

# Michael L. Raymer, Ph.D.

# CURRICULUM VITÆ

**Associate Professor**  
Dept. of Computer Science & Engineering  
Wright State University  
Dayton, OH 4531-0001

**Hire date: Sept 1, 2000**  
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## EDUCATION

<b>Institution</b>	<b>Concentration, Degree</b>	<b>Date</b>
Michigan State University	Computer Science, Ph.D.	2000
Michigan State University	Computer Science, M.S.	1995
Colorado State University	Computer Science, B.S.	1991

## ACADEMIC EXPERIENCE

<b>Institution</b>	<b>Position</b>	<b>Date</b>
Wright State University	Full faculty member of the Biomedical science Ph.D. program	2003+
Wright State University	Full faculty member of the Environmental Sciences Ph.D. program	2005+
Wright State University	Full member of the Graduate Faculty	2001+
Wright State University	Assistant Professor, Department of Computer Science and Engineering	2000+
Michigan State University	Graduate Research Assistant, Dept. of Biochemistry	1994-2000
Michigan State University	Graduate Research Assistant, Dept. of Computer Science	1993-1994

## PROFESSIONAL AND ACADEMIC HONORS

<b>Title of Award</b>	<b>Granting Association</b>	<b>Date</b>
Early Career Achievement Award	College of Engineering and Computer Science, Wright State University	2002-2003
Outstanding Teaching	College of Engineering and Computer Science, Wright State University	2002-2003
Outstanding Teaching	College of Engineering and Computer Science, Wright State University	2001-2002
Outstanding Teaching	College of Engineering and Computer Science, Wright State University	2000-2001
Ohio Teaching Excellence Program	Wright State University	2002-2003
Finn Wold Travel Award	The Protein Society	1998
Student Travel Grant	American Crystallographic Association	1995
DeVlieg Fellowship	Michigan State University	1993
Distinguished Performance Award	Los Alamos National Laboratory	1992
Summa Cum Laude	Colorado State University	1991
Mohilner Scholarship	Colorado State University	1990
President's Scholarship	Colorado State University	1987
Boettcher Foundation Scholarship	The Boettcher Foundation	1987-1991

**PROFESSIONAL MEMBERSHIP**

Association	Status	Date
IEEE Computer Society	Member	2002+
Phi Beta Kappa National Honor Society	Member	1991+

**OTHER PROFESSIONAL EXPERIENCE**

Association	Status	Date
Los Alamos National Laboratory	Technical Staff Member	1992-1996
Los Alamos National Laboratory	Staff Research Assistant	1991-1992
Reynolds Electrical and Engineering Company	Programmer	1990

**GRANTS AND CONTRACTS****External Grants and Contracts**

- M. Raymer (WSU PI), "Ohio Consortium for Bioinformatics," Ohio Board of Regents, Choose Ohio First Scholarship Program Award COFSP-08-15, \$235,000 September 2008 – September 2012.
- N. Reo and M. Raymer, "NMR-Based Metabolomics in Toxicology Research", Co-PI (10% effort), U.S. Air Force – AFRL, \$91, 830, September 2007 – August 2008.
- N. Klingbeil, K. Rattan, D. Reynolds, M. Raymer, and R. Mercer, "A National Model for Engineering Mathematics Education," Co-PI, NSF CCLI Award #DUE-0817332, \$2,000,000, July 2006 – July 2009.
- N. Klingbeil, K. Rattan, D. Reynolds, M. Raymer, and R. Mercer, "A National Model for Engineering Mathematics Education," Co-PI, NSF CCLI Award #DUE-0618571, \$500,000, July 2006 – July 2009.
- N. Klingbeil, R. Mercer, K. Rattan, M. Raymer, and D. Reynolds "A National Model for Engineering Mathematics Education", Co-PI, NSF/EDU Award #EEC-0343214, \$100,000, September 2003 – August, 2005.
- D. Millhorn, T. Boat, R. Fyffe, et al. "A genome research institute in Ohio," Ohio BRTT Grant. Award amount: \$1,700,000. PI on subcomponent grant under this award. Subcomponent award amount: \$427,642. Period: January 2003 – January 2005.
- M. Raymer, T. Doom, and D. Krane. "Crossing the interdisciplinary barrier: An integrated undergraduate program in bioinformatics," PI, NSF CISE Research Infrastructure Grant #EIA-0122582. Award amount: \$552,056. Period: September 2001 - August 2004.
- T. Doom, J. Gallagher, M. Raymer. "Cluster Computing for Bioinformatics and Biocontrol," Ohio Shared Computing Center Resources Grant. Award amount: A cluster of eight two-processor systems valued at ~\$50,000. Period: Sept 2001+.

**Internal Grants and Contracts**

- M. Raymer, "Investigation of codon usage biases and gene expressivity, a proposal to the National Institutes of Health", Wright State University Research Initiation Award #282026, \$10,000, April 2007 – June 2008.
- A. Sheth, M. Raymer, N. Reo, "Advanced Data Management Resource for Biomedical Research", Wright State University Major Collaboration Grant (# pending), \$30,000, May 2007 – June 2008.
- J. McDougal, D. Cool, M. Raymer, and B. Foy, "Proteomics with Chlorpyrifos Skin Contact", Major Collaboration Grant, Wright State University, \$48,000, May, 2003 – June, 2004, Co-investigator: 10% participation.
- K. Grasman, A. Burton, W. Carmichael, D. Krane, M. Morris, M. Raymer, and J. McDougal, "Proposals to the Biomedical Research & Technology Transfer Commission and/or the US Environmental Protection Agency to develop environmental health assessments using toxicogenomic technologies", Major Collaboration Grant, Wright State University, \$55,000, May 2002 – June, 2003.

