

List of publications

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1 Patents (3)

3. M. Méchali, C. Cayrou, P. Coulombe, **E. Rivals**, P. Prorok, *Purification process of nascent DNA*, patent n° US 2019 / 0093149, March 28th 2019.
2. M. Méchali, C. Cayrou, P. Coulombe, **E. Rivals**, P. Prorok, *Purification process of nascent DNA*, patent n° US 20150267208 (2015).
1. M. Méchali, C. Cayrou, P. Coulombe, **E. Rivals**, *Purification process of nascent DNA*, patent n° US 61/238 315 (2011) and European patent EP2473623 (2012).

2 International journals (54 + 7)

54. B. Cazaux, **E. Rivals**, *Hierarchical Overlap Graph*, *Information Processing Letters* 155, doi: [10.1016/j.ip1.2019.105862](https://doi.org/10.1016/j.ip1.2019.105862), 2020.
53. Oldfield AJ, Henriques T, Kumar D, Burkholder AB, Cinghu S, Paulet D, Bennett BD, Yang P, Scruggs BS, Laverder CA, **Rivals E**, Adelman K, Jothi R. *NF-Y controls fidelity of transcription initiation at gene promoters through maintenance of the nucleosome-depleted region. Nature Communications* Jul 11;10(1):3072. doi: [10.1038/s41467-019-10905-7](https://doi.org/10.1038/s41467-019-10905-7), 2019.
52. B. Cazaux, G. Castel, **E. Rivals**, *AquaPony: visualization and interpretation of phylogeographic information on phylogenetic trees*, *Bioinformatics* 35 (17), 3163-3165, btz011, doi: [10.1093/bioinformatics/btz011](https://doi.org/10.1093/bioinformatics/btz011), 2019.
51. B. Cazaux, T. Lecroq, **E. Rivals**, *Linking indexing data structures to de Bruijn Graphs: construction and update*, *J. of Computer and System Sciences* 104: 165-183, doi:[10.1016/j.jcss.2016.06.008](https://doi.org/10.1016/j.jcss.2016.06.008), 2019.
50. T. Marschall, M. Marz, . . . , **E. Rivals**, . . . et al., *Computational Pan-Genomics: Status, Promises and Challenges*, *Briefings in Bioinformatics*, doi: [10.1093/bib/bbw089](https://doi.org/10.1093/bib/bbw089), (online 2016), Vol 19(1), p. 118-135, 2018.
49. B. Cazaux, **E. Rivals**, *Relationship between superstring and compression measures: new insights on the greedy conjecture*, *Discrete Applied Mathematics* doi: [10.1016/j.dam.2017.04.017](https://doi.org/10.1016/j.dam.2017.04.017), Vol. 245, p. 59-64, 2018.
48. A. Diwedi, C. Reynes, A. Kuehn, DB. Roche, N. Khim, M. Hebrard, S. Milanese, **E. Rivals**, R. Frutos, D. Menard, CB. Mamoun, J. Colinge, E. Cornillot, *Functional analysis of Plasmodium falciparum subpopulations associated with artemisinin resistance in Cambodia*, *Malaria Journal* 16:493, DOI: [10.1186/s12936-017-2140-1](https://doi.org/10.1186/s12936-017-2140-1) 2017.
47. X. Argout, G. Martin, G. Droc, O. Fouet, K. Labadie, **E. Rivals**, J.M. Aury, C. Lanaud, *The cacao Criollo genome v2.0: an improved version of the genome for genetic and functional genomic studies*, *BMC Genomics* 18:730, DOI: [10.1186/s12864-017-4120-9](https://doi.org/10.1186/s12864-017-4120-9) 2017.

