 2005

Faculty Member, Tenth Annual Course on 3D Microscopy of Living Cells, University of British Columbia, Vancouver, BC, June 16-24, 2005

Invited Faculty Member, Short Course on High-Content Analysis, Society for Biomolecular Sciences Conference 2005, Geneva, Switzerland, September 11, 2005

Invited Tutorial “Image Analysis of Subcellular Patterns for High Throughput Screening and Systems Biology,” International Society for Analytical Cytology XXIII Congress, Quebec City, Quebec, Canada, May 20, 2006

Invited Tutorial “Basics of Machine Learning for Image or Flow (Cytometry),” International Society for Analytical Cytology XXIII Congress, Quebec City, Quebec, Canada, May 20, 2006

Invited Faculty Member, Short Course on High-Content Analysis, Society for Biomolecular Sciences Conference 2006, Seattle, Washington, September 17, 2006

Faculty Member, Machine Learning Department Autumn Course on Data Mining from Text and Image, Pittsburgh, PA, September 27, 2006

Invited Tutorial “Machine Learning Approaches to Information Extraction from Text and Images in Biomedical Journal Articles,” International Association of Science and Technology for Development Biomed 2007 and Signal Processing, Pattern Recognition, and Applications 2007, Innsbruck, Austria, February 15, 2007

Invited Faculty Member, IV Interactive Course in Cytometry, Modena, Italy, March 6-9, 2007
Faculty Member, Twelfth Annual Course on 3D Microscopy of Living Cells, University of British Columbia, Vancouver, BC, June 29-July 2, 2007
Invited Faculty Member, Short Course on High-Content Analysis, Society for Biomolecular Sciences Conference 2008, St. Louis, Missouri, April 6, 2008
Faculty Member, Thirteenth Annual Course on 3D Microscopy of Living Cells, University of British Columbia, Vancouver, BC, June 28-30, 2008
Short Course, “Machine Learning Approaches to Biological Research: Bioimage Informatics and Beyond”, Freiburg Institute for Advanced Studies, Freiburg, Germany, September 29-October 1, 2008
Selected Tutorial “Automated Proteome-wide Determination and Modeling of Subcellular Location”, Sixth Conference on Computational Methods in Systems Biology, Rostock, Germany, October 12, 2008
Invited Faculty Member, V Advanced Course in Cytometry, Modena, Italy, March 3-8, 2009
Invited Speaker, EMBO Practical Course on Light Microscopy of Living Cells, Oeiras, Portugal, May 29-June 5, 2009
Lecture on Advanced Image Analysis, Life Cell Imaging Workshop, Zentrum für Biosystems Analyse, Freiburg, Germany, July 14, 2009
Short Course, “Bioimage Informatics: Automated Image Analysis and Modeling”, Biogem, Ariano Irpino, Italy, July 7-9, 2010
Invited Faculty Member, International Symposium in Applied Bioimaging, Porto, Portugal, September 20-21, 2012
Invited Faculty Member, EMBO Practical Course on “Intravital Microscopy, Flow Cytometry and Cell Sorting”, Berlin, Germany, July 7-12, 2013
Instructor and Co-Organizer, MMBioS Workshop on “Computational Methods for Spatially Realistic Microphysiological Simulations”, Pittsburgh, April 28-30, 2014
Instructor and Co-Organizer, MMBioS Workshop on “Computational Methods for Spatially Realistic Microphysiological Simulations”, Pittsburgh, April 27-29, 2015
Instructor, Bioinformatics Course, University of Freiburg, July 20-24, 2015
Instructor and Co-Organizer, MMBioS Workshop on “Computational Methods for Spatially Realistic Microphysiological Simulations”, Pittsburgh, June 1-3, 2016
Instructor, Bioinformatics Course, University of Freiburg, July 24-27, 2016
Instructor and Co-Organizer, MMBioS Workshop on “Computational Methods for Spatially Realistic Microphysiological Simulations”, Pittsburgh, June 26-28, 2017
Instructor and Co-Organizer, MMBioS Workshop on “Computational Methods for Spatially Realistic Microphysiological Simulations”, Seattle, Washington, March 7-9, 2018
Instructor and Co-Organizer, MMBioS Workshop on “Cell Modeling”, Pittsburgh, May 8-10, 2019
Instructor and Co-Organizer, MMBioS Virtual Workshop on “Cell Modeling”, Pittsburgh, June 22-26, 2020
Session Chair, Convergence in Oncology Summit, Lausanne, September 23-25, 2020

PROFESSIONAL SOCIETIES

American Institute for Medical and Biological Engineering (Fellow), American Society for Cell Biology (Emeritus Member), Institute of Electrical and Electronic Engineers (IEEE, Fellow), International Society for Advancement of Cytometry (Past President), International Society for Computational Biology (Senior Member)

BOOKS

1. Applications of Fluorescence in the Biomedical Sciences (1986) D. L. Taylor, A. S. Waggoner, R. F. Murphy, F. Lanni, R. Birge (eds.), Alan R. Liss, Inc., New York.
2. Endosomes and Lysosomes: A Dynamic Relationship (1993) B. Storrie and R. F. Murphy (eds.), JAI Press.
3. Bioinformatics Research and Development: Second International Conference, BIRD 2008, Vienna, Austria, July 7-9, 2008 Proceedings (Communications in Computer and Information Science) (2008) M. Elloumi, J. Küng, R. Murphy, K. Schneider, C. Toma (eds.), Springer, Berlin.
4. New Trends in Image Analysis and Processing, ICIAP 2013 Workshops: Naples, Italy, September 2013, Proceedings (Lecture Notes in Computer Science) (2013) A. Petrosino, L. Maddalena, P. Pala, V. Cantoni, M. Ceccarelli, R. F. Murphy, A. Del Bimbo, M. Pantic, C. Grana, J. Oomen, G. Serra, M. Leo, D. P. Mandic, G. Pirlo, M. Fairhurst, D. Impedovo (eds.), Springer, Heidelberg.
5. Imaging Cell Signaling. Methods in Molecular Biology, vol 2800. C. Wuelfing and R.F. Murphy, (eds) Humana, New York, NY.

PATENTS

R.F. Murphy, A. Rao, E. Glory-Afshar, J.Y. Newberg, S. Bhavani, A. Kumar. Identifying Location Biomarkers. U.S. patent number 9,092,850 (WO 2012100190).

PUBLICATIONS

These papers have received over 14,000 citations and a Hirsch index (h-index) of 60.

1. R. F. Murphy and J. Bonner (1975). Alkaline Extraction of Non-Histone Proteins from Rat Liver Chromatin. *Biochim. Biophys. Acta* 405:62-66.
2. J. M. Gottesfeld, R. F. Murphy and J. Bonner (1975). Structure of Transcriptionally Active Chromatin. *Proc. Natl. Acad. Sci. USA* 72:4404-4408.
3. R. B. Wallace, T. D. Sargent, R. F. Murphy and J. Bonner (1977). Physical Properties of Chemically Acetylated Rat Liver Chromatin. *Proc. Natl. Acad. Sci. USA* 74:3244-3248.
4. J. Bonner, R. B. Wallace, T. D. Sargent, R. F. Murphy and S. K. Dube (1977). The Expressed Portion of Eukaryotic Chromatin. *Cold Spring Harbor Symp. Quant. Biol.* 42:851-857.
5. R. F. Murphy, R. B. Wallace and J. Bonner (1978). Altered Nucleosome Spacing in Newly Replicated Chromatin from Friend Leukemia Cells. *Proc. Natl. Acad. Sci. USA* 75:5903-5907.
6. R. B. Wallace, J. Schaeffer, R. F. Murphy, T. Hiroso, K. Itakura and J. Bonner (1979). Hybridization of Synthetic Oligodeoxyribonucleotides to ϕ X174 DNA: The Effect of Single Base Pair Mismatch. *Nucleic Acids Res.* 6:3543-3557.
7. R. F. Murphy, W. R. Pearson and J. Bonner (1979). Computer Programs for Analysis of Nucleic Acid Hybridization, Thermal Denaturation and Gel Electrophoresis Data. *Nucleic Acids Res.* 6:3911-3921.
8. R. F. Murphy, R. B. Wallace and J. Bonner (1980). Isolation of Newly-Replicated Chromatin by Using Shallow Metrizamide Gradients. *Proc. Natl. Acad. Sci. USA* 77:3336-3340.
9. R. F. Murphy (1980). Chromosomal Protein-DNA Interactions. Doctoral Thesis. California Institute of Technology.