- G. Alter, D. Krane, M. Raymer, and P. Seybold, "A proposal to the National Science Foundation (NSF) to study high resolution molecular topology of nucleotide excision repair", Major Collaboration Grant, Wright State University, \$30,000, May 2002 – June, 2003.
- D. Krane, M. Raymer, T. Doom, and O. Garcia. "Commercialization of forensic DNA typing expertise," Wright State University Technology Commercialization Grant #664723. Award amount: \$99,951. Period: September 2001 - August 2002.
- M. Raymer, "A Bioinformatics-Based Approach for the Identification of Promising Drug Leads", PI, Research Challenge Award, Wright State University: \$25, 000, March, 2001 – February, 2002.

## BRIEF BIO

Michael L. Raymer graduated in 1991 from Colorado State University with a B.S. degree in Computer Science. He obtained an M.S. degree in Computer Science from Michigan State University in 1995, and a Ph.D. degree in Computer Science from Michigan State University in 2000. While at Michigan State, his research crossed the boundaries between computer science and biochemistry. He worked in the Protein Structural Analysis and Design Laboratory, directed by Dr. Leslie Kuhn, and also in the Genetic Algorithms Research and Applications laboratory, directed by Dr. Bill Punch and Dr. Erik Goodman. His work in both labs was directed at developing algorithms to analyze and predict interactions between proteins and water molecules. He is currently an associate professor of computer science and engineering at Wright State University, a member of the faculty of the Biomedical Sciences Ph.D. program and the Environmental Science Ph.D. program, and co-founder and Senior Systems Engineer for Forensic Bioinformatic Services, Inc. (FBS). At FBS, Dr. Raymer co-directs an active research program investigating statistical, biological, and technical issues related to the analysis and interpretation of forensic DNA evidence. Dr. Raymer is also a principal coordinator of the undergraduate program in bioinformatics at Wright State University, the first such program in the nation to be funded by the National Science Foundation. He is co-author of the textbook *Fundamental Concepts of Bioinformatics*, the first undergraduate textbook in bioinformatics, available from Benjamin Cummings publishers.

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## PRINTED SCHOLARSHIP

### Textbook

D. Krane and M. Raymer (2003), *Fundamental Concepts in Bioinformatics*, Benjamin Cummings, Jan. 2003. ISBN 0-8053-4633-3

### Technical articles under review

- M. Westrick, N. DelRaso, D. Mahle, M. Raymer, A. Neuforth, and N. Reo (2008). "Dose and Time Response Metabolomic Analyses of  $\alpha$ -Naphthylisothiocyanate Toxicity in the Rat." *Submitted to Chemical Research in Toxicology*.
- D. Paoletti, D. Krane, T. Doom, and M. Raymer (2008), "Inferring the Number of Contributors to Mixed DNA Profiles." *Submitted to IEEE Transactions on Computational Biology and Bioinformatics. TCBB-2008-11-0196*.
- J. Gilder, T. Doom, M. Raymer, K. Inman, and D. Krane (2008). "Resolution of forensic DNA mixtures." *Submitted to Forensic Science International: Genetics, October 2008*.

### Technical articles published in peer-reviewed journals

- Raiford, Douglas W., Doom, Travis E., Krane, Dan E., & Raymer, Michael E. 2009. A genetic optimization approach for isolating translational efficiency bias. *Accepted for publication in IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 11 February, 2009. IEEE computer Society Digital Library, IEEE Computer Society, <<http://doi.ieeecomputersociety.org/10.1109/TCBB.2008.65>>.
- P. Anderson, N. Reo, N. DelRaso, T. Doom, and M. Raymer (2008), "Gaussian binning: A new kernel-based method for processing NMR spectroscopic data for metabolomics," *Metabolomics*, 4:3, September, 2008.

- D. Raiford, E. Heizer, R. Miller, H. Akashi, M. Raymer, and D. Krane (2008), "Do amino acid biosynthetic costs constrain protein evolution in *Saccharomyces cerevisiae*?" *Journal of Molecular Evolution*, **67**:6, 621-30, December, 2008.
- Raiford, Douglas W., Krane, Dan E., Doom, Travis E., & Raymer, Michael L. 2008a. Automated isolation of translational efficiency bias that resists the confounding effect of GC(AT)-content. *Accepted for publication in EEE/ACM Transactions on Computational Biology and Bioinformatics*, 19 June 2008. Digital Library. IEEE Computer Society, 30 June 2008, < <http://doi.ieeecomputersociety.org/10.1109/TCBB.2008.65>>.
- C. Rowland, R. V. Van Trees, M. Taylor, M. Raymer and D. Krane (2006), "Was the Shawnee War Chief Blue Jacket a Caucasian?" *Ohio Journal of Science*, **106**:4, 2006.
- E. Heizer, D. Raiford, M. Raymer, T. Doom, R. Miller and D. Krane (2006), "Amino Acid Cost and Codon Usage Biases in Six Prokaryotic Genomes: A Whole Genome Analysis." *Molecular Biology and Evolution*, June 2006, **23**:9, 1670–1680.
- D. Paoletti, T. Doom, M. Raymer, and D. Krane. "Assesing the implications for close relatives in the event of similar but non-matching DNA profiles." *Jurimetrics* , **46**:2, Winter, 2006, 161–175.
- D. Paoletti, T. Doom, C. Krane, M. Raymer, and D. Krane (2005), "Empirical Analysis of the STR profiles resulting from conceptual mixtures." *Journal of Forensic Sciences*, **50**:6, November 2005, 1361–1366.
- J. Gilder, S. Ford, T. Doom, M. Raymer, and D. Krane (2004), "Systematic differences in electropherogram peak heights reported by different version of the Genescan® software." *Journal of Forensic Science*, **49**:1, January 2004, 92–85.
- D. Sweeney, M. Raymer, and T. Lockwood (2003), "Antidiabetic and antimalarial biguanide drugs are metal-interactive antiproteolytic agents." *Biochemical Pharmacology*, **66**:4, 663-677.
- T. Doom, M. Raymer, D. Krane, and O. Garcia (2003), "Crossing the interdisciplinary barrier: A baccalaureate computer science option in bioinformatics." *IEEE Transactions on Education*, **46**:3, 387–393, August, 2003.
- M. Raymer, T. Doom, A. Kuhn, and W. Punch (2003), "Knowledge Discovery in Biological Datasets Using a Hybrid Bayes Classifier/Evolutionary Algorithm." *IEEE Transactions on Systems, Man, and Cybernetics*, **33**:5, 802–813, October, 2003.
- M. Raymer, W. Punch, E. Goodman, L. Kuhn, and A. Jain (2000), "Dimensionality Reduction Using Genetic Algorithms." *IEEE Transactions on Evolutionary Computation*, **4**, 164–171.
- M. Raymer, P. Sanschagrin, W. Punch, S. Venkataraman, E. Goodman, and L. Kuhn (1997), "Predicting Conserved Water-Mediated and Polar Ligand Interactions in Proteins Using a K-nearest-neighbors Genetic Algorithm." *Journal of Molecular Biology*, **265**, 445–464.

