1. Name, Position and Academic Department

Charles E. Lawrence
Professor of Applied Mathematics
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2. Home Address

108 Long Pasture Way
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3. Education

1967	B.S.	Rensselaer Polytechnic Institute	Physics
1971	Ph.D.	Cornell University	Applied Operations Research and Statistics in Environmental Engineering

Dissertation topic: “Population Dynamics”

4. Professional Appointments

1971 -1975	Assistant Professor, Systems Engineering and Operations Research and Statistics, Rensselaer Polytechnic Institute.
1971-1975	Consultant to the Ministry of Maternal and Child Health, Dominican Republic.
1975 -1981	Director of Operations Research and Statistics, Division of Epidemiology, New York State Department of Health.
1981-2003	Chief of the Biometrics/Bioinformatics Laboratory, Wadsworth Center for Laboratories and Research, New York State Department of Health.
1985-1992	Statistical Consultant, Harrison Radiator Division General Motors Corp.
1992-1996	Visiting Scientist, National Center for Biotechnology Information, NLM-NIH.
2000-2003	Research Professor, Computer Science Department, Rensselaer Polytechnic Institute. (one day per week)
2004-2006	Director of the Center for Computational Molecular Biology, and Professor of Applied Mathematics, Brown University.
2004-present	Professor of Applied Mathematics and Center for Computational Molecular Biology, Brown University

5. Completed Publications

c. **Refereed journal articles**

1. Using controls to limit false discovery in the era of big data(2018) , Matthew M. Parks, Benjamin J. Raphael and Charles E. Lawrence, BMC Bioinformatics, 19:323, https://doi.org/10.1186/s12859-018-2356-2

2. Characterization and visualization of RNA secondary structure Boltzmann ensemble via information theory (2018), Luan Lin, Wilson H McKerrow, Bryce Richards, Chukiat Phonsom and Charles E Lawrence, BMC Bioinformatics, 2018, accepted

3. Autoregressive Statistical Modeling of a Peru Margin Multi-Proxy Holocene Record Shows Correlation Not Cause, Flickering Regimes and Persistence , (2018) Seonmin Ahn, Baylor Fox-Kemper, Timothy Herbert, Charles Lawrence, In review

4. The Role of Uncertainty in Estimating Lead/Lag Relationships in Marine Sedimentary Archives: A Case Study From the Tropical Pacific (2017), D. Khider, Ahn, L. E. Lisiecki2, C. E. Lawrence , and M. Kienast, Paleoceanography, Volume 32, Issue 11, 1275, DIO: 10.1002/2016PA003057

5. A probabilistic Pliocene–Pleistocene stack of benthic δ^{18}O using a profile hidden Markov model (2017), Seonmin Ahn Deborah Khider Lorraine E Lisiecki Charles E Lawrence, *Dynamics and Statistics of the Climate System*, Volume 2, Issue 1

6. Predicting RNA hyper-editing with a novel tool when unambiguous alignment is impossible, McKerrow, WH. Savva, YA. Rezael, A, Reenan, RA, Lawrence, CE. (2017), *BMC Genomics* 18:522, DOI 10.1186/s12864-017-3898-9

7. Guang, AF. Zapata, F. Howison, M. Lawrence, CE. Dunn, CW. An Aitergrated Perspective on Phylogenetic Workflows. Trends in Ecology and Evolutions, Volume 31, Issue 2, p116–126, 2016, DOI: 10.1016/j.tree.2015.12.007

8. Detecting non-allelic homologous recombination from high-throughput sequencing data, (2015) Matthew M Parks, Charles E Lawrence, and Benjamin J Raphael. Genome Biology, 16:72, DOI 10.1186/s13059-015-0633

9. Probabilistic sequence alignment of stratigraphic records (2014), Luan Lin, Deborah Khider, Lorraine E. Lisiecki, and Charles E. Lawrence, Paleoceanography, 29(10): 976-9898, □ DOI: 10.1002/2014PA002713

10. The Bayesian Change Point and Variable Selection Algorithm: Application to the δ18O Proxy Record of the Plio-Pleistocene (2014) Ruggieri, Eric, Lawrence, C. E., Journal of Computational and Graphical Statistics, *Volume 23, Number 1, Pages 87–110 DOI: 10.1080/10618600.2012.707852*

11. Genome-Wide Analysis of A-to-I RNA Editing via Single Molecule Sequencing in *Drosophila,* (2013) Georges St. Laurent, Michael R. Tackett, Sergey Nechki, Dmitry Shtokalo, Denis Antonets, Yiannis A. Savva, Rachel Maloney, Philipp Kapranov, Charles E. Lawrence, and Robert A. Reenan, Nature Structural and Molecular Biology, 20(11):1333-9. doi: 10.1038/nsmb.2675.

