Ming-Ying Leung
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Director, Bioinformatics and Computational Science Programs
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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
1989-2003 : Assistant and Associate Professor, Division of Mathematics and Statistics, The University of Texas at San Antonio
1993   : Visiting Research Fellow, Department of Statistics, University of California at Berkeley and Department of Pharmaceutical Chemistry, University of California at San Francisco
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
2013-   : Director, Computational Science Program, The University of Texas at El Paso

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
1990-   : Journal Referee for Annals of Applied Statistics, BioEssays, Biophysical Journal, BMC Bioinformatics, Communications in Statistics, International J. of Neural Systems, Mathematical Bioscience, INFORMS Journal on Computing, Journal of Bioinformatics and Computational Biology, Journal of Cellular Biochemistry, Methodology and Computing in Applied Probability, Nucleic Acids Research, PLOS
1990-   : Grant Reviewer for NSF, NIH, USDA, Research Council of Hong Kong
2004   : Professor Y.C. Wong Visiting Lectureship, University of Hong Kong
2007-2008 : Outstanding Performance Award, Office of Research and Sponsored Programs, UTEP
2008-2010 : Member, The University of Texas System Computational Biology Workgroup for the Cancer Prevention and Research Institute of Texas
2009-   : Member, NIH-RCMI Translational Research Network Translational Informatics Subcommittee
2010-   : Advisory Committee Member for the Campus Office of Undergraduate Research Initiatives (COURI), UTEP
2013-   : Mentor, National Alliance for Doctoral Studies in the Mathematical Sciences
2014-   : Internal Advisory Committee member, BUILDing Undergraduate SCHOLARS, UTEP
2017   : Student Choice Award for Outstanding Teaching, Department of Mathematical Sciences, UTEP
2023   : Grand Marshall of Winter 2023 Commencement for the Wood L. Hunt College of Business and College of Science, UTEP

2023- : Interactive Exhibit organizer for the annual El Paso Science Festival
2024- : Abstract reviewer for annual RCMI National Conference

Leadership in Academia, Professional Societies, and Community

2002-2003 : Editorial Board Member, Advances and Applications in Statistics
2002-2004 : Co-chair, Organizing Committee for the International Workshop on Statistical Methods in Microarray Data Analysis, Institute of Mathematical Sciences, National University of Singapore
2005 : Chair, Joint Session in Bioinformatics, 2005 INFORMS Annual Meeting
2005-2007 : External Advisory Board Member, NSF and HHMI funded "Talent Expansion in Quantitative Biology" project at East Tennessee State University
2007-2013 : Associate Editor, INFORMS Journal on Computing
2008 : Chair, Invited paper session in Stochastic Models for Biological Processes, International Workshop on Applied Probability, July 2008, Compiegne, France
2008- : Co-organizer for the annual Joint UTEP/NMSU Workshop on Mathematics, Computer Science, and Computational Sciences
2008- : Director of BBRC Bioinformatics Computing Core Facility, UTEP
2009- : Committee Member for NIH-RCMI Translational Research Network Translational Informatics
2010 : Chair, Session on Stochastic Models for Biological Systems, 2010 INFORMS Annual Meeting
2011 : Chair for invited Session Computational Methods in Biomolecular and Phylogenetic Analyses, International Federation of Operational Research Societies (IFORS) Conference, July 2011, Melbourne, Australia.
2011 : Chair for invited Cluster on Computational Biology, Institute for Operations Research and Management Science (INFORMS) Annual Conference, November 2011, Charlotte.
2012- : Organizer, Joint UTEP/NMSU Workshop on Mathematics, Computer Science, and Computational Sciences
2019-2020: Data Science Session Organizer and Chair for American Mathematical Society Central Sectional Conference
2021-2022: Special Session Organizer and Chair for American Mathematical Society Central Sectional Conference: (i) Mathematical and Computational Methods in Omics Research, (ii) Methods and Applications in Data Science
2022 : External Reviewer for the Computational and Data Science PhD Program, Middle Tennessee State University

Selected Publications

Leung, M.Y., Blaisdell, B.E., Burge, C., 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 Underrepresentation 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 *Scan Statistics and Applications,* pp.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, in *Encyclopedia of Measurement and Statistics,* pp.865-868, 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.

