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 Excellence at Ecole Polytechnique. This unique experience, including work over four summers as an undergraduate in biochemistry labs, provides for an interest and familiarity with the mathematical, algorithmic and physical chemical issues that concern the research in computational biology – especially RNA and protein structural bioinformatics. He has co-written 2 books, co-edited 4 books, and published 108 peer-reviewed articles in journal or book chapters, many of which are single-authored mathematics papers (hence leading to lower publication count than in physical sciences). Since 2005, Clote has published 61 papers (on average 5.5 per year) in the journals Bioinformatics, RNA, NAR, PLoS Comp Biol, PLoS ONE, Proteins, Proteomics, J Comp Biol, JBCB, etc. In Munich, he led the establishment of a PhD program in bioinformatics in 1999. His 2000 book, *Computational Molecular Biology: An Introduction,* has been used at MIT, RPI, University of Washington, etc. His 2005 ISMB tutorial, "*RNA: Algorithms for structure prediction and gene finders*", was ranked as the best tutorial among 14 invited tutorials. From June 20-24, 2011 and July 6-10, 2014, Clote co-organized the "Summer School on Computational Methods for RNA", held at Boston College. The summer school attracted graduate students, postdocs, faculty from MIT and other local universities, University of Rochester,, Brown University, Cold Spring Harbor Lab, New England Biolabs, and University Autonoma of Madrid.

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 2011.
Founder and co-organizer (with B. Berger), Bioinformatics Seminar, Mathematics Department & CSAIL, MIT, 2000-2010.

Service and editorial work:
Ad hoc member of numerous NIH study sections and NSF panels. Ad hoc reviewer for NSERC (Canada), ANR (France), and Alexander von Humboldt Foundation, DAAD (German funding agency), Austrian and Czech funding agencies.
Associate Editor, *Journal of Mathematical Biology* (2005-present)
Editorial Board: *International Journal of Knowledge Discovery in Bioinformatics,* 2008 - present.
Frontiers in Non-Coding RNA , a specialty of Frontiers in Genetics (2010-present). *Frontiers Molecular Bioscience* 2014-present. *Open Bioinformatics Journal,* 2008 - present. *Open Statistics & Probability Journal,* 2008 - present. *Guest associate editor: Supplement of BMC Bioinformatics - Italian Bioinformatics Conference 2006. Notre Dame Journal of Formal Logi*c (1991-2003). Section editor: *Modern Programming Paradigms in Biology,* pages 3489—3654, *Wiley Encyclopedia of Bioinformatics,* in the 8-volume encyclopedia, *Genetics, Genomics, Proteomics and Bioinformatics (2005), Computer Science Logic,* by P. Clote and H. Schwichtenberg (Eds.), 14th International Workshop, CSL 2000, Springer Lecture Notes in Computer Science 1862, ISBN 3-540-67895-6, August 2000. *Feasible Mathematics II*, by P. Clote and J. Remmel (Eds.), Birkhäuser Inc (1995). *Arithmetic, proof theory and computational complexity*, by P. Clote and J. Krajicek (Eds.),

Honors

Aug 2013-July 2014 Guggenheim Fellowship in Applied Mathematics.
Jun 2008- May 2012 Digiteo Chair of Excellence at Ecole Polytechnique and Université Paris-Sud.
2003 Alpha Sigma Nu Book Award in 2003 for Boolean Functions and Computation Models, P. Clote and E. Kranakis, Springer-Verlag (2002).
1992-93 Alexander von Humboldt Foundation for research at Technische Universität Berlin.
1974-75 Fulbright Fellowship.
1973 Nomination to Sigma Xi Scientific Research Society.

Postdoctoral and doctoral students – current location indicated.

Amirhossein Bayegan (BC), J.A. Garcia Martin (Madrid), E. Senter (software engineer, Google), I. Dotu (Universidad Politecnica de Cataluña), F. Lou (SanValley Biotechnology Inc.), B. Raman (Mentor Graphics, Grenoble), A. Lorenz (JWP Inc., Ohio), Y. Ding (University of Pennsylvania), F. Ferre (University of Rome "La Sapienza"), J. Waldispuhl (McGill University), R. Backofen (Universität Freiburg), Th. Altenkirch (Nottingham University), R. Matthes (CNRS, Toulouse), J. Johannsen (Ludwig-Maximilians-Universität München).