12. Assessing the validity and reproducibility of genome scale predictions, (2013) Lauren A. Sugden 1_, Michael R. Tackett 2, Yiannis A. Savva 3, William A. Thompson 1, Charles E. Lawrence, Bioinformatics, 15;29(22):2844-51. doi: 10.1093/bioinformatics/btt508 Vol. 29 no. 22.

13. Auto-regulatory RNA editing fine-tunes mRNA re-coding and complex behavior in *Drosophila*, (2012) Yiannis A. Savva1, James E.C Jepson1, Asli Sahin1, Arthur U. Sugden, Jacquelyn S. Dorsky, Lauren Alpert, Charles Lawrence, Robert A. Reenan, Nature Communications 3:790 | DOI: 10.1038/ncomms1789 | www.nature.com/naturecommunications

14. On efficient calculations for Bayesian variable selection, (2012) Eric Ruggieri, and Charles E. Lawrence, *Computational Statistics and Data Analysis,* 56: 1319-1332, doi:10.1016/j.csda.2011.09.026

15. RNAG: a new Gibbs sampler for predicting RNA secondary structure for unaligned sequences, (2011) Donglai Wei, Lauren V. Alpert and Charles E. Lawrence, *Bioinformatics*, Vol. 27 no. 18, pages 2486–2493 doi:10.1093/bioinformatics/btr421

16. Chromatin remodeling in the aging genome of Drosophila (2010), Jason G. Wood,1 Sara Hillenmeyer,1 Charles Lawrence,2 Chengyi Chang,1 Suzanne Hosier,1 Will Lightfoot,1 Eric Mukherjee,1 Nan Jiang,1 Christoph Schorl,1 Alexander S. Brodsky,1 Nicola Neretti1,3 and Stephen L. Helfand, Aging Cell 9:971-778

17. Change point method for detecting regime shifts in paleoclimatic time series: Application to δ-O^{18} time series of the Plio-Pleistocene, Paleoceanography, (2009) Ruggieri, E., T. Herbert, K. T. Lawrence, and C. E. Lawrence 24, PA1204, doi:10.1029/2007PA001568.

18. Exact Calculation of Distributions on Integers, with Application to Sequence Alignment (2009), Newberg LA. Lawrence CE. Journal of Computational Biology, 16(1): 1-18

19. Centroid estimators for inference in high-dimensional discrete spaces (2008) Luis E. Carvalho, and Charles E. Lawrence, *PNAS: USA*, 105: 3209–3214

20. Automated mapping of large-scale chromatin structure in ENCODE. (2008) Lian H, Thompson WA, Thurman R, Stamatoyannopoulos JA, Noble WS, Lawrence CE. *Bioinformatics*. 1;24(17):1911-6. Epub 2008 Jun 30.

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26. PhyloScan: Identification of transcription factor binding sites using cross-species evidence (2007) C Steven Carmack, Lee Ann McCue, Lee A Newberg, and Charles E Lawrence, (in press) *Algorithms for Molecular Biology, 2:1* doi:10.1186/1748-7188-2-1

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28. Clustering of RNA secondary structures with application to messenger RNAs, (2006) Ye Ding Y, Chan CY, and Lawrence CE, Journal of Molecular Biology, 359: 554–571

29. The Relative Inefficiency of Sequence Weights Approaches in Determining a Nucleotide Position Weight Matrix (2005), Newberg, LA. MuCue, LA. and Lawrence, CE. *Statistical Applications in Genetics and Molecular Biology*, 4(1) DOI: 10.2202/1544-6115.1135

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42. Bayesian Clustering with Variable and Transformation Selections (with discussion). Liu JS, Zhang JL, Palumbo H, Lawrence CE. *Bayesian Statistics*, 7:249-275, Bernardo JM, Berger JO, David AP, Smith AFM. (eds). Oxford: Clarendon Press, 2003.

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44. An Application of Nonlinear Optimization in Molecular Biology. Ecker JG, Kupferschmid M, Lawrence CE, Reilly AA, Scott ACH. *Eur J Oper Res*, 138: 452-458, 2002.

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46. Identification of a Novel Class in the Alpha/Beta Hydrolase Fold Superfamily: the N-myc Differentiation-Related Proteins. Shaw E, McCue LA, Lawrence CE, Dordick JS. *Proteins* 47(2):163-168, 2002.

47. Factors Influencing the Identification of Transcription Factor Binding Sites by Cross Species Comparison. McCue LA, Thompson W, Carmack CS, Lawrence CE. *Genome Res,* 12:1523-532, 2002.