10. R. F. Murphy, J. R. Daban and C. R. Cantor (1981). Flow Cytofluorometric Analysis of the Nuclear Division Cycle of Physarum Polycephalum Plasmodia. *Cytometry* 2:26-30.
11. R. F. Murphy, E. D. Jorgensen and C. R. Cantor (1982). Kinetics of Histone Endocytosis in Chinese Hamster Ovary Cells: A Flow Cytofluorometric Analysis. *J. Biol. Chem.* 257:1695-1701.
12. R. F. Murphy, S. Powers, M. Verderame, C. R. Cantor and R. Pollack (1982). Flow Cytofluorometric Analysis of Insulin Binding and Internalization by Swiss 3T3 Cells. *Cytometry* 2:402-406.
13. R. Haas, R. F. Murphy and C. R. Cantor (1982). Testing Models of the Arrangement of DNA Inside Bacteriophage Lambda by Crosslinking the Packaged DNA. *J. Mol. Biol.* 159:71-92.
14. P. L. McNeil, R. F. Murphy, F. Lanni and D. L. Taylor (1984). A Method for Incorporating Macromolecules into Adherent Cells. *J. Cell Biol.* 98:1556-1564.
15. R. F. Murphy, S. Powers and C. R. Cantor (1984). Endosome pH Measured in Single Cells by Dual Fluorescence Flow Cytometry: Rapid Acidification of Insulin to pH 6. *J. Cell Biol.* 98:1757-1762.
16. R. F. Murphy, S. Powers, C. R. Cantor and R. Pollack (1984). Reduced Insulin Endocytosis in Serum Transformed Fibroblasts Demonstrated by Flow Cytometry. *Cytometry* 5:275-280.
17. W. Hiddemann, J. Schumann, M. Andreeff, B. Barlogie, C. J. Herman, R. C. Leif, B. H. Mayall, R. F. Murphy, A. A. Sandberg (1984). Convention on Nomenclature for DNA Cytometry. *Cytometry* 5:445-446.
18. R. F. Murphy and T. M. Chused (1984). A Proposal for a Flow Cytometric Data File Standard. *Cytometry* 5:553-555.
19. R. F. Murphy, D. B. Tse, C. R. Cantor and B. Pernis (1984). Acidification of Internalized Class I MHC Antigen by T Lymphoblasts. *Cell. Immunol.* 88:336-342.
20. R. F. Murphy, E. Bisaccia, C. R. Cantor, C. Berger and R. L. Edelson (1984). Internalization and Acidification of Insulin by Activated Human Lymphocytes. *J. Cell. Physiol.* 121:351-356.
21. P. L. Wollenzien, C. F. Hui, C. Kang, R. F. Murphy and C. R. Cantor (1984) RNA structure, Free and on the Ribosome, as Revealed by Chemical and Enzymatic Studies. In: **Mechanisms of Protein Synthesis**, Bernek, (ed.), Springer-Verlag, Berlin.
22. P. L. McNeil, A. L. Kennedy, A. S. Waggoner, D. L. Taylor and R. F. Murphy (1985). Light Scattering Changes During Chemotactic Stimulation of Human Neutrophils: Kinetics Followed by Flow Cytometry. *Cytometry* 6:7-12.
23. R. F. Murphy (1985). Automatic Identification of Subpopulations in Flow Cytometric List Mode Data Using Cluster Analysis. *Cytometry* 6:302-309.
24. P. L. Wollenzien, R. F. Murphy, C. R. Cantor, A. Expert-Bezancon and D. H. Hayes (1985). Structure of the E. coli 16S rRNA. Psoralen Crosslinks and N-Acetyl-N²-(p-Glyoxylylbenzoyl) Cystamine Crosslinks Detected by Electron Microscopy. *J. Mol. Biol.* 184:67-80.
25. C. R. Cantor, D. B. Tse, J. McDowell, R. Murphy, and B. Pernis (1985). Internalization of Histocompatibility Antigens Studied by Flow Cytometry. In: **Cell Biology of the Major Histocompatibility Complex**, B. Pernis & H. J. Vogel (eds.), Academic Press, New York, pp. 165-172.
26. R. F. Murphy (1985). Analysis and Isolation of Endocytic Vesicles by Flow Cytometry and Sorting: Demonstration of Three Kinetically Distinct Compartments Involved in Fluid-Phase Endocytosis. *Proc. Natl. Acad. Sci. USA* 82:8523-8526.
27. M. Fechheimer, C. Denny, R. F. Murphy, and D. L. Taylor (1986). Measurement of cytoplasmic pH in Dictyostelium discoideum by using a new method for introducing macromolecules into living cells. *Eur. J. Cell Biol.* 40:242-247.

28. R. F. Murphy (1986). Flow Cytometry in Cell Biology. In: **Applications of Fluorescence in the Biomedical Sciences**, D. L. Taylor, A. S. Waggoner, R. F. Murphy, F. Lanni, R. Birge (eds.), Alan R. Liss, Inc., New York, pp. 525-530.
29. R. F. Murphy and M. Roederer (1986). Flow Cytometric Analysis of Endocytic Pathways. In: **Applications of Fluorescence in the Biomedical Sciences**, D. L. Taylor, A. S. Waggoner, R. F. Murphy, F. Lanni, R. Birge (eds.), Alan R. Liss, Inc., New York, pp. 545-566.
30. C. C. Cain and R. F. Murphy (1986). Growth Inhibition of 3T3 Fibroblasts by Lysosomotropic Amines: Correlation with Effects on Intravesicular pH but Not Vacuolation. *J. Cell. Physiol.* 129:65-70.
31. M. Roederer and R. F. Murphy (1986). Cell-By-Cell Autofluorescence Correction for Low Signal-to-Noise Systems: Application to EGF Endocytosis by 3T3 Fibroblasts. *Cytometry* 7:558-565.
32. M. Roederer, R. Bowser, and R. F. Murphy (1987). Kinetics and Temperature Dependence of Exposure of Endocytosed Material to Proteolytic Enzymes and Low pH: Evidence for a Maturation Model for the Formation of Lysosomes. *J. Cell. Physiol.* 131:200-209.
33. S. Taylor, M. Roederer, and R. F. Murphy (1987). Flow Cytometric DNA Analysis of Adrenocortical Tumors in Children. *Cancer* 59:2059-2063.
34. D. M. Sipe and R. F. Murphy (1987). High resolution kinetics of transferrin acidification in Balb/c 3T3 cells: Exposure to pH 6 followed by temperature-sensitive alkalinization during recycling. *Proc. Natl. Acad. Sci. USA* 84:7119-7123.
35. R. A. Preston, R. F. Murphy, and E. W. Jones (1987). Apparent Endocytosis of FITC-Dextran by *Saccharomyces cerevisiae* Reflects Uptake of Low Molecular Weight Impurities, not Dextran. *J. Cell Biol.* 105:1981-1987.
36. C. C. Cain and R. F. Murphy (1988). A Chloroquine-resistant Swiss 3T3 Cell Line with a Defect in Late Endocytic Acidification. *J. Cell Biol.* 106:269-277.
37. S. Taylor, J. Blatt, J. Costantino, M. Roederer, and R. F. Murphy (1988). Flow Cytometric DNA Analysis of Neuroblastoma and Ganglioneuroma: a 10-year Retrospective Study. *Cancer* 62:749-754.
38. R. F. Murphy (1988). Processing of Endocytosed Material. **Adv. Cell Biol.** 2:159-180.
39. C. C. Cain, D. M. Sipe and R. F. Murphy (1989). Regulation of Endocytic pH by the Na^+/K^+ -ATPase in Living Cells. *Proc. Natl. Acad. Sci. USA* 86:544-548.
40. M. Roederer, R. W. Mays and R. F. Murphy (1989). Effect of Confluence on Endocytosis by 3T3 Fibroblasts: Increased Rate of Pinocytosis and Accumulation of Residual Bodies. *Eur. J. Cell Biol.* 48:37-44.
41. C. R. Abramowsky, S. R. Taylor, A. H. Anton, A. Berk, M. Roederer and R. F. Murphy (1989). Flow Cytometry DNA Ploidy Analysis and Catecholamine Secretion Profiles in Neuroblastoma. *Cancer* 63:1752-1756.
42. R. B. Wilson and R. F. Murphy (1989). Flow Cytometric Analysis of Endocytic Compartments. **Methods Cell Biol.** 31:293-317.
43. R. F. Murphy (1989). Flow Cytometric Analysis of Ligand Binding and Endocytosis. In: **Microspectrofluorometry of Single Cells**, E. Kohen and J. G. Hirschberg (eds.), Academic Press, New York, pp. 363-376.
44. R. F. Murphy, M. Roederer, D. M. Sipe, C. Cain, and R. Bowser (1989). Determination of the Biochemical Characteristics of Endocytic Compartments by Flow Cytometric and Fluorometric Analysis of Cells and Organelles. In: **Flow Cytometry: Advanced Research and Clinical Applications**, Volume II, A. Yen (ed.), CRC Press, Boca Raton, FL, pp. 221-254.
45. R. A. Preston, R. F. Murphy and E. W. Jones (1989). Assay of Vacuolar pH in Yeast and Identification of Acidification-defective Mutants. *Proc. Natl. Acad. Sci. USA* 86:7027-7031.

46. R. F. Murphy (1990). Ligand Binding, Endocytosis, and Processing. In: **Flow Cytometry and Sorting, Second Edition**, M. R. Melamed, T. Lindmo, M. L. Mendelsohn (eds.), Wiley-Liss, Inc., New York, pp. 355-366.
47. R. Bowser and R. F. Murphy (1990). Kinetics of Hydrolysis of Endocytosed Substrates by Mammalian Cultured Cells: Early Introduction of Lysosomal Enzymes into the Endocytic Pathway. *J. Cell. Physiol.* 143:110-117.
48. M. Roederer, J. Barry, R. B. Wilson and R. F. Murphy (1990). Endosomes Can Undergo an ATP-dependent Density Increase in the Absence of Dense Lysosomes. *Eur. J. Cell Biol.* 51:229-234.
49. P. N. Dean, C. B. Bagwell, T. Lindmo, R. F. Murphy, and G. C. Salzman (1990). Data File Standard for Flow Cytometry. *Cytometry* 11:323-332.
50. D. M. Sipe, A. Jesurum and R. F. Murphy (1991). Absence of Na⁺,K⁺-ATPase Regulation of Endosomal pH in K562 Erythroleukemia Cells: Analysis via Inhibition of Transferrin Recycling by Low Temperatures. *J. Biol. Chem.* 266:3469-3474.
51. D. M. Sipe and R. F. Murphy (1991). Binding to Cellular Receptors Results in Increased Iron Release from Transferrin at Mildly Acidic pH. *J. Biol. Chem.* 266:8002-8007.
52. C. C. Cain, R. B. Wilson and R. F. Murphy (1991). Isolation by Fluorescence-Activated Cell Sorting of Chinese Hamster Ovary Cell Lines with Pleiotropic, Temperature-Conditional Defects in Receptor Recycling. *J. Biol. Chem.* 266:11746-11752.
53. R. F. Murphy (1991). Maturation Models for Endosome and Lysosome Biogenesis. *Trends Cell Biol.* 1:77-82.
54. R. F. Murphy, M. Roederer, D. M. Sipe, C. C. Cain and R. B. Wilson (1992). Endosomal pH Regulation and the Maturation Model for Lysosome Biogenesis. In: **Endocytosis: From Cell Biology to Health, Disease and Therapy** (Proceedings of the NATO Advanced Research Workshop on Endocytosis), P. J. Courtoy (ed.), NATO ASI Series H, Vol. 62, Springer Verlag, pp. 91-95.
55. R. E. Valdes-Perez, H. A. Simon, and R. F. Murphy (1992) Discovery of pathways in science. Proceedings of the ML92 Workshop on Machine Discovery, J. Zytkow (ed.), Aberdeen, Scotland, pp. 51-57.
56. R. F. Murphy (1992) Scatchard analysis by flow cytometry. In: **Flow Cytometry and Cell Sorting**, A. Radbruch (ed.), Springer Verlag, Berlin, pp. 59-62.
57. R. F. Murphy (1992) Ligand acidification by non-adherent cells. In: **Flow Cytometry and Cell Sorting**, A. Radbruch (ed.), Springer Verlag, Berlin, pp. 124-129.
58. S. A. Brockman and R. F. Murphy (1993) Endosomal and Lysosomal Hydrolases. In: **Biological Barriers to Protein Delivery** (Pharmaceutical Biotechnology, Vol. 4), K. L. Audus and T. J. Raub (eds.), Plenum Press, New York, pp. 51-70.
59. R. F. Murphy (1993) Models of Endosome and Lysosome Traffic. **Adv. Cell Mol. Biol. Memb.** 1:1-17.
60. R. F. Murphy, J. Schmid and R. Fuchs (1993) Endosome maturation: Insights from somatic cell genetics and cell-free analysis. *Biochem. Soc. Trans.* 21:716-720.
61. R. B. Wilson, C. C. Mastick and R. F. Murphy (1993). A Chinese Hamster Ovary Cell Line with a Temperature-Conditional Defect in Receptor Recycling is Pleiotropically Defective in Lysosome Biogenesis. *J. Biol. Chem.* 268:25357-25363.
62. M. Bucci, T. W. Moyer, C. M. Brown, R. B. Wilson and R. F. Murphy (1994). The receptor-recycling and lysosome biogenesis mutant Tft1.11 belongs to a new complementation group, End6. *Somatic Cell Mol. Genet.* 20:47-54.
63. S. A. Brockman and R. F. Murphy (1994). Isolation and Analysis of Somatic Cell Mutants with Defects in Endocytic Traffic. **Methods Cell Biol.** 42:131-148.