46. R. Blanc-Mathieu, M. Krasovec, M. Hébrard, S. Yau, E. Desgranges, J. Martin, W. Schackwitz, A. Kuo, G. Salin, C. Donnadieu, Y. Desdevises, S. Sanchez-Ferandin, H. Moreau, **E. Rivals**, I. Grigoriev, N. Grimsley, AC Eyre-Walker, G. Piganeau, *Population genomics of picophytoplankton unveils novel chromosome hypervariability*, *Science Advances*, Vol. 3, no. 7, e1700239, DOI: 10.1126/sciadv.1700239, July 2017.
45. J. Baaijens, A.Z. El Aabidine, **E. Rivals**, A. Schönhuth (co-corresponding authors), *De novo assembly of viral quasispecies using overlap graphs*, *Genome Research* 27: 835-848, 2017.
44. D. Paulet, A. David, **E. Rivals**, *Ribo-seq enlightens Codon Usage Bias*, *DNA Research* dsw062. doi: 10.1093/dnares/dsw062, 2017.
43. A. Limasset, B. Cazaux, **E. Rivals**, P. Peterlongo, *Read mapping on de Bruijn Graphs*, *BMC Bioinformatics* doi:10.1186/s12859-016-1103-9, 17:237, 2016.
42. L. Salmela, R. Walve, **E. Rivals**, E. Ukkonen, *Accurate selfcorrection of errors in long reads using de Bruijn graphs*, *Bioinformatics*, (online 2016) doi: 10.1093/bioinformatics/btw321, 33 (6): 799-806, 2017.
41. B. Cazaux, **E. Rivals**, *A linear time algorithm for shortest cyclic cover of strings* doi: 10.1016/j.jda.2016.05.001, *Journal of Discrete Algorithms*, vol. 37, p. 56–67, 2016.
40. Y. Le Bras, O. Collin, C. Monjeaud, V. Lacroix, **E. Rivals**, C. Lemaitre, V. Miele, G. Sacomoto, C. Marchet, B. Cazaux, A. Zine El Aabidine, L. Salmela, S. Alves-Carvalho, A. Andrieux, R. Uricaru, P. Peterlongo *Colib' read on Galaxy: A tools suite dedicated to biological information extraction from raw NGS reads*, *Giga-Science*, Feb 11;5:9. eCollection 2016.
39. B. Cazaux, **E. Rivals**, *The power of greedy algorithms for approximating Max-ATSP, Cyclic Cover, and superstrings* doi:10.1016/j.dam.2015.06.003, PSC 2014 Special Issue, online in 2015 *Discrete Applied Mathematics*, Vol. 212, p. 48–60, 2016.
38. R. Uricaru, C. Michotey, H. Chiapello, **E. Rivals**, *YOC, a new strategy for pairwise alignment of collinear genomes*, *BMC Bioinformatics*, doi:10.1186/s12859-015-0530-3, 16:111, 2015.
37. C. Keyser, C. Hollard, A. Gonzalez, L. Fausser, **E. Rivals**, A. Alexeev, A. Riberon, E. Crubézy, B. Ludes, *The ancient Yakuts: a population genetic enigma*, in press *Philosophical Transactions of the Royal Society series B*, doi: 10.1098/rstb.2013.0385, Jan 19;370(1660), 2015.
36. R. Blanc-Mathieu, B. Verhelst, E. Derelle, S. Rombauts, G. Piganeau, F-Y. Bouget, I. Carré, A. Château, AC Eyre-Walker, N. Grimsley, H. Moreau, B. Piegu, **E. Rivals**, Y. van de Peer, W. Schackwitz, *An improved genome of the model marine alga *Ostreococcus tauri* unfolds by assessing Illumina read de novo assemblies*, *BMC Genomics* 15:1103 doi:10.1186/1471-2164-15-1103 2014.
35. L. Salmela, **E. Rivals**, *LoRDEC: accurate and efficient long read error correction*, *Bioinformatics*, doi:10.1093/bioinformatics/btu538, 30(24), p. 3506-3514, 2014.
34. B. Cazaux, **E. Rivals**, *Reverse Engineering of Compact Suffix Trees and Links: a Novel Algorithm* vol. 28, String-Masters 2012 & 2013 Special Issue, p. 9-22 *J. Discrete Algorithms*, 2014.
33. J. Buard, **E. Rivals**, D. Dunoyer de Segonzac, C. Garres, P. Caminade, B. de Massy, P. Boursot, *Diversity of Prdm9 ZnF array in wild mice unravels new facets of the evolutionary turnover of this coding minisatellite*, *PLOS One* doi: 10.1371/journal.pone.0085021, 2014.
32. N. Philippe, E. Bou Samara, A. Boueux, F. Rufflé, Q. Bai, A. Mancheron, J. Devos, **E. Rivals**, T. Commes, *Combining DGE and RNA-Sequencing data to identify new polyA+ non-coding transcripts in the human genome*, *Nucleic Acids Research*, 42(5):2820-2832. doi: 10.1093/nar/gkt1300, 2014.
31. N. Philippe, M. Salson, T. Commes, **E. Rivals**, *CRAC: an integrated approach to the analysis of RNA-seq reads*, *Genome Biology*, 14:R30, 2013.
30. **E. Rivals**, N. Philippe, M. Salson, M. Léonard, T. Commes, T. Lecroq, *A Scalable Indexing Solution to Mine Huge Genomic Sequence Collections*, *ERCIM News*, 89, p. 20-21, 2012.