48. BALSA: Bayesian Algorithm for Local Sequence Alignment. Webb BJ, Liu JS, Lawrence CE. *Nucleic Acids Res,* 30(5):1268-1277, 2002.

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http://lib.stat.cmu.edu/bayesworkshop/2001/invited.html#liu.

50. Statistical Prediction of Single-Stranded Regions in RNA Secondary Structure and Application to Predicting Effective Antisense Target Sites and Beyond. Ding Y, Lawrence CE. *Nucleic Acids Res,* 29(5):1034-1046, 2001.

51. Phylogenetic Footprinting of Transcription Factor Binding Sites in Proteobacterial Genomes. McCue LA, Thompson W, Carmack CS, Ryan MP, Liu JS, Derbyshire V, Lawrence CE. *Nucleic Acids Res,* 29:774-782, 2001.

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53. Human-Mouse Genome Comparison to Locate Human Regulatory Sites. Wasserman WW, Palumbo M, Thompson W, Fickett JW, Lawrence CE. *Nature-Genetics,* 26(2):225-228, 2000.

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57. Markovian Structures in Biological Sequence Alignments Author(s): Jun S. Liu, Andrew F. Neuwald, Charles E. Lawrence Source: Journal of the American Statistical Association, 94:1-15, 1999

58. Bayesian Inference on Biopolymer Models. Liu JS, Lawrence CE. *Bioinformatics*, (invited paper) 15:38-52, 1999.

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60. Motifs and Structural Fold of the Cofactor Binding Site of Human Glutamate Decarboxylase. Qu K, Martin DL, Lawrence CE. *Protein Sci*, 7:1092-1105, 1998.

61. Bayesian Adaptive Sequence Alignment Algorithms. Zhu J, Liu JS, Lawrence CE. *Bioinformatics*, 14:25-39, 1998.

62. Bayesian Adaptive Alignment and Inference. Zhu J, Liu J, Lawrence CE. Proceedings of the Fifth International Conference on Intelligent Systems for Molecular Biology, *ISMB,* 5:358-368, 1997.

63. Extended Homology Prediction for Motif Structure by Multiple Sequence Alignment. Qu K, Lawrence CE. *Mathematical Modeling & Scientific Computing,* Vol. 8, 1997.

64. Identification and Characterization of Two Groups of Congenital Hypothyroid Infants: Implications for Newborn Screening. Auger IE, Bellisario R, Koerner-Rabatoy S, Lawrence CE. *Early Human Develop,* 44:235-245, 1997.

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71. Statistical Models for Multiple Sequence Alignment: Unification and Generalizations. Liu JS, Lawrence CE. *Proceedings American Statistical Association, Statistical Computing Section*, 21:1-8, 1995.

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94. Distribution of Accessible Surfaces of Amino Acids in Globular Proteins. Lawrence C, Auger I, Mannella C. *Proteins: Structure, Function, and Genetics*, 2:153-161, 1987.

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99. Broken Appointments at a Neighborhood Health Center: Emphasis on Weather. Morse D, Coulter M, Napodano RJ, Hwang HL, Lawrence CE. *Med Care*, 22(9):813, 1984.

100. Polychlorinated Biphenyls: Influence on Birthweight and Gestation. Taylor PR, Lawrence CE, Hwang HL, Paulson AS. *Am J Public Health*, 74(10):1153-1154, 1984.

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b. chapters in books

1. A Gibbs Sampler for the Detection of Subtle Motifs in Multiple Sequences. Lawrence CE, Altschul S, Wootton J, Boguski M, Neuwald AF, Liu JS. Proceedings of the Twenty-Seventh Annual Hawaii International Conference on System Sciences, 5:245-254, 1994.

2. Empirical Estimation of Exposure in Retrospective Epidemiologic Studies. Lawrence, CE, Taylor, P. Environmental Epidemiology, Lewis Publishers, Inc., Kopfler F., Craun G. eds., 1986.

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h. papers read

Referee for:

Bioinformatics
Nucleic Acids Research
Genome Research
PLoS Computational Biology
Biometrics
Nature Genetics
PNAS Proceedings of the National Academy of Sciences in the USA
Cell

k. White papers

Sequencing of Multiple Strains of *Shewanella*, Facultative Metal-Reducing Gamma Proteobacteria. Fredrickson, J., Kolker, E., Lawrence, CE., McCue, LA., DiChristina, T., Nealson, K. For Consideration by the U.S. Department of Energy, Office of Biological and Environmental Research, 2003.