64. L.C. Seamer, C.B. Bagwell, L. Barden, D. Redelman, G.C. Salzman, J.C. Wood, R.F. Murphy (1997). Proposed new data file standard for flow cytometry, version FCS 3.0. *Cytometry* 28:118-122.
65. S. L. Rybak, F. Lanni and R. F. Murphy (1997). Theoretical considerations on the role of membrane potential in the regulation of endosomal pH. *Biophys. J.* 73:674-687.
66. M. V. Boland, M. K. Markey and R. F. Murphy (1997). Classification of Cellular Protein Localization Patterns Obtained via Fluorescence Microscopy. *Proceedings of the 19th Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, pp. 594-597.
67. M. V. Boland and R. F. Murphy (1998). Multivariate Analysis. In: **Current Protocols in Cytometry**, pp. 10.8.1-10.8.21.
68. S. L. Rybak and R. F. Murphy (1998). Primary Cell Cultures from Murine Kidney and Heart Differ in Endosomal pH. *J. Cell. Physiol.* 176:216-222.
69. M. V. Boland, M. K. Markey and R. F. Murphy (1998). Automated Recognition of Patterns Characteristic of Subcellular Structures in Fluorescence Microscopy Images. *Cytometry* 33:366-375.
70. N. Bayer, D. Schober, E. Prehla, R. F. Murphy, D. Blass, and R. Fuchs (1998). Effect of bafilomycin A1 and nocodazole on endocytic transport in HeLa cells: Implications for viral uncoating and infection. *J. Virol.* 72:9645-9655.
71. D. Schober, N. Bayer, R.F. Murphy, E. Wagner, and R. Fuchs (1998). Establishment of an assay to determine adenovirus-induced endosome rupture required for receptor-mediated gene delivery. *Gene Therapy Mol. Biol.* 3:1-9.
72. M. K. Markey, M. V. Boland and R. F. Murphy (1999). Towards Objective Selection of Representative Microscope Images. *Biophys. J.* 76:2230-2237.
73. M. V. Boland and R. F. Murphy (1999). Automated Analysis of Patterns in Fluorescence Microscope Images. *Trends Cell Biol.* 9:201-202.
74. R. F. Murphy and M. V. Boland (1999). Pattern Analysis Meets Cell Biology. *Microsc. Microanal.* 5 (Suppl. 2: Proceedings):510-511.
75. M. V. Boland and R. F. Murphy (1999). After Sequencing: Quantitative Analysis of Protein Localization. *IEEE Eng. Med. Biol. Mag.* 18(5):115-119.
76. R. F. Murphy (1999). Scatchard analysis by flow cytometry. In: **Flow Cytometry and Cell Sorting, 2nd Ed.**, A. Radbruch (ed.), Springer Verlag, Berlin, pp. 82-85.
77. R. F. Murphy (1999) Ligand acidification by non-adherent cells. In: **Flow Cytometry and Cell Sorting, 2nd Ed.**, A. Radbruch (ed.), Springer Verlag, Berlin, 186-193.
78. S. L. Rybak and R. F. Murphy (2000). Measurement of Ligand Acidification Kinetics for Adherent and Non-Adherent Cells. In: **In Living Color: Protocols in Flow Cytometry and Cell Sorting** (R. Diamond and S. DeMaggio, eds.), pp. 496-523.
79. R. F. Murphy, M. V. Boland and M. Velliste (2000). Towards a Systematics for Protein Subcellular Location: Quantitative Description of Protein Localization Patterns and Automated Analysis of Fluorescence Microscope Images. *Proc Int Conf Intell Syst Mol Biol* 8:251-259.
80. R. F. Murphy, M. Velliste, J. Yao, and G. Porreca (2001). Searching Online Journals for Fluorescence Microscope Images Depicting Protein Subcellular Location Patterns. *Proceedings of the 2nd IEEE International Symposium on Bio-Informatics and Biomedical Engineering (BIBE 2001)*, pp. 119-128.
81. M. V. Boland and R. F. Murphy (2001). A Neural Network Classifier Capable of Recognizing the Patterns of all Major Subcellular Structures in Fluorescence Microscope Images of HeLa Cells. *Bioinformatics* 17:1213-1223.

82. S.A. Jesch, A.J. Mehta, M. Velliste, R.F. Murphy and A.D. Linstedt (2001). Mitotic Golgi is in a Dynamic Equilibrium Between Clustered and Free Vesicles Independent of the ER. *Traffic* 2:873-884.
83. E.J.S. Roques and R.F. Murphy (2002). Objective evaluation of differences in protein subcellular distribution. *Traffic* 3:61-65.
84. C.A. Telmer, P.B. Berget, B. Ballou, R.F. Murphy, and J.W. Jarvik (2002) Epitope tagging genomic DNA using a CD-tagging Tn10 Minitransposon. *Biotechniques* 32:422-430.
85. K. Huang, J. Lin, J.A. Gajnak, and R.F. Murphy (2002). Image Content-based Retrieval and Automated Interpretation of Fluorescence Microscope Images via the Protein Subcellular Location Image Database. *Proceedings of the 2002 IEEE International Symposium on Biomedical Imaging (ISBI 2002)*, pp. 325-328.
86. M. Velliste and R.F. Murphy (2002). Automated Determination of Protein Subcellular Locations from 3D Fluorescence Microscope Images. *Proceedings of the 2002 IEEE International Symposium on Biomedical Imaging (ISBI 2002)*, pp. 867-870.
87. R. F. Murphy, M. Velliste and G. Porreca (2002). Robust Classification of Subcellular Location Patterns in Fluorescence Microscope Images. *Proceedings of the 2002 IEEE International Workshop on Neural Networks for Signal Processing (NNSP 12)*, pp. 67-76.
88. J. H. Price, A. Goodacre, K. Hahn, L. Hodgson, E. A. Hunter, S. Krajewski, R. F. Murphy, A. Rabinovich, J. C. Reed, and S. Heynen (2002). Advances in Molecular Labeling, High Throughput Imaging and Machine Intelligence Portend Powerful Functional Cellular Biochemistry Tools. *J. Cell. Biochem. Supp.* 39:194-210.
89. X. Chen, M. Velliste, S. Weinstein, J.W. Jarvik and R.F. Murphy (2003). Location proteomics - Building subcellular location trees from high resolution 3D fluorescence microscope images of randomly-tagged proteins. *Proc. SPIE* 4962: 298-306.
90. K. Huang, M. Velliste, and R. F. Murphy (2003). Feature reduction for improved recognition of subcellular location patterns in fluorescence microscope images. *Proc. SPIE* 4962: 307-318.
91. W.W. Cohen, R. Wang and R.F. Murphy (2003). Understanding Captions in Biomedical Publications. *Proceedings of the Ninth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD-2003)*, pp. 499-504.
92. Z. Kou, W.W. Cohen and R.F. Murphy (2003). Extracting information from text and images for location proteomics. *Proceedings of the Third ACM SIGKDD Workshop on Data Mining in Bioinformatics (BIOKDD03)*, pp. 2-9.
93. R.F. Murphy, M. Velliste, and G. Porreca (2003). Robust Numerical Features for Description and Classification of Subcellular Location Patterns in Fluorescence Microscope Images. *J. VLSI Sig. Proc.* 35: 311-321.
94. S. Puri, H. Telfer, M. Velliste, R.F. Murphy, and A.D. Linstedt (2004). Dispersal of Golgi matrix proteins during mitotic Golgi disassembly. *J. Cell Sci.* 117:451-456.
95. R. F. Murphy (2004). Automated Interpretation of Subcellular Location Patterns. *Proceedings of the 2004 IEEE International Symposium on Biomedical Imaging (ISBI 2004)*, pp. 53-56.
96. K. Huang and R. F. Murphy (2004). Automated Classification of Subcellular Patterns in Multicell images without Segmentation into Single Cells. *Proceedings of the 2004 IEEE International Symposium on Biomedical Imaging (ISBI 2004)*, pp. 1139-1142.
97. K. Huang and R.F. Murphy (2004). Boosting accuracy of automated classification of fluorescence microscope images for location proteomics. *BMC Bioinformatics* 5:78.
98. R. F. Murphy (2004). Automated Interpretation of Protein Subcellular Location Patterns: Implications for Early Cancer Detection and Assessment. *Annals of the New York Academy of Science* 1020:124-131.