### **Papers published in official proceedings of peer-reviewed conferences**

- Cooper, G. and Raymer, M. (2009), "Improving Remote Homology Detection Using Sequence Properties and Position Specific Scoring Matrices." *The 2009 International Conference on Bioinformatics and Computational Biology (BIOCOMP '09)*, Las Vegas, NV. July 13-16, 2009. *Acceptance rate: 27%*
- Klingbeil, N., Rattan, K., Raymer, M., Reynolds, D., Mercer, R., Kukreti, A. and Randolph, B., 2007, "A National Model for Engineering Mathematics Education," *Proceedings 2007 ASEE Annual Conference & Exposition*, Honolulu, HI, June, 2007.
- Kelly, B. J., Anderson, P. E., Reo, N. V., DelRaso, N. J. , Doom, T. E., and Raymer, M. L. (2007). "A proposed statistical protocol for the analysis of metabolic toxicological data derived from NMR spectroscopy." *In Proceedings of the 7th IEEE International Conference on Bioinformatics and Bioengineering (BIBE 2007)*, volume II, pages 1414-1418, Cambridge - Boston, Massachusetts, USA IEEE Computer Society.
- Raiford, D. W., Krane, D. E., Doom, T. E., and Raymer, M. L. (2007). "A multi-objective genetic algorithm that employs a hybrid approach for isolating codon usage bias indicative of translational efficiency." *In Proceedings of the 7<sup>th</sup> IEEE International Conference on Bioinformatics and Bioengineering (BIBE 2007)*, volume I, pages 278–285, Cambridge - Boston, Massachusetts, USA (Conference Center at Harvard Medical School). IEEE Computer Society.
- D. Raiford, D. Krane, T. Doom, and M. Raymer, (2007). "A multi-objective genetic algorithm that employs a hybrid approach for isolating codon usage bias indicative of translational efficiency." *Proceedings of*

