

LISTE D'ARTICLES pour ASB 2007-08.

Pour d'autres propositions d'articles, contactez moi.

Détermination des gènes sur les séquences

C.B. Burge and S. Karlin. Finding the genes in genomic DNA. *J. Mol. Bio*, 268:78–94, 1997.

M. Burset and R. Guigo. Evaluation of gene structure prediction programs. *Genomics*, 34:353–367, 1996.

S.Djebali , F.Delaplace, H.Roest Crolius, Exogean: a framework for annotating protein-coding genes in eukaryotic genomic DNA, *Genome Biology* 2006, 7.

Recherche de motifs sur les séquences

Algorithme MEME:

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* Alberto Policriti, Nicola Vitacolonna, Structured Motifs Search, *Journal of Computational Biology*, 2005

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Multiple Alignment

* Chuong B. Do, Mahathi S.P. Mahabhashyam, Michael Brudno, and Serafim Batzoglou, ProbCons: Probabilistic consistency-based multiple sequence alignment, *Genome Research*, 2005

* Ariel S. Schwartz, and Lior Pachter, Multiple alignment by sequence annealing, *Bioinformatics*, Vol. 23 ECCB 2006, pages e24–e29

Charles E. Lawrence, Stephen F. Altschul, Mark S. Boguski, Jun S. Liu, Andrew F. Neuwald, and John C. Wootton. Detecting subtle sequence signals: a Gibbs sampling strategy for multiple alignment. *Science*, 262:208–214, 8 October 1993.

* Cedric Notredame, Desmond G. Higgins, Jaap Heringa, T-Coffee: A Novel Method for Fast and Accurate Multiple Sequence Alignment, *J. Mol. Biol.* (2000) 302, 205±217.

Détermination de signaux sur les promoteurs

* van Helden, J., André, B. & Collado-Vides, J. (1998). Extracting regulatory sites from the upstream region of yeast genes by computational analysis of oligonucleotide frequencies. *J Mol Biol* 281(5), 827-42.

* van Helden, J., Rios, A. F. & Collado-Vides, J. (2000). Discovering regulatory elements in intergenic sequences by analysis of spaced dyads. *Nucleic Acids Res.* 28(8):1808-18.

* van Helden, J. (2004). Metrics for comparing regulatory sequences on the basis of pattern counts. *Bioinformatics*, 2004 20(3):399-406.

* N.Rajewsky, M.Vergassola, U.Gaul, E.Siggia, Computational detection of genomic *cis*-regulatory modules applied to body patterning in the early *Drosophila* embryo, *BMC Bioinformatics* 2002, 3:30.

Analyse statistique des génomes et génomique comparative

- * D.Kreil, C.Ouzounis, Identification of hydrophilic species by the amino-acids composition deduced from their genomes, *Nucleic Acids Research*, 1608-1615, 2001.
- * A.Carbone, A.Zinovyev, F.Képès, Codon Adaptation Index as a measure of dominating codon bias, *Bioinformatics*, 19:2005-2015, 2003.
- * Kira S. Makarova, L. Aravind, Michael Y. Galperin, Nick V. Grishin, Roman L. Tatusov, Yuri I. Wolf, and Eugene V. Koonin, Comparative Genomics of the Archaea (Euryarchaeota): Evolution of Conserved Protein Families, the Stable Core, and the Variable Shell, *Genome Research* 9:608–628, 1999
- * Fredj Tekaiiaa, Edouard Yeramianb, Bernard Dujon, Amino acid composition of genomes, lifestyles of organisms, and evolutionary trends: a global picture with correspondence analysis, *Gene*, 297, 51–60, 2002.
- * Rickard Sandberg, Gösta Winberg, Carl-Ivar Bränden, Alexander Kaske, Ingemar Ernberg, and JoakimCöster, Capturing Whole-Genome Characteristics in Short Sequences Using a Naïve Bayesian Classifier, *Genome Research*, 11:1404–1409, 2001.
- * Patrick J. Deschavanne, Alain Giron, Joseph Vilain, Guillaume Fagot, and Bernard Fertil, Genomic Signature: Characterization and Classification of Species Assessed by Chaos Game Representation of Sequences, *Mol. Biol. Evol.* 16(10):1391–1399. 1999
- * Dina Sokol, Gary Benson and Justin Tojeira, Tandem repeats over the edit distance, *Bioinformatics*, Vol. 23 ECCB 2006, pages e30–e35.

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- * O. Perriquet , H. Touzet and M. Dauchet, Finding the common structure shared by two homologous RNAs, *Bioinformatics*, 19:1, 108–116,2003.
- * Christian Haslinger, Peter F. Stadler, RNA Structures with Pseudo-knots: Graph-theoretical, Combinatorial, and Statistical Properties, *Bulletin of Mathematical Biology* (1999) 61, 437–467.
- * Engelen S and Tahi F., Predicting RNA secondary structure by the comparative approach: how to select the homologous sequences, *BMC Bioinformatics* 2007, 8:464.

DNA design in nanotechnology

- * A.Brenneman, A.Condon, Strand design for biomolecular computation, *Natural Computing*, 287:1, 39–58, 2002.
- * D.Tulpan, H.Hoos, A.Condon , Stochastic local search algorithms for DNA word design, *Lecture Notes In Computer Science*; Vol. 2568, the 8th International Workshop on DNA Based Computers: DNA Computing, 229 – 241, 2002

Méthode « Evolutionary Trace » pour la détection de sites d'interaction entre protéines

- * O. Lichtarge and M. Sowa, Evolutionary predictions of binding surfaces and interactions, *Current Opinion in Structural Biology* 2002, 12:21–27

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