99. A. K. Singh, B. S. Manjunath, and R. F. Murphy (2004) Design of a Distributed Database for BioMolecular Images. *SIGMOD Record* 33(2).
100. Y. Hu and R. F. Murphy (2004). Automated Interpretation of Subcellular Patterns from Immunofluorescence Microscopy. *J. Immunol. Methods* 290:93-105.
101. R. F. Murphy (2004). Automated Determination of Subcellular Location from Confocal Microscope Images. *Microsc. Microanal* 10 (Suppl. 2):1242-1243.
102. K. Huang and R. F. Murphy (2004). From Quantitative Microscopy to Automated Image Understanding. *J. Biomed. Optics* 9:893-912.
103. X. Chen and R.F. Murphy (2004). Robust Classification of Subcellular Location Patterns in High Resolution 3D Fluorescence Microscope Images. *Proceedings of the 26th Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, pp. 1632-1635.
104. K. Huang and R. F. Murphy (2004). Data Mining Methods for a Systematics of Protein Subcellular Location. In: **Data Mining in Bioinformatics** (J.T.L. Wang, M.J. Zaki, H.T.T. Toivonen, and D. Shasha, eds.) , Springer-Verlag (London), pp. 143-187.
105. R. F. Murphy, Z. Kou, J. Hua, M. Joffe, and W. W. Cohen (2004). Extracting and Structuring Subcellular Location Information from On-line Journal Articles: The Subcellular Location Image Finder. *Proceedings of the IASTED International Conference on Knowledge Sharing and Collaborative Engineering (KSCE 2004)*, pp. 109-114.
106. X. Chen and R. F. Murphy (2004). Location Proteomics: Determining the Optimal Groupings of Proteins according to their Subcellular Location Patterns as determined from Fluorescence Microscope Images. *Proceedings of the 38th Asilomar Conference on Signals, Systems and Computers*, pp. 50-54.
107. M. Brabec, D. Schober, E. Wagner, N. Bayer, R.F. Murphy, D. Blaas, and R. Fuchs (2005). Opening of size selective pores in endosomes during human rhinovirus serotype 2 *in vivo* uncoating monitored by single organelle flow analysis. *J. Virol.* 79: 1008-1016.
108. X. Chen and R. F. Murphy (2005). Automated interpretation of protein subcellular location. *Biophotonics Intl* 12(3):34-35.
109. T.E. Merryman Jr., J. Kovacevic, E. Garcia Osuna, and R. F. Murphy (2005). Adaptive Multirate Data Acquisition of 3D Cell Images. *Proceedings of ICASSP 2005*, pp. II-133-136.
110. G. Baravalle, D. Schober, M. Huber, N. Bayer, R.F. Murphy and R. Fuchs (2005). Transferrin recycling and transport to lysosomes is differentially affected by bafilomycin, nocodazole and low temperature. *Cell Tissue Res.* 320:99-113.
111. R.F. Murphy (2005). Location Proteomics: A Systems Approach to Subcellular Location. *Biochem. Soc. Trans.* 33:535-538.
112. X. Chen and R. F. Murphy (2005). Objective Clustering of Proteins Based on Subcellular Location Patterns. *J. Biomed. Biotech.* 2005(2):87-95.
113. Z. Kou, W.W. Cohen and R.F. Murphy (2005). High-recall protein entity recognition using a dictionary. *Bioinformatics* 21:i266-i273 (Proceedings of 13th Annual International Conference on Intelligent Systems in Molecular Biology; only 13% of submitted papers accepted).
114. P. Nair, B.E. Schaub, K. Huang, X. Chen, R.F. Murphy, J.M. Griffith, H.J. Geuze, and J. Rohrer (2005). Characterization of the TGN Exit Signal of the human Mannose 6-Phosphate Uncovering Enzyme. *J. Cell Sci.* 118:2949-2956.
115. R.F. Murphy (2005). Location Proteomics: Providing Critical Information for systems Biology. *Bioforum Europe*, 4/2005, pp. 40-41.
116. R.F. Murphy (2005). Location Proteomics. *GIT Imaging & Microscopy*, 2/2005, pp. 17-19.

117. T. Zhao, M. Velliste, M.V. Boland, and R.F. Murphy (2005). Object Type Recognition for Automated Analysis of Protein Subcellular Location. *IEEE Trans. Image Proc.* 14:1351-1359.
118. R.F. Murphy (2005). Cytomics and Location Proteomics: Automated Interpretation of Subcellular Patterns in Fluorescence Microscope Images. *Cytometry* 67A:1-3.
119. G. Valet, R.F. Murphy, J.P. Robinson, A. Tárnok and A. Kriete (2006). Cytomics – from cell states to predictive medicine. **In: Computational Systems Biology** (A. Kriete and R. Eils, eds.), Elsevier Academic Press (Burlington, Massachusetts), pp. 363-381.
120. S.-C. Chen, and R.F. Murphy (2006). A Graphical Model Approach to Automated Classification of Protein Subcellular Location Patterns in Multi-Cell Images. *BMC Bioinformatics* 7:90.
121. T. Zhao and R.F. Murphy (2006). Automated Interpretation of Subcellular Location Patterns from Three Dimensional Confocal Microscopy. **In: Handbook of Biological Confocal Microscopy, Third Edition** (J.W. Pawley, ed.), Springer, pp. 818-828.
122. S.-C. Chen, G. Gordon, and R.F. Murphy (2006). A Novel Approximate Inference Approach to Automated Classification of Protein Subcellular Location Patterns in Multi-Cell Images. *Proceedings of the 2006 IEEE International Symposium on Biomedical Imaging (ISBI 2006)*, pp. 558-561.
123. T. Zhao, S. Soto, and R.F. Murphy (2006). Improved Comparison of Protein Subcellular Location Patterns. *Proceedings of the 2006 IEEE International Symposium on Biomedical Imaging (ISBI 2006)*, pp. 562-565.
124. L. Coulot, H. Kirschner, A. Chebira, J.M.F. Moura, J. Kovacevic, E. Garcia Osuna, and R.F. Murphy (2006). Topology Preserving STACS Segmentation of Protein Subcellular Location Images. *Proceedings of the 2006 IEEE International Symposium on Biomedical Imaging (ISBI 2006)*, pp. 566-569.
125. Y. Hu, J. Carmona, and R.F. Murphy (2006). Application of Temporal Texture Features to Automated Analysis of Protein Subcellular Locations in Time Series Fluorescence Microscope Images. *Proceedings of the 2006 IEEE International Symposium on Biomedical Imaging (ISBI 2006)*, pp. 1028-1031.
126. X. Chen, and R.F. Murphy (2006). Automated Interpretation of Protein Subcellular Location Patterns. *International Review of Cytology* 249:193-227.
127. X. Chen, M. Velliste, and R.F. Murphy (2006). Automated Interpretation of Subcellular Patterns in Fluorescence Microscope Images for Location Proteomics. *Cytometry* 69A:631-640.
128. Y.-L. Wang, K.M. Hahn, R.F. Murphy, and A.F. Horwitz (2006). From imaging to understanding: Frontiers in Live Cell Imaging, Bethesda, MD April 19-21, 2006 (Meeting Review). *J. Cell. Biol.* 174:1-4.
129. R.F. Murphy (2006). Putting proteins on the map (News and Views). *Nature Biotech.* 24:1223-1224.
130. S.-C. Chen, T. Zhao, G.J. Gordon, and R.F. Murphy (2006). A Novel Graphical Model Approach to Segmenting Cell Images. *Proceedings of the 2006 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB '06)*, pp. 1-8.
131. Z. Kou, W.W. Cohen, and R.F. Murphy (2007). A Stacked Graphical Model for Associating Sub-Images with Sub-Captions. *Pacific Symposium on Biocomputing* 12:257-268.
132. E. Glory and R.F. Murphy (2007). Automated Subcellular Location Determination and High Throughput Microscopy. *Developmental Cell* 12:7-16.

- 133.X. Chen and R.F. Murphy (2007). Interpretation of Protein Subcellular Location Patterns in 3D Images Across Cell Types and Resolutions. *Lecture Notes in Bioinformatics (LNBI 4414)*:328-342.
- 134.R.F. Murphy (2007). Systematic Description Of Subcellular Location For Integration With Proteomics Databases And Systems Biology Modeling. *Proceedings of the 2007 IEEE International Symposium on Biomedical Imaging (ISBI 2007)*, pp. 1052-1055.
- 135.J. Hua, O.N. Ayasli, W.W. Cohen, and R.F. Murphy (2007). Identifying Fluorescence Microscope Images in Online Journal Articles Using Both Image and Text Features. *Proceedings of the 2007 IEEE International Symposium on Biomedical Imaging (ISBI 2007)*, pp. 1224-1227.
- 136.E. Garcia Osuna, J. Hua, N.W. Bateman, T. Zhao, P.B. Berget and R.F. Murphy (2007). Large-Scale Automated Analysis of Protein Subcellular Location Patterns in Randomly-Tagged 3T3 Cells. *Annals Biomed. Eng.* 35:1081-1087.
- 137.A. Chebira, Y. Barbotin, C. Jackson, T. Merryman, G. Srinivasa, R.F. Murphy, and J. Kovacevic (2007). A multiresolution approach to automated classification of protein subcellular location images. *BMC Bioinformatics* 8:210.
- 138.T. Zhao, S.-C. Chen, and R.F. Murphy (2007). Location Proteomics. In: **Introduction to Systems Biology**. (S. Choi, ed.), Humana Press, pp. 196-214.
- 139.S.-C. Chen, T. Zhao, G. J. Gordon, and R. F. Murphy (2007). Automated Image Analysis of Protein Localization in Budding Yeast. *Bioinformatics* 23:i66-i71 (Proceedings of 15th Annual International Conference on Intelligent Systems in Molecular Biology; only 16% of submitted papers accepted).
- 140.E. Garcia Osuna and R.F. Murphy (2007). Automated, Systematic Determination of Protein Subcellular Location using Fluorescence Microscopy. In: **Subcellular Proteomics: From Cell Deconstruction to System Reconstruction** (E. Bertrand and M. Faupel, eds.), Springer, pp. 263-278.
- 141.C. Jackson, R.F. Murphy and J. Kovacevic (2007). Efficient Acquisition and Learning of Fluorescence Microscopy Data Models. *Proceedings of 2007 IEEE International Conference on Image Processing*, pp. VI-245-VI-248.
- 142.T. Zhao and R.F. Murphy (2007). Automated Learning of Generative Models for Subcellular Location: Building Blocks for Systems Biology. *Cytometry* 71A:978-990.
- 143.Y. Qian and R.F. Murphy (2008). Improved Recognition of Figures containing Fluorescence Microscope Images in Online Journal Articles using Graphical Models. *Bioinformatics* 24:569-576.
- 144.G. K. Rohde, A. Ribeiro, K. N. Dahl, and R. F. Murphy (2008). Deformation-based nuclear morphometry: capturing nuclear shape variation in HeLa Cells. *Cytometry*, 73A:341-350.
- 145.S.-C. Chen, G. J. Gordon, and R.F. Murphy (2008). Graphical Models for Structured Classification, with an Application to Interpreting Images of Protein Subcellular Location Patterns. *J. Machine Learning Res.* 9:651-682.
- 146.J. Newberg and R.F. Murphy (2008). A Framework for the Automated Analysis of Subcellular Patterns in Human Protein Atlas Images. *J. Proteome Res.* 7: 2300-2308.
- 147.E. Glory, J. Newberg, and R.F. Murphy (2008). Automated Comparison Of Protein Subcellular Location Patterns Between Images Of Normal And Cancerous Tissues. *Proceedings of the 2008 IEEE International Symposium on Biomedical Imaging (ISBI 2008)*, pp. 304-307.
- 148.R.F. Murphy (2008). Automated Proteome-Wide Determination Of Subcellular Location Using High Throughput Microscopy. *Proceedings of the 2008 IEEE International Symposium on Biomedical Imaging (ISBI 2008)*, pp. 308-311.