Recent research grants

1. NSF DBI-1262439, Aug 1, 2013 – July 31, 2018, "ABI Innovation: Engineering molecular scissors by computational design with experimental validation".
2. Guggenheim Fellowship in Applied Mathematics, Aug 1, 2013 – July 31, 2014.
3. NSF DMS-1016618, Sep 15, 2010 -- Aug 31, 2013, "Energy parameters and novel algorithms for an extended nearest neighbor energy model of RNA".
4. NSF DMS-0817971, Sep 2008 - Aug 2011. Project "Physically modeling cross-hybridization error in gene expression microarrays by a novel Boltzmann partition function algorithm for probe-specific position-dependent free energy".
5. Foundation Digiteo - Triangle de la Physique, June 1, 2008 -- May 31, 2012. Funding covers summer salary as "Digiteo Chair of Excellence", annual salaries for 2 postdoctoral associates and 2 graduate students for research at Ecole Polytechnique (Paris) and Université Paris-Sud (Orsay). Project title "RNAomics", June 1, 2008 -- May 31, 2012.
6. Deutscher Akademischer Austauschdienst (DAAD), research visiting professor, Max Planck Institut für Molekulare Genetik (Berlin), July 2008, Aug 2009.
7. NSF DBI-0543506, Apr 2006 -- Mar 2011. Biological Databases and Informatics. Project "RNA-parafold: Algorithms and Web Server for parametric aspects of RNA secondary structure".

12 Most recent Publications (from 108 papers, 2 books and 4 edited books)

1. P. Clote, A. Bayegan. RNA folding kinetics using Monte Carlo and Gillespie algorithms. J Math Biol, in press (2017), arXiv article ID 1707.03922.
2. Bayegan AH and Clote P. "An IP algorithm for RNA folding trajectories", Workshop on Algorithms in Bioinformatics (WABI 2017), August 21-23, 2017, Boston, MA.
3. Bayegan AH, Garcia-Martin JA, and Clote P. New tools to analyze overlapping coding regions. BMC Bioinformatics. 2016 Dec 13;17(1):530.
4. Garcia-Martin JA, Bayegan AH, Dotu I, and Clote P. RNAdualPF: software to compute the dual partition function with sample applications in molecular evolution theory. BMC Bioinformatics, Bioinformatics. 2016 Oct 19;17(1):424.
5. Garcia-Martin JA, Dotu I, Fernandez-Chamorro J, Lozano G, Ramajo J, Martinez-Salas E, Clote P. RNAiFold2T: Constraint Programming design of thermo-IRES switches. Bioinformatics. 2016 Jun 15;32(12):i360-i368. doi: 10.1093/bioinformatics/btw265.
6. Javier Fernandez-Chamorro, Gloria Lozano, Juan Antonio Garcia-Martin, Jorge Ramajo, Ivan Dotu, Peter Clote, and Encarna Martinez-Salas. Designing synthetic RNAs to determine the relevance of structural motifs in picornavirus IRES elements. Nature Scientific Reports, 6:24243, DOI: 10.1038/srep24243, 07 April 2016.
7. Garcia-Martin JA, Clote P. RNA Thermodynamic Structural Entropy. PLoS One.

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.

9. 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. Clote P. Computational Methods for Understanding Riboswitches, Methods in Enzymology., Vol 553, ed. Donald H. Burke and Shi-Jie Chen, Elsevier Inc., ISSN 0076-6879, 287-307, 2015.

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

1. Genetics, Genomics, Proteomics and Bioinformatics Section editor of Bioinformatics, *Modern Programming Paradigms in Biology*, in the 8-volume encyclopedia entitled Genetics, Genomics, Proteomics and Bioinformatics (2005), ISBN-13 978-0-470-84974-3.
2. *Computational Molecular Biology: An Introduction* , P. Clote and R. Backofen, Japanese translation (2005), 272 pages, ISBN 4-320-05615-9.
3. *Boolean Functions and Computation Models,* 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 & Sons, Ltd., 286 pages (2000), ISBN 0-471-87251-2 (hardback) and ISBN 0-471-87251-0 (paperback). BibTeX entry
5. *Computer Science Logic*, by P. Clote and H. Schwichtenberg (Eds.), 14th International Workshop, CSL 2000, Springer Lecture Notes in Computer Science 1862, ISBN 3-540-67895-6, August 2000.
6. *Feasible Mathematics II*, Birkhäuser Inc., eds. P. Clote and J. Remmel, in series *Progress in Computer Science and Applied Logic*, Volume 13, (1995) 447 pages.
7. *Arithmetic, Proof Theory and Computational Complexity* , Oxford University Press, eds. P. Clote and J. Krajicek, in series *Oxford Logic Guides*, volume 23, (1993) 428 pages.
8. Research monograph translation, *Theory of Relations*, by R. Fraissé, North Holland (1986), 397 pages, translator P. Clote (French into English).