- the Seventh IEEE Symposium on Bioinformatics and Bioengineering (BIBE 2007)*, Cambridge - Boston, Massachusetts, USA. IEEE Computer Society.
- B.J. Kelly, P.E. Anderson, N.V. Reo, N.J. DeRaso, T.E. Doom, and M.L. Raymer. "Comparison of Statistical Techniques for the Analysis of Metabolic Toxicological Data Derived from NMR Spectroscopy." *Ohio Collaborative Conference on Bioinformatics (OCCBIO) 2007*, Miami University, Oxford, OH, July 9-11, 2007.
- D. Raiford, D. Krane, T. Doom, and M. Raymer (2006), "Isolation and visualization of codon usage biases." In *Proceedings of the 6th IEEE Symposium on Bioinformatics and Bioengineering (BIBE 2006)*, Washington D.C., October 2006, 179–182.
- D. Raiford, M. Raymer, E. Heizer, and D. Krane (2006), "An Investigation of Codon Usage Bias Including Visualization and Quantification in Organisms Exhibiting Multiple Biases." *Ohio Collaborative Conference on Bioinformatics (OCCBIO) 2006*, Athens, OH. June 2006.
- S. Ramachandran, T. Doom, M. Raymer, and D. Krane. "ALU elements as time series genomic data." *Proceedings of Ohio Collaborative Conference on Bioinformatics (OCCBIO) 2006*, Athens, OH. June 2006.
- Klingbeil, N.W., Mercer, R.E., Rattan, K.S., Raymer M.L. and Reynolds, D.B., 2006, "Redefining Engineering Mathematics Education at Wright State University," *Proceedings 2006 ASEE Annual Conference & Exposition*, Chicago, IL, June 2006.
- P. Anderson, D. Raiford, D. Sweeney, T. Doom and M. Raymer (2005), "A Stochastic Model of Protease-Ligand Reactions." *Proceedings of the IEEE Symposium on Bioinformatics and Bioengineering (BIBE 2005)*, October 2005, 306–310.
- N. Klingbeil, R. Mercer, K. Rattan, M. Raymer, D. Reynolds (2005), "The WSU Model for Engineering Mathematics Education." *ASEE Annual Conference Proceedings*, Portland, Oregon. *In press*.
- N. Klingbeil, R. Mercer, K. Rattan, M. Raymer, D. Reynolds (2005), "Work in progress – The WSU model for engineering mathematics education." *35<sup>th</sup> ASEE/IEEE Frontiers in Education Conference*, Indianapolis, IN. *In press*.
- M. Peterson, T. Doom, M. Raymer (2005), "GA-Facilitated KNN Classifier Optimization with Varying Similarity Measures." *Proceedings of the 2005 IEEE Congress on Evolutionary Computation (CEC 2005)*, **3**, 2506–2513.
- M. Peterson, M. Raymer, G. Lamont (2005), "Balanced Accuracy for Feature Subset Selection with Genetic Algorithms." *Proceedings of the 2005 IEEE Congress on Evolutionary Computation (CEC 2005)*, **3**, 2514–2521.
- N. Klingbeil, R. Mercer, K. Rattan, M. Raymer and D. Reynolds (2005), "Redefining Engineering Mathematics Education at Wright State University." *Proceedings of the 2005 ASEE North Central Conference*, Ada, OH, April 2005. *Winner: Overall Best Paper Award*.
- M. Raymer, M. Peterson and T. Doom (2004), "Knowledge Discovery in Large Biological Data Sets Using Hybrid Classifier/Evolutionary Algorithms." *Proceedings the 36<sup>th</sup> Symposium on the Interface: Computational Biology and Bioinformatics*, Baltimore, MD, May 26 – 29, 2004.
- G. Kramer, J. Gallagher, and M. Raymer (2004), "On the Relative Efficacies of \*cGA Variants for Intrinsic Evolvable Hardware: Population, Mutation, and Random Immigrants." in *Proc 2004 NASA/DoD Conference on Evolvable Hardware*. IEEE Press, 2004.
- N. Klingbeil, R. Mercer, K. Rattan, M. Raymer, and D. Reynolds (2004), "Rethinking Engineering Mathematics Education: A Model for Increased Retention, Motivation and Success in Engineering." *ASEE Annual Conference Proceedings*, Salt Lake City (UT), pp. 12169-12180, June 2004.
- M. Peterson, T. Doom, and M. Raymer (2004), "GA-facilitated knowledge discovery and pattern recognition optimization applied to the biochemistry of protein solvation." *Proceedings of ACM Genetic and Evolutionary Computation Conference (GECCO) 2004*, Seattle (WA), pp. 426-437, June 2004.
- G. Cooper, M. Raymer, T. Doom, D. Krane, and N. Futamura (2004), "Indexing genomic databases." *Proceedings of 2004 IEEE international symposium on Bioinformatics and Bioengineering (BIBE)*, Taichung (Taiwan), pp. 587-591, May 2004.
- J. Gilder, D. Krane, T. Doom and M. Raymer (2003), "Identifying patterns in DNA change." *Proceedings of the 2003 Midwest Artificial Intelligence and Cognitive Science Conference (MAICS 2003)*, **34**, 78–84.

- M. Peterson, T. Doom, and M. Raymer (2002), "GA-facilitated cosine classifier optimization with application to the biochemistry of protein-water interactions." *International Conference on High Performance Computing, (HPC-Asia 2002)*, Bangalore (India), December 2002.
- T. Doom, M. Raymer, D. Krane, and O. Garcia (2002), "A Proposed Undergraduate Bioinformatics Curriculum for Computer Scientists." *Proceedings of the ACM Special Interest Group on Computer Science Education (SIGCSE 2002)*, Covington, KY, February, 2002.
- M. Raymer, A. Kuhn, and W. Punch (2001), "Knowledge Discovery in Biological Datasets Using a Hybrid Bayes Classifier/Evolutionary Algorithm." *Proceedings of the 2<sup>nd</sup> IEEE International Symposium on Bioinformatics and Bioengineering (BIBE 2001)*, 236–245.
- D. Sweeney, G. Alter, M. Raymer, and T. Doom (2001), "Profile Combinatorics for Fragment Selection in Comparative Protein Structure Modeling." *Proceedings of the 2<sup>nd</sup> IEEE International Symposium on Bioinformatics and Bioengineering (BIBE 2001)*, 271–278.
- J. Gilder, M. Raymer, and T. Doom (2001), "PocketMol: A Molecular Visualization Tool for the PocketPC." *Proceedings of the 2<sup>nd</sup> IEEE International Symposium on Bioinformatics and Bioengineering (BIBE 2001)*, 11–14.
- M. Raymer, W. Punch, E. Goodman, P. Sanschagrín, and L. Kuhn (1997), "Simultaneous Feature Scaling and Selection Using a Genetic Algorithm." in *Proceedings of the Seventh International Conference on Genetic Algorithms (T. Bäck, ed.)*, Morgan Kaufmann Publishers, San Francisco, pp. 561–567.
- M. Raymer, W. Punch, E. Goodman, and L. Kuhn (1996), "Genetic Programming for Improved Data Mining – Application to the Biochemistry of Protein Interactions." in *Genetic Programming 1996: Proceedings (J. R. Koza, D. E. Goldberg, D. B. Fogel, and R. L. Riolo, eds.)*, MIT Press, Cambridge, MA, pp. 275–381.