149. G. K. Rohde, W. Wang, T. Peng, and R.F. Murphy (2008). Deformation-Based Nonlinear Dimension Reduction: Applications To Nuclear Morphometry. *Proceedings of the 2008 IEEE International Symposium on Biomedical Imaging (ISBI 2008)*, pp. 500-503.
150. L. P. Coelho and R.F. Murphy (2008). Identifying Subcellular Locations from Images of Unknown Resolution. *Communications in Computer and Information Science 13*:235-242.
151. W. Hendee, K. Cleary, R. Ehman, G. Fullerton, W. Grundfest, J. Haller, C. Kelley, A. Meyer, R. F. Murphy, W. Phillips, V. Torchlin (2008). Bioengineering and Imaging Research Opportunities Workshop V: A White Paper on Imaging and Characterizing Structure and Function in Native and Engineered Tissues. *Radiology 248*:342-347.
152. J. Newberg, J. Hua, and R.F. Murphy (2009). Location Proteomics: Systematic Determination of Protein Subcellular Location. In: **Systems Biology (Methods in Molecular Biology Volume 500)**, I. Maly (ed.), Humana Press, pp. 313-332.
153. J. H. Boysen, S. Fanning, J. Newberg, R. F. Murphy, and A. P. Mitchell (2009) Detection of protein-protein interactions through vesicle targeting. *Genetics 181*:33-39.
154. A. Shariff, G. K. Rohde, and R. F. Murphy (2009) Indirect learning of generative models for microtubule distribution from fluorescence microscope images. *Proceedings of the ICML-UAI-COLT 2009 Workshop on Automated Interpretation and Modeling of Cell Images (Cell-Image Learning 2009)*.
155. L. P. Coelho and R. F. Murphy (2009) Unsupervised Unmixing of Subcellular Location Patterns. *Proceedings of the ICML-UAI-COLT 2009 Workshop on Automated Interpretation and Modeling of Cell Images (Cell-Image Learning 2009)*.
156. A. Ahmed, A. Arnold, L. P. Coelho, J. Kangas, A.-S. Sheikh, E. Xing, W. Cohen, and R. F. Murphy (2009) Structured Literature Image Finder. *Proceedings of the Ninth Annual Meeting of the ISMB BioLINK Special Interest Group*, pp. 209-212.
157. L. P. Coelho, A. Shariff, and R. F. Murphy (2009) Nuclear Segmentation In Microscope Cell Images: A Hand-Segmented Dataset And Comparison Of Algorithms. *Proceedings of the 2009 IEEE International Symposium on Biomedical Imaging (ISBI 2009)*, pp. 518-521.
158. T. Peng, Wei Wang, G. K. Rohde, R. F. Murphy (2009) Instance-Based Generative Biological Shape Modeling. *Proceedings of the 2009 IEEE International Symposium on Biomedical Imaging (ISBI 2009)*, pp. 690-693.
159. J. Y. Newberg, J. Li, A. Rao, E. Lundberg, F. Ponten, M. Uhlen and R. F. Murphy (2009) Automated Analysis Of Human Protein Atlas Immunofluorescence Images. *Proceedings of the 2009 IEEE International Symposium on Biomedical Imaging (ISBI 2009)*, pp. 1023-1026.
160. A. Ahmed, E. Xing, W. Cohen, and R. F. Murphy (2009) Structured Correspondence Topic Models for Mining Captioned Figures in Biological Literature. *Proceedings of the Fifteenth ACM SIGKDD Conference on Knowledge Discovery and Data Mining (KDD-2009)*, pp. 39-47.
161. C. Jackson, R. F. Murphy, and J. Kovacevic (2009) Intelligent Acquisition and Learning of Fluorescence Microscope Data Models, *IEEE Trans Image Proc.* 18:2071-2084.
162. T. E. Buck, A. Rao, L. P. Coelho, M. Fuhrman, J. W. Jarvik, P. B. Berget, and R. F. Murphy (2009) Protein Localization Dependence on Cell Cycle Inferred from Static, Asynchronous Images. *Proceedings of the 31st Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, pp. 1016-1019.
163. S. Huh, D. Lee and R. F. Murphy (2009) Efficient framework for automated classification of subcellular patterns in budding yeast. *Cytometry 75A*:934-940.
164. J. Spidlen, W. Moore, D. Parks, M. Goldberg, C. Bray, V. Cordioli, P. Gorombey, B. Hyun, M. Hubbard, R. Lefebvre, R. Leif, M. Naivar, D. Novo, L. Ostruszka, A. Treister, J. Wood, R. F. Murphy, M. Roederer, D. Sudar, R. Zigon, and R. R. Brinkman (2010) Data File

- Standard for Flow Cytometry: Version FCS 3.1. *Cytometry* 75A:97-100.
- 165.T. Peng, G.M.C. Bonamy, E. Glory-Afshar, D. R. Rines, S. K. Chanda, and R. F. Murphy (2010) Determining the distribution of probes between different subcellular locations through automated unmixing of subcellular patterns. *Proc. Natl. Acad. Sci. U.S.A.* 107:2944-2949.
- 166.A. Shariff, G. K. Rohde and R. F. Murphy (2010) A Generative Model of Microtubule Distributions, and Indirect Estimation of its Parameters from Fluorescence Microscopy Images. *Cytometry* 77A:457-466.
- 167.E. Glory-Afshar, E. Garcia Osuna, B. Granger, and R. F. Murphy (2010) A Graphical Model To Determine The Subcellular Protein Location In Artificial Tissues, *Proceedings of the 2010 IEEE International Symposium on Biomedical Imaging (ISBI 2010)*, pp. 1037-1040.
- 168.L. P. Coelho, E. Glory-Afshar, J. Kangas, S. Quinn, A. Shariff, and R. F. Murphy (2010) Principles of Bioimage Informatics: Focus on machine learning of cell patterns. *Lecture Notes in Computer Science* 6004:8-18.
- 169.L. P. Coelho, A. Ahmed, A. Arnold, J. Kangas, A.-S. Sheikh, E. Xing, W. Cohen, and R. F. Murphy (2010) Structured Literature Image Finder: Extracting, Information from Text and Images in Biomedical Literature. *Lecture Notes in Computer Science* 6004:23-32.
- 170.L. P. Coelho, T. Peng, and R. F. Murphy (2010) Quantifying the distribution of probes between subcellular locations using unsupervised pattern unmixing. *Bioinformatics* 26:i7-i12 (Proceedings of 18th Annual International Conference on Intelligent Systems in Molecular Biology; only 19% of submitted papers accepted).
- 171.A. Ahmed, A. Arnold, L. P. Coelho, J. Kangas, A.-S. Sheikh, E. Xing, W. Cohen, and R. F. Murphy (2010) Structured Literature Image Finder: Parsing Text and Figures in Biomedical Literature. *Web Semantics: Science, Services and Agents on the World Wide Web* 8:151-154.
- 172.Y. Hu, E. Garcia Osuna, J. Hua, T. S. Nowicki, R. Stolz, C. McKayle and R. F. Murphy (2010) Automated Analysis of Protein Subcellular Locations in Time Series Images. *Bioinformatics* 26:1630-1636.
- 173.R. F. Murphy (2010) Communicating Subcellular Distributions. *Cytometry* 77A:686-692.
- 174.A. Shariff, J. Kangas, L.P. Coelho, S. Quinn and R.F. Murphy (2010) Automated Image Analysis for High Content Screening and Analysis. *J. Biomolec. Screening* 15:726-734.
- 175.A.-S. Sheikh, A. Ahmed, A. Arnold, L. P. Coelho, J. Kangas, E. P. Xing, W. Cohen, and R. F. Murphy (2010) Structured literature image finder: Open source software for extracting and disseminating information from text and figures in biomedical literature. Carnegie Mellon University School of Computer Science Technical Report CMU-CB-09-101.
- 176.T. Lin, R.F. Murphy, and Z. Bar-Joseph (2011) Discriminative Motif Finding for Predicting Protein Subcellular Localization. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 8:441-51.
- 177.A. Shariff, R.F. Murphy, and G. Rohde (2011) Automated Estimation of Microtubule Model Parameters from 3-D Live Cell Microscopy Images. *Proceedings of the 2011 IEEE International Symposium on Biomedical Imaging (ISBI 2011)*, pp. 1330-1333.
- 178.A. Rao and R.F. Murphy (2011) Determination of Protein Location Diversity Via Analysis of Immunohistochemical Images from the Human Protein Atlas. *Proceedings of the 2011 IEEE International Symposium on Biomedical Imaging (ISBI 2011)*, 1727-1729.
- 179.T. Lin, Z. Bar-Joseph, and R. F. Murphy (2011) Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs. *Lecture Notes in Bioinformatics (Proceedings of RECOMB 2011)* 6577:204-221.
- 180.T. Peng and R.F. Murphy (2011) Image-derived, Three-dimensional Generative Models of Cellular Organization. *Cytometry* 79A:383-391.
- 181.R. F. Murphy (2011) An active role for machine learning in drug development. *Nature Chemical Biology* 7:327-330.