29. C. Cayrou, P. Coulombe, A. Vigneron, S Stanojcik, O Ganier, I Peiffer, **E. Rivals**, A Puy, S. Laurent-Chabalier, R. Desprat, M. Mechali, *Genome-scale analysis of metazoan replication origins reveals their organization in specific but flexible sites defined by conserved features*, *Genome Research*, 21(9), p. 1438-49, Sep. 2011.
28. R. Uricaru, A. Mancheron, **E. Rivals**, *Novel definition and algorithm for chaining fragments with proportional overlaps*, *J. of Computational Biology*, Vol. 18(9), p. 1141-54, 2011.
27. N. Philippe, M. Salson, T. Lecroq, M. Léonard, T. Commes, **E. Rivals**, *Querying large read collections in main memory: a versatile data structure*, *BMC Bioinformatics*, 12, p. 42, 2011.
26. A. Mancheron, R. Uricaru, **E. Rivals**, *An Alternative Approach to Multiple Genome Comparison*, *Nucleic Acids Research*, Vol. 39, No. 15, p. e101, 2011.
25. Z. Shao, **E. Rivals**, N. Zhao, S. Lek, J. Chang, P. Berrebi, *Evolutionary process of a tetranucleotide microsatellite locus in *Acipenseriforms**, *J. of Genetics*, Vol. 90(2), p. 217-227, 2011.
24. **E. Rivals**, A. Mancheron, R. Uricaru, *Reliable Bacterial Genome Comparison Tools*, *ERCIM News*, Vol. 82, p. 17-18, 2010.
23. S. Leclercq, **E. Rivals**, P. Jarne, *DNA slippage occurs at microsatellite loci without minimal threshold length in humans : a comparative genomic approach*, *Genome Biology & Evolution*, vol. 2, p. 325-335, 2010.
22. J.R. Hernandez Mora, **E. Rivals**, H. Mireau, F. Budar, *Sequence analysis of two alleles reveals that intra-and intergenic recombination played a role in the evolution of the radish fertility restorer (*Rfo*)*, *BMC Plant Biology*, vol. 10:35, 2010.
21. N. Philippe , A. Boureux, L. Bréhèlin, J. Tarhio, T. Commes, **E. Rivals**, *Using reads to annotate the genome: influence of length, background distribution, and sequence errors on prediction capacity*, *Nucleic Acids Research*, 37(15):e104, 2009.
20. F. Nicolas, **E. Rivals**, *Hardness of Optimal Spaced Seed Design*, *Journal of Computer and System Sciences*, 74, p. 831-849, 2008.
19. E. Adebiyi, **E. Rivals**, *Detection of Recombination in Variable Number Tandem Repeat Sequences*, *South African Computer Journal (SACJ)*, 39, p. 1-7, 2007.
18. **E. Rivals** , A. Boureux, M. Lejeune, F. Ottones, O. Pecharromàn-Pérez, J. Tarhio, F. Pierrat, F. Ruffle, T. Commes, J. Marti, *Transcriptome Annotation using Tandem SAGE Tags*, *Nucleic Acids Research*, 35(17):e108, 2007.
17. F. Bonhomme, **E. Rivals**, A. Orth, G.R. Grant, A. J. Jeffreys, P.R.J. Bois *Species wide distribution of highly polymorphic minisatellite markers suggests past and present genetic exchanges among House Mouse subspecies*, *Genome Biology*, 8(5):R80, 2007.
16. S. Leclercq, **E. Rivals**, P. Jarne, *Detecting microsatellites within genomes: different solutions with different algorithms*, *BMC Bioinformatics*, 8, p. 125, 2007.
15. F. Nicolas, **E. Rivals**, *Longest Common Subsequence Problem for Unoriented and Cyclic Strings*, *Theoretical Computer Science*, 370, p. 1-18, 2007.
14. S. Bérard, F. Nicolas, J. Buard, O. Gascuel, **E. Rivals**, *A Fast and Specific Alignment Method for Minisatellite Maps*, *Evolutionary Bioinformatics Online*, 2, p. 327-344, 2006.
13. **E. Rivals**, C. Bruyère, C. Toffano-Nioche, A. Lecharny, *Formation of the Arabidopsis pentatricopeptide family*, *Plant Physiology*, 141, p. 825-839, 2006.
12. F. Nicolas, **E. Rivals**, *Hardness Results for the Center and Median String Problems under the Weighted and Unweighted Edit Distances*, *J. of Discrete Algorithms*, 3(2-4), p. 390-415, 2005.
11. O. Delgrange, **E. Rivals**, *STAR: an algorithm to Search for Tandem Approximate Repeats*, *Bioinformatics*, Vol. 20, No. 16, p. 2812-2820, 2004.
10. **E. Rivals**, *A Survey on Algorithmic Aspects of Tandem Repeat Evolution*, *International Journal on Foundations of Computer Science*, Vol. 15, No. 2, p. 225-257, 2004.

