

# List of publications

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## 1 Patent (1)

1. M. Méchali, C. Cayrou, P. Coulombe, **E. Rivals**, *Purification process of nascent DNA*, patent n° US 61/238 315.

## 2 International journals (29 + 4)

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. Ottonnes, O. Pecharromàn-Pérez, J. Tarhio, F. Pierrat, F. Ruffle, T. Commes, J. Martí, *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 (4)

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 (11)

11. **Eric Rivals**, *CRAC: A multi-purpose program to analyse large read collections*, *Analyse bio-informatique des données NGS*, Institut Pasteur, Lille, 7 décembre 2011.
10. **Eric Rivals**, *An integrated approach to read analysis*, *LIX Bioinformatics Symposium 2010*, Ecole Polytechnique, Paris, 8-10 Novembre 2010.
9. **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.
8. **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.
7. **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.
6. **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.
5. **Eric Rivals**, *Combinatorics of Periods in Strings*, *Workshop on Algorithms on Words*, Turku, Finlande, 28-30 mars 2007.
4. **Eric Rivals**, *Tandem Repeats Analysis*, *South African Bioinformatics Workshop*, Johannesburg, Afrique du Sud, 28-30 janvier 2007.
3. **Eric Rivals**, *Analyse des génomes: quels enjeux algorithmiques ?*, *Rencontres des ASTI : Sciences et Technologies de l'Information*, Clermont-Ferrand, 24 au 26 octobre 2005.
2. **Eric Rivals**, *Histoire de duplications et répétitions en tandem*, *Journées Montoises d'Informatique Théorique*, Montpellier, septembre 2002.
1. **Eric Rivals**, *Apports futurs de la bioinformatique*, *Colloque AUF-AUPELF "Des modèles biologiques à l'amélioration des plantes"*, Montpellier, 3-5 juillet 2000.

### 4 Communications in international conferences with proceedings (17)

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. Adebisi, **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 (11)

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](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  
download <http://www.mpi-sb.mpg.de/~{ }stburk/research.html>; 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.