**Articles in magazines, letters, book reviews, abstracts, and other publications**

- P. Anderson, N. Reo, N. DelRaso, and M. Raymer (2008). "Gaussian binning for processing NMR spectroscopic data for metabolomics." *U.S. Army Center for Health Promotion and Preventive Medicine 11th Annual Force Health Protection Conference*, August 9-11, 2008. Albuquerque, NM.
- N. Reo, A. Neuforth, W. Couch, M. Raymer, P. Anderson, D. Mahle, and N. DelRaso (2007). "A time and dose response metabonomics study of d-serine toxicity in rats." *Society of Toxicology 47<sup>th</sup> annual meeting*, March 16–20, 2008.
- P. Anderson, L. Mitchell, D. Sweeney, T. Christian, M. Raymer, and G. Alter, "Protein Structure Probing through Chemical Modification", Poster and abstract: *Ohio Collaborative Conference on Bioinformatics (OCCBIO) 2006*, June 2006.
- M. Raymer (2005), "Book Review: Evolutionary Computation in Bioinformatics." *Genetic Programming and Evolvable Machines*, **6**, 229-230.
- M. Peterson, T. Doom, and M. Raymer (2005), "GA-facilitated classifier optimization with varying similarity measures." *Proceedings of ACM Genetic and Evolutionary Computation Conference (GECCO) 2005*, April 2005.
- D. Krane, T. Doom, L. Mueller, M. Raymer, W. Shields and W. Thompson (2004), "Commentary on: Budowle B, Shea B, Niezgoda S, Chakraborty R. CODIS STR loci data from 41 sample populations. *J. Forensic Sci* 2001; 46:453-489." *Journal of Forensic Science*, Dec. 2004.
- T. Doom, M. Raymer, and D. Krane (2004), "Bioinformatics: Where Biology meets Computer Science." *IEEE Potentials*, **23**:1, 24–27, February/March, 2004.
- D. Krane, M. Raymer, and T. Doom (2003), "An interdisciplinary undergraduate bioinformatics curriculum for biological scientists." *Journal of College Science Teaching*, XXXII:296.
- W. Thompson, S. Ford, T. Doom, M. Raymer, and D. Krane (2003), "Evaluating forensic DNA evidence: Breaking open the black box (how to review electronic data)." *The Champion*, (XXVII:3), 25-28.
- W. Thompson, S. Ford, T. Doom, M. Raymer, and D. Krane (2003), "Evaluating forensic DNA evidence: Essential elements of a competent defense review." *The Champion*, (XXVII:2), 16-25.
- J. Gilder, M. Raymer, and T. Doom. "PocketMol: A Molecular Visualization Program for the Pocket PC." Abstract and poster at the Symposium on Bioinformatics for Drug-Development, Toledo (OH), November 2001.
- M. Peterson, M. Raymer, and T. Doom. "Prediction Enhancement of Protein-Water Binding Conservation through Evolutionary Computation." Abstract and poster at the Symposium on Bioinformatics for Drug-Development, Toledo (OH), November 2001.

D. Sweeney, T. Doom, and M. Raymer. "Profile Combinatorics for Fragment Selection in Comparative Protein Structure Modeling." Abstract and poster at the Symposium on Bioinformatics for Drug-Development, Toledo (OH), November 2001.

### **Theses and Dissertations Directed**

*Algorithmic Techniques Employed in the Isolation of Codon Usage Biases in Prokaryotic Genomes*, Douglas W. Raiford III, Ph.D. Dissertation, Spring 2008.

*Evolutionary Methodology for Optimization of Image Transforms Subject to Quantization Noise*, Michael Peterson, Spring 2008.

*A computational framework for analyzing chemical modification and limited proteolysis experiments for high confidence protein structure determination*, Paul Anderson, M.S. Thesis, Fall 2006.

*Multivariate Analysis of Prokaryotic Amino Acid Usage Bias: A Computational Method for Understanding Building Block Selection in Primitive Organisms*, Doug Raiford, M.S. Thesis, Summer, 2005.

*Male-driven substitutional evolution in humans*, Balasubramanian Abiramikumar, M.S. Thesis, Summer, 2004.

*Application of alternative regression methods to quantitative structure-based analysis of drug binding affinity*, Prashanth Athri, M.S. Thesis, Fall, 2003.

*Developing an expert system and discovering new standards for forensic DNA analysis*, Jason Gilder, M.S. thesis, Spring, 2003.

*EC-Facilitated cosine-based knn classifier optimization as applied to protein solvation*, Michael Peterson, M.S. thesis, Spring, 2003.

*Statistical boundaries for recognizing positive selection in mammalian orders using nucleotide substitution rates*, Sundeep Anand, M.S. Thesis, Spring, 2003.

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## **OTHER SCHOLARSHIP**

### **Patents and licensing agreements**

- T. Doom, M. Raymer, O. Garcia, D. Krane (inventors). Exclusive license agreement with Forensic Bioinformatic Services, Inc. (licensee) for the use of the Genophiler software and related technology developed at Wright State University, July 19, 2002.
- D. Krane, T. Doom, M. Raymer, and O. Garcia. "Computerized analysis of forensic DNA evidence", U.S. patent application, Docket No. WRU 0233 PA, April 25, 2003.
- D. Krane, T. Doom, M. Raymer, "A satisfiability approach for mixture deconvolution", (provisional patent application filed, Spring 2005).

### **Selected workshops, seminars, panels, and invited presentations**

M. L. Raymer (2008), "Introduction to Bioinformatics." Invited seminar for the Miami University Workshop on Algorithms and Data Analysis for Bioinformatics. Miami University, Oxford OH, May 14-15, 2008.

M. L. Raymer (2008), "Fundamental Concepts of Bioinformatics." Invited tutorial for the *Ohio Collaborative Conference on Bioinformatics (OCCBIO)*, University of Toledo, Ohio, July 2008.

S. Sahoo, M. Raymer, C. Henson, A. Sheth and W. York (2008) *Ontology driven Semantic Provenance for Heterogeneous Biomimics Experimental Data*. Oral presentation at the *Ohio Collaborative Conference on Bioinformatics (OCCBIO)*, University of Toledo, OH, July 2008.