9. **E. Rivals**, S. Rahmann, *Combinatorics of Periods in Strings*, *J. of Combinatorial Theory series A*, 104(1), p. 95-113, 2003.
8. S. Rahmann, **E. Rivals**, *On the Distribution of the Number of Missing Words in Random Texts*, *Combinatorics, Probability and Computing*, p. 73-87, vol. 12, 2003.
7. S. Bérard, **E. Rivals**, *Comparison of Minisatellites*, *J. of Computational Biology*, p. 357-372, vol. 10(3-4), 2003.
6. S. Haas, T. Beissbarth, **E. Rivals**, A. Krause, M. Vingron, *GeneNest: automated generation and visualization of gene indices*, *Trends in Genetics*, p. 521-2, vol. 16(11), 2000.
5. J.-S. Varré, J.-P. Delahaye, **E. Rivals**, *The Transformation Distance: a Dissimilarity Measure Based on Movements of Segments*, *Bioinformatics*, p. 194-202, vol. 15(3), 1999.
4. E. Bornberg-Bauer, **E. Rivals**, M. Vingron, *Strategies for Identifying Leucine Zippers*, *Nucleic Acids Research*, p. 2740-2746, vol. 26(11), 1998.
3. **Eric Rivals**, Jean-Paul Delahaye, *Optimal Representation in Average using Kolmogorov Complexity*, *Theoretical Computer Science*, p. 261-287, vol. 200(1-2), 1998.
2. **E. Rivals**, O. Delgrange, J-P. Delahaye, M. Dauchet, M-O. Delorme, Hénaut A., Ollivier E., *Detection of significant patterns by compression algorithms: the case of Approximate Tandem Repeats in DNA sequences*, *CABIOS (Computer Applications in BIOSciences)*, p. 131-136, vol. 13(2), 1997.
1. **E. Rivals**, M. Dauchet, J-P. Delahaye, O. Delgrange, *Compression and genetic sequences analysis*, *Biochimie*, p. 315-322, vol. 78(4), 1996.

2.1 Conference Abstracts in Journals (7)

7. N. Philippe, M. Salson, T. Commes, **E. Rivals**, *A combinatorial and integrated method to analyse RNA-seq reads*, *EMBnet Journal*, 17(Supp. B):11, mar 2012.
6. N. Philippe, M. Salson, F. Rufflé, E. Bou Samara, A. Boureux, T. Commes, **E. Rivals**, *Digital gene expression data, cross-species conservation and noncoding RNA*, *EMBnet Journal*, 17(Supp. B):32, mar 2012.
5. N. Philippe, M. Salson, T. Lecroq, M. Léonard, T. Commes, **E. Rivals**, *Read Indexing*, *EMBnet Journal*, 17(Supp. B):45, mar 2012.
4. N. Philippe, M. Salson, F. Rufflé, E. Bou Samara, A. Boureux, T. Commes, **E. Rivals**, *Prediction of chimeric RNA from RNA sequencing*, *Bulletin du cancer*, 98(Sp. Iss. 5):S45, oct 2011.
3. N. Philippe, F. Rufflé, E. Bou Samara, A. Boureux, T. Commes, **E. Rivals**, *ARN sequencing, conservation and non-coding ARN*, *Bulletin du cancer*, 97(Sp. Iss. 4):S44, oct 2010.
2. N. Philippe, A. Boureux, L. Bréhèlin, J. Tarhio, T. Commes, **E. Rivals**, *Estimation of sequence errors and capacity of genomic annotation in transcriptomic and DNA-protein interaction assays based on next generation sequencers*, *Cellular Oncology*, 31(2):145-6, 2009.
1. A. Boureux, L. Bréhèlin, **E. Rivals**, T. Commes, *New approaches based on high throughput sequencing and bioinformatics to study the transcriptomes of leukemic stem cells*, *Bulletin du cancer*, 96(Sp. Iss. 3):S33, oct 2009.

3 Keynote speaker (22)

22. **E. Rivals**, *Searching for probabilistic motifs in a pan-genome graph* Workshop *Computational Pan-Genomics*, 30 September – 2 October 2019, Bielefeld University, Germany.
21. **E. Rivals**, *Enjeux computationnels de la pan-génomique* *Computational Pan-Genomics* Journée Pangénomique végétale GIS Biotechnologies Vertes 1 July 2019, INRA Paris.

