

IFT6291-BIN6000: Banque d'articles

Note: Si l'un des articles de la liste vous intéresse et que vous n'arrivez pas à obtenir le fichier .pdf, communiquez avec moi par courriel et je vous l'enverrai.

Alignement, séquences:

- M. Crochemore, G.M. Landau, M. Ziv-Ukelson, *A Sub-quadratic Sequence Alignment Algorithm for Unrestricted Cost*, In Proc. 13th Annual ACM/SIAM Symposium on Discrete Algorithms (SODA'02), pages 679-688, 2002.
- M. Kinsella and V. Bafna, *Combinatorics of the Breakage-Fusion-Bridge Mechanism*, Journal of Computational Biology, Vol.19(6), pp.662 – 678, 2012.
- L. Marsan et M.F. Sagot, *Extracting structured motifs using suffix tree- Algorithms and application to promoter consensus identification*, in S. Minoru and R. Shamir (eds.), RECOMB 2000, Tokyo, Japon, Proceedings of the Fourth Annual International Conference on Computational Molecular Biology, pages 210-219, ACM Press, 2000.
- N. Pisanti, M. Crochemore, R. Grossi et M.F. Sagot, *Bases of Motifs for Generating Repeated Patterns with Wild Cards*, IEEE/ACM Transactions on Computational Biology and Bioinformatics 2(1) 40-50, 2005.
- M.F. Sagot, A. Viari, J. Pothier et H. Soldano, *Finding Flexible Patterns in Text - An Application to 3D Molecular Matching*, Comput. Application in the BIO-Sciences, 11:59–70, 1994.

Réarrangements de génomes:

- M.P. Béal, A. Bergeron, S. Corteel, M. Raffinot, *An Algorithmic View of Gene Teams*, Theoretical Computer Science , 320(2-3), pp. 955–418, 2004.
- A. Bergeon, J. Mixtacki and J. Stoye, *On Computing the Breakpoint Reuse Rate in Rearrangement Scenarios*, Lecture Notes in Computer Science 5267, pp.226-240, 2008.
- A. Bergeron, J. Mixtacki et J. Stoye, *A New Linear Time Algorithm to Compute the Genomic Distance Via the Double Cut and Join Distance*, Theoretical Computer Science, 410 (51), pp. 5300-5316, 2009.
- P. Holloway, K. Swenson, D. Ardell and N.El-Mabrouk, *Evolution of Genome Organization by Duplication and Loss: an Alignment approach*, RECOMB 2012.

- M.F. Sagot et E. Tannier, *Perfect Sorting by Reversals*, Proceedings of 11th Computing and Combinatorics (COCOON'05) Annual International Conference, Lecture Notes in Computer Science, vol. 3595, pages 42-51, 2005.
- D. Sankoff and M. Blanchette, *The median problem for breakpoints in comparative genomics*, Lecture Notes in Computer Science 1276, pp.251–263, 1997.

Structures:

- J. Allali et M.F. Sagot, *A Multiple Graph Layers Model with Application to RNA Secondary Structures Comparison*, String Processing and Information Retrieval (SPIRE) 2005.
- N. El-Mabrouk, M.Raffinot, J.E. Duchesne, M. Lajoie et N. Luc, *Approximate Matching of Structured Motifs in DNA Sequences*, Journal of Bioinformatics and Computational Biology, Vol. 3, No. 2, pp. 317–342, 2005.
- A. Lamiable, F. Quessette, S. Vial, D. Barth et A. Denise, *An Algorithmic Game-Theory Approach for Coarse-Grain Prediction of RNA 3D Structure*, IEEE/ACM Transactions on Computational Biology and Bioinformatics, vol. 10, no. 1, pp. 193-199, 2013.