D. Homer, M. Raymer and N. V. Reo (2008), "Statistical Population Thresholding: A novel non-linear thresholding method for peak and baseline selection in biological spectra containing thermally generated noise." WSU Biomedical Sciences Program Research Retreat, D. H. Ponitz Sinclair Center, Sinclair Community College, Dayton, OH. May 19, 2008. (Platform presentation).

M. L. Raymer (2007), "Charting the winds of evolutionary change: Bioinformatics methods for identifying bias in prokaryotic codon usage." Invited talk for Indiana University Southeast, College of Natural Sciences. November, 2007.

M. L. Raymer (2007), "CSI Revisited: The Science of Forensic DNA Analysis." Invited talk for the IEEE Computer Society, Dayton Chapter. August 2007. Dayton, OH.

# **Michael L. Raymer, Ph.D.**      **CURRICULUM VITÆ**

- M. L. Raymer (2007), "Fundamental Concepts of Bioinformatics." Invited tutorial for the *Ohio Collaborative Conference on Bioinformatics (OCCBIO) 2007*, Miami University, Oxford, OH. July 9-11, 2007.
- Klingbeil, N.W., Mercer, R.E., Rattan, K.S., Raymer M.L. and Reynolds, D.B. (2007), "Engineering Mathematics Education at Wright State University: A Model for Increasing Student Success in Engineering," *Dayton Engineering Sciences Symposium*, October, 2007.
- Klingbeil, N.W., Mercer, R.E., Rattan, K.S., Raymer M.L. and Reynolds, D.B., (2007) "The Wright State Model for Engineering Mathematics Education: Uncorking the First-Year Bottleneck," *A Dialogue on Engineering Education II: The Role of the First Year, ASEE First Year Engineering Workshop*, Notre Dame, IN, July 2007.
- Klingbeil, N.W., Mercer, R.E., Rattan, K.S., Raymer M.L. and Reynolds, D.B. (2007), "A National Model for Engineering Mathematics Education," *ASEE Southeastern Section Conference*, Louisville, KY, April 2007.
- Klingbeil, N.W., Mercer, R.E., Rattan, K.S., Raymer M.L. and Reynolds, D.B. (2007), "Engineering Mathematics Education at Wright State University: Uncorking the First-Year Bottleneck," *26th Annual Conference on the First-Year Experience, National Resource Center for the First-Year Experience & Students in Transition*, Addison, TX, February 2007.
- D. A. Mahle, N. J. DelRaso, M. L. Raymer, A. E. Neuforth, M. Westrick and N. V. Reo (2006), "Combined Urine and Plasma Metabolomic Analysis of  $\alpha$ -Naphthylisothiocyanate (ANIT) Liver Toxicity in the Rat." Presented at *2nd Annual Meeting of the Metabolomic Society*, Boston, MA, June 2006.
- M. L. Raymer, G. Alter, P. Anderson, D. Sweeney and L. Mitchell (2006), "Computational and Experimental Methods for High Confidence Protein Structure Prediction." Invited presentation for the *Ohio Collaborative Conference on Bioinformatics (OCCBIO) 2006*, Athens, OH. June 2006.
- M. L. Raymer (2006), "Fundamental Concepts of Bioinformatics." Invited tutorial for the *Ohio Collaborative Conference on Bioinformatics (OCCBIO) 2006*, Athens, OH. June 2006.
- M. L. Raymer (2005), "Beyond CSI: The Science and Engineering of Forensic DNA Analysis and Interpretation", Invited presentation for the Dayton, OH chapter of the IEEE, July 2005.
- M. L. Raymer, M. Peterson and T. E. Doom (2004), "Knowledge Discovery in Large Biological Data Sets Using Hybrid Classifier/Evolutionary Algorithms." Invited presentation at the *36th Symposium on the Interface: Computational Biology and Bioinformatics*, Baltimore, MD, May 26 – 29, 2004.
- J. R. Gilder, S. Ford, M. Raymer, T. E. Doom and D. E. Krane (2003), "Differences in electropherogram peak heights reported by different versions of the Genescan(R) software." *14th International Symposium on Human Identification*. Promega. Phoenix, AZ. September 29 - October 2, 2003.
- M. Raymer, D. Krane and T. Doom (2003), *NSF workshop on incorporating genomics into the undergraduate curriculum II*. Invited talk, Wheaton College, Norton, MA., June 2003.
- M. Raymer, D. Krane, and T. Doom (2002), *NSF workshop on incorporating genomics into the undergraduate curriculum*. Invited talk, Wheaton College, Norton, MA., June 2002.
- M. Raymer (2002), "Visualization in Bioinformatics." Invited presentation for the Ohio Supercomputing Center/Wright State University Summer Institute for Advanced Computation, Dayton, OH.
- M. Peterson, M. Raymer, and T. Doom (2001), "Prediction Enhancement of Protein-Water Binding Conservation through Evolutionary Computation." Presented at the *Symposium on Bioinformatics for Drug Development*, Toledo, OH, November 16–17, 2001.
- J. Gilder, M. Raymer, and T. Doom (2001), "PocketMol: A Molecular Visualization Program for the Pocket PC." Presented at the *Symposium on Bioinformatics for Drug Development*, Toledo, OH, November 16–17, 2001.
- D. Sweeney, M. Raymer, and T. Doom (2001), "Profile Combinatorics for Fragment Selection in Comparative Protein Structure Modeling." Presented at the *Symposium on Bioinformatics for Drug Development*, Toledo, OH, November 16–17, 2001.
- M. Raymer (2001), "Computational Biology for Drug Design: Understanding how proteins and waters interact." Invited talk for the Ohio Supercomputing Center's *Summer Institute for Advanced Computation*, Dayton, OH, August, 2001.
- M. Raymer (2001), "Molecular graphics: visualization of proteins." Invited talk for the Ohio Supercomputing Center's *Summer Institute for Advanced Computation*, Dayton, OH, August, 2001.
- M. L. Raymer (2000), "An Overview of Bioinformatics and Computational Biology." Invited presentation for the Statewide Users' Group of the Ohio Supercomputer Center, Cincinnati, OH, November 2000.