20. **E. Rivals**, *High performance text indexing and applications in life sciences*, UK-France Bilateral International Meeting on High Performance Computing and Biomathematics Chicheley, UK, on the 20-21 Feb. 2019
19. **E. Rivals**, *Indexing data structures*, 7th Workshop on Monte-Carlo Methods and Big Data, Heidelberg, Allemagne, 10-11 feb. 2017.
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18. **E. Rivals**, *LoRDEC: a tool for correcting errors in long sequencing reads*, Montpellier Omics Days 2016, Montpellier, 8-9 feb. 2016.
17. **E. Rivals**, *La fouille des données (data mining)*, 16ème *Rencontre E. Markiewicz*, CHU J. Bordet, Bruxelles, Belgique, 14 nov. 2015.
16. **E. Rivals**, *LoRDEC: a tool for correcting errors in long sequencing reads*, German Conference in Bioinformatics 2015, Dortmund, Allemagne, 27-30th sep. 2015.
15. **E. Rivals**, *Correction of long sequencing reads: a novel approach*, Annual Symposium From Nucleotides to Networks 2015, Gand, Belgique, 21 may 2015.
14. **E. Rivals**, *Défis computationnels des séquençage et phénotypage haut-débit en science de la vie*, Journée Big Data, Strasbourg, 7 nov. 2014.
13. **Eric Rivals**, *Building the Assembly De Bruijn Graph from an Implicit Suffix Tree*, *Workshop on the Storage, Search and Annotation of Multiple Similar Genomes*, Univ. Bielefeld, Bielefeld, Allemagne, 9-10 décembre, 2013.
12. **Eric Rivals**, *CRAC: A multi-purpose program to analyse large read collections*, *Analyse bio-informatique des données NGS*, Institut Pasteur, Lille, 7 décembre 2011.
11. **Eric Rivals**, *An integrated approach to read analysis*, *LIX Bioinformatics Symposium 2010*, Ecole Polytechnique, Paris, 8-10 Novembre 2010.
10. **Eric Rivals**, *Investigating the transcriptomic repertoire based on High Throughput Sequencing data*, *Colloque 2009 du GDR de Bioinformatique Moléculaire*, Institut Henri Poincaré, Paris, 12-13 Novembre 2009.
9. **Eric Rivals**, *La comparaison de séquences de génomes complets et l'amélioration de la sensibilité dans les approches par ancrés*, *Groupe de Travail en Génomique Comparative*, Nantes, 8 juin 2009.
8. **Eric Rivals**, *Estimation of sequence errors and prediction capacity in transcriptomic and DNA-protein interaction assays*, *Journée thématique : nouveaux séquenceurs (NGS)*, Rennes, 2 avril 2009.
7. **Eric Rivals**, *L'analyse de marqueurs minisatellites variables suggèrent de fréquents échanges génétiques entre sous-espèces de la souris commune*, *Bioinformatique, modélisation des systèmes biologiques*, Institut Henri Poincaré, Paris, 4-5 octobre 2007.
6. **Eric Rivals**, *Combinatorics of Periods in Strings*, *Workshop on Algorithms on Words*, Turku, Finlande, 28-30 mars 2007.
5. **Eric Rivals**, *Tandem Repeats Analysis*, *South African Bioinformatics Workshop*, Johannesburg, Afrique du Sud, 28-30 janvier 2007.
4. **Eric Rivals**, *Analyse des génomes: quels enjeux algorithmiques ?*, *Rencontres des ASTI : Sciences et Technologies de l'Information*, Clermont-Ferrand, 24 au 26 octobre 2005.
3. **Eric Rivals**, *Histoire de duplications et répétitions en tandem*, *Journées Montoises d'Informatique Théorique*, Montpellier, septembre 2002.
2. **Eric Rivals**, *Apports futurs de la bioinformatique*, *Colloque AUF-AUPELF "Des modèles biologiques à l'amélioration des plantes"*, Montpellier, 3-5 juillet 2000.

3.1 Invited speaker in training schools (5)

5. **E. Rivals**, *Indexing data structures*, Summer School Open access, Open data, Université de Strasbourg, June 19-21, 2018.
4. **E. Rivals**, *Data mining*, *Rencontres de Venise: Peut-on Mathématiser le vivant ?* Venise, Italie, 8-9 jan. 2016.
3. **Eric Rivals**, *Development of novel tools for NGS (RNASeq/DNASeq) analysis*, EMBO course *High-throughput next generation sequencing applied to infectious diseases*, Institut Pasteur, Tunis, 15-25 septembre 2014.
2. **Eric Rivals**, *Analyse de séquençage haut débit : besoins et solutions algorithmiques*, EPIT 2014 *École de Printemps d'Informatique Théorique*, Oléron, 11-16 mai 2014.
1. **Eric Rivals**, *Analysis of genomic data from high throughput sequencing: concepts and basic methods*, *Analyse bio-informatique des données NGS*, Cargese, 17-21 octobre 2011.