Journal Articles (108)

13. P. Clote, A. Bayegan. RNA folding kinetics using Monte Carlo and Gillespie algorithms. J Math Biol, in press (2017), arXiv article ID 1707.03922.
14. Bayegan AH and Clote P. "An IP algorithm for RNA folding trajectories", Workshop on Algorithms in Bioinformatics (WABI 2017), August 21-23, 2017, Boston, MA.
15. Bayegan AH, Garcia-Martin JA, and Clote P. New tools to analyze overlapping coding regions. BMC Bioinformatics. 2016 Dec 13;17(1):530.
16. Garcia-Martin JA, Bayegan AH, Dotu I, and Clote P. RNAdualPF: software to compute the dual partition function with sample applications in molecular evolution theory. BMC Bioinformatics, Bioinformatics. 2016 Oct 19;17(1):424.
17. Garcia-Martin JA, Dotu I, Fernandez-Chamorro J, Lozano G, Ramajo J, Martinez-Salas E, Clote P. RNAiFold2T: Constraint Programming design of thermo-IRES switches. Bioinformatics. 2016 Jun 15;32(12):i360-i368. doi: 10.1093/bioinformatics/btw265.
18. Javier Fernandez-Chamorro, Gloria Lozano, Juan Antonio Garcia-Martin, Jorge

Ramajo, Ivan Dotu, Peter Clote, and Encarna Martinez-Salas. Designing synthetic RNAs to determine the relevance of structural motifs in picornavirus IRES elements. Nature Scientific Reports, 6:24243, DOI: 10.1038/srep24243, 07 April 2016.

19. Garcia-Martin JA, Clote P. RNA Thermodynamic Structural Entropy. PLoS One. 2015 Nov 10;10(11):e0137859. doi: 10.1371/journal.pone.0137859.

20. 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.

21. 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).

22. 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.

23. Clote P. Computational Methods for Understanding Riboswitches, Methods in Enzymology., Vol 553, ed. Donald H. Burke and Shi-Jie Chen, Elsevier Inc., ISSN 0076-6879, 287-307, 2015.

24. Senter E, Clote P. Fast, approximate kinetics of RNA folding. J Comp Biol, Vol. 22, No. 2, February 2015: 124-144.

25. 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.

26. Clote P. Expected degree of RNA secondary structure networks. J Comp Chem 2015 Jan 15;36(2):103-17.

27. 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.

28. Y. Ding, W.A. Lorenz, I. Dotu, E. Senter, P. Clote. Computing the probability of RNA hairpin and multiloop formation. J Comput Biol. 2014 Mar;21(3):201-18. doi: 10.1089/cmb.2013.0148. Epub 2014 Feb 21.

29. Ivan Dotu, Vinodh Mechery, Peter Clote. Energy parameters and novel algorithms for an extended nearest neighbor energy model of RNA. PLoS One PLoS One. 2014 Feb 21;9(2):e85412. doi: 10.1371/journal.pone.0085412.

30. Clote P, Kranakis E, Krizanc D. Asymptotic number of hairpins of saturated RNA secondary structures. Bull Math Biol. 2013 Dec;75(12):2410-30. doi: 10.1007/s11538-013-9899-1.

31. Dotu I, Lozano G, Clote P, Martinez-Salas E. Using RNA inverse folding to identify IRES-like structural subdomains. RNA Biol. 2013 Dec 1;10(12):1842-52. doi: 10.4161/rna.26994.