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.

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., Gultyaev, 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, *OR/MS Today,* 36(3).

Cruz-Cano, R., Chew, D.S.H., Choi, K.P., and Leung, M.Y. (2010) Least-Squares Support Vector Machine Approach to Viral Replication Origin Prediction, *INFORMS J. Computing* 22(3), 457-470.

Rosskopf, J.J.; Upton, J.H.III, Rodarte, L., Romero, T.A., Leung, M.Y., Taufer, M. and Johnson, K.L. (2010) A 3' terminal stem-loop structure in Nodamura virus RNA2 forms an essential cis-acting signal for RNA replication. *Virus Research* 150(1-2):12-21.

Schaubert, K.L., Price, D.A., Salkowitz, J.R., Sewell, A.K., Sidney, J, Asher, T.E., Blondelle, S.E., Adams, S., Marincola, F.M., Joseph, A., Sette, A., Douek, D.C., Ayyavoo, V, Storkus, W., Leung, M.Y., Ng, H.L., Yang, O.O., Goldstein, H., Wilson, D.B., Kan-Mitchell, J. (2010) Generation of robust CD8(+) T-cell responses against subdominant epitopes in conserved regions of HIV-1 by repertoire mining with mimotopes. *Eur. J. Immunol.* 40(7):1950-1962.

Licon, A., Taufer, M., Leung, M.Y., Johnson, K.L. (2010) A Dynamic Programming Algorithm for Finding the Optimal Segmentation of an RNA Sequence in Secondary Structure Predictions. In: Proceedings of the 2nd International Conference on Bioinformatics and Computational Biology 2010 (BICoB-2010), pp.165-170. Honolulu, Hawaii.

Zheng, J., Fuentes, O., Leung, M.Y., and Jackson, E. (2010) Mammogram Compression Using Super-Resolution. In J. Martí, A. Oliver, J. Freixenet, and R. Martí (Eds.), Vol. 6136, pp.46-53, Springer-Verlag, Berlin: Lecture Notes in Computer Science. Available at link.springer.com/chapter/10.1007/978-3-642-13666-5_7.

Cruz-Cano, R., Lee, M.L.T., and Leung, M.Y. (2012) Logic Minimization and Rule Extraction for Identification of Functional Sites in Molecular Sequences. BioData Mining, 5(10), 1-21. Available at biodatamining.org/content/5/1/10.

Aguilar-Bonavides, C., Leung, M.Y., Nakayasu, E. S., Lopes, F. G., Almeida, I. C., (2012). Computational tool for large-scale GPIomic analysis. In: Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine, ACM, New York, NY, pp. 585-587. Available at doi.org/10.1145/2382936.2383029.

Yehdego, D.T., Zhang, B., Taufer, M., Kodimala, V.K.R., Vegesna, R., Viswakula, S., Johnson, K. L., and Leung, M.Y. (2012) Secondary Structure Predictions for Long RNA Sequences. In: Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine, ACM, New York, NY, pp. 545-547. Available at doi.org/10.1145/2382936.2383016.

Yehdego, D.T., Zhang, B., Kodimala, V.K.R., Johnson, K.L., Taufer, M., Leung, M.Y., (2013) Secondary Structure Predictions for Long RNA Sequences Based on Inversion Excursions and MapReduce. In: Proceedings of the 12th IEEE International Workshop on High Performance Computational Biology (HiCOMB 2013), Boston, MA, pp. 1-10. Available at doi.org/10.1109/IPDPSW.2013.109.