4 Communications in international conferences with proceedings (30)

30. B. Cazaux, **E. Rivals**, *Linking BWT and XBW via Aho-Corasick Automaton: Applications to Run-Length Encoding*, *30th International Conference Combinatorial Pattern Matching (CPM)* LIPICs series, vol. 128(24), doi: [10.4230/LIPIcs.CPM.2019.24](https://doi.org/10.4230/LIPIcs.CPM.2019.24), 2019.
29. D. Martin, V. Maillol, **E. Rivals**, *Fast and accurate genome-scale identification of DNA-binding sites*, *IEEE Int. Conf. on Bioinformatics and Biomedicine (BIBM2018)* doi: [10.1109/BIBM.2018.8621093](https://doi.org/10.1109/BIBM.2018.8621093), 2018.
28. B. Cazaux, **E. Rivals**, *Superstrings with multiplicities* doi: [10.4230/LIPIcs.CPM.2018.21](https://doi.org/10.4230/LIPIcs.CPM.2018.21), *Proc. of the 29th Annual Symposium on Combinatorial Pattern Matching (CPM)*, LIPICs series, vol. 105(21), 2018.
27. B. Cazaux, S. Juhel, **E. Rivals**, *Superstring Graph: a new approach for genome assembly* doi: [10.4230/LIPIcs.SEA.2018.18](https://doi.org/10.4230/LIPIcs.SEA.2018.18), *Proc. of the 17th International Symposium on Experimental Algorithms (SEA)*, LIPICs series, vol. 103(18), 2018.
26. S. Pulicani, P. Simonaitis, **E. Rivals**, K.M. Swenson, *Rearrangement Scenarios Guided by Chromatin Structure*, *Comparative Genomics RECOMB-CG*, LNCS vol. 10572, p. 141–155, 2017
25. R. Cánovas, **E. Rivals**, *Full Compressed Affix Tree Representations*, in *27th Data Compression Conference (DCC)*, IEEE Computer Society Press, p. 102–111, 2017.
24. B. Cazaux, G. Sacamoto, **E. Rivals**, *Superstring Graph: a new approach for genome assembly*, *Algorithmic Aspects in Information and Management*, Lecture Notes in Computer Science (LNCS) series, Volume 9778, p. 39–52, 2016.
23. L. Salmela, R. Wave, **E. Rivals**, E. Ukkonen, *Accurate selfcorrection of errors in long reads using de Bruijn graphs*, *RECOMB-SEQ satellite conference*, <http://recomb2016.bioinformatics.ucla.edu/recomb-seq-schedule/>, 2016.
22. B. Cazaux, R. Cánovas, **E. Rivals**, *Shortest DNA cyclic cover in compressed space*, in *9th Data Compression Conference (DCC)*, IEEE Computer Society Press, doi: [10.1109/DCC.2016.79](https://doi.org/10.1109/DCC.2016.79), 536-545, 2016.
21. B. Cazaux, T. Lecroq, **E. Rivals**, *Construction of a de Bruijn Graph for Assembly from a Truncated Suffix Tree*, in *9th International Conference on Language and Automata Theory and Applications*, Lecture Notes in Computer Science (LNCS) Vol. 8977, pp. 109-120, 2015.
20. B. Cazaux, **E. Rivals**, *Approximation of greedy algorithms for Max-ATSP, Maximal Compression, Maximal Cycle Cover, and Shortest Cyclic Cover of Strings*, in *Prague Stringology Conference*, Czech Technical University in Prague, isbn: 978-80-01-05547-2, p. 148–161, 2014.
19. B. Cazaux, T. Lecroq, **E. Rivals**, *From Indexing Data Structures to de Bruijn Graphs*, *Proc. of the 25th Annual Symposium on Combinatorial Pattern Matching (CPM)*, Lecture Notes in Computer Science (LNCS) Vol. 8486, p. 89–99, 2014.

18. N. Välimäki, **E. Rivals**, *Scalable and Versatile k-mer Indexing for High-Throughput Sequencing Data*, 9th International Symposium on Bioinformatics Research and Applications (ISBRA), Lecture Notes in Bioinformatics (LNBI), Springer Verlag, Z. Cai et al. (Eds.), LNBI 7875, p. 237–248, 2013.
17. P. Riou, A. Chateau, **E. Rivals**, *Approximate Common Intervals in Multiple Genome Comparison*, IEEE International Conference Bioinformatics & Biomedicine, IEEE Computer Society, p. 131-134, 2011.
16. R. Uricaru, A. Mancheron, **E. Rivals**, *Novel definition and algorithm for chaining fragments with proportional overlaps*, RECOMB Comparative Genomics, Lecture Notes in Computer Science (LNCS), Springer-Verlag, Vol. 6398, p. 161-172, 2010.
15. **E. Rivals**, L. Salmela, P. Kiiskinen, P. Kalsi, J. Tarhio, *MPSCAN: fast localisation of multiple reads in genomes*, Proc. 9th Workshop on Algorithms in Bioinformatics, Lecture Notes in Bioinformatics (LNBI), Springer-Verlag, Vol. 5724, p. 246-260, 2009.
14. E. Adebiyi, **E. Rivals**, *On the Detection of Recombination in Minisatellite Data*, Proc. of the 1st Southern African Bioinformatics Workshop, p. 25-32, S. Hazelhurst, M. Ramsay editors, Johannesburg, 28-30 Jan 2007.
13. O. Bodini, **E. Rivals**, *Tiling an Interval of the Discrete Line*, Proc. 17th Annual Symposium on Combinatorial Pattern Matching (CPM), LNCS vol. 4009, p. 117-28, G. Valiente, M. Levenshtein editors, Springer-Verlag, Berlin, 2006.
12. F. Nicolas, **E. Rivals**, *Hardness of Optimal Spaced Seed Design*, Proc. 16th Annual Symposium on Combinatorial Pattern Matching (CPM), LNCS vol. 3537, p. 144-55, A. Apostolico, M. Crochemore, K. Park editors, Springer-Verlag, Berlin 2005.
11. O. Delgrange, **E. Rivals**, *Modular Data Compression to Optimally Locate Regular Segments in Sequences. Application to DNA Sequence Analysis* au 26th Symposium on Information Theory in the Benelux (IT05), p. 105-12, J. Cardinal, N. Cerf, O. Delgrange, O. Markowich Eds, ISBN 90-71048-21-7, Bruxelles, Mai 2005.
10. F. Nicolas, **E. Rivals**, *Complexities of the Median and Center String Problems*, Proc. 14th Annual Symposium on Combinatorial Pattern Matching (CPM), LNCS vol. 2676, p. 315-27, R. Baeza-Yates, E. Chavez, M. Crochemore editors, Springer-Verlag, Berlin, 2003.
9. S. Bérard, **E. Rivals**, *Comparison of Minisatellites*, 6th International Conference on Computational Molecular Biology (RECOMB02), p. 67-76, ACM Press, Washington, 2002.
8. **Eric Rivals**, Sven Rahmann, *Combinatorics of Periods in Strings* Proc. 28th International Colloquium on Automata, Languages, and Programming, Lecture Notes in Computer Science vol. 2076, p. 615-26., P. Orejas, P. G. Spirakis, J. van Leuween editors, Springer Verlag, Berlin, 2001.
7. Sven Rahmann, **Eric Rivals**, *Exact and Efficient Computation of the Expected Number of Missing and Common Words in Random Texts*, Proceedings of the 11th Annual Symposium on Combinatorial Pattern Matching, Lecture Notes in Computer Science, Number 1848, p. 375-87, Springer-Verlag, Berlin, 2000.
6. S. Burkhardt, A. Crauser, P. Ferragina, H.-P. Lenhof, **E. Rivals**, M. Vingron, *q-gram Based Database Searching Using a Suffix Array (QUASAR)*, Proc. of the 3rd International Conference on Computational Molecular Biology (RECOMB99), p. 77-83, ACM Press, Washington, 1999.
5. O. Delgrange, M. Dauchet, **E. Rivals**, *Location of Repetitive Regions in Sequences By Optimizing A Compression Method*, Proc of the 4th Pacific Symposium on Biocomputing (PSB), p. 254-65, Hawaii, 4-9 janvier 1999.
4. J.-S. Varré, J.-P. Delahaye, **E. Rivals**, *The Transformation Distance: a Dissimilarity Measure Based on Movements of Segments*, à la German Bioinformatics Conference, Cologne, du 7-11 octobre 1998.
3. **E. Rivals**, M. Dauchet, J.-P. Delahaye, O. Delgrange, *Fast Discerning Repeats in DNA Sequences with a Compression Algorithm*, Proc. of the 8th Workshop on Genome and Informatics (GIW97), vol. (8), p. 215-26, Universal Academic Press, Tokyo, Japan 1997.
2. **E. Rivals**, J.-P. Delahaye, M. Dauchet, O. Delgrange, *A Guaranteed Compression Scheme for Repetitive DNA Sequences*, Proceedings of the 6th Data Compression Conference, p. 453, IEEE Computer Science Press, Snowbird, Utah, 1996.

1. **E. Rivals**, O. Delgrange, J-P. Delahaye, M. Dauchet, *A First Step Towards Chromosome Analysis by Compression Algorithms*, Proc. of the IEEE Symposium on *Intelligence in Neural and Biological Systems (INBS)*, p. 233-9, IEEE Computer Science Press, Herndon (VA), 1995.

5 Chapter in a book (2)

2. **Eric Rivals**, L. Salmela, J. Tarhio, *Exact Search Algorithms for Biological Sequences*, pages 1-22 dans *ALGORITHMS IN COMPUTATIONAL MOLECULAR BIOLOGY: TECHNIQUES, APPROACHES AND APPLICATIONS*, Editeurs scientifiques M. Elloumi, A.Y. Zomaya, ISBN : 978-0470505199, Wiley Series in Bioinformatics, Wiley, 2010.
1. **Eric Rivals**, *Apports futurs de la bioinformatique*, pages 65-75 dans *DES MODÈLES BIOLOGIQUES À L'AMÉLIORATION DES PLANTES*, Editeur scientifique S. Hamon, ISSN : 0767-2896, ISBN : 2-7099-1472-7, IRD Editions Collection "Colloques et Séminaires", 892 pages Paris, 2001.

6 Softwares (20)

20. *AQUAPONY*: an interactive visualisation tool for phylogenies with ancestral annotations and trait evolution scenarios
access <http://www.atgc-montpellier.fr/aquapony>; publication: (52).
19. *Motif*: a web-service for searching binding sites in whole genomes
access <http://www.atgc-montpellier.fr/motif>; Communication: (29).
18. *SAVAGE*: a de novo assembly for viral quasispecies
access <https://bitbucket.org/jbaaijens/savage>; publication (46).
17. *RSCU_{RS}*: an R program for assessing synonymous codon usage bias from Ribo-sequencing data
access <http://www.lirmm.fr/~rivals/rscu>; publication (45).
16. *YOC*: pairwise whole genome alignment <https://github.com/ruricar/YOC>; publication (38).
15. *LoRDEC*: hybrid, accurate, and efficient long read error correction
access <http://www.atgc-montpellier.fr/lordec>; publication (36).
14. *GS_check*: an application framework for comparing automatically the results of NGS data analyses.
13. *Compressed Gk arrays*: a C++ library implementing a compressed indexing data structure for NGS reads.
communication (18)
12. *CRAC*: a program to analyse RNA sequencing reads obtained from deep sequencing.
access <http://crac.gforge.inria.fr/>; publication (31)
11. *Gk arrays*: a C++ library for indexing huge collection of Next Generation Sequencing read collections.
access <http://www.atgc-montpellier.fr/gkarrays/>; see publication (27)
10. *QOD*: Comparison of complete genomes based on segmentation by similarity.
access <http://www.atgc-montpellier.fr/qod/>; see publication (26)
9. *MPscan*: fast localisation of multiple reads in genomes, related to publication Rivals et al., WABI, LNCS 2009
access <http://atgc.lirmm.fr/mpscan>; see communication (27)
8. *TandemSAGE*: identification of SAGE tags in tandem in genomes
access <http://www.lirmm.fr/~rivals/GENOMICS>; see publication (18)
7. *PPR*: detection and annotation of protein PPR motifs with Hidden Markov models
access <http://atgc.lirmm.fr/PPR>; see communication (27)

6. *MS_Align*: alignment of variable tandem repeat sequences
access http://atgc.lirmm.fr/ms_align; see publications (7), (14)
5. STAR (Search for Approximate Tandem Repeats): locate tandem repeats in genomes
access <http://atgc.lirmm.fr/star>; see publication (11)
4. *GeneNest*: gene index and EST clustering for Human, mouse, *C. elegans*, and *Arabidopsis*
access <http://genenest.molgen.mpg.de>; see publication (6)
3. *Transformation Distance*: alignment free sequence comparison with rearrangements
access <http://www.lifl.fr/~varre/TD>; see publication (5)
2. *2ZIP*: detection "Leucine zipper" protein domains
access <http://2zip.molgen.mpg.de>; see publication (4)
1. *QUASAR*: fast local similarity search tool; see communication (7)

7 Doctoral and habilitation thesis

2. **E. Rivals**, *Algorithmes d'analyse de séquences en bioinformatique. Périodicité et répétitions*, Habilitation thesis in computer science, Université de Montpellier II, 2005.
1. **E. Rivals**, *Algorithmes de compression et applications à l'analyse de séquences génétiques*, Doctoral thesis in computer science, Université de Lille I, 1996.