32. Clote P, Kranakis E, Krizanc D. Asymptotic structural properties of quasi-random saturated structures of RNA. Algorithms Mol Biol. 2013 Oct 25;8(1):24. doi: 10.1186/1748-7188-8-24..

33. Juan Antonio Garcia-Martin, Peter Clote, Ivan Dotu. RNAiFold: A web server for RNA inverse folding and molecular design. Nucleic Acids Research Web Server Issue, 2013, doi: 10.1093/nar/gkt280.

34. E. Senter, S. Sheik, I. Dotu, Y. Ponty, P. Clote. Using the Fast Fourier Transform to Accelerate the Computational Search for RNA Conformational Switches (2-

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. Maximum expected accuracy structural neighbors of an RNA secondary structure. BMC Bioinformatics BMC Bioinformatics. 2012 Apr 12;13 Suppl 5:S.

40. 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.

42. Feng Lou, Alain Denise and Peter Clote. A new approach to suboptimal pairwise sequence alignment. IASTED conference CompBio 2011, July 11-13, 2011, Cambridge, UK.

43. P. Bochet, F. Rüheimer, T. Guina, P. Brooks, D. Goodlett, P. Clote, B. Schwikowski. Fragmentation-free LC-MS can identify hundreds of proteins. *Proteomics*, 2011 Jan;11(1):22-32.

44. Feng Lou and Peter Clote. Maximum expected accurate structural neighbors of an RNA secondary structure. Proceedings of 1st IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS), Feb 3-5, 2011, 123-128, Orlando, FL,
ISBN 978-1-61284-851-8, doi 10.1109/ICCABS.2011.5729865.

45. W.A. Lorenz, P. Clote. Computing the partition function for kinetically trapped RNA secondary structures. Public Library of Science One (PLoS ONE), (2011) PLoS ONE 6(1): e16178. doi:10.1371/journal.pone.0016178.

46. Ivan Dotú, Manuel Cebrián, Pascal Van Hentenryck and Peter Clote. On Lattice Protein Structure Prediction Revisited. IEEE/ACM Transactions on Computational Biology and Bioinformatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB), Volume 8 Issue 6, November 2011, 1620-1632, IEEE Computer Society Press Los Alamitos, CA, http://doi.ieeecomputersociety.org/10.1109/TCBB.2011.41

47. I. Dotú, W.A. Lorenz, P. Van Hentenryck, P. Clote. RNA Structural Segmentation. Pac Symp Biocomput. 2010:57-68.

48. I. Dotú, W.A. Lorenz, P. Van Hentenryck, P. Clote. Computing folding pathways between RNA secondary structures. Nucleic Acids Res. 2010 Mar 1;38(5):1711-

22.

49. Feng Lou, Peter Clote. Thermodynamics of RNA structures by Wang-Landau sampling. ISMB 2010, *Bioinformatics* 2010 Jun 15;26(12):i278-86.

50. Peter Clote, Evangelos Kranakis, Danny Krizanc, Bruno Salvy. Asymptotics of Canonical and Saturated RNA Secondary Structures. Clote P, Kranakis E, Krizanc D, Salvy B. J Bioinform Comput Biol. 2009 Oct;7(5):869-93.

51. Peter Clote; Evangelos Kranakis; Danny Krizanc. Asymptotics of Canonical RNA Secondary Structures. 9th IEEE Conference on Bioinformatics and Bioengineering (BIBE 2009). June 22-24, 2009 Taichung, Taiwan.

52. Jerome Waldispühl, Srinivas Devadas, Bonnie Berger, Peter Clote. RNAmutants: A web server to explore the mutational landscape of RNA secondary structures Nucleic Acids Res. 2009 Jul;37(Web Server issue):W281-6. Epub 2009 Jun 16.

53. Jerome Waldispühl, Srinivas Devadas, Bonnie Berger, Peter Clote. Efficient algorithms for probing the RNA mutation landscape. PLoS Comput Biol. 2008 Aug 8;4(8):e1000124.