- 182.C. Jackson, E. Glory, R. F. Murphy and J. Kovacevic (2011) Model building and intelligent acquisition with application to protein subcellular location classification. *Bioinformatics* 27:1854-1859.
- 183.T. Lin, Z. Bar-Joseph, and R. F. Murphy (2011) Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs. *Journal of Computational Biology* 18: 1709-1722.
- 184.R. F. Murphy (2012) CellOrganizer: Image-derived Models of Subcellular Organization and Protein Distribution. *Methods in Cell Biology* 110: 179-193.
- 185.J. Li, L. Xiong, J. Schneider, and R.F. Murphy (2012) Protein Subcellular Location Pattern Classification in Cellular Images Using Latent Discriminative Models. *Bioinformatics* 28, i32-39 (Proceedings of 20th Annual International Conference on Intelligent Systems in Molecular Biology; only 13% of submitted papers accepted).
- 186.B.H. Cho, I. Cao-Berg, J.A. Bakal, and R.F. Murphy (2012) OMERO.searcher: Content-based image search for microscope images. *Nature Methods* 9:633-634.
- 187.K.W. Eliceiri, M.R. Berthold, I.G. Golberg, L. Ibanez, B.S. Manjunath, M.E. Martone, R.F. Murphy, H. Peng, A.L. Plant, B. Roysam, N. Stuurmann, J.R.Swedlow, P. Tomancak, and A.E. Carpenter (2012) Biological Imaging Software Tools. *Nature Methods* 9:697-710.
- 188.T.E. Buck, J. Li, G.K. Rohde, and R.F. Murphy (2012) Towards the virtual cell: Automated approaches to building models of subcellular organization 'learned' from microscopy images. *Bioessays* 34:791-799.
- 189.J. Li, A. Shariff, M. Wiking, E. Lundberg, G.K. Rohde and R.F. Murphy (2012) Estimating microtubule distributions from 2D immunofluorescence microscopy images reveals differences among human cultured cell lines. *PLoS ONE* 7:e0050292.
- 190.J. Li, J.Y. Newberg, M. Uhlén, E. Lundberg, and R.F. Murphy (2012) Automated Analysis and Reannotation of Subcellular Locations in Confocal Images from the Human Protein Atlas. *PLoS ONE* 7:e0050514.
- 191.S. Weber, M.L. Fernández-Cachón, J. M. Nascimento, S. Knauer, B. Offermann, R.F. Murphy, M. Boerries, and H. Busch (2013) Label-free detection of neuronal differentiation in cell populations Using High-Throughput Live-Cell Imaging of PC12 Cells. *PLoS ONE* 8: e56690.
- 192.C. Stadler, E. Rexhepaj, V.R. Singan, R.F. Murphy, R. Pepperkok, M. Uhlén, J.C. Simpson, and E. Lundberg (2013) Immunofluorescence and fluorescent protein-tagging are complementary techniques with high correlation for subcellular investigation of the human proteome in mammalian cells. *Nature Methods* 10: 315-323.
- 193.L. P. Coelho, J. D. Kangas, A. Naik, E. Osuna-Highley, E. Glory-Afshar, M. Fuhrman, R. Simha, P. B. Berget, J. W. Jarvik, and R. F. Murphy (2013) Determining the subcellular location of new proteins from microscope images using local features. *Bioinformatics* 29: 2343-2349.
- 194.K.T. Roybal, P. Sinai, P. Verkade, R. F. Murphy, and Christoph Wülfing (2013) The actin-driven spatiotemporal organization of signaling in T cells activated by antigen presenting cells. *Immunological Reviews* 256: 133-147.
- 195.A. W. Naik, J. D. Kangas, C. J. Langmead and R. F. Murphy (2013) Efficient Modeling and Active Learning Discovery of Biological Responses. *PLoS ONE* 8: e83996. doi:10.1371/journal.pone.0083996.
- 196.A. Gough, T. Lezon, J. Faeder, C. Chennubhotla, R. F. Murphy, R. Critchley-Thorne and D. L. Taylor (2014) High-Content Analysis with Cellular and Tissue Systems Biology: A Bridge between Cellular Biology and Tissue-Based Diagnostics. **In: The Molecular Basis of Cancer, 4th edition** (J. Mendelsohn, J. W. Gray, P. M. Howley, M. A. Israel, and C. B. Thompson, eds.), pp. 369-392.
- 197.R. F. Murphy (2014) A new era in bioimage informatics. *Bioinformatics* 30:1353.

198. J.D. Kangas, A.W. Naik, and R.F. Murphy (2014) Efficient discovery of responses of proteins to compounds using active learning. *BMC Bioinformatics* 15:143.
199. A. Kumar, A. Rao, S. Bhavani, J.Y. Newberg, R. F. Murphy (2014) Automated Analysis of Immunohistochemical Images Identifies Candidate Location Biomarkers for Cancers. *Proc. Natl. Acad. Sci. U.S.A.* 111:18249-18254.
200. M. Temerinac-Ott, A. W. Naik, and R. F. Murphy (2015) Deciding when to stop: Efficient experimentation to learn to predict drug-target interactions. *BMC Bioinformatics* 16:213 (also selected for oral presentation in the Proceedings track of RECOMB 2015; only 20% of submitted papers accepted). doi: 10.1186/s12859-015-0650-9
201. G. R. Johnson, T. E. Buck, D. P. Sullivan, G. K. Rohde and R. F. Murphy (2015) Joint Modeling of Cell and Nuclear Shape Variation. *Mol. Biol. Cell* 26:4046-4056. doi: 10.1091/mbc.E15-06-0370
202. G. R. Johnson, J. Li, A. Shariff, G.K.Rohde, and R.F. Murphy (2015) Automated Learning of Subcellular Pattern Variation among Punctate Proteins and of a Generative Model of their Distributions in Relation to Microtubules. *PLoS Computational Biology* 11(12): e1004614. doi:10.1371/journal.pcbi.1004614
203. R. M. Donovan, J.-J. Tapia, D. P. Sullivan, J. R. Faeder, R. F. Murphy, M. Dittrich, D. M. Zuckerman (2016) Unbiased Rare Event Sampling in Spatial Stochastic Systems Biology Models Using A Weighted Ensemble Of Trajectories. *PLoS Computational Biology* 12(2):e1004611. doi:10.1371/journal.pcbi.1004611
204. R. F. Murphy (2016) Building Cell Models and Simulations from Microscope Images. *Methods* 96:33-39. doi:10.1016/j.ymeth.2015.10.011
205. A.W. Naik, J.D. Kangas, D. P. Sullivan, and R. F. Murphy (2016) Active Machine Learning-driven Experimentation to Determine Compound Effects on Protein Patterns, *eLife* 5:e10047. doi:10.7554/eLife.10047.
206. K. T. Roybal, T. E. Buck, X. Ruan, B. H. Cho, D. J. Clark, R. Ambler, H. M. Tunbridge, J. Zhang, P. Verkade, C. Wülfing, and R. F. Murphy (2016) Computational spatiotemporal analysis identifies WAVE2 and Cofilin as joint regulators of costimulation-mediated T cell actin dynamics. *Science Signaling* 9:rs3. doi: 10.1126/scisignal.aad4149.
207. Y. Li, T. D. Majarian, A. W. Naik, G. R. Johnson, and R. F. Murphy (2016) Point process models for localization and interdependence of punctate cellular structures. *Cytometry* 89A:633-643. doi: 10.1002/cyto.a.22873.
208. B. Diedrich, K.G. Rigbolt, M. Röring, R. Herr, S. Kaeser-Pebernard, C. Gretzmeier, R.F. Murphy, T. Brummer, and J. Dengjel (2017) Discrete cytosolic macromolecular BRAF complexes exhibit distinct activities and composition. *EMBO J* 36:646–663. doi: 10.15252/emj.201694732.
209. R. Ambler, X. Ruan, R.F. Murphy, and C. Wülfing (2017) Systems Imaging of the immune synapse. The Immune Synapse: Methods and Protocols, *Methods in Molecular Biology*, vol. 1584 (C. T. Baldari and M. L. Dustin, eds.), pp. 409-421. doi: 10.1007/978-1-4939-6881-7_25.
210. G. R. Johnson, J. D. Kangas, A. Dovzhenko, R. Trojok, K. Voigt, T. D. Majarian, K. Palme, and R. F. Murphy (2017) A Method for Characterizing Phenotypic Changes in Highly Variable Cell Populations and its Application to High Content Screening of *Arabidopsis thaliana* Protoplasts. *Cytometry* 91A:326-335. doi: 10.1002/cyto.a.23067.
211. C. Gretzmeier, S. Eiselein, G. R. Johnson, R. Engelke, H. Nowag, M. Zarei, V. Küttner, A. C. Becker, K. T. G. Rigbolt, M. Høyer-Hansen, J. S. Andersen, C. Münz, R. F. Murphy, and J. Dengjel (2017) Degradation of protein translation machinery by amino acid starvation-induced macroautophagy. *Autophagy* 13:1064-1075. doi: 10.1080/15548627.2016.1274485
212. X. Ruan, C. Wülfing, and R. F. Murphy (2017) Image-based Spatiotemporal Causality