Aguilar-Bonavides, C., Cardenas, G. A., Nakayasu, E. S., Lopes, F. G., Almeida, I. C., Leung, M.Y., (2013) Automatic Annotation of GPI Structures Using Grid Computing. (pp. 1-6). Honolulu, Hawaii: Proceedings of the 5th International Conference on Bioinformatics and Computational Biology (BICoB 2013).

Zhang, B., Yehdego, D. T., Johnson, K. L., Leung, M.Y., Taufer, M. (2013) Enhancement of accuracy and efficiency for RNA secondary structure prediction by sequence segmentation and MapReduce. BMC Structural Biology, 13 (Suppl. 1)(S3), 1-24. Available at biomedcentral.com/1472-6807/13/S1/S3.

Guerrero, F., Kellogg, A., Ogrey, A. N., Heekin, A. M., Barrero, R., Bellgard, M. I., Dowd, S. E., Leung, M.Y. (2016) Prediction of G protein-coupled receptor encoding sequences from the synganglion transcriptome of the cattle tick, *Rhipicephalus microplus*. *Ticks and Tick-borne Diseases*. 7(5), 670-677. Available at doi.org/10.1016/j.ttbdis.2016.02.014.

Leung, M.Y., Knapka, J.A., Wagler, A.E., Rodriguez, G., Kirken, R.A. (2016) OncoMiner: A pipeline for bioinformatics analysis of exonic sequence variants in cancer. In: Big Data Analytics in Genomics, Wong, K.C. (Ed.), pp. 373-396, Springer, New York. Available at link.springer.com/chapter/10.1007/978-3-319-41279-5_12.

Munoz, S., Guerrero, F., Kellogg, A., Heekin, A. M., Leung, M.Y. (2017) Bioinformatic prediction of G protein-coupled receptor encoding sequences from the transcriptome of the foreleg, including the Haller's organ, of the cattle tick, *Rhipicephalus australis*. PLOS ONE 12(2):e0172326. Available at doi.org/10.1371/journal.pone.0172326.

Leung, M.Y. (2017) Scan Statistics Applications in Genomics. In: Handbook of Scan Statistics, Glaz, J. and Koutras, M.V. (Eds.); Springer, New York. Available at doi.org/10.1007/978-1-4614-8414-1_42-1.

Rivas, J.A., Mohl, J.E., Van Pelt, R.S., Leung, M., Wallace, R.L., Gill, T. E. and Walsh, E. J. (2018) Evidence for regional aeolian transport of freshwater micro metazoans in arid regions. Limnology and Oceanography Letters. Available at doi.org/10.1002/lol2.10072.

Vasquez, M., Mohl, J.E., Leung, M.Y. (2018) Parsing Next Generation Sequencing Data in Parallel Environments for Downstream Genetic Variation Analysis. Journal of Computational Science Education 9(2):37-45. Available at doi.org/10.22369/issn.2153-4136/9/2/5.

Patil, A. R., Ayivor, F., Mohl, J. E., Leung, M.Y., Kim, S. (2019) Analyzing epigenetics data using feature ranking with various classifiers. Computational and Mathematical Biophysics, 7, 98-120. doi.org/10.1515/cmb-2019-0008.

Begum, K., Mohl, J. E., Ayivor, F.*, Perez, E. E.*, Leung, M.Y., (2020). GPCR-PEnDB: A database of protein sequences and derived features to facilitate prediction and classification of G protein-coupled receptors. *Database*. academic.oup.com/database/article/doi/10.1093/database/baaa087/5995841.

Mohl, J. E., Gerken, T., Leung, M.Y., (2020). ISOGlyP: de novo prediction of isoform specific mucin-type O-glycosylation. *Glycobiology*. doi.org/10.1093/glycob/cwaa067.

Wang, B., Mohl, J. E., Leung, M.Y., (2020). Computational Prediction of Functional Effects for Cancer Related Genetic Sequence Variants. (pp. 2999-3001). Seoul: IEEE International Conference on Bioinformatics and Biomedicine (BIBM). doi.ieeecomputersociety.org/10.1109/BIBM49941.2020.9313326.