54. Ivan Dotú, Manuel Cebrián, Pascal Van Hentenryck and Peter Clote. Protein Structure Prediction With Large Neighborhood Constraint Programming Search. pp 82-96, *Principles and Practice of Constraint Programming*, 14th International Conference, CP 2008, Sydney, Australia, September 14-18, 2008, Proceedings Series: Lecture Notes in Computer Science Subseries: Programming and Software Engineering , Vol. 5202 Stuckey, Peter J. (Ed.) 2008, XVII, 648 p., Softcover ISBN: 978-3-540-85957-4

55. Y. Ponty, R. Istrate, E. Porcelli, P. Clote. LocalMove: Computing on-lattice fits for biopolymers. Nucleic Acids Res. 2008 Jul 1;36(Web Server issue):W216-22.

56. I. Dotú, M. Cebrián, P. Van Hentenryck, P. Clote. A Local Search Approach to Protein Structure Prediciton on the Face Centered Cubic Lattice. Twenty-Third Association for the Advancement of Artificial Intelligence Conference on Artificial Intelligence (AAAI-08), July 13-17, 2008, pp 241-246.

57. W.A. Lorenz, Y. Ponty and P. Clote. Asymptotics of RNA shapes. J Comput Biol. 2008 Jan-Feb;15(1):31-63.

58. P. Clote. Introduction to special issue on RNA. J Math Biol. 2008 Jan;56(1-2):3-13.

59. Modeling ensembles of transmembrane beta-barrel proteins, J. Waldispühl, C.W. O'Donnell, S. Devadas, P. Clote, B. Berger, Proteins. 2007 Nov 14;71(3):1097-1112.

60. Asymptotic expected number of base pairs in optimal secondary structure for random RNA using the Nussinov-Jacobson energy model, P. Clote, E. Kranakis, D. Krizanc and L. Stacho, *Discrete Applied Mathematics*, special issue in Bioinformatics (eds S. Istrail and P. Pevzner), 157(6-7):759-787 (2007).

61. Boltzmann probability of RNA structural neighbors and riboswitch detection. , Eva Freyhult; Vincent Moulton; Peter Clote, Bioinformatics. 2007 Aug 15;23(16):2054-62. Epub 2007 Jun 14.

62. Asymptotics of RNA shapes. W.A. Lorenz, Y. Ponty and P. Clote. *J Comput Biol. 2008 Jan-Feb;15(1):31-63.*

63. DIAL: a web server for the pairwise alignment of two RNA three-dimensional structures using nucleotide, dihedral angle and base-pairing similarities , F. Ferre;

Y. Ponty; W. A. Lorenz; Peter Clote Nucleic Acids Res. 2007 Jul 1;35(Web Server issue):W659-68. Epub 2007 Jun 13.

64. RNAbor: A web server for RNA structural neighbors. E. Freyhult, V. Moulton, P. Clote. Nucleic Acids Res. 2007 Jul 1;35(Web Server issue):W305-9. Epub 2007 May 25.

65. Computing the partition function and sampling for saturated secondary structures of RNA, with respect to the Turner energy model, J. Waldispühl, P. Clote, *J Comput Biol* 2007 Mar;14(2):190-215.

66. Combinatorics of saturated secondary structures of RNA, P. Clote, *J Comp Biol.* 13(9):1640-1657 (2006).

67. Predicting transmembrane beta-barrels and interstrand residue interactions from sequence, J. Waldispühl, B. Berger, P. Clote, J.-M. Steyaert, *Proteins* 65(1):61-74 (2006).

68. transFold: a Web Server for predicting the structure and residue contacts of transmembrane beta-barrels, J. Waldispühl, B. Berger, P. Clote, J.-M. Steyaert, *Nucleic Acids Res.* 34(Web Server Issue):189-193 (2006).

69. BTW: A web server for Boltzmann time warping of gene expression time series, F. Ferr{\`e}, P. Clote, *Nucleic Acids Res.* 34(Web Server issue):W482-5 (2006).

70. DiANNA1.1webServer DiANNA 1.1: An extension of the DiANNA web server for ternary cysteine classification, F. Ferre, P. Clote, *Nucleic Acids Res.* 34(Web Server issue):W182-5 (2006).

71. Symmetric time warping, Boltzmann pair probabilities and functional genomics , P. Clote, J. Straubhaar, *J Math Biol.* 53(1):135-61 (2006).

72. Energy landscape of k-point mutants of an RNA molecule P. Clote, J. Waldispuhl, B. Behzadi, J.-M. Steyaert, *Bioinformatics* 21(22):4140-4147 (2005).

