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#### Refereed Publications

1. 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
2. The Bayesian Change Point and Variable Selection Algorithm: Application to the  $\delta^{18}\text{O}$  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](https://doi.org/10.1080/10618600.2012.707852)
3. 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.
4. 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.
5. Auto-regulatory RNA editing fine-tunes mRNA re-coding and complex behavior in *Drosophila*, (2012) Yiannis A. Savva<sup>1</sup>, James E.C Jepson<sup>1</sup>, Asli Sahin<sup>1</sup>, 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](http://www.nature.com/naturecommunications)
6. 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](https://doi.org/10.1016/j.csda.2011.09.026)
7. 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
8. Ruggieri, E., T. Herbert, K. T. Lawrence, and C. E. Lawrence (2009), Change point method for detecting regime shifts in paleoclimatic time series: Application to  $\delta\text{-O}^{18}$  time series of the Plio-Pleistocene, *Paleoceanography*, 24, PA1204, doi:10.1029/2007PA001568
9. Exact Calculation of Distributions on Integers, with Application to Sequence Alignment (2009), Newberg LA. Lawrence CE. *Journal of Computational Biology*, 16(1): 1-18
10. Centroid estimators for inference in high-dimensional discrete spaces (2008) Luis E. Carvalho, and Charles E. Lawrence, *PNAS: USA*, 105: 3209–3214
11. [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.

12. Measuring Global Credibility with Application to Local Sequence Alignment, (2008) Webb-Robertson BJM, McCue LA, and Lawrence CE. *PLoS Computational Biology* 4(5): e1000077 doi:10.1371/journal.pcbi.1000077.
13. Using the Gibbs Motif Sampler for phylogenetic footprinting. (2007), [Thompson W](#), [Conlan S](#), [McCue LA](#), [Lawrence CE](#). *Methods Mol Biol*. 2007;395:403-24.
14. Effect of target secondary structure on RNAi efficiency. (2007) Shao Y, Chan CY, Maliyekkel A, Lawrence CE, Roninson IB, Ding Y. *RNA*. 2007 Oct;13(10):1631-40.
15. The Gibbs Centroid Sampler, (2007) Thompson WA, Newberg, LA, Conlan SP, McCue, LA, Lawrence, CE. *Nucleic Acids Res*, 2007 35(Web Server issue):W232-W237.
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17. 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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