Mohl, J. E., Gerken, T., Leung, M.Y., (2020). Predicting mucin-type O-Glycosylation using enhancement value products from derived protein features. *Journal of Theoretical and Computational Chemistry, 19*(3), 2040003. doi.org/10.1142/S0219633620400039.

Dankwah, K. O., Mohl, J. E., Begum, K., Leung, M.-Y. (2021). Understanding the binding of the same ligand to GPCRs of different families (pp. 2494-2501). IEEE International Conference on Bioinformatics and Biomedicine. https://doi.org/10.1109/BIBM52615.2021.9669761.

Patil, A. R., Leung, M.-Y., Roy, S. (2021). Identification of Hub Genes in Different Stages of Colorectal Cancer through an Integrated Bioinformatics Approach. *Int. J. Environ. Res. Public Health, 18*, 5564. doi.org/10.3390/ijerph18115564.

Gadad, B., Medrano, J., Diaz-Pacheco, V., Ramos, E., Yang, B., Leung, M.-Y., Thompson, P., Mellios, N., Jha, M., Trivedi, M. (2021). Whole-Transcriptome Brain Expression and Exon-Usage Profiling in Major Depression and Suicide. Biological Psychiatry, 89(9), S120-S121. https://doi.org/10.1016/j.biopsych.2021.02.311.

Dankwah, K.O., Mohl, J.E., Begum, K., Leung, M.-Y., (2022) What Makes GPCRs from Different Families Bind to the Same Ligand? Biomolecules 12(7):863. Available at doi.org/10.3390/biom12070863.

Gadad, B., Medrano, J., Ramos, E., Ruiz-Velasco, A., Leung, M.-Y., Thompson, P. (2023). Protein-Coding Transcriptome in Major Depressive Disorder and Suicidality: Distinct Pathways Regulating Myelination, Lipid Biogenesis, and Extracellular Matrix Pathways. Biological Psychiatry, 93(9), S291. https://doi.org/10.1016/j.biopsych.2023.02.726.

Grant, A. H., Rodriguez, A. C., Rodriguez Moncivais, O. J., Sun, S., Li, L., Leung, M.-Y., Kirken, R. A., Rodriguez, G. (2023). JAK1 Pseudokinase V666G Mutant Dominantly Impairs JAK3 Phosphorylation and IL-2 Signaling. International Journal of Molecular Sciences, 24 (7), 6805. https://doi.org/10.3390/ijms24076805.

Data Analytic Pipelines, Websites, Education and Research Modules

Bioinformatics Education for Agricultural Science (BEAS) Curriculum Modules: First Release in 2012; Updated Version Available at bioinformatics.utep.edu/agriculture/curriculum.

Bioinformatics Information Modules for Education and Research (BIMER): First Release in 2000; Updated Version Available at math.utep.edu/Faculty/mleung/BIMER.

Isoform Specific O-Glycosylation Prediction (ISOGlyP): First Release in 2014; Updated Version Available at isoglyp.utep.edu.

OncoMiner Pipeline for Bioinformatics Analysis of Genetic Sequence Variants in Cancer: First Release in 2016; Updated Version Available at oncominer.utep.edu

Probability Research Information Statistics Education Modules (PRISEM): First Release in 2001; Updated Version Available at math.utep.edu/Faculty/mleung/PRISEM.

Ribonucleic Acid Virtual Laboratory (RNAVLab) for Sequence Analysis, Structure Prediction, and Databases: First Release in 2008; Updated Version Available at rnavlab.utep.edu.

Undergraduate Participation in Bioinformatics Training (UPBiT) Curriculum Modules: First Release in 2010; Updated Version Available at bioinformatics.utep.edu/UPBiT/curriculum.

Selected Invited Presentations

Leung, M.Y. "Computational insights into G protein-coupled receptor ligand binding," Mini Symposium on Integrated Biotechnology for Sustainable Development, The Centre for Transdisciplinary Biotechnology Research, University of Columbo, Sri Lanka (December 2, 2022).