73. An efficient algorithm to compute the landscape of locally optimal RNA secondary structures with respect to the Nussinov-Jacobson energy model , P. Clote, *Journal of Computational Biology 12*(1) 2005 83--101.

74. Structural RNA has lower folding energy than random RNA of the same dinucleotide frequency , P. Clote, F. Ferre, E. Kranakis, D. Krizanc, *RNA RNA*, 11(5):578-591 (2005).

75. Asymptotic expected number of base pairs in optimal secondary structure for random RNA using the Nussinov-Jacobson energy model, P. Clote, E. Kranakis, D. Krizanc and L. Stacho. Discrete Applied Mathematics 155(6-7): 759-787 (2007).

76. Disulfide connectivity prediction using secondary structure information and diresidue frequencies" , F. Ferre and P. Clote, *Bioinformatics* 21(10):2336-2346 (2005).

77. On realizing shapes in the theory of RNA neutral networks , P. Clote, L. Gasieniec, R. Kolpakov, E. Kranakis, D. Krizanc, *J. Theoretical Biology* 236(2): 216-227 (2005).

78. RNALOSS: A web server for RNA locally optimal secondary structures , P. Clote, *Nucleic Acids Research*, web server W1-W5 (2005).

79. DiANNA: a web server for disulfide connectivity prediction , F. Ferre, P. Clote, *Nucleic Acids Research*, Nucleic Acids Res. 2005 Jul 1;33(Web Server issue):W230-232.

80. Solving the Fisher-Wright and coalescence problems with a discrete Markov chain analysis , S.R. Buss and P. Clote, *Advances in Applied Probability*, 36(3), 1175-1197 (2004).

81. "Reverse mathematics of some topics from algorithmic graph theory" , P. Clote, J. Hirst, *Fundamenta Mathematica* 157(1), 1-13 (1998).

82. "Nondeterministic stack register machines", P. Clote, *Theoretical Computer Science* 178 (June 1997) 37-76.

83. "Note on monotonic complexity of 2-REF" , P. Clote, *Information Processing Letters* 57, 117-123 (1996).

84. "Cutting planes, connectivity and threshold logic", S.R. Buss, P. Clote, *Archive for Mathematical Logic* 35, 33-62 (1995). See additional supplement.

85. "Cutting plane and Frege proofs", P. Clote, *Information and Computation*, 121(1) 103-122 (1995).

86. ALOGTIME and a conjecture of S.A. Cook", P. Clote, in Proceedings of *IEEE Logic in Computer Science* (LICS), Philadelphia PA, June 1990, journal version in *Annals of Mathematics and Artificial Intelligence* 6 (1992) 57-106.

87. "Bounded arithmetic for NC, ALOGTIME, L and NL", P. Clote, G. Takeuti, *Annals of Pure and Applied Logic* 56 73-117 (1992).

88. "A time-space hierarchy between P and NP", P. Clote, *Mathematical Systems Theory* 25 77-92 (1992).

89. "On some formalized consistency statements in arithmetic", P. Clote, P. Hájek, J.B. Paris, *Archive for Mathematical Logic* 30(4) 201-221 (1991).

90. "Boolean functions, invariance groups, and parallel complexity", P. Clote, E. Kranakis, *SIAM J. Comput.* 20 (3) 553-590 (1991), extended abstract appeared in the *Proceedings of Structure in Complexity Theory*, Fourth Annual IEEE sponsored conference (1989), 55-65.

91. "The metamathematics of scattered linear orderings", P. Clote, *Archive for Mathematical Logic* 29 9-20 (1989).

92. "A note on the MacDowell-Specker Theorem", P. Clote, *Fundamenta Mathematicae* 127 (1986), 163-170.

93. "Members of PI$_1$ classes", P. Clote, D. Cenzer, R. Smith, R. Soare, S. Wainer, *Annals of Pure and Applied Logic* 31 (1986), 145-161.

94. "On the finite containment problem for Petri nets", P. Clote, *Theoretical Computer Science* 43 (1986), 99-105.

95. "A generalization of the limit lemma and clopen games", P. Clote, *Journal of Symbolic Logic* 51 (1986), 273-291.

96. "Sharp bounds on ordinal comparison maps", P. Clote, *Archiv für Mathematische Logik und Grundlagenforschung* 25 (1985), 99-107.

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