# 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, Computer Science, Freie Universität Berlin. Apr-July 2014 Visiting Professor, Bioinformatics, Max Planck Institute for Molecular Genetics, Berlin. Jan-Mar 2014 Visiting Associate in Biology and Bioengineering, California Institute of Technology. June 2012 Visiting Professor, l'Université Paris-Est Créteil 2008–2011 (summers) Digiteo Chair of Excellence, Ecole Polytechnique and Université Paris—Sud. Aug 2008,Jan and Aug 2009 Max Planck Institut for Molecular Genetics, Berlin. July 2007 Visiting Professor, National University of Singapore. May -June 2007 Max Planck Institut for Molecular Genetics, Berlin. June 2003 Visiting Professor, Insitut Henri Poincaré (Mathematics, Paris). Sep – Dec 2000 Massachusetts Institute of Technology (Mathematics).

### **Brief Bio**

Clote, a 2014 Guggenheim Fellow in Applied Mathematics, has an unusual background, having held faculty positions in Mathematics, Computer Science and Biology in France, Germany and the United States, including the tenured Gentzen Computer Science Chair in Munich, and a visiting Digiteo Chair of

### **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.
- 4) "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

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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).
- 10. 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.
- 11.

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12. Senter E. Dotu I, Clote P. RNA folding pathways and kinetics using 2D energy landscapes. J Math Biol. 2015 Jan;70(1-2):173-96.

# Full Publication List of Peter G. Clote

# Books

- <u>Genetics, Genomics, Proteomics and Bioinformatics</u> 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. <u>BibTeX entry</u>
- 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</u> <u>structural neighbors of an RNA secondary structure.</u> BMC Bioinformatics BMC Bioinformatics. 2012 Apr 12;13 Suppl 5:S.
- 40. Peter Clote, Stefan Dobrev, Ivan Dotu, Evangelos Kranakis. Danny Krizanc, Jorge Urrutia. <u>On the Page Number of Secondary Structures with Pseudoknots.</u> J Math Biol. 2012 Dec;65(6-7):1337-57. doi: 10.1007/s00285-011-0493-6.
- P. Clote, Y. Ponty, J.-M. Steyaert. <u>Expected distance between terminal</u> <u>nucleotides of RNA secondary structures.</u> 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

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- 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. <u>"A safe recursion scheme for exponential time"</u>, 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. <u>"Biologically significant sequence alignments using Boltzmann</u> probabilities", P. Clote (2003). After submission, I learned that this result was discovered about one year earlier by Mueckstein, Hofacker, Stadler.
- 130. <u>"Vax Pascal and Hypercard implementation of an assembler for a parallel random access machine"</u>, 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.

