

Ming-Ying Leung

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Education

1980:	University of Hong Kong	B.Sc.	Mathematics
1983:	University of Hong Kong	M.Phil.	Mathematics
1988:	Stanford University	M.S.	Computer Science
1989:	Stanford University	Ph.D.	Mathematics

Positions

1980-1983: Teaching Assistant, Department of Mathematics, University of Hong Kong
 1983-1989: Research Assistant and Teaching Fellow, Department of Mathematics, Stanford University
 1989-1993: Assistant Professor, Division of Mathematics, Computer Science, and Statistics, The University of Texas at San Antonio (UTSA)
 1993: Visiting Research Fellow, Department of Statistics, University of California at Berkeley and Department of Pharmaceutical Chemistry, University of California at San Francisco
 1993-2003: Associate Professor, Division of Mathematics and Statistics, UTSA
 2001-2002: Visiting Associate Professor, Department of Statistics, Rice University
 2003- : Professor, Department of Mathematical Sciences, and Director, Bioinformatics Program, The University of Texas at El Paso (UTEP)

Honors and Services

1986-1987: Andrew Mellon Foundation Research Award, Institute of Population and Resource Studies, Stanford University
 1990-1991: Consultant for the mathematical molecular biology groups at the University of Southern California and Stanford University
 2002-2004: Co-chair of the organizing committee for an international workshop on Statistical Methods in Microarray Data Analysis, Institute of Mathematical Sciences, National University of Singapore
 2004: Professor Y.C. Wong Visiting Lectureship, University of Hong Kong
 2005: Chair, Joint Session in Bioinformatics, INFORMS Annual Meeting 2005
 2005- : External Advisory Board for the NSF and HHMI funded "Talent Expansion in Quantitative Biology" project at East Tennessee State University
 2007- : Editorial Board, INFORMS Journal on Computing
 2008: Chair, Invited paper session in Stochastic Models for Biological Processes, International Workshop on Applied Probability, July 2008, Compiègne, France
 2008 - : Member of The University of Texas System Computational Biology Workgroup for the Cancer Prevention and Research Institute of Texas
 2008 - : Director, Bioinformatics Computing Laboratory, Core Facility of Border Biomedical Research Center, UTEP
 2009 - : Member of the NIH-RCMI Translational Research Network Translational Informatics Subcommittee

Selected Publications

- Leung, M.Y., Burge, C., Blaisdell, B.E., and Karlin, S., (1991) An Efficient Algorithm for Identifying Matches with Errors in Multiple Long Molecular Sequences, *J. Mol. Biol.* 221, 1367-1378.
- Leung, M.Y., Schachtel, G., and Yu, H.S., (1994) Scan Statistics and DNA Sequence Analysis: The Search for an Origin of Replication in a Virus, *Nonlinear World* 1, 445-471.
- Leung, M.Y., Marsh, G.M., and Speed, T.P. (1996) Over and Under Representation of Short Oligonucleotides in Herpes Virus Genomes. *J. Computational Biology*, 3(3), 345-360.
- Leung, M.Y. and Yamashita, T.E. (1999) Applications of the Scan Statistic in DNA Sequence Analysis, in *Recent Developments in Scan Statistics and Applications*, 269-286. Ed. Balakrishnan, N. and Glaz, J., Birkhauser Publishers.
- Grosu, D., Chronopoulos, A.T., and Leung, M.Y. (2002) Load Balancing in Distributed Systems: An Approach Using Cooperative Games. *Proceedings of the 16th IEEE International Parallel and Distributed Processing Symposium, Fort Lauderdale, Florida, USA*, IEEE Computer Science Press, 52-61.
- Chew, D.S.H., Choi, K.P., Heidner, H., and Leung, M.Y. (2004) Palindromes in SARS and Other Coronaviruses, *INFORMS J. Comp.* 16(4), 331-340.
- Leung, M.Y., Choi, K.P., Xia, A. and Chen, L.H.Y. (2005) Nonrandom Clusters of Palindromes in Herpesvirus Genomes, *J. Computational Biology* 12(3), 331-354.
- Chew, D.S.H., Choi, K.P., and Leung, M.Y. (2005) Scoring Schemes of Palindrome Clusters for More Sensitive Prediction of Replication Origins in Herpesviruses, *Nucleic Acids Research* 33 (15), e134.
- McMullin, B.T., Leung, M.Y., Shanbag, A.S., McNulty, D., Mabrey, J.D., and Agrawal, C.M. (2006) Correlating Subjective and Objective Descriptors of Ultra High Molecular Weight Wear Particles from Total Joint Prostheses. *Biomaterials* 27, 752-757.
- Leung, M.Y. (2006) Scan Statistics for Detecting Clusters, in *Encyclopedia of Measurement and Statistics*, S11-14, Salkind, N.J., Editor, SAGE Publications, Thousand Oaks.
- Chew, D.S.H., Leung, M.Y., and Choi, K.P. (2007) AT Excursion: a New Approach to Predict Replication Origins in Viral Genomes by Locating AT-rich Regions. *BMC Bioinformatics* 8, 163.
- Araiza, R., Taufer, M., and Leung, M.Y. (2007) Towards Optimal Scheduling for Global Computing under Probabilistic, Interval, and Fuzzy Uncertainty, with Potential Applications to Bioinformatics. *Proceedings of the 2007 Annual Meeting of the North American Fuzzy Information Processing Society*, June 2007, San Diego, California, USA, 520-525.
- Taufer, M., Solorio, T., Licon, A., Mireles, D., and Leung, M.Y. (2008) On the Effectiveness of Rebuilding RNA Secondary Structures from Sequence Chunks. In: *Proceedings of the Seventh IEEE International Workshop on High Performance Computational Biology (HiCOMB'08)*, April 2008, Miami, Florida, USA.
- Grosu, D., Chronopoulos, A.T., and Leung, M.Y. (2008) Cooperative Load Balancing in Distributed Systems. *Concurrency and Computation: Practice and Experience* 20:1953-1976.
- Chew, D.S.H., Choi, K.P., and Leung, M.Y. (2008) Stochastic Approaches to Predict Replication Origins in DNA Viral Genomes. In: *Proceedings of the 2008 International Workshop for Applied Probability*, July 2008, Compiègne, France.
- Taufer, M., Leung, M.Y., Solorio, T., Licon, A., Mireles, D., and Johnson, K.L. (2008) RNAVLab: A Virtual Laboratory for Studying RNA Secondary Structures Based on Grid Computing Technology, *Parallel Computing* 34: 661-680.
- Taufer, M., Licon, A., Araiza, R., Mireles, D., Gulyaev, A., Van Batenburg, F.H.D., and Leung, M.-Y. (2009) PseudoBase++: An Extension of PseudoBase for Easy Searching, Formatting, and Visualization of Pseudoknots *Nucleic Acids Research* 37(Database Issue):D127-135.
- Cruz-Cano, R. and Leung, M.Y. (2009) Comparison of Feature Selection Techniques for Viral DNA Replication Origin Prediction. *Proceedings of the 2009 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, March, 2009, Nashville, Tennessee, USA, 128-134.
- Greenberg, H.J., Holder, A.G., Leung, M.Y., and Schwartz, R. (2009) Computational Biology and Medical Applications: Opportunities for Operations Research, *ORMS Today*, 36(3), available at <http://www.lionhrtpub.com/orms/orms-6-09/frbiomedicine.html>