- L. A. Kuhn, V. Schnecke, M. L. Raymer, and P. C. Sanschagrin (1999), "How proteins fold, flex, and bind other molecules." Workshop on Computational and Theoretical Biology, Michigan State University, April, 1999.
- M. L. Raymer, D. Holstius, P. C. Sanschagrin, L. A. Kuhn (1998), "Identifying the Determinants of Conserved Protein Solvation." Presentation at *Protein Society Symposium*, San Diego, CA, July 1998.
- M. L. Raymer, P. C. Sanschagrin, W. F. Punch, E. D. Goodman, and L. A. Kuhn (1998), "Elucidating the Determinants of Conserved Protein Surface Solvation Using a Genetic Algorithm and Nearest Neighbor Classifier." Presentation at *UCSF/MDI Conference on Molecular Recognition in Drug Design: Docking and Scoring*, San Francisco, California, February 1998.
- M. L. Raymer, W. F. Punch, E. D. Goodman, P. C. Sanschagrin, and L. A. Kuhn (1997), "Simultaneous Feature Extraction and Selection Using a Masking Genetic Algorithm." Presentation at the *Seventh International Conference on Genetic Algorithms (ICGA)*, July 1997.
- M. L. Raymer, W. F. Punch, P. C. Sanschagrin, E. D. Goodman, and L. A. Kuhn (1997), "Discovering the Chemistry of Conserved First-Shell and Active-Site Hydration in Proteins Using Pattern Classification with a Genetic Algorithm." Presentation at *Protein Society Symposium*, Boston, Massachusetts, July 1997.
- M. L. Raymer, W. F. Punch, E. D. Goodman, and L. A. Kuhn (1996), "Genetic Programming for Improved Data Mining – Application to the Biochemistry of Protein Interactions." Presentation at *Genetic Programming 1996: the First Annual Conference*, Stanford University, Palo Alto, California, July 1996.
- M. L. Raymer (1996), "Learning From Nature - Genetic Algorithms Applied to Protein Recognition." Presentation for the Macromolecular Structural Techniques Group at Michigan State University, January, 1996.
- M. L. Raymer, W. F. Punch, E. D. Goodman, P. C. Sanschagrin, and L. A. Kuhn (1996), "Pattern Recognition Using Evolutionary Algorithms Applied to Understanding Water-Mediated Recognition in Proteins." Presented at *Sandia National Laboratory Workshop on Computational Molecular Biology*, Albuquerque, New Mexico, March 1996.
- M. L. Raymer, S. Venkataraman, W. F. Punch, E. D. Goodman, and L. A. Kuhn (1995), "Predicting Conserved Water-Mediated Interactions in Protein Active Sites." Invited presentation at the *American Crystallographic Association Annual Meeting*, Montreal, Quebec, Canada, July 1995.
- M. L. Raymer, W. F. Punch, E. D. Goodman, M. Pei, and L. A. Kuhn (1995), "Prediction of Conserved Water Sites Between Independently Solved Protein Structures Using a Genetic Algorithm and a K Nearest Neighbor Classifier." *West Coast Protein Crystallography Workshop*, Pacific Grove, California, March 1995.
- L. A. Kuhn, P. C. Sanschagrin, and M. L. Raymer (1997), "Using Cluster Analysis to Identify Conserved Binding Sites in Proteins." Presentation at the *Protein Society Symposium*, Boston, Massachusetts, July 1997.
- L. A. Kuhn, W. B. Anderson, C. E. Barkham, M. L. Raymer, and P. C. Sanschagrin (1997), "Implications of Structural Comparison of Prostaglandin Synthase Isozymes and Ribonucleotide Reductase for Understanding their Specificity and Catalysis." Presentation at the *American Heart Association, Michigan Affiliate Cardiovascular Research Forum*, Ann Arbor, September 1997.
- P. C. Sanschagrin, M. L. Raymer, and L. A. Kuhn (1997), "Cluster Analysis of Multiple Serine Protease Structures Identifies Conserved Water Sites Involved in Structure and Specificity." Presentation at *West Coast Protein Crystallography Workshop*, Pacific Grove, California, March 1997.
- L. A. Kuhn, M. L. Raymer, P. C. Sanschagrin, E. D. Goodman, and W. F. Punch (1996), "Resolving Water-Mediated and Polar Ligand Recognition Using Genetic Algorithms." Presented at the *International Conference on Protein Folding and Design*, National Institutes of Health, Bethesda, Maryland, April 1996.
- L. A. Kuhn, M. L. Raymer, W. F. Punch, P. C. Sanschagrin, and E. D. Goodman (1996), "Predicting and Analyzing Determinants of Water-Mediated Ligand Recognition." Presented at the *International Union of Crystallography Congress and General Assembly*, Seattle, Washington, August 1996.
- L. A. Kuhn, M. L. Raymer, W. F. Punch, P. C. Sanschagrin, and E. D. Goodman (1996), "Predicting and Analyzing Determinants of Water-Mediated Ligand Recognition." *International Union of Crystallography Congress and General Assembly*, Seattle, Washington, August 1996.
- L. A. Kuhn, M. L. Raymer, P. C. Sanschagrin, E. D. Goodman, and W. F. Punch III (1995), "Genetic Algorithm Prediction of Water-mediated Ligand Interactions and the Implications for the Chemistry of

Water Binding.” Invited talk for the Program in Mathematics and Molecular Biology Symposium: From DNA to Protein Structure and Function, Santa Fe, NM, November, 1995.