Leung, M.Y. "Identifying Novel Prostate Cancer-Associated Genes and Their Protein Interaction Networks," Precision in the Science of Medicine (PRiSM) Seminar Series, Department of Medicine, The University of Texas Health Science at San Antonio, San Antonio, TX (October 2, 2022).

Leung, M.Y. "Identifying Novel Prostate Cancer-Associated Genes from Whole-Exome Sequencing Data," The Epidemiology and Biostatistics Seminar at the Indiana University School of Public Health, Bloomington, IN (May 2, 2022).

Leung, M.Y., AMS Central Fall Sectional Meeting, The University of Texas at El Paso, El Paso, TX, "Protein-protein interaction network models for identifying cancer-related genes," American Mathematical Society. (September 17, 2022).

Leung, M.Y., NMSU Department of Mathematical Sciences Colloquium, "Statistical models for predicting functional effects of genetic sequence variants in cancer," New Mexico State University at Las Cruces. (November 6, 2020).

Leung, M.Y., AMS Central Fall Virtual Sectional Meeting, "Scan statistics for finding inversion clusters in genomic sequences," American Mathematical Society. (September 12, 2020).

Mohl, J. E., Gerken, T., Leung, M.Y., AMS Central Fall Virtual Sectional Meeting, "Using derived protein feature enhancement values to calculate the propensity for mucin-type O-glycosylation with the ISOGlyP program," American Mathematical Society. (September 12, 2020).

Leung, M.Y., Mohl, J. E., GlyGen Monthly Talks, "ISOGlyP: de novo prediction of isoform specific mucin-type O-glycosylation," www.glygen.org, Online. (April 7, 2020).

Leung, M.Y., Mean and Variance of Inversion Counts in Nucleotide Sequences. The 8th International Workshop on Applied Probability (IWAP2016), Toronto, Canada. (June 22, 2016).

Leung, M.Y., Identifying Inversion Clusters in Viral Genomes by Scan Statistics. The 8th International Workshop on Applied Probability (IWAP2016), Toronto, Canada. (June 20, 2016).

Ongoing Research Support

2023-2028: Cancer Prevention & Research Institute of Texas (CPRIT)/Texas Tech University – HSC, El Paso, Texas – "Impact of Cancer Outcomes in Hispanics (ICOHN)"; $68,323, Sub-Award PI

2019-2025: NIMHD (RCMI) – "Border Biomedical Research Center: Research Infrastructure Core"; $1,461,063, Co-Director

Past Research Support

2014-2019: NIH (U01)/Case Western University – "Initiation and Regulation of Mucin Type O-glycosylation"; $190,720, Subcontract PI

2014-2019: NIH – "Border Biomedical Research Center: Bioinformatics Core Facility"; $505,376, Bioinformatics Core Director

2014-2017: NIH – "Mechanisms in Viral RNA Replication Complex Assembly: Novel Targets For Antivira"; $453,000, Co-I

2012-2016: USDA – "Bioinformatics Education for Agricultural Science"; $295,000, PI

2010-2016: NSF – "Recruiting and Keeping Undergraduate Students in the Sciences"; $552,000, Co-PI

2009-2016: NSF Interdisciplinary Training for Undergraduates in Biological and Mathematical Sciences (UBM) – "UBM Institutional: Undergraduate Training in Bioinformatics"; $870,000, PI

2009-2014: NIH/NCRR – "Border Biomedical Research Center: Bioinformatics Computing Core Facility"; $279,605, Bioinformatics Core Director

2008-2013: NIH (MARC) – "Enhancement of Quantitative Science in Biology Curricula"; $1,187,256, Co-PI

2008-2013: NSF Mathematical Sciences – "Mathematical Models for RNA"; $415,632, PI

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

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

2006-2010: THECB Norman Hackerman Advanced Research Program, $99,982 and $117,780, 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