- Inference for Protein Signaling Networks. *Bioinformatics* 33:i217-i224 (Proceedings of 25th Annual International Conference on Intelligent Systems in Molecular Biology; only 16% of submitted papers accepted). doi: 10.1093/bioinformatics/btx258.
- 213.P. Spealman, A.W. Naik, G.E. May, S. Kuersten, L. Freeberg, R.F. Murphy, and J. McManus (2018) Conserved non-AUG uORFs revealed by a novel regression analysis of ribosome profiling data. *Genome Research* 28:214-222. doi: 10.1101/gr.221507.117
- 214.L. Han, R. F. Murphy, and D. Ramanan (2018) Learning Generative Models of Tissue Organization with Supervised GANs. *Proceedings of the 2018 IEEE Winter Conf. on Applications of Computer Vision*, pp. 682-690. doi: 10.1109/WACV.2018.00080.
- 215.T. Majarian, I. Cao-Berg, X. Ruan, and R. F. Murphy (2019) CellOrganizer: Learning and Using Cell Geometries for Spatial Cell Simulations. Modeling Biomolecular Site Dynamics, pp. 251-264. doi: 10.1007/978-1-4939-9102-0_11.
- 216.T. D. Majarian, R.F. Murphy, and S.S. Lakdawala (2019) Learning the sequence of influenza A genome assembly during viral replication using point process models and fluorescence in situ hybridization. *PLoS Computational Biology* 15 (1), e1006199 doi: 10.1371/journal.pcbi.1006199 (also bioRxiv 322966; doi: <https://doi.org/10.1101/322966>)
- 217.X. Ruan and R. F. Murphy (2019) Evaluation of methods for generative modeling of cell and nuclear shape. *Bioinformatics* 35 :2475-2489. doi: 10.1093/bioinformatics/bty983.
- 218.J. Lugo-Martinez, J. Dengjel, Z. Bar-Joseph, and R. F. Murphy (2019) Integration of heterogeneous experimental data improves global map of human protein complexes. Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics, pp. 144-153. doi: 10.1145/3307339.3342150
- 219.The HuBMAP Consortium (2019) The human body at cellular resolution: the NIH Human Biomolecular Atlas Program. *Nature* 574:187-192. doi: 10.1038/s41586-019-1629-x
- 220.D. J. Clark, L.E. McMillan, S.L. Tan, G. Bellomo, C. Massou, H. Thompson, L. Mykhaylechko, D. Alibhai, X. Ruan, K.L. Singleton, M. Du, A.J. Hedges, P.L. Schwartzberg, P. Verkade, R.F. Murphy, and C. Wülfing (2019) Transient protein accumulation at the center of the T cell antigen presenting cell interface drives efficient IL-2 secretion. *eLife* 8:e45789. doi: 10.7554/eLife.45789 (also bioRxiv 296616; doi: <https://doi.org/10.1101/296616>)
- 221.Y.-Y. Xu, H.-B. Shen and R. F. Murphy (2019) Learning complex subcellular distribution pattern of proteins via analysis of immunohistochemistry images. *Bioinformatics* 36(6):1908-1914. doi: 10.1093/bioinformatics/btz844
- 222.X. Ruan, G. R. Johnson, I. Bierschenk, R. Nitschke, M. Boerries, H. Busch, and R. F. Murphy (2019) Image-derived Models of Cell Organization Changes During Differentiation and Drug Treatments. *Molecular Biology of the Cell* 31(7):655-666. doi: 10.1091/mbc.E19-02-0080 (also bioRxiv 522763; doi: <https://doi.org/10.1101/522763>)
- 223.H. Sun and R. F. Murphy (2020) An Improved Matrix Completion Algorithm For Categorical Variables: Application to Active Learning of Drug Responses. *Proceedings of the ICML 2020 Workshop on Real World Experiment Design and Active Learning*. https://realworldml.github.io/files/cr/15_SunAndMurphyRevised.pdf
- 224.R. Ambler, G. L. Edmunds, S. L. Tan, S. Cirillo, J. I. Pernes, X. Ruan, J. Huete Carrasco, C.C.W. Wong, J. Lu, J. Ward, G. Toti, A. J. Hedges, S.J. Dovedi, R. F. Murphy, D. J. Morgan and C. Wülfing (2020) PD-1 suppresses the maintenance of cell couples between cytotoxic T cells and tumor target cells within the tumor. *Science Signaling* 13:eaau4518. doi: 10.1126/scisignal.aau4518
- 225.Y.-Y. Xu, H. Zhou, R. F. Murphy, and H.-B. Shen (2021) Consistency and variation of protein subcellular location annotations. *PROTEINS: Structure, Function, and Bioinformatics* 89(2):242-250. doi: 10.1002/prot.26010

- 226.M. E. Johnson, A. Chen, J. R. Faeder, P. Henning, I. I. Moraru, M. Meier-Schellersheim, R. F. Murphy, T. Prüstel, J. A. Theriot, and A. M. Uhrmacher (2021) Quantifying the roles of space and stochasticity in computer simulations for cell biology and cellular biochemistry. *Molecular Biology of the Cell* 32(2):91-210. doi: 10.1091/mbc.E20-08-0530
- 227.H. Sun and R. F. Murphy (2021) Evaluation of categorical matrix completion algorithms: toward improved active learning for drug discovery. *Bioinformatics* 37(20):3538–3545. doi: 10.1093/bioinformatics/btab322
- 228.H. Sun, X. Fu, S. Abraham, S. Jin and R. F. Murphy (2022) Improving And Evaluating Deep Learning Models Of Cellular Organization. *Bioinformatics* 38(23): 5299-5306. doi: 10.1093/bioinformatics/btac688
- 229.H. Chen and R. F. Murphy (2022) Evaluation of cell segmentation methods without reference segmentations. *Molecular Biology of the Cell* 34:ar50:1-11. doi: 10.1091/mbc.E22-08-0364
- 230.H. Sun, A. W. J. Soh, L. E. Mitchell, C. G. Pearson, R. F. Murphy (2022) Basal body organization and cell geometry during the cell cycle in *Tetrahymena thermophila*. *Molecular Biology of the Cell* 34:ar53:1-13. doi: 10.1091/mbc.E22-11-0508
- 231.J. C. Schaff, A. Lakshminarayana, R. F. Murphy, F.T. Bergmann, A. Funahashi, D. P. Sullivan, L. P. Smith (2023) SBML Level 3 Package: Spatial Processes, Version 1, Release 1. *Journal of Integrative Bioinformatics*, pp. 20220054. doi:10.1515/jib-2022-0054.
- 232.J. Lu, A. Veler, B. Simonetti, T. Raj, P. H. Chou, S. J. Cross, A. M. Phillips, X. Ruan, L. Huynh, A. D. Dowsey, D. Ye, Robert F. Murphy, P. Verkade, P. J. Cullen, and C. Wuelfing (2023) Five inhibitory receptors display distinct vesicular distributions in T cells. *Cells* 12:2558. doi:10.3390/cells12212558
- 233.H. Sun, J. Li and R. F. Murphy (2024) Expanding the coverage of spatial proteomics: a machine learning approach. *Bioinformatics* 40(2):btae062, doi:10.1093/bioinformatics/btae062
- 234.H. Sun and R.F. Murphy (2024) Learning Morphological, Spatial, and Dynamic Models for Cellular and Subcellular Components. In: Wuelfing, C., Murphy, R.F. (eds) *Imaging Cell Signaling. Methods in Molecular Biology*, vol 2800. Humana, New York, NY. doi:10.1007/978-1-0716-3834-7_16
- 235.J. Hoffman, S. Zheng, H. Zhang, R.F.Murphy, and K.N.Dahl (2024) Image-based discrimination of the early stages of mesenchymal stem cell differentiation. *Molecular Biology of the Cell* 35(8):ar103. doi: 10.1091/mbc.E24-02-0095.
- 236.K. Börner, P. D. Blood, J. C. Silverstein, M. Ruffalo, R. Satija, S. A. Teichmann, G. Pryhuber, R. S. Misra, J. Purkerson, J. Fan, J. W. Hickey, G. Molla, C. Xu, Y. Zhang, G. Weber, Y. Jain, D. Qaurooni, Y. Kong, HRA Team (including R. F. Murphy), A. Bueckle, and B. W. Herr II (2024) Human BioMolecular Atlas Program (HuBMAP): 3D Human Reference Atlas Construction and Usage. *Nature Methods*, in press. bioRxiv <https://doi.org/10.1101/2024.03.27.587041>

TRAINEES

Past Ph.D. students

1. Dr. Mario Roederer, Biological Sciences Ph.D. 1988, postdoctoral fellow, senior postdoctoral fellow, and Research Scientist with Dr. Leonard Herzenberg, Stanford University (1988-2000); currently Director, Flow Cytometry Core, Vaccine Research Center, NIAID, NIH
2. Dr. David M. Sipe, Biological Sciences (Biochemistry/Biophysics Program) Ph.D. 1990, postdoctoral fellow with Dr. Jerry Kaplan, University of Utah (1990-1991); Senior Scientist,

Gull Labs, Inc. (1997-1998), Senior Scientist, Lumenal Technologies, L.P. (1999-2000), currently Senior Researcher with Dr. Alan Waggoner, Carnegie Mellon University.

3. Dr. Cynthia Corley Cain Mastick, Biological Sciences Ph.D. 1990, postdoctoral fellow with Dr. Gustav Lienhard, Dartmouth Medical School (1991-1992) and Dr. Alan Saltiel, Parke-Davis Pharmaceutical (1993-1995); Senior Scientist, Parke-Davis Pharmaceutical Research Division (1995-1998); Assistant Professor, Department of Biochemistry, University of Nevada, Reno (1998-2003); currently Associate Professor, Department of Biochemistry, University of Nevada, Reno
4. Dr. Sandra A. Brockman, Biological Sciences Ph.D. 1994, postdoctoral fellow with Dr. Harvey Lodish, Whitehead Institute, Massachusetts Institute of Technology (1994-1997); Technical Specialist, Hamilton, Brook, Smith and Reynolds, PC, Boston, MA (1997-2002); currently Associate, Hamilton, Brook, Smith and Reynolds, PC, Boston, MA
5. Dr. Sheree L. Rybak, Biological Sciences Ph.D. 1997, postdoctoral fellow with Dr. Gary Thomas, Vollum Institute, Oregon Health & Science University (1997-1998); Technical Consultant, Klarquist Sparkman Campbell Leigh & Whinston, LLP, Portland, OR (1998-2003); currently Attorney, Klarquist Sparkman Campbell Leigh & Whinston, LLP, Portland, OR
6. Dr. Michael V. Boland, Biomedical Engineering Ph.D. 1999, completed M.D./Ph.D. program, University of Pittsburgh Medical School (1999-2001), Intern, University of Pittsburgh Medical School (2001-2002); Resident, Department of Ophthalmology and Visual Sciences, University of Iowa (2003-2005); Assistant Professor, Department of Ophthalmology, Johns Hopkins University; currently Associate Professor
7. Dr. E. John Meharr (deceased), Biological Sciences Ph.D. 2001, postdoctoral fellow with Dr. Humphrey Gardner (1998-1999) and Dr. Martin Lotz (1999-2000), Scripps Research Institute
8. Dr. Meel Velliste, Biomedical Engineering Ph.D. 2002 (Thesis: Image Interpretation Methods for a Systematics of Protein Subcellular Location), currently postdoctoral fellow with Dr. Andrew Schwartz, Department of Neurobiology, University of Pittsburgh, 2002-2006; Research Assistant Professor, University of Pittsburgh, 2006-2013; currently Vice President of Engineering, Fivetran, 2013-
9. Dr. Kai Huang, Computational and Statistical Learning M.S., 2003, Biological Sciences Ph.D. 2004 (Thesis: Data Mining Approaches for Interpreting Protein Subcellular Location Patterns in Fluorescence Microscope Images), currently Associate, Fixed Income and Derivatives Department, Credit Suisse First Boston, New York
10. Dr. Xiang Chen, Computational and Statistical Learning M.S., 2004, Biological Sciences Ph.D., 2005 (Automated interpretation of protein subcellular location patterns in 3D images), postdoctoral fellow, Yale University, New Haven, Connecticut, 2005-2010; currently Bioinformatics Research Scientist at St. Jude Children's Research Hospital