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## ACADEMIC SERVICE

- Ad hoc Academic Services Committee, Wright State University, 2008-2009.
- Curriculum Committee, Biomedical Sciences Ph.D. Program, Wright State University, 2007-2008.
- Admissions Committee, Biomedical Sciences Ph.D. Program, Wright State University, 2005-2007 (*Chair: 2006-2007*), 2008-2009.
- Steering Committee, Department of Computer Science and Engineering, 2005-2008 (*Chair: 2007-2008*).
- Ad-hoc search committee for Recruitment Officer, Department of Computer Science and Engineering, 2006.
- Undergraduate Studies Committee, Department of Computer Science and Engineering, 2005-2006, 2007-2008, *Chair 2008-2009*.
- Chair, Applications Area Committee, Department of Computer Science and Engineering, 2004-2005.
- Admissions Committee, Biomedical Sciences Ph.D. Program, Wright State University, 2004-2005.
- Ad-hoc Program Assessment and Planning Committee, Department of Computer Science and Engineering, 2004-2005.
- Ph.D. Qualifiers Committee (Architecture and Computer Science Math), Department of Computer Science and Engineering, 2003-present.
- Graduate Studies Committee, Department of Computer Science and Engineering, 2004-2005.
- Faculty search committee, Department of Computer Science and Engineering, 2002-2005.
- Ad-hoc math solutions committee, College of Engineering and Computer Science, 2003-2005.
- Faculty Advisor, Wright State University Tae Kwon Do Club, 2002 – 2006.
- Faculty Advisor, Wright State University Go Club, 2008 – present.

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## PROFESSIONAL SERVICE

- Co-director: Research Infrastructure – Ohio Consortium for Bioinformatics. <http://ohiobioinformaticsconsortium.com>
- Member, Department of Homeland Security Life Sciences and Technology Expert Survey Group, United States of America Department of Homeland Security, 2008.
- Program committee, *Sixth European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO)* 2008, 2009.
- Associate Editor, *The International Journal of Computational Bioscience*, Acta Press, 2008.
- Editorial Board, *The International Journal of Computational Biology and Drug Design*, Inderscience publishing, 2007, 2008.
- Editorial Board, *Open Cybernetics and Systemics Journal*, Bentham Science Publishers, 2007.
- Editorial Board: *International Journal of Computational Intelligence in Bioinformatics and Systems Biology (IJCIBSB)*, 2007.
- Poster Chair and Program Committee member, *IEEE 7<sup>th</sup> Symposium on Bioinformatics and Bioengineering (BIBE 2007)*.
- Reviewer, *Third Indian International Conference on AI (IICAI)*, 2007.
- Reviewer, *International Journal of AI Tools*, 2007.
- Program Committee, *Ohio Collaborative Conference on Bioinformatics (OCCBIO)*, 2007, 2008.
- Panelist, National Science Foundation CISE Pathways to Revitalized Undergraduate Education (CPATH), 2007.
- Program Committee, *2007 International Conference on Bioinformatics and Computational Biology (BIOCOMP'07)*.
- Program Committee, *Fifth European Conference on Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics (EvoBIO 2007)*, 11-13 April 2007, Valencia, Spain.
- Program Chair, Bioinformatics: *IEEE 6<sup>th</sup> Symposium on Bioinformatics and Bioengineering (BIBE 2006)*.

- Program Committee: Biological Applications Track, *ACM Genetic and Evolutionary Computation Conference (GECCO)*, 2006, 2007.
- Conference organizer: *The Science of DNA Profiling – Forensic Bioinformatics Annual Conference*, 2001 – 2007.
- Program Committee, *ACM Genetic and Evolutionary Computation Conference (GECCO)*, 2005.
- Reviewer, *Bioinformatics* (Oxford), 2006, 2007, 2008.
- Reviewer, *Journal of Heuristics*, 2005.
- Reviewer, *Pattern Analysis and Applications*, 2005.
- Reviewer, *IEEE Transactions on Evolutionary Computation*, 2005 – 2007.
- Reviewer, *IEEE Transactions on Neural Networks*, 2004, 2005.
- Reviewer, *IEEE Transactions on Systems, Man, and Cybernetics*, 2003, 2004, 2005.
- Reviewer, *IEEE Transactions on Knowledge Discovery and Data Engineering*, 2004.
- Reviewer, *Genetic Programming and Evolvable Machines*, 2003, 2004.
- Textbook reviewer, Oxford University Press, 2006.
- Textbook reviewer for John Wiley and Sons, 2004.
- Textbook reviewer for Thompson Publishing, 2004.
- NSF/CISE REU-SITE review panel member, November, 2003.
- Reviewer, 3<sup>rd</sup> *IEEE International Symposium on Bioinformatics and Bioengineering (BIBE 2003)*.
- NSF/CISE CAREER review panel member, December, 2002.
- NSF/CISE CRCD review panel member, January 24, 2002.
- Program committee, 2<sup>nd</sup> *IEEE International Symposium on Bioinformatics and Bioengineering (BIBE 2001)*.
- Reviewer, *Journal of Computer-Aided Molecular Design* (Kluwer Academic Publishers), 2002.
- Reviewer, *IEEE Transactions on Knowledge and Data Engineering*, 2002.
- Reviewer, *Journal of Intelligent Automation and Soft Computing*, 2001.
- IEEE Computer Society, Member, 2002–present.

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**CONSULTING**

- Consulting senior systems engineering consultant and founding partner of Forensic Bioinformatic Services (<http://www.bioforensics.com>) (2002-present).