6. Research Grants

a. Current grants

08/10 – 07/16 “IGERT reverse ecology integration of genomes, organisms, and environments”
Collaborating Participant NSF $5,275,683

9/16 – 9/21 “COBRE Computational Biology of Human Disease”, NIH, Mentor

b. Pending

04/17 – 04/20 Collaborative Proposal: Bringing the Late Pleistocene into focus: Better estimates of ages and ocean circulation through data-model comparison, Principle Investigator, NSF, $251,645

c. Completed grants

09/10 – 09/14 ” CMG Collaborative Research: Probabilistic Stratigraphic Alignment and
Principle investigator Dating of Paleoclimate Data”
NSF proposal#: 1025438, Approved for funding starting 9/30/2010-9/30/2014 , $603,526

01/11 – 12/15 “Computational approaches for structural variation studies”
Co-Principle Investigator NIH –R01 $2,477,7600

05/09 – 05/13 “Bayesian computational approaches for gene regulation studies of bioethanol
Principal investigator and biohydrogen production.”
DE-FG02-04ER63942, $445,000

09/04-08/09 "Development of Bioinformatics and Experimental Technologies for
Principal Investigator Identification of Prokaryotic Regulatory Networks"
DOE: DE-FG02-04ER63942 Direct: $1,451,530

07/03-06/08 "Rational Design Tools for Antisense Nucleic Acids"
Co-PI NIH/NIGMS: RO1 GM068726 Direct: $760,000

10/01-09/06 "Identification and Characterization of Transcription Regulation
Co-PI Networks in Environmentally Significant Species"
DOE: DEFG0201ER63204 Direct: $1,162,135

12/99-11/06 "Detecting Subtle Sequence Signals in Genomic Sequence",
Principal Investigator NIH: R01-HG01257 Direct: $1,185,529

07/02-06/05 "Statistical Tools for RNA Folding Prediction and Antisense Design for
Co-PI High Throughput Functional Genomics" Direct: $395,640

10/01-12/04 "Bioinformatics Center Extramural Construction Facilities Grant"
Scientific Director NIH: C06 RR14537-01A2 Direct: $1,394,032
of the Center (Wadsworth Research Office) JH Galivan, PI

7. Service

i. University

2016	Tenure and Promotions Review Committee, Applied Mathematics, Chair
2016	Promotion Review Committee, Applied Mathematics, member
2009-2017	Graduate Admission Committee, Center for Computational Molecular Biology
2008-2015	Prager fellowship review committee, Division of Applied mathematics
2008-2017	Division of Applied Mathematics under graduate advisor
2008-2014	Division of Applied Mathematics under graduate curriculum committee
2008-2009	Faculty Search Committee, Center for Computational Molecular Biology
2007-2008	Faculty Search Committee, Center for Computational Molecular Biology
2006-2007	Faculty Search Committee, Center for Computational Molecular Biology
2007-2008	Faculty Search Committee, Division of Applied Mathematics
2005-2006	Faculty Search Committee, Chair: Center for Computational Molecular Biology
2004-present	Undergraduate Curriculum committee, Division of applied mathematics
2004-2005	Faculty Search Committee, Chair: Center for Computational Molecular Biology
2004-Present	Curriculum Committee, Center for Computational Molecular Biology

ii. Profession

02/05 – 1/10	Associate Editor, Public Library of Science (PLoS) Computational Biology
02/05	Editorial Board, Bioinformatics and Computational Biology
03/05	Genomic Sciences Graduate Program Review Team, North Carolina State University
Various	Ad Hoc Study Section Member, LIM-NIH and NHGRI-NIH
09/99-09/03	Permanent member Genome Research Review Committee (NHGRI-NIH)

iii. Community

8. Academic Honors

Fellow of the American Statistical Association

Mitchell Prize for outstanding applied Bayesian statistics paper in the year 2000

Centroid estimators for inference in high-dimensional discrete spaces (2008), Luis E. Carvalho, and Charles E. Lawrence, *PNAS: USA*, 105: 3209–3214. Reported as a must read paper in the Faculty of 1000.

Exact Calculation of Distributions on Integers, with Application to Sequence Alignment, Newberg and Lawrence, J. Computational Biology (January, 2009), selected as a highlighted article.

Visiting faculty, Institute of Pure and Applied Mathematics, UCLA 10/00, & 12/00

Rensselaer Alumni Association Fellow

Member American Statistical Association

Member International Society for Computational Biology

Member Sigma Xi

9. Teaching

a) Statistical Inference in Computational Molecular Biology and Genomics (Brown: APAM108O)
b) Operations Research Deterministic models (Brown: APAM 1210)
c) Inference in Molecular Biology (Brown: APAM 2820)
d) Statistical Inference I (Brown: APAM 1650)
e) Computational Probability and Statistics (Brown: APMA1690)