Cruz-Cano, R., Chew, D.S.H., Choi, K.P., and Leung, M.Y. (2009) Least-Squares Support Vector Machine Approach to Viral Replication Origin Prediction, *INFORMS J. Computing* (to appear).

Online Modules and Software Development

BIMER: Bioinformatics Information Modules; www.math.utep.edu/Faculty/mleung/BIMER

MOLPAC: UNIX-based Molecular Package for multiple sequence comparisons in C++

OGPET: O-Glycosylation Prediction Electronic Tool; <http://ogpet.utep.edu>

PRISEM: Probability Research Information Modules; www.math.utep.edu/Faculty/mleung/PRISEM

PseudoBase++: Database search engine for RNA pseudoknots; <http://pseudobaseplusplus.utep.edu>

RNAVLab: Virtual Laboratory for RNA Structure Predictions; <http://rnavlab.utep.edu>

Ongoing Research Support

2009-2014: NSF Interdisciplinary Training for Undergraduates in Biological and Mathematical Sciences (UBM) – “UBM Institutional: Undergraduate Training in Bioinformatics”; \$870,000, PI

2008-2013: NIH (MARC) – “Enhancement of Quantitative Science in Biology Curricula”; \$1,196,016, Co-PI

2008-2012: NIH (R01) – “Mapping Novel Subdominal B*5701 Epitopes in Conserved Regions of the HIV Proteome”; \$2,353,543; Co-I

2008-2012: NSF Mathematical Sciences – “Mathematical Models for RNA”; \$415,632, PI

2008-2010: Texas Higher Education Coordinating Board Advanced Research Program – “Probabilistic Models for Inversions in Viral RNA Sequences”; \$117,780, PI

2007-2011: NIH Support for Continuous Research Excellence (SCORE) Grant – “Computational Prediction of RNA Viral Genome Structures”; \$606,952, Subproject PI

Past Research Support

2006-2008: Texas Higher Education Coordinating Board Advanced Research Program, \$99,982, PI

2005-2007: NIH/Pittsburgh Supercomputer Center; \$79,968, Subcontract PI

2005-2007: IBM Shared University Research (SUR) Awards Program; \$600,000, Subproject Co-PI

2003-2007: NIH Support for Continuous Research Excellence (SCORE) Grant; \$475,946, Subproject PI

2004-2006: NSF Major Research Instrumentation; \$207,152, Co-I

2004-2005: UTEP Advance GRA Grant; \$4,400, Co-PI

2004-2005: NIH Minority Access to Research Careers (MARC) Program; \$54,000, Subproject Co-I

2001-2003: NIH Support for Continuous Research Excellence (SCORE) Grant; \$147,798, Subproject PI

2000-2003: NSF Course, Curriculum, and Laboratory Improvement Grant; \$122,351, PI

1996-1999: NSF Research Improvement in Minority Institutions Grant (RIMI); \$134,863, Co-PI

1992-1994: Texas Higher Education Coordinating Board Advanced Research Program; \$74,852, PI

1991-1995: San Antonio Area Foundation Research Grants, \$9,500 (1992); \$13,775 (1994), PI

1991-1993: NSF Research Grant, Probability and Statistics Program; \$70,352, PI

1990-1992: Texas Higher Education Coordinating Board Advanced Research Program; \$90,000, PI