11. Dr. Juchang Hua, Computational and Statistical Learning M.S., 2006, Biological Sciences Ph.D., 2007 (Image databases for automated determination of protein subcellular locations), currently Goldman Sachs, New York
12. Dr. Yanhua Hu, Biological Sciences Ph.D., 2007 (Automated Analysis of Protein Subcellular Locations in Time Series Images)
13. Dr. Ting Zhao, Biomedical Engineering Ph.D., 2007 (Generative Models of Protein Subcellular Location Patterns), postdoctoral fellow with Dr. Eugene Myers, Janelia Farm Research Campus, Howard Hughes Medical Institute 2007-2009; Assistant Professor, Qiushi Academy for Advanced Studies, Zhejiang University 2009-2012; Currently Senior Software Engineer, Howard Hughes Medical Institute, Janelia Farm Research Campus
14. Dr. Shann-Ching Chen, Biomedical Engineering Ph.D., 2007 (Graphical Model Approaches to Segmentation and Classification for Analysis of Protein Subcellular Location Patterns), postdoctoral fellow with Dr. Gaudenz Danuser, Scripps Research Institute, La Jolla, California 2007-2009; Bioinformatics Research Scientist, St. Jude's Children's Research Hospital, 2009-2013; Currently Staff Scientist, Bioinformatics, Life Technologies.
15. Dr. Elvira (Garcia) Osuna Highley, Biomedical Engineering Ph.D., 2007 (Automated Analysis of the Subcellular Location of Proteins in NIH3T3 and CaCo2 Cells Using Fluorescence Microscope Images), currently postdoctoral fellow with Dr. Phillip Campbell, Carnegie Mellon University
16. Dr. Justin Y. Newberg, Biomedical Engineering Ph.D., 2009 (Frameworks for Classifying Proteins Across Human Cells Lines and Tissues), currently postdoctoral fellow with Dr. Michael Mancini, Baylor College of Medicine
17. Dr. Tienho Lin, Language Technology Ph.D., 2011 (Learning Cellular Sorting Pathways Using Protein Interactions and Sequence Motifs), currently postdoctoral fellow with David Heckerman at Microsoft Research (joint with Ziv Bar-Joseph)
18. Dr. Tao Peng, Biomedical Engineering Ph.D., 2011 (Image-derived Generative Models for Three-dimensional Cellular Organization); 2011-2013; Software Engineer, Bing Indexing and Knowledge team, Microsoft; currently Staff Scientist at Opera Solutions
19. Dr. Luis Pedro Coelho, Computational Biology Ph.D., 2011 (Modeling the space of subcellular location patterns using images and other sources of information), currently postdoctoral fellow with Musa Mhlanga at University of Lisbon
20. Dr. Aabid Shariff, Computational Biology Ph.D. 2012 (Learning Generative Models of Microtubule Distributions), currently Senior Scientist, Image Analysis and Computational Biology, GrassRoots Biotechnology, Durham, NC (joint with Gustavo Rohde)
21. Dr. Jieyue Li, Biomedical Engineering Ph.D. 2012 (Automated Learning of Subcellular Location Patterns in Confocal Fluorescence Images from Human Protein Atlas), currently Machine Learning Expert, ZestFinance, Los Angeles, CA

22. Dr. Joshua D. Kangas, Computational Biology Ph.D., 2013 (Active Learning for Drug Discovery), Chief Science Officer, Quantitative Medicine, LLC; currently Assistant Teaching Professor, Carnegie Mellon University
23. Dr. Armaghan Naik, Computational Biology Ph.D., 2013 (Efficient Modeling and Active Learning of Biological Responses: Learning without Prior Knowledge), Lane Fellow in Computational Biology, Carnegie Mellon University, 2013-2016; currently Director and Head of Design Sciences, FluNXT, Sanofi Pasteur
24. Dr. Taraz Buck, Computational Biology Ph.D., 2013 (Automated Construction of Dynamic Models of Subcellular Structure), postdoctoral fellow in Computational Biology, Carnegie Mellon University
25. Dr. Devin P. Sullivan, Computational Biology Ph.D., 2015 (Image-derived generative modeling of complex cellular organization in both space and time), postdoctoral fellow with Dr. Emma Lundberg, Stockholm, Sweden
26. Dr. Gregory R. Johnson, Computational Biology Ph.D., 2016 (Image-derived Models of the Organization of Cellular Components), Machine Learning Scientist, Allen Institute for Cell Science, Seattle, WA
27. Dr. Xiongtao Ruan, Computational Biology Ph.D., 2019 (Computational Methods for Image-derived Modeling of Cell Shape and Organization Dynamics), currently postdoctoral fellow with Gokul Upadhyayula and Eric Betzig, University of California, Berkeley
28. Dr. Aparna Kumar, Computational Biology Ph.D., 2021 (Automated analysis of protein subcellular location in immunohistochemistry images for cancer diagnosis).
29. Dr. Haoran Chen, Computational Biology Ph.D., 2023 (Learning complex spatial relationships from tissue and cell images).
30. Dr. Huangqingbo (Paul) Sun, Computational Biology Ph.D., 2024 (Explorations of Spatial Cellular Patterns at Proteomic Level).
31. Dr. Gary Robert Wilkins, Biological Sciences Ph.D., 2024 (Mapping Protein Complex Function with Cell Type Resolution)

Past M.S. students

Edward Roques, M.S. in Computational Biology, Dec. 2001; currently at Atto Bioscience, Rockville, MD (June 2003-)

Swapnil Prakash Uganlawar (M.S. in Computational Biology)

Amol Shanbhag, M.S. in Biomedical Engineering, Sep. 2006; currently at Microsoft, Pullman, WA (September 2006-)

Ivan Cao-Berg, M.S. in Computational Biology, May 2009; currently Senior Research Programmer, Carnegie Mellon University

Gregory Johnson, M.S. in Biomedical Engineering, May 2012; received Ph.D. in Computational Biology under my supervision; currently Machine Learning Scientist, Allen Institute for Cell Science (February 2016-)

Jingyi Wang, M.S. in Biomedical Engineering, May 2017

Sun Uk Kim, M.S. in Biomedical Engineering, May 2018

Kelvin Liu, M.S. in Computational Biology, December 2018

Huangqinbo Sun, M.S. in Automated Science, May 2021

Past Postdoctoral fellows

Dr. Russell B. Wilson, October 1987-May 1991, Assistant Professor of Pathology, Tulane University Medical School (1991-1995); currently President, Autoimmune Technologies, Inc., New Orleans, LA

Dr. Peter C. Kulakosky, November 1989-May 1991, postdoctoral fellow, Insect Science Center, University of Arizona (1991-1997); currently at Boyce Thompson Institute for Plant Research

Dr. Bruce Taillon, March 1993-September 1993, postdoctoral fellow, Washington University (1993-1997); currently Senior Scientist, Vyrex Corp.

Dr. Estelle Glory, October 2006-July 2010, currently on maternity leave.

Dr. Arvind Rao (Lane Fellow), July 2008-June 2011, Assistant Professor of Bioinformatics, University of Texas Southwestern Medical Center (2011-)

Dr. Baek-Hwan Cho, December 2008-February 2012, Research Staff, Samsung Advanced Institute of Technology (2012-)

Dr. Seung-Il Huh, March 2013-December 2013, Google Laboratories (2013-)

Dr. Felix Reisen (co-mentor), January 2013-August 2014

Dr. Maja Temerinac-Ott, May 2013-April 2016, Postdoctoral Fellow, University of Strasbourg (2016-)

Dr. Armaghan Naik (Lane Fellow in Computational Biology), 2013-2016; currently Director and Head of Design Sciences, FluNXT, Sanofi Pasteur

Dr. Jose Lugo-Martinez (Lane Fellow in Computational Biology), 2017-2021; currently Assistant Professor of Computer Science, University of Puerto Rico-Rio Pedras

Past Visiting Graduate Students

Dr. Johannes Schmid, February 1993-March 1993, Dept. of General and Experimental Pathology, University Vienna, Vienna, Austria, Ph.D. 1994; currently Ao. Univ. Prof. DI., Dept. of Vascular Biology and Thrombosis Research and Competence Center Bio-Molecular Therapeutics

Dr. Daniela Schober, January 1994-March 1994, Dept. of General and Experimental Pathology, University Vienna, Vienna, Austria

Dr. Ying Li, September 2014-March 2015, State Key Laboratory of Information Engineering in Surveying, Mapping and Remote Sensing, Wuhan University, Wuhan, China

Dr. Yingying Xu, September 2015-October 2016, Institute of Image Processing & Pattern Recognition, School of Electronics, Information and Electrical Engineering, Shanghai Jiaotong University, Shanghai, China

Past Visiting Scientists

Dr. Moshe Yaacobi, July 1986-September 1986, Chemistry Lecturer, Practical Engineering College of Beer Sheva, Beer Sheva, Israel

Dr. Andrea Fattorossi, November 1993-December 1993, Head, Department of Hygiene and Immunology, Aerospace Medical Center, Divisione Aerea Studi Ricerche e Sperimentazioni, Rome, Italy

Dr. Yuntao Qian, January 2006-December 2006, Professor, College of Computer Science, Zhejiang University, Hangzhou, China

Dr. Tim Nattkemper, April 2008, University of Bielefeld, Germany

Dr. Hagit Shatkay, School of Computing, Queen's University, Kingston, Ontario, Canada

Dr. Dechang Xu, Food Science & Engineering School, Harbin Institute of Technology, China

Dr. Jianwei Zhang, College of Computer Science and Engineering, ^[1]_[SEP]South China Univ. of Technology, Guangzhou, China

Dr. Zhaowen Qiu, Institute of Information and Computer Engineering, Northeast Forestry University of China, Harbin, China

Dr. Liqiang Pan, Harbin Institute of Technology, China

Dr. Long Liu, Xi'an University of Technology

Dr. Jörn Dengjel, University of Fribourg, Switzerland