

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 Article submitted to international journals, preprints (2)

2. Sangsoo Park, Sung Gwan Park, Bastien Cazaux, Kunsoo Park, **E. Rivals**. *A Linear Time Algorithm for Constructing Hierarchical Overlap Graphs*. ArXiv CoRR doi: [2102.12824](https://doi.org/2102.12824) (2021) accepted at CPM 2021.
1. D. Paulet, A. David, **E. Rivals**. *RNA-Ribo Explorer: interactive mining and visualisation of Ribosome profiling data* bioRxiv doi: [2021.03.23.436679](https://doi.org/2021.03.23.436679) 2021.

3 International journals (57 + 7)

57. S. Relier, J. Ripoll, H. Guilloit, A. Amalric, F. Boissière, J. Vialaret, A. Attina, F. Debart, A. Choquet, F. Macari, V. Marchand, Y. Motorin, E. Samalin, J.-J. Vasseur, J. Pannequin, F. Aguilo, E. Crapez, C. Hirtz, **E. Rivals**, A. Bastide, A. David
FTO-mediated cytoplasmic m6Am demethylation adjusts stem-like properties in colorectal cancer cell
Nature Communication 12, p. 1716 doi:[10.1038/s41467-021-21758-4](https://doi.org/10.1038/s41467-021-21758-4), 2021.
56. G.E. Scholz, B. Linard, N. Romashchenko, **E. Rivals**, F. Pardi.
Rapid screening and detection of inter-type viral recombinants using phylo-k-mers
Bioinformatics, btaa1020; doi: [10.1093/bioinformatics/btaa1020](https://doi.org/10.1093/bioinformatics/btaa1020), 2020.
55. B. Linard, N. Romashchenko, F. Pardi, **E. Rivals**, *PEWO: a collection of workflows to benchmark phylogenetic placement*, *Bioinformatics* 35 (17), 3163-3165, btz011, doi: [10.1093/bioinformatics/btaa657](https://doi.org/10.1093/bioinformatics/btaa657), 2020.
54. B. Cazaux, **E. Rivals**, *Hierarchical Overlap Graph*, *Information Processing Letters* 155, doi: [10.1016/j.ipl.2019.105862](https://doi.org/10.1016/j.ipl.2019.105862), 2020.
53. Oldfield AJ, Henriques T, Kumar D, Burkholder AB, Cinghu S, Paulet D, Bennett BD, Yang P, Scruggs BS, Lavelander 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. Donnadiou, 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](https://doi.org/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](https://doi.org/10.1101/164848), 2017.
44. D. Paulet, A. David, **E. Rivals**, *Ribo-seq enlightens Codon Usage Bias*, *DNA Research* dsw062. doi: [10.1093/dnares/dsw062](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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. Piegou, **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](https://doi.org/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. Boureux, 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. Bréhélin, 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. Ottonnes, O. Pecharromàn-Pérez, J. Tarhio, F. Pierrat, F. Rufflé, 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.

3.1 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.

4 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.
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.

4.1 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.

5 Communications in international conferences with proceedings (31)

31. S. Park, B. Cazaux, K. Park, **E. Rivals**, *Efficient Construction of Hierarchical Overlap Graphs*, *String Processing and Information Retrieval (SPIRE)*, Lecture Notes in Computer Science, vol 12303., p. 277–290, Springer, Cham. doi:10.1007/978-3-030-59212-7_20, 2020.
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, 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, 2018.
28. B. Cazaux, **E. Rivals**, *Superstrings with multiplicities* doi: 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**, *Practical lower and upper bounds for the Shortest Linear Superstring* doi: 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.
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