Curriculum vitae of Peter G. Clote

Professor of Biology with courtesy appointment in Computer Science Boston College, 140 Commonwealth Avenue, Chestnut Hill, MA 02467

Education

1985: Doctorat d'Etat en Mathématiques, Université Paris 7 (France).

1979: PhD in Mathematics, Duke University, Durham, NC.

1975: Fulbright Fellow, Mathematics, Universität Köln.

1973: Sc. B. in Mathematics, Massachusetts Institute of Technology, Cambridge, MA.

Professional Appointments

2002— Professor, Department of Biology, Boston College Courtesy appointment in Computer Science. 1995–2000 Gerhard-Gentzen Chair, Institut für Informatik, Ludwig-Maximilians-Universität München. 1987–2002 Professor, Department of Computer Science, Boston College. 1984–1987 Associate Professor, Department of Computer Science, Boston College. 1979–1984 Assistant Professor, Département de Mathématiques, Université Paris 7 (France).

Visiting Positions in the past 10 years

Apr-July 2014 Visiting Professor,

Recent invited talks

- 1) "Network properties of RNA secondary structures", invited talk at Canadian Discrete and Algorithmic Mathematics (CanaDAM) Ryerson University, Toronto, June 12-15, 2017
- 2) "Designing RNA molecules" at Proteomics and Genomics Conference, Costa Rica, Oct 18-22, 2016.
- 3) "High Performance Computing in RNA Bioinformatics" at 19th IEEE High Performance Extreme Computing, 17 Sept, 2015, Waltham, MA.
- "Network properties of the ensemble of RNA structures" at WABI 2015, IEEE BCB/WABI 2015, Sep 10, 2015
- 5) "Conformational entropy and network properties of RNA secondary structures", University of Massachusetts at Boston, Oct 28, 2015

Synergetic Activities

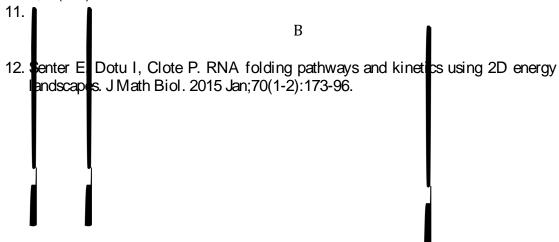
Outreach and transfer of research:

Organizer of NSF-funded "RNA Summer School", June 13-17, 2016, as well as in June 2014 and July

Recent re earc rant B A AB

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- 2015 Nov 10;10(11):e0137859. doi: 10.1371/journal.pone.0137859.
- 8. Clote P, Bayegan A. Network Properties of the Ensemble of RNA Structures. PLoS One. 2015 Oct 21;10(10):e0139476. doi: 10.1371/journal.pone.0139476.
- P. Clote. Abstract: Network properties of the ensemble of RNA structures. 15th International Workshop, WABI 2015, Atlanta, GA, USA, September 10-12, 2015. Eds. Mihai Pop, Hélène Touzet, Eds. Lecture Notes in Bioinformatics, Springer Verlag, pp 3-5, ISBN 978-3-662-48220-9 (2015).
- Garcia-Martin JA, Dotu I, Clote P. RNAiFold 2.0: a web server and software to design custom and Rfam-based RNA molecules. Nucleic Acids Res. 2015 Jul 1;43(W1):W513-21.



Full Publication List of Peter G. Clote

Books

- Genetics, Genomics, Proteomics and Bioinformatics Section editor of Bioinformatics, <u>Modern Programming Paradigms in Biology</u>, in the 8-volume encyclopedia entitled <u>Genetics, Genomics, Proteomics and Bioinformatics</u> (2005), ISBN-13 978-0-470-84974-3.
- 2. <u>Computational Molecular Biology: An Introduction</u>, P. Clote and R. Backofen, Japanese translation (2005), 272 pages, ISBN 4-320-05615-9.
- 3. <u>Boolean Functions and Computation Models</u>, P. Clote and E. Kranakis, Springer-Verlag, 601 pages (2002), ISBN 3-540-59436-1. BibTeX entry
- 4. Computational Biology: an Introduction, P. Clote and R. Backofen, John Wiley

Ramajo, Ivan Dotu, Peter Clote, and Encarna Martinez-

- page abstract). M. Deng et al. (Eds.): RECOMB 2013, LNBI 7821, pp. 264–265, 2013. Springer-Verlag Berlin Heidelberg 2013.
- 35. Juan Antonio Garcia-Martin, Peter Clote, Ivan Dotu. RNAiFold: A constraint programming algorithm for RNA inverse folding and molecular design. J Bioinform Comput Biol 11(2): 1350001, 2013.
- 36. E. Senter, S. Sheik, I. Dotu, Y. Ponty, P. Clote. Using the Fast Fourier Transform to accelerate the computational search for RNA conformational switches. PLoS One. 2012 7(12):e50506. doi: 10.1371/journal.pone.0050506. Epub 2012 Dec 19.
- 37. E. Fusy and P. Clote. Combinatorics of locally optimal RNA secondary structures. J Math Biol. 2012 Dec 22. [Epub ahead of print]
- 38. Zarringhalam K, Meyer MM, Dotu I, Chuang JH, Clote P. Integrating chemical footprinting data into RNA secondary structure prediction. PLoS One. 2012;7(10):e45160. doi: 10.1371/journal.pone.0045160
- 39. Peter Clote, Feng Lou, William A. Lorenz. <u>Maximum expected accuracy structural neighbors of an RNA secondary structure.</u> BMC Bioinformatics BMC Bioinformatics. 2012 Apr 12;13 Suppl 5:S.
- Peter Clote, Stefan Dobrev, Ivan Dotu, Evangelos Kranakis. Danny Krizanc, Jorge Urrutia. On the Page Number of Secondary Structures with Pseudoknots. J Math Biol. 2012 Dec;65(6-7):1337-57. doi: 10.1007/s00285-011-0493-6.
- 41. P. Clote, Y. Ponty, J.-M. Steyaert. Expected distance between terminal nucleotides of RNA secondary structures. J Math Biol. 2012 Sep;65(3):581-99. Epub 2011 Oct 9.

22.

49. Feng Lou, Peter Clote. Thermodynamics of RNA structures by Wang-Landau sampling. ISMB 2010,

Y. Ponty; W. A. Lorenz; Peter Clote Nucleic Acids Res. 2007 Jul 1;35(Web Server issue):W659-

80. Solving the Fisher-Wright and coalescence problems with a discrete Markov

Encyclopedia of Bioinfor

- 113. <u>"Evolution as a computational engine"</u>, R. Backofen, P. Clote, *Computer Science Logic*, Aug 25-29, 1997, Springer Lecture Notes in Computer Science 14114, pp. 35--55, Denmark (1997).
- 114. "A safe recursion scheme for exponential time", P. Clote, Logical Foundations of Computer Science (LFCS'97)

Science Professional Publications (not peer reviewed)

Publications in Computer Science Professional Publications (not peer reviewed)

128. <u>"Aktuelles Schlagwort Bioinformatik",</u> Rolf Backofen, Francois Bry, Peter Clote, Hans-Peter Kriegel, Thomas Seidl and Klaus Schulz, Informatik Spektrum, Okt. 1999 (in German).

Unpublished Tech Reports

129. "Biologically significant sequence alignments using Boltzmann probabilities", P. Clote (2003). After submission, I learned that this result was discovered about one year earlier by Mueckstein, Hofacker, Stadler.

130. "Vax Pascal and Hypercard implementation of an assembler for a parallel random access machine", P. Clote and A. Lai, Technical Report BCCS-91-9, 22 October 1991, 61 pages. Unpublished technical report for simulation programs for parallel SIMD